NDSL
National Digital Science Library

감귤육종소재은행

Gene & Material Bank for Citrus Breeding

주관연구기관	제주대학교
연구책임자	김재훈
발행년월	2012-02
주관부처	교육과학기술부
사업관리기관	한국연구재단
NDSL URL	http://www.ndsl.kr/ndsl/search/detail/report/reportSearchResultDetail.do?cn=TRKO201300010795
IP/ID	14.49.138.138
이용시간	2017/11/03 13:30:34

저작권 안내

① NDSL에서 제공하는 모든 저작물의 저작권은 원저작자에게 있으며, KISTI는 복제/배포/전송권을 확보하고 있습니다.

② NDSL에서 제공하는 콘텐츠를 상업적 및 기타 영리목적으로 복제/배포/전송할 경우 사전에 KISTI의 허락을 받아야 합니다.

③ NDSL에서 제공하는 콘텐츠를 보도, 비평, 교육, 연구 등을 위하여 정당한 범위 안에서 공정한 관행에 합치되게 인용할 수 있습니다.

④ NDSL에서 제공하는 콘텐츠를 무단 복제, 전송, 배포 기타 저작권법에 위반되는 방법으로 이용할 경우 저작권법 제136조에 따라 5년 이하의 징역 또는 5천만 원 이하의 벌금에 처해질 수 있습니다.

KiSTi
www.kisti.re.kr

연구소재지원사업('07년 선정) 최종보고서

양식A 101

① 부처사업명(대)	원천기술개발사업	보안등급(보안, 일반)	일반
② 사 업 명(중)	바이오의료기술개발사업	공개가능여부(공개, 비공개)	공개
③ 세부사업명(소)	연구소재지원사업		
④ 과제성격(기초, 응용, 개발)	기초	④-1 실용화 대상여부(실용화, 비실용화)	비실용화
⑤ 과 제 명	국문	감귤육종소재은행	
	영문	Gene & Material Bank for Citrus Breeding	
⑥ 주관연구기관	제주대학교		
⑦ 협동연구기관			
⑧ 주관연구책임자	성 명	김재훈	직급(직위) 부교수
	소속부서	생명자원과학대학 생명공학부	전 공 생화학

⑨ 연구개발비 및 참여연구원수 (단위: 천원, M·Y)

년 도	정부출연금 (A)	기업체부담금			정부외 출연금 (B)	상대국 부담금 (F)	합계 G=(A+B+E)	참여 연구원 수
		현금 (C)	현물 (D)	소계 E=(C+D)				
1차년도	100,000			0				13
2차년도	91,000			0				15
3차년도	94,000			0				12
4차년도	102,300							12
5차년도	122,300							9
합계	509,600	0	0	0	0	0	0	61

⑩ 총연구기간	2007.4.1 - 2012.2.29 (59개월)			
⑪ 참여기업	중소기업수	대기업수	기타	계
				0
⑫ 국제공동연구	상대국연구기관수	상대국연구개발비	상대국연구책임자수	

관계규정과 모든 지시사항을 준수하면서 이 연구개발사업을 성실히 수행하고자 아래와 같이 단계보고서와 연구계획서를 제출합니다.

2012 년 월 일

주관연구책임자 : 김 재 훈 (인)

주관연구기관장 : (인)

교 육 과 학 기 술 부 장 관 귀하

IP : 14.49.138.138, 2017-11-03 13:30:33

<연구결과_한글 요약문 >

양식A201

연구목적 및 내용 (500자내외)	감귤유전자와 감귤 변이주를 비롯한 분자육종 핵심소재를 개발하고 이들 소재의 유지관리 및 활용지원 체계를 구축하여 감귤 및 기타작물의 육종연구에 제공하고자 함.
연구결과 (1000자내외)	I. 소재 개발 가. 유전자 라이브러리 제작 나. 유전자 염기서열 결정 다. 유전자 아미노산서열, 기능, 발현 profile 분석 라. 유전자 Full-length cDNA 클로닝 마. 유전자 발현단백질 제조 및 구조분석 바. 감귤 유전자 DNA 유전자 칩 제작 사. 감귤 변이주 확보 아. 분자육종 기초소재 개발 자. 재래감귤 게놈 염기서열 분석 II. 관리 및 활용지원 체계 가. 소재(DNA, 단백질, 유전자원식물)의 유지 및 품질관리 체계 구축 나. 소재정보 데이토베이스 구축 및 Update 다. Online/Offline Service System 구축 라. 소재활용 교육훈련체계 구축(교육프로그램 개발 및 운영) 마. 감귤육종연구자 네트워크 구축(감귤육종연구회 운영 등)
기대효과 (500자내외) (응용분야 및 활용범위 포함)	가. 감귤육종 기초연구 지원 나. 일반작물 분자육종 기초연구 지원 다. 국제 감귤유전체 컨소시엄 지원 라. 감귤돌연변이육종사업(감귤클러스터사업) 지원 마. GMO환경위해성평가기관사업 지원 바. 아열대원예산업연구소(SHRI)-형질전환식물연구사업 지원 사. 농업진흥청 감귤시험장 감귤육종 지원 아. 제주도 농업기술원 감귤 유전체 분석 지원 자. 기업체 감귤 유용유전자 이용 기술개발 지원 차. 고품질 감귤 생산 및 지역 경제 활성화 지원

중심어	감귤	육종	유전자
	라이브러리	유전자 칩	데이터베이스
	국제감귤컨소시엄	유전자조작식물	연구네트워크

IP : 14.49.138.138, 2017-11-03 13:30:33

차 례

Ⅰ. 소재은행 개요 1

1. 목 적 1

2. 주요연혁 1

3. 연구소재은행 사업개요 1

1) 주요사업 1

2) 소재 및 소재은행의 중요성 2

3) 소재은행의 역할 및 기능 3

4) 소속대학 특성화에의 기여정도 4

5) 범국가적인 자원은행으로서의 역할범위 4

4. 운영체제 요약 5

5. 5년간 사업비 현황 6

6. 주요사업 추진성과 및 목적 달성도 6

1) 년차별 추진목표 및 달성도 6

2) 기초연구 육성 기반 확충에의 기여도 8

Ⅱ. 연구 소재 서비스 기반 구축 및 운영 관리 9

1. 연구소재 확보, 관리, 분양체제의 효율성과 개방성 9

1) 연구소재 수집 . 관리 . 분양 체제 9

2) 서비스 측면에서의 효율성과 개방성 11

3) 연구소재의 활용 촉진을 위한 노력 13

4) 연구소재은행 운영지침서 마련 29

2. 소재은행의 국내 . 외적인 위상 제고를 위한 노력 및 실적 30

3. 인력기반 구축 46

1) 조직 및 운영체계도 46

2) 소재은행장의 적정성 47

3) 운영요원 확보 및 활용 51

4. 시설과 공간의 확보 52

1) 주요 시설현황 52

2) 주요 장비 보유현황 53

Ⅲ. 사업 수행(연구) 실적 54

1. 연구소재 확보 . 관리실적 54

1) 년차별 추진목표 및 달성도 54

2) 연구소재 종류별 구체적인 확보현황을 연도별 비교 54

IP : 14.49.138.138, 2017-11-03 13:30:33

3) 사업지원으로 인한 연구소재의 개발, 수집 및 관리실적 59
4) 연구소재의 확보 및 보존절차, 방법, 품질관리 67
2. 연구소재분양 실적 71
1) 분양실적 71
2) 연구소재의 분양절차 및 방법 72
3) 연구소재 분양에 따른 효과분석 72
3. 연구소재 정보 관리 실적 73
4. 소재은행 관련으로 발표된 연구성과 74
IV. 운영 및 재정 기반 구축 94
1. 운영 및 재정 기반 구축 94
1) 자금집행체제 94
2) 대학지원금 95
3) 재원조달 및 집행의 타당성 96
V. 애로 및 건의사항 96
[기타 제출사항]
첨부자료 1. 보유 감귤 유전자의 기능 추정 정보 98
첨부자료 2. Microarray Data 345
첨부자료 3. 보유 연구소재 목록 : 전체 염기서열 정보 348
첨부자료 4. 현재 보유하고 있는 감귤 유전자원 식물체 363
첨부자료 5. 발표자료 367
첨부자료 6. 분양신청양식 398
첨부자료 7. 학술지 발표논문 404
첨부자료 8. 분양실적 521
첨부자료 9. 학술지 발표 논문 내역서 584
첨부자료 10. 자체평가의견서 586
첨부자료 11. 개인정보 활용동의서 592

IP : 14.49.138.138, 2017-11-03 13:30:33

Ⅰ. 연구소재은행 개요

1. 목적

본 소재은행은 감귤 유전자/유전자원과 감귤 캘러스, 감귤 변이주를 비롯한 분자육종 핵심 소재를 개발하고 이들 소재의 유지관리 및 활용지원 체계를 구축하여 감귤 및 기타작물의 육종연구에 제공하며, 감귤류 유전자 및 정보를 안정적으로 제공하여 관련연구의 시너지 효과를 극대화 하고 연구 네트워크를 형성하여 신품종 감귤 생산을 통한 국제 경쟁력을 강화하는데 목적이 있다.

2. 주요 연혁

·2002년 09월 과학기술부/과학재단 지정“아열대·열대식물유전자은행” 설립
·2003년 06월 감귤유전자 기초라이브러리/데이터베이스 구축
·2003년 07월 전용공간확보[유전자 유지관리실+데이터베이스 관리실]-아열대원예산업연구소건물
·2003년 09월 홈페이지 개설/기술요원(최수정)채용
·2004년 07월 한국과학재단 “아열대·열대생물유전자은행”으로 명칭변경 승인
·2005년 02월 “아열대·열대생물유전자은행” 학칙기구로 승격
·2005년 04월 베트남 National Institute for Plant Protection (NIPP)와 국제협력 협정 체결
·2005년 06월 “아열대·열대생물유전자은행” 센터 대학규정 제정
·2005년 10월 센터장 변경: 생명자원과학대학 생명과학부 김재훈 교수 취임
·2007년 04월 국가지정연구소재 ‘감귤육종소재은행’ 출범
·2007년 08월 ISBER(International Society for Biological and Environmental Repositories)가입
·2008년 02월 감귤육종 전담 연구원(진성범 박사)채용
·2009년 01월 중국 상구 대학교와 국제협력 협정
·2009년 07월 국가지정연구소재 ‘감귤유전자원소재은행’으로 명칭 변경
·2011년 06월 차세대바이오그린 21사업 선정
·2011년 12월 미국 플로리다 대학과 국제협력 협정

3. 연구소재은행 사업 개요

1) 주요사업

IP : 14.49.138.138, 2017-11-03 13:30:33

가. 소재확보 및 개발

- 유전자 라이브러리 제작
- 유전자 염기서열 결정
- 유전자 아미노산서열, 기능, 발현 profile 분석
- 유전자 Full-length cDNA 클로닝
- 유전자 발현단백질 제조 및 구조 분석
- 감귤 유전자 DNA microarray 제작
- 감귤 변이주 확보
- 분자육종 기초소재 개발
- 유전자원 과실/식물체 확보
- 제주도 재래감귤(병귤) 게놈 염기서열 개발 및 확보

나. 관리 및 활용지원 체계

- 소재(DNA, 단백질, 유전자원식물)의 유지 및 품질관리 체계 구축
- 소재정보 DB 구축 및 Update
- Online/Offline Service System 구축
- 소재활용 교육훈련체계 구축(교육프로그램 개발 및 운영)
- 감귤육종연구자 네트워크 구축(감귤육종연구회 운영 등)

2) 소재 또는 소재은행의 중요성

□ 감귤은 국내 과수 생산량에 있어서 연평균 6000억 원의 규모로 1위를 차지하고 있을 만큼 중요한 작물이다. 하지만 2011년 한미 FTA가 체결됨에 따라 오렌지수입개방으로 인하여 철폐 시점인 2022년까지 연평균 750억 원 감소할 것으로 추정할 만큼 가장 피해가 우려되는 작물 중 하나이다. 따라서 품질 개선을 통한 경쟁력 강화가 무엇보다 절실한 상황이며, 그에 따른 고품질 감귤 생산이 시급한 실정이다.

□ 현재 국내에서 재배되고 있는 대부분의 감귤 품종들은 일본에서 도입된 것으로 국제식물신품종 보호동맹 협약(UPOV)에 따라 큰 피해가 우려되는 작물로서 국산 품종의 개발이 시급한 실정이다. 그러나 국내에는 유전자 및 유전정보의 체계적 개발이 이루어지고 있지 않아 감귤신품종 육성연구에 걸림돌이 되고 있다.

□ 감귤류는 제주도 산업에 있어 중요할 뿐만 아니라 국가적으로 유전자원으로서도 가치가 매우 크기 때문에, 미국, 일본을 중심으로 감귤유전체연구국제컨소시엄이 조직되어 2007년부터 유전체규명을 위한 구체적 사업이 추진되고 있어 국가 간 유전체개발 경쟁력 강화를 위한 컨

IP : 14.49.138.138, 2017-11-03 13:30:33

소시엄 참여와 유전체정보의 효율적 활용을 위한 기반구축이 시급한 상황이며, 국내에는 지각, 병귤 등을 포함한 12 품종의 재래감귤 품종이 있으나 멸종위기에 직면하고 있어 육종소재의 보존차원에서 이들 재래감귤에 대한 유전자 및 유전정보의 확보와 안정적 유지관리가 필요한 실정이다.

3) 소재은행의 역할 및 기능

□ 본 소재은행은 국내에서 주로 생산되고 있는 고품질 감귤품종과 멸종위기에 직면하고 있는 재래감귤품종들의 cDNA 라이브러리를 제작 하고 염기서열등을 분석함으로써 유전자원을 수집/유지하는 기능을 수행하고 있으며, 대량 염기서열 분석시스템을 이용하여 감귤유전자의 서열정보를 대량으로 수집하고 database화함으로써 감귤을 비롯한 과수 작물의 유전공학/분자생물학적 연구를 위한 기초 자료를 제공하고 있을 뿐 아니라 분자육종을 위한 신규유전자의 발굴 기능도 수행하고 있다.

□ 감귤의 cDNA 라이브러리 및 분석유전자의 클론을 연구자들에게 분양제공 하여 연구자들이 분자육종 또는 생명공학적 연구에 바로 활용할 수 있도록 해줌으로써 개개의 연구자들이 필요한 유전자들을 직접 선발해야하는데 소요되는 시간과 비용을 절감해 주고 있다.

□ 감귤의 유전자 염기서열 및 발현 정보 등의 제공은 실제 감귤을 비롯한 과수 작물의 다양한 생명공학적 접근에 기초가 될 뿐 아니라 개개의 연구자들이 이러한 다양한 정보들을 직접 수집하기 위하여 소요해야 하는 시간과 비용을 절감해 줌은 물론 중복 연구/투자의 비효율성도 해소되도록 하고 있다.

□ 재래감귤은 항산화, 항바이러스 등 고부가가치가 있는 기능성 물질 등이 많이 함유하고 있는 것으로 보고되고 있다. 따라서, 최근 연구자들은 재래감귤 과실로부터 고 기능성 물질에 대한 연구를 함에 있어 재래감귤의 과실을 많이 찾고 있다. 하지만 재래감귤은 제주도에만 자생하는 감귤이며 수확시기가 다르기 때문에 외부의 연구자들은 재래감귤 시료를 확보하기 힘들다. 따라서 재래감귤에 대한 과실을 시기별 확보하여 분양함으로써 외부 연구자들의 연구에 중요한 재료를 제공하고 있다

□ 감귤의 cDNA 라이브러리, 유전자 클론 및 서열정보 외에도 감귤의 DNA microarray 분석정보, 돌연변이주 및 이들의 유전자 발현정보, 단백질 발현분석 정보 등을 database화하여 제공함으로써 감귤을 비롯한 과수 작물의 생리 및 물질대사 연구에 중요한 기초 정보를 제공하고 있다.

□ 분자생물학적 기초소재의 cDNA 라이브러리, 유전자클론 및 서열정보는 기초소재의 특성을 이해하는데 뿐만 아니라 감귤을 비롯한 각종 작물의 분자생물학적 신품종개발에 중요한 재분화계 확립과 목표유전자 발굴에도 중요한 역할을 하고 있다.

IP : 14.49.138.138, 2017-11-03 13:30:33

4) 소속대학 특성화에의 기여 정도

□ 본 대학에서는 감귤에 관련된 연구 활성화를 위하여 감귤화훼과학기술센터(농림부지원)를 설치 운영하고 있으며, 본 대학의 아열대원예산업연구소에서는 핵심사업으로써 “GM식물연구” 사업을 추진함과 동시에 2007년부터 9년간의 GM식물 개발 연구를 포함하는 “아열대 GM식물 개발” 중점연구소사업(한국연구재단)을 유치하여 2단계 진행 중에 있다. 또한 본 대학에서는 제주도와 함께 감귤클러스터사업(2005-2014)을 진행하는 등 감귤산업 육성을 위한 다각적인 연구 사업을 진행하고 있다. 따

라서 이러한 대학 기관들의 연구사업과 연계하여 볼 때 본 소재은행의 핵심 소재인 감귤 유전자 및 유전자 정보 등은 상기 센터 및 연구사업의 활성화에 크게 기여하여 본 대학의 연구 활성화에 중추적인 역할을 할 수 있을 것으로 기대된다.

□ 본 대학에서는 제주대학교 중장기 종합발전계획(2001.5.31)에 따라, 해양과학분야, 관광산업분야와 더불어 아열대생물산업분야를 특성화분야로 선정하여 집중 육성하고 있는데, 본 소재은행에서 제공하는 감귤의 유전자 및 서열정보, 발현정보 등은 아열대생물산업분야의 핵심 소재라 할 수 있으며, 특히 감귤의 경우는 지역적 차원에서도 매우 중요한 작물이기 때문에 제주대학교의 아열대생물산업분야 특성화의 핵심이라 할 수 있어 본 소재은행의 설립/운영은 제주대학교 종합발전계획을 추진함에 있어 매우 중요한 역할을 하고 있다.

5) 범국가적인 자원은행으로서의 역할 범위

□ 현재 국내 과수산업은 2011년 FTA 협상 등으로 인한 농산물시장이 개방됨에 따라 많은 위협을 받고 있다. 특히 제주에서 주로 재배되고 있는 제주산업의 핵심작물인 감귤은 가장 큰 위협에 처해있으며, 그 외 사과, 배, 포도, 감 등도 그 피해가 점차 확산될 것으로 예상되고 있다. 이에 따라 국내 과수산업의 국제경쟁력 강화를 위한 다양한 노력들이 전개되고 있고, 고품질 과일생산을 위한 신품종개발 연구들도 많이 이루어지고 있지만 현재까지 감귤을 비롯한 과수의 분자생물학적 연구 기반은 아주 미흡한 실정이다. 국내에서 본 소재은행과 가장 유사한 사업을 수행하고 있는 기관으로는 한국연구재단의 특수소재은행사업으로 지원되고 있는 「한국의 식물 DNA 은행」인데 이 은행에서는 감귤류를 비롯한 각종 식물의 DNA를 genomic DNA 형태로 보유하고 있어 본 소재은행에서 개발/제공하고 있는 발현 유전자(cDNA) 정보와는 본질적인 차이가 있고, 본 소재은행에서 제공하는 DNA microarray 분석 데이터와 각종 감귤 변이주에 대한 정보등은 본 소재은행의 특화된 부분이라 할 수 있다. 따라서 본 소재은행에서 핵심소재로 제공하고 있는 감귤류 유전자 정보들은 국내에서 유일무이 하다고 할 수 있어 국내의 감귤 관련 연구에 중추적인 역할을 할 수 있을 것이다. 또한 국내의 과수에 대한 분자생물학적 연구기반이 빈약하다는 점을 고려하여 볼 때, 본 소재은행이 확보/제공하고 있는 감귤류

IP : 14.49.138.138, 2017-11-03 13:30:33

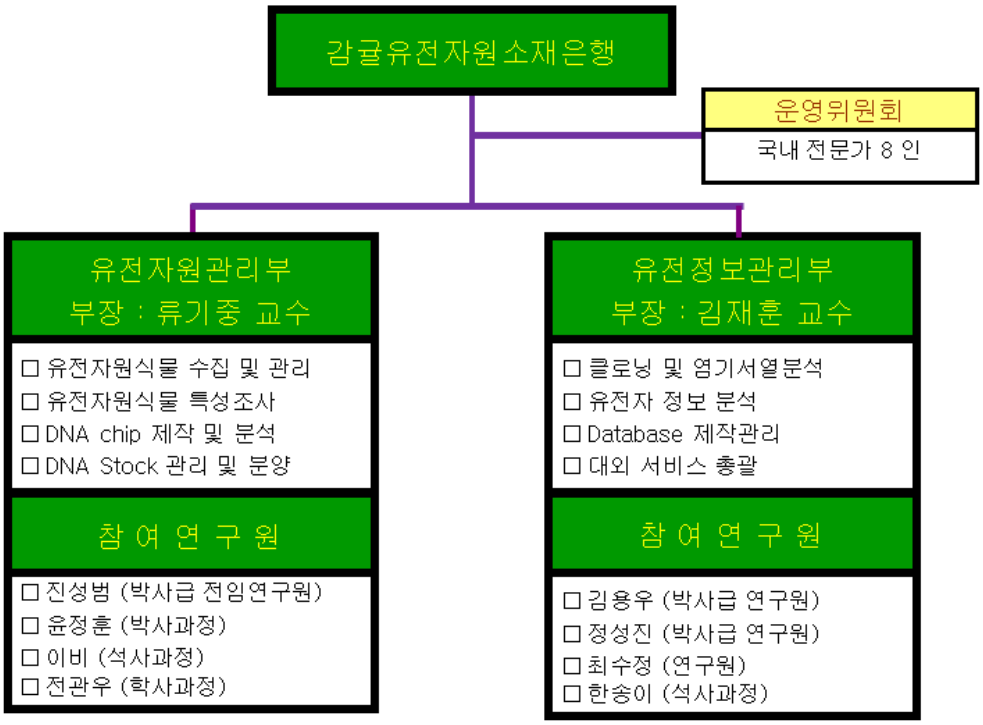
의 발현유전자 정보들은 국내의 목본류를 비롯한 과수의 연구기반으로써도 중요한 역할을 할 수 있을 것으로 기대되고 있다.

□ 제주도내의 난지연구소와 농업기술원을 비롯한 일부 감귤 관련 연구기관에서는 전통적인 감귤 재배 및 생리에 중심을 둔 연구를 진행하고 있어 본 사업을 통하여 개발/제공되는 감귤류의 유전자 및 분석 정보들은 이러한 연구에 시너지 효과를 줄 수 있을 것으로 예상된다.

□ 국제감귤게놈콘소시움에서 2007년 7월부터 Citrus Genome Project 시행계획을 수립하여 진행하고 있는데, 2011년 본 소재은행은 차세대바이오그린 21 감귤유전체 사업에 선정됨에 따라서 본 사업을 통하여 감귤 유전자의 확보, 유전자정보 database 구축 및 그에 따른 연구 인프라를 확보함으로써 Citrus Genome Project에 참여하고 분담업무를 성공적으로 수행할 수 있는 기반이 마련될 것이며 그에 따른 국가 위상도 제고 될 것이다.

4. 운영체제 요약(조직 및 인력)

본 소재은행은 유전자원관리부, 유전정보관리부로 나뉘어 운영되고 있다. 각부에는 부장(운영위원) 1인이 배치되어 부서 운영에 관한 사항들을 관리/감독하고 있으며, 그에 따른 운영요원이 각각 2-3인 배치되어 실무를 전담하고 있다. 또한 본 소재은행에서는 전담 행정요원 1인을 배치하여 소재의 분양 접수 및 처리, 홈페이지 관리, 행정 및 재정 업무 등을 전담하게 함은 물론 효과적인 홍보 전략 등도 모색하게 하여 은행 활성화를 꾀하고 있다.



<사업수행의 운영체계>

IP : 14.49.138.138, 2017-11-03 13:30:33

- 2003년 9월 아열대 열대유전자은행 유전정보관리 연구원 (최수정 연구원)
- 2008년 2월 감귤육종 전담 연구원(진성범 박사, 감귤육종)

5. 5년간 사업비 현황:

[표 1] 사업비 현황 : 연도별/재원별 (단위 : 백만 원)

재원	1차년도	2차년도	3차년도	4차년도	5차년도
정부지원금	100	91	94	102,3	122.3

6. 주요 사업 추진 성과 및 목적 달성도

1) 년차별 추진목표 및 달성도

추진내용	내용	달성도				
		1차년도	2차년도	3차년도	4차년도	5차년도
1) 식물재료 수집/ 유지	감귤 유전자원 식물 수집 및 유지 관리	100	100	100	100	100
2) cDNA library, 염기서열 분석 및 database 확충	cDNA library 제작, cDNA 염기서열분석 및 유전자정보분석 database구축	100	100	100	100	100
3) 분양실적	감귤 유전자 정보 및 클론 분양	95	100	100	99	100
4) 시설·장비 확충	유전자 분석 프로그램확충 및유전자보관 장비 구입	95	100	100	100	99
5) 서비스 환경 추진	홈페이지구축 및 데이터베이스 업그레이드	100	100	100	100	100
6) 운영	감귤육종연구회 개최 및 운영위원회의 개최	100	100	100	100	100

. 가. 연구소재 확보실적

① 멸종위기에 있는 제주도 자생 감귤인 진귤, 병귤, 청귤, 편귤, 동정귤, 소유자, 당유자, 지각, 홍귤, 사두감, 빈귤 과 같은 12 품종들을 비롯한 86개의 감귤 유전자원 식물체를 국내 내부 혹은 외부 기관으로 부터 확보하여 유지시키고 있으며, 또한 품종별 시기에 따라서 과실을 매년 확보하여 분양하고 있다. 과실 현재 보유량은 약 432개이며, 이는 분양되는 양에 따라 다소 변동된다. 또한 현재 감귤 callus cell line 궁천, 상야조생, 하례조생, 네블오렌지, 청도온주 등 8 품종 확보하여 유지하고 있다.

② 본 소재은행의 보유 EST와 public DB인 Genbank에 보고된 Citrus EST를 수집하여

IP : 14.49.138.138, 2017-11-03 13:30:33

174,228개의 추정 전사물 (transcript)에 대한 정보를 확보한 후 이 유전자들 중 중복을 고려하여 67,881개의 고유유전자서열을 선택하였다. 이들 중 유전자의 방향을 알 수 있는 54,355개에 대하여 각각 4개의 primer를 계획하여 217,420개의 primer를 제작하였고, 방향이 불분명한 유전자 13,682개에 대해서는 두 방향으로 하여 4개씩을 계획하여 109,456개의 primer를 설계한 후 300K 감귤 DNA chip 제작하였고, 이를 이용하여 다양한 품종에 대하여 분석을 실시하였고, data를 확보하였다.

③ 정우 식품으로부터 제주도 자생 시로미 유묘 전초의 cDNA 라이브러리 2.0×10^4 클론을 기탁받았고,. 1155 개의 유전자 염기서열 정보를 기탁 받았다. 시로미에는 감귤에 포함되어 있는 것과 유사한 기능성 물질들이 다량 포함되어 있어 감귤유전자와의 비교를 통하여 기능성 유전자 발굴에 도움을 줄 것으로 기대하고 있다.

④ 감귤류 9 품종에 대한 cDNA 라이브러리를 확보하고 있으며, 이 9.4×10^6개의 cDNA 라이브러리 클론에 대한 20,010개의 염기서열 결정 유전자 클론을 확보 하고 있다. 이들 중에 기능이 밝혀지지 않은 고유유전자 (unkown gene)는 11,868개이며 기능이 추정되고 있는 5,265개 유전자가 포함되어 있다.

⑤ 감귤류에서 glycosyltransferase와 관련된 유전자 28개와 유사 유전자 5개를 비롯한 33개의 클론과 GeneBank에 등록한 miraculin-like protein(FJ532030, FJ532031) 유전자 2개 그리고 Ethylene responsive element binding protein(FJ544914, FJ544915, FJ544916) 유전자 3 그리고 온주밀감 cDNA 라이브러리로부터 카로티노이드 생합성 과 관련된 zeta carotenoid desaturase(ZDS) 유전자와 geranylgeranyl diphosphate synthesis(GGPS)유전자에 대하여 Full-length gene을 확보하였고, 유전자 서열분석을 실시하였다. 또한, 개화유전자와 관련된 CIFT2 Full-length cDNA 염기서열분석에 대한 정보 및 클론 등을 확보하여 기능 연구를 실시하고 있다.

나. 연구소재 분양실적

① cDNA 라이브러리는 국내 외부기간에서 각각의 유전자에 대하여 5-10ml 씩을 5점 분양하였고, 내부기관은 각각의 유전자에 대하여 5-10ml 씩 4점 분양하였다. cDNA 클론은 국내 외부기관인 감귤연구소, 제주도 농업기술원, 바이오스펙트럼, 바이오애그 종 다양성 연구소를 비롯한 외부 연구자들에게 3,477점, 운영위원회 및 공동연구자들 포함한 내부기관 연구자들에게 2,052점을 분양하였다. 염기서열 정보 분양은 국내 외부기관인 감귤연구소, 제주도 농업기술원, 바이오스펙트럼, 바이오애그, 종다양성 연구소를 비롯한 외부기관에 8,853점 공동연구자들을 포함한 내부기관 연구자에게 4,650점을 분양하였다. 또한 상동성조사정보는 국내 외부기관 바이오애그 기업체에 2,401점을 분양하였다.

② 감귤 캘러스 cell line은 국내 외부기관인 감귤 시험장에 온주밀감 3품종(궁천조생, 상

IP : 14.49.138.138, 2017-11-03 13:30:33

야조생, 하례조생)을 포함한 총 6품종의 감귤 캘러스 cell line을 분양하였고, 전라남도 한방산업 진흥원에 당유자를 포함한 7품종의 감귤 캘러스 cell line을 분양하였으며, 인삼소재은행 소속 연구원에게 감귤 8품종 각각에 대한 식물소재(잎)를 분양하고, 내부기관의 공동연구자인 김소미 교수 연구실에 온주밀감을 비롯한 여러 품종의 식물소재(잎) 35개를 분양하였다. 또한, 그리고 감귤 과실은 국내 외부기관인 식품연구소에서 제주도 재래감귤 진귤을 비롯한 124개의 미숙• 성숙과실 그리고 경상대 화학과 신성철 교수 연구실에 병귤을 비롯한 273개의 미숙• 성숙과실을 분양하였다. 또한, 부산하이테크소재연구부에 271개 미숙• 성숙과실을 분양하였다.

2) 기초연구 육성 기반 확충에의 기여도

가. 감귤 육종 기초연구 : 감귤 과실로부터 얻어진 EST 정보는 과실의 품질 및 기능성 향상을 위한 유전정보의 기초 자료로 활용되며, 현재 재배되고 있는 대부분의 감귤류들은 전통적인 육종 방법으로 얻어진 것들이어서 이들의 EST 정보는 발현 유전자 정보임은 물론 전통교배로 얻을 수 있는 품종에 대한 정보를 예측하는 데에도 중요한 자료가 된다. 또 300K DNA micorarray 분석은 감귤이 보유하고 있다고 추정되는 모든 유전자에 대한 발현 분석을 실시하는 것으로 품종간의 분자적 수준에서의 차이를 DB화하여 EST data와 더불어 감귤 육종에 필요한 유전형질 분석에 활용될 뿐만 아니라 분자육종에 필요한 목표 유전자를 발굴하는 데에도 활용될 수 있다. 감귤 돌연변이주에 대한 유전정보 분석 또한 품종간의 특성을 좀 더 특화된 형태로 보여줄 것으로 기대되고 있다.

나. 감귤 생리 및 물질 대사 연구 : 다양한 유전자들이 관여하는 감귤류의 생리특성과 물질 대사를 심도 있게 규명하는 것은 매우 어려운 일이나, EST 정보와 DNA micorarray와 같은 총체적인 정보의 이용/분석을 전통적인 연구에 적용함으로써 종합적이고 다각적인 접근이 가능하며, 감귤류에는 헤스페리딘, 나린진 등의 유용한 성분이 있어 기능성 약제 등으로써 활용되고 있고, 과피 추출물에 다량으로 존재하는 플라보노이드를 이용한 화장품 개발에 이용하고 있는데, 이와 같은 특유한 물질의 생합성 및 분해대사 연구에도 활용도가 높고, 고유한 물질의 생물공학적 생산에도 이용될 수 있다. 또한 특정물질대사와 관련이 예상되는 유전자에 대해서는 아미노산 서열 분석, profile 정보 분석, 단백질 발현 등을 통하여 생리 및 물질 대사에 관한 기능 확인이 가능하다.

다. 분자육종용 신규유전자 : 멸종위기에 있는 1재래 감귤류 12품종에 존재하는 고유한 유전자를 발굴하고, 아미노산 서열 분석과 도메인 분석, profile 정보 등을 이용하여 유전자의 기능을 밝히고, 이들에 대한 종간의 발현 양상을 비교함으로써 분자 육종에서 필요한 신규 유전자 발굴이 가능하다.

라. 돌연변이육종 : 감귤의 EST 정보와 DNA micorarray 분석 정보 등은 2005년부터 2014

IP : 14.49.138.138, 2017-11-03 13:30:33

년까지 3단계 사업으로 진행 중인 감귤클러스터사업(돌연변이육종사업)의 일환인 돌연변이 개체 선발 및 변이개체의 생리대사 연구에 중요한 기초 자료가 될 것이다.

마. 감귤 구조 및 기능 유전체 연구 : 감귤유전자의 EST 연구 내용과 cDNA 데이타베이스는 국제적으로 진행되고 있는 감귤게놈 프로젝트의 성공적인 수행과 완전한 유전자의 배열을 파악하는데 공헌함은 물론 이를 토대로 한 품종 간 염기서열 식별(비교 유전체학)이나 실제로 생체 내에서 어떠한 기능을 담당하고 있는지를 알아내는 기능유전체 연구에도 기여할 것이다.

바. GMO 작물개발 및 환경위해성평가 : 제주대학교 아열대원예산업연구소에서는 핵심사업으로 GMO 식물연구사업을 추진하고 있는데 식물재분화 관련 유전자는 식물의 형질전환계 확립에 활용되며, 내충성유전자와 기타 기능성 유전자의 full length cDNA는 GMO 작물의 개발에 직접 활용될 것이다. 또한 제주대학교는 농림부의 GMO 작물환경위해성평가기관으로 지정되어 있는데 유전자, 단백질 등 본 은행의 소재는 GMO 작물의 분자생물학적 특성과 Gene flow 등 주요 환경위해성 평가지표의 protocol 개발 및 분석에 활용될 수 있다.

Ⅱ. 연구 소재 서비스 기반 구축 및 운영 관리

1. 연구소재 확보, 관리, 분양체제의 효율성과 개방성

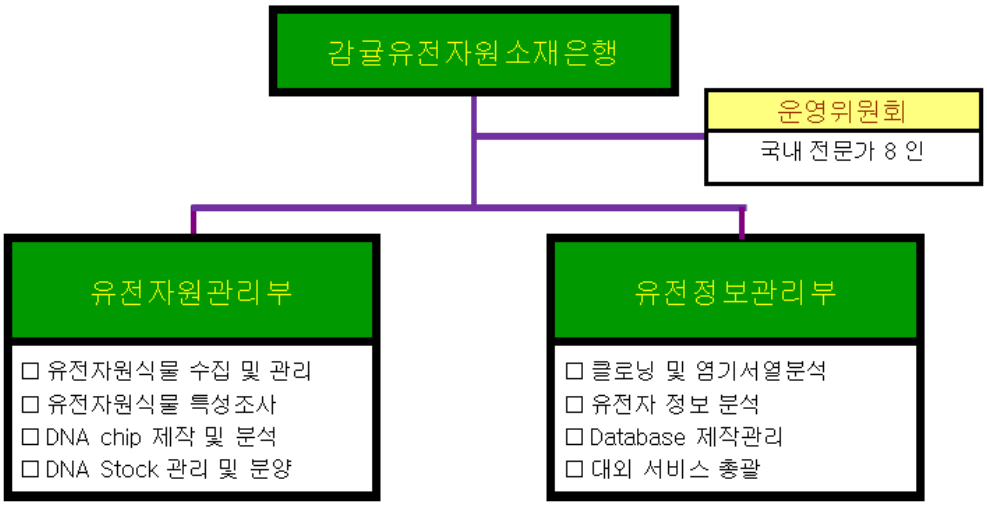
1) 연구소재 수집·관리·분양 체제

본 소재은행은 8인의 국내 전문가로 구성된 운영위원회와 유전자원관리부, 유전정보관리부의 2개 관리부로 구성/운영되고 있다. 연구소재의 선정과 수집, 관리 및 분양에 따른 전반적인 사항은 운영위원회를 통하여 결정되고 그에 따른 세부지침은 각각의 관리부에 전달되어 시행되고 있다.

연구소재는 감귤류를 중심으로 감귤 육종에 유용한 정보 및 유전자원의 확보에 중점을 두어 선정하고 있다.

□사업수행의 운영체계

IP : 14.49.138.138, 2017-11-03 13:30:33



가) 연구소재 수집체제

유전자원 관리부는 운영위원회에서 선정한 유전자원들을 수집하고 관리하며, 동시에 유전자 DNA chip 제작 및 분석을 관리한다. 또한 유전자 염기결정 클론에 대한 보관 유지 및 분양 등을 관리한다. 감귤 유전자원 식물체나 과실 등은 도내 감귤 시험장이나 농업기술원에 공문 등을 통해 매년 정기적으로 5-6월 봄에 확보하고 있다. 현재 감귤유전자원 식물체는 약 80여 품종을 확보하고 있으며, 과실인 경우는 재래감귤 12품종에 대해서 각각 성숙시기별 확보하고 있으며, 온주밀감을 포함한 9개 감귤 라이브러리에 대한 유전자 염기서열 결정 클론을 매년 하고 있다.

또한 감귤 국제 컨소시엄에 동참하기 위하여, 현재 감귤 유전체 사업으로써 제주도 재래감귤(병귤)에 대한 라이브러리 제작 및 게놈 분석을 수행하고 있다.

나) 연구소재 관리 체제

감귤 유전자원 식물체는 봄에 확보한 감귤 접수를 약 3년 정도 재배된 탱자 대목에 접목을 통해 독립된 감귤유전자원 하우스에서 고유의 번호를 부여하여 유지/관리한다, 매년 정기적으로 확보되는 감귤 과실은 -80℃ 초저온 냉동고에 품종별 그리고 성숙시기별 구별하여 고유의 번호를 부여하여 보관한다.

유전자원관리부에서 수집된 유전자원 중 라이브러리 제작이 요구되어지는 자원은 유전정보관리부로 전달되고 라이브러리 제작 형태를 결정하여 라이브러리 제작을 실시하고, 클론 및 염기서열 확보 량을 고려하여 일정 클론을 선발/정제한 후 각 클론에 대한 염기서열을 대량 염기서열 분석시스템으로 분석한다. 유전정보관리부에서는 high-quality의 염기서열만을 선발한 후 CAP3 프로그램으로 중복도를 고려한 고유염기서열 수집 및 과발현 유전자를 선발하고, 고유염기서열정보는 Blastx 프로그램으로 Genbank의 유전자들과 상동성조사를 수행하여 각각의 유전자들에 대한 잠재적 기능을 부여하는 일들을 수행한 후에 이러한 정보들을 데이터베이스

IP : 14.49.138.138, 2017-11-03 13:30:33

화 하여 홈페이지의 데이터베이스에 추가한다. 확보된 cDNA 라이브러리 및 염기결정 클론은 2set 이상을 만들어 1set는 명지대학교 내 GG바이오 -80℃ 초저온 냉동고에 보관하며 보관하고 있으며, 각 클론들은 감귤품종에 따라 고유의 번호를 부여하여 필요에 따라 사용하며, 특히 확보된 클론에 대해 데이터베이스화해 관리한다.

다) 연구소재 분양 체제

연구소재의 분양신청은 홈페이지, 전화, 팩스, 이메일 등을 통하여 전담 은행원 및 행정요원에게 접수되고 있다. 유전자클론, 염기서열 정보, 유전자 정보 등의 접수 사항은 분양요구 형태에 따라 유전자원관리부, 유전정보관리부에 전달되어 빠른 시간 내에 분양이 진행될 수 있도록 하고 있다

① 이용자격, 권한, 회원제 운영

감귤을 대상으로 하여 연구하고자 하는 모든 연구, 회사, 공익기관, 법인은 감귤유전자원 소재은행의 간단한 회원가입절차를 통하여 회원자격을 획득하게 된다. 회원의 경우 연구결과의 공유, 정보 분양(염기서열 정보 등) 기타의 우선권을 갖게 한다.

② 분 양

소재은행의 분양 신청서 양식의 서류접수에 의해 분양 (첨부자료 <분양신청서 양식>)

- 유전자원 식물체 및 과실에 대한 분양은 유전자원 관리부에 전달되어 빠른 시간 내에 분양이 진행될 수 있도록 하고 있다.
- 유전자클론 분양이 진행될 시에는 클론 분양과 동시에 각 클론에 대한 E. coli stock, plasmid 증폭 및 정제 등도 수행하여 차후 분양의 효율성도 증대시키고 있다.
- 유전자 염기결정클론 및 염기서열 정보는 현재는 무상으로 분양하고 있다.
- 유전자원 과실의 외부 분양인 경우 일부는 무상으로 분양을 하거나 일부는 착불을 통해 분양하고 있다.

2) 서비스 측면에서의 효율성과 개방성

○ 홈페이지 구축

본 소재은행이 계속적으로 확보하고 있는 연구소재(유전자 라이브러리, 유전자 클론, 유전자 정보 등)들은 감귤유전자원소재은행 홈페이지(http://citrus.jejunu.ac.kr/)를 통하여 모두 제공되고 있어 관련 연구자는 누구나 홈페이지 접속만으로 확보소재들의 정보를 확인할 수 있도록 하였다. 홈페이지는 포털 사이트에서 쉽게 검색이 가능하도록 되어 있어 누구나 손 쉽게 접근할 수 있도록 되어 있다. 또한 홈페이지의 회원가입을 통하여 web 상에서 분양신청을 할 수 있게 하여 분양 절차를 간소화함은 물론 최대한 빠른 시간 내에 분양이 이루어 질 수 있도록 하였는데, 홈페이지의 회원가입은 간단한 개인정보만을 입력하면 누구나 할 수 있도록 되어 있

IP : 14.49.138.138, 2017-11-03 13:30:33

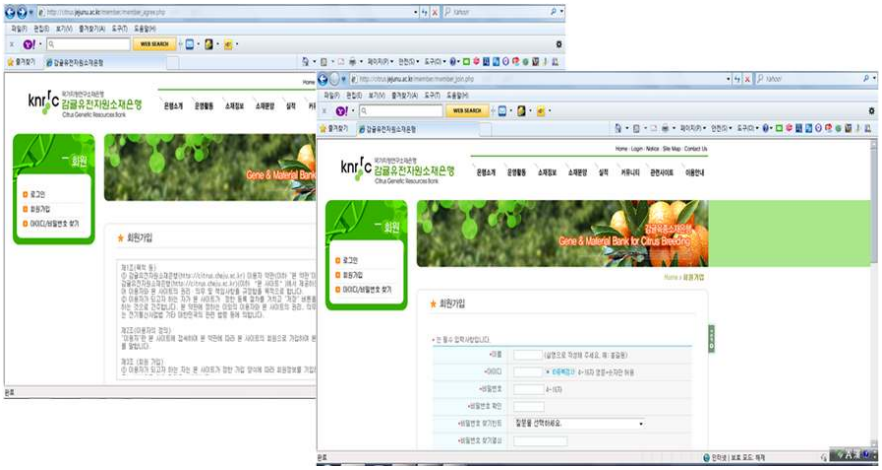
으며 관리자의 승인절차만 거치면 쉽게 정회원이 될 수 있다. 정보 분양(염기서열 정보 등)의 경우는 분양이 접수되는 즉시 승인절차만 거치면 web 상에서 바로 신청 정보를 볼 수 있도록 하여 최대한 빠른 시간 내에 수요자들이 정보를 활용할 수 있도록 하였고 유전자 클론의 분양은 체계적으로 최대한 빠른 시간 내에 수요자들에게 공급할 수 있도록 클론 분양 접수 후 매주 수요일에 분양하고 있으며, 유전자원 식물체 및 과실에 대한 분양도 빠른 시간 내에 공급할 수 있도록 성숙 시기별 과실을 확보하여 분양하고 있다.



<검색페이지>

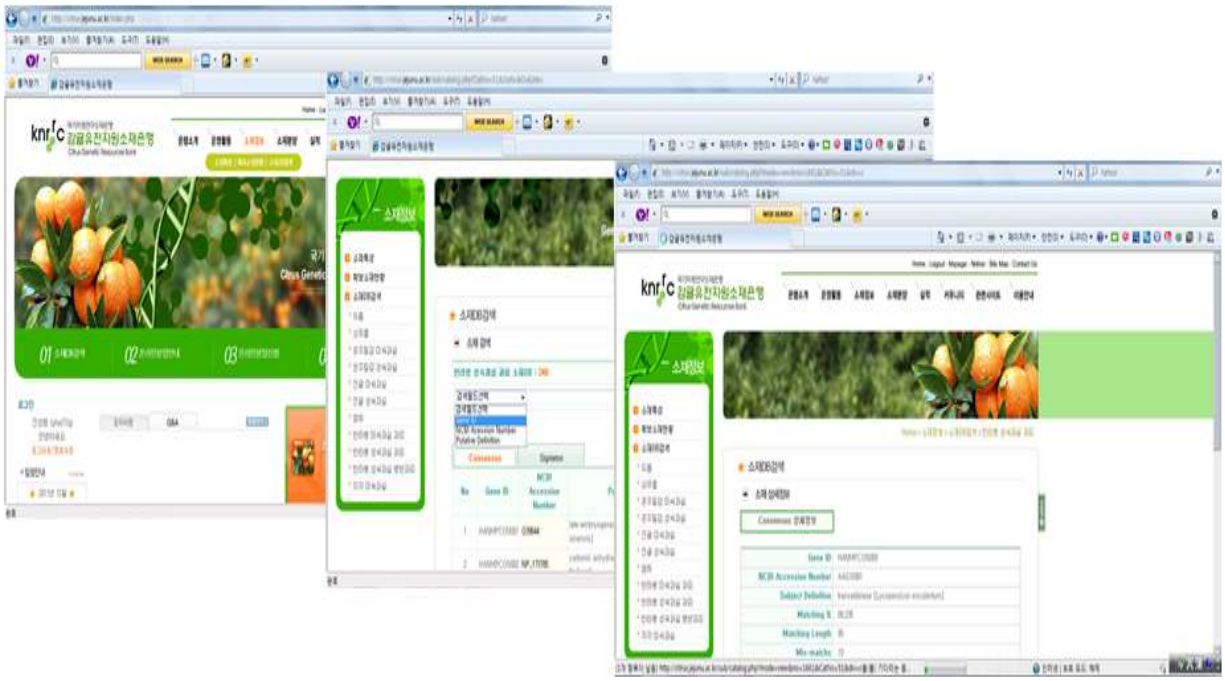


<감귤유전자원소재은행 홈페이지(http://Citrus.jejunu.ac.kr/)>



< 회원가입>

IP : 14.49.138.138, 2017-11-03 13:30:33



<분양신청>

3) 연구소재의 활용 촉진을 위한 노력

① 인터넷 홈페이지 활용

인터넷 홈페이지를 구축함으로서 최근 연구자들의 동향에 대한 정보(세미나 등)를 공유하고 간단한 절차를 통한 홈페이지 가입을 통하여 감귤 유전자원의 검색 및 분양 신청이 온라인상에서 가능하도록 하였다.



IP : 14.49.138.138, 2017-11-03 13:30:33

② 감귤육종연구회 운영

2007년 12월 11일 “감귤육종연구회”가 설립된 이래 최근까지 총 23회의 정기적인 모임을 수행하였으며, 감귤소재 및 육종 등에 관한 최근 정보들에 교환으로써 논문발표 및 실험결과들에 대하여 교환하고, 감귤 전문가들을 초빙하여 세미나를 개최 하였다. 또한, 본 소재은행이 확보하고 있는 소재들의 활용도 및 활용 범위 등에 관하여 세밀하게 검토/논의하여 활용가치가 높은 소재들을 선정하고 감귤 분자육종 소재로 직접 활용할 수 있도록 관련연구자들의 활용 촉진을 위한 홍보도 하였으며 계속적인 홍보를 통하여 도내 감귤관련연구기관 및 연구자들의 가입을 적극적으로 홍보하고 있다.

감귤육종연구회 운영실적(총 8회 운영)				
구분	일시	장소	주제	내용
1회	2008. 03. 18	생명대 세미나실	The citrus fruit Proteome 및 논문발표	1) Proteomic tool를 이용한 Citrus fruit의 발현 단백질 동정. 2) LC MS/MS를 이용한 발현단백질의 동정. 3) 당·산대사와 당·산 운반에 관여하는 단백질들 동정. * 논문제목: The citrus fruit proteome: insights into citrus fruit metabolism.
2회	2008. 04. 15	생명대 세미나실	감귤형질전환 계획 및 논문발표	1) 감귤 형질전환계획 - 감귤 캘러스세포 확보/ 금귤 기내배양조건 확립 2) 균주확보 - EHA105/ LBA4404 3) 형질전환에 사용할 유전자 - 형광유전자(GFP)/ 제초제저항성 유전자(bar)/ 개화촉진 유전자(CiFT) * 논문제목: High efficient transgenic plant regeneration from embryogenic calluses of *Citrus sinensis.*
3회	2008. 05. 20	생명대 세미나실	Microarray를 이용한 citrus 과육 숙성에 관여하는 유전자들의 발현 비교 및 논문발표	1) 감귤의 생장· 숙성에 이르는 단계별로 발현되는 유전자위 발현차이 Microarray를 이용한 분석 2) 과육의 성장과 숙성에 중요한 유전자들 확인 3) 유전자의 발현 real time RT/PCR를 이용한 재확인 * 논문제목: Global analysis of gene expession during development and ripening of citrus fruit flesh. A proposed mechanism for citric acid utilization.
4회	2008. 07. 22	생명자원과학대학 세미나실	현재까지의 실험결과 발표 및 감귤 전문가 초청 세미나	1) 흥진, 궁천 캘러스 세포 확보 및 증식 2) 금귤 조직배양 조건 확립 3) 도입유전자 구성 4) 유전자도입 protocol 5) 궁천조생/상야조생간의 유전자 발현양상 비교분석 6) 감귤연구소 안현주 박사 세미나 발표
5회	2008. 08. 08	생명대 세미나실	실험상 문제점들 및 논문발표	온주밀감 캘러스 세포 유전자 도입함에 있어 문제점 체크 및 해결방법 * 논문제목: Plant Regeneration from protoplasts isolated from Embryogenic callus of Satsuma.

IP : 14.49.138.138, 2017-11-03 13:30:33

6회	2008. 09. 12	생명대 세미나실	현재까지의 실험진행사항 및 논문발표	1) 궁천 callus cell line 확보 2) Miraculin 유전자 온주밀감 캘러스 세포내 도입 3) GFP 도입 온주밀감 캘러스 세포내 선발 4)금귤에서 Miraculin 유전자 도입여부 PCR로 확인 * 논문제목: An inproved procedure for Agrobac-terium-mediated transformation of trifoliata-orange via indirect organogenesis.
7회	2008. 10. 06	생명대 세미나실	제 11회 국제 감귤학회 발표 포스터 검토, 온주밀감 신품종 개발 및 최신논문발표,	1) 온주밀감 신품종 개발 2) 제 11회 국제감귤학회 참가 발표 포스터 확인 - 2008. 10.21-30 - 중국 우한 * 논문제목: GFP expression as an indicator of somatic hybrids between transgenic satsuma mandarin and calamondin at embryoid stage.
8회	2008. 11. 20	생명대 세미나실	실험진행사황 및 논문발표	1) Microarray의 결과를 이용한 유전자 발현차이 분석 2) 진귤 성숙과실 cDNA 라이브러리 제작 3) 과육의 성장과 숙성에 중요한 유전자 확인/발현분석 * 논문제목: comparafive analysis among cittrus cultivars by DNA Microarray

감귤육종연구회 운영실적(총 5회 운영)				
구분	**일시**	**장소**	**주제**	**내용**
1회	2009. 03. 18	생명대 세미나실	감귤형질전환 계획 및 논문발표	1) 감귤 형질전환계획 - 온주밀감 캘러스세포 재확보 2) 형질전환에 사용할 유전자 - GGPS 유전자 * 논문제목: “Gene stacking in 1-year-cycling APETALA1 citrus plants for a rapid revaluation of transgenic in reproductive tissues”
2회	2009. 05. 15	생명대 세미나실	단백질 발현분석 항체 개발 및 논문발표	1) 미라클린 유전자 도입에 따른 형질전환체 단백질 발현 여부 확인 위한 미라클린항체 개발 2) 단백질 발현 벡터 재확인 * 논문제목: Introductopn of citrus blight-associated gene info Carrizo citrange[Citrus sinensis(L.) Osbc.x Poncirus trifoliata (L.) Raf. by Agrobacterium-mediated transformation
3회	2009. 07. 15	생명대 세미나실	2009년 미국 식물학회 참석 및 논문발표	1) 2009 미국 식물학회 참석에 따른 포스터 검토 * 논문제목: comparison of endoplasmic reticulum targeted and non-targeted cytoplasmic GFP as a selectable marker in citrus protoplast transformation
4회	2009. 09. 18	생명대 세미나실	형질전환체 감귤류 확보에 따른 유지/온주밀감 캘러스 재 확보	1) 미라클린 유전자 도입 형질전환체 단백질 발현여부 확인 2) 온주밀감 캘러스 세포 재확보
5회	2009. 11. 20	생명대 세미나실	실험결과사황	1) Microarray의 결과를 이용한 상야조생과 궁천조생간에 발현 유전자 차이 분석 2) 지각 성숙과실 cDNA 라이브러리 제작 3) 형질전환 감귤류 확보

IP : 14.49.138.138, 2017-11-03 13:30:33

감귤육종연구회 운영실적(총 5회 운영)				
구분	일시	장소	주제	내용
1회	2010. 03. 12	생명대 세미나실	2010년 실험계획 및 논문발표	○ 감귤 조직배양 및 형질전환 실험계획 - 감귤 캘러스 세포 확보 - 유용 유전자 개발 - ERF 유전자, 카로티노이드생합성유전자, 미라클린 생합성유전자 * 논문제목: Regeneration and characterization of transgenic kumquat plants containing the Arabidopsis APETALA1 gene
2회	2010. 05. 11	생명대 세미나실	2010년 생화학분자생물학회 참석 및 논문발표	○ 2010 생화학분자생물학회 참석에 따른 포스터 검토 * 논문제목: Optimization of fermentation parameters for production of ethanol from kinnow waste and banana peels by simulataneous saccharification and fermentation
3회	2010. 07. 05	생명대 세미나실	논문발표/실험사항 및 논의	○ Bio 에탄올 관련하여 실험상 문제점 등 ○ 감귤 육종과 관련하여 미라클린 생산에 있어 특허 및 논문 관련하여 토의 * 논문제목: DUSP12B/TMDP inhibits stress-activated MAPKs and suppresses AP-1 dependent gene expression
4회	2010. 09. 29	생명대 세미나실	미라클린 유전자 도입 형질전환 감귤 식물체 감미테스트 및 논문발표	○ 미라클린 유전자 도입 형질전환 감귤 식물체 - 미라클린 항체를 이용한 단백질 발현 분석 - 미라클린 유전자 발현 여부에 따른 감미테스트 * 논문제목: Bifunctional selection-reporter systems for genetic transformation of citrus: mannose- and kanamycin-based systems
5회	2010. 11. 19	생명대 세미나실	2010년 졸업논문 발표 준비 및 paper 준비	○ 박사 학위 졸업논문 발표준비 - 에드난 - 일시 2010년 12월 7일 오후 4시 - 장소 RRC 세미나실 발표제목: Functional Expression of Miraculin, a Taste-modifying Protein, in *Citrus unshiu* Marc.and characterization of three novel citrus ERF genes ○ 2010년 paper 준비 - Expression of Miraculin Protein in Transgenic Youngpa Kumquat Plant - Functional Expression of Miraculin a Taste-modifying Protein in Transgenic Miyagawa Wase Satsuma Mandarin(*Citrus unshiu* Marc.) - Expression Profiling of Cultivar-related Genes in Satsuma mandarins,Miyagawa wase and Ueno wase - Agrobacterium-mediated transformation using embryogenic calluses in Satsuma mandarin(*Citrus unshiu* Marc.)cv.Miyagawa wase

IP : 14.49.138.138, 2017-11-03 13:30:33

감귤육종연구회 운영실적(총 5회 운영)				
구분	일시	장소	주제	내용
1회	2011. 03. 03	생명대 세미나실	실험발표 및 논문발표	○ 감귤 ADH 유전자 관련된 실험결과 발표 ○ 재래귤 11품종 캘러스 유도와 관련된 실험계획 보고 ○ 병귤 cDNA cloning 관련된 결과 발표 * 논문제목: Functional analysis of a cinnamyl alcohol dehydrogenase involved in lignin biosynthesis in wheat
2회	2011. 05. 13	생명대 세미나실	실험결과 발표 및 논문발표	○ 재래귤 callus 유도에 관련된 실험결과 발표 ○ 미라클린 형질전환체 논문 발표와 관련된 보고서 발표 ○ 병귤 cDNA합성과 관련된 결과발표 * 논문제목: EST sequencing from embryogenic cyclamen pericum cell cultures identifices a high proportion of Transscripts homologous to plant genes involved in somatic embryogenesis
3회	2011. 07. 05	생명대 세미나실	논문발표/실험사항 및 논의	○ Bio 에탄올 관련하여 실험상 문제점 등 ○ 감귤 육종과 관련하여 미라클린 생산에 있어 특허 및 논문 관련하여 토의 * 논문제목: DUSP13/TMDP inhibits stress-activated MAPKs and suppresses AP-1 dependent gene expression
4회	2010. 09. 02	생명대 세미나실	논문발표/실험사항 말표	○ 미라클린 생산과 관련된 실험 Data 정리 및 논문투고 준비관련된 상의 ○ ADH와 관련된 실험 실행사항 ○ 재래귤 캘러스 유도와 관련된 실험사항 * 논문제목: Production of Recombinant Miraculin using Transgenic Tomatoes in a closed cultivation system
5회	2011. 11. 03	생명대 세미나실	실험결과 발표 및 논문발표	○ 미라클린 현탁배양 및 조류독감 현탁배양 system 확립에 따른 결과 및 특허 관련된 보고서 작성 ○ 제주도 재래감귤 체세포배 형성 캘러스 유도에 대한 논문 발표 및 정리 ○ 알콜분해효소와 관련된 실험논의 * 논문제목: Localization of flavonoid enzymes in Arabidopsis roots

③ 국제 심포지엄 개최 및 전단지 배포(2007. 04. 01-2012. 02. 29)

구분	일시	장소	행사명	연 사
1	2008. 02. 29	아열대원예산업연구소	“한일교류 식물과학 심포지움”	이토 유키히로(일본동북대학교 농학부 조교수)
2	2009. 12. 10	아열대원예산업연구소	“2009 한.중 국제학술 심포지엄 개최”	이토 유키히로(일본동북대학교 농학부 조교수)
3	2009. 10 22 - 24	제주 그랜드호텔	“2009 International Sym-posium and Annual Meeting of the KSABC”	
4	2011. 12. 06-07	제주대학교 국제교류회관	“한미 국제 심포지움 과수유전체연구 최근동향과방향”	Fred Gmitter교수(플로리다대학) 외 3인

IP : 14.49.138.138, 2017-11-03 13:30:33

④ 전문인 초청 세미나,워크샵 개최 및 전단지 배포(2007. 04.-2012. 02. 29)

구분	일시	장소	행사명	연 사
1	2007. 05. 11-12	아열대원예산업연구센터	"국제감귤게놈프로젝트"에 관한 세미나"	임용표(충남대)
2	2007. 09. 03	아열대원예산업연구센터	"Gibberellic acid regulates abscisic acid-induced inhibition of stomatal opening by light in Arabidopsis"	고창효박사(부산대)
3	2007. 10. 26	아열대원예산업연구센터	"Functional screening of human genes in zebrafish"	김철희박사(충남대)
4	2007. 11. 10	아열대원예산업연구센터	"Production and Characterization of Genetically Engineered Creeping Bentgrass (*Agrostispalustris*)"	김정일박사(전남대)
5	2007. 12. 27	아열대원예산업연구센터	"생명과학분야 연구동향 및 발전방안"	민태선박사(한국과학재단)
6	2008. 03. 20	아열대원예산업연구센터	"감귤바이오 에탄올의 발전과 전망"	배현종(전남대학교)
10	2008. 06. 24	아열대원예산업연구센터	"제주도에서의 바이오 에탄올 생산"	김용우 박사(바이오스펙트럼 천연물연구소 소장)
11.	2008. 07. 22	생명과학대학 세미나실	"세포융합기술을 이용한 감귤육종" 세미나	안현주

구분	일시	장소	행사명	연 사
12	2008. 11. 12	아열대원예산업연구센터	"Regulation of Knox gene expression in rice"	이토 유키히로(일본 동북대학교 조교수)
13	2009. 01. 15	아열대원예산업연구센터	"Occurrence Situation and Control Strategy for Greenhouse Tomato Disease in Shangqiu"	Hong Quanchun Ph. D. (Assistant prof., Dept. of life Science, Shang-qiu Normal University, HENAN, CHINA)
14	2009. 02. 25	아열대원예산업연구센터	"Introduction of plants in Vietnam"	Ph.D. Tran The Bach Deputy Head, Departme-nt of Botany Institute of Ecology and Biological Resources 18 Hoang Qu-oc Viet, Cau Giay, Han-oi, Vietnam
15	2009. 04. 17	아열대원예산업연구소	"Germplasm Management and Characte-rization of Woody Ornamental Landscape Plants New Approache"	노승문박사 (전 영남대학교 교수, 전 매릴랜드 대학교연구 교수, 현 농무성 화훼 연구실 연구원)
16	2009. 06. 05	아열대원예산업연구소	"The antioxodant gene Mdhar plays an important role in protecting cells from various oxidative stress"	윤호성 박사(경북대학교 생물학과)
17	2009. 06. 23	아열대원예산업연구소	"A role of a 14-3-3 protein in programmed cell and disease resistance"	오창식 박사(Boyce Thompson Institute for Plant Research,Ithace NY 14850,USA)

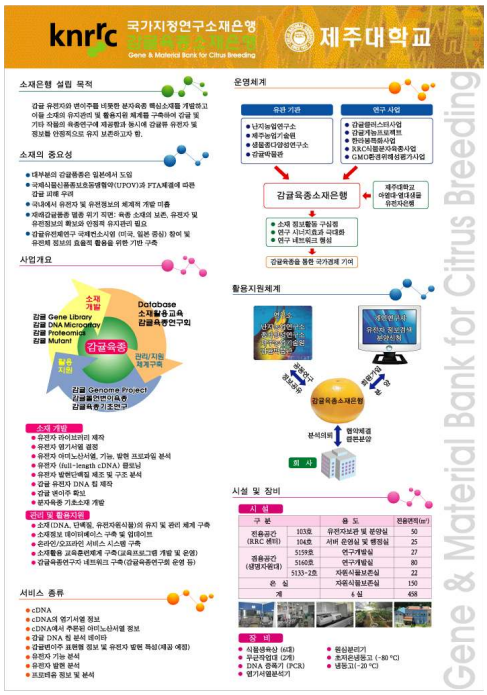
IP : 14.49.138.138, 2017-11-03 13:30:33

18	2009. 06. 29	아열대원예산업연구소	“면역질환의 제어를 위한 식품소재의 검색”	이상한소장(경북대 식품생물산업연구소) 외 권택규교수(계명의대 면역학교실)
19	2009. 09. 17	아열대원예산업연구소	“통합 연구재단의 생명과학분야 R&D 방향 및 사업”	김건수 단장[한국연구재단 생명과학단],김정회
20	2009. 09. 17	아열대원예산업연구소	“ Evolution of Technology; Case of Bio-based Xylitol”	김정회 교수, KAIST 생명과학과
21	2009. 12. 19	아열대원예산업연구소	“저탄소 녹색성장 추진방안”세미나	오영출 전문위원(녹생성장위원회)

구분	일시	장소	행사명	연 사
22	2010. 02. 10	아열대원예산업연구소	Molecular Pharming	고석민박사
23	2010. 03. 15	아열대원예산업연구소	“Regulation of Transcription Elongation by NELF in Drosophila and HIV”	이찬효박사님(보스턴 의과대학)
24	2010. 07. 29	아열대원예산업연구소	“About Limonene”세미나	이민재 (주)넥스캠
25	2010. 09. 03-04	제주대학교 국제교류회관	2010년 제1회 식물거점센터 워크숍	
26	2011. 02. 27	아열대원예산업연구소	“연구계획서 작성방법”	민태선 박사(한국연구재단)
27	2011. 03. 22	아열대원예산업연구소	“Physiological characterization for gene function in transgenic plants as a case”	고창효박사(감귤육종 및 농업연구소 부소장)
28	2011. 05. 17	아열대원예산업연구소	“유전자재조합식품바로알기”	김현경박사(식양청 신소재식품과, 보건연구관)
29	2011. 08. 18	아열대원예산업연구소	“환경에 대한 이해: 왜 중요한가?”	김호일 박사(충남대)
30	2011. 10. 06	아열대원예산업연구소	“Construction of Arabidopsis expression library and study on the phyB supressing mutant”	서수정 박사(한국생명공학연구원)
31	2011. 10. 17	아열대원예산업연구소	“세계 식량공급의 문제와 전망”	Prof. John Perry GUSTAFSON (UNIVERSITY OF MISSOURI, 전공: Wheat Biology
32	2011. 10. 25	아열대원예산업연구소	“감귤품종 육종 및 기술개발”	윤 수현 박사(감귤시험장)
33	2011. 11. 07	아열대원예산업연구소	“Structural studies of Influenza RNA-polymerase for novel drug design”	Sam-Yong Park (Yokohama City University, Professor of protein crystallography)

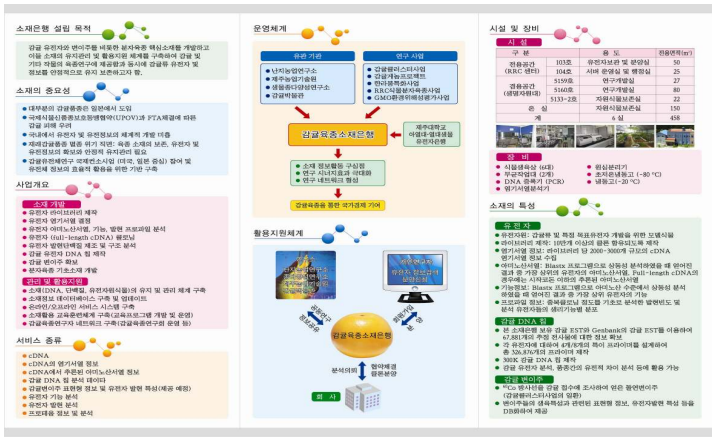
IP : 14.49.138.138, 2017-11-03 13:30:33

[홍보 포스터] 2007. 04. 01-2012. 02.





[홍보 유인물] 2007. 04. 01-2012. 02. 29





IP : 14.49.138.138, 2017-11-03 13:30:33

[국제 심포지움 개최]

- 제목 : "한일교류 식물과학 심포지움"
- 일시 : 2008년 2월 29일
- 장소 : 아열대원예산업연구센터

- 특강 1 : Molecular identification and spaceflight experiments for the studies of the gravity-influenced growth in plants
  (연사: Takahashi Hideyuki 일본동북대학교)
- 특강 2 : Floral organ development in nongrass monocots.
  (연사: Kanno Akira 일본동북대학교)
- 특강 3 : The collection, preservation and evaluation of *Zoysia* grass as genetic resource
  (연사: Akashi Ryo 미야자키대학)
- 특강 4 : Targeting of proteins to the chloroplast outer envelope membranes
  (연사: 황인환 포항공대학교)
- 특강 5 : Control of ginsenoside biosynthesis in *Panax ginseng*
  (연사: 최용의 강원대학교)
- 특강 6 : Characteristics of rice mutants resistant to 5-methyltryptophan
  (연사: Tohukairin Hideyoshi 일본동북대학교)

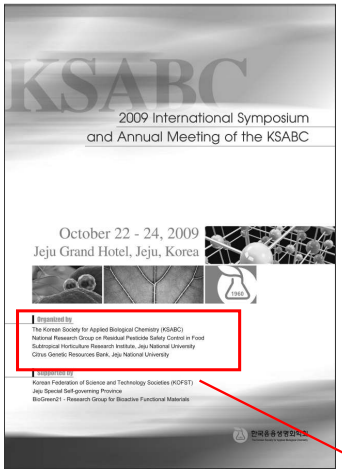


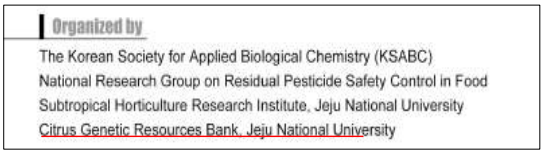




IP : 14.49.138.138, 2017-11-03 13:30:33

• 제목 : “2009 International Symposium and Annual Meeting of the KSABC”
• 일시 : 2009년 10월 22일 - 10월 24일
• 장소 : 제주 그랜드호텔
• 주최 : (사)한국응용생명화학회, 제주대학교 아열대원예산업연구소, 한국보건산업진흥원
국가잔류농약안전관리연구사업단, 제주대학교 감귤유전자원소재은행





* 국제학술대회를 제주대학교의 감귤유전자원소재은행에 대한 지원으로 공동 개최 하였음,
* 학회기간동안 28명의 연사 발표, 240명의 회원이 참가한 대규모 학술회의 였으며, 관련연구자들의 정보교류 및 감귤유전자원소재은행의 직접적인 홍보가 되었음.

• 제목 : “2009 한.중 국제학술 심포지엄 개최”
연사 : 이토 유키히로(일본동북대학교 농학부 조교수)
일시 : 2009년 12월 10일(목) 10:00-12:00
장소 : 아열대원예산업연구소 세미나실



IP : 14.49.138.138, 2017-11-03 13:30:33

• 제목 : “The Trend and Strategy of Fruit Tree Genomics Research”
• 일시 : 2011년 12월 06일 - 12월 07일
• 장소 : 제주대학교 국제교류회관
• 주체 : 제주대학교 감귤유전자원소재은행
제주대학교 재래감귤 유전체 연구사업
제주대학교 아열대원예산업연구소
• 후원 : 농촌진흥청 Post 바이오그린 차세대유전체연구사업단

특강 1. 한국 과수육종의 현황과 발전방안(신용억 박사, 농촌진흥청)
특강 2. Genetic history and NGS data application for genome analysis (최익영 박사, 서울대학교)
특강 3. The Haploid Mandarin and Diploid Sweet Orange Genome Sequences (Freed Gmitter 교수, 플로리다 대학)
특강 4. 한국 감귤유전체 연구동향과 방향(김재훈 교수, 제주대학교)



[워크샵 및 세미나 개최]

• 제목 : “국제감귤게놈프로젝트”에 관한 세미나
연사 : 임용표(충남대)
일시 : 2007년 05월 11일
장소 : 아열대원예산업연구센터



IP : 14.49.138.138, 2017-11-03 13:30:33

제목: “감귤 조직배양 및 형질전환 문제점”
연사: 진성범 박사 (감귤소재은행)
일시: 2008년 07월 22일
장소: 생명자원과학대학 세미나실

제목: “세포융합기술을 이용한 감귤육종”
연사: 안현주 박사 (감귤연구소)
일시: 2008년 07월 22일
장소: 생명자원과학대학 세미나실



• 제목 : “Germplasm Management and Characterization of Woody Ornamental Landscape Plants New Approache”

연사 : 노승문박사
(전 영남대학교 교수, 전 매릴랜드 대학교연구 교수, 현 농무성 화훼 연구실 연구원)
일시 : 2009년 4월 17일 10:00
장소 : 제주대학교 아열대원예산업연구소, 2층 세미나실



• 제목 : “통합 연구재단의 생명과학분야 R&D 방향 및 사업”
연사 : 김건수 단장[한국연구재단 생명과학단],김정회
일시 : 2009년 09월 17일(목) 10:00-12:00
장소 : 제주대학교 아열대원예산업연구소, 2층 세미나실



IP : 14.49.138.138, 2017-11-03 13:30:33

• 제목 : “Evolution of Technology; Case of Bio-based Xylitol”
연사 : 김정회 교수, KAIST 생명과학과
일시 : 2009년 09월 17일(목) 10:00-12:00
장소 : 제주대학교 아열대원예산업연구소, 2층 세미나실



• 제목 : “저탄소 녹색성장 추진방안”세미나
연사 : 오영출 전문위원(녹생성장위원회)
일시 : 2009년 12월 19일(토) 오후 4시
장소 : 아열대원예산업연구소 세미나실



• 제목 : “Regulation of Transcription Elongation by NELF in Drosophila and HIV”
연사 : 이찬효박사님(보스턴 의과대학)
일시 : 2010년 03월 15일(월), 13:00
장소 : 제주대학교 아열대원예산업연구소, 2층 세미나실



IP : 14.49.138.138, 2017-11-03 13:30:33

• 제목 : “About Limonene”
연사 : 이민재(주)넥스캠
일시 : 2010년 07월 29일
장소 : 제주대학교 아열대원예산업연구소, 2층 세미나실



• 제목 : “Physiological characterization for gene function in transgenic plants as a case study”
연사 : 고창효박사(감귤육종 및 농업연구소 부소장)
일시 : 2011년 03월 22일
장소 : 제주대학교 아열대원예산업연구소, 2층 세미나실



• 제목 : “환경에 대한 이해: 왜 중요한가?”
연사 : 김호일박사(충남대)
일시 : 2011년 08월 18일
장소 : 제주대학교 아열대원예산업연구소, 2층 세미나실



IP : 14.49.138.138, 2017-11-03 13:30:33

• 제목 : “세계 식량공급의 문제와 전망”
연사 : Prof. John Perry GUSTAFSON (University of Missouri)
일시 : 2011년 10월 17일
장소 : 제주대학교 아열대원예산업연구소, 2층 세미나실



• 제목 : “감귤 품종 육종 및 기술 개발”
연사 : 윤수현 박사(감귤시험장)
일시 : 2011년 10월 25일
장소 : 제주대학교 아열대원예산업연구소, 2층 세미나실



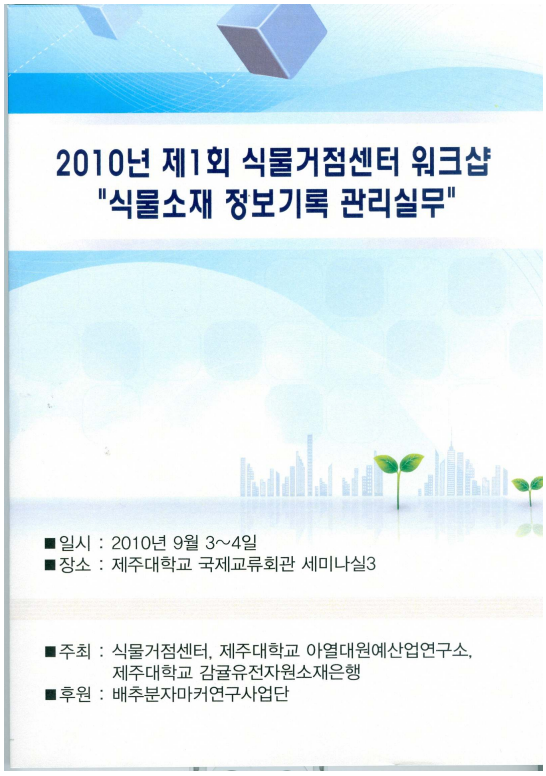
• 제목 : “Regulation of Transcription Elongation by NELF in Drosophila and HIV”
연사 : 이찬효박사님(보스턴 의과대학)
일시 : 2010년 3월 15일(월), 13:00
장소 : 제주대학교 아열대원예산업연구소, 2층 세미나실



IP : 14.49.138.138, 2017-11-03 13:30:33

[워크샵]

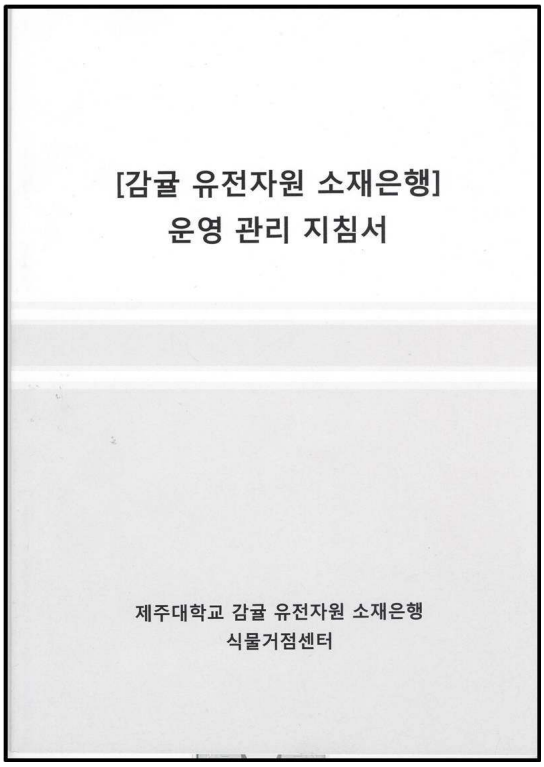
- 제목 : “2010년 제 1회 식물거점센터 워크샵”
  일시 : 2010년 9월 3일 - 9월 4일
  장소 : 제주대학교 국제교류회관 세미나실
  주최 : 식물거점센터, 제주대학교 감귤유전자원소재은행



IP : 14.49.138.138, 2017-11-03 13:30:33

4) 연구소재은행 운영지침서 마련

본 연구소재은행은 소재은행 운영관리 지침서를 참고하여 유전자/유전자원을 확보하며 보존절차 및 분양등을 수행한다. 유전자/유전자원들은 유전자원관리부에서 확보 및 보존하며, 유전자원관리부에서 확보된 유전자원 중 라이브러리 제작이 요구되어지는 자원은 라이브러리관리부로 전달되고 라이브러리관리부에서는 라이브러리 제작 형태를 결정하여 라이브러리 제작을 실시한다. 클론 및 염기서열 확보량을 고려하여 일정 클론을 선발/정제한 후 각 클론에 대한 염기서열을 대량 염기서열 분석시스템으로 분석함과 동시에 분양을 대비한 클론도 확보/보관하고 있다. 또한 연구소재의 품질관리 역시 소재은행 운영관리 지침서를 참고하여 유전자는 1달에 약 5건씩 유전자 품질검사를 수행하고 있고, 유전자원 캘러스세포들은 6개월 간격으로 재분화를 유도하여 재분화능을 확인하며, 캘러스세포들은 2년에 한번씩 새로 만든다.



IP : 14.49.138.138, 2017-11-03 13:30:33

2. 소재은행의 국내·외적인 위상 제고를 위한 노력 및 실적

○ 교육 및 홍보 행사 참가(2007. 04. 01-2012. 02. 29)

구분	일시	장소	행사명	참가자
1	2007. 09. 06	국회의사당	세계 연구소재은행 현황 국가지정연구소재은행-연구의 출발점	부경환
2	2007. 09. 14	생물종다양성연구소	2007년 바이오 아일랜드 제주포럼	부경환
3	2008. 08. 19	서울 여자대학교 인문사회관1층 108호	제 2회 연구소재은행 워크샵	진성범, 김재훈
4	2008. 09. 04-05	국회의사당	2008년 국가연구소재은행 국제 심포지움및 전시회	진성범,김재훈
5	2009. 03. 20	서울 여자대학교 인문사회관1층 108호	국가지정연구소재은행 협의회 참석	김재훈, 진성범
6	2009. 04. 20-21	서울 국회의사당	국회 심포지엄 및 전시회 참석	김재훈, 진성범, 윤정훈
7	2009. 06. 15	서울 여자대학교	국가연구소재은행 중앙센터 워크숍 참석	김재훈, 진성범
8	2009. 07. 08	충남대	유전자소재 보관 및 분리 워크숍 참석	김재훈, 진성범
9	2009. 08. 28	서울 여자대학교	국가연구소재중앙센터 워크숍참석	김재훈, 진성범
10	2009. 12. 16-17	제주 그랜드호텔	2009 제3회 연구소재은행 워크숍 참석	김재훈, 류기중,진성범,최수정, 윤정훈, 고유라
11	2010. 03. 05	서울산업대학교	2010년 제 1차 연구소재중앙센터교육프로그램참석	진성범
12	2010. 04. 09	서울 산업대학교	2010 제 1회 연구소재중앙센터 워크숍참석	김재훈, 진성범
13	2010. 04. 26	서울 국회의사당	2010 제 4회 국회 국제 심포지엄 및 전시회 참석	진성범, 이비
14	2010. 07. 02	서울 산업대학교	2010 제 2회 연구소재중앙센터 교육프로그램 참석	진성범
15	2010. 06. 17-19	서울 aT센터	생명 산업대전 참석	진성범
16	2010. 06. 18-19	수원	연구협의 참석	류기중
17	2010. 07. 26-27	부산 해운대	2010 제 2회 연구소재중앙센터 워크숍 참석	김재훈, 진성범
18	2010. 10. 19-21	중국	한 중 국제공동 세미나 참석	김재훈
19	2010. 11. 26	대전	2010 제 3회 연구소재중앙센터 교육프로그램 참석	김재훈, 진성범
20	2010. 12. 22	수원 경희대학교	제 2회 거점소재 은행 워크샵 참석	김재훈, 진성범
21	2011. 01. 21	서울테크노파크 602호	2011 제1회 연구소재은행 교육프로그램-은행운영과 소재관리	진성범
22	2011. 05. 31	국회의사당	2011년 국가연구소재은행 국제 심포지움및 전시회	진성범,이비
23	2011. 08. 26	서울역 GLORY 대회의실	2011 제2회 연구소재중앙센터 교육프로그램-은행운영과 소재관리 II	진성범,한송이
24	2012. 02 02-03	강원도 홍천 대명 비발디파크 리조트	2012 제1회 연구소재은행 교육프로그램-유전자원의 관리와 활용	진성범,한송이, 김재훈

IP : 14.49.138.138, 2017-11-03 13:30:33

○국내, 국제협력 (2007. 04. 01-2012. 02. 29)

구분	일자	제목	이름	기관
1	2007. 10. 12	소재기탁협의서	시로미 유전자 및 유전서열정보	정우식품
2	2007. 03.	국가지정연구소재은행 사업지원 확약서		제주대학교총장
3.	2007. 03. 01	협약서	이효연	아열대원예산업연구소
4.	2009. 01. 19	국제협력	Hon Quanchun	중국 상구 대학교
5	2009. 12. 21	컨소시엄구성협약서	이연희	재단법인 연구소재중앙센터
6	2011.12. 06-07	국제협력	Fred Gmitter	미국 플로리다 대학교

○국내, 국제 학회참석 및 발표(2007. 04. 01-2012. 02. 29)

구분	일시	장소	학회	참가자
1	2007. 08. 13		ISBER 가입	김재훈
2	2008. 05. 18	미국 maryland	국제 ISBER 학회 참석	김재훈, 류기중
3	2008. 10. 21	대구	2008년 한국응용생명화학회	윤정훈
4	2008. 10. 21-30	중국	2008년 국제 감귤학회	진성범, 부경환, 김재훈, 류기중
5	2009. 07-23	미국(하와이)	2009 미국 식물학회 참석 및 발표	김재훈, 류기중
6	2009. 09. 22-23	서울 코엑스	국제 ISBER 학회 참석	김재훈, 진성범, 윤정훈,
7	2009. 10. 22-24	제주그랜드호텔	한국응용생명화학회 추계학술대회	
8	2010. 05. 18	서울	생화학분자생물학회 참석	김재훈, 진성범, 윤정훈, 에드난
9	2010. 10. 28-30	일본	제2회 ANRRC 참가	김재훈, 정성진
10	2011. 04. 15	경희대	한국응용생명화학회	진성범
11	2011. 05. 16-18	서울	한국생화학 분자생물학회	한송이
12	2011. 10. 20-22	제주	한국응용생명과학회	류기중
13	2011. 10. 27-28	부산	한국생명과학회	한송이, 이비

IP : 14.49.138.138, 2017-11-03 13:30:33

○도내· 외 교육 홍보(2007. 04. 01-2012. 02. 29)

구분	일시	장소	행사명
1	2007. 11. 22-24	삼무힐랜드	“아열대 친환경 생물산업 페스티벌” 전시홍보부스운영
2	2008. 04. 12	아열대원예산업연구소	여고생 생명공학 교실(4회)
3	2008. 10. 30-11. 01	제주칼호텔	2008 아열대친환경 생물산업 페스티발
4	2009. 08. 13-14	아열대원예산업연구소	GMO 제작 및 평가
5	2009. 08. 22-23	아열대원예산업연구소	생명공학 교실 심화반
6	2009. 12. 26	아열대원예산업연구소	“도내 고교과학반초청 생명공학교실”
7	2010. 06. 26	아열대원예산업연구소	여고생생명공학교실(20명 참가)
8	2010. 08. 09-17	아열대원예산업연구소	2010GMO 연수강좌
9	2011. 06. 19	과천과학관	과천초등학생교육
10	2011. 06. 25	아열대원예산업연구소	여고생 생명공학교실 기초반(2회)
11	2011. 08. 06	아열대원예산업연구소	여고생 생명공학교실 심화반
12	2011. 10. 30	과천과학관	과천초등학생교육

IP : 14.49.138.138, 2017-11-03 13:30:33

[국내, 국제협력]

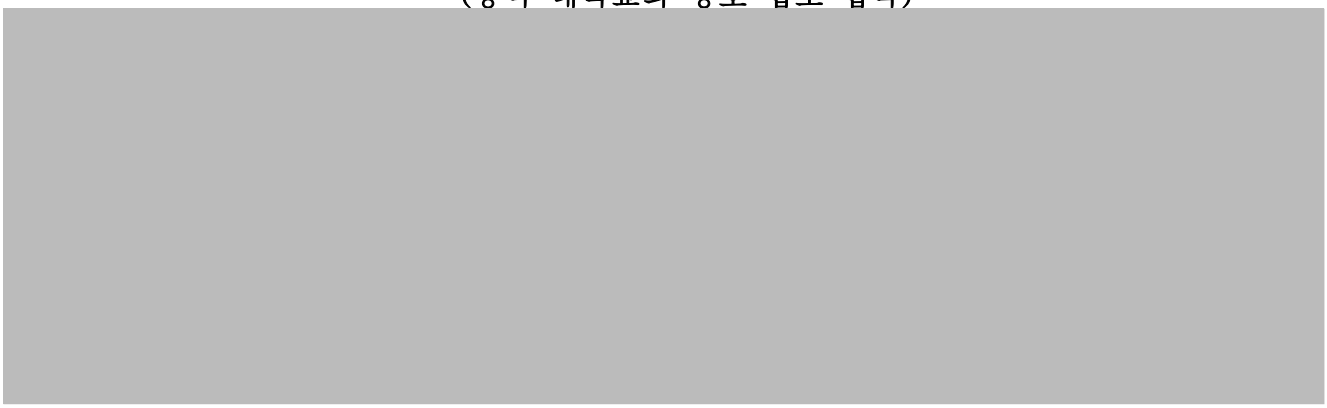
(한미국제협력)



(사업지원확약서)



(중국 대학교와 상호 협조 협약)



IP : 14.49.138.138, 2017-11-03 13:30:33

(중점연구소사업과 상호 협조 협약) (컨소시엄 구성 협약) (소재기탁 협약)



[국제학회참석]

(국제 생물환경 은행 협회에 가입)

(제 11회차 국제 감귤학회 참석 2008년 10월 23일 중국우한)

IP : 14.49.138.138, 2017-11-03 13:30:33



(2009년 07월 17일 미국식물학회 참석)



(2009년 09월 22일 국제 ISBR 학회참석)



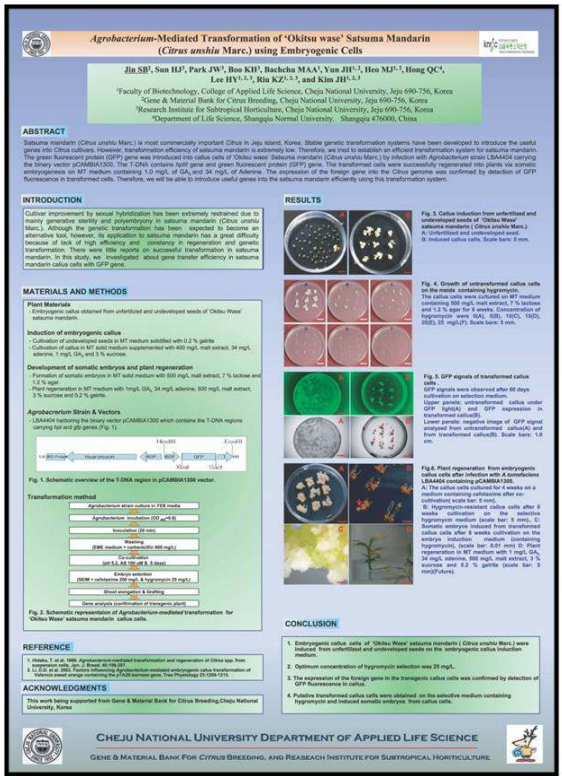
(2010년 10월 28일-30일 ANRRC참가 및 발표)

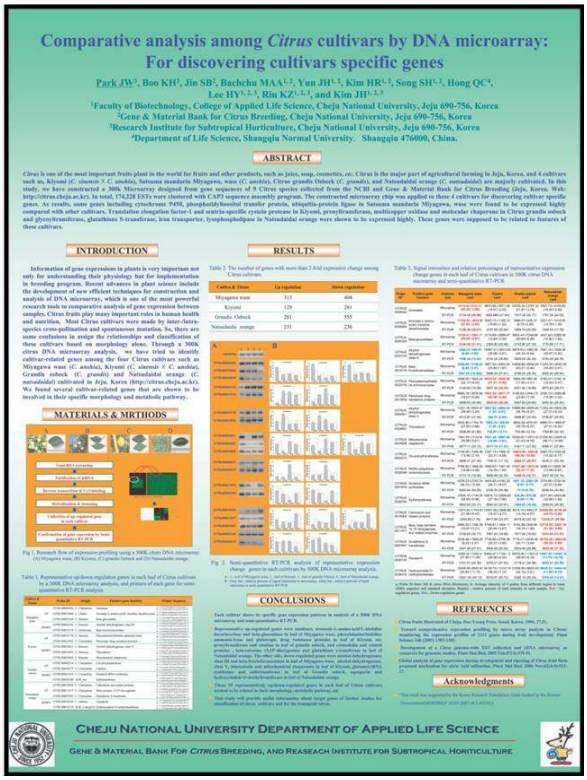
IP : 14.49.138.138, 2017-11-03 13:30:33



[국내 국제 학회 발표 포스터]

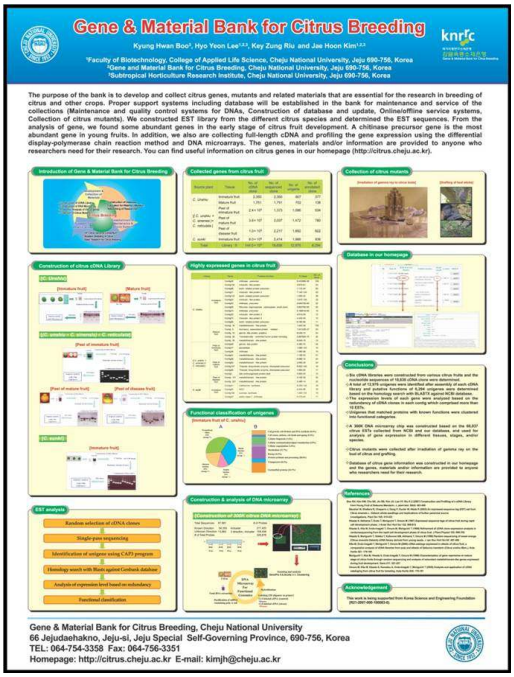
(11회차 국제 감귤학회 포스터)





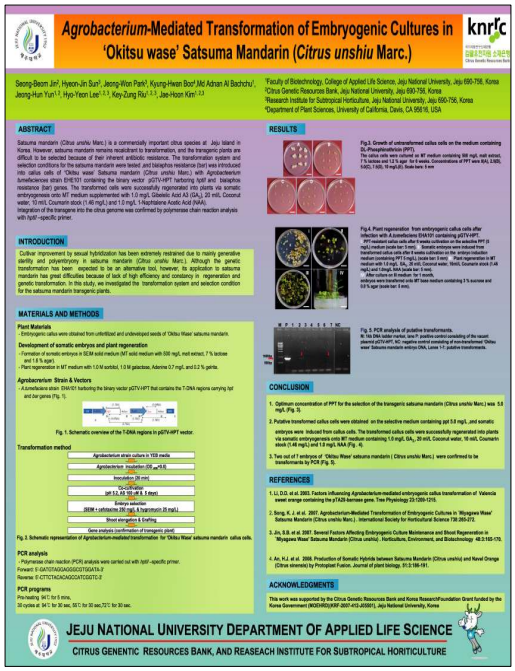
IP : 14.49.138.138, 2017-11-03 13:30:33

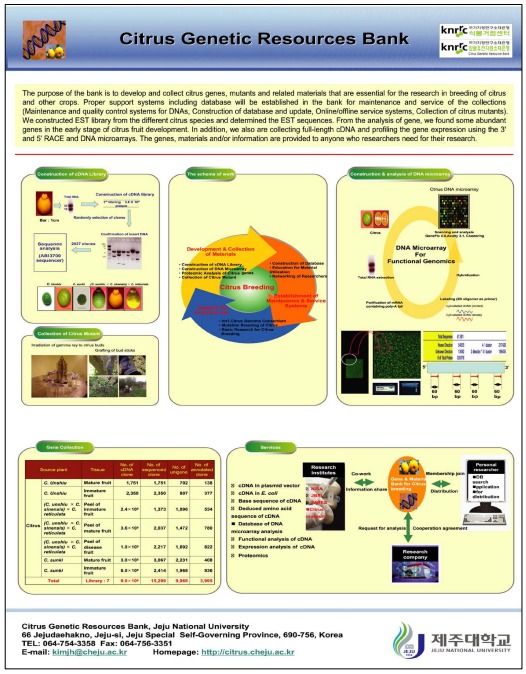
(ISBR 국제학회 포스터:2008. 5.18 미국 maryland) (응용 생명학회 포스터:2008. 10. 21 대구)





(2009년미국식물 학회 포스터) (2009 국제 ISBR 학회 포스터)





IP : 14.49.138.138, 2017-11-03 13:30:33

Functional expression of the taste-modifying protein, miraculin, in transgenic Miyagawa Wase Satsuma Mandarin (*Citrus unshiu* Marc.)

Md. Adnan Al Bachchu[1,2], Seong-Beom Jin[2], Fei Li[1], Jeong-Won Park[3], Hyeon-Jin Sun[3], Hyo-Yeon Lee[1,2,3], Key-Zung Riu[1,2,3], Jae-Hoon Kim[1,2,3]*

[1]Faculty of Biotechnology, College of Applied Life Sciencee, Jeju National University, Jeju 690-756, Korea, [2]Citrus Genetic Resources Bank, Jeju National University, Jeju 690-756, Korea,[3]Research Institute for Subtropical Horticulture, Jeju National University, Jeju 690-756, Korea

ABSTRACT

Miraculin gene, a taste modifying proteins which has the unusual property of being able to modify a sour taste into a sweet taste, was introduced under the control of 35S promoter into the Miyagawa Wase Satsuma mandarin (*Citrus unshiu* Marc.) callus by *Agrobacterium*-mediated transformation to produce citrus transgenic plant. Satsuma Mandarin is one of the choicest citrus varieties grown widely and commercially in Korea (especially in Jeju Island) and Japan. Satsuma mandarin is known o be recalcitrant to transformation. In this study, we constructed the transformation system and selection conditions for the Satsuma mandarin. Our protocol resulted in a reasonable transformation efficiency of 22%. Transformations of miraculin gene were identified by Polymerase Chain Reaction (PCR) and integration of miraculin gene in transgenic Miyagawa Wase plants genome was confirmed by Southern blot analysis. Genetically stable expression was confirmed by Western blot analysis. To investigate the expressed protein is correctly modified in the transgenic plants, we analyzed the dimerization and N-glycosylation of recombinant miraculin gene in transgenic Miyagawa Wase Satsuma mandarin(*Citrus unshiu* Marc) plants.

INTRODUCTION

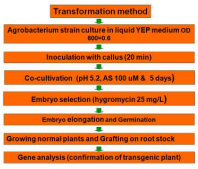
Miraculin is a taste-modifying protein found in the miracle fruit (*Richadella dulcifica*), a native West African shrub. Indigenous peoples often use the berries of this shrub to improve the palatability of acidic foods and beverages. But now a days, these proteins have been used in many food processing industry as sweetening agents, flavor enhancers, and animal fodder supplements. These proteins can act at extremely low concentrations (1) and currently interest has been increasing in miraculin due to this amazing taste-modifying property. But, commercial feasibility of miraculin is very low because of the plants tropical origin. Recently, some microorganism, such as *E. coli* (2), *Aspergillus oryzae* (3) was used as a host for expressing miraculin and the recombinant protein did exhibit taste-modifying properties. Some crop species including lettuce(4), tomato (5) and strawberry (6) successfully expressed recombinant miraculin, however, in subsequent generations, stable miraculin expression was observed in tomato and strawberry but silencing of the transgene occurred in lettuce, In this study, we expressed the taste-modifying protein miraculin, in the perennial plants Miyagawa Wase Satsuma Mandarin, is one of the choicest citrus variety grown widely and commercially in Korea and Japan, To best our knowledge, this is the first report to produce transgenic Miyagawa Wase plants containing miraculin gene.

MATERIALS & METHODS

***Agrobacterium* Strain & Vectors :** EHA105 harboring the binary vector Pcambia1300 which contains the T-DNA regions carrying hygromycin and miraculin gene (Fig. 1)



Fig 1. Schematic representation of the binary vector pcambia1300 with its position of different enzymes of citrus genetic transformation. RB-Right border, LB-Left border, NOS-ter- Terminator of nopaline synthase gene, Mir-Miraculin gene, 35SP-35S promoter of cauliflower mosaic virus, Hyg- Hygromycin, PolyA- Polyclonal A.



PCR analysis : Polymerase chain reaction (PCR) analysis was carried out with Miraculin –specific primer:
Forward: 5-TTTTCTAGAATGAAGGAATTAACAATGCT-3
Reverse: 5- TTTGAGCTCTTAGAAGTATACGGTTTTGT-3 and hygromycin specific primer:
Forward: 5-CTTCTACACAGCCATCGGTCCAGA-3
Reverse: 5- GATGTAGGAGGGCGTGGATATGTC-3
PCR programs: Pre-heating 94˚C for 5min, 30 cycles at 94˚C for1min, 50˚C for 1min, 72˚C for 1min and final 720C for10 mins.
Western Blot Analysis : Miraculin polyclonal antibody (Primary antibody – Miraculin R2 Final anti-serum (Ab Frontier) and Secondary antibody – Donkey anti-rabbit IgG-HRP)
Analysis of post translational modification of the recombinant miraculin expressed in the transgenic Miyagawa Wase plants: Dimerizaion of the transgenic plants protein were done by western blot. SDS-PAGE was confirmed under non-reducing and reducing conditions. Glycosylation confirmed by western blot using *E. coli* protein containing miraculin protein and transgenic Miyagawa Wase plant protein.

RESULTS

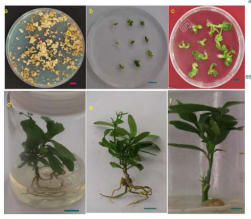


Fig 2. Regeneration of the Miyagawa Wase embryogenic calluses after agrobacterium-mediated genetic transformation. (a) The resistant embryos (green) growing on hygromycin selection medium after 6 weeks of culture. (b) Heart shaped embryos on embryo elongation medium after 3 weeks of culture. (c) Germinated embryos on germination medium after 4 weeks of culture. (d) Transgenic plants on MT medium containing 3.0% sucrose and 0.8% agar after 6 weeks of culture. (e) Transgenic plants showing well developed shoot and root. (f) Shoot-tip grafting in-vitro on rootstock.

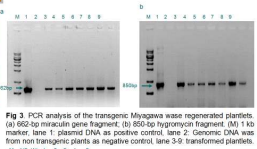


Fig 3. PCR analysis of the transgenic Miyagawa wase regenerated plantlets. (a) 662-bp miraculin gene fragment, (b) 850-bp hygromycin fragment. (M) 1 kb marker, lane 1: plasmid DNA as positive control, lane 2: Genomic DNA was from non transgenic plants as negative control, lane 3-9: transformed plantlets.

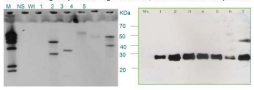


Fig 4. Southern blot analysis of transgenic plants. M=DIG-labeled DNA molecular weight marker, NS= no sample, Wt= wild type, lane1-5= transgenic plants.

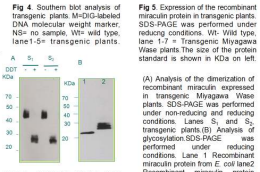


Fig 6. Analysis of the post translational modification of recombinant miraculin expressed in transgenic Miyagawa Wase plants.

Fig 5. Expression of the recombinant miraculin protein in transgenic plants. SDS-PAGE was performed under reducing conditions. Wt- Wild type, lane 1-7 = Transgenic Miyagawa Wase plants.The size of the protein standard is shown in KDa on left.

(A) Analysis of the dimerization of recombinant miraculin expressed in transgenic Miyagawa Wase plants. SDS-PAGE was performed under non-reducing and reducing conditions. Lanes S_1 and S_2 transgenic plants.(B) Analysis of glycosylation.SDS-PAGE was performed under reducing conditions. Lane 1 Recombinant miraculin protein from *E. coli* lane2 Recombinant miraculin protein from transgenic plant, The size of the protein standard is shown in KDa on the left.

CONCLUSIONS

- We constructed the transformation system and selection conditions for the Miyagawa Wase (*Citrus unshiu* Marc).
  a. Optimum concentration of hygromycin selection was 25mg/L.
  b. Our protocol resulted in a reasonable transformation efficiency of 22%.
- Presence of miraculin gene was confirmed by polymerase chain reaction with both the miraculin specific and hygromycin specific primer (Figure 3).
- Integration of miraculin gene in transgenic plants genome was confirmed by Southern blot analysis (Fig. 4)
- Expression of miraculin protein was detected by western blot analysis (Fig. 5).
- Post translational modification of the recombinant miraculin gene expressed in transgenic Miyagawa Wase was shown by dimerization and glycosylation (Fig. 6)
- To best our knowledge, this is the first report to produce transgenic Miyagawa Wase plants containing miraculin gene.

REFERENCES

Kurihara K, Beidler L, M (1969) Mechanism of the action of taste-modifying protein. *Nature* 222: 1176–1179.
Matsuyama,T, Satoh,M, Nakata, R, Takashi Aoyama2, Hiroyasu Inoue. 2009. Functional expression of miraculin, a taste-modifying protein in *Escherichia coli*. J. Biochem. 145(4):445–450
Ito K, Asakura T, Morita Y, Nakajima K, Koizumi A, Shimizu- Ibuka A, Masuda K, Ishiguro M, Terada T, Maruyama J, Kitamoto K, Misaka T, Abe K (2007) Microbial production of sensory-active miraculin. *Biochem Biophys Res Commu* 360:407–411
Sun HJ, Cui M, Ma B, Ezura H (2006) Functional expression of taste-modifying protein miraculin in transgenic lettuce. *FEBS Lett* 580: 620–626.
Sun HJ, Kataoka H, Yano M, Ezura H (2007) Genetically stable expression of functional miraculin, a new type of alternative sweetener, in transgenic tomato plants. *Plant Biotechnol J* 5: 768–777.
Sugaya T, Yano M, Sun hJ, Hirai T, Ezura H (2008) Transgnic Strawberry expressing the taste-modifying Protein miraculin, *Plant Biotechnol J* 25: 329–333.

Acknowledgments

◆ These work were supported from Citrus Genetic Resources Bank, Jeju National University, and National Research Foundation of Korea funded by the Ministry of Education, Science and Technology, (NRF-2009-0094060).

CHEJU NATIONAL UNIVERSITY DEPARTMENT OF APPLIED LIFE SCIENCE
Citrus Genetic Resources Bank and Research Institute of Subtropical Horticulture

IP : 14.49.138.138, 2017-11-03 13:30:33

[도내 학생교육 및 홍보]

(아열대친환경 생물산업 페스티발: 2008년 10월 .31-11월 01일 제주 칼호텔)



• 제목 : "도내 고교과학반초청 생명공학교실"
일시 : 2009년 12월 26일(목)
장소 : 아열대원예산업연구소 세미나실



• 제목 : "여고생 생명공학 교실"
일시 : 2010년 06월 26일
참가자: 서귀포연고, 중앙여고, 남녕고 총 26명



IP : 14.49.138.138, 2017-11-03 13:30:33

[도외학생교육]

(과천초등학생교육:2011. 06.19, 10.30)



○ 도내 외 언론 및 인터넷 홍보 2007년 4.1-2011.

구분	일시	행사명	비 고
1	2007. 04. 24	KCTV 인터뷰 (“DNA로 신품종”, 2007년 4월 24일)	
2	2007. 04 .28	YTN 인터뷰 (“감귤 신품종으로 FTA 극복”, 2007년 4월 28일)	
3	2008. 08. 01	인터넷 검색엔진 홍보	네이버
4	2008. 10. 21	김재훈 교수 세계 인명사전 등재	제민일보,한라일보
5	2011. 06. 21	제주도,제주감귤 유전체 사업 유치	(제주투데이,시사제주,제주일보
6	2011. 12. 11	제주감귤산업 미래 유전자 해독에 달렸다	제주일보

[도내 홍보]

KCTV 인터뷰(“DNA로 신품종”, 2007년 04월 24일)



YTN 인터뷰(“감귤 신품종으로 FTA 극복”,2007년 04월 28일)



IP : 14.49.138.138, 2017-11-03 13:30:33



제주일보

경제

제주 병귤 유전체 해독 눈 앞에 다가왔다



제주人 제주in 이야기

"감귤의 미래 유전자에 달렸다"

자생 품종 '병귤' 유전자 해독 나서

현재 1단계 분석…완전 판독 '눈앞'

"FTA 종자 전쟁 이겨내기 위해

감귤의 확고한 입지 강도록 최선"



YTN

"감귤 신품종으로 FTA 극복"

Jejusori.net

제주시수입 UFTA 대비

사회

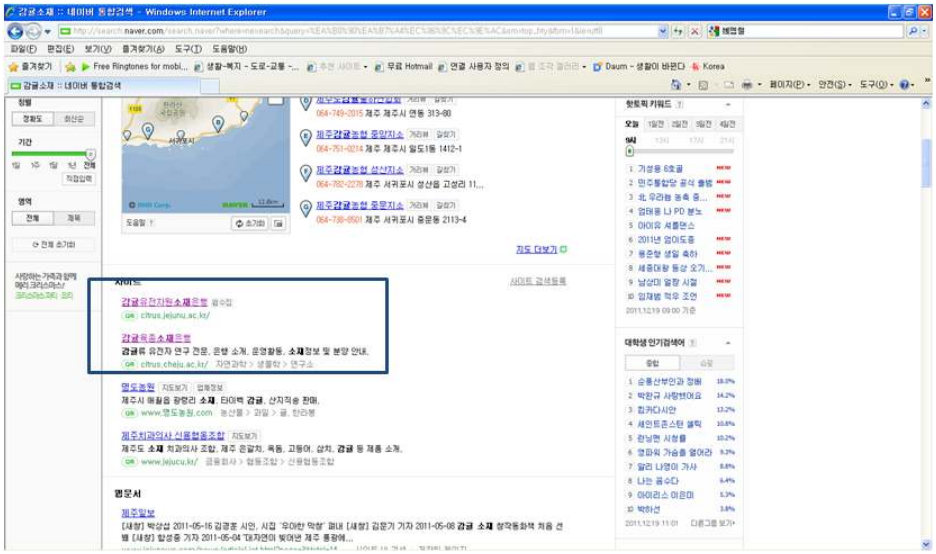
제주대, 재래감귤 병귤의 380만 유전자 염기서열 밝힌다!

IP : 14.49.138.138, 2017-11-03 13:30:33

(인터넷 검색엔진 홍보)



검색어 : 감귤, 국가지정연구소재은행



IP : 14.49.138.138, 2017-11-03 13:30:33

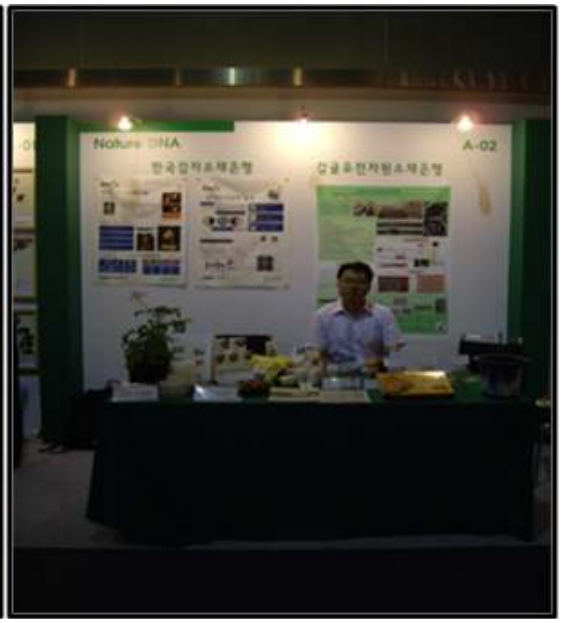
(홍보 책자)





(2010 생명 산업대전 참가)





IP : 14.49.138.138, 2017-11-03 13:30:33

(제 11회차 국제 감귤학회 포스터발표: 2008년 10월 23일 중국우한)



(2008 국회 심포지움 및 전시회 참가)



IP : 14.49.138.138, 2017-11-03 13:30:33

(2010 국회 심포지엄 및 전시회 참가)



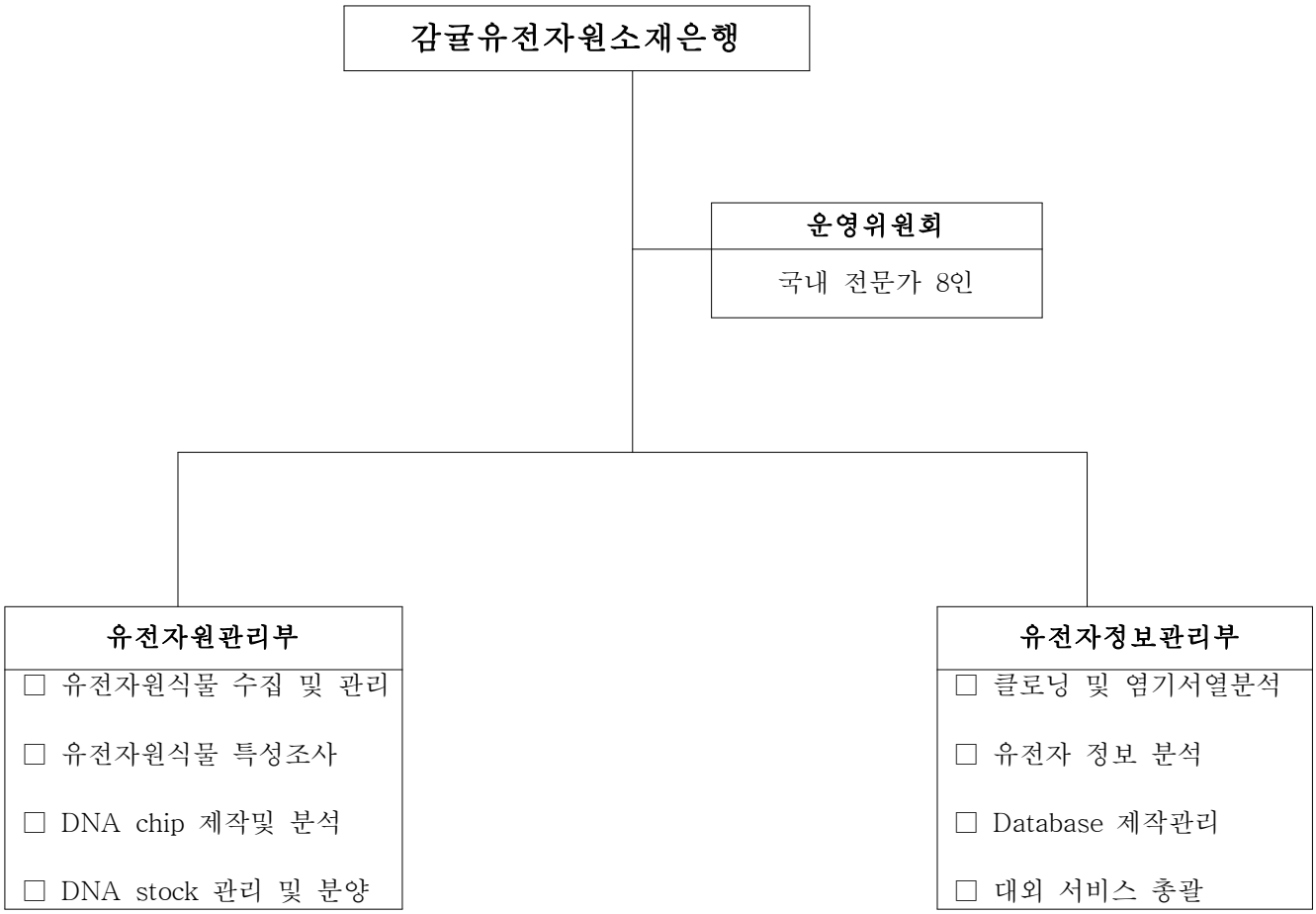
(2011 국회 심포지엄 및 전시회 참가)



IP : 14.49.138.138, 2017-11-03 13:30:33

3. 인력기반 구축

1) 조직 및 운영체계도



운영위원회 구성

성 명	소 속	직 급	임 무	전 공
김재훈	제주대학교 생명공학부			
이선주	제주대학교 화학과			
류기중	제주대학교 생명공학부			
남백희	명지대학교 생명과학정보학부			
이효연	제주대학교 생명공학부			
김소미	제주대학교 생명공학부			
김인중	제주대학교 생명공학부			
임평옥	제주대학교 생명공학부			
이동선	제주대학교 생명공학부			

IP : 14.49.138.138, 2017-11-03 13:30:33

○ **운영위원회 활용**

사업계획, 추진방향 등 본 소재은행의 운영과 관련된 전반적인 사항들은 대부분 운영위원회의 협의를 거쳐 결정되고 있고, 감귤 육종에 활용가치가 높은 유전자원 선정은 소재은행의 특성화 및 가치 함양을 위하여 매우 중요하기 때문에 운영위원회에서 결정하고 있다. 그 외에도 유전자 클론, database 등의 관리와 분양 업무에 관한 전반적인 사항들은 운영위원회의 협의를 거쳐 결정되고 있다.

2) 소재은행장의 적정성

○ 제주대학교 아열대/열대생물유전자은행 은행장의 직무를 수행하면서 본 소재은행의 핵심소재인 감귤의 genomics, proteomics, metabolics 등에 관한 이론적인 지식과 연구경험을 겸비하여 왔으며, 이를 바탕으로 보유소재를 활용한 다양한 연구방안을 모색함과 동시에 관련 연구자 및 연구기관과의 지속적인 협의를 통하여 소재의 활용을 촉진하고 활용 범위를 확대해 나가고 있다.

○ 감귤 유전자의 300K DNA microarray 칩을 국내 최초로 개발하여 감귤 유전자의 기능 및 발현 분석, 생리현상 분석, 돌연변이 분석 등 감귤 관련 분자생물학적 연구의 중요한 기반을 마련하였다.

○ 국제감귤게놈콘소시엄에 참가하여 2007년 7월부터 시행되고 있는 Citrus Genome Project의 참여 발판을 마련하였으며, 관계자들과 긴밀한 연락을 통하여 본 소재은행이 확보하고 있는 감귤 소재의 가치를 국제적으로 홍보함과 동시에 Project 참여 기반을 마련하고자 노력하였고, 2008년 10월 중국에서 개최된 제11회 국제 감귤학회에서 개최된 감귤 게놈 운영위원회에 참가하여 본 소재은행을 국제적으로 홍보하였다.

○ 감귤돌연변이(제주감귤클러스터)육종사업에 참여하고 있어 감귤 300K DNA microarray를 비롯한 보유소재들의 활용 촉진을 위한 노력을 기울이고 있다.

○ 소재은행장은 세계 3대 인명사전에 속하는 미국 마르퀴스 후즈후(Marquis Who's Who)에서 발행하는 '과학과 공학' 인명사전 2008-2009판에 등재됨으로써 소재은행의 국제적 위상을 높이고 있다.

○ 보유소재의 정보를 다각도에서 분석하여 식물의 분자생물학적 이해와 연구에 보유소재의 활용가치를 극대화 할 수 있도록 노력하고 있으며 이와 관련된 전문 연구자를 섭외하여 데이터를 새롭게 활용할 수 있는 방안도 모색하고 있다.

IP : 14.49.138.138, 2017-11-03 13:30:33

○ 2011년 제주도 감귤 유전체 사업을 유치함으로써 도내 언론에 감귤 유전자원 소재은행을 널리 홍보하였으며, 국제 감귤게놈콘소시엄에 참여할 수 있는 기반을 구축하였다. 또한, 미국 플로리다 대학과 MOU 협정을 체결하였고, 한미 국제 감귤 유전체 심포지엄을 성공적으로 개최 하였다.

가. 과제 참여 실적

과제명	지원기관	연구비(원)	연구기간 (부터-까지)	역할
감귤육종소재은행	교육과학기술부		2007.04.01-2012.02.29	책임
제주재래귤(병귤)의 연관지도작성 및 표준유전체 연구기반구축	농림수산식품부		2011.02.01-2012.12.31	책임

나. 연구업적

(1) 특허

(출원)

(2) 논문

○ 국제 학술지 및 SCI급

1) Kyung Hwan Boo, Dae Woon Kim, Somi Kim Cho, Seong Beom Jin, **Jae Hoon Kim**, Hyo Yeon Lee, and Key Zung Riu*. Construction and Profiling of a cDNA Library from Young Fruit of Satsuma Mandarin. Journal of Plant Biology, August 50(4) : 403-409 (2007)(sci)

2) Jeong-Won Park, Kyung-Hwan Boo, Seong-Beom Jin, Md. Adnan Al Bachchu, Su-Hyun Yun, Yong-Woo Kim, Dong-Sun Lee, Hyo-Yeon Lee, Key-Zung Riu, and **Jae-Hoon Kim***.
Expression Profiling of Cultivar -related Genes in Satsuma Mandarins, Miyagawa Wase and Ueno Wase. J. Korean Soc. Appl. Biol. Chem. 53(6), 691-701(2010)

3) Kyung Hwan BOO, Doseung LEE, Gyeong Lyong JEON, Seung Hee KO, Somi K. CHO, **Jae Hoon KIM**, Se Pill PARK, Quanchun HONG, Sang-Han LEE, Dong-Sun LEE and Key Zung RIU. Distribution and Biosynthesis of 20-Hydroxyecdysone in Plants of Achyranthes japonica Nakai. Biosci. Biotechnol. Biochem, 74(11), 2226-2231 (2010)

4) Jin-Man Lee, Jong-Guk Kim, Tae-Ho Kim, Do S. Lee, **Jae H. Kim**, Somi K. Cho, Key Z. Riu, Dong-SunLee, Sang-HanLee. Nonactin hinders intra cellular glycosylationin virus-infected baby hamster kidney cells. Molecular Medicine REPORTS 3:115-119 (2010)

IP : 14.49.138.138, 2017-11-03 13:30:33

5) Doseung Lee, Kyung-Hwan Boo, Jin-Kyu Woo, Gyeong-Lyong Jeon, Jin-Man Lee, Sang-Han Lee, **Jae Hoon Kim**, Dong-Sun Lee1*, Key Zung Riu*. Production Conditions for Bruceanol B, an Antibiotic that Generates Oxygen Radical. J. Korean Soc. Appl. Biol. Chem. 54(1), 128-131 (2011)

6) Doseung Lee, Seong-Cheol Kim, Donghern Kim, **Jae Hoon Kim**, Se Pill Park, Youn-Chul Ryu, Minyoung Kim, Somi Kim Cho, Key Zung Riu, and Dong-Sun Lee*. Screening of Phellinus linteus, a Medicinal Mushroom, for Anti-viral Activity. J. Korean Soc. Appl. Biol. Chem. 54(3), 475-478 (2011)

7) Hae Gyeong Kim, Gon-Sup Kim, Jung Han Lee, Semin Park, Won Young Jeong, Yun-Hi Kim, **Jae Hoon Kim**, Soo Taek Kim,Young Ah Cho, Won Sup Lee, Soo Jung Lee, Jong Sung Jin, Sung Chul Shin. Determination of the change of flavonoid componentsas the defence materials of Citrus unshiu Marc. fruit peel against Penicillium digitatum by liquid chromatography coupled with tandem mass spectrometry. Food Chemistry 12849- 45 (2011)

8) Hae Gyeong Kim, Gon-Sup Kim, Semin Park, Jung Han Lee, On Nuri Seo, Soo Jung Lee, **Jae Hoon Kim**, Jae-Han Shim, A.M.AbdEl-Aty, Jong Sung Jin and Sung Chul Shin. Flavonoid profiling in three citrus varieties native to the Republic of Korea using liquid chromatography coupled witht an demmas sspectrometry: contribution to over all antioxidant activity. Biomedical Chromatography, 26(4) 464-470(2012)

9) Md. Adnan Al Bachchu, Seong Beom Jin, Jeong Won Park, Hyeon Jin Sun, Su Hyun Yun, Hyo Yeon Lee, Dong Sun Lee, Quan Chun Hong, Yong Woo Kim and Key Zung Riu, and **Jae Hoon Kim**. Agrobacterium-mediated transformation using embryogenic calli in Satsuma mandarin (CitrusunshiuMarc.) cv. Miyagawa wase. Hort. Environ. Biotechnol. 52(2): 170-175 (2011)

10) Mohammad Adnan Al Bachchu, Seong-Beom Jin, Jeong-Won Park, Kyung-Hwan Boo, Hyeon-Jin Sun, Yong-Woo Kim, Hyo-Yeon Lee, Key-Zung Riu, **Jae-Hoon Kim***.Functional Expression of Miraculin, a Taste-modifying Protein in Transgenic Miyagawa Wase Satsuma Mandarin (CitrusunshiuMarc.). J. Korean Soc. Appl. Biol. Chem. 54(1), 24-29 (2011)

11) Doseung Lee, Jin-Kyu Woo, Donghern Kim, Minyoung Kim, Somi K. Cho, **Jae Hoon Kim**, Se Pill Park, Hyo Yeon Lee, Key Zung Riu, Dong-Sun Lee. Antiviral Activity of Methylelaiophylin, an α-Glucosidase Inhibitor. J. Microbiol. Biotechnol. 21(3): 263-266 (2011)

○ 국내 학술지 및 비SCI급

1) **Jae-Hoon Kim**,Jeong-HunYun.InhibitoryEffectofPlantExtracts on VHR Dual Specificity Protein Phosphatase. J. Appl. Biol. Chem. 50(4), 301-303 (2007)

2) **Jae-Hoon Kim*** and Dae-GwinJeong. Proteomic Identification of Proteins Interacting with a Dual Specificity Protein Phosphatase, VHZ. J. Appl. Biol. Chem. 50(2), 58-62(2007)

IP : 14.49.138.138, 2017-11-03 13:30:33

3) Somi K. Cho,Young-Mee Kim, Minyoung Kim, Doseung Lee, **Jae Hoon Kim**, Se Pill Park, Key Zung Riu and Dong-Sun Lee Expression and Isolation of Limonoid UDP-glucosyltransferase, a Bitterness-
reducing Enzyme, in *E.coli* KoreanJ Food Preserv 18(2), 208-211(2011)

<미국 마르퀴스 후즈후(Marquis Who's Who) 2008-2009 등재>

IP : 14.49.138.138, 2017-11-03 13:30:33

3) 운용요원 확보 및 활용

[표 2] 운영요원 확보 및 활용 현황

(단위 : 천 원)

구분	신분 및 임무	학력 및 전공	근무기간
A	박사,라이브러리	박사, 식물대사공학	2007. 04. 01-2010. 02 .28
B	박사, 라이브러리	박사, 식물분자육종	2008. 02. 28-2012. 02. 29
C	박사, 유전정보관리부	박사, 분자유전	2010. 08. 01-2010. 01. 31
D	박사과정, 데이터베이스관리	석사, 식물병리학	2007. 10. 01-2011. 08. 31
E	박사과정, 유전자원관리	석사, 곤충학	2008. 05. 01-2011. 02. 28
F	석사과정,라이브러리관리	학사	2007. 09. 01-2009. 02. 28
G	석사과정, 유전정보관리부	학사, 생명공학	2011. 03. 01-2012. 02. 29
H	석사과정, 유전자원관리	학사, 생명공학	2011. 03. 01-2012. 02. 29
I	학부생, 유전자원관리	고졸	2007. 04. 01 -2007. 06. 30
J	학부생, 유전자원관리	고졸	2007. 04. 01-2008. 10.31
K	학부생, 데이터베이스	고졸	2007. 04. 01-2008. 02. 28
L	학부생, 라이브러리관리	고졸	2007. 04. 01-2009. 02. 28

○ 인력활용 현황

본 소재은행은 1차년도에서 4차년도까지는 유전자원관리부, 라이브러리관리부, 데이터베이스관리부로 나뉘어 운영되어 왔으며, 각부에는 부장(운영위원) 1인이 배치되어 부서 운영에 관한 사항들을 관리/감독하고, 그에 따른 운영요원이 각각 2-3인 배치되어 실무를 전담하여 왔다. 또한 본 소재은행에서는 전담 행정요원 1인을 배치하여 소재의 분양 접수 및 처리, 홈페이지 관리, 행정 및 재정 업무 등을 전담하게 함은 물론 효과적인 홍보 전략 등도 모색하게 하여 은행 활성화를 꾀하여 왔으나, 최근 5차년도에 들어서는 체계적이면서 효과적인 유전자원 관리부와 유전정보 관리부로 통합하여 관리운영하고 있다.

IP : 14.49.138.138, 2017-11-03 13:30:33

4. 시설과 공간의 확보

1) 주요 시설현황

구 분		용 도	수용 인원	전용면적 (m^2)
원예산업연구소	104호	Server 운영실 및 행정실 행정실	1	25
	114호	유전자기능성 연구 배양실	1	20
생명자원과학대학 (생명자원대)	5147호	연구개발실	1	80
	5153호	유전자원 보존 및 분양	1	22
온실		유전자원보존온실I	1	150
		유전자원보존온실II	1	297
분자육종실		감귤분자육종실	2	20
계		7실	8	614


[유전자원 보존 온실 I]


[유전자원 보존온실 II]


[분자육종실]


[연구개발실]


[유전자원 보존]

○ 제주대학교 아열대 농업생명과학연구소

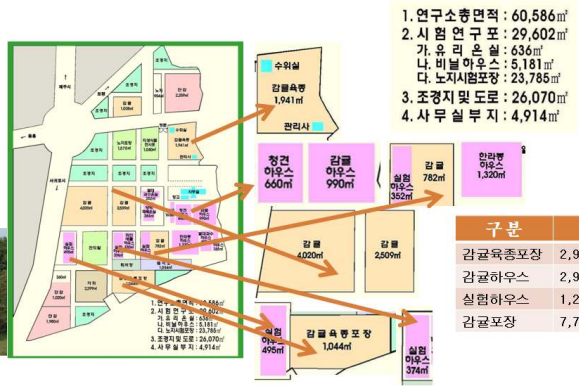

실험하우스


육종포장


한라봉하우스


관리연구동


감귤하우스



구분	면적
감귤육종포장	2,985 (m^2)
감귤하우스	2,970 (m^2)
실험하우스	1,221 (m^2)
감귤포장	7,750 (m^2)

IP : 14.49.138.138, 2017-11-03 13:30:33

2) 주요 장비 보유현황

[표 3] 주요 시설 및 장비 보유 현황

명 칭	용도	수량	구입가격 (단위:천원)	도입시기	도입재원
소재 보관/분양실	소재(유전자 등) 보관/분양	1실			
서버 운영 및 행정실	서버/홈페이지 관리, 행정	1실			
연구개발실	라이브러리 제작 등	2실			
온실	유전자원 식물체 관리/유지	1실		2008	대학
온실	유전자원 식물체 관리/유지	1실			대학
조직배양실	식물조직배양/형질전환	1실	15,000	2008	대학
조직배양실	유전자원식물 조직배양	1실			대학
무균상	유전자원 분양 및 유지	1대	4,000	2008	대학
저온배양기	식물 형질전환	1대	3,000	2008	대학
교반 배양기	식물 형질전환	1대	3,000	2008	대학
컴퓨터	홈페이지 관리	1대	1,742	2008	재단 지원
Semi-Dry Blotters	유전자 발현 분석	1대	2,228	2008	재단 지원
Deep Freezer	시료보관	1대	9,900	2008	대학
액체질소통	유전자분리 및 시료보관	1대	3,000	2004	대학
자동전원공급장치	초저온냉동고 무정전 유지	1대	50,000	2003	대학
centrifuger	물질 분리	4대	총10,000	2003	대학
무균상	식물 조직배양	1대	2,420	2003	대학
Deep Freezer	시료 보관	1대	1,000	2002	대학
PCR 기기	유전자 증폭	3대	총 7,000	2000-2002	대학
식물생육상	유전자원식물재배 및 유지	3대	총100,000	2001	대학
UV/VIS spectrophotometer	활성 측정	1대	총 46,000	1999-2000	대학
HPLC	물질분리	1대	17,354	1996	대학
CO_2 incubator	세포배양	2대	총3,000	1999	타 연구비
pH meter	용액 준비	1대	2,500	1997	타 연구비
water bath	온도 조절	2대	총4,222	1998	대학
Deep Freezer	시료 보관	1대	14,345	1997	대학
Co_2 Cold Lab chamber	유전자 발현 분석	1대	4,900	2009	대학
shaking incubator	유전자분석	1대	2,320	1996-2009	대학
Hybridization Inculbator	물질 분석	1대	2,600	2009	대학
원심분리기	유전자 분양	1대	300	2009	대학
저온배양기	세포배양	1대	3,000	2008	대학
Deep Freezer	시료 보관	1대	10,000	2010	대학
PCR 기기	유전자증폭/분석	1대	5,800	2011	타연구비

IP : 14.49.138.138, 2017-11-03 13:30:33

Ⅲ. 사업 수행(연구) 실적

1. 연구소재 확보·관리실적

1). 년차별 추진목표 및 달성도

추진내용	내용	달성도				
		1차년도	2차년도	3차년도	4차년도	5차년도
1) 식물재료 수집/ 유지	유전자원 식물 수집 및 관리/유지	80	100	100	100	100
2) 유전자원 확보 및 database 확충	- 감귤 cDNA 라이브러리제작 - cDNA 염기서열 분석 - 유전자 정보 분석 - Database 구축	100 90 80	100 100 100	100 100 100	100 100 100	100 100 100
3) 시설·장비 확충	Deep Freezer 및 기타 실험 장비 구입	95	100	100	100	99
4) 서비스 환경 강화	- Web Site 구성 강화 - 소재정보 분석 서비스 강화 - 소재활용 관련 세미나/ 심포지움 개최	100 70 90	100 100 100	100 100 100	100 100 100	100 100 100
5) 운영	- 사업기획 - 사업평가	80 80	100 100	100 100	100 100	100 100

2). 연구소재 종류별 구체적인 확보현황을 연도별 비교

가. 1차년도 ('07.04~'08.02)

○ 감귤 유전자 DNA microarray[첨부파일]

- 감귤류 고유염기서열 유전자정보 67,881개 확보
  (보유 EST와 Genbank에 보고된 Citrus EST 활용)
- 감귤 유전자 67,881개에 대한 Oligomer Chip 제작용 primer 326,876개 설계
- 감귤 유전자 발현분석용 300K Oligomer Chip 제작 및 확보
- 300K Oligomer Chip을 이용한 발현분석 data 확보
  * 당유자 잎 과발현 유전자 1,823개
  * 청견 잎 과발현 유전자 1,701개

○ 유전자 라이브러리

[감귤류: 2종]

- 온주밀감 일남1호 과실 full-length cDNA 라이브러리

IP : 14.49.138.138, 2017-11-03 13:30:33

- 한라봉 과실 full-length cDNA 라이브러리

[분자육종 기초소재: 1종]

- 시로미 유묘 전초 cDNA 라이브러리 : 2.0×10^4 클론 (정우식품 기탁)

○ 유전자 염기서열 정보[첨부파일]

[감귤류: 105]

- 감귤류 glycosyltransferase 유전자 클론의 삽입유전자 전체 염기서열분석 : 41
- 클론 분양 후 삽입유전자 전체 염기서열 분석 결과를 기탁 받은 유전자 : 65

[분자육종 기초소재: 1,176]

- 시로미 유묘 유전자 (정우식품 기탁) : 1,155
- 클론 분양 후 삽입유전자 전체 염기서열 분석 결과를 기탁 받은 유전자 : 21

○ 유전자 아미노산서열 및 기능 정보

[감귤류: 105]

- 감귤류 glycosyltransferase 유전자 클론의 삽입유전자 전체 염기서열 분석 : 41
- 클론 분양 후 삽입유전자 전체 염기서열 분석 결과를 기탁 받은 유전자 : 65

[분자육종 기초소재: 355]

- 시로미 유묘 유전자 (정우식품 기탁) : 334
- 클론 분양 후 삽입유전자 전체 염기서열 분석 결과를 기탁 받은 유전자 : 21

○ Full-length cDNA 클론[첨부파일]

[감귤류: 33]

- 감귤류 glycosyltransferase 유전자 : 17
- 클론 분양 후 재기탁 받은 감귤 유전자 : 11
- 클론 분양 후 재기탁 받은 기타 유전자 : 5

나. 2차년도('08.03~'09.02)

○ 유전자 라이브러리

[감귤류: 1종]

- 진귤 성숙과실 cDNA 라이브러리

○ 유전자 염기서열 정보

[감귤류: 3,067개 유전자]

- 진귤 성숙과실 유전자 클론의 염기서열 분석 : 3,067

IP : 14.49.138.138, 2017-11-03 13:30:33

○ 유전자 염기서열 상동성 조사정보

[감귤류: 2,231개 유전자]
- 진귤 성숙과실 유전자 클론의 상동성 조사정보 : 2,231

○ 유전자 아미노산서열 및 기능정보

[감귤류: 408개 유전자]
- 진귤 성숙과실 유전자 클론의 삽입유전자 전체 염기서열 분석 : 408

○ Full-length cDNA 클론[첨부파일]

[감귤류: 5 개 유전자]
- 감귤류 miraculin-like protein 유전자 : 2
- 감귤류 Ethylene responsive element binding protein 유전자: 3
- GeneBank 등록
- Miraculin-like protein: (FJ532030,FJ532031)
- Ethylene responsive element binding protein: (FJ544914,FJ544915,FJ544916)

다. 3차년도 ('09.03~'10.02)

○ 유전자 라이브러리

[감귤류: 1종]
- 지각 미숙과실 cDNA 라이브러리 (1set: $4x10^5$)

○ cDNA 클론분석[별첨]

[감귤류: 1종]
- 지각 미숙과실 유전자 클론분석 : 2,301

○ 유전자 염기서열 정보

[감귤류: 1종]
- 지각 미숙과실 유전자 염기서열 정보 : 900

○ Full-length cDNA 염기서열분석

IP : 14.49.138.138, 2017-11-03 13:30:33

[온주밀감: 2 개 유전자]

- zeta carotenoid desaturase (ZDS) 유전자
- geranylgeranyl diphosphate synthesis(GGPS) 유전자

라. 4차년도 ('10.03~'10.12)

○ 유전자 라이브러리

[감귤류: 1종]

- 병귤 미숙과실 cDNA 라이브러리 (1set: $4x10^5$추정)

○ cDNA 클론분석[첨부파일]

[감귤류: 1종]

- 병귤 미숙과실 유전자 클론분석 : 1,000
- 온주밀감 미숙과실 CiFT2 유전자 : 1
- 진귤 성숙과실 클론분석 : 1,000

○ 유전자 염기서열 정보

[감귤류: 1종]

- 병귤 미숙과실 유전자 염기서열 정보 : 1,000

○ Full-length cDNA 염기서열분석

[온주밀감: 1 개 유전자]

- 온주밀감 미숙과실 CiFT2 유전자 : 1

마. 5차년도 ('11.03~'12.02.)

○ cDNA 클론분석[첨부파일]

[감귤류: 1종]

- 진귤 성숙과실 유전자 클론 분석 : 67
- 병귤 미숙과실 유전자 염기서열 정보 : 1,500

○ 유전자 염기서열 정보

[감귤류: 2종]

- 병귤 미숙과실 유전자 염기서열 정보 : 1,500
- 지각 미숙과실 유전자 염기서열 정보 : 360

IP : 14.49.138.138, 2017-11-03 13:30:33

[표 4] 연구소재 확보 실적

(단위 : 천 원)

년도	소재종류	단위	국내						국외		합계	
			자체		외부기관		계					
			개수	금액	개수	금액	개수	금액	개수	금액	개수	금액
1차년도	300K 감귤 DNA chip	개	3	3,000			3	3,000			3	3,000
	유전자원식물	개	6종	(60)			6	(60)			6	(60)
	cell line	개										
	cDNA 라이브러리	개	1	3,000			1	3,000			1	3,000
	cDNA 클론	클론	41	4,100	1,155	115,500	1,196	119,600			1,196	119,600
	염기서열정보	클론	41	820	1,241	2,482	1,282	3,302			1,282	3,302
	상동성조사정보	클론	91	1,820	1,241	24,820	1,332	26,640			1,332	26,640
2차년도	유전자원식물	개	9	(90)	13	(130)	24	(240)			24	(240)
	cell line	개	8	4,000			8	4,000			8	4,000
	cDNA 라이브러리	개	1	3,000			1	3,000			1	3,000
	cDNA 클론	클론	2,000	200,000			2,000	200,000			2,000	200,000
	염기서열정보	클론	3,067	61,340			3,067	61,340			3,067	61,340
	상동성조사정보	클론	2,231	44,620			2,231	44,620			2,231	44,620
3차년도	유전자원식물	개			13	(130)	13	(130)			13	(130)
	cell line	개	8	4,000			8	4,000			8	4,000
	cDNA 라이브러리	개	1	3,000			1	3,000			1	3,000
	cDNA 클론	클론	2,301	230,100			2,301	230,100			2,301	230,100
	염기서열정보	클론	902	18,040			902	18,040			902	18,040
4차년도	유전자원식물	개	1	(10)	50	(50)	51	(510)			51	(510)
	cell line	개										
	과실	개			768	(768)	768	(768)			768	(768)
	cDNA 라이브러리	개	1	3,000			1	3,000			1	3,000
	cDNA 클론	클론	2,001	200,100			2,001	200,100			2,001	200,100
	염기서열정보	클론	1,001	20,020			1,001	20,020			1,001	20,020
5차년도	유전자원식물	개			2	(20)	2	(20)			2	(20)
	cell line	개	5	2,500			5	2,500			5	2,500
	과실	개			310	(310	310	(310)			310	(310)
	cDNA 라이브러리	개										
	cDNA 클론	클론	1,567	156,700			1,567	156,700			1,567	156,700
	염기서열정보	클론	360	7,200			360	7,200			360	7,200
합계			15,647	970,520	4,793	144,210	20,442	1,115,200			20,442	1,115,200

- 인간 유전체 사업단 자료를 근거로 하여 아래와 같이 산출하였다.
- 300K 감귤 DNA chip : 100 만원, 유전자원 식물 : 개당 1000원, 라이브러리 : 300 만원, cDNA 클론 : 10 만원, 염기서열정보 및 상동성 조사 정보 : 2 만원, 유전자원 식물 : 만원, cell line 50만원, 과실 : 1000 원

IP : 14.49.138.138, 2017-11-03 13:30:33

3) 사업지원으로 인한 연구소재의 개발, 수집 및 관리 실적

가. 1차년도(2007. 4.1-2008. 2.28)

○ **유전자원 수집** : 감귤류 과실의 유전자원을 확보하기 위하여 일남1호, 흥진, 궁천, 한라봉, 청견, 등의 미숙 또는 성숙과실을 수집하여 유지/보관하고 있다.

○ **감귤의 full-length cDNA 라이브러리 확보** : 본 소재은행이 확보하고 있는 감귤류 유전자클론들은 full-length cDNA와 partial cDNA가 혼재해 있어 실제 수요자들이 필요로 하는 유전자가 partial cDNA인 경우는 이 정보만을 이용할 수 있기는 하나 full-length cDNA를 선발해야 하는 일들이 빈번하여 이를 해소하기 위한 방안으로 본 소재은행에서 수요자가 원하는 full-length cDNA를 직접 선발하여 공급하거나 또는 수요자들이 쉽게 full-length cDNA를 선발할 수 있는 라이브러리를 제공할 목적으로 온주밀감 일남1호와 한라봉 과실에 대한 full-length cDNA 라이브러리를 제작하였다. Full-length cDNA 라이브러리는 온주밀감 일남1호와 한라봉 과실로부터 전체 RNA를 분리한 후 mRNA 정제용 kit(Qiagen)와 full-length cDNA 라이브러리 제작용 kit(Invitrogen)를 이용하여 mature mRNA의 5'에 특정 adaptor가 달려 있는 cDNA를 합성하여 제작하였다.

그림 1은 일남1호와 한라봉의 full-length cDNA 라이브러리를 제작한 후 라이브러리 제작이 잘 되었는지를 확인하기 위하여 감귤의 GAPDH 클로닝 여부 및 5' & 3' RACE를 실시하여 전기영동한 사진인데, 그림에 보여 진 것과 같이 이 두 라이브러리에는 GAPDH 유전자가 full-length로 존재하는 것이 확인되었다. 따라서 이들 두 라이브러리는 온주밀감 일남1호와 한라봉의 각종 유전자에 대한 full-length cDNA를 선발하는데 활용도가 높은 것으로 확인되었다.

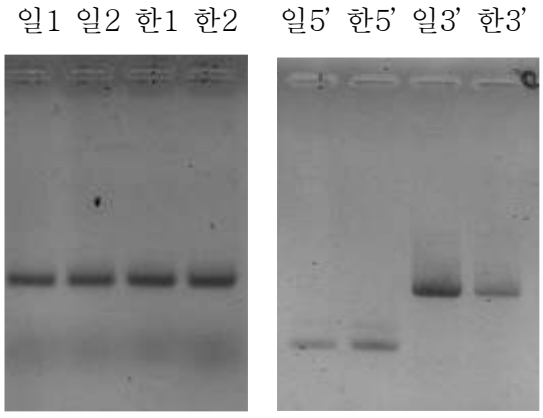


그림 1. Full-length cDNA 라이브러리 제작여부 확인

○ **유용유전자 선발** : 감귤류에는 flavonoid를 비롯한 다양한 기능성 화합물들이 존재하는데 이러한 화합물들의 활성은 glycosyltransferase에 의해 다양하게 변화되기 때문에 glycosyltransferase 관련 유전자들은 감귤류에 존재하는 기능성물질의 생물공학적 생산에 매우 중요하다. 또한 이 유전자들은 감귤의 당도 및 기능성물질의 함량과도 관련이 있어 감귤 분자육종의 목표유전자

IP : 14.49.138.138, 2017-11-03 13:30:33

로도 활용이 가능하다. 따라서 감귤의 glycosyltransferase 관련 유전자들을 다량 발굴하기 위하여 본 소재은행이 보유하고 있는 감귤류의 glycosyltransferase 관련 유전자 클론 41종의 삽입유전자 전체 염기서열을 분석하였다. 그 결과 glycosyltransferase 관련 유전자 17종의 full-length cDNA 염기서열을 확인하였다(첨부자료 참조).

○ **기자재 확충 :** 확보 유전자들의 발현 분석을 수행할 목적으로 Semi-dry blotters를 구입하였으며, 홈페이지 관리, 분양 업무, 홍보 사업 등을 원활히 수행하기 위해 업무전용 컴퓨터를 구입하였다.

○ **전문인력 양성 :** 감귤의 full-length cDNA 라이브러리 제작 전과정, 유전자정보 분석과 관련된 bioinformatics tool의 활용에 관한 실습 등을 학부 운영요원들에게 지도하여 유전자 및 유전자 정보를 이해하고 연구에 활용할 수 있는 인력양성의 기회도 마련되었다.

나. 2차년도(2008. 3.1-2009. 2.28)

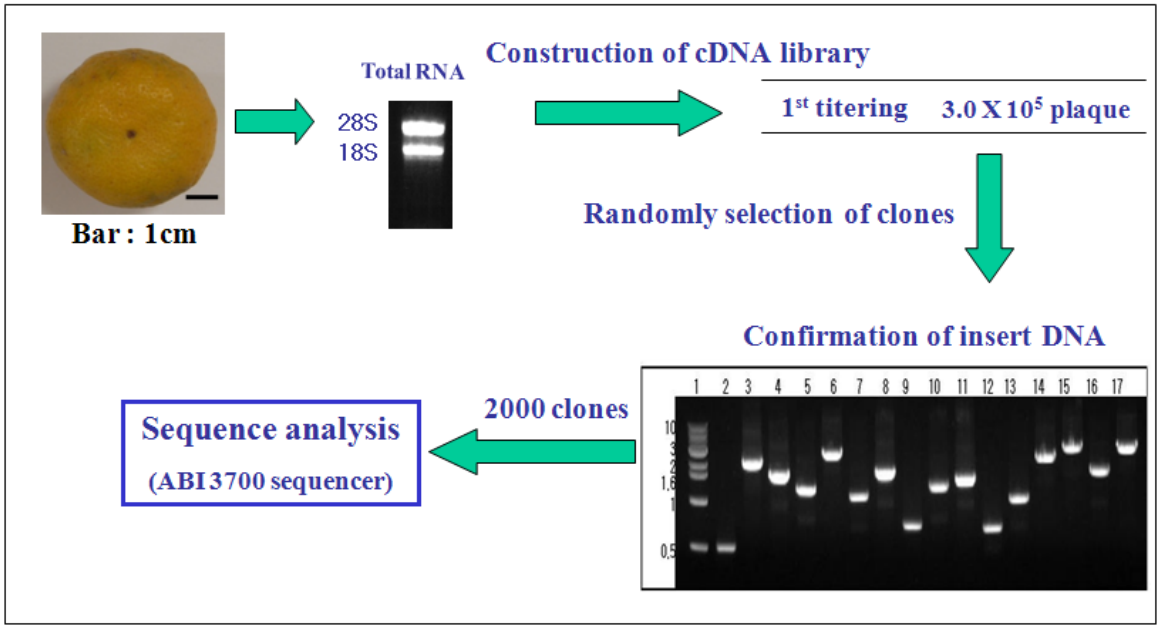
○ **유전자원 수집 :**

■ 유전자원 보존 및 유용유전자 발굴 목표를 위해 현재 도내에 남아 있는 재래감귤 감자, 유자, 동정귤, 청귤, 지각, 병귤 등 13 품종을 확보하여 유지 보관 하고 있다. 또한, 감귤류 과실의 유전자원을 계속적인 확보를 위하여 당유자, 사두감, 금감, 불수감, 병귤, 하귤, 성전온주, 상야조생, 삼보감 등 9 품종의유전자원 식물체를 수집하여 유지/보관하고 있다. 또한, 분자육종 재료 및 분양을 위해서 궁천, 홍진 온주밀감 캘러스 세포를 기내에서 배양하여 확보/유지하고 있다.

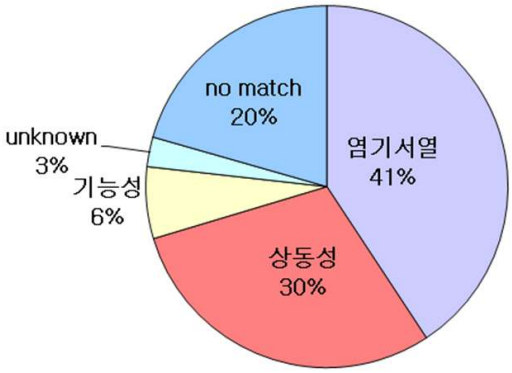
■ 부산대학교 성해영교수로부터 Cocktail grafpruit 감귤의 접수를 기탁 받아 탱자 대목에 접목을 한 후 하우스에서 유지/보관하고 있다.

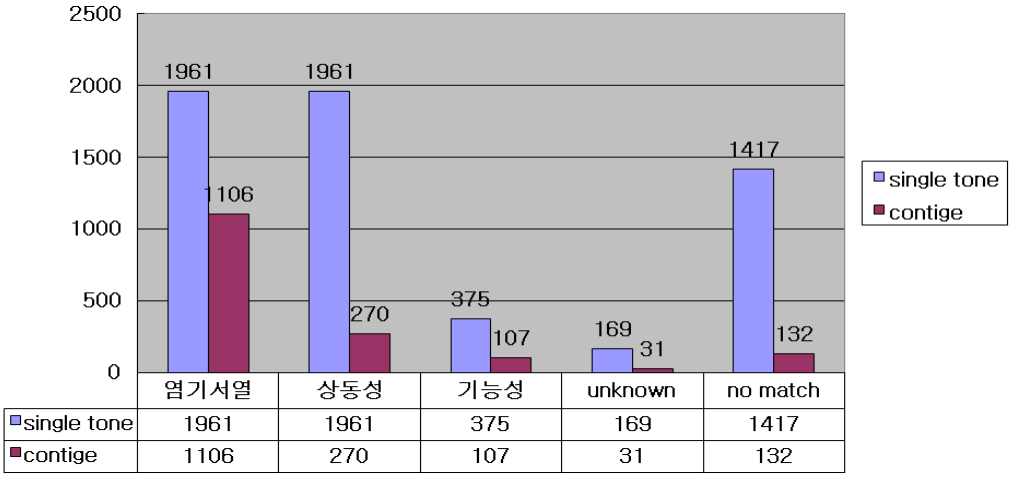
○ **진귤성숙과실 라이브러리 제작:** 감귤유전자원으로는 재래품종 중 유용성분이 밝혀져 있거나 품종이 멸종위기에 있어 유전자원 확보가 시급한 품종 중 진귤성숙과실을 목표유전자개발에 활용하였다. 유전자 라이브러리는 식물체(주로 과실)의 total RNA로부터 mRNA 만을 정제한 후 이를 주형으로 ZAP-cDNA synthesis kit로 이중가닥 cDNA를 합성한 후에 ZAP-cDNA Gigapack III Gold Cloning Kit를 이용하여 bacteriophage에 packaging 하여 제작한다. 라이브러리는 profile 분석 외에 특정 유전자의 선발 또는 스크리닝이 가능하도록 라이브러리 당 10만개 이상의 클론이 되도록 제작하였다. 2,000 cDNA 클론에 대한 염기서열, 아미노산서열 및 기능성 정보를 분석한 결과 의 염기서열 3,067개, unigene은 2,231 그리고 기능추정 염기서열 정보는 408개였다.

IP : 14.49.138.138, 2017-11-03 13:30:33



<진귤 성숙과실 라이브러리 제작과정>





	염기서열	상동성	기능성	unknown	no match
single tone	1961	1961	375	169	1417
contige	1106	270	107	31	132

<진귤 성숙과실 유전자 염기서열 상동성 및 기능성분석>

IP : 14.49.138.138, 2017-11-03 13:30:33

○ **유용유전자 선발 :**

■ 감귤류에는 조기 숙성 및 개화에 관련하는 유전자로 추정된 Ethylene responsive element binding protein와 당과 관련된 miraculin-like protein 유전자가 있다. 감귤류의 조기 숙성에 관여하는 중간 매개 유전자라고 추정되는 이 Ethylene responsive element binding protein 유전자는 감귤류의 유년성 문제를 해결할 수 있을 것으로 사료되어 감귤 분자육종의 목표유전자로도 활용이 가능하다. 따라서 감귤류의 Ethylene responsive element binding protein 유전자 클론 3종의 삽입유전자에 대한 전체 염기서열을 분석하였다. 그 결과 Ethylene responsive element binding protein 관련 유전자 full-length cDNA 염기서열을 확인하였고 GeneBank에 등록하였다(첨부자료 참조).

■ 당도 이외에 곰팡이 저항성과도 관련된 것으로 알려져 있는 miraculin 유전자는 신맛을 단맛으로 느끼게 해주는 물질인데, 본 소재은행에서는 miraculin-like protein 유전자 2종의 full-length cDNA를 cloning 하였다. 이 miraculin-like protein 유전자들은 감귤의 당도 및 곰팡이 저항성과도 관련이 있어 감귤 분자육종의 목표유전자로도 활용이 가능하다. 따라서 miraculin-like protein 유전자 2종의 full-length cDNA 염기서열을 cloning 및 분석하였다. 그 결과 miraculin-like protein 관련 유전자 2종의 full-length cDNA 염기서열을 확인하였고 GeneBank에 등록하였다(첨부자료 참조).

○ **감귤 유전자원 분양 :** 온주밀감 궁천조생, 흥진조생 2개품종에 대한 캘러스 세포와 금귤등의 묘종을 바이오스펙트럼 기업체에 분양하였다. 또한 아열대산업연구소에 온주밀감 궁천조생과 흥진조생 2개 품종에 대한 캘러스 세포를 분양하였다.

○ **기자재 확충 :** 소재은행이 보유한 유전자를 가지고 분자육종을 수행하기 위하여 유전자원의 유지/증식을 위한 배양실 및 육종하는데 필요한 무균대 저온 배양기 등을 확보하였다.

○ **전문인력 양성 :** 감귤의 full-length cDNA 라이브러리 제작 전과정, 유전자정보 분석과 관련된 bioinformatics tool의 활용에 관한 실습 등을 학부 운영요원들에게 지도하여 유전자 및 유전자 정보를 이해하고 연구에 활용할 수 있는 인력양성의 기회도 마련하였고, 소재은행의 보유소재를 이용하여 감귤 육종을 수행할 수 있는 식물 육종 전공자(Post-Doc.)를 전임연구원으로 확보하였다.

다. 3차년도(2009. 3.1-2010. 2.28)

○ **유전자원 수집 :** 유전자원 보존 및 유용유전자 발굴 목표를 위해 현재 도내에 남아 있는 재래감귤 중 편귤 1 품종을 확보하여 유지 보관 하고 있으며, 감귤류 과실의 유전자원을 계속적인 확보를 위하여 탐라,하례,일남일호,상도,궁천,흥진,청견,클래멘타인,Sweer 오렌지, 레몬, 남감20호 등의 12품종을 수집하여 유지/보관하고 있다. 분자육종 재료 및 분양을 위해서 흥진,궁

IP : 14.49.138.138, 2017-11-03 13:30:33

천,의 미발육 종자로부터 재차 유기한 캘러스 세포 와 삼보감,탱자,유자,칵테일,하례, 금감 등 8 품종의 세포주를 기내에서 배양하여 확보/유지하고 있다.



<감귤 유전자원>

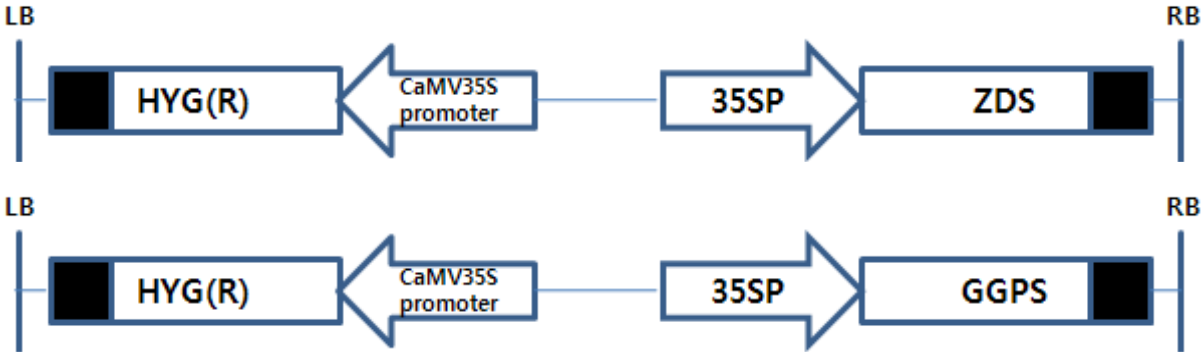
○ **지각미숙과실 라이브러리 제작** : 감귤유전자 라이브러리 제작에는 제주 재래품종이면서 유용성분이 있는 것으로 보고되어 있는 지각미숙과실을 목표유전자개발에 활용하였다. 소재은행에서 확보한 지각 미숙과실의 유전자 라이브러리는 식물체(주로 과실)의 total RNA로부터 mRNA 만을 정제한 후 이를 주형으로 ZAP-cDNA synthesis kit로 이중가닥 cDNA를 합성한 후에 ZAP-cDNA Gigapack III Gold Cloning Kit를 이용하여 bacteriophage에 packaging 하여 제작한다. 라이브러리는 40만개 이상의 클론이 되도록 제작하였고 2,301개의 클론에 대한 염기서열을 확보하였다.



<지각 미숙과실>

IP : 14.49.138.138, 2017-11-03 13:30:33

○ **유용유전자 선발 :** licopen 물질은 플라보노이드계의 하나이면서 항암 작용을 하는 것으로 알려져 있다. 이 licopen 물질 합성에 관여하는 것으로 알려진 zeta carotenoid desaturase (ZDS) 와 geranylgeranyl diphosphate synthesis(GGPS) 유전자를 온주밀감의 cDNA 라이브러리로부터 전체 염기서열을 확인하였고, 감귤 분자육종의 목표유전자로도 활용이 가능하다 사료되어 식물 형질전환 벡터에 재구성 한 후 형질전환에 사용하고 있다.



<카로티노이드 생합성 유전자(ZDS 와 GGPS) 식물형질전환 벡터 재구성>

○ **감귤 유전자원 분양 :** 재래감귤 지각 그리고 청귤 등 재래감귤 4 품종을 동물 생리활성물질 은행에 2회에 걸쳐서 지원하였다. 또한, 온주밀감 궁천조생, 홍진조생 2 품종에 대한 현탁배양 캘러스 세포를 바이오스펙트럼 기업체에 분양하였다.

○ **기자재 확충 :** 확보 유전자들의 발현 분석을 수행할 목적으로 Co_2 cold chember를 구입하였으며, 감귤세포배양및 육종에 필요한 shaking incubater등을 확보하였다.

○ **전문인력 양성 :** 감귤의 full-length cDNA 라이브러리 제작 전과정, 유전자정보 분석과 관련된 bioinformatics tool의 활용에 관한 실습 등을 학부 운영요원들에게 지도하여 유전자 및 유전자 정보를 이해하고 연구에 활용할 수 있는 인력양성의 기회를 마련하고 있다. 또한, 2011. 2. 본 소재은행의 은행원인 에드난 알바츄 및 단방맨 이 박사학위를 받았다.

라. 4차년도(2010. 3.1-2011. 2.28)

○ **유전자원수집 :** 유전자원 보존 및 유용유전자 발굴 목표를 위해 현재 도내에 보유하고 있는 암기, 강본 극조생 등 51 품종 확보하여 탱자 대목에 접목을 한 후 하우스에서 유지/보관하고 있다. 또한, 감귤류 과실의 유전자원을 계속적인 확보를 위하여 재래감귤 12품종을 포함한 총 15품종의 과실의 유전자원을 수집하여 유지/보관하고 있다.

○ **병귤 미숙과실 라이브러리 제작 :** 감귤유전자원으로는 재래품종 중 유용성분이 밝혀져 있거나 품종이 멸종위기에 있어 유전자원 확보가 시급한 품종 중 병귤 미숙과실을 목표유전자개발에 활용하였다. 유전자 라이브러리는 그림 2에서 보는 것과 같이 식물체(주로 과실)의 total RNA로부터 mRNA 만을 정제한 후 이를 주형으로 In-Fusion^{TM} SMARTer^{TM} cDNA Library

IP : 14.49.138.138, 2017-11-03 13:30:33

Construction kit로 이중가닥 cDNA를 합성한 후에 In-Fusion™ Advantage PCR Cloning Kit를 이용하여 E.coli에 insertion 하여 제작한다. 라이브러리는 profile 분석 외에 특정 유전자의 선발 또는 스크리닝이 가능하도록 라이브러리 당 10만개 이상의 클론이 되도록 제작하였고, 1,000 의 cDNA 클론에 대한 염기서열 정보를 분석 하였다. 또한, 2008년 진귤 성숙과실 염기서열 1,000개에 대한 클론을 확보하였다.

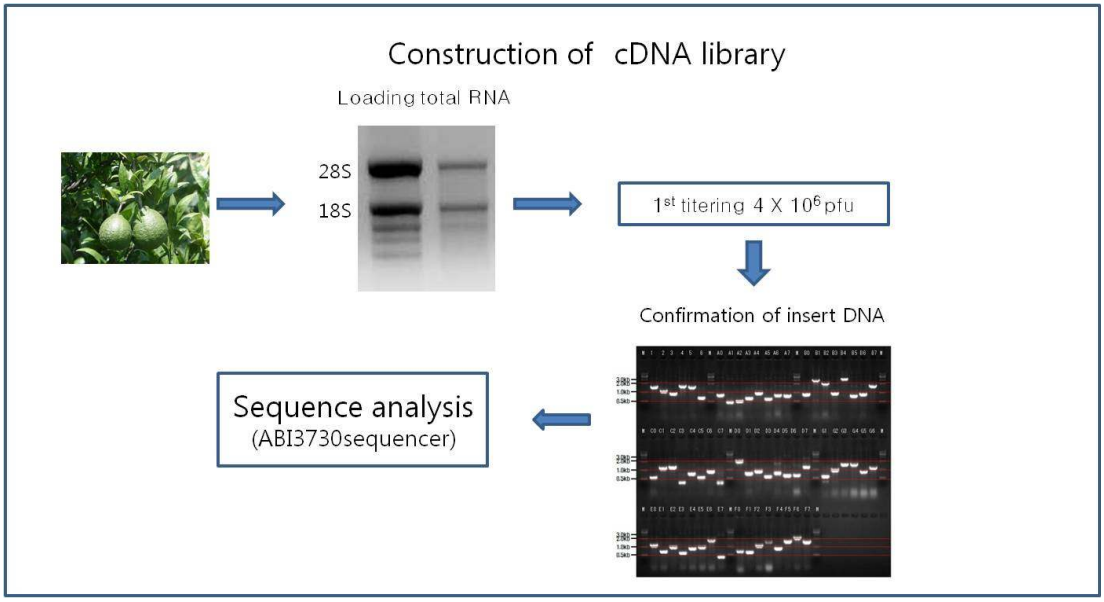


그림 2. 병귤 미숙과실 라이브러리 제작과정

○ 유용유전자 선발 :

■ 감귤류를 포함한 모든 식물체는 다양한 스트레스 저항성 또는 항산화에 관련된 많은 유전자들을 가지고 있다. 그 중에서 엽록체, 세포질, 미토콘드리아등의 식물체 전반에 존재하는 prenyltranserase 유전자는 단백질의 prenylation에 관여하여 단백질의 능력을 배가시키는 기능을 가지고 있는 것으로 알려져 있다. 이 유전자는 여러 종류의 감귤류 중 특히 당유자에서 높게 발현된다는 것을 microarray 연구를 통하여 확인하였다. 그리고 당유자와 병귤에서 prenyltransferase 유전자의 기능을 확인하기 위하여 2종의 Full-length cDNA 염기서열을 확인하였다.

■ Prenyltransferase 뿐 아니라 2종의 Alcohol dehydrogenase (ADH) 유전자 또한 microarray 연구를 통하여 당유자에서 특이적으로 발현되는 유전자로 밝혀졌다. ADH는 탈수, 저온, 등의 환경에서 강하게 발현된다고 알려져 있다. 이 ADH 유전자들 또한 Full-length cDNA 염기서열을 확인하였다.

○ 감귤 유전자원 분양 : 내부기관의 공동연구자인 김소미 교수 연구실에 온주밀감을 비롯한 여러 품종의 식물소재(잎) 35개를 분양하였고 재래감귤 지각 및 8품종에 대한 과실 124개의 미숙● 성숙과실를 한국식품 연구원에 분양하였으며, 경상대학교에서 병귤을 267개를 분양하였다.

IP : 14.49.138.138, 2017-11-03 13:30:33

또한 감귤연구소에 온주밀감 궁천조생 1개 품종에 대한 캘러스 세포를 분양하였고 인삼 소재은행 연구원에게 탱자를 비롯한 감귤 8품종에 대한 감귤 잎을 분양하였다.

○ **기자재 확충 :** 확보한 유전자 및 유전자원 과실들의 유지 보관을 위한 목적으로 Deep Freezer를 구입하였으며, 원할 한 유전자 분석을 위한 GENETYX 프로그램을 업그레이드 하였다. 또한, 소재은행이 보유한 유전자를 가지고 분자육종을 수행하여 얻어진 분자육종 감귤에 대한 순화 과정을 수행하기 위하여 식물생육장치를 확보하였다.

○ **전문인력 양성 :** 감귤의 full-length cDNA 라이브러리 제작 전과정, 유전자정보 분석과 관련된 bioinformatics tool의 활용에 관한 실습 등을 학부 운영요원들에게 지도하여 유전자 및 유전자 정보를 이해하고 연구에 활용할 수 있는 인력양성의 기회를 마련하였다.

마. 5차년도(2011. 3.1-2012.2.29)

○ **유전자원수집 :** 유전자원 보존 및 유용유전자 발굴 목표를 위해 현재 도내에 보유하고 있는 병감, Minneola Tangelo 2 품종 확보하여 탱자 대목에 접목을 한 후 하우스에서 유지하고 있다. 감귤 캘러스 세포 궁천, 하례, 상야 조생 캘러스와 재래감귤 당유자, 병귤등 총 5품에 대한 캘러스를 유도하고 기내에서 유지/보관하고 있다. 또한, 감귤류 과실의 유전자원을 계속적인 확보를 위하여 재래감귤 12품종에 대한 과실의 유전자원을 수집하여 유지/보관하고 있다.

○ **유전자 확보 :** 2008년 진귤 성숙과실 염기서열 67개에 대한 클론을 확보하였고, 2010년 병귤 미숙과실에 대한 염기서열 1,500개 대한 클론을 확보하였다. 또한, 3차년도에 확보한 지각 미숙과실 클론에 대한 염기서열 360개를 분석하였다.

○ **유용유전자 선발 : 본** 소재은행에서 보유하고 있는 Citrus 300K DNA microarray 칩을 이용하여, 다양한 외부의 스트레스에 내성을 나타내는 유전자로 알려진 2개의 Alcohol dehydrogenase (ADH) 유전자가 재래감귤의 한 품종인 당유자에서 특이적으로 높게 발현된다는 것을 확인하고 병귤에서 ADH 유전자의 Full-length cDNA RT-PCR법을 이용하여 염기서열 정보 확보 후 감귤의 다양한 조직에서의 ADH 유전자 발현패턴을 확인하였다. 또한 확보한 아미노산 서열을 바탕으로 기존에 밝혀진 ADH 유전자들과의 상동성 조사를 수행하여 genomic DNA 분석을 통해 ADH 유전자의 구조를 밝혀내었다(첨부자료 참조).

○ **감귤 유전자원 분양 :** 재래감귤 병귤 및 5품종에 대한 과실 271개를 한국기초과학지원연구원 부산센터 하이테크소재 연구부에 분양하였고 감귤시험장에 상야조생, 하례조생을 포함한 총 5품종 캘러스 cell line에 대해서 분양하였으며, 전라남도 한방산업 진흥원에 당유자를 포함한 7품종의 감귤 캘러스 cell line을 분양하였다. 또한 경상대 신성철 교수가 병귤 과실 4개를 분양하였다.

IP : 14.49.138.138, 2017-11-03 13:30:33

○ **전문인력 양성 :** 본 소재은행의 감귤 분자육종에 대한 전문지식을 갖고 있는 이비 은행원을 “제주도 재래감귤류 12품종에 대한 캘러스 유도”에 대한 논문 발표를 통해 2012. 2월 초에 배출하였다.

○ **감귤 유전자 지도 작성 :** 유전체 분석을 위한 재래감귤 병귤 genomic DNA 라이브러리를 제작 하였고 comparative genomics를 이용한 재래감귤의 유용 유전자 대량 확보 하였다.

4) 연구소재의 확보 및 보존절차, 방법, 품질관리

가.감귤유전자/유전자원의확보

제주도 재래감귤 12품종의 유전자 및 유전자원을 확보하기 위하여 감귤품종별 성숙시기에 따라서 과실 및 유전자원 식물체를 확보한다. 소재확보를 위해서 전정가위(감귤 접수 자르거나 과실 따는데 사용) 보호 장갑, 비닐 주머니(확보한 접수 및 과실을 담아 운반하거나 보관할 때 이용), 흡습지 및 화장지(절취한 접수부분이 말라버리는 것을 방지하는데 이용) 그리고 액체질소나 드라이아이스 (RNA파괴되는것 방지)를 준비한다.



<유전자/유전자원확보>

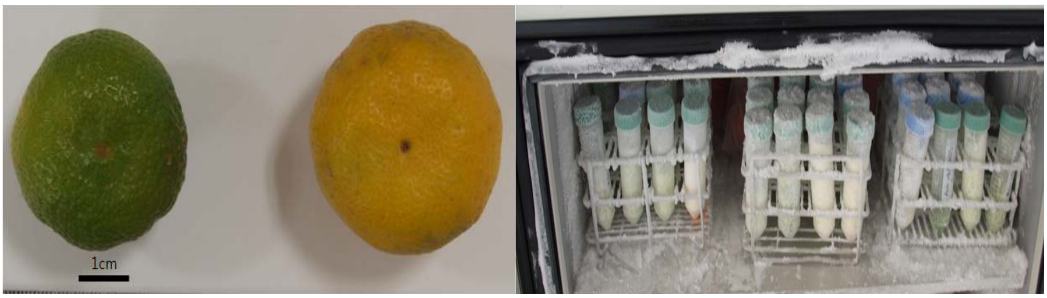
나.소재보관

유전자 라이브러리 제작을 위해 확보한 과실 중 일부는 사진 촬영 후 과실 전체를 절단하여 50ml 원심분리 튜브에 나누어서 넣은 후 -80℃에서 보관한다. 나머지 과실은 저장 box 내에 일정양 -80℃에서 보관한다. 수집한 접수는 즉시 탱자 대목에 접목을 수행하거나 2-3일간 4℃ 냉장고에 보관해 두었다가 수행한다.

IP : 14.49.138.138, 2017-11-03 13:30:33



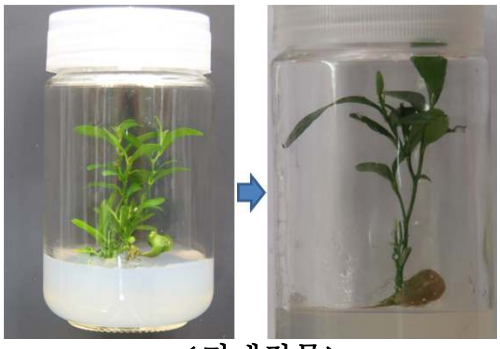
<유전자/유전자원과실보관>



<유전자라이브러리제작유전자원보관>

다.감귤접수접목

- **기내접목:** 3-4월경 확보한 탱자나 시쿠아사의 종자를 MT 기본배지에 배양하여, 지상부가 약 7 cm이상 생육했을 때 유자 및 시쿠아사의 지상부를 3-4cm 절단한 후 측면으로 약 1 cm정도 깎아 내고, 접수로 사용될 식물체의 한 면을 약 0.3 cm정도 깎아 내린 후 대목에 끼어 MT 배지에서 16시간 광주기와 약 1,000 Lux이하의 광도, 25±2℃로 보정된 배양실에서 배양한다.



<기내접목>

IP : 14.49.138.138, 2017-11-03 13:30:33

- **기외접목:** 2월경 구입한 탱자 종자를 *in vivo* 상의 배양토에 배양하여, 지상부가 약 7 cm이상 생육했을 때 탱자대목의 지상부를 3-4cm 절단한 후 측면으로 약 1 cm정도 깎아 내고, 접수로 사용될 유전자원의 액아부분이 2-3개 남도록 자르고 한 면을 약 0.3 cm정도 깎아 내린 후 대목에 끼어 파라필름으로 감싼 후 온실에 서 배양한다.



<기외접목>

다. 보존절차 및 품질관리

장기보존용 유전자는 영구보존용으로 나누어 명지대 GG 바이오에 1 set를 장기 보존하고 있으며, -80℃의 장기저온저장고에서 보존한다. 보존기한은 50년에서 최대 100년이다. 소재 관리자는 유전자 클론의(특성검사용과 분양용) 수량을 고려하여 총 보존 수량을 결정하며 보존 수량이 30ul 이하이면 다시 유전자를 형질전환 시켜 분리 정제하여 보존한다.

구분	보존구분	보존기간	보존온도	용도
장기보존용	장기보존	100년	-80℃	영구보존용
운용	중기보존	30-50년	-80℃	분양용,관리용. 연구용
중복보존용	장기보존	100년	-80℃	중복보존용

신규 유전자/유전자원을 등록할 때는 은행등록번호, 위치번호의 부여체계에 따라 신규 번호를 부여하고 생산관리대장, 등록관리대장과 보존관리대장에 기록한다. 유전자의 은행등록번호는 유전자/유전자원 소재명와 위치번호를 조합하여 부여한다. 감귤 품종명 최대 5글자 이내로 구성한다. 일련번호는 최대 6자릿수 이내의 아라비아 숫자로 알파벳으로 구성하고 유전자원 소재등록순서에 따라 순차적으로 부여한다.

예) YHANP-01-R-M06

한라봉 미숙과실 01번 384plate M06번 위치시료

IP : 14.49.138.138, 2017-11-03 13:30:33

과실인 경우는 유전자 소재은행(CGRB)명을 기입하고 감귤 품종 일련번호를 아라비아숫자로 구성한다.

예) CGRB15

CGRB: 유전자소재은행명 15번: 감귤품종명(당유자)

유전자/유전자원은 1달 주기로 유전자 정기 정검을 수행하며, 식물거점센터와 공유하여 분기별로보유하고 있는 유전자의 정기적인 유전자의 정도관리를 실시하며 결과는 정도관리대장과 정도관리결과표에 기록한다. 폐기 대상 소재는 별도로 구획된 안전한 장소 또는 용기에 보관하여야 한다. 예를 들면 배양물, tip, 배지 등의 오염 폐기물 또는 잠재적 감염성 소재는 반드시 멸균뚜껑이 있는밀폐용기에 보관하였다가 감압멸균을 통해 폐기처리한다.

IP : 14.49.138.138, 2017-11-03 13:30:33

2. 연구소재분양 실적

1) 분양실적

[표 5] 연구소재 분양 실적

(단위 : 천 원)

년도	분양내역	국내						국외		합계	
		자체		외부기관		계					
		개수	금액	개수	금액	개수	금액	개수	금액	개수	금액
1차년도	300K 감귤 DNA chip										
	유전자원식물										
	cell line										
	cDNA 라이브러리	1	3,000	2	6,000	3	9,000			3	9,000
	cDNA 클론	291	29,100	64	6,400	355	35,500			355	35,500
	염기서열정보	3,095	61,900	5,366	107,320	8,461	169,220			8,461	169,220
	상동성조사정보			2,401	48,020	2,401	48,020			2,401	48,020
2차년도	유전자원식물										
	cell line										
	cDNA 라이브러리	2	6,000	2	6,000	4	12,000			4	12,000
	cDNA 클론	428	42,800	404	40,400	832	83,200			832	83,200
	염기서열정보	587	11,740	735	14,700	1,322	26,440			1,322	26,440
3차년도	유전자원식물										
	cell line										
	cDNA 라이브러리	1(1,700)	3,000	1(41,000)	3,000	2(42,700)	6,000			2(42,700)	6,000
	cDNA 클론	767	76,700	1,429	142,900	2,196	219,600			2,196	219,600
	염기서열정보	390	7,800	1,098	21,960	1,488	29,760			1,488	29,760
4차년도	유전자원식물	35	350	8	(80)	43	430			43	430
	cell line			1	500	1	500			1	500
	과실			391	(391)	391	(391)			391	(391)
	cDNA 라이브러리										
	cDNA 클론	252	25,200	773	77,300	1,025	102,500			1,025	102,500
	염기서열정보	273	5,460	851	17,020	1,124	22,480			1,124	22,480
5차년도	유전자원식물										
	cell line			12	6,000	12	6,000			12	6,000
	과실			275	(275)	275	(275)			275	(275)
	cDNA 라이브러리										
	cDNA 클론	314	31,400	807	80,700	1,121	112,100			1,121	112,100
	염기서열정보	305	6,100	803	16,060	1,108	22,160			1,100	22,160
합계		6,741	310,550	15,423	595,026	22,164	905,576			32,064	905,576

(09.8.19 진성범 온주밀감라이브러리 1 set 분양(1,751클론), 09. 9.11 윤수현 한라봉 병반 1 plate(라이브러리를 plate에 깔아서 41,000클론 분양)

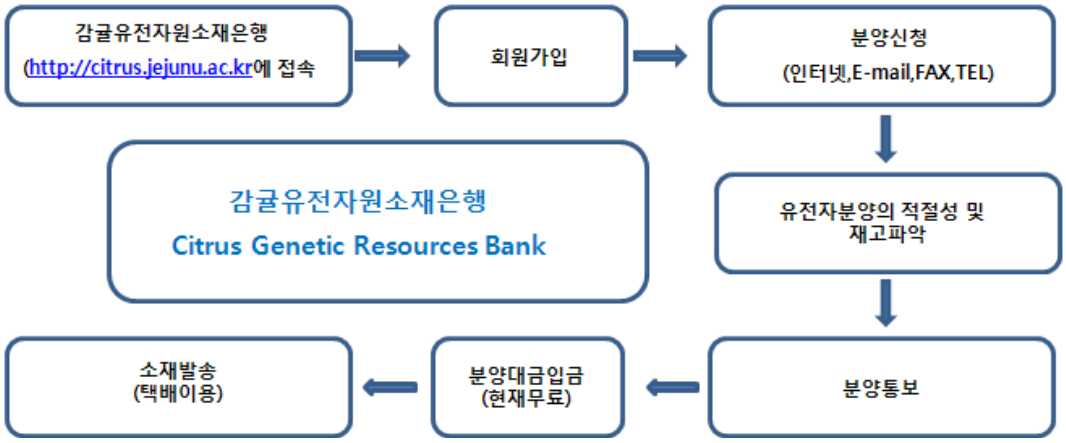
- 인간 유전체 사업단 자료를 근거로 하여 아래와 같이 산출하였다.

- 300K 감귤 DNA chip : 100 만원, 유전자원 식물 : 개당 만원, 라이브러리 : 300만원, cDNA 클론 : 10만원, 염기서열 정보 및 상동성 조사 정보 : 2만원, 식물 세포주 : plate당 50만원, 과실: 개당 1,000원

IP : 14.49.138.138, 2017-11-03 13:30:33

2) 연구소재의 분양절차 및 방법

○ 연구소재의 분양절차는 홈페이지(http://citrus.jejunu.ac.kr), 전화, 팩스, 이메일 등을 통하여 전담 행정요원에서 접수되고 있다. 접수사항은 유전자클론, 염기서열 정보, 유전자 정보 등 분양요구 형태에 따라 라이브러리관리부 또는 데이터베이스관리부에 전달되어 빠른 시간 내에 분양이 진행될 수 있도록 하고 있으며, 관련된 연구자 들은 누구나 홈페이지 접속만으로 확보 소재들의 정보를 확인할 수 있도록 하였다. 또한 홈페이지의 회원가입은 간단한 개인정보만을 입력함으로써 누구나 회원가입 할 수 있도록 되어 있으며 관리자의 승인절차만 거치면 쉽게 정회원이 될 수 있도록 하였고, web 상에서 분양신청을 할 수 있게 하여 분양 절차를 간소화 함으로써 최대한 빠른 시간 내에 분양이 이루어 질 수 있도록 하였는데, 유전자 정보 분양(염기서열 정보 등)인 경우는 분양이 접수되는 즉시 승인절차만 거치면 web 상에서 바로 신청 정보를 볼 수 있도록 하여 최대한 빠른 시간 내에 수요자들이 정보를 활용할 수 있도록 하였으며, 유전자 클론의 분양은 체계적으로 최대한 빠른 시간 내에 수요자들에게 공급하기 위해서 클론 분양 접수 후 매주 수요일에 분양하였다. 또한 유전자원 식물체나 과실인 경우는 부패가 되지 않도록 드라이아이스가 첨가된 ice 박스에 밀봉한 후 수요자에게 택배를 통해 분양하였다.



<분양절차>

3) 연구소재 분양에 따른 효과 분석

■ 감귤 관련 연구의 분자생물학적 기반은 무엇보다도 유전자 및 서열정보라 할 수 있는데 본 소재은행에서 cDNA 라이브러리를 제작하고 일정량의 유전자 클론 및 유전자 정보들을 수집하여 감귤 관련 연구자들의 요구에 따라 분양해 주고 있기 때문에 개개의 연구자들이 연구 소재 및 정보들을 직접 선발/수집하는데 소요되는 많은 시간, 노력 그리고 비용 등을 최소화하여 연구의 효율을 극대화 하고 있다.

■ 현재 침체위기에 놓여 있는 제주 감귤산업을 극복하기 위하여 고품질 감귤 생산 신품종 개발, 감귤이 함유하고 있는 약리활성/기능성 물질의 생물공학적 생산 등과 관련된 연구들이 활발히 진행되고 있는데, 본 소재은행에서 제공하는 유전자 및 서열정보 및 유전자원 식물체들은

IP : 14.49.138.138, 2017-11-03 13:30:33

이러한 연구에 있어서 필수적인 것들이어서 감귤과 관련된 생물공학적, 분자생물학적 연구의 중요한 기반이 되고 있다.

■ 감귤 클러스터사업의 일환으로 방사선 돌연변이를 이용한 신품종개발 사업이 진행되고 있는데, 본 소재은행에서 제공하는 300K 감귤 DNA microarray 분석 data는 돌연변이체의 유전자적 변이를 확인하는 것뿐만 아니라 본 대학에서 유치한 “중점연구사업(학술진흥재단)”에도 중요한 자료가 되고 있다.

■ 소재 분양 등에 따른 학술발표, 논문발표 등의 연구 성과 도출 효율의 증진은 관련 연구의 활성화에 기여할 뿐 아니라 본 소재은행의 가치 함양과 홍보에도 효과가 클 것이다.

■ 분양된 유전자 및 유전자원(과실)을 이용한 연구결과는 지속적으로 발표되고 있으며, 국제적으로 인정받는 결정적 계기가 될 것이다.

3. 연구소재 정보 관리 실적

○ 연구소재의 정보관리 현황 및 중앙센터 DB에 소재 정보 탑재 여부

2개의 DB서버로 안정성과 보안을 위해 웹서버는 따로 분리해서 운영하고 있으며, 확보된 유전자들의 유전자 정보 등은 모두 일관성 있게 관리하고 편리하게 검색하기 위해 모든 자료를 DB화하고 있다. 모든 유전자 정보에 대해서는 고유 accession 번호를 부여하고, 수집 확보한 감귤 유전자원에 대해서도 accession 번호를 부가하여 지속적으로 데이터베이스 시스템에 업데이트 되어 전산망을 통하여 그 실체를 확인 할 수 있도록 하고 있으며, Homepage는 DB서버와 물리적으로 분리되어 작동되고 있으며, 일반인과 전문가 누구나 접속하여 이용 할 수 있도록 개방 운영체계로 운영되어 이들 이용자의 편의를 최대한 도모 하도록 서비스를 제공하고 있다. 인터넷 상에서 홈페이지(http://citrus.jejunu.ac.kr)를 통해 본 소재은행에서 소장중인 감귤 관련 유전자 정보 등을 검색할 수 있도록 하고 있다. 중앙센터 DB에 소재 정보 탑재 여부에 있어, 지난해 말 본 소재은행에서 보유하고 있는 9개 유전자원 라이브러리 중 지각 과 최근에 확보한 병귤 미숙과실을 제외한 나머지 8개 유전자원 라이브러리 에 대한 유전자 정보 등 모든 자료를 중앙센터 DB에 탑재 하였다. 현재 병귤 미숙과실은 DB화 진행 중 이다.



<감귤류유전자원라이브러리>

IP : 14.49.138.138, 2017-11-03 13:30:33

4. 소재은행 관련으로 발표된 연구 성과

가. 발표논문

<1차년도(2007. 04-2008. 02)논문실적>

(국외 SCI)

-소재은행관련

1) Kyung Hwan Boo, Dae Woon Kim, Somi Kim Cho, Seong Beom Jin, Jae Hoon Kim, Hyo Yeon Lee, and Key Zung Riu* Construction and Profiling of a cDNA Library from Young Fruit of Satsuma Mandarin. Journal of Plant Biology, August 50(4) : 403-409 (2007)

(국내 비SCI)

-소재은행관련

1) Hyun Jeong Oh*, Hyo Min Ahn, Kyoung Ha So, Sang Suk Kim, Pil Yong Yun, Gyeong Lyong Jeon, and KeyZungRiu.Chemical and Antimicrobial Properties of Essential Oils from Three Coniferous Trees Abies koreana, Cryptomeria japonica, and Torrey anucifera. J. Appl. Biol. Chem. 50 (3), 164-169 (2007)

(국내 비SCI)

-소재은행 비관련

1) Hyun Jeong Oh,*, Hyo Min Ahn, Sang Suk Kim, Pil Yong Yun, Gyeong Lyong Jeon, Young Hwan Ko and Key Zung Riu. Composition and Antimicrobial Activities of Essential Oils in the Peel of Citrus Fruits. J. Appl. Biol. Chem. 50(3), 148-154 (2007)

2) Jae-Hoon Kim, Jeong-Hun Yun. Inhibitory Effect of Plant Extracts on VHR Dual Specificity Protein Phosphatase. J. Appl. Biol. Chem. 50(4), 301-303 (2007)

3) Jae-Hoon Kim* and Dae-Gwin Jeong. Proteomic Identification of Proteins Interacting with a Dual Specificity Protein Phosphatase, VHZ. J. Appl. Biol. Chem. 50(2), 58-62 (2007)

4) Kyung Hwan Boo, Hana Kim, Key Zung Riu, Youn Woo Kim, Moonjae Cho and Somi Kim Cho,, Analysis of the Limonoid Contents of Dangyuja (Citrus spp.) by Liquid Chromatography-mass Spectrometry (LC-MS). J. Korean Soc. Appl. Biol. Chem. 50(3), 238-243 (2007)

<4차년도(2010. 03-2011. 02)논문실적>

(국내 SCI)

-소재은행관련

1) Jeong-Won Park, Kyung-Hwan Boo, Seong-Beom Jin, Md. Adnan Al Bachchu, Su-Hyun Yun,

IP : 14.49.138.138, 2017-11-03 13:30:33

Yong-Woo Kim, Dong-Sun Lee, Hyo-Yeon Lee, Key-Zung Riu, and Jae-Hoon Kim*. Expression Profiling of Cultivar-related Genes in Satsuma Mandarins, Miyagawa Wase and Ueno Wase. J. Korean
Soc. Appl. Biol. Chem. 53(6), 691-701 (2010)

2) Kyung Hwan BOO, Doseung LEE, Gyeong Lyong JEON, Seung Hee KO, Somi K. CHO, Jae Hoon
KIM, Se Pill PARK, Quanchun HONG, Sang-Han LEE, Dong-Sun LEE and Key Zung RIU. Distribution
and Biosynthesis of 20-Hydroxyecdysone in Plants of Achyranthes japonica Nakai. Biosci. Biotechnol.
Biochem, 74(11), 2226-2231 (2010)

(국외 SCI)
-소재은행 비관련

1) Jin-Man Lee, Jong-Guk Kim, Tae-Ho Kim, Do S. Lee, Jae H. Kim, Somi K. Cho, Key Z. Riu, Dong-Sun Lee, Sang-Han Lee. Nonactin hinders intracellular glycosylation in virus-infected baby hamster
kidney cells. Molecular Medicine REPORTS 3: 115-119 (2010)

<5차년도(2011. 03-2012. 02)논문실적>

(국외 SCI)
-소재은행관련

1) Hae Gyeong Kim, Gon-Sup Kim, Jung Han Lee, Semin Park, Won Young Jeong, Yun-Hi Kim, JaeHoonKim,Soo Taek Kim, Young Ah Cho, Won Sup Lee, Soo Jung Lee ,Jong Sung Jin, Sung Chul
Shin. Determination of the change of flavonoid components as the defence materials of Citrus unshiu Marc .fruit peel against Penicillium digitatum by liquid chromatography coupled with tandem mass spectrometry. Food Chemistry 12849- 45 (2011)

2) Hae Gyeong Kim, Gon-Sup Kim, Semin Park, Jung Han Lee, On Nuri Seo, Soo Jung Lee, Jae Hoon Kim, Jae-Han Shim, A. M. Abd El-Aty, Jong Sung Jin and Sung Chul Shin. Flavonoid profiling in three citrus varieties native to the Republic of Korea using liquid chromatography coupled with tandem mass spectrometry: contribution to overall antioxidant activity. Biomedical Chromatography, 26(4) 464-470(2012)

3) Hongtao Wang, Min-Kyeoung Kim, Yeon-Ju Kim, Hee-Neoung Lee, Haizhu Jin, Jiayu Chen, Deok-Chun Yang. Molecular authentication of the Oriental medicines Pericarpium Citri Reticulatae and Citri Unshius Pericarpium using SNP markers. Gene 494: 92-95(2012)

(국내 SCI)
-소재은행관련-

IP : 14.49.138.138, 2017-11-03 13:30:33

1) Md. Adnan Al Bachchu, Seong Beom Jin, Jeong Won Park, Hyeon Jin Sun, Su Hyun Yun, Hyo Yeon Lee, Dong Sun Lee, Quan Chun Hong, Yong Woo Kim and Key Zung Riu, and Jae Hoon Kim. Agrobacterium-mediated transformation using embryogenic calli in Satsuma mandarin (Citrus unshiu Marc.) cv. Miyagawa wase. Hort. Environ. Biotechnol. 52(2):170-175 (2011)

2) Mohammad Adnan Al Bachchu, Seong-Beom Jin, Jeong-Won Park, Kyung-Hwan Boo, Hyeon-Jin Sun, Yong-Woo Kim, Hyo-Yeon Lee, Key-Zung Riu, Jae-Hoon Kim*. Functional Expression of Miraculin, a Taste-modifying Protein, in Transgenic Miyagawa Wase Satsuma Mandarin (Citrus unshiu Marc.). J. Korean Soc. Appl. Biol. Chem. 54(1), 24-29 (2011).

(국내 SCI)

-소재은행 비관련

1) Kyung-Hwan Boo, Doseung Lee, Jin-Kyu Woo, Seung Hee Ko, Eun-Hyoung Jeong,Quanchun Hong, Key Zung Riu1*, Dong-Sun Lee*. Anti-bacterial and Anti-viral Activity of Extracts from Paeonia lactiflora Roots. J. Korean Soc. Appl. Biol. Chem. 54(1), 132-135(2011)

2) Doseung Lee, Kyung-Hwan Boo, Jin-Kyu Woo, Fangmeng Duan, Keun-Hwa Lee,Taeg Kyu Kwon4, Hyo Yeon Lee, Key Zung Riu, and Dong-Sun Lee*. Anti-bacterial and Anti-viral Activities of Extracts from Terminalia chebula Barks. J. Korean Soc. Appl. Biol. Chem. 54(2), 295-298 (2011)

3) Doseung Lee, Jin-Kyu Woo, Donghern Kim, Minyoung Kim, Somi K. Cho, Jae Hoon Kim, Se Pill Park, Hyo Yeon Lee, Key Zung Riu, Dong-Sun Lee. Antiviral Activity of Methylelaiophylin, an α-Glucosidase Inhibitor. J. Microbiol. Biotechnol. 21(3): 263~266 (2011)

4) Key Zung Riu*. Production Conditions for Bruceanol B, an Antibiotic that Generates Oxygen Radical. J. Korean Soc. Appl. Biol. Chem. 54(1), 128-131 (2011)

5) Doseung Lee, Kyung-Hwan Boo, Jin-Kyu Woo, Quanchun Hong,Somi K. Cho, Se Pill Park, Dong-Sun Lee, and Key Zung Riu. Trafficking Inhibition of Bruceanol B as a Radical-Producing Antibiotic. J. Korean Soc. Appl. Biol. Chem. 54(2), 299-301 (2011)

6) Doseung Lee, Seong-Cheol Kim, Donghern Kim, Jae Hoon Kim, Se Pill Park, Youn-Chul Ryu, Minyoung Kim, Somi Kim Cho, Key Zung Riu, and Dong-Sun Lee* . Screening of Phellinus linteus, a Medicinal Mushroom, for Anti-viral Activity. J. Korean Soc. Appl. Biol. Chem. 54(3), 475-478 (2011)

7) Doseung Lee,Jin-Kyu Woo, Donghern Kim, Minyoung Kim, Somi K. Cho, Jae Hoon Kim, Se Pill Park, Hyo Yeon Lee, Key Zung Riu, Dong-Sun Lee. Antiviral Activity of Methylelaiophylin, an α-Glucosidase Inhibitor. J. Microbiol. Biotechnol. 21(3), 263-266 (2011)

(국내 비SCI)

-소재은행관련

IP : 14.49.138.138, 2017-11-03 13:30:33

1) Somi K. Cho,Young-Mee Kim, Minyoung Kim, Doseung Lee, Jae Hoon Kim, SePill Park, Key Zung
Riu and Dong-Sun Lee Expression and Isolation of Limonoid UDP-glucosyltransferase, a Bitterness-reducing Enzyme, in *E.coli* Korean J Food Preserv 18(2), 208-211(2011)

(국내 비SCI)

-소재은행 비관련

1) Young Mee Kim, Do Seung Lee, Deokhyoon Jeon, Yeonwoo Song, Dong-Sun Lee, Key Zung Ryu, Moonjae Cho, Dong Hoon Lee and Somi Kim Cho Analysis of Expression Pattern of the Limonoid UDP-glucosyltransferase Gene as an Indicator for Delayed Bitterness from the Citrus Endemic in Jeju Korean J Food Preserv 18(2), 208-211 (2011)

나. 특허출원

번 호	특 허 명	출원일	출원번호
1			
2			

IP : 14.49.138.138, 2017-11-03 13:30:33

[표 6] 소재은행 관련으로 발표된 성과(논문 수)

년도	국내								국외				계			
	자체				외부기관											
	SCI		비SCI		SCI		비SCI		SCI		비SCI		SCI		비SCI	
	소재은행 표시	소재은행 미표시	소재은행 표시	소재은행 미표시	소재은행 표시	소재은행 미표시	소재은행 표시	소재은행 미표시	소재은행 표시	소재은행 미표시	소재은행 표시	소재은행 미표시	소재은행 표시	소재은행 미표시	소재은행 표시	소재은행 미표시
1차년도	1		2	1				2					1		2	3
2차년도																
3차년도																
4차년도					1				1	1			2	1		
5차년도	3		1		3	2	1		5				11	2		
합계	4		3	1	4	2	1	2	6	1			14	3	2	3

□ DNA microarray를 이용한 기능 유전자 분석

○ **DNA microarray를 이용한 품종 간 발현 유전자 분석:** 본 소재은행이 보유하고 있는 EST 와 public 데이터베이스인 GeneBank에 보고된 Citrus EST를 이용하여 Citrus 유전자 분석을 통해 얻어진 67,881개의 unigene을 가지고 Citrus 300k DNA Chip을 제작하였다. 이 감귤 유전자 칩은 “중점연구사업(학술진흥재단)”에 이용되도록 지원하였고, 이 감귤 유전자 칩을 이용하여 궁천조생, 청견, 당유자 와 하귤의 과실 및 잎에서 mRNA의 발현량의 차이를 비교 분석하는데 도움을 주었다(첨부자료 참조). 분석된 Chip 데이터에 의하면 각 품종별로 mRNA의 발현량을 비교 분석한 결과 2배 이상 차이가 나는 것으로 추정되는 유전자들을 찾아내었다.

품종	up regulation	Down regulation
궁천	313	404
청견	129	281
당유자	281	555
하귤	231	236

< 감귤품종간 mRNA의 발현량이 2배 이상 차이나는 유전자>

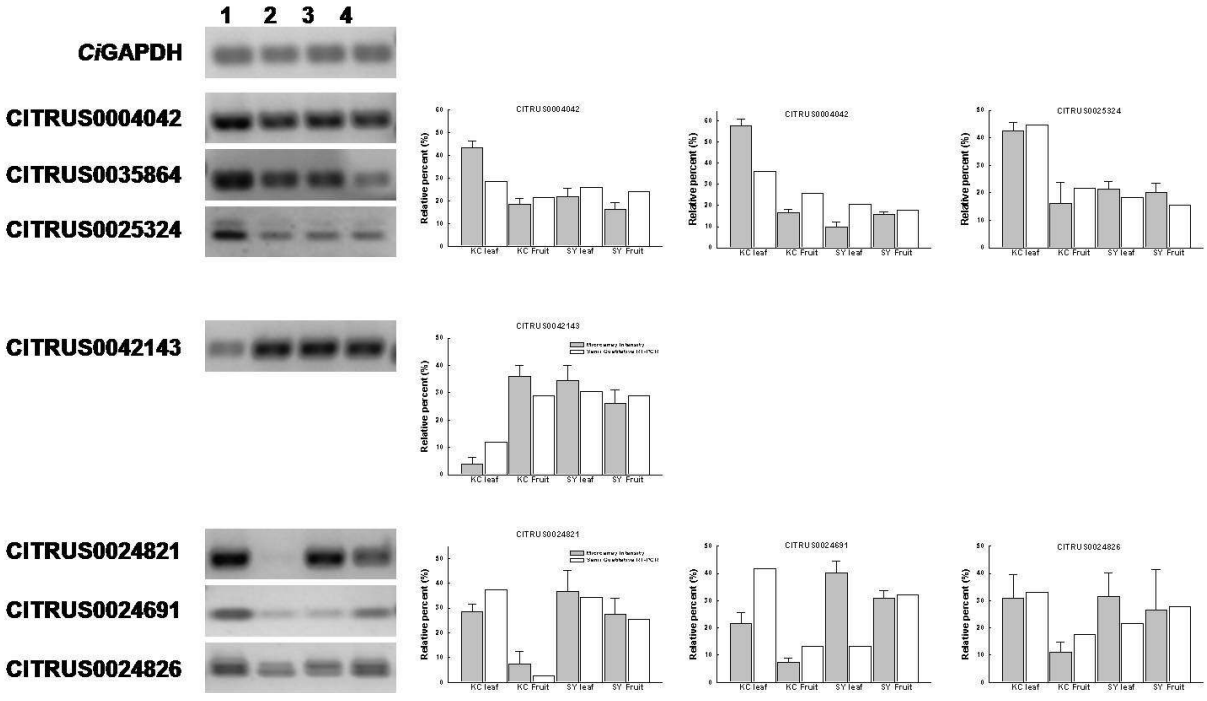
또한, Semi-quantitative RT-PCR 분석을 통하여 microarray 분석에서의 각 품종간에 발

IP : 14.49.138.138, 2017-11-03 13:30:33

현이 많거나 적은 것으로 분석된 결과와 동일한 양상의 결과를 확인할 수 있었다.

Probe ID[a]	Putative gene function	Analysis tool	Miyagawa wase Leaf	Kiyomi Leaf	Gradis osbeck Leaf	Natsudaidai orange Leaf
CITRUS 0004042	Amidases	Microarray	19775.84±6752.72[b] (43.42±3.08)	8672.68±3871.08 (18.61±2.55)	10039.34±3787.30 (21.67±3.78)	7907.72±4154.85 (16.30±2.82)
		RT-PCR	2134.39 (28.68)	1602.689 (21.54)	1917.39 (25.77)	1787.39 (24.02)
CITRUS 0035864	Aromatic-L-amino-acid/L-histidine decarboxylase	Microarray	11706.05±4932.80 (57.83±2.93)	3303.73±1163.12 (16.65±1.52)	1866.57±559.37 (9.73±2.55)	3221.47±1414.93 (15.78±1.35)
		RT-PCR	3156.46 (36.01)	2247.46 (25.64)	1804.75 (20.59)	1558.04 (17.78)
CITRUS 0025324	Beta-glucosidase	Microarray	15738.27±10901.77 (55.69±8.91)	3174.66±2989.47 (10.84±3.32)	6803.44±7248.69 (20.68±6.28)	3427.62±2288.38 (12.80±1.95)
		RT-PCR	3140.80 (31.41)	2355.80 (23.56)	2732.80 (27.33)	1770.68 (17.71)
CITRUS 0042143	Alcohol dehydrogenase, class III	Microarray	1208.33±980.01 (6.86±2.60)	10567.01±2673.65 (35.96±3.91)	9979.93±1980.59 (34.33±5.64)	7581.10±1938.56 (25.97±5.20)
		RT-PCR	1556.34 (12.02)	3734.04 (28.85)	3929.04 (30.35)	3725.04 (28.78)
CITRUS 0024821	Alcohol dehydrogenase, class V	Microarray	12221.06±6930.47 (28.48±3.20)	3857.92±4004.54 (7.25±5.41)	14958.88±6050.63 (36.78±8.37)	11253.34±5542.28 (27.51±6.33)
		RT-PCR	4012.87 (37.40)	284.51 (2.65)	3696.87 (34.45)	2736.87 (25.50)
CITRUS 0024691	Thioredoxin	Microarray	4905.90±1704.76 (21.65±3.88)	1603.10±328.62 (7.25±5.41)	8802.59±878.20 (36.78±8.37)	6890.01±1688.67 (27.51±6.33)
		RT-PCR	2328.80 (41.65)	732.97 (13.11)	734.68 (13.14)	1794.80 (32.10)
CITRUS 0024826	Mitochondrial chaperonin,	Microarray	15851.89±15124.94 (30.88±8.61)	7421.34±9697.40 (10.98±3.91)	15009.62±14572.43 (31.43±8.76)	21258.49±23839.25 (26.71±14.59)
		RT-PCR	4877.11 (33.13)	2577.70 (17.51)	3167.11 (21.52)	4098.41 (27.84)
CITRUS 0002214	Cis-prenyltransferase	Microarray	3139.09±1048.36 (13.46±2.10)	2397.14±1569.72 (20.31±4.58)	14879.65±549.28 (66.29±10.85)	2483.70±1555.22 (10.32±4.77)
		RT-PCR	2609.21 (27.20)	1700.51 (17.73)	2865.21 (29.87)	2416.21 (25.19)

< Microarray의 signal intensity와 각 품종별 semi-qantitative RT-PCR의 결과>



<각 품종별 RT-PCR 분석결과>

○ DNA microarray를 이용한 아조변이 관련 유전자 분석 : 감귤 유전자 분석을 통해 얻어낸 67,881개의 unigene을 이용하여 제작된 300K DNA chip을 이용하여, 온주밀감 풍종중 주된 품종인 궁천조생 과 궁천조생의 아조변이인 상야 조생의 잎과 과실로 부터 분석된 chip 데이

IP : 14.49.138.138, 2017-11-03 13:30:33

터에서 각 품종간의 그리고 조직간의 비교를 통해 mRNA의 발현량이 2배 이상차이가 나는 것으로 추정되는 유전자들을 분석하였다. 그 결과 발현차이를 보이는 유전자의 수에서 동일한 품종내에서 잎과 과실간의 비교에서는 두 품종 모두 차이를 보이는 유전자의 수는 비교적 유사한 것으로 나타났다. 그러나 두 품종의 과실간의 비교에서는 궁천조생에 비해 상야조생의 과실에서 발현량이 많은 유전자가 많은 것으로 나타났다. 이러한 결과는 궁천조생으로부터 변이된 상야조생의 과실에서 보다 많은 유전자의 발현이 변이된 것으로 추정된다

A

궁천조생과 상야조생간의 비교	
	No. of genes
궁천조생의 잎	2,745
상야조생의 잎	2,120
궁천조생의 과실	474
상야조생의 과실	1,315

B

동일 품종내에서 잎와 과실간의 비교	
	No. of genes
궁천조생의 잎	9,770
궁천조생의 과실	7,880
상야조생의 잎	8,527
상야조생의 과실	7,828

<Microarray를 이용한 온주밀감 두 품종간의 발현차이를 보이는 유전자의 수>

(A; 두 품종의 동일한 조직간의 비교, B; 품종내에서 조직간의 비교)

또한, 차이를 보이는 유전자들의 기능적 분류에서도 두 품종은 유사한 보이는 것으로 나타났으나, Translation, ribosomal structure and biogenesis에 관련된 유전자는 두 품종간 잎간의 비교에서 특이적으로 많은 것으로 나타났다.

<두품종의 동일한 조직간의 비교에서 발현차이를 보이는 유전자의 COG functional 그룹>

COG	COG Definition	궁천 잎	상야 잎	궁천 과실	상야 과실
INFORMATION STORAGE AND PROCESSING					
J	Translation, ribosomal structure and biogenesis	46 (1.68)	79 (3.73)	9 (1.90)	27 (2.05)
A	RNA processing and modification	58 (2.11)	26 (1.23)	2 (0.42)	10 (0.76)
K	Transcription	41 (1.49)	44 (2.08)	3 (0.63)	10 (0.76)
L	Replication, recombination and repair	9 (0.33)	9 (0.42)	0 (0.00)	1 (0.08)
B	Chromatin structure and dynamics	8 (0.29)	12 (0.57)	1 (0.21)	2 (0.15)
Sub total		**162 (5.90)**	**170 (8.02)**	**15 (3.16)**	**50 (3.80)**
CELLULAR PROCESSING AND SIGNALING					
D	Cell cycle control, cell division, chromosome partitioning	16 (0.58)	15 (0.71)	0 (0.00)	6 (0.46)
Y	Nuclear structure	8 (0.29)	0 (0.00)	0 (0.00)	2 (0.15)
V	Defence mechanisms	11 (0.44)	9 (0.42)	3 (0.63)	3 (0.23)

IP : 14.49.138.138, 2017-11-03 13:30:33

T	Signal transduction mechanisms	81 (2.95)	55 (2.59)	4 (0.84)	29 (2.21)
M	Cell wall/membrane/envelope biogenesis	13 (0.47)	5 (0.23)	1 (0.21)	5 (0.38)
N	Cell motility	0 (0.00)	0 (0.00)	0 (0.00)	0 (0.00)
Z	Cytoskeleton	19 (0.69)	12 (0.57)	2 (0.42)	12 (0.91)
W	Extracellular structure	2 (0.07)	1 (0.05)	0 (0.00)	1 (0.08)
U	Intracellular trafficking, secretion and vesicular transport	63 (2.30)	38 (1.79)	4 (0.84)	14 (1.06)
O	Posttranslational modification, protein turnover, chaperones	97 (3.53)	87 (4.10)	18 (3.80)	58 (4.41)
Sub total		**310 (11.29)**	**222 (10.47)**	**32 (6.75)**	**130 (9.89)**
METABOLISM					
C	Energy production and conversion	50 (1.82)	40 (1.89)	6 (1.27)	35 (2.66)
G	Carbohydrate transport and metabolism	59 (2.15)	47 (2.22)	8 (1.69)	40 (3.04)
E	Amino acid transport and metabolism	36 (1.31)	28 (1.32)	11 (2.32)	25 (1.90)
F	Nucleotide transport and metabolism	2 (0.07)	5 (0.24)	1 (0.21)	3 (0.23)
H	Coenzyme transport and metabolism	9 (0.33)	9 (0.42)	1 (0.21)	10 (0.76)
I	Lipid transport and metabolism	35 (1.28)	34 (1.60)	3 (0.63)	19 (1.44)
P	Inorganic ion transport and metabolism	24 (0.87)	23 (1.08)	3 (0.63)	12 (0.91)
Q	Secondary metabolites biosynthesis transport and metabolism	56 (2.04)	31 (1.46)	13 (2.74)	33 (2.51)
Sub total		**271 (9.87)**	**217 (10.24)**	**46 (9.70)**	**177 (13.46)**
POORLY CHARACTERIZED					
R	General function prediction only	182 (6.63)	113 (5.33)	14 (2.95)	65 (4.94)
S	Function unknown	15 (0.55)	30 (1.42)	4 (0.84)	23 (1.75)
Sub total		**197 (7.18)**	**143 (6.75)**	**18 (3.80)**	**88 (6.69)**
Not classified COGs categories		1,805 (65.76)	1,368 (64.53)	363 (76.58)	870 (66.16)
Total		**2,745**	**2,120**	**474**	**1,315**

□ 감귤육종 위한 항체 개발

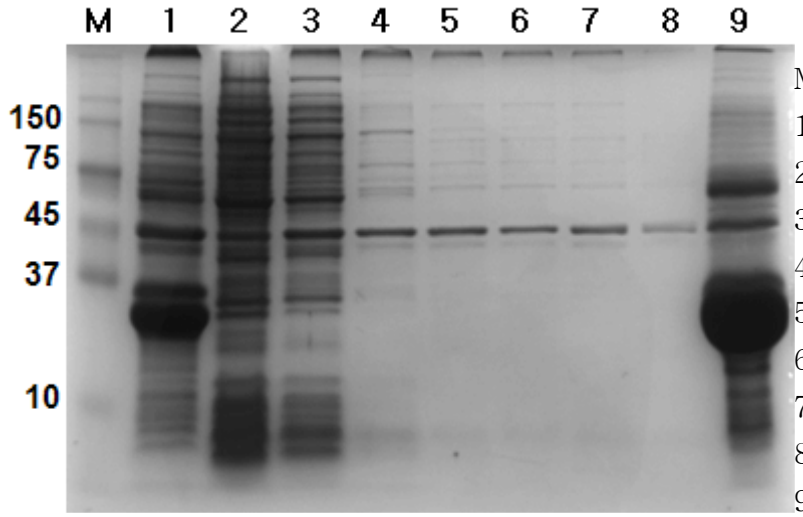
○ Miraculin Antibody 제작

Miraculin단백질은 서아프리카가 원산지인 Richadella dulcifica (Miracle fruit)에 분리된 단백질로서 신맛을 단맛으로 느끼게하는 taste modify 활성을 가지고 있는 것으로 알려져 있는데, 현재 소재은행은행에서는 이미 금귤과 온주밀감(궁천조생) 캘러스에 miraculin 유전자를 도입하였다. 이에 miraculin 단백질의 antibody 제작을 통해 식물체에서의 miraculin 단백질의 발현을 확인하고자, Miraculin 단백질을 대장균 발현 시스템에서 대량 발현시키고 rabbit을 이용하여 polyclonal antibody를 제작하여 형질전환 식물체에서 miraculin 단백질 발현 확인에 이용하였다.

IP : 14.49.138.138, 2017-11-03 13:30:33

○ Miraculin 단백질의 과발현 시스템

Miraculin 유전자를 대장균 과발현 vector인 pET15b에 cloning하고, BL21(DE3) host에 형질전환 하였다. 단백질의 발현은 37℃에서 1 mM IPTG를 이용하여 miraculin 단백질의 대량 발현을 유도하였다. 그 결과 IPTG에의해 miraculin 단백질이 대량으로 발현되는 것을 확인 할 수 있었으나, 발현된 단백질은 insoluble로 inclusion body를 형성하여 침전되었다. Suluble 단백질로의 발현을 유도하기위하여 induction 온도, IPTG 농도, induction 시간 등의 조건을 달리해 보았으나, inclusion body가 형성되는 것으로 확인되어 inclusion body 정제를 통해 가능한 순수한 miraculin 단백질을 분리하였다. 분리된 단백질을 이용하여 rabbit을 이용하여 polyclonal antibody를 제작에 이용하였다.



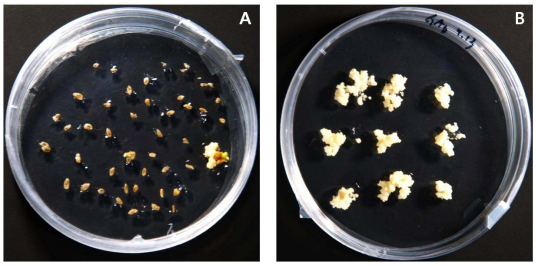
< Miraculin over-expression과 inclusion body 정제>

□ 신품종 감귤 개발을 위한 감귤 분자육종

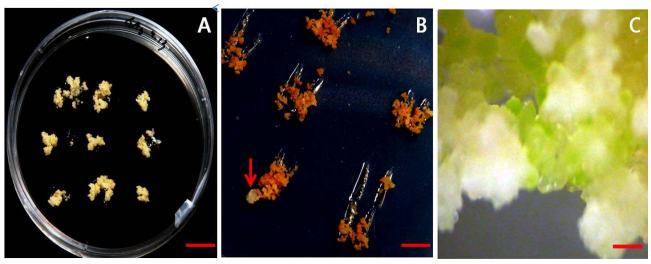
○ **분자육종기법을 이용한 감귤육종:** 감귤은 목본으로서 유년성이 10년 이상이나 되며, 조직배양 과 형질전환이 어려운 점 때문에, 온주밀감 품종에 대한 조직배양과 형질전환에 대한 연구가 많이 되어있지 않다. 형질전환 감귤체를 얻었다는 보고가 현재까지 없을 정도로 매우 어려운 감귤류 중 하나인데 본 소재은행에서는 온주밀감(궁천조생)의 미발육 종자에서 얻어진 캘러스 세포를 가지고 캘러스유기조건, embryogenic cell line 확보방법, 식물체재분화조건 및 형질전환 시스템을 완전히 구축하였다(그림 7). 또한, 기존의 *Agrobacterium*을 이용한 감귤형질전환 방법들과는 다른 형질전환 방법과는 더 효과적인 형질 방법을 구축하였다. 본 소재은행에서 형광유전자(GFP)가 도입된 온주밀감 형질전환식물체를 만들었으며, 라이코펜 합성 전구체로 알려진 GGPS 와 ZDS 유전자를 온주밀감 캘러스 세포에 도입하여 유전자 도입여부를 확인하였고, 신

IP : 14.49.138.138, 2017-11-03 13:30:33

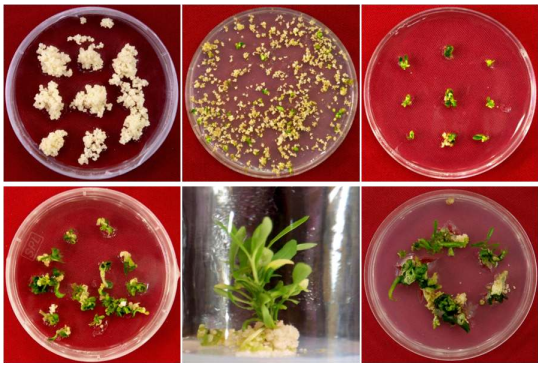
맛을 단맛으로 느끼게 해주는 단백질인 미라클린 유전자가 도입된 온주밀감(궁천조생), 금귤 형질전환식물체를 만들었다. 미라클린 유전자가 도입된 온주밀감(응용생명과학회지와 원예학회지에 투고됨 첨부파일 참조) 과 금귤 형질전환식물체는 유전자 도입에 따른 단백질 발현여부와 감미테스트를 수행하여 감미 활성여부를 확인하였다.(현재 국내 원예학회지에 투고하여 수정 중 이다).



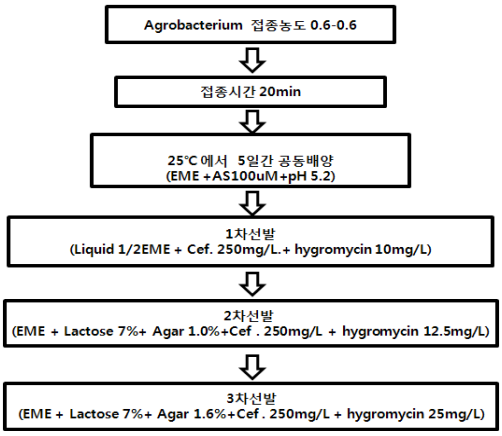
<온주밀감 궁천 품종에서 캘러스 유도(A) 및 증식(B)>



<온주밀감 형질전환체 선발 캘러스 세포(A) 및 형질전환체 선발(B). 체세포배 유도(C)>

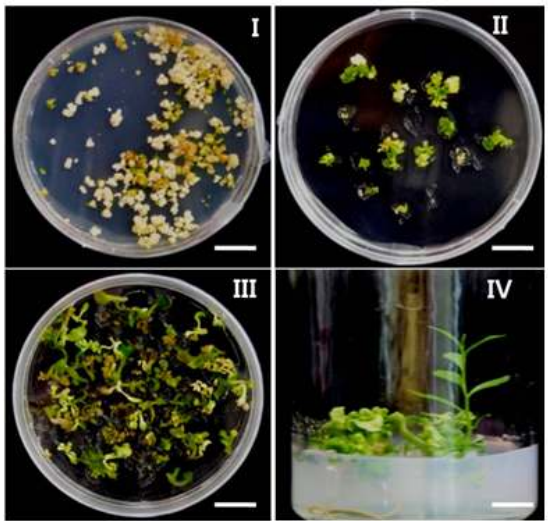


<캘러스 배유도 배증식 식물체>

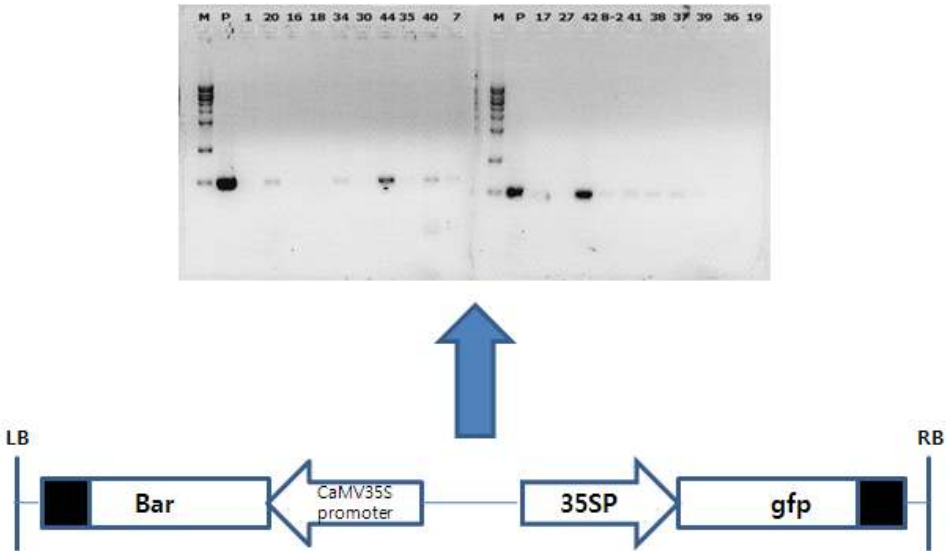


<형질전환방법>

IP : 14.49.138.138, 2017-11-03 13:30:33

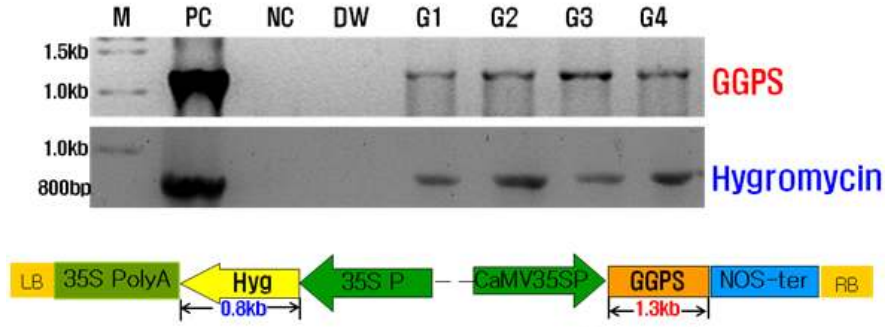


<형질전환 방법 구축>



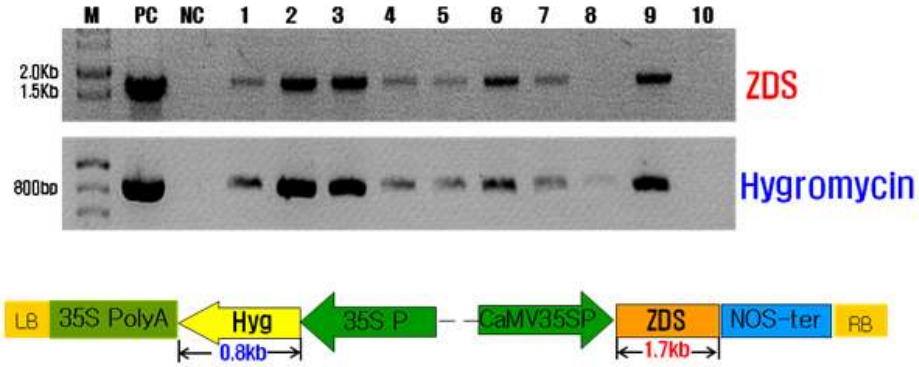
<GFP 유전자 도입 온주밀감 형질전환체 PCR 분석>

IP : 14.49.138.138, 2017-11-03 13:30:33



pCAMBIA1300 GGPS 벡터 구성도

<GGPS 유전자 도입 온주밀감 형질전환체 PCR 분석>

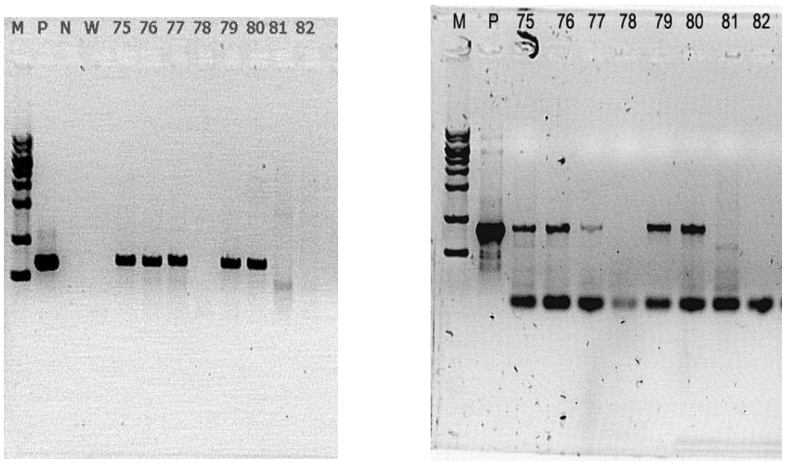


pCAMBIA1300 ZDS 벡터 구성도

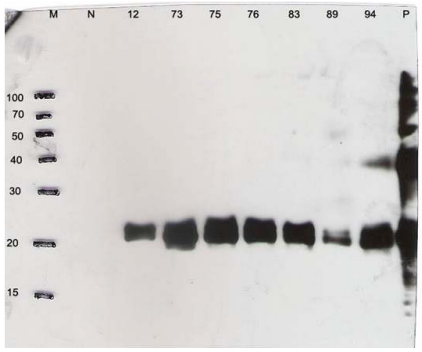
<ZDS 유전자 도입 온주밀감 형질전환체 PCR 분석>

IP : 14.49.138.138, 2017-11-03 13:30:33

가) 나)



<미라클린 유전자 도입 온주밀감 형질전환체 PCR 분석>
A) 미라클린, 나) 하이그로마이신



<미라클린 유전자 도입 온주밀감 형질전환체 단백질 발현분석>



<미라클린 유전자 도입 온주밀감 형질전환체 식물체>

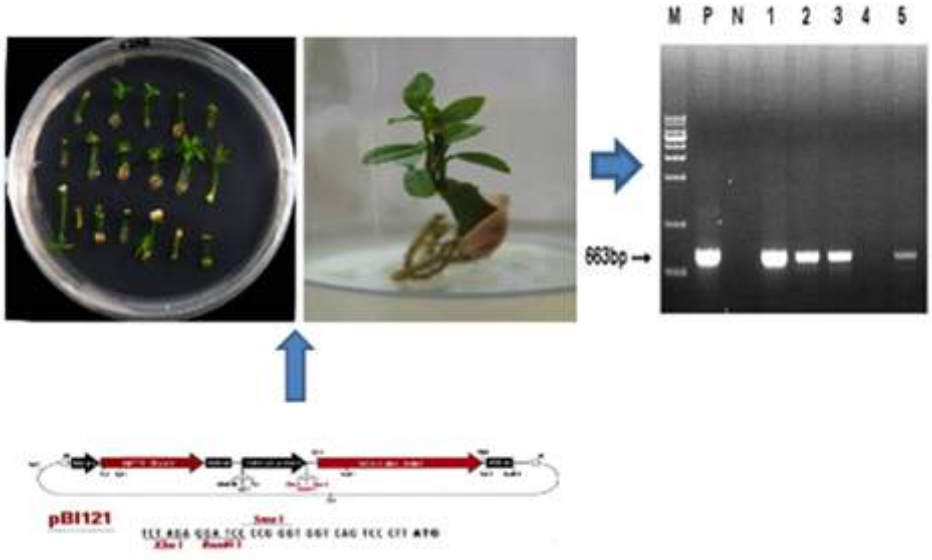
IP : 14.49.138.138, 2017-11-03 13:30:33



<미라클린 유전자 도입 온주밀감 형질전환체 기내점목>

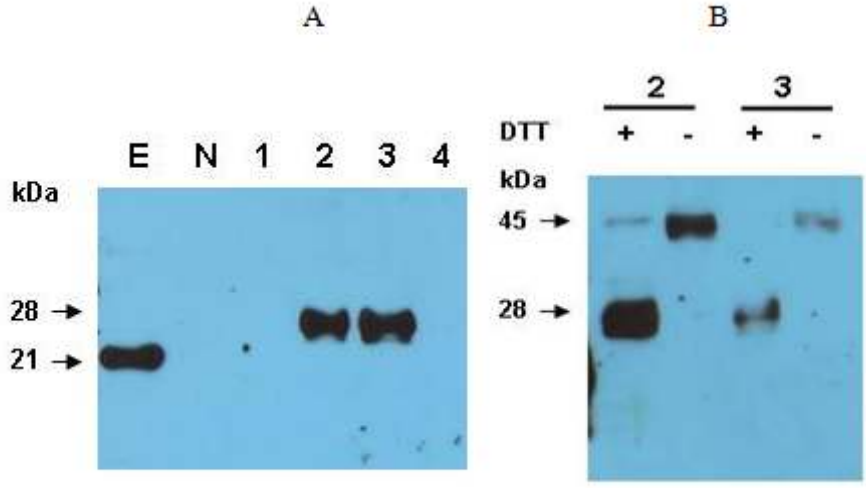
Source materials	Weight of Leaves tissue (g)	Induced sweetness (SEV) (M)
Miyagawa Wase Leaves tissue	1	0.28 ± 0.02

<온주밀감 Miraculin 감미 테스트>



<형질전환 금귤 식물체로부터 미라클린 유전자 도입 확인>

IP : 14.49.138.138, 2017-11-03 13:30:33

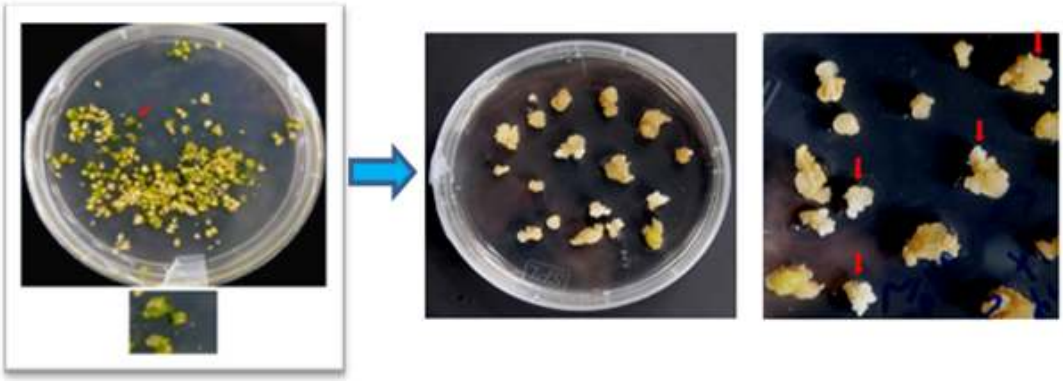


<형질전환 금귤 식물체로부터 미라클린 단백질 발현 분석>

Source material	Weight of leaf tissue (g)	Induced sweetness(SEV)(M)
Fortunella leaf tissue	0.25	0.28±0.05

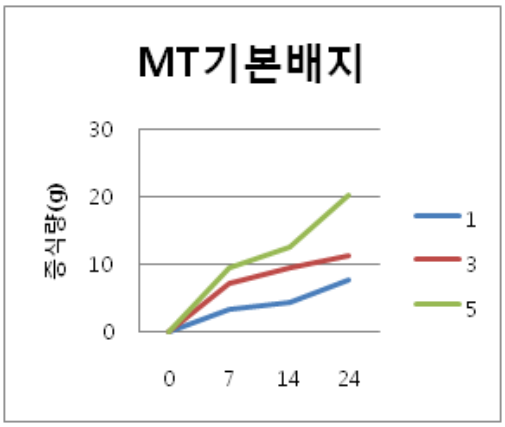
<형질전환 금귤 식물체로부터 미라클린 단백질 활성 감미테스트>

○ 감귤 캘러스 세포를 이용하여 고 기능성 물질 및 고부가가치인 항체 등을 생산하기 위하여 네블오렌지 캘러스 세포에 미라클린 단백질 유전자와 조류독감 항체 합성 유전자를 도입하여 세포현탁배양 기법을 응용하여 미라클린 단백질 발현을 갖고 있는 캘러스 세포 및 조류 독감 유전자가 발현되는 감귤 캘러스 세포를 대량 생산하고 있다 (현재 특허출원 중임).

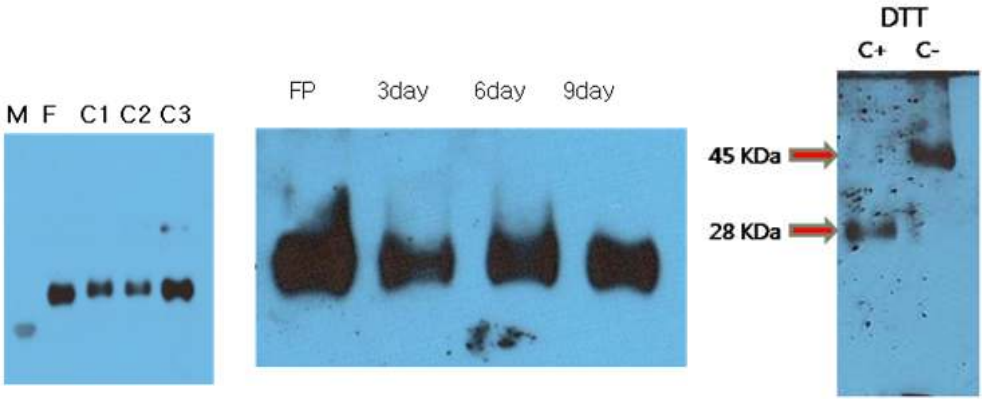


< 형질전환체 선발 체세포배-> 캘러스 유도>

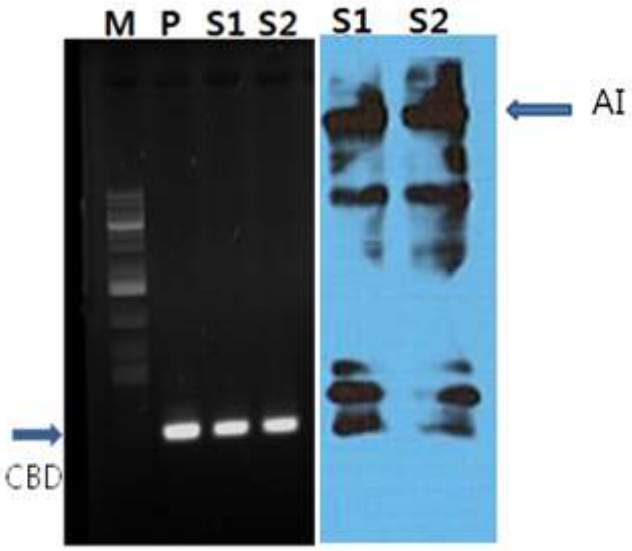
IP : 14.49.138.138, 2017-11-03 13:30:33



< 배양기간에 따른 캘러스 세포 증식율>



< 미라클린 단백질 분석 및 세대간 유전적 안정성>

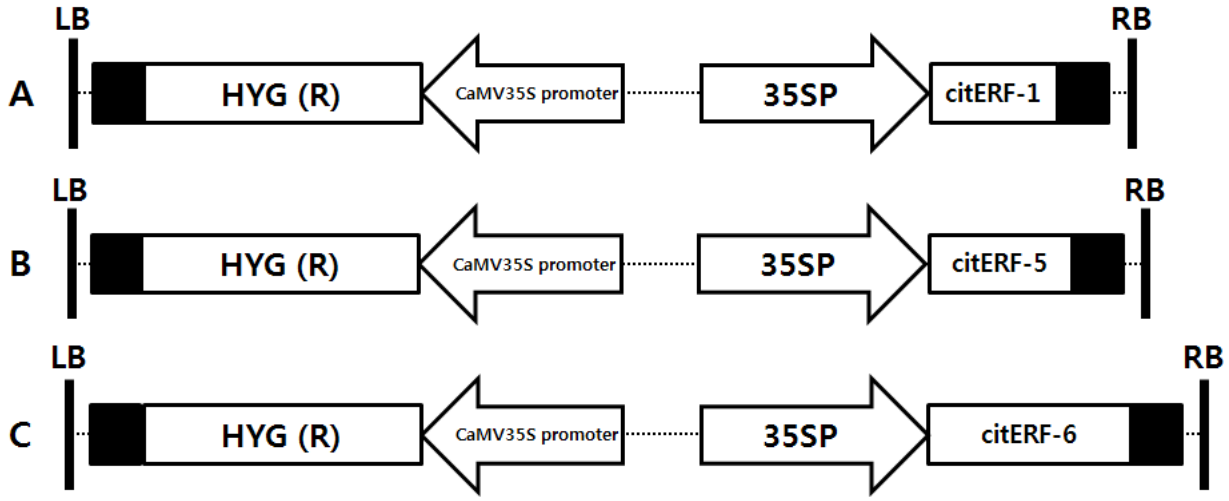


< 조류 독감 유전자 도입 및 단백질 분석>

IP : 14.49.138.138, 2017-11-03 13:30:33

○ 모델 실물인 Arabidopsis를 이용한 감귤 ERF 유전자의 기능연구

본 소재은행의 DB에서 확보한 감귤ERF(citERF)유전자들의 기능연구를 위하여 binary vector인 pCAMBIA 1300에 cloning(그림 13)하여 모델 식물인 Arabidopsis에 도입하여 T3세대에서 citERF-1, citERF-5 그리고 citERF-6에 대한 염 농도 저항성 여부를 검토하기 위하여 MS 기본배지에 0, 100, 120 mM NaCl 농도를 달리하여 뿌리의 신장여부를 실험 하였다. T3 세대에서 citERF-1, citERF-5 보다 citERF-6가 염농도에 저항성을 보이는 것을 확인 할 수 있었다

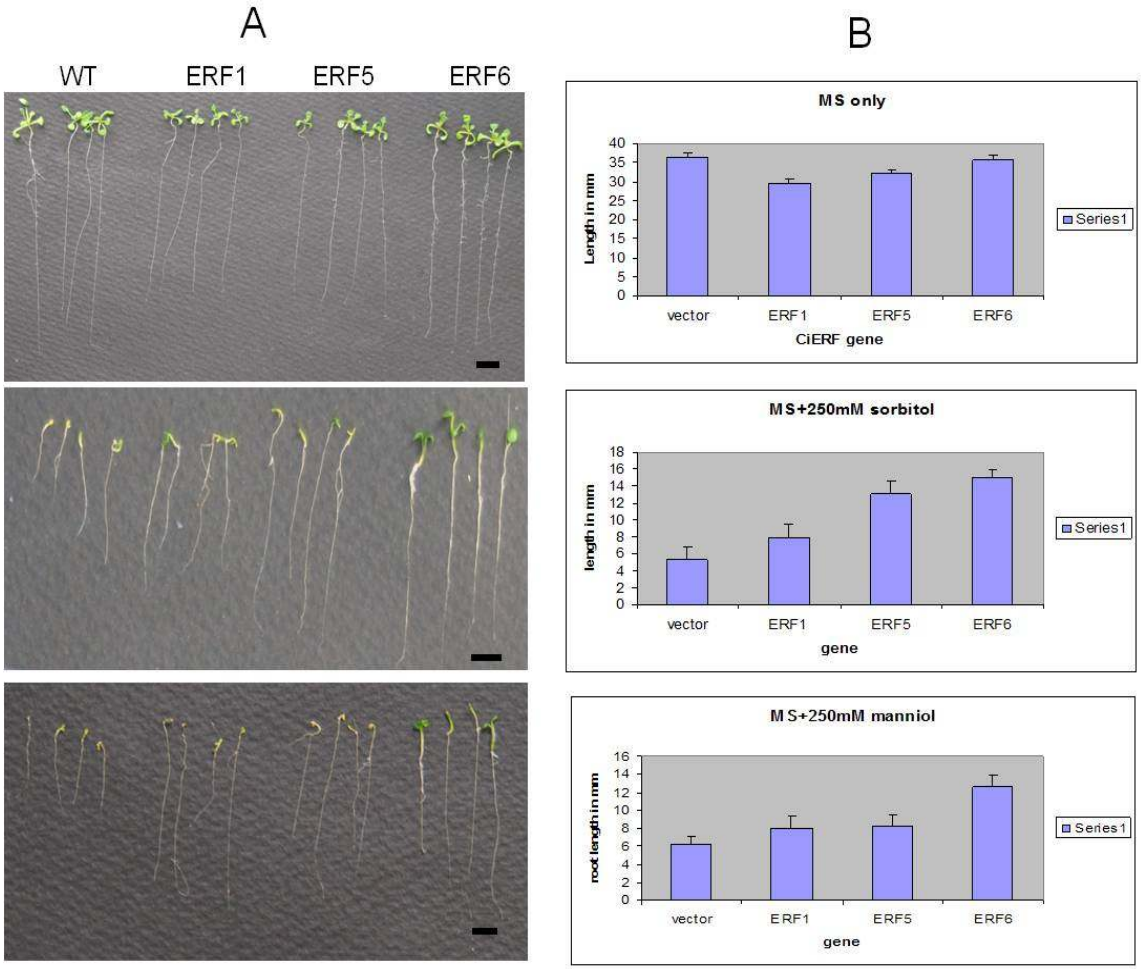


<pCAMBIA-citERF vector map>



<citERF를 도입한 Arabidopsis>

IP : 14.49.138.138, 2017-11-03 13:30:33



<염농도 처리에 따른 T3 Arabidopsis의 뿌리 신장>

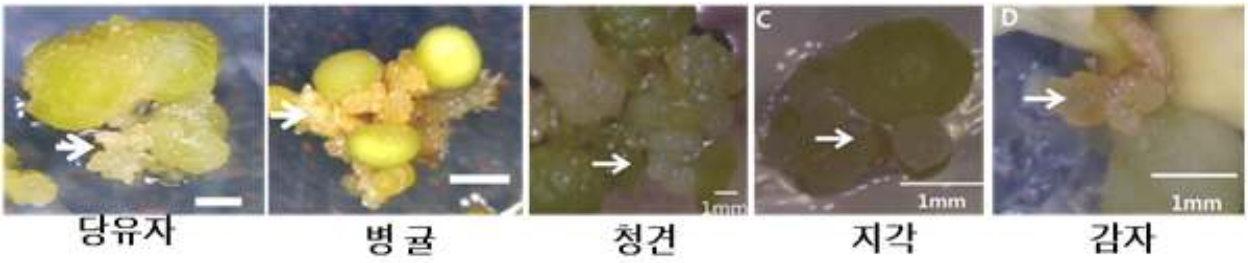
□ 재래감귤 캘러스 세포 유도

○ 제주도 재래감귤 12품종에 대한 배주 배양을 통하여 5종류의 배지조성에 따라 캘러스 세포를 유도하였다.

Medium	MS I			MS II			MS III			EME			1/2 EME		
Common name	Normal callus derived from embryo	Abnormal callus derived from ovule	Embryo	Normal callus derived from embryo	Abnormal callus derived from ovule	Embryo	Normal callus derived from embryo	Abnormal callus derived from ovule	Embryo	Normal callus derived from embryo	Abnormal callus derived from ovule	Embryo	Normal callus derived from embryo	Abnormal callus derived from ovule	Embryo
Kamja	0	0	6	0	0	0	0	0	0	0	0	0	1	0	7
Dangyooja	0	0	2	0	0	1	5	0	10	0	0	5	0	0	11
Dongjeongkyool	0	0	2	0	10	0	0	7	0	0	0	6	0	0	7
Byungkyool	0	0	3	1	0	9	0	0	0	0	3	1	0	0	2
Binkyool	0	0	4	0	0	3	0	0	0	0	0	2	0	0	12
Sadookam	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Yooja	0	0	5	0	1	9	0	0	16	0	0	2	0	0	1
Jikak	2	0	21	0	0	13	0	0	3	1	0	7	0	0	6
Jinkyool	1	0	3	1	0	6	1	3	12	0	0	4	0	3	6
Cheongkyool	2	6	13	4	17	20	1	3	11	3	0	12	6	0	31
Pyunkyool	0	0	3	0	0	7	0	0	12	0	0	0	0	0	0
Hongkyool	0	1	5	0	0	5	0	0	17	3	4	8	0	0	20

Embryogenic callus.
비정상 Callus(Embryogenic callus가 아님).
일반 Embryo.

IP : 14.49.138.138, 2017-11-03 13:30:33

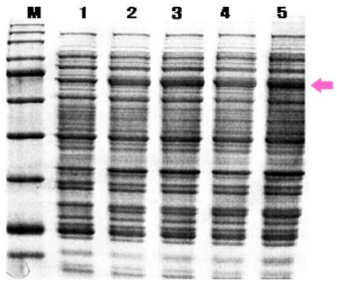


< 재래감귤 품종별 캘러스 유도>

□ 기능성 유전자 선발

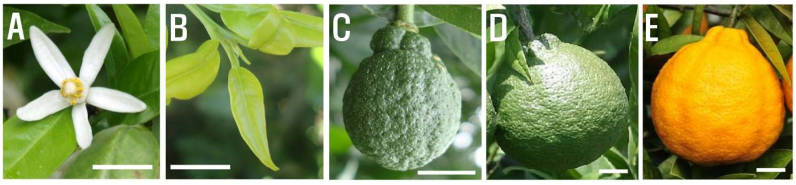
○황산화 등 기능성 유전자 한라봉 EST 유전자로부터 cloning 한 감귤 flavonoid glycosyltra-

nsferase의 활성을 보기 위해서 단백질 발현 백터인 pGX에 cloning 한 후 DE3 rosetta2에 형질전환 하였고, 현재 단백질 상에서 발현여부를 확인하였다.



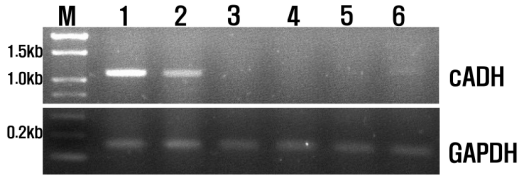
<flavonoid glycosyltransferase단백질 분석>

○ 본 연구소재은행의 300K microarray 결과를 가지고 두개의 ADH V가 1086 bp에 362 aa 그리고 ADH III가 1125 bp에 375 aa의 크기를 갖는 ADH를 분리하였다. 염기서열을 이용하여 각각의 유연관계를 비교분석한 결과 ADH V는 애기장대의 cinnamyl alcohol dehydrogenase-like protein과 90% 이상의 상동성을 보였다. Cinnamyl alcohol dehydrogenase (CAD)는 식물의 세포벽 구성 성분인 리그닌 생합성에서 중요한 효소로서 작용하는 유전자임이 보고되어 있는데, 병귤의 조직별 발현량상을 분석한 결과 병귤의 꽃과 잎에서 발현량이 과실에 비해 상대적으로 높다는 것을 확인하였다.



<병귤의 각 조직과 과실의 단계별 발달 과정>

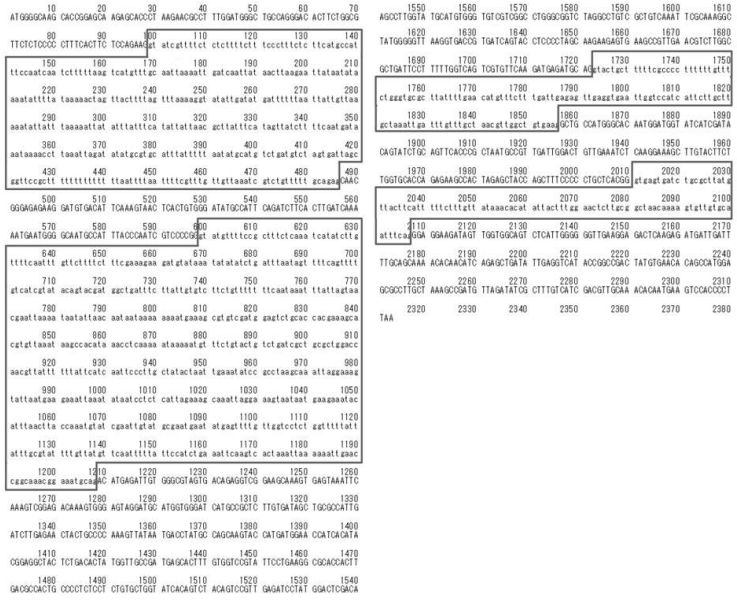
IP : 14.49.138.138, 2017-11-03 13:30:33



<병귤의 각 조직에서 추출한 RNA를 이용한 CAD 유전자 발현패턴>

1: 꽃잎, 2: 어린 잎, 3-5: 미성숙 과실, 6: 성숙 과실, M: DNA 마커

○ 병귤 CAD 유전자의 게놈 DNA 구조 분석을 위해 병귤의 어린 잎에서 추출한 게놈 DNA PCR을 수행한 결과, 약 2.3kb의 염기서열 분석 결과를 통해 5개의 exon과 4개의 intron 구조를 갖고있는 것을 확인하였다.

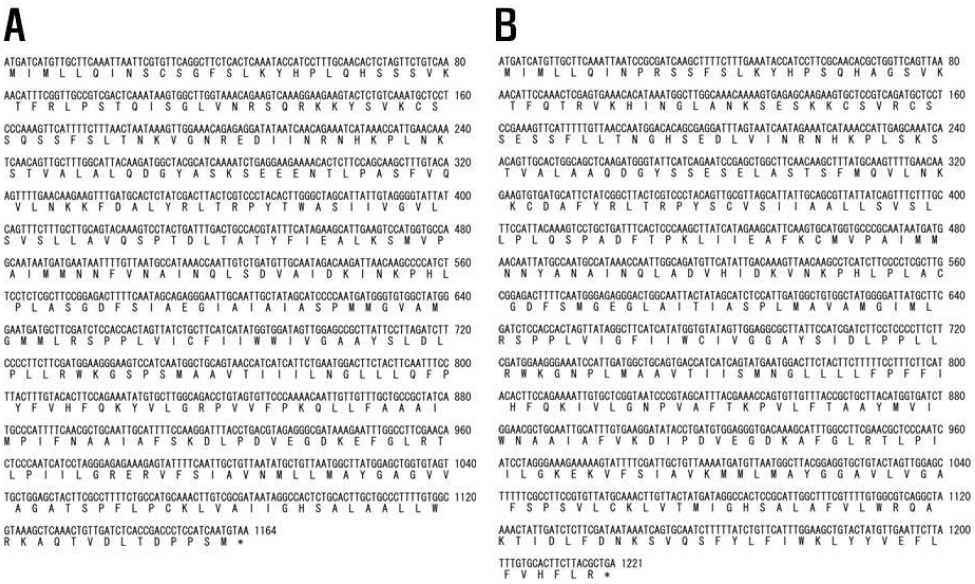


<병귤 CAD 유전자의 게놈 구조>

(박스로 표시된 부분이 intron 영역으로 4개 intron의 총 길이는 1,226bp임)

○ 다양한 스트레스 저항성 또는 항산화 단백질의 prenylation에 관여하는 pathway의 중요 효소로서 목적 단백질의 능력을 배가시키는 기능을 가지고 있는 것으로 보고되어 있는 재래 감귤류 중 당유자에서 높게 발현된다는 것으로 확인된 prenyltransferase 유전자를 RT- PCR법을 이용하여 full-length cDNA에 대한 염기서열 정보를 확인하였다.

IP : 14.49.138.138, 2017-11-03 13:30:33



<병귤 (A)과 당유자 (B)에서 분리한 prenyltransferase의 full-length 염기서열 및 아미노산 서열>

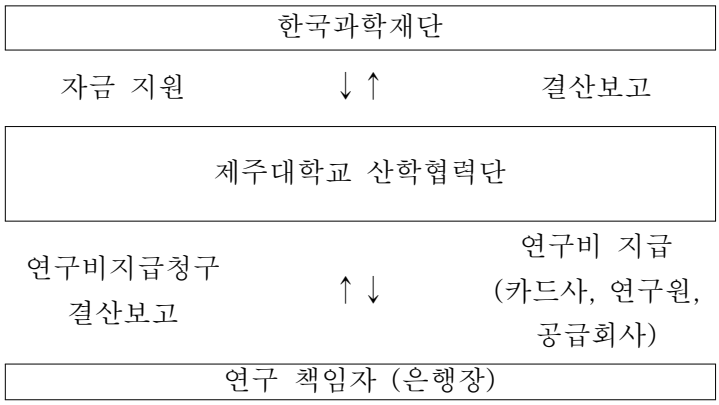
Ⅳ. 운영 및 재정 기반 구축

1.운영 및 재정 기반 구축

1) 자금 집행 체제

한국과학재단에서 지급되는 정부지원금은 정부연구개발 연구비 관리 최상위 등급인 A+을 받은 제주대학교 산학협력단에서 일괄 관리/집행하고 있으며, 연구비(카드) 사용에 따른 집행은 구비서류를 작성하여 산학협력단에 지급 청구함으로써 처리되고 있다.

제주대학교에서 지원되는 대응자금의 경우는 은행 운영에 필요한 기자재를 선정하여 요청하면 산학협력단에서 소정의 절차를 거쳐 기자재를 구입한 후 은행에 배치해 주고 있다.



IP : 14.49.138.138, 2017-11-03 13:30:33

2) 대학지원금

대학의 연구소재은행사업의 지원 확약에 의해 매년 10,000,000원씩 2007-2011년까지 지원받음.

<연구비 집행실적(대학지원금)>

구 분	1차년도 (2007년)	2차년도 (2008년)	3차년도 (2009년)	4차년도 (2010년)	5차년도 (2011년)
대학 지원금	초저온 냉동고: 9,900천원	크린벤치: 4,000천원 교반배양기: 3,000천원 저온배양기: 3,000천원	Digital Cold lab Chamber: 4,900천원 Shaking Incubator: 2,200천원 Hybridization Incubator: 2,600천원 원심분리기: 300천원	초저온 냉동고: 10,000천원	재료비: 10,000천원

■ 자금의 집행체계

-운영비: 한국연구과학재단을 통한 정부지원으로 운영

- 학교측으로부터 행정적인 도움 및 기자재와 공간을 제공

-매년 10,000천원씩 현금 지원으로 기자재 및 재료 구입

■ 예산집행은 제주대학교 산학협력단의 중앙전산시스템을 이용하여 연구비관리규정에 의거 투명하게 집행하였음.

IP : 14.49.138.138, 2017-11-03 13:30:33

3) 재원조달 및 집행의 타당성

《 사업비 확보 및 집행 현황 》

(단위 : 천 원)

연도	이월	정부지원금	계	집행금액	집행잔액	집행내역
2007						
2008						
2009						
2010						
2011						
계						

Ⅴ. 애로 및 건의사항

① 감귤로부터 유용한 유전자와 프로모터를 분리하여 품종 육성에 응용하기 위해서는 다양한 library의 제작, DNA chip과 gel blot을 이용한 발현 분석, 기능분석, 형질 전환체를 이용한 생리기능 규명 등의 작업이 필요하며, 이러한 단계를 통해 목표로 하는 정보를 얻기 위해서는 다년간의 연구가 요구된다. 현재 지원되고 있는 정부지원금으로는 본 소재은행의 주 소재인 감귤 유전자 및 서열정보를 확보하는데 어려움이 많다. 일반적으로 한 가지 소재에 대한 라이브러리 제작, 염기서열 결정 클론 2000개 유전자 확보, 서열정보 분석, database 구축 등에 소요되는 비용이 약 3000-4000만원정도인 것을 감안하면, 실제 연간 정부지원금으로는 한 가지 시료에 대한 유전자 소재를 확보하기도 어렵다.

② 소재은행의 관리 및 활용지원 체계는 소재(DNA, 단백질, 유전자원식물)의 유지 및 품질관리 체계 구축, 소재정보 DB 구축 및 Update, Online/Offline Service System 구축, 소재활용 교육훈련체계 구축(교육프로그램 개발 및 운영), 감귤육종연구자 네트워크 구축(감귤육종연구회 운영 등)등이 관리 활용되고 있으나 현재 과제에 지원된 예산으로는 감귤육종소재의 확충 관리하는데 어려움이 있다.

[기타 제출 사항]

○ 보유 연구소재 목록, 종류별 분양 실적, 발표 논문 내역서

- 확보하고 있는 소재의 현황 및 분양 실적을 구체적으로 파악할 수 있도록 연구소재 목록(**[표 7]**) 및 이를 이용한 발표 논문 실적(**[표 8]**)을 이용하여 제시

IP : 14.49.138.138, 2017-11-03 13:30:33

※ 설명 부분은 삭제 후 제출해 주시기 바라며, 기타 결과에 참고가 되는 자료가 있을 경우 첨부하여 주시기 바랍니다.

IP : 14.49.138.138, 2017-11-03 13:30:33

[기타 제출 사항]

첨부자료 1. 《보유 감귤 유전자의 기능 추정 정보》

1) 온주밀감미숙과실

Clone No.	Accession No.	Definition of Putative homologue[Organism]	Matching %	Matching Length	E-value
CT--07-F-L02.ab1	1909359A	ribosomal protein S19 [Solanum tuberosum]	93.9394	33	5.97E-11
CT--07-F-L04.ab1	1909359A	ribosomal protein S19 [Solanum tuberosum]	95.4545	66	9.36E-31
CT--04-F-L09.ab1	1909359B	ribosomal protein L7 [Solanum tuberosum]	92.3077	39	1.83E-07
CT--02-F-M20.ab1	1APX_A	Chain A, Crystal Structure Of Recombinant Ascorbate Peroxidase	95.2381	63	1.68E-17
CT--02-F-M03.ab1	2114378A	aminolevulinate dehydratase [Lycopersicon esculentum]	94.6237	93	3.20E-44
CT--07-F-N15.ab1	A46304	homeotic protein HAT4 - Arabidopsis thaliana	56	100	7.43E-20
CT--02-F-H02.ab1	A47557	S-like ribonuclease RNS2 - Arabidopsis thaliana	55.8824	34	0.00488481
CT--04-F-G06.ab1	A57478	serine O-acetyltransferase - watermelon	88.8889	99	1.16E-44
CT--01-F-F21.ab1	A60671	tubulin alpha chain - sea urchin	100	25	2.99E-07
CT--01-F-C14.ab1	AAA18550	putative, proteolipid subunit of vacuolar H+ ATPase [Zea mays]	100	28	3.52E-07
CT--04-F-B04.ab1	AAA56908	homeobox protein [Arabidopsis thaliana]	42.1488	121	7.84E-09
CT--04-F-C08.ab1	AAA80678	small GTP-binding protein [Lycopersicon esculentum]	83.5821	67	1.23E-26
CT--06-F-E03.ab1	AAA96253	GF14omega isoform [Arabidopsis thaliana]	87.5	40	4.28E-14
CT--03-F-N24.ab1	AAA99934	vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]	95.0495	101	5.67E-27
CT--04-F-G15.ab1	AAB05871	PAPS-reductase-like protein [Catharanthus roseus]	88.8889	45	3.38E-16
CT--06-F-B17.ab1	AAB17193	laccase [Liriodendron tulipifera]	86.747	83	2.90E-42
CT--02-F-G17.ab1	AAB62892	catalase-1 [Nicotiana glutinosa]	83.7209	43	3.66E-16
CT--07-F-O06.ab1	AAB62947	LTCOR11 [Lavatera thuringiaca]	69.3548	62	3.87E-24
CT--01-F-H05.ab1	AAB64207	elongation factor 1-alpha [Zea mays]	98.4496	129	3.23E-69
CT--07-F-B06.ab1	AAB65494	hypothetical protein; 51018-49636 [Arabidopsis thaliana]	71.4286	77	6.96E-27
CT--05-F-A15.ab1	AAB70426	Strong similarity to 60S ribosomal protein L17 . EST gb|AA042332 comes from this gene. [Arabidopsis thaliana]	100	33	2.06E-12
CT--07-F-A08.ab1	AAB70433	Similar to Babesia aldo-keto reductase . [Arabidopsis thaliana]	58.4158	101	2.99E-26
CT--04-F-L02.ab1	AAB80624	Strong similarity to Arabidopsis ATHSAR1 . ESTs gb|T44122,gb|N65276,gb|AA041135 come from this gene. [Arabidopsis thaliana]	69.8113	53	4.48E-08
CT--05-F-O01.ab1	AAB86513	putative ribosomal protein S4 [Arabidopsis thaliana]	92	75	6.37E-35
CT--06-F-P02.ab1	AAB97312	salt stress inducible small GTP binding protein Ran1 homolog [Arabidopsis thaliana]	100	36	0.000220963
CT--01-F-P09.ab1	AAC09388	xyloglucan endotransglycosylase precursor [Actinidia deliciosa]	80.2469	81	3.03E-39
CT--02-F-D16.ab1	AAC09388	xyloglucan endotransglycosylase precursor [Actinidia deliciosa]	84.4262	122	2.10E-64
CT--03-F-L05.ab1	AAC12797	adenosine triphosphatase; c-subunit of V-ATPase [Vigna radiata]	100	65	4.01E-21
CT--02-F-C24.ab1	AAC15992	chlorophyll a/b binding protein [Oryza sativa]	95.8904	73	5.08E-36
CT--04-F-J16.ab1	AAC16012	polyubiquitin [Elaeagnus umbellata]	98.1818	110	3.19E-55
CT--05-F-A11.ab1	AAC24588	late embryogenesis-like protein [Prunus armeniaca]	86.2069	29	2.52E-07
CT--07-F-P21.ab1	AAC32121	probable 40S ribosomal protein S15 [Picea mariana]	100	67	6.29E-33
CT--07-F-E14.ab1	AAC32140	probable ubiquitin activating enzyme 2 [Picea mariana]	54.5455	33	2.88E-06

IP : 14.49.138.138, 2017-11-03 13:30:33

CT--07-F-F02.ab1	AAC34983	light harvesting chlorophyll A/B binding protein [Prunus persica]	76.7442	129	8.85E-50
CT--02-F-A18.ab1	AAC36058	calmodulin [Oryza sativa]	100	59	8.34E-27
CT--05-F-H01.ab1	AAC72543	unknown [Oryza sativa] [Oryza sativa]	52.4272	103	9.62E-24
CT--01-F-D04.ab1	AAD03486	MADS1 [Corylus avellana]	77.5	40	8.16E-12
CT--03-F-K12.ab1	AAD09518	NTGP4 [Nicotiana tabacum]	72.1649	97	4.84E-29
CT--02-F-E22.ab1	AAD24540	vacuole-associated annexin VCaB42 [Nicotiana tabacum]	82.1782	101	1.30E-41
CT--01-F-G23.ab1	AAD25793	Belongs to PF|00583 Acetyltransfersase family. [Arabidopsis thaliana]	94.2857	35	7.70E-13
CT--01-F-B21.ab1	AAD27590	elongation factor 1-alpha 1; EF-1-alpha1 [Lilium longiflorum]	100	29	3.23E-09
CT--06-F-L04.ab1	AAD27878	chlorophyll a/b binding protein CP29 [Vigna radiata]	72.2222	72	8.74E-19
CT--04-F-N10.ab1	AAD27882	chlorophyll a/b-binding protein CP24 precursor [Vigna radiata]	90.7563	119	8.82E-61
CT--07-F-A11.ab1	AAD33072	secretory peroxidase [Nicotiana tabacum]	55.8824	34	0.00492078
CT--01-F-N04.ab1	AAD39034	MADS-box protein MADS3 [Nicotiana sylvestris]	95.7746	142	9.41E-71
CT--03-F-D11.ab1	AAD43150	Unknown Protein [Arabidopsis thaliana]	54.902	51	1.40E-10
CT--05-F-E12.ab1	AAD50034	Very similar to SRG1 [Arabidopsis thaliana]	36.9565	46	0.00149445
CT--01-F-G17.ab1	AAF13094	unknown protein [Arabidopsis thaliana]	96.2264	53	6.02E-23
CT--04-F-A18.ab1	AAF13094	unknown protein [Arabidopsis thaliana]	95.3488	43	4.51E-17
CT--05-F-P10.ab1	AAF16753	F3M18.15 [Arabidopsis thaliana]	42.0455	88	2.35E-09
CT--06-F-H23.ab1	AAF17236	adenosine-5'-phosphosulfate kinase [Zea mays]	86.2069	29	2.78E-12
CT--01-F-K10.ab1	AAF21428	suppressor of K+ transport growth defect-like protein [Mesembryanthemum crystallinum]	74.4681	47	2.83E-13
CT--01-F-G14.ab1	AAF24583	F22C12.2 [Arabidopsis thaliana]	96	50	3.20E-22
CT--05-F-C10.ab1	AAF27917	nascent polypeptide associated complex alpha chain [Pinus taeda]	88.6364	44	1.65E-14
CT--03-F-L20.ab1	AAF34800	60S ribosomal protein L35 [Euphorbia esula]	96.1538	78	8.41E-35
CT--04-F-I23.ab1	AAF37726	LMW heat shock protein [Euphorbia esula]	60.4938	81	1.18E-18
CT--03-F-H09.ab1	AAF40462	ESTs gb|T76891 and gb|T21582 come from this gene. [Arabidopsis thaliana]	55	60	1.27E-08
CT--04-F-L04.ab1	AAF48120	nbA gene product [Drosophila melanogaster]	50	32	0.0416569
CT--02-F-F15.ab1	AAF60293	chaperonin 21 precursor [Lycopersicon esculentum]	80	70	8.60E-28
CT--06-F-K03.ab1	AAF61440	papain-like cysteine proteinase isoform I [Ipomoea batatas]	97.2603	73	6.90E-39
CT--07-F-D21.ab1	AAF63200	caffeic acid O-3-methyltransferase [Populus tomentosa]	41.7722	158	7.56E-20
CT--07-F-E10.ab1	AAF63824	hypothetical protein [Arabidopsis thaliana]	77.3585	53	2.24E-12
CT--07-F-E12.ab1	AAF63824	hypothetical protein [Arabidopsis thaliana]	76.087	46	1.02E-08
CT--07-F-P01.ab1	AAF64170	plastid ribosomal protein S9 precursor [Spinacia oleracea]	69.2982	114	2.59E-36
CT--03-F-B20.ab1	AAF64457	ribosomal protein L18 [Oreochromis niloticus]	100	15	0.0949927
CT--06-F-B01.ab1	AAF65155	2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase [Catharanthus roseus]	45.283	106	2.46E-11
CT--04-F-A14.ab1	AAF71695	phospholipid transfer protein [Aerides japonica]	70.2703	37	6.21E-08
CT--04-F-L03.ab1	AAF73016	ubiquitin conjugating protein [Avicennia marina]	97.9452	146	4.00E-82
CT--06-F-P15.ab1	AAF78279	Contains similarity to unknown protein F27F5.5 gi|7767655 from Arabidopsis thaliana F27F5 gb|AC007915 and contains a DedA PF|00597 domain. EST gb|T44906 comes from this gene	44.8276	58	2.93E-06
CT--02-F-G19.ab1	AAF78382	T10O22.21 [Arabidopsis thaliana]	71.831	71	3.27E-27
CT--06-F-D02.ab1	AAF79239	F10B6.22 [Arabidopsis thaliana]	72.9412	85	3.74E-30
CT--05-F-A05.ab1	AAF79517	F21D18.7 [Arabidopsis thaliana]	57.1429	77	7.82E-17
CT--07-F-H18.ab1	AAF80655	It is a member of an Uncharacterised protein family PF|01894. ESTs gb|T43915, gb|AA395185 and gb|AI997079 come from this gene.	87.7193	57	5.97E-25

IP : 14.49.138.138, 2017-11-03 13:30:33

		[Arabidopsis thaliana]			
CT--04-F-O24.ab1	AAF82212	Contains similarity to an unknown protein F7A7_100 gi|7327817 from Arabidopsis thaliana BAC F7A7 gb|AL161946. ESTs gb|N65842, gb|F19836 and gb|AI993679 come from this gene	60.6897	145	5.55E-47
CT--06-F-I20.ab1	AAF82212	Contains similarity to an unknown protein F7A7_100 gi|7327817 from Arabidopsis thaliana BAC F7A7 gb|AL161946. ESTs gb|N65842, gb|F19836 and gb|AI993679 come from this gene	87.1795	39	1.06E-15
CT--02-F-A11.ab1	AAF97276	Contains similarity to RING-H2 finger protein RHG1a from Arabidopsis thaliana gb|AF079183 and contains a Zinc finger PF|00097 domain. EST gb|AV522036 comes from this gene	67.3077	52	1.65E-18
CT--07-F-M23.ab1	AAF98369	patatin-like protein 3 [Nicotiana tabacum]	55.8824	68	2.92E-16
CT--02-F-O10.ab1	AAF99846	Unknown protein [Arabidopsis thaliana]	64	50	0.000655512
CT--03-F-G06.ab1	AAG09086	Unknown Protein [Arabidopsis thaliana]	100	28	5.88E-09
CT--01-F-E24.ab1	AAG10600	MYB-related transcription factor PHAN1 [Pisum sativum]	75.2294	109	9.47E-44
CT--02-F-P12.ab1	AAG13068	Similar to cytokinin oxidase [Arabidopsis thaliana]	69.8413	126	1.16E-44
CT--07-F-F05.ab1	AAG23847	RUB1 conjugating enzyme [Lycopersicon esculentum]	85.7143	49	1.49E-19
CT--07-F-E24.ab1	AAG27431	QM-like protein [Elaeis guineensis]	79.0123	81	3.56E-30
CT--02-F-E02.ab1	AAG34813	glutathione S-transferase GST 23 [Glycine max]	69.697	33	1.14E-07
CT--02-F-F23.ab1	AAG34872	In2-1 protein [Glycine max]	76.8595	121	3.52E-53
CT--02-F-O06.ab1	AAG38522	lectin-related protein precursor [Citrus x paradisi]	44.6154	130	1.23E-20
CT--07-F-L24.ab1	AAG38522	lectin-related protein precursor [Citrus x paradisi]	100	61	3.38E-28
CT--01-F-O11.ab1	AAG40371	AT4g27960 [Arabidopsis thaliana]	97.8947	95	1.67E-51
CT--02-F-P11.ab1	AAG40386	AT5g02160 [Arabidopsis thaliana]	87.2727	55	1.38E-21
CT--06-F-N11.ab1	AAG52341	hypothetical protein; 86186-84430 [Arabidopsis thaliana]	59.7826	92	4.14E-23
CT--07-F-A13.ab1	AAG59894	phosphoethanolamine N-methyltransferase [Lycopersicon esculentum]	77.7778	36	2.23E-11
CT--06-F-J12.ab1	AAK00965	putative ubiquitin-conjugating enzyme E2 [Oryza sativa]	100	23	1.74E-06
CT--06-F-P04.ab1	AAK01235	minor allergen hazelnut profilin [Corylus avellana]	95.4545	44	3.85E-18
CT--04-F-E10.ab1	AAK16172	putative glucosyltransferase [Oryza sativa]	52.1277	94	1.47E-23
CT--02-F-C23.ab1	AAK25760	ribosomal protein L33 [Castanea sativa]	91.4894	94	3.60E-46
CT--05-F-N09.ab1	AAK25904	unknown protein [Arabidopsis thaliana]	82.1429	28	2.91E-07
CT--01-F-O10.ab1	AAK27801	60S ribosomal protein L21 [Oryza sativa]	100	28	2.06E-09
CT--01-F-K15.ab1	AAK31146	unknown [Arabidopsis thaliana]	55.814	43	0.000545211
CT--04-F-I24.ab1	AAK38665	stem secoisolariciresinol dehydrogenase [Forsythia x intermedia]	67.8261	115	5.47E-38
CT--04-F-M06.ab1	AAK43709	ribosomal protein L32 [Mercurialis annua]	77.907	86	7.29E-31
CT--02-F-L04.ab1	AAK48956	Unknown protein [Arabidopsis thaliana]	83.7209	43	3.42E-17
CT--03-F-B24.ab1	AAK49947	TGF-beta receptor-interacting protein 1 [Phaseolus vulgaris]	95.6522	115	3.20E-60
CT--01-F-L10.ab1	AAK52587	Putative NADPH-dependent oxidoreductase [Oryza sativa]	54.7945	73	1.72E-20
CT--07-F-D11.ab1	AAK52587	Putative NADPH-dependent oxidoreductase [Oryza sativa]	61.6071	112	2.95E-37
CT--01-F-P14.ab1	AAK55776	Putative small nuclear ribonucleoprotein G [Oryza sativa]	86.2069	29	1.26E-06
CT--03-F-N11.ab1	AAK55776	Putative small nuclear ribonucleoprotein G [Oryza sativa]	84.6154	26	8.82E-05
CT--01-F-F11.ab1	AAK58693	sinapyl alcohol dehydrogenase [Populus tremuloides]	59.4203	69	8.01E-14
CT--04-F-H06.ab1	AAK62446	putative fructokinase [Arabidopsis thaliana]	76.1905	105	2.67E-41
CT--06-F-O21.ab1	AAK68809	similar to GTP-binding protein [Arabidopsis thaliana]	64.0625	64	1.13E-15
CT--02-F-I18.ab1	AAK93649	unknown protein [Arabidopsis thaliana]	72.3077	65	1.76E-24
CT--07-F-I18.ab1	AAK93649	unknown protein [Arabidopsis thaliana]	70	30	6.73E-07
CT--06-F-N10.ab1	AAK94781	gamma hydroxybutyrate dehydrogenase [Arabidopsis thaliana]	77.1429	70	5.24E-16

IP : 14.49.138.138, 2017-11-03 13:30:33

CT--05-F-F14.ab1	AAK95282	AT4g03280/F4C21_21 [Arabidopsis thaliana]	72.3077	130	7.63E-51
CT--01-F-F17.ab1	AAK95517	cyclase [Nicotiana tabacum]	57.1429	105	4.73E-27
CT--04-F-E05.ab1	AAL06348	submergence induced protein-like protein [Musa acuminata]	53.8462	26	0.00101745
CT--03-F-E06.ab1	AAL09401	ribosomal protein [Petunia x hybrida]	82.6923	52	8.16E-12
CT--03-F-C22.ab1	AAL14412	At1g12410/F5O11_7 [Arabidopsis thaliana]	68.0851	47	1.25E-13
CT--05-F-O11.ab1	AAL14412	At1g12410/F5O11_7 [Arabidopsis thaliana]	59.0909	88	7.13E-31
CT--02-F-O19.ab1	AAL16282	At1g18030/T10F20_3 [Arabidopsis thaliana]	53.3784	148	6.03E-27
CT--03-F-F05.ab1	AAL24258	At1g47530/F16N3_20 [Arabidopsis thaliana]	65.625	32	9.72E-05
CT--05-F-D11.ab1	AAL24269	AT5g51550/K17N15_10 [Arabidopsis thaliana]	87.7358	106	1.85E-42
CT--02-F-H21.ab1	AAL32441	Fe-superoxide dismutase precursor [Medicago sativa]	81.3953	43	1.36E-15
CT--01-F-F03.ab1	AAL35979	extensin-like protein [Cucumis sativus]	72.7273	22	0.00403855
CT--02-F-D06.ab1	AAL38267	unknown protein [Arabidopsis thaliana]	77.9221	77	8.62E-23
CT--01-F-I18.ab1	AAL38757	unknown protein [Arabidopsis thaliana]	66.1538	130	1.42E-34
CT--02-F-J16.ab1	AAL38841	unknown protein [Arabidopsis thaliana]	81.25	32	3.26E-09
CT--06-F-F21.ab1	AAL38852	unknown protein [Arabidopsis thaliana]	42.6087	115	4.74E-12
CT--06-F-G17.ab1	AAL49750	aquaporin-like protein [Petunia x hybrida]	96.8254	63	5.17E-31
CT--05-F-P20.ab1	AAL62421	ADP-RIBOSYLATION FACTOR -like protein [Arabidopsis thaliana]	97.2973	74	1.64E-35
CT--01-F-J23.ab1	AAL79831	cystatin [Sandersonia aurantiaca]	85.7143	63	7.18E-25
CT--01-F-M11.ab1	AAL86003	putative E2, ubiquitin-conjugating enzyme UBC7 [Arabidopsis thaliana]	86.4286	140	3.46E-65
CT--07-F-D23.ab1	AAL86003	putative E2, ubiquitin-conjugating enzyme UBC7 [Arabidopsis thaliana]	90	50	2.09E-19
CT--01-F-G24.ab1	AAL91164	unknown protein [Arabidopsis thaliana]	78.125	32	1.25E-06
CT--01-F-F19.ab1	AAL91176	eukaryotic translation initiation factor [Arabidopsis thaliana]	97.561	41	2.87E-16
CT--02-F-L14.ab1	AAL93042	hypothetical protein [Dictyostelium discoideum]	38.0952	63	0.00991388
CT--01-F-B16.ab1	AAM10318	MFL8.1/MFL8.1 [Arabidopsis thaliana]	70	40	4.20E-11
CT--02-F-O21.ab1	AAM12880	GTP-binding protein [Helianthus annuus]	99.2188	128	3.12E-74
CT--06-F-N04.ab1	AAM12880	GTP-binding protein [Helianthus annuus]	100	18	0.00455881
CT--05-F-O06.ab1	BAA23657	EF-1 alpha [Oryza sativa]	95.122	41	2.15E-23
CT--04-F-O16.ab1	BAA31561	metallothionein-like protein [Citrus unshiu]	100	39	7.20E-15
CT--07-F-F17.ab1	BAA81870	ESTD24835 corresponds to a region of the predicted gene.~Similar to Arabidopsis thaliana chromosome II BAC T06D20 genomic sequence, complete sequence. [Oryza sativa]	59.322	59	2.42E-14
CT--04-F-E21.ab1	BAA87043	N-hydroxycinnamoyl/benzoyltransferase [Ipomoea batatas]	61.1511	139	3.11E-46
CT--02-F-C22.ab1	BAA88636	elicitor-inducible LRR receptor-like protein EILP [Nicotiana tabacum]	52.459	61	3.63E-11
CT--05-F-P12.ab1	BAA89230	wts2L [Citrullus lanatus]	37.3913	115	1.71E-07
CT--06-F-B04.ab1	BAA90806	ESTs C26000,AU082130 correspond to a region of the predicted gene.~Similar to mRNA for zinc-finger protein [Oryza sativa]	49.0909	55	2.97E-11
CT--02-F-P09.ab1	BAA92699	type 2A protein phosphatase-3 [Vicia faba]	91.7293	133	3.13E-63
CT--01-F-I01.ab1	BAA96453	F1-ATPase [Pyrus pyrifolia]	90.9091	44	2.15E-14
CT--04-F-G04.ab1	BAA97477	gb|AAF17201.1~gene_id:F2O15.9~similar to unknown protein [Arabidopsis thaliana]	69.1176	68	2.09E-17
CT--07-F-M24.ab1	BAB01889	ER lumen protein-retaining receptor-like protein [Arabidopsis thaliana]	85.1064	47	6.94E-15
CT--03-F-L11.ab1	BAB02761	cytochrome c oxidoreductase-like [Arabidopsis thaliana]	48.1481	54	0.000340775
CT--06-F-L18.ab1	BAB02809	contains similarity to EH domain containing proteins~gene_id:MQC12.3 [Arabidopsis thaliana]	77.2152	79	2.18E-31
CT--01-F-A19.ab1	BAB09444	gene_id:MSI17.3~unknown protein [Arabidopsis thaliana]	54.5455	44	0.0236219

IP : 14.49.138.138, 2017-11-03 13:30:33

CT--04-F-L06.ab1	BAB09970	contains similarity to chalcone-flavonone isomerase ~gene_id:K18I23.7 [Arabidopsis thaliana]	69.1489	94	1.29E-27
CT--04-F-K02.ab1	BAB10495	gene_id:K21I16.3~unknown protein [Arabidopsis thaliana]	68.9655	29	0.000215199
CT--04-F-N06.ab1	BAB10495	gene_id:K21I16.3~unknown protein [Arabidopsis thaliana]	63.5294	85	3.34E-20
CT--07-F-K07.ab1	BAB10643	cleavage stimulation factor subunit 1-like protein [Arabidopsis thaliana]	82.7586	29	8.37E-06
CT--03-F-M14.ab1	BAB11028	gene_id:MUL8.23~pir||S77152~similar to unknown protein [Arabidopsis thaliana]	70.3704	27	0.00321842
CT--03-F-I01.ab1	BAB11233	6-phosphogluconolactonase-like protein [Arabidopsis thaliana]	60.2564	78	5.37E-20
CT--07-F-P22.ab1	BAB11233	6-phosphogluconolactonase-like protein [Arabidopsis thaliana]	57.971	69	3.89E-24
CT--01-F-A18.ab1	BAB11565	14-3-3 protein GF14 [Arabidopsis thaliana]	84.058	138	2.52E-61
CT--03-F-J04.ab1	BAB17821	vf14-3-3c protein [Vicia faba]	96.1538	52	4.07E-22
CT--07-F-G16.ab1	BAB20580	response regulator 5 [Zea mays]	88.3721	43	7.69E-14
CT--04-F-D05.ab1	BAB32723	contains ESTs AU030293,AU030294~similar to Arabidopsis thaliana chromosome 4, F9D16.100~unknown protein [Oryza sativa]	75.6098	82	1.10E-30
CT--02-F-P10.ab1	BAB32914	contains ESTs AU029632,AU162277~similar to Arabidopsis thaliana chromosome 3 T6K12.29~unknown protein [Oryza sativa]	76.2712	59	1.92E-23
CT--02-F-L02.ab1	BAB40128	hypothetical protein~similar to Arabidopsis thaliana F13M22.18 [Oryza sativa]	80.7692	26	4.10E-05
CT--02-F-I02.ab1	BAB40142	plasma membrane intrinsic protein 1-1 [Pyrus communis]	67.2414	58	1.44E-19
CT--07-F-B18.ab1	BAB40143	plasma membrane intrinsic protein 2-2 [Pyrus communis]	83.1169	77	3.66E-23
CT--02-F-N05.ab1	BAB59136	casein kinase II alpha [Triticum aestivum]	88.8889	18	0.0636322
CT--01-F-J14.ab1	BAB60678	geranylgeranyl diphosphate synthase [Hevea brasiliensis]	43.5644	101	4.97E-15
CT--07-F-H16.ab1	BAB63491	contains ESTs AU100716,AU029967,C26395~hypothetical protein~similar to Arabidopsis thaliana chromosome 2, At2g25910 [Oryza sativa]	85.7143	35	1.84E-10
CT--02-F-B16.ab1	BAB64099	putative photosystem II subunit precursor [Oryza sativa]	87.3684	95	7.59E-44
CT--04-F-D13.ab1	BAB67953	putative auxin-induced protein [Oryza sativa]	61.0169	59	6.05E-13
CT--04-F-N07.ab1	BAB67953	putative auxin-induced protein [Oryza sativa]	47.7612	67	5.30E-06
CT--05-F-B04.ab1	BAB67953	putative auxin-induced protein [Oryza sativa]	55.9322	59	3.75E-11
CT--04-F-D03.ab1	BAB78597	copper/zinc superoxide dismutase [Bruguiera gymnorrhiza]	89.0244	82	3.38E-31
CT--07-F-F13.ab1	BAB88934	glucosyltransferase NTGT3 [Nicotiana tabacum]	50	126	8.33E-25
CT--07-F-M10.ab1	BAB88939	Rurm1 [Oryza sativa]	72.5275	91	2.67E-31
CT--03-F-H24.ab1	BAB89352	1-aminocyclopropane-1-carboxylate oxidase [Diospyros kaki]	93.1818	44	1.20E-25
CT--03-F-K13.ab1	CAA09042	40S ribosomal protein S6 [Cicer arietinum]	90	60	4.11E-12
CT--03-F-I08.ab1	CAA09603	20S proteasome beta subunit [Cicer arietinum]	87.1795	39	1.40E-14
CT--07-F-O15.ab1	CAA11553	2-oxoglutarate dehydrogenase E2 subunit [Arabidopsis thaliana]	90.4762	42	2.14E-16
CT--02-F-C09.ab1	CAA12199	caffeoyl-CoA 3-O-methyltransferase [Populus balsamifera subsp. trichocarpa]	85.2459	61	1.27E-24
CT--05-F-I15.ab1	CAA18194	putative protein [Arabidopsis thaliana]	87.5	56	1.50E-08
CT--02-F-P20.ab1	CAA63107	ribosomal protein L23 [Spinacia oleracea]	98.5507	69	2.26E-20
CT--07-F-B01.ab1	CAA66034	peroxidase [Populus balsamifera subsp. trichocarpa]	55.5556	36	0.0110759
CT--02-F-M10.ab1	CAA67969	MADS5 protein [Betula pendula]	75	28	0.000175379
CT--07-F-I22.ab1	CAA75386	3-deoxy-D-arabino-heptulosonate 7-phosphate synthase; 2-dehydro-3-deoxyphosphoheptonate aldolase [Morinda citrifolia]	87.8788	33	4.07E-10
CT--02-F-H10.ab1	CAB09799	hypothetical protein [Citrus x paradisi]	97.2973	37	8.77E-15
CT--06-F-A01.ab1	CAB42658	iron sulfur subunit of succinate dehydrogenase and ribosomal protein S14 [Zea mays]	72.3404	94	5.86E-33
CT--02-F-I12.ab1	CAB45387	NAD-malate dehydrogenase [Nicotiana tabacum]	86.8421	38	3.76E-11
CT--02-F-G20.ab1	CAB72130	heat shock protein 70 [Cucumis sativus]	87.234	47	1.00E-07
CT--02-F-K20.ab1	CAB85625	putative ripening-related protein [Vitis vinifera]	70.4225	71	4.24E-25

IP : 14.49.138.138, 2017-11-03 13:30:33

CT--03-F-O11.ab1	CAB90214	putative elongation factor 1 beta [Hordeum vulgare subsp. vulgare]	85.5072	69	4.35E-28
CT--04-F-B13.ab1	CAB90214	putative elongation factor 1 beta [Hordeum vulgare subsp. vulgare]	84.7222	72	9.28E-30
CT--02-F-P05.ab1	CAC12882	O-linked GlcNAc transferase like [Nicotiana tabacum]	85	40	5.00E-12
CT--02-F-L10.ab1	CAC34489	putative protein [Arabidopsis thaliana]	66.2162	74	1.83E-17
CT--01-F-L21.ab1	CAC39061	putative protein [Oryza sativa]	87.0968	31	2.14E-08
CT--03-F-O04.ab1	CAC39071	DnaJ-like protein [Oryza sativa]	64.5161	62	8.21E-12
CT--05-F-C09.ab1	CAC83750	reversibly glycosylated polypeptide [Gossypium hirsutum]	74.4681	47	2.98E-13
CT--03-F-H15.ab1	CAC84489	putative translation factor [Pinus pinaster]	88.4956	113	3.85E-48
CT--04-F-E23.ab1	CAC84547	dicarboxylate/tricarboxylate carrier [Nicotiana tabacum]	94.5946	37	4.43E-15
CT--04-F-G01.ab1	CAC86996	ATP citrate lyase b-subunit [Lupinus albus]	83.8983	118	7.11E-52
CT--03-F-N04.ab1	CAD21142	ribosome-associated protein [Neurospora crassa]	49.1803	122	7.16E-31
CT--02-F-A06.ab1	H71409	hypothetical protein - Arabidopsis thaliana	41.5094	159	6.63E-18
CT--02-F-L06.ab1	JC2511	beta-tubulin R2242 - rice	100	42	1.03E-18
CT--02-F-H14.ab1	NP_027545	expressed protein [Arabidopsis thaliana]	86.6667	45	2.58E-23
CT--02-F-N15.ab1	NP_084540	hypothetical protein MGC6623 [Mus musculus]	91.5663	83	6.69E-41
CT--04-F-F17.ab1	NP_171963	putative K+ channel, beta subunit [Arabidopsis thaliana]	86.6667	75	8.61E-31
CT--02-F-N14.ab1	NP_172094	salt-tolerance protein [Arabidopsis thaliana]	54.6512	86	1.05E-17
CT--04-F-G08.ab1	NP_172638	Avr9 elicitor response-like protein [Arabidopsis thaliana]	41.4286	70	5.17E-05
CT--02-F-B17.ab1	NP_172893	DNA-binding protein p24, putative [Arabidopsis thaliana]	69.2308	52	1.77E-18
CT--04-F-D14.ab1	NP_173079	hypothetical protein [Arabidopsis thaliana]	72.7273	55	6.58E-33
CT--04-F-M03.ab1	NP_173114	NADH:ubiquinone oxidoreductase, putative [Arabidopsis thaliana]	100	17	0.0134538
CT--02-F-A02.ab1	NP_173261	pathogenesis-related group 5 protein, putative [Arabidopsis thaliana]	66.6667	72	2.36E-24
CT--02-F-G12.ab1	NP_173387	GSH-dependent dehydroascorbate reductase 1, putative [Arabidopsis thaliana]	75.8621	87	1.53E-34
CT--03-F-F17.ab1	NP_173923	transmembrane protein, putative [Arabidopsis thaliana]	79.0323	62	4.11E-22
CT--03-F-J18.ab1	NP_174108	hypothetical protein [Arabidopsis thaliana]	36.7347	49	0.0928019
CT--02-F-F20.ab1	NP_174210	19S proteosome subunit 9, putative [Arabidopsis thaliana]	91.1111	90	8.81E-41
CT--06-F-D04.ab1	NP_174351	coatomer-like protein, epsilon subunit [Arabidopsis thaliana]	84.375	96	1.85E-34
CT--01-F-I08.ab1	NP_174376	hypothetical protein [Arabidopsis thaliana]	60	55	5.86E-12
CT--05-F-L01.ab1	NP_175482	unknown protein [Arabidopsis thaliana]	90.9091	44	2.98E-18
CT--07-F-I24.ab1	NP_175517	histone H2A, putative [Arabidopsis thaliana]	100	76	6.65E-26
CT--03-F-L18.ab1	NP_175576	epsilon subunit of mitochondrial F1-ATPase [Arabidopsis thaliana]	89.8551	69	5.05E-32
CT--03-F-B09.ab1	NP_175641	protein kinase, putative [Arabidopsis thaliana]	87.8049	41	3.20E-14
CT--01-F-B12.ab1	NP_175669	signal peptidase subunit, putative [Arabidopsis thaliana]	94.9153	59	3.63E-26
CT--07-F-D12.ab1	NP_175963	photosystem I subunit V precursor, putative [Arabidopsis thaliana]	94.5946	37	6.17E-28
CT--01-F-E12.ab1	NP_176075	integral membrane protein, putative [Arabidopsis thaliana]	80	70	3.33E-27
CT--01-F-E20.ab1	NP_176291	ferrodoxin precursor [Arabidopsis thaliana]	89.2857	28	2.01E-08
CT--01-F-C23.ab1	NP_176395	symbiosis-related protein, putative [Arabidopsis thaliana]	92.0354	113	2.07E-54
CT--02-F-P07.ab1	NP_176568	unknown protein [Arabidopsis thaliana]	57.2414	145	1.16E-42
CT--04-F-G18.ab1	NP_178073	phosphoglycerate kinase, putative [Arabidopsis thaliana]	94.5652	92	1.23E-43
CT--02-F-D13.ab1	NP_178163	hypothetical protein [Arabidopsis thaliana]	84.9057	53	6.54E-21

IP : 14.49.138.138, 2017-11-03 13:30:33

CT--02-F-J06.ab1	NP_178204	unknown protein [Arabidopsis thaliana]	68.1818	22	6.19E-05
CT--03-F-L06.ab1	NP_178453	putative esterase [Arabidopsis thaliana]	42.8571	49	3.18E-05
CT--03-F-K02.ab1	NP_179558	copia-like retroelement pol polyprotein [Arabidopsis thaliana]	100	31	1.30E-12
CT--05-F-A24.ab1	NP_179646	putative heat shock protein [Arabidopsis thaliana]	65.3846	52	1.37E-14
CT--05-F-C23.ab1	NP_179713	putative triosephosphate isomerase [Arabidopsis thaliana]	100	18	0.0231644
CT--04-F-P09.ab1	NP_179822	putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	37.6623	77	1.19E-09
CT--01-F-N06.ab1	NP_180719	40S ribosomal protein; contains C-terminal domain [Arabidopsis thaliana]	94.4444	126	2.88E-61
CT--05-F-H17.ab1	NP_180831	putative cytochrome b5 [Arabidopsis thaliana]	86.6667	45	2.98E-31
CT--02-F-J24.ab1	NP_180879	mitochondrial chaperonin [Arabidopsis thaliana]	68.1818	44	1.06E-10
CT--05-F-J21.ab1	NP_180909	hypothetical protein [Arabidopsis thaliana]	52.2727	88	7.20E-17
CT--04-F-J21.ab1	NP_181046	putative thioredoxin [Arabidopsis thaliana]	60.8696	46	3.48E-09
CT--05-F-K22.ab1	NP_181057	glycine decarboxylase complex H-protein [Arabidopsis thaliana]	80.5755	139	6.01E-60
CT--01-F-I16.ab1	NP_181187	putative fructose bisphosphate aldolase [Arabidopsis thaliana]	89.7959	49	5.92E-18
CT--04-F-F12.ab1	NP_181196	putative receptor-like protein kinase [Arabidopsis thaliana]	75.8621	29	2.26E-06
CT--01-F-N23.ab1	NP_181277	putative protein translocase [Arabidopsis thaliana]	70	30	0.000991503
CT--06-F-H04.ab1	NP_181674	ERD15 protein [Arabidopsis thaliana]	76.9231	65	2.20E-26
CT--03-F-I23.ab1	NP_181827	putative APG isolog protein [Arabidopsis thaliana]	44.8598	107	7.29E-26
CT--04-F-D01.ab1	NP_181874	60S ribosomal protein L38 [Arabidopsis thaliana]	94.2029	69	1.05E-31
CT--01-F-I04.ab1	NP_182109	putative AT-hook DNA-binding protein [Arabidopsis thaliana]	42.3913	92	1.79E-06
CT--02-F-K09.ab1	NP_186983	unknown protein [Arabidopsis thaliana]	72	25	0.0112211
CT--02-F-M07.ab1	NP_187142	putative mitogen activated protein kinase kinase [Arabidopsis thaliana]	45.5224	134	1.02E-22
CT--06-F-B05.ab1	NP_187420	putative P-protein: chorismate mutase, prephenate dehydratase [Arabidopsis thaliana]	91.3043	23	5.26E-05
CT--07-F-P13.ab1	NP_187780	hypothetical protein [Arabidopsis thaliana]	69.6429	56	1.01E-15
CT--01-F-B19.ab1	NP_187865	unknown protein [Arabidopsis thaliana]	73.1707	41	3.86E-10
CT--06-F-N03.ab1	NP_188422	hypothetical protein [Arabidopsis thaliana]	41.1765	102	2.74E-06
CT--01-F-K22.ab1	NP_189339	hypothetical protein [Arabidopsis thaliana]	66.6667	66	3.46E-21
CT--02-F-C04.ab1	NP_189421	50S ribosomal protein L12-A [Arabidopsis thaliana]	57.5758	66	1.63E-11
CT--02-F-N09.ab1	NP_189984	ribosomal S29 -like protein [Arabidopsis thaliana]	87.5	56	4.77E-26
CT--04-F-L22.ab1	NP_189996	putative protein [Arabidopsis thaliana]	53.8462	130	7.78E-33
CT--03-F-O24.ab1	NP_190278	dUTP pyrophosphatase-like protein [Arabidopsis thaliana]	79.3103	29	9.28E-06
CT--03-F-H16.ab1	NP_190735	putative protein [Arabidopsis thaliana]	60.4651	43	4.76E-06
CT--04-F-O05.ab1	NP_191007	putative protein [Arabidopsis thaliana]	80.2469	81	1.68E-27
CT--03-F-J08.ab1	NP_191507	fructokinase-like protein [Arabidopsis thaliana]	81.0526	95	3.67E-39
CT--01-F-C10.ab1	NP_191681	putative protein [Arabidopsis thaliana]	61.6438	73	5.87E-19
CT--02-F-F12.ab1	NP_191705	RING finger protein [Arabidopsis thaliana]	57.9832	119	4.72E-29
CT--02-F-I05.ab1	NP_191721	exonuclease RRP41 [Arabidopsis thaliana]	80	25	0.00113106
CT--01-F-L22.ab1	NP_192056	putative water channel protein [Arabidopsis thaliana]	82.7586	87	4.55E-39
CT--03-F-E07.ab1	NP_192170	tryptophan synthase alpha 1-like protein [Arabidopsis thaliana]	84.6154	39	3.42E-11
CT--01-F-O21.ab1	NP_192230	putative xyloglucan endotransglycosylase [Arabidopsis thaliana]	64.5833	96	5.84E-34
CT--07-F-O24.ab1	NP_192634	putative phi-1-like phosphate-induced protein [Arabidopsis thaliana]	67.1875	64	4.80E-21

IP : 14.49.138.138, 2017-11-03 13:30:33

CT--01-F-H18.ab1	NP_193202	RNA polymerase II fifth largest subunit like protein [Arabidopsis thaliana]	66.3793	116	9.60E-45
CT--04-F-J11.ab1	NP_193313	SYBL1 like protein [Arabidopsis thaliana]	65.3543	127	4.05E-37
CT--04-F-N24.ab1	NP_193718	putative protein [Arabidopsis thaliana]	56.1404	171	4.48E-41
CT--04-F-L14.ab1	NP_194071	water channel - like protein [Arabidopsis thaliana]	97.1429	35	1.22E-14
CT--03-F-J22.ab1	NP_194296	putative protein [Arabidopsis thaliana]	46.3415	41	0.00254915
CT--06-F-E04.ab1	NP_194319	putative acidic ribosomal protein [Arabidopsis thaliana]	86.9565	46	2.13E-14
CT--07-F-L13.ab1	NP_194377	putative protein [Arabidopsis thaliana]	57.5	40	8.41E-08
CT--07-F-N14.ab1	NP_194791	putative protein [Arabidopsis thaliana]	71.9298	57	5.04E-13
CT--04-F-N12.ab1	NP_194842	putative protein [Arabidopsis thaliana]	78.8732	71	1.38E-21
CT--01-F-L12.ab1	NP_195013	putative protein [Arabidopsis thaliana]	44.1176	34	0.00733129
CT--03-F-P16.ab1	NP_195072	putative protein [Arabidopsis thaliana]	61.1111	144	1.33E-32
CT--02-F-L22.ab1	NP_195662	GTP-binding - like protein [Arabidopsis thaliana]	93.1034	29	5.80E-09
CT--03-F-I16.ab1	NP_195825	putative protein [Arabidopsis thaliana]	45.4545	132	4.97E-17
CT--07-F-J01.ab1	NP_195891	putative protein [Arabidopsis thaliana]	73.6111	72	2.37E-33
CT--01-F-O02.ab1	NP_196069	putative protein [Arabidopsis thaliana]	74.0741	54	2.86E-16
CT--01-F-I17.ab1	NP_196082	8-amino-7-oxononanoate synthase - like protein [Arabidopsis thaliana]	64.7059	102	2.44E-34
CT--01-F-O14.ab1	NP_196578	-hydroxymyristoyl- dehydratase -like protein [Arabidopsis thaliana]	94.9153	59	4.26E-25
CT--02-F-P08.ab1	NP_196652	putative protein [Arabidopsis thaliana]	46.25	80	8.10E-11
CT--06-F-G11.ab1	NP_196822	NAM-like protein [Arabidopsis thaliana]	37.9747	79	6.51E-07
CT--07-F-A23.ab1	NP_196845	putative protein [Arabidopsis thaliana]	87.8049	41	1.06E-23
CT--02-F-E08.ab1	NP_197406	putative protein [Arabidopsis thaliana]	70.4	125	1.86E-36
CT--01-F-H24.ab1	NP_197430	phospholipase - like protein [Arabidopsis thaliana]	75	116	1.64E-51
CT--01-F-O06.ab1	NP_197483	putative protein [Arabidopsis thaliana]	86.6667	30	6.11E-06
CT--01-F-L08.ab1	NP_198197	PS I antenna protein Lhca2 fragment [Arabidopsis thaliana]	94.1176	85	1.05E-44
CT--05-F-F12.ab1	NP_198418	putative protein [Arabidopsis thaliana]	95.7447	47	5.37E-19
CT--01-F-A20.ab1	NP_198627	anti-silencing factor 1-like protein [Arabidopsis thaliana]	90	60	1.52E-28
CT--06-F-A16.ab1	NP_198790	ribosomal protein L5 - like [Arabidopsis thaliana]	89.2857	112	6.60E-58
CT--07-F-G05.ab1	NP_198824	putative protein [Arabidopsis thaliana]	73.5294	34	1.75E-14
CT--02-F-N04.ab1	NP_199196	aluminum-induced protein-like [Arabidopsis thaliana]	78.125	64	8.25E-23
CT--06-F-C22.ab1	NP_199326	ras-related GTP-binding protein RHA1 [Arabidopsis thaliana]	94.8052	77	2.12E-35
CT--03-F-F16.ab1	NP_199373	putative protein [Arabidopsis thaliana]	78	50	4.06E-16
CT--01-F-N10.ab1	NP_199544	palmitoyl-protein thioesterase precursor-like [Arabidopsis thaliana]	50	46	2.72E-06
CT--04-F-C17.ab1	NP_199598	putative protein [Arabidopsis thaliana]	81.5789	76	7.78E-33
CT--01-F-F16.ab1	NP_199683	putative protein [Arabidopsis thaliana]	59.8214	112	3.44E-33
CT--05-F-I09.ab1	NP_199687	60S ribosomal protein L13a [Arabidopsis thaliana]	75	40	2.71E-10
CT--04-F-A05.ab1	NP_200119	putative protein [Arabidopsis thaliana]	82.7586	29	3.12E-15
CT--03-F-E12.ab1	NP_200265	putative protein [Arabidopsis thaliana]	28.9855	69	0.0367528
CT--04-F-K09.ab1	NP_200311	FH protein interacting protein FIP2 [Arabidopsis thaliana]	83.7209	86	1.44E-36
CT--04-F-A04.ab1	NP_200560	CCHH finger protein 2-like protein [Arabidopsis thaliana]	74.4186	86	1.74E-24
CT--03-F-O08.ab1	NP_200632	bis-triphosphatase-like; also similar to fragile histidine triad [Arabidopsis thaliana]	75	44	2.24E-12

IP : 14.49.138.138, 2017-11-03 13:30:33

CT--04-F-K21.ab1	NP_200632	bis-triphosphatase-like; also similar to fragile histidine triad [Arabidopsis thaliana]	78.3784	111	7.02E-46
CT--05-F-C11.ab1	NP_200632	bis-triphosphatase-like; also similar to fragile histidine triad [Arabidopsis thaliana]	54.5455	33	0.0416569
CT--01-F-A02.ab1	NP_201035	putative protein [Arabidopsis thaliana]	58.9286	56	5.80E-11
CT--04-F-G23.ab1	NP_201231	phi-1-like protein [Arabidopsis thaliana]	80	90	7.03E-39
CT--06-F-B24.ab1	NP_201242	beta-ureidopropionase [Arabidopsis thaliana]	83.6957	92	8.30E-43
CT--02-F-O23.ab1	NP_229486	conserved hypothetical protein [Thermotoga maritima]	48.7179	39	0.0409626
CT--04-F-H24.ab1	NP_249984	hypothetical protein [Pseudomonas aeruginosa]	31.25	96	0.00020644
CT--04-F-K12.ab1	NP_310552	putative transport protein [Escherichia coli O157:H7]	100	171	1.86E-82
CT--01-F-G12.ab1	NP_502933	Y7A9C.3,p [Caenorhabditis elegans]	31.8841	69	0.0371207
CT--07-F-F21.ab1	NP_563698	expressed protein [Arabidopsis thaliana]	51.4563	103	1.45E-19
CT--01-F-F18.ab1	NP_563780	expressed protein [Arabidopsis thaliana]	90.9091	55	2.68E-25
CT--02-F-H12.ab1	NP_563823	expressed protein [Arabidopsis thaliana]	67.1053	76	8.70E-24
CT--03-F-D18.ab1	NP_564150	expressed protein [Arabidopsis thaliana]	79.2208	77	1.72E-31
CT--06-F-H02.ab1	NP_564308	Expressed protein [Arabidopsis thaliana]	62.8866	97	9.30E-27
CT--01-F-K02.ab1	NP_564334	expressed protein [Arabidopsis thaliana]	35.4545	110	2.34E-07
CT--01-F-P18.ab1	NP_564482	expressed protein [Arabidopsis thaliana]	51.7857	56	1.60E-07
CT--03-F-J23.ab1	NP_564507	expressed protein [Arabidopsis thaliana]	66.6667	48	2.21E-27
CT--02-F-O18.ab1	NP_564748	expressed protein [Arabidopsis thaliana]	40.5797	69	4.16E-05
CT--01-F-D14.ab1	NP_564819	expressed protein [Arabidopsis thaliana]	96.1538	26	1.41E-06
CT--03-F-E17.ab1	NP_564933	Expressed protein [Arabidopsis thaliana]	41.1765	51	0.00146973
CT--02-F-F06.ab1	NP_564974	expressed protein [Arabidopsis thaliana]	60.7143	84	7.95E-18
CT--03-F-M08.ab1	NP_565029	expressed protein [Arabidopsis thaliana]	70	70	4.91E-21
CT--01-F-D16.ab1	NP_565057	Expressed protein [Arabidopsis thaliana]	74.6032	63	2.52E-07
CT--06-F-I11.ab1	NP_565076	expressed protein [Arabidopsis thaliana]	41.2371	97	1.34E-11
CT--06-F-N15.ab1	NP_565206	expressed protein [Arabidopsis thaliana]	43.6364	55	3.19E-07
CT--01-F-O17.ab1	NP_565284	NAM -like protein [Arabidopsis thaliana]	87.931	116	4.83E-57
CT--03-F-F14.ab1	NP_565294	expressed protein [Arabidopsis thaliana]	84.8485	66	1.50E-18
CT--06-F-E01.ab1	NP_565336	expressed protein [Arabidopsis thaliana]	83.3333	90	1.74E-21
CT--01-F-N03.ab1	NP_565409	expressed protein [Arabidopsis thaliana]	65.8537	41	1.16E-11
CT--07-F-B11.ab1	NP_565561	expressed protein [Arabidopsis thaliana]	88.3721	43	7.10E-14
CT--06-F-I22.ab1	NP_565834	E2, ubiquitin-conjugating enzyme, putative [Arabidopsis thaliana]	88.7324	71	5.96E-33
CT--03-F-J16.ab1	NP_565836	ubiquitin extension protein [Arabidopsis thaliana]	100	34	9.32E-15
CT--01-F-L05.ab1	NP_566014	expressed protein [Arabidopsis thaliana]	68.9655	58	4.65E-15
CT--07-F-O04.ab1	NP_566526	expressed protein [Arabidopsis thaliana]	64.4444	90	1.86E-26
CT--06-F-C04.ab1	NP_566535	putative ribosomal protein [Arabidopsis thaliana]	92.7711	83	5.29E-42
CT--03-F-P22.ab1	NP_566677	expressed protein [Arabidopsis thaliana]	75	44	5.23E-12
CT--07-F-C06.ab1	NP_566691	expressed protein [Arabidopsis thaliana]	44.2623	61	3.98E-07
CT--05-F-K11.ab1	NP_566715	putative selenocysteine methyltransferase [Arabidopsis thaliana]	80.5556	36	7.10E-10
CT--06-F-J03.ab1	NP_566858	expressed protein [Arabidopsis thaliana]	43.4343	99	9.18E-23
CT--04-F-O02.ab1	NP_567154	putative YABBY3 axial regulator [Arabidopsis thaliana]	51.6779	149	1.02E-31

IP : 14.49.138.138, 2017-11-03 13:30:33

CT--02-F-E23.ab1	NP_567663	HSP associated protein like [Arabidopsis thaliana]	87.8049	41	2.93E-14
CT--01-F-P13.ab1	NP_567726	expressed protein [Arabidopsis thaliana]	48.8889	45	0.00811379
CT--04-F-G22.ab1	NP_567832	Expressed protein [Arabidopsis thaliana]	76.7857	56	1.76E-16
CT--03-F-P04.ab1	NP_567835	mRNA cleavage factor subunit - like protein [Arabidopsis thaliana]	71.831	71	4.14E-26
CT--04-F-N18.ab1	NP_567871	predicted protein [Arabidopsis thaliana]	52	75	3.18E-10
CT--07-F-O08.ab1	NP_567872	predicted protein [Arabidopsis thaliana]	73.7705	61	1.11E-20
CT--01-F-N16.ab1	NP_567979	putative protein [Arabidopsis thaliana]	81.8182	44	1.28E-13
CT--07-F-G23.ab1	NP_567984	putative protein [Arabidopsis thaliana]	100	23	7.06E-15
CT--01-F-P17.ab1	NP_568013	putative protein [Arabidopsis thaliana]	70	40	1.72E-08
CT--05-F-O12.ab1	NP_568040	expressed protein [Arabidopsis thaliana]	74.6667	75	2.15E-36
CT--01-F-A12.ab1	NP_568046	putative thaumatin-like protein [Arabidopsis thaliana]	67.8571	112	1.01E-40
CT--04-F-P03.ab1	NP_568103	putative protein [Arabidopsis thaliana]	55.2632	38	0.00131653
CT--04-F-I18.ab1	NP_568115	Expressed protein [Arabidopsis thaliana]	71.4286	63	3.12E-21
CT--02-F-G18.ab1	NP_568331	Expressed protein [Arabidopsis thaliana]	51.6484	91	1.38E-21
CT--01-F-H06.ab1	NP_568392	expressed protein [Arabidopsis thaliana]	79.5455	44	2.11E-21
CT--06-F-L24.ab1	NP_568699	Expressed protein [Arabidopsis thaliana]	53.5714	56	1.40E-10
CT--01-F-O24.ab1	NP_568727	Expressed protein [Arabidopsis thaliana]	80	40	2.67E-11
CT--07-F-P10.ab1	NP_568906	putative protein [Arabidopsis thaliana]	70.2128	47	4.98E-13
CT--07-F-P12.ab1	NP_568906	putative protein [Arabidopsis thaliana]	75.7576	33	4.07E-07
CT--07-F-A10.ab1	NP_568976	expressed protein [Arabidopsis thaliana]	88.4058	69	2.53E-32
CT--06-F-D22.ab1	NP_596201	hypothetical F-box domain protein [Schizosaccharomyces pombe]	28.9474	114	8.09E-10
CT--07-F-J11.ab1	O04885	LACTOYLGLUTATHIONE LYASE	85.7143	49	1.80E-21
CT--01-F-M24.ab1	O23787	Thiazole biosynthetic enzyme, chloroplast precursor	100	44	1.73E-18
CT--06-F-G23.ab1	O48922	CYTOCHROME P450 98A2	81.0127	79	1.51E-34
CT--07-F-B16.ab1	O49884	60S RIBOSOMAL PROTEIN L30	91.0891	101	3.85E-50
CT--03-F-A19.ab1	O50003	60S RIBOSOMAL PROTEIN L12	91.4894	47	5.24E-18
CT--07-F-F23.ab1	O81263	Thymidine kinase	86.6667	30	2.03E-05
CT--01-F-K23.ab1	O81363	40S ribosomal protein S4	81.1594	69	3.43E-26
CT--04-F-P16.ab1	O81363	40S ribosomal protein S4	92.1053	76	2.72E-62
CT--05-F-I20.ab1	P26518	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC	88.7097	124	1.42E-59
CT--02-F-B05.ab1	P28643	3-oxoacyl-[acyl-carrier protein] reductase, chloroplast precursor	81.25	32	2.20E-08
CT--06-F-B02.ab1	P34091	60S RIBOSOMAL PROTEIN L6	82.9268	41	4.63E-13
CT--03-F-F04.ab1	P35694	Brassinosteroid-regulated protein BRU1 precursor	69.697	99	1.73E-32
CT--04-F-L11.ab1	P42056	36 kDa outer mitochondrial membrane protein porin	94.3662	71	6.18E-32
CT--03-F-K18.ab1	P42553	DNA BINDING PROTEIN S1FA	67.5676	74	0.0143173
CT--05-F-M12.ab1	P42896	ENOLASE	82.1782	101	3.67E-42
CT--03-F-H21.ab1	P46277	G2/mitotic-specific cyclin 1	68.8172	93	1.12E-31
CT--03-F-H12.ab1	P48495	Triosephosphate isomerase, cytosolic	85.3659	82	5.39E-34
CT--04-F-D22.ab1	P49198	40S RIBOSOMAL PROTEIN S3A	88.4615	78	1.65E-31
CT--01-F-L15.ab1	P52424	Phosphoribosylformylglycinamidine cyclo-ligase, chloroplast precursor	76.6667	30	1.92E-08

IP : 14.49.138.138, 2017-11-03 13:30:33

CT--04-F-E12.ab1	P93847	60S RIBOSOMAL PROTEIN L10	87.0968	62	6.24E-26
CT--03-F-C09.ab1	Q03666	PROBABLE GLUTATHIONE S-TRANSFERASE	70.9677	62	1.02E-21
CT--04-F-H04.ab1	Q08069	40S ribosomal protein S8	92.7273	55	8.00E-24
CT--07-F-C05.ab1	Q40519	Photosystem II 10 kDa polypeptide, chloroplast precursor	88.2353	68	1.13E-23
CT--05-F-E11.ab1	Q41387	Photosystem II reaction center W protein, chloroplast precursor	59.1837	98	4.73E-19
CT--05-F-K23.ab1	Q42463	DCL PROTEIN, CHLOROPLAST PRECURSOR	89.5522	67	8.13E-31
CT--02-F-G03.ab1	Q43019	NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR	69.0476	42	3.63E-11
CT--06-F-I19.ab1	Q43019	NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR	69.6429	56	6.72E-18
CT--07-F-N19.ab1	Q43814	Ornithine carbamoyltransferase, chloroplast precursor	53.5211	71	1.03E-12
CT--02-F-L12.ab1	Q43843	Ribulose-phosphate 3-epimerase, chloroplast precursor	91.6667	72	1.92E-31
CT--02-F-P18.ab1	Q96499	60S RIBOSOMAL PROTEIN L44	100	105	2.25E-58
CT--01-F-A15.ab1	Q9SLQ8	Oxygen-evolving enhancer protein 2, chloroplast precursor	81.4433	97	7.46E-38
CT--03-F-P13.ab1	Q9SP55	Vacuolar ATP synthase subunit G	94.8276	58	1.26E-23
CT--05-F-C12.ab1	Q9XF97	60S ribosomal protein L4	88.3721	43	2.69E-09
CT--02-F-O22.ab1	Q9ZT05	Photosystem I reaction center subunit X, chloroplast precursor	95.7447	47	4.89E-27
CT--03-F-I21.ab1	Q9ZWQ9	Flavonol synthase	97.619	126	1.34E-65
CT--01-F-M03.ab1	S22522	chlorophyll a/b-binding protein precursor - Japanese black pine	78.7234	141	3.14E-55
CT--05-F-G06.ab1	S28827	chlorophyll a/b-binding protein type I - common tobacco	87.5	56	1.83E-22
CT--07-F-L22.ab1	S65062	fiber protein E6 - upland cotton	50.8197	61	9.27E-07
CT--07-F-J05.ab1	T01782	GDP dissociation inhibitor - common tobacco	89.7436	78	3.65E-62
CT--04-F-M02.ab1	T04077	probable ribosomal protein L9 - rice	88.6792	53	5.03E-20
CT--07-F-E02.ab1	T05707	phosphate transport protein G7, mitochondrial - soybean	88.7324	71	1.58E-23
CT--02-F-L08.ab1	T07086	acid phosphatase - soybean	43.3962	106	3.02E-18
CT--06-F-M02.ab1	T07780	remorin - potato	89.2308	65	2.72E-26
CT--03-F-M11.ab1	T09399	caffeoyl-CoA O-methyltransferase - alfalfa	80	75	1.39E-25
CT--02-F-B06.ab1	T09541	transketolase TKT1 precursor, chloroplast [validated] - pepper	92.1053	38	1.44E-12
CT--01-F-B03.ab1	T09704	probable arginine/serine-rich splicing factor - alfalfa	77.6119	134	6.30E-55
CT--03-F-M23.ab1	T10106	chitinase precursor - sweet orange	68.932	103	1.83E-30
CT--02-F-J08.ab1	T10106	chitinase precursor - sweet orange	100	50	2.10E-24
CT--03-F-G10.ab1	T10173	24-sterol C-methyltransferase - castor bean	91.8919	37	1.02E-12
CT--03-F-H22.ab1	T10174	hypothetical protein - castor bean	72.7273	121	1.97E-44
CT--04-F-C14.ab1	T10790	peroxidase - upland cotton	91.3462	104	1.82E-51
CT--01-F-C01.ab1	T31611	hypothetical protein Y50E8A.g - Caenorhabditis elegans	33.3333	69	0.00189551
CT--01-F-H04.ab1	T50847	hypothetical protein 110K5.11 [imported] - sorghum	85.7143	28	9.40E-06
CT--04-F-C20.ab1	T51098	hypothetical protein p85RF [imported] - Prunus armeniaca	68.4211	76	1.25E-19
CT--04-F-H21.ab1	XP_064564	similar to mucin [Homo sapiens]	27.3585	106	0.0416569

Consensus Number	Accession No.	Definition of Putative homologue[Organism]	Matching %	Matching Length	E-value
Contig1	Q06652	Probable phospholipid hydroperoxide glutathione peroxidase	95.238	42	8.64E-25
Contig2	BAB02135	gb|AAF15936.1~gene_id:MLD15.10~similar to unknown protein [Arabidopsis thaliana]	66.327	98	1.00658E-2

IP : 14.49.138.138, 2017-11-03 13:30:33

					0
Contig3	No hits found				
Contig4	AAF34767	60S acidic ribosomal protein P0 [Euphorbia esula]	86.364	44	1.81E-16
Contig5	No hits found				
Contig6	No hits found				
Contig7	AAF65512	ADP-ribosylation factor [Capsicum annuum]	99.123	114	1.10E-95
Contig8	CAC80550	cyclophilin [Ricinus communis]	93.711	159	1.25E-77
Contig9	NP_187557	unknown protein [Arabidopsis thaliana]	88.571	35	2.67E-12
Contig10	P12469	Chlorophyll A-B binding protein C, chloroplast precursor	68.041	97	1.02E-29
Contig11	NP_567774	Expressed protein [Arabidopsis thaliana]	62.069	174	1.02E-42
Contig12	No hits found				
Contig13	No hits found				
Contig14	NP_187531	putative 60S acidic ribosomal protein P0 [Arabidopsis thaliana]	81.053	95	2.31E-38
Contig15	NP_191088	ribosomal L23a - like protein [Arabidopsis thaliana]	82.828	99	1.38295E-38
Contig16	No hits found				
Contig17	NP_564405	zinc-finger protein, putative [Arabidopsis thaliana]	81.818	22	1.58E-03
Contig18	AAF64525	histone H1 variant [Lycopersicon chilense]	70.115	87	1.71E-28
Contig19	Q08069	40S ribosomal protein S8	91.549	71	1.60884E-31
Contig20	AAG38518	miraculin-like protein 2 [Citrus x paradisi]	98.969	97	4.61E-50
Contig21	CAA10101	ribosomal protein S28 [Prunus persica]	96.078	51	7.63365E-21
Contig22	S28420	ubiquitin / ribosomal protein CEP52 - wood tobacco	99.219	128	3.25719E-68
Contig23	AAD27882	chlorophyll a/b-binding protein CP24 precursor [Vigna radiata]	91	100	9.33E-51
Contig24	No hits found				
Contig25	AAL49933	AT5g58420/mqj2_10 [Arabidopsis thaliana]	87.234	47	1.81E-19
Contig26	AAK71233	S-adenosylmethionine synthetase [Brassica juncea]	96.825	63	1.42E-30
Contig27	No hits found				
Contig28	NP_566182	expressed protein [Arabidopsis thaliana]	63.235	68	4.06E-22
Contig29	BAB64099	putative photosystem II subunit precursor [Oryza sativa]	84.906	53	4.44E-21
Contig30	No hits found				
Contig31	AAG38518	miraculin-like protein 2 [Citrus x paradisi]	99.576	236	7.141E-124
Contig32	NP_568867	Expressed protein [Arabidopsis thaliana]	89.474	76	7.91E-39
Contig33	No hits found				
Contig34	NP_175640	60S ribosomal protein L37, putative [Arabidopsis thaliana]	92.537	67	1.33267E-32
Contig35	Q9XJ57	Chalcone synthase 2	96.552	145	4.16093E-75
Contig36	AAG38518	miraculin-like protein 2 [Citrus x paradisi]	95.918	98	3.38463E-56
Contig37	BAB86520	ribosomal protein L28-like [Oryza sativa]	76.389	144	3.02E-57
Contig38	BAB84008	ascorbate peroxidase [Brassica oleracea]	93.478	46	4.41258E-09
Contig39	AAA86982	caffeic acid O-methyl transferase [Chrysosplenium americanum]	50	94	2.23101E-21
Contig40	No hits found				
Contig41	No hits found				

IP : 14.49.138.138, 2017-11-03 13:30:33

Contig42	NP_567338	Expressed protein [Arabidopsis thaliana]	60.714	140	4.00E-48
Contig43	AAB68045	polyubiquitin [Fragaria x ananassa]	97.368	38	1.31E-16
Contig44	NP_191670	ribosomal protein S27 [Arabidopsis thaliana]	93.827	81	1.14E-34
Contig45	AAD34458	Skp1 [Medicago sativa]	85.256	156	7.18E-65
Contig46	T10106	chitinase precursor - sweet orange	95.238	105	8.44388E-56
Contig47	NP_188923	early light-induced protein [Arabidopsis thaliana]	83.146	89	2.99E-37
Contig48	BAB02572	gene_id:F4B12.9~unknown protein [Arabidopsis thaliana]	56.25	80	1.38E-18
Contig49	AAK25752	calmodulin [Castanea sativa]	100	84	2.87E-41
Contig50	O65781	UDP-glucose 4-epimerase GEPI48	91.045	67	3.63E-31
Contig51	No hits found				
Contig52	AAG27431	QM-like protein [Elaeis guineensis]	76.786	56	3.37E-20
Contig53	T10106	chitinase precursor - sweet orange	95.536	112	5.65072E-60
Contig54	AAG38517	miraculin-like protein [Citrus x paradisi]	100	229	7.91E-129
Contig55	BAB20645	contains EST AU164600~hypothetical protein [Oryza sativa]	96.429	28	1.81E-20
Contig56	NP_197516	ribosomal protein L7Ae-like [Arabidopsis thaliana]	93.75	128	1.02E-52
Contig57	NP_568915	actin depolymerizing factor 3 - like protein [Arabidopsis thaliana]	92.857	42	1.90E-14
Contig58	No hits found				
Contig59	NP_567244	predicted NADH dehydrogenase 24 kD subunit [Arabidopsis thaliana]	83.621	116	9.49E-51
Contig60	Q40250	Ribulose bisphosphate carboxylase small chain, chloroplast precursor	76.271	177	3.80076E-80
Contig61	No hits found				
Contig62	AAL09401	ribosomal protein [Petunia x hybrida]	86.538	52	3.85666E-13
Contig63	AAD29676	plasma membrane MIP protein [Zea mays]	87.5	136	1.30E-63
Contig64	No hits found				
Contig65	Q9XHS0	40S ribosomal protein S12	86.538	52	7.7529E-22
Contig66	Q9ZSW9	Translationally controlled tumor protein homolog	92.857	168	3.46767E-74
Contig67	Q96499	60S RIBOSOMAL PROTEIN L44	99.01	101	1.43168E-55
Contig68	AAL67601	putative cinnamoyl-CoA reductase [Oryza sativa]	53.623	69	4.53E-12
Contig69	No hits found				
Contig70	AAL04507	glutaredoxin [Tilia platyphyllos]	77.57	107	3.80E-44
Contig71	No hits found				
Contig72	AAG38518	miraculin-like protein 2 [Citrus x paradisi]	62.963	81	3.06E-47
Contig73	T10106	chitinase precursor - sweet orange	88.281	128	5.16941E-63
Contig74	AAG38518	miraculin-like protein 2 [Citrus x paradisi]	46.119	219	4.40E-40
Contig75	AAF76226	14-3-3 protein [Populus x canescens]	82.609	23	0.0895766
Contig76	AAB51394	tonoplast intrinsic protein bobTIP26-2 [Brassica oleracea var. botrytis]	84.706	85	1.76E-39
Contig77	AAC12797	adenosine triphosphatase; c-subunit of V-ATPase [Vigna radiata]	100	35	0.000802948
Contig78	BAA95845	Similar to Arabidopsis thaliana low temperature and salt responsive protein LTI6B. [Oryza sativa]	80.702	57	3.54076E-21
Contig79	AAC15992	chlorophyll a/b binding protein [Oryza sativa]	97.297	37	2.19E-22
Contig80	AAF71817	putative aquaporin PIP1-1 [Vitis berlandieri x Vitis rupestris]	92.453	53	7.44765E-24
Contig81	P42055	34 kDa outer mitochondrial membrane protein porin	85.065	154	2.8399E-73

IP : 14.49.138.138, 2017-11-03 13:30:33

Contig82	No hits found				
Contig83	BAA92155	glycine-rich protein [Citrus unshiu]	100	31	2.30E-10
Contig84	NP_201067	putative protein [Arabidopsis thaliana]	58.108	74	6.05E-06
Contig85	T10106	chitinase precursor - sweet orange	90.361	166	1.7481E-77
Contig86	AAG38522	lectin-related protein precursor [Citrus x paradisi]	100	155	8.78E-85
Contig87	T06096	hypothetical protein T5J17.70 - Arabidopsis thaliana	73.469	98	3.15728E-23
Contig88	AAG38522	lectin-related protein precursor [Citrus x paradisi]	87.097	62	1.11E-24
Contig89	AAL06948	AT5g02040/T7H20_90 [Arabidopsis thaliana]	83.019	53	1.42E-25
Contig90	No hits found				
Contig91	AAD27575	hypothetical protein [Sorghum bicolor]	84.314	51	4.11E-19
Contig92	Q9XJ57	Chalcone synthase 2	100	88	1.02544E-36
Contig93	NP_568698	expressed protein [Arabidopsis thaliana]	47.525	101	7.54597E-15
Contig94	AAF34799	40S ribosomal protein S16 [Euphorbia esula]	94.444	90	2.42107E-43
Contig95	JQ1287	glyceraldehyde-3-phosphate dehydrogenase , cytosolic - Arabidopsis thaliana	95.385	65	4.44279E-29
Contig96	No hits found				
Contig97	CAB51835	l1332.6 [Oryza sativa]	73.438	64	5.57E-21
Contig98	No hits found				
Contig99	No hits found				
Contig100	BAB12722	gamma tonoplast intrinsic protein [Pyrus communis]	85.714	140	2.01E-52
Contig101	No hits found				
Contig102	AAK96474	At1g31330/T19E23_1 [Arabidopsis thaliana]	88.06	67	1.55E-29
Contig103	AAM66110	putative inorganic pyrophosphatase [Arabidopsis thaliana]	86.42	81	1.56E-34
Contig104	No hits found				
Contig105	AAD21625	putative chlorophyll a/b-binding protein [Phalaenopsis sp. 'KCbutterfly']	97.468	79	1.73328E-57
Contig106	BAA83471	Csf-3 [Cucumis sativus]	92	25	5.89475E-07
Contig107	No hits found				
Contig108	NP_201307	annexin [Arabidopsis thaliana]	78.667	75	3.86E-28
Contig109	NP_198121	putative protein [Arabidopsis thaliana]	54.545	99	7.76E-25
Contig110	AAF79634	F5O11.12 [Arabidopsis thaliana]	80	70	8.50E-28
Contig111	NP_568154	putative protein [Arabidopsis thaliana]	47	100	3.00E-17
Contig112	No hits found				
Contig113	CAC20221	ribosomal protein L2 [Glycine max]	97.436	39	9.64096E-25
Contig114	No hits found				
Contig115	AAL82519	putative transmembrane protein [Oryza sativa]	72.727	99	8.28776E-39
Contig116	BAB09970	contains similarity to chalcone-flavonone isomerase ~gene_id:K18I23.7 [Arabidopsis thaliana]	67.416	89	1.11E-24
Contig117	No hits found				
Contig118	No hits found				
Contig119	AAF80615	F2D10.18 [Arabidopsis thaliana]	71.304	115	4.33564E-37
Contig120	AAF19544	F23N19.15 [Arabidopsis thaliana]	66.667	33	0.00137217
Contig121	CAA71132	ubiquitin extension protein [Solanum tuberosum]	97.727	88	9.15E-31

IP : 14.49.138.138, 2017-11-03 13:30:33

Contig122	BAA06335	peroxidase [Populus kitakamiensis]	71.429	56	5.30E-16
Contig123	AAG38522	lectin-related protein precursor [Citrus x paradisi]	87.097	62	1.05E-24
Contig124	AAM15999	glycine-rich RNA binding protein [Zea mays]	74.51	51	4.05506E-27
Contig125	No hits found				
Contig126	No hits found				
Contig127	NP_563969	expressed protein [Arabidopsis thaliana]	96.667	30	3.8541E-09
Contig128	AAL32688	plasma membrane intrinsic protein 1C [Arabidopsis thaliana]	93.333	60	3.36E-53
Contig129	O24111	40S RIBOSOMAL PROTEIN S5	88.235	119	2.42E-48
Contig130	AAC77930	similar to ribosomal protein L32 [Medicago sativa]	96.552	29	1.10E-07
Contig131	No hits found				
Contig132	NP_192395	predicted protein of unknown function [Arabidopsis thaliana]	78.182	55	6.52427E-19
Contig133	AAA80593	chlorophyll a/b binding protein [Solanum tuberosum]	100	79	7.22E-41
Contig134	AAG38517	miraculin-like protein [Citrus x paradisi]	96.364	110	3.87E-61
Contig135	CAC27136	40S ribosomal protein S2 [Picea abies]	78.378	74	4.27E-27
Contig136	BAB33422	putative senescence-associated protein [Pisum sativum]	76.712	73	9.37E-37
Contig137	No hits found				
Contig138	AAG40023	At2g20820 [Arabidopsis thaliana]	58.333	72	3.17845E-17
Contig139	NP_564059	expressed protein [Arabidopsis thaliana]	68.675	83	2.22E-33
Contig140	AAM77651	cp10-like protein [Gossypium hirsutum]	64.22	109	4.75E-25
Contig141	No hits found				
Contig142	No hits found				
Contig143	AAD48913	caffeate O-methyltransferase [Liquidambar styraciflua]	59.184	49	4.76E-10
Contig144	BAB93221	putative 60S RIBOSOMAL PROTEIN L36 [Oryza sativa]	79.091	110	5.47E-45
Contig145	No hits found				

2) 온주밀감성숙과실

Clone No.	Accession No.	Definition of Putative homologue[Organism]	Matching %	Matching Length	E-value
MCT--04-R-M13.ab1	NP_201415	20S proteasome alpha subunit D2 (PAD2) [Arabidopsis thaliana]	90.426	94	6.76E-32
MCT--03-R-N17.ab1	AAQ22726	40S ribosomal protein S25 [Glycine max]	97.183	71	1.29551E-30
MCT--01-R-K12.ab1	NP_191670	40S ribosomal protein S27 (RPS27B) [Arabidopsis thaliana]	94.186	86	4.23E-37
MCT--01-R-F19.ab1	F84857	60S ribosomal protein L11B [imported] - Arabidopsis thaliana	94.667	75	9.97311E-25
MCT--06-R-J22.ab1	NP_179635	60S ribosomal protein L14 (RPL14A) [Arabidopsis thaliana]	86.17	94	1.85E-38
MCT--01-R-C02.ab1	Q9ATF5	60S ribosomal protein L18a	96.429	140	1.39E-75
MCT--03-R-G07.ab1	NP_190560	60S ribosomal protein L26 (RPL26A) [Arabidopsis thaliana]	90.411	146	6.38496E-54
MCT--04-R-B20.ab1	AAQ72789	60S ribosomal protein L5 [Cucumis sativus]	89.437	142	1.18E-68
MCT--06-R-E18.ab1	BAB85987	Acyl-CoA-binding protein [Panax ginseng]	93.023	86	2.0951E-40
MCT--01-R-N24.ab1	BAB84008	ascorbate peroxidase [Brassica oleracea]	92.308	65	3.50E-10
MCT--07-R-J18.ab1	NP_191968	asparaginase 2 family [Arabidopsis thaliana]	56.757	37	3.37429E-06

IP : 14.49.138.138, 2017-11-03 13:30:33

MCT--01-R-M07.ab1	AAK55703	At2g04520/T1O3.7 [Arabidopsis thaliana]	93.458	107	4.24E-54
MCT--06-R-G03.ab1	AAK91370	At2g21620/F2G1.11 [Arabidopsis thaliana]	68.056	72	2.18E-25
MCT--06-R-K17.ab1	AAL77705	AT4g18710/F28A21_120 [Arabidopsis thaliana]	94.34	106	1.24404E-51
MCT--01-R-N16.ab1	AAL06879	AT5g07010/MOJ9_18 [Arabidopsis thaliana]	64.567	127	3.63E-43
MCT--02-R-H11.ab1	AAO24535	At5g58240 [Arabidopsis thaliana]	67.742	155	4.45658E-53
MCT--07-R-C12.ab1	NP_566518	autophagy protein APG8H (AtAPG8i) [Arabidopsis thaliana]	82.927	82	3.29447E-34
MCT--02-R-N08.ab1	NP_191376	Bet1/Sft1-related SNARE (AtBS14a) [Arabidopsis thaliana]	85.849	106	2.27169E-46
MCT--07-R-B15.ab1	T07844	BURP domain-containing protein - rape	42.553	94	1.55E-13
MCT--04-R-P21.ab1	NP_198590	C2 domain-containing protein [Arabidopsis thaliana]	75.904	83	2.52478E-31
MCT--04-R-E09.ab1	AAC49708	caffeic acid O-methyltransferase	64	50	4.55326E-12
MCT--04-R-F21.ab1	BAC78828	caffeic acid O-methyltransferase [Rosa chinensis var. spontanea]	51.095	137	1.41E-32
MCT--04-R-P22.ab1	AAL91506	caffeic acid O-methyltransferase II [Nicotiana tabacum]	48.193	83	1.03E-13
MCT--04-R-K07.ab1	NP_187630	calmodulin, putative [Arabidopsis thaliana]	63.281	128	2.69504E-36
MCT--02-R-D09.ab1	T09793	carbonate dehydratase (EC 4.2.1.1) 1a - Populus tremula x Populus tremuloides	68	100	5.10626E-19
MCT--06-R-K04.ab1	AAL87023	cell wall protein Exp4 precursor [Mirabilis jalapa]	94.34	53	5.89733E-24
MCT--06-R-J24.ab1	P08221	Chlorophyll A-B binding protein of LHCII type I, chloroplast precursor (CAB) (LHCP)	95.536	112	2.23532E-57
MCT--03-R-M13.ab1	AAC15460	cold-regulated LTCOR12 [Lavatera thuringiaca]	70.37	81	6.64E-30
MCT--03-R-P14.ab1	AAL56612	cystatin [Vigna radiata]	70.313	64	3.49E-14
MCT--02-R-M19.ab1	AAL66291	cysteine synthase [Glycine max]	89.831	118	3.93E-54
MCT--01-R-L02.ab1	AAO41731	cytoplasmic ribosomal protein S14 [Brassica napus]	93.284	134	4.80E-57
MCT--04-R-K04.ab1	BAA33801	cytosolic phosphoglycerate kinase 1 [Populus nigra]	88.889	126	1.83E-53
MCT--02-R-G12.ab1	AAL67991	dehydration-induced protein RD22-like protein [Gossypium hirsutum]	68.182	88	1.0248E-29
MCT--02-R-L08.ab1	AAP56259	dehydrin [Citrus sinensis]	54.839	31	1.01E-07
MCT--04-R-D02.ab1	NP_180353	dTDP-glucose 4-6-dehydratase -related [Arabidopsis thaliana]	90.647	139	3.86761E-69
MCT--01-R-J23.ab1	NP_192763	endomembrane-localized small heat shock protein [Arabidopsis thaliana]	67.47	83	3.16E-27
MCT--07-R-J21.ab1	CAA48763	envelope glycoprotein [Spleen focus-forming virus]	100	51	9.80E-25
MCT--03-R-M10.ab1	AAQ08191	eukaryotic translation initiation factor 5A isoform I [Hevea brasiliensis]	95.522	134	2.90E-71
MCT--03-R-L23.ab1	BAC67188	expansin [Pyrus communis]	69.697	33	4.74322E-13
MCT--03-R-N06.ab1	BAC66694	expansin [Vitis labrusca x Vitis vinifera]	87.2	125	1.16632E-47
MCT--02-R-O12.ab1	NP_181300	expansin, putative (EXP3) [Arabidopsis thaliana]	60.684	117	3.60133E-34
MCT--01-R-M13.ab1	AAO29946	expressed protein [Arabidopsis thaliana]	71.429	140	1.38E-47
MCT--03-R-H05.ab1	NP_197221	expressed protein [Arabidopsis thaliana]	84.615	130	1.68E-51
MCT--02-R-B20.ab1	NP_191814	expressed protein [Arabidopsis thaliana]	47.917	96	1.88E-21
MCT--03-R-M05.ab1	NP_683315	expressed protein [Arabidopsis thaliana]	73.913	46	2.49E-13
MCT--03-R-N16.ab1	NP_564163	expressed protein [Arabidopsis thaliana]	70.968	124	8.67E-35
MCT--02-R-J13.ab1	NP_568440	expressed protein [Arabidopsis thaliana]	65.854	41	3.72E-08
MCT--04-R-P12.ab1	NP_191147	expressed protein [Arabidopsis thaliana]	49.275	138	2.88E-28
MCT--06-R-N18.ab1	NP_565875	expressed protein [Arabidopsis thaliana]	80.882	68	3.64368E-28
MCT--02-R-N03.ab1	NP_850928	expressed protein [Arabidopsis thaliana]	61.111	36	6.64E-10
MCT--02-R-G10.ab1	NP_196493	expressed protein [Arabidopsis thaliana]	73.043	115	1.04E-46

IP : 14.49.138.138, 2017-11-03 13:30:33

MCT--01-R-L19.ab1	NP_195683	expressed protein [Arabidopsis thaliana]	75	88	1.21E-37
MCT--02-R-O06.ab1	NP_566678	expressed protein [Arabidopsis thaliana]	50.943	53	3.58E-07
MCT--01-R-N22.ab1	NP_568143	expressed protein [Arabidopsis thaliana]	77.381	84	8.40E-30
MCT--07-R-J23.ab1	AAP34362	fiber protein Fb15 [Gossypium barbadense]	71.91	89	1.48E-36
MCT--06-R-J03.ab1	ADSPAC	fructose-bisphosphate aldolase (EC 4.1.2.13), cytosolic - spinach	91.667	108	8.47E-62
MCT--03-R-J04.ab1	NP_201098	GDSL-motif lipase/hydrolase protein [Arabidopsis thaliana]	75.926	162	1.78477E-68
MCT--07-R-G17.ab1	AAC78466	glutathione peroxidase [Zantedeschia aethiopica]	91.209	91	2.69E-44
MCT--01-R-P08.ab1	AAF65767	glutathione S-transferase [Euphorbia esula]	70.748	147	9.37E-53
MCT--04-R-F03.ab1	NP_175517	histone H2A, putative [Arabidopsis thaliana]	87.692	65	1.77E-25
MCT--04-R-G01.ab1	NP_175683	histone H2A, putative [Arabidopsis thaliana]	88.393	112	1.06E-34
MCT--06-R-D02.ab1	O22582	Histone H2B	96.907	97	2.65E-41
MCT--01-R-G03.ab1	P82888	Histone H4	98.718	78	4.90E-36
MCT--02-R-P16.ab1	P40619	HMG1/2-like protein	68	75	3.5923E-22
MCT--07-R-B05.ab1	AAQ97809	HSPC038 protein [Danio rerio]	38.571	70	3.02E-06
MCT--06-R-G18.ab1	AAD25944	hypothetical EIF-2-Alpha [Arabidopsis thaliana]	95.122	123	5.88E-52
MCT--04-R-G08.ab1	AAF23279	hypothetical protein [Arabidopsis thaliana]	70.213	47	1.79051E-08
MCT--06-R-B08.ab1	AAG60133	hypothetical protein [Arabidopsis thaliana]	66.667	111	4.84E-30
MCT--01-R-E18.ab1	NP_187206	hypothetical protein [Arabidopsis thaliana]	45.946	74	6.91245E-15
MCT--04-R-C07.ab1	CAB61744	hypothetical protein [Cicer arietinum]	65.421	107	3.47E-31
MCT--02-R-J10.ab1	CAB09799	hypothetical protein [Citrus x paradisi]	99.265	136	9.45614E-77
MCT--07-R-O06.ab1	CAC84114	hypothetical protein [Gossypium hirsutum]	68.75	128	4.60E-33
MCT--01-R-P03.ab1	D86180	hypothetical protein [imported] - Arabidopsis thaliana	89.855	69	4.48E-18
MCT--04-R-O17.ab1	C86390	hypothetical protein T1K7.26 - Arabidopsis thaliana	73.585	53	1.18E-15
MCT--01-R-E10.ab1	P52578	Isoflavone reductase homolog (CP100)	78.621	145	4.88E-57
MCT--01-R-N14.ab1	AAK08102	mago nashi-like protein [Oryza sativa]	93.617	94	3.44E-45
MCT--07-R-A20.ab1	BAA31562	metallothionein-like protein [Citrus unshiu]	98.113	53	7.50E-25
MCT--07-R-C05.ab1	BAA31562	metallothionein-like protein [Citrus unshiu]	50	62	3.7894E-08
MCT--07-R-P08.ab1	BAA31562	metallothionein-like protein [Citrus unshiu]	54.839	62	6.60899E-12
MCT--02-R-E09.ab1	AAK21969	myo-inositol 1-phosphate synthase [Avicennia marina]	100	27	4.55E-08
MCT--03-R-M04.ab1	AAK83083	nuclear matrix protein 1 [Lycopersicon esculentum]	92.553	94	3.95E-43
MCT--03-R-A08.ab1	CAE04574	OSJNBb0039L24.13 [Oryza sativa (japonica cultivar-group)]	82.143	84	2.40E-26
MCT--04-R-H07.ab1	NP_915490	P0005H10.15 [Oryza sativa (japonica cultivar-group)]	81.69	71	1.10E-34
MCT--07-R-M16.ab1	BAC15791	P0466H10.24 [Oryza sativa (japonica cultivar-group)]	59.259	54	3.85E-14
MCT--03-R-D21.ab1	NP_915424	putative 60S RIBOSOMAL PROTEIN L36 [Oryza sativa (japonica cultivar-group)]	80.198	101	4.59E-41
MCT--07-R-M11.ab1	AAF23294	putative ascorbate peroxidase [Arabidopsis thaliana]	81.69	71	1.14E-43
MCT--04-R-C09.ab1	AAL69381	putative DEAD/DEAH box helicase [Narcissus pseudonarcissus]	92.857	112	8.36478E-56
MCT--03-R-B16.ab1	AAO33591	putative early light induced protein [Arachis hypogaea]	56.25	144	2.69749E-33
MCT--03-R-K24.ab1	AAP45162	putative Mob1/phocein family protein [Solanum bulbocastanum]	86.792	53	1.19E-20
MCT--07-R-L22.ab1	AAM64992	putative phi-1-like phosphate-induced protein [Arabidopsis thaliana]	66.364	110	2.49E-26
MCT--01-R-C18.ab1	NP_180930	putative related to microbial divalent cation tolerance proteins [Arabidopsis thaliana]	62.963	162	6.28E-44

IP : 14.49.138.138, 2017-11-03 13:30:33

MCT--03-R-B24.ab1	AAR01683	putative ribosomal protein L13a [Oryza sativa (japonica cultivar-group)]	86.842	38	1.52E-11
MCT--06-R-B18.ab1	CAB85625	putative ripening-related protein [Vitis vinifera]	61.957	92	5.29E-26
MCT--07-R-N10.ab1	CAC69854	putative thioredoxin m2 [Pisum sativum]	75	56	2.92E-25
MCT--01-R-K04.ab1	AAP40643	putative triose-phosphate isomerase [Gossypium barbadense]	87.209	86	8.37779E-38
MCT--07-R-D16.ab1	CAC39038	putative vesicle-associated membrane protein (VAMP) [Oryza sativa]	56.923	65	2.15E-09
MCT--06-R-F16.ab1	P52902	Pyruvate dehydrogenase E1 component alpha subunit, mitochondrial precursor (PDHE1-A)	75.969	129	3.20904E-51
MCT--02-R-O11.ab1	BAA96072	ribosomal protein L29 [Panax ginseng]	86.667	60	2.00E-25
MCT--03-R-L03.ab1	AAA34366	ribosomal protein L41	98.684	76	3.84E-39
MCT--02-R-C02.ab1	AAG61120	ribulose-1,5-bisphosphate carboxylase/oxygenase activase 1 [Gossypium hirsutum]	69.173	133	2.29154E-41
MCT--06-R-G17.ab1	AAL67493	senescence-associated putative protein [Narcissus pseudonarcissus]	67.213	61	1.21E-17
MCT--02-R-K07.ab1	2205248A	Ser/Thr kinase	70.588	119	4.90E-43
MCT--04-R-H13.ab1	CAC03600	splicing factor SC35 [Arabidopsis thaliana]	83.908	87	2.35707E-34
MCT--02-R-O14.ab1	Q43636	Thioredoxin H-type (TRX-H)	89.565	115	2.59E-55
MCT--02-R-K22.ab1	DAA00281	TPA: putative phytosulfokine peptide precursor [Glycine max]	52.459	61	4.33E-10
MCT--07-R-K18.ab1	NP_195256	transporter - related [Arabidopsis thaliana]	75.455	110	4.52E-46
MCT--06-R-J14.ab1	NP_199900	ubiquitin-conjugating enzyme, putative [Arabidopsis thaliana]	80.303	132	6.26E-60
MCT--04-R-O19.ab1	Q43070	UDP-glucose 4-epimerase (Galactowaldenase) (UDP-galactose 4-epimerase)	75	32	1.13E-09
MCT--02-R-I10.ab1	AAM63827	unknown [Arabidopsis thaliana]	60.432	139	4.90E-36
MCT--02-R-P06.ab1	AAM63417	unknown [Arabidopsis thaliana]	60.274	73	1.05E-21
MCT--03-R-B18.ab1	AAM65809	unknown [Arabidopsis thaliana]	71.429	35	2.91522E-08
MCT--03-R-H21.ab1	AAM65826	unknown [Arabidopsis thaliana]	57.6	125	2.56E-36
MCT--06-R-M15.ab1	AAM64507	unknown [Arabidopsis thaliana]	76.471	51	4.54E-18
MCT--06-R-A22.ab1	AAF34768	unknown [Euphorbia esula]	55.556	126	6.11E-30
MCT--06-R-M21.ab1	BAC43661	unknown protein [Arabidopsis thaliana]	85.333	75	6.96E-30
MCT--03-R-N08.ab1	BAC43625	unknown protein [Arabidopsis thaliana]	72.115	104	3.22E-43
MCT--02-R-I17.ab1	AAK71543	unknown protein [Oryza sativa (japonica cultivar-group)]	39.796	98	8.44E-09
MCT--04-R-F15.ab1	NP_913548	unnamed protein product [Oryza sativa (japonica cultivar-group)]	51.515	66	7.89612E-12
MCT--04-R-G23.ab1	CAC33000	urease accessory protein G [Solanum tuberosum]	86.29	124	6.93E-61
MCT--02-R-L04.ab1	Q9SP55	Vacuolar ATP synthase subunit G (V-ATPase G subunit) (Vacuolar proton pump G subunit)	95.96	99	4.24E-36
MCT--01-R-O07.ab1	P49043	Vacuolar processing enzyme precursor (VPE)	100	86	1.86E-45
MCT--04-R-E13.ab1	AAB01195	VP16 transactivation domain (modified)	73.684	38	9.11E-06
MCT--01-R-O10.ab1	NP_566182	zinc finger (C2H2 type) protein family [Arabidopsis thaliana]	66.176	68	1.26E-22

IP : 14.49.138.138, 2017-11-03 13:30:33

Clone No.	Accession No.	Definition of Putative homologue[Organism]	Matching %	Matching Length	E-value
Contig1	Q06652	Probable phospholipid hydroperoxide glutathione peroxidase	95.238	42	8.64E-25
Contig2	BAB02135	gb|AAF15936.1~gene_id:MLD15.10~similar to unknown protein [Arabidopsis thaliana]	66.327	98	1.00658E-20
Contig3	No hits found				
Contig4	AAF34767	60S acidic ribosomal protein PO [Euphorbia esula]	86.364	44	1.81E-16
Contig5	No hits found				
Contig6	No hits found				
Contig7	AAF65512	ADP-ribosylation factor [Capsicum annuum]	99.123	114	1.10E-95
Contig8	CAC80550	cyclophilin [Ricinus communis]	93.711	159	1.25E-77
Contig9	NP_187557	unknown protein [Arabidopsis thaliana]	88.571	35	2.67E-12
Contig10	P12469	Chlorophyll A-B binding protein C, chloroplast precursor	68.041	97	1.02E-29
Contig11	NP_567774	Expressed protein [Arabidopsis thaliana]	62.069	174	1.02E-42
Contig12	No hits found				
Contig13	No hits found				
Contig14	NP_187531	putative 60S acidic ribosomal protein P0 [Arabidopsis thaliana]	81.053	95	2.31E-38
Contig15	NP_191088	ribosomal L23a - like protein [Arabidopsis thaliana]	82.828	99	1.38295E-38
Contig16	No hits found				
Contig17	NP_564405	zinc-finger protein, putative [Arabidopsis thaliana]	81.818	22	1.58E-03
Contig18	AAF64525	histone H1 variant [Lycopersicon chilense]	70.115	87	1.71E-28
Contig19	Q08069	40S ribosomal protein S8	91.549	71	1.60884E-31
Contig20	AAG38518	miraculin-like protein 2 [Citrus x paradisi]	98.969	97	4.61E-50
Contig21	CAA10101	ribosomal protein S28 [Prunus persica]	96.078	51	7.63365E-21
Contig22	S28420	ubiquitin / ribosomal protein CEP52 - wood tobacco	99.219	128	3.25719E-68
Contig23	AAD27882	chlorophyll a/b-binding protein CP24 precursor [Vigna radiata]	91	100	9.33E-51
Contig24	No hits found				
Contig25	AAL49933	AT5g58420/mqj2_10 [Arabidopsis thaliana]	87.234	47	1.81E-19
Contig26	AAK71233	S-adenosylmethionine synthetase [Brassica juncea]	96.825	63	1.42E-30
Contig27	No hits found				
Contig28	NP_566182	expressed protein [Arabidopsis thaliana]	63.235	68	4.06E-22
Contig29	BAB64099	putative photosystem II subunit precursor [Oryza sativa]	84.906	53	4.44E-21
Contig30	No hits found				
Contig31	AAG38518	miraculin-like protein 2 [Citrus x paradisi]	99.576	236	7.141E-124
Contig32	NP_568867	Expressed protein [Arabidopsis thaliana]	89.474	76	7.91E-39
Contig33	No hits found				
Contig34	NP_175640	60S ribosomal protein L37, putative [Arabidopsis thaliana]	92.537	67	1.33267E-32
Contig35	Q9XJ57	Chalcone synthase 2	96.552	145	4.16093E-75
Contig36	AAG38518	miraculin-like protein 2 [Citrus x paradisi]	95.918	98	3.38463E-56
Contig37	BAB86520	ribosomal protein L28-like [Oryza sativa]	76.389	144	3.02E-57
Contig38	BAB84008	ascorbate peroxidase [Brassica oleracea]	93.478	46	4.41258E-09
Contig39	AAA86982	caffeic acid O-methyl transferase [Chrysosplenium americanum]	50	94	2.23101E-21

IP : 14.49.138.138, 2017-11-03 13:30:33

Contig40	No hits found				
Contig41	No hits found				
Contig42	NP_567338	Expressed protein [Arabidopsis thaliana]	60.714	140	4.00E-48
Contig43	AAB68045	polyubiquitin [Fragaria x ananassa]	97.368	38	1.31E-16
Contig44	NP_191670	ribosomal protein S27 [Arabidopsis thaliana]	93.827	81	1.14E-34
Contig45	AAD34458	Skp1 [Medicago sativa]	85.256	156	7.18E-65
Contig46	T10106	chitinase precursor - sweet orange	95.238	105	8.44388E-56
Contig47	NP_188923	early light-induced protein [Arabidopsis thaliana]	83.146	89	2.99E-37
Contig48	BAB02572	gene_id:F4B12.9~unknown protein [Arabidopsis thaliana]	56.25	80	1.38E-18
Contig49	AAK25752	calmodulin [Castanea sativa]	100	84	2.87E-41
Contig50	O65781	UDP-glucose 4-epimerase GEPI48	91.045	67	3.63E-31
Contig51	No hits found				
Contig52	AAG27431	QM-like protein [Elaeis guineensis]	76.786	56	3.37E-20
Contig53	T10106	chitinase precursor - sweet orange	95.536	112	5.65072E-60
Contig54	AAG38517	miraculin-like protein [Citrus x paradisi]	100	229	7.91E-129
Contig55	BAB20645	contains EST AU164600~hypothetical protein [Oryza sativa]	96.429	28	1.81E-20
Contig56	NP_197516	ribosomal protein L7Ae-like [Arabidopsis thaliana]	93.75	128	1.02E-52
Contig57	NP_568915	actin depolymerizing factor 3 - like protein [Arabidopsis thaliana]	92.857	42	1.90E-14
Contig58	No hits found				
Contig59	NP_567244	predicted NADH dehydrogenase 24 kD subunit [Arabidopsis thaliana]	83.621	116	9.49E-51
Contig60	Q40250	Ribulose bisphosphate carboxylase small chain, chloroplast precursor	76.271	177	3.80076E-80
Contig61	No hits found				
Contig62	AAL09401	ribosomal protein [Petunia x hybrida]	86.538	52	3.85666E-13
Contig63	AAD29676	plasma membrane MIP protein [Zea mays]	87.5	136	1.30E-63
Contig64	No hits found				
Contig65	Q9XHS0	40S ribosomal protein S12	86.538	52	7.7529E-22
Contig66	Q9ZSW9	Translationally controlled tumor protein homolog	92.857	168	3.46767E-74
Contig67	Q96499	60S RIBOSOMAL PROTEIN L44	99.01	101	1.43168E-55
Contig68	AAL67601	putative cinnamoyl-CoA reductase [Oryza sativa]	53.623	69	4.53E-12
Contig69	No hits found				
Contig70	AAL04507	glutaredoxin [Tilia platyphyllos]	77.57	107	3.80E-44
Contig71	No hits found				
Contig72	AAG38518	miraculin-like protein 2 [Citrus x paradisi]	62.963	81	3.06E-47
Contig73	T10106	chitinase precursor - sweet orange	88.281	128	5.16941E-63
Contig74	AAG38518	miraculin-like protein 2 [Citrus x paradisi]	46.119	219	4.40E-40
Contig75	AAF76226	14-3-3 protein [Populus x canescens]	82.609	23	0.0895766
Contig76	AAB51394	tonoplast intrinsic protein bobTIP26-2 [Brassica oleracea var. botrytis]	84.706	85	1.76E-39
Contig77	AAC12797	adenosine triphosphatase; c-subunit of V-ATPase [Vigna radiata]	100	35	0.000802948
Contig78	BAA95845	Similar to Arabidopsis thaliana low temperature and salt responsive protein LTI6B. [Oryza sativa]	80.702	57	3.54076E-21
Contig79	AAC15992	chlorophyll a/b binding protein [Oryza sativa]	97.297	37	2.19E-22

IP : 14.49.138.138, 2017-11-03 13:30:33

Contig80	AAF71817	putative aquaporin PIP1-1 [Vitis berlandieri x Vitis rupestris]	92.453	53	7.44765E-24
Contig81	P42055	34 kDa outer mitochondrial membrane protein porin	85.065	154	2.8399E-73
Contig82	No hits found				
Contig83	BAA92155	glycine-rich protein [Citrus unshiu]	100	31	2.30E-10
Contig84	NP_201067	putative protein [Arabidopsis thaliana]	58.108	74	6.05E-06
Contig85	T10106	chitinase precursor - sweet orange	90.361	166	1.7481E-77
Contig86	AAG38522	lectin-related protein precursor [Citrus x paradisi]	100	155	8.78E-85
Contig87	T06096	hypothetical protein T5J17.70 - Arabidopsis thaliana	73.469	98	3.15728E-23
Contig88	AAG38522	lectin-related protein precursor [Citrus x paradisi]	87.097	62	1.11E-24
Contig89	AAL06948	AT5g02040/T7H20_90 [Arabidopsis thaliana]	83.019	53	1.42E-25
Contig90	No hits found				
Contig91	AAD27575	hypothetical protein [Sorghum bicolor]	84.314	51	4.11E-19
Contig92	Q9XJ57	Chalcone synthase 2	100	88	1.02544E-36
Contig93	NP_568698	expressed protein [Arabidopsis thaliana]	47.525	101	7.54597E-15
Contig94	AAF34799	40S ribosomal protein S16 [Euphorbia esula]	94.444	90	2.42107E-43
Contig95	JQ1287	glyceraldehyde-3-phosphate dehydrogenase , cytosolic - Arabidopsis thaliana	95.385	65	4.44279E-29
Contig96	No hits found				
Contig97	CAB51835	l1332.6 [Oryza sativa]	73.438	64	5.57E-21
Contig98	No hits found				
Contig99	No hits found				
Contig100	BAB12722	gamma tonoplast intrinsic protein [Pyrus communis]	85.714	140	2.01E-52
Contig101	No hits found				
Contig102	AAK96474	At1g31330/T19E23_1 [Arabidopsis thaliana]	88.06	67	1.55E-29
Contig103	AAM66110	putative inorganic pyrophosphatase [Arabidopsis thaliana]	86.42	81	1.56E-34
Contig104	No hits found				
Contig105	AAD21625	putative chlorophyll a/b-binding protein [Phalaenopsis sp. 'KCbutterfly']	97.468	79	1.73328E-57
Contig106	BAA83471	Csf-3 [Cucumis sativus]	92	25	5.89475E-07
Contig107	No hits found				
Contig108	NP_201307	annexin [Arabidopsis thaliana]	78.667	75	3.86E-28
Contig109	NP_198121	putative protein [Arabidopsis thaliana]	54.545	99	7.76E-25
Contig110	AAF79634	F5O11.12 [Arabidopsis thaliana]	80	70	8.50E-28
Contig111	NP_568154	putative protein [Arabidopsis thaliana]	47	100	3.00E-17
Contig112	No hits found				
Contig113	CAC20221	ribosomal protein L2 [Glycine max]	97.436	39	9.64096E-25
Contig114	No hits found				
Contig115	AAL82519	putative transmembrane protein [Oryza sativa]	72.727	99	8.28776E-39
Contig116	BAB09970	contains similarity to chalcone-flavonone isomerase ~gene_id:K18I23.7 [Arabidopsis thaliana]	67.416	89	1.11E-24
Contig117	No hits found				
Contig118	No hits found				
Contig119	AAF80615	F2D10.18 [Arabidopsis thaliana]	71.304	115	4.33564E-37

IP : 14.49.138.138, 2017-11-03 13:30:33

Contig120	AAF19544	F23N19.15 [Arabidopsis thaliana]	66.667	33	0.00137217
Contig121	CAA71132	ubiquitin extension protein [Solanum tuberosum]	97.727	88	9.15E-31
Contig122	BAA06335	peroxidase [Populus kitakamiensis]	71.429	56	5.30E-16
Contig123	AAG38522	lectin-related protein precursor [Citrus x paradisi]	87.097	62	1.05E-24
Contig124	AAM15999	glycine-rich RNA binding protein [Zea mays]	74.51	51	4.05506E-27
Contig125	No hits found				
Contig126	No hits found				
Contig127	NP_563969	expressed protein [Arabidopsis thaliana]	96.667	30	3.8541E-09
Contig128	AAL32688	plasma membrane intrinsic protein 1C [Arabidopsis thaliana]	93.333	60	3.36E-53
Contig129	O24111	40S RIBOSOMAL PROTEIN S5	88.235	119	2.42E-48
Contig130	AAC77930	similar to ribosomal protein L32 [Medicago sativa]	96.552	29	1.10E-07
Contig131	No hits found				
Contig132	NP_192395	predicted protein of unknown function [Arabidopsis thaliana]	78.182	55	6.52427E-19
Contig133	AAA80593	chlorophyll a/b binding protein [Solanum tuberosum]	100	79	7.22E-41
Contig134	AAG38517	miraculin-like protein [Citrus x paradisi]	96.364	110	3.87E-61
Contig135	CAC27136	40S ribosomal protein S2 [Picea abies]	78.378	74	4.27E-27
Contig136	BAB33422	putative senescence-associated protein [Pisum sativum]	76.712	73	9.37E-37
Contig137	No hits found				
Contig138	AAG40023	At2g20820 [Arabidopsis thaliana]	58.333	72	3.17845E-17
Contig139	NP_564059	expressed protein [Arabidopsis thaliana]	68.675	83	2.22E-33
Contig140	AAM77651	cp10-like protein [Gossypium hirsutum]	64.22	109	4.75E-25
Contig141	No hits found				
Contig142	No hits found				
Contig143	AAD48913	caffeate O-methyltransferase [Liquidambar styraciflua]	59.184	49	4.76E-10
Contig144	BAB93221	putative 60S RIBOSOMAL PROTEIN L36 [Oryza sativa]	79.091	110	5.47E-45
Contig145	No hits found				

3) 한라봉 미숙과피

Clone No.	Accession No.	Definition of Putative homologue[Organism]	Matching %	Matching Length	E-value
YHANP--01-R-M06.ab1	Q8L5K3	(R)-limonene synthase 1 ((+)-limonene synthase 1)	97.541	122	1.22E-64
YHANP--02-R-N15.ab1	CAC21424	12-oxophytodienoate reductase 3 [Lycopersicon esculentum]	73.239	71	8.69E-23
YHANP--03-R-G13.ab1	BAD12174	14-3-3 d-2 protein [Nicotiana tabacum]	91.736	121	5.10E-58
YHANP--01-R-H07.ab1	Q96451	14-3-3-LIKE PROTEIN B (SGF14B)	94.444	90	2.63E-40
YHANP--01-R-B24.ab1	AAN15459	26S proteasome AAA-ATPase subunit RPT5a [Arabidopsis thaliana]	98.113	106	1.62331E-53
YHANP--01-R-E17.ab1	NP_175120	26S proteasome regulatory complex subunit p42D, putative [Arabidopsis thaliana]	90.476	147	9.47E-70
YHANP--01-R-I17.ab1	A41370	2-dehydro-3-deoxy-phosphoheptonate aldolase (EC 4.1.2.15) 1 - Arabidopsis thaliana	58.427	89	3.19E-23
YHANP--02-R-C21.ab1	AAM65197	2-dehydro-3-deoxyphosphoheptonate aldolase [Arabidopsis thaliana]	73.856	153	2.76E-61
YHANP--04-R-B22.ab1	NP_176216	3' exoribonuclease family domain 1-containing protein [Arabidopsis thaliana]	74.825	143	8.91871E-50
YHANP--03-R-P11.	P49313	30 kDa ribonucleoprotein, chloroplast precursor (CP-RBP30)	70.968	155	1.14E-49

IP : 14.49.138.138, 2017-11-03 13:30:33

ab1					
YHANP--04-R-I21.ab1	P49198	40S RIBOSOMAL PROTEIN S3A	85.841	113	4.11E-51
YHANP--02-R-L15.ab1	AAM65672	4-coumarate-CoA ligase-like protein [Arabidopsis thaliana]	76.154	130	3.63316E-37
YHANP--04-R-P18.ab1	AAM60860	4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis protein, putative [Arabidopsis thaliana]	69.231	39	7.31E-09
YHANP--04-R-C13.ab1	AAM62519	50S ribosomal protein L3 [Arabidopsis thaliana]	61.039	77	8.17784E-10
YHANP--01-R-M22.ab1	P27684	50S ribosomal protein L40, chloroplast precursor (CL40)	49.451	91	2.35E-07
YHANP--03-R-K24.ab1	NP_564555	5-methylthioribose kinase family [Arabidopsis thaliana]	79.2	125	6.98E-52
YHANP--04-R-P14.ab1	NP_181933	6,7-dimethyl-8-ribityllumazine synthase / DMRL synthase / lumazine synthase / riboflavin synthase [Arabidopsis thaliana]	68.75	128	1.01007E-42
YHANP--02-R-H10.ab1	P46287	60S RIBOSOMAL PROTEIN L11 (L5)	99.254	134	4.35E-70
YHANP--02-R-L19.ab1	AAR83868	60S ribosomal protein L12 [Capsicum annuum]	94.286	140	1.85E-67
YHANP--04-R-M03.ab1	AAQ72789	60S ribosomal protein L5 [Cucumis sativus]	90.968	155	5.07E-76
YHANP--02-R-I13.ab1	NP_187967	60S ribosomal protein L7 (RPL7D) [Arabidopsis thaliana]	87.903	124	9.34E-44
YHANP--02-R-D20.ab1	BAB83610	6b-interacting protein 1 [Nicotiana tabacum]	64.228	123	5.29E-41
YHANP--02-R-E09.ab1	AAG50592	ABC transporter, putative [Arabidopsis thaliana]	45.333	150	1.44E-30
YHANP--03-R-G19.ab1	T09670	abscisic acid activated protein - alfalfa	64.286	42	5.45E-13
YHANP--01-R-H13.ab1	AAG49361	ACC oxidase [Citrus sinensis]	100	144	9.45E-78
YHANP--02-R-K06.ab1	CAC39078	acetylglutamate kinase-like protein [Oryza sativa]	68.354	79	3.9088E-15
YHANP--01-R-J06.ab1	NP_567449	acid phosphatase survival protein SurE, putative [Arabidopsis thaliana]	66.867	166	2.18156E-56
YHANP--02-R-C15.ab1	NP_565146	ACT domain containing protein [Arabidopsis thaliana]	60.759	158	3.21E-44
YHANP--04-R-A16.ab1	AAO38821	actin [Oryza sativa (japonica cultivar-group)]	100	126	3.33E-70
YHANP--04-R-C08.ab1	T50670	actin bundling protein ABP135 [imported] - trumpet lily	74.172	151	2.52E-61
YHANP--02-R-N18.ab1	AAD23407	actin depolymerizing factor [Populus x canescens]	93.75	64	5.38E-28
YHANP--02-R-M01.ab1	CAA05979	adenine nucleotide translocator [Lupinus albus]	98.734	79	1.18468E-30
YHANP--03-R-C14.ab1	AAD56042	ADP-glucose pyrophosphorylase large subunit [Citrus unshiu]	100	34	1.98334E-11
YHANP--03-R-G01.ab1	NP_191788	ADP-ribosylation factor [Arabidopsis thaliana]	84.559	136	4.36E-59
YHANP--04-R-N09.ab1	NP_190556	ADP-ribosylation factor, putative [Arabidopsis thaliana]	98.095	105	5.70897E-54
YHANP--03-R-O09.ab1	AAO61677	AKIN beta2 [Medicago truncatula]	77.358	159	5.94085E-70
YHANP--01-R-C21.ab1	AAA98987	alcohol dehydrogenase 2b	86.765	68	5.06E-29
YHANP--03-R-C01.ab1	NP_563770	aldo/keto reductase family protein [Arabidopsis thaliana]	80.556	108	1.44E-46
YHANP--04-R-P17.ab1	NP_566777	allene oxide cyclase, putative / early-responsive to dehydration protein, putative / ERD protein, putative [Arabidopsis thaliana]	52.817	142	1.69E-26
YHANP--02-R-B02.ab1	AAK48972	alpha NAC-like protein [Arabidopsis thaliana]	95.652	46	5.87054E-18
YHANP--03-R-J14.ab1	NP_563831	amidase family protein [Arabidopsis thaliana]	74.39	82	1.81E-28
YHANP--03-R-G18.ab1	BAD19146	ankyrin repeat protein-like [Oryza sativa (japonica cultivar-group)]	81.29	155	1.81E-63
YHANP--02-R-E22.ab1	AAM61215	anthranilate N-benzoyltransferase [Arabidopsis thaliana]	51.19	84	3.00E-20
YHANP--02-R-N16.ab1	AAF66599	apyrase [Arabidopsis thaliana]	64.754	122	9.74E-40
YHANP--03-R-B14.ab1	S57614	ARP protein - Arabidopsis thaliana	69.281	153	1.2353E-55
YHANP--01-R-O23.ab1	AAA86689	ascorbate peroxidase	94.681	94	1.38E-36
YHANP--03-R-P21.ab1	BAB20972	aspartic proteinase 4 [Nepenthes alata]	80.247	162	2.81E-67
YHANP--04-R-C17.ab1	AAL24250	At1g19180/T29M8_5 [Arabidopsis thaliana]	70.27	37	2.38E-07
YHANP--02-R-C24.ab1	AAL24250	At1g19180/T29M8_5 [Arabidopsis thaliana]	36.232	138	1.68E-13

IP : 14.49.138.138, 2017-11-03 13:30:33

YHANP--03-R-P23.ab1	AAP21223	At1g48300 [Arabidopsis thaliana]	55.435	92	6.10E-19
YHANP--01-R-K06.ab1	AAO42832	At2g03440 [Arabidopsis thaliana]	51.613	93	7.73247E-06
YHANP--01-R-D20.ab1	AAL38378	At2g13540/T10F5.8 [Arabidopsis thaliana]	69.032	155	1.3858E-57
YHANP--02-R-J21.ab1	AAK50114	At2g20140/T2G17.6 [Arabidopsis thaliana]	98.113	53	8.40E-15
YHANP--01-R-N18.ab1	AAL09731	At2g32240/F22D22.1 [Arabidopsis thaliana]	51.786	56	7.39E-06
YHANP--01-R-C04.ab1	AAM19833	At2g43410/T1O24.15 [Arabidopsis thaliana]	36.42	162	3.63E-08
YHANP--02-R-P16.ab1	AAT06481	At3g23540 [Arabidopsis thaliana]	59.74	77	4.12946E-20
YHANP--03-R-N14.ab1	AAG40343	AT4g13930 [Arabidopsis thaliana]	91.25	80	6.76E-38
YHANP--02-R-N09.ab1	AAL14388	AT4g15940/dl4011w [Arabidopsis thaliana]	84.733	131	6.30E-61
YHANP--01-R-P18.ab1	AAL77677	AT4g24270/T22A6_100 [Arabidopsis thaliana]	63.057	157	2.84E-45
YHANP--04-R-M10.ab1	AAK32887	AT4g24840/F6I7_50 [Arabidopsis thaliana]	71.918	146	3.2227E-40
YHANP--03-R-N15.ab1	AAG40400	AT4g27650 [Arabidopsis thaliana]	78.261	138	6.83E-50
YHANP--01-R-J07.ab1	AAL47484	AT5g10020/T31P16_9 [Arabidopsis thaliana]	77.193	57	9.00E-18
YHANP--02-R-G15.ab1	AAK50066	AT5g20410/F5O24_300 [Arabidopsis thaliana]	82.069	145	5.77E-66
YHANP--03-R-C21.ab1	AAL77697	AT5g20480/F7C8_70 [Arabidopsis thaliana]	44	150	3.40E-29
YHANP--03-R-F03.ab1	AAL15302	AT5g25900/T1N24_23 [Arabidopsis thaliana]	73.77	122	1.70E-45
YHANP--02-R-E19.ab1	AAK74003	AT5g39790/MKM21_80 [Arabidopsis thaliana]	75.676	37	1.80E-07
YHANP--03-R-E02.ab1	AAS76701	At5g48720 [Arabidopsis thaliana]	49.682	157	3.18E-33
YHANP--03-R-P14.ab1	CAC27141	ATP synthase beta chain precursor [Picea abies]	100	23	3.55E-06
YHANP--02-R-K09.ab1	P29685	ATP synthase beta chain, mitochondrial precursor	77.885	104	1.7437E-33
YHANP--01-R-G13.ab1	P26360	ATP synthase gamma chain, mitochondrial precursor	98.413	63	1.06E-26
YHANP--03-R-M12.ab1	NP_177679	ATP-dependent protease La (LON) domain-containing protein [Arabidopsis thaliana]	80.808	99	4.6586E-27
YHANP--02-R-H16.ab1	AAM91657	auxin response factor 1 [Arabidopsis thaliana]	83.636	55	2.16938E-20
YHANP--01-R-P05.ab1	AAP06759	auxin response factor-like protein [Mangifera indica]	71.698	106	1.7888E-37
YHANP--04-R-B06.ab1	AAP06759	auxin response factor-like protein [Mangifera indica]	69.369	111	1.84E-34
YHANP--02-R-L02.ab1	P40691	Auxin-induced protein PCNT115	79.747	158	4.40E-67
YHANP--01-R-O19.ab1	AAS75891	auxin-repressed protein [Solanum virginianum]	75.325	77	1.17568E-17
YHANP--03-R-G14.ab1	AAP03882	Avr9/Cf-9 rapidly elicited protein 276 [Nicotiana tabacum]	67.097	155	4.03205E-57
YHANP--03-R-J08.ab1	NP_915318	B1088C09.19 [Oryza sativa (japonica cultivar-group)]	47.917	144	7.85E-30
YHANP--02-R-L23.ab1	BAC05570	B1097D05.21 [Oryza sativa (japonica cultivar-group)]	85.811	148	2.47E-65
YHANP--03-R-B04.ab1	AAG01117	BAC19.2 [Lycopersicon esculentum]	34.328	134	1.94E-12
YHANP--03-R-E12.ab1	NP_180818	barren family protein [Arabidopsis thaliana]	63.636	55	4.33E-12
YHANP--04-R-F10.ab1	AAN03626	BEL1-related homeotic protein 29 [Solanum tuberosum]	50.575	87	5.01E-14
YHANP--02-R-O16.ab1	AAN03627	BEL1-related homeotic protein 30 [Solanum tuberosum]	78.71	155	1.69487E-61
YHANP--01-R-G09.ab1	AAG10793	beta-carotene hydroxylase [Citrus unshiu]	100	96	3.55E-34
YHANP--02-R-O03.ab1	AAN86822	beta-cyanoalanine synthase [Betula pendula]	75.893	112	1.56E-43
YHANP--01-R-N21.ab1	NP_176049	beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative [Arabidopsis thaliana]	87.821	156	2.3278E-76
YHANP--02-R-J07.ab1	BAB02059	blue copper-binding protein-like [Arabidopsis thaliana]	49.18	61	7.84E-10
YHANP--03-R-H03.ab1	NP_680660	BTB/POZ domain-containing protein [Arabidopsis thaliana]	79.452	73	8.79E-26
YHANP--02-R-E12.ab1	2119166A	caffeic acid O-methyltransferase	82.759	116	1.62E-53

IP : 14.49.138.138, 2017-11-03 13:30:33

YHANP--02-R-E24.ab1	AAS83524	caffeine synthase 1 [Camellia sinensis var. sinensis]	56.209	153	1.01E-42
YHANP--04-R-D13.ab1	NP_195026	calcineurin B-like protein 10 (CBL10) [Arabidopsis thaliana]	82.474	97	6.67278E-41
YHANP--03-R-P17.ab1	NP_195026	calcineurin B-like protein 10 (CBL10) [Arabidopsis thaliana]	41.935	62	4.5332E-06
YHANP--01-R-I20.ab1	NP_196037	calcium-binding EF hand family protein [Arabidopsis thaliana]	81.25	96	2.45E-40
YHANP--04-R-B24.ab1	NP_566657	calcium-binding EF hand family protein [Arabidopsis thaliana]	66.667	132	3.37E-49
YHANP--01-R-I19.ab1	NP_173259	calcium-binding protein, putative [Arabidopsis thaliana]	67.424	132	5.59E-46
YHANP--03-R-D02.ab1	NP_174807	calcium-dependent protein kinase 2 (CDPK2) [Arabidopsis thaliana]	88.462	156	2.75E-77
YHANP--03-R-N18.ab1	AAB86496	calmodulin [Zea mays]	100	47	2.74E-19
YHANP--03-R-D18.ab1	NP_201045	calmodulin-binding family protein [Arabidopsis thaliana]	42.69	171	3.94E-26
YHANP--01-R-A05.ab1	AAL76166	candidate plant disease resistance protein [Glycine max]	58.394	137	8.55E-42
YHANP--02-R-C05.ab1	T09793	carbonate dehydratase (EC 4.2.1.1) 1a - Populus tremula x Populus tremuloides	83.019	159	1.0522E-52
YHANP--04-R-K09.ab1	NP_567928	carbonic anhydrase family protein / carbonate dehydratase family protein [Arabidopsis thaliana]	62.162	37	4.9455E-10
YHANP--03-R-E11.ab1	AAM63923	carnitine racemase like protein [Arabidopsis thaliana]	70.807	161	2.77E-51
YHANP--03-R-L16.ab1	CAA57522	cathepsin B-like cysteine proteinase [Nicotiana rustica]	78.899	109	1.01755E-49
YHANP--02-R-D12.ab1	NP_567952	CBS domain-containing protein [Arabidopsis thaliana]	52.903	155	6.93E-33
YHANP--02-R-H07.ab1	S52663	ccr protein - Citrus paradisi	100	135	2.74E-71
YHANP--03-R-G06.ab1	CAA70572	CDPK-related protein kinase [Arabidopsis thaliana]	69.565	161	1.69E-32
YHANP--03-R-M14.ab1	AAL25130	cellulose synthase-like protein OsCslE2 [Oryza sativa]	50.476	105	4.82E-24
YHANP--02-R-P20.ab1	AAQ18797	central motor kinesin 1 [Gossypium hirsutum]	86.538	156	8.77E-71
YHANP--04-R-B16.ab1	1H1Y_A	Chain A, The Structure Of The Cytosolic D-Ribulose-5-Phosphate 3-Epimerase From Rice Complexed With Sulfate	84.956	113	2.26E-53
YHANP--02-R-M23.ab1	AAL91367	chimera1 [synthetic construct]	78.218	101	4.90E-42
YHANP--01-R-F18.ab1	AAO45885	chlorophyll a/b-binding protein precursor [Citrus limon]	99.213	127	8.57E-71
YHANP--01-R-K10.ab1	P27518	Chlorophyll a-b binding protein 151, chloroplast precursor (LHCII type II CAB-151) (LHCP)	94.783	115	2.81E-48
YHANP--04-R-E09.ab1	NP_191434	citrate synthase, glyoxysomal, putative [Arabidopsis thaliana]	72.656	128	6.60584E-47
YHANP--03-R-E23.ab1	NP_565912	complex 1 family protein / LVR family protein [Arabidopsis thaliana]	68.966	87	1.00E-23
YHANP--03-R-E17.ab1	AAM64362	contains similarity to ethylene responsive element binding factor [Arabidopsis thaliana]	49.351	154	3.98E-31
YHANP--02-R-K05.ab1	AAM61381	contains similarity to peroxisomal membrane carrier protein [Arabidopsis thaliana]	85.075	67	6.27214E-20
YHANP--04-R-N18.ab1	NP_196946	copine-related [Arabidopsis thaliana]	71.429	63	2.43E-12
YHANP--04-R-N03.ab1	NP_565206	copine-related [Arabidopsis thaliana]	75	48	8.61E-18
YHANP--03-R-E15.ab1	AAR82925	coronatine-insensitive 1 [Lycopersicon esculentum]	72.414	87	2.91E-35
YHANP--02-R-B08.ab1	AAN62336	CTV.2 [Poncirus trifoliata]	70.866	127	2.77E-47
YHANP--02-R-L04.ab1	NP_199674	cyclin family protein [Arabidopsis thaliana]	77.333	150	8.49146E-66
YHANP--02-R-J09.ab1	AAL51087	cyclophilin [Glycine max]	88.608	79	9.30E-37
YHANP--04-R-J23.ab1	NP_568727	cyclopropyl isomerase (CPI1) [Arabidopsis thaliana]	86.047	43	1.54E-23
YHANP--02-R-A06.ab1	AAG38521	cystatin-like protein [Citrus x paradisi]	100	118	2.15E-63
YHANP--01-R-G17.ab1	NP_564126	cysteine endopeptidase, papain-type (XCP2) [Arabidopsis thaliana]	68.675	83	3.02E-26
YHANP--02-R-G02.ab1	AAF72202	cysteine protease inhibitor [Manihot esculenta]	61.616	99	8.04E-24
YHANP--01-R-L07.ab1	T10944	cysteine proteinase (EC 3.4.22.-) precursor - spring vetch	73.418	79	3.28E-28
YHANP--03-R-E14.ab1	CAA04703	cytochome b5 [Olea europaea]	57.692	52	4.33E-09
YHANP--02-R-C12.ab1	NP_198679	cytochrome B561 family protein [Arabidopsis thaliana]	77.966	118	5.06E-47

IP : 14.49.138.138, 2017-11-03 13:30:33

YHANP--03-R-I11.ab1	NP_173935	cytochrome B561 family protein [Arabidopsis thaliana]	72.152	158	6.44051E-61
YHANP--03-R-I12.ab1	P26291	Cytochrome B6-F complex iron-sulfur subunit, chloroplast precursor (Rieske iron-sulfur protein) (RISP)	70.085	117	5.92158E-43
YHANP--02-R-D06.ab1	T03634	cytochrome P450 - common tobacco	67.32	153	2.79228E-58
YHANP--01-R-L10.ab1	CAA04117	cytochrome P450 [Helianthus tuberosus]	46.667	135	1.4694E-32
YHANP--01-R-D11.ab1	O49858	Cytochrome P450 82A3 (P450 CP6)	59.524	42	1.05E-06
YHANP--01-R-F15.ab1	NP_190897	cytochrome P450, putative [Arabidopsis thaliana]	39.655	116	5.1507E-14
YHANP--03-R-B15.ab1	NP_173149	cytochrome P450, putative [Arabidopsis thaliana]	52.703	74	1.47E-17
YHANP--01-R-J12.ab1	NP_188087	cytochrome P450, putative [Arabidopsis thaliana]	51.938	129	1.22E-35
YHANP--03-R-J02.ab1	NP_194922	cytochrome P450, putative [Arabidopsis thaliana]	71.25	80	2.73113E-27
YHANP--02-R-G16.ab1	AAT40507	cytoplasmic ribosomal protein S13 [Solanum demissum]	98.519	135	1.95E-70
YHANP--03-R-A24.ab1	AAO41731	cytoplasmic ribosomal protein S14 [Brassica napus]	93.6	125	6.98E-52
YHANP--03-R-B12.ab1	AAO41731	cytoplasmic ribosomal protein S14 [Brassica napus]	95.172	145	3.37E-65
YHANP--01-R-G20.ab1	CAB55566	cytosolic phosphoglucose isomerase [Clarkia gracilis]	85.246	61	1.05E-23
YHANP--01-R-N10.ab1	CAA10694	D1-processing protease [Arabidopsis thaliana]	75	80	1.60E-27
YHANP--03-R-O16.ab1	AAF75749	dehydration-induced protein ERD15 [Lycopersicon esculentum]	58.929	112	4.60181E-30
YHANP--03-R-I01.ab1	NP_193537	dehydration-responsive family protein [Arabidopsis thaliana]	85.987	157	4.34E-78
YHANP--02-R-B16.ab1	AAL26909	dehydration-responsive protein RD22 [Prunus persica]	64.286	42	2.12E-13
YHANP--01-R-G21.ab1	AAL32062	deoxy-D-xylulose-5-phosphate synthase [Morinda citrifolia]	87.805	41	9.63E-14
YHANP--02-R-L14.ab1	NP_190926	diaminopimelate epimerase family protein [Arabidopsis thaliana]	83.333	90	1.46E-27
YHANP--04-R-B09.ab1	NP_683441	disease resistance protein (CC-NBS-LRR class), putative [Arabidopsis thaliana]	43.617	94	4.95E-08
YHANP--01-R-M02.ab1	NP_176113	disease resistance-responsive protein-related / dirigent protein-related [Arabidopsis thaliana]	55.769	104	2.42E-28
YHANP--04-R-L07.ab1	NP_195128	DJ-1 family protein [Arabidopsis thaliana]	64.286	56	2.24E-13
YHANP--02-R-E11.ab1	NP_564626	DJ-1 family protein [Arabidopsis thaliana]	62.581	155	4.95E-45
YHANP--02-R-H14.ab1	BAC81662	DNA binding with one finger 5 protein [Pisum sativum]	61.818	110	4.74E-36
YHANP--02-R-O08.ab1	NP_563854	DNA polymerase delta subunit 4 family [Arabidopsis thaliana]	64.286	126	5.74E-38
YHANP--04-R-P22.ab1	BAB02486	DNA topoisomerase VI subunit B-like protein [Arabidopsis thaliana]	88.991	109	2.38E-39
YHANP--03-R-N09.ab1	NP_200849	DNA-binding family protein [Arabidopsis thaliana]	52.991	117	1.18743E-22
YHANP--04-R-G20.ab1	NP_187752	DNAJ heat shock N-terminal domain-containing protein / cell division protein-related [Arabidopsis thaliana]	55.446	101	1.15E-19
YHANP--03-R-H09.ab1	NP_564336	double-stranded DNA-binding family protein [Arabidopsis thaliana]	83.193	119	1.09024E-47
YHANP--01-R-B23.ab1	AAP13820	DVL5 [Arabidopsis thaliana]	92.308	26	1.37787E-07
YHANP--02-R-P18.ab1	AAD25856	dynamin-like protein [Arabidopsis thaliana]	83.974	156	1.65E-69
YHANP--02-R-O18.ab1	AAQ73529	early flowering 3 [Mesembryanthemum crystallinum]	46.809	94	4.14E-12
YHANP--03-R-B22.ab1	NP_567575	early-responsive to dehydration stress protein (ERD3) [Arabidopsis thaliana]	84.932	146	1.30112E-73
YHANP--04-R-L16.ab1	BAB13711	elicitor inducible protein [Nicotiana tabacum]	82.759	29	3.52E-07
YHANP--04-R-L06.ab1	AAK62346	elicitor-inducible cytochrome P450 [Nicotiana tabacum]	63.478	115	9.07E-32
YHANP--02-R-L22.ab1	AAL79774	elongation factor 1 alpha [Saccharum hybrid cultivar CP65-357]	96.774	62	3.15E-28
YHANP--01-R-A20.ab1	BAC23049	Elongation factor 1-alpha [Solanum tuberosum]	96.835	158	2.20E-85
YHANP--03-R-E21.ab1	A96602	elongation factor EF-2 [imported] - Arabidopsis thaliana	90.244	41	2.62E-13
YHANP--02-R-I12.ab1	BAC22691	endo-1,4-beta-D-glucanase [Pyrus communis]	90	60	2.16E-25
YHANP--02-R-I01.ab1	NP_193002	endomembrane protein 70, putative [Arabidopsis thaliana]	92.157	51	4.92554E-20

IP : 14.49.138.138, 2017-11-03 13:30:33

YHANP--03-R-L14.ab1	NP_178306	endomembrane protein 70, putative [Arabidopsis thaliana]	95.062	81	7.17E-36
YHANP--01-R-I06.ab1	NP_188674	endoribonuclease L-PSP family protein [Arabidopsis thaliana]	72.258	155	8.43E-53
YHANP--04-R-B14.ab1	CAB65283	Enod93 protein [Medicago sativa subsp. x varia]	67.568	74	6.10E-23
YHANP--03-R-J07.ab1	Q9ZTN2	ER lumen protein retaining receptor (HDEL receptor) (PGP169-12)	88.462	130	1.61785E-67
YHANP--01-R-B18.ab1	NP_199234	ERF domain protein 9 (ERF9) [Arabidopsis thaliana]	34.356	163	1.92E-09
YHANP--04-R-H21.ab1	BAD01556	ERF-like protein [Cucumis melo]	62.963	54	1.13E-10
YHANP--01-R-K23.ab1	NP_566801	esterase/lipase/thioesterase family protein [Arabidopsis thaliana]	61.957	92	6.02E-24
YHANP--01-R-F21.ab1	NP_910315	ESTs AU082454(S3638),D41267(S3638) correspond to a region of the predicted gene.~Similar to Arabidopsis thaliana DNA chromosome 4, BAC clone T5K18; hypothetical protein (AL022580) [Oryza sativa (japonica cultivar-group)]	67.785	149	3.58E-48
YHANP--02-R-N23.ab1	CAD21849	ethylene responsive element binding protein [Fagus sylvatica]	62.658	158	8.36704E-40
YHANP--02-R-N19.ab1	AAK58599	ethylene-induced esterase [Citrus sinensis]	71.233	73	4.15E-25
YHANP--01-R-H18.ab1	NP_191427	ethylene-responsive transcriptional coactivator, putative [Arabidopsis thaliana]	85.612	139	2.56E-62
YHANP--02-R-E04.ab1	AAS07262	eukaryotic peptide chain release factor subunit 1-3 (eRF1-3) [Oryza sativa (japonica cultivar-group)]	97.452	157	4.05355E-84
YHANP--03-R-G11.ab1	AAQ08191	eukaryotic translation initiation factor 5A isoform I [Hevea brasiliensis]	92.683	82	5.42336E-39
YHANP--03-R-G17.ab1	Q9AXQ5	Eukaryotic translation initiation factor 5A-2 (eIF-5A 2)	98.684	76	1.08084E-63
YHANP--03-R-I07.ab1	NP_565058	eukaryotic translation initiation factor-related [Arabidopsis thaliana]	71.429	49	1.44314E-11
YHANP--02-R-P19.ab1	NP_197952	exonuclease family protein [Arabidopsis thaliana]	63.636	110	5.86E-32
YHANP--01-R-N15.ab1	NP_187125	expressed protein (SWP1) [Arabidopsis thaliana]	80.625	160	1.28E-64
YHANP--04-R-J01.ab1	NP_176911	expressed protein [Arabidopsis thaliana]	54.412	68	2.08E-07
YHANP--04-R-O04.ab1	NP_568340	expressed protein [Arabidopsis thaliana]	63.38	71	1.60E-11
YHANP--01-R-L03.ab1	NP_680687	expressed protein [Arabidopsis thaliana]	32.258	186	5.98E-21
YHANP--02-R-O20.ab1	NP_973572	expressed protein [Arabidopsis thaliana]	75	56	1.52E-21
YHANP--02-R-K02.ab1	NP_683424	expressed protein [Arabidopsis thaliana]	46.617	133	3.99E-23
YHANP--01-R-B04.ab1	NP_194153	expressed protein [Arabidopsis thaliana]	81.25	64	3.67133E-26
YHANP--01-R-F14.ab1	NP_565718	expressed protein [Arabidopsis thaliana]	70.69	58	1.01373E-19
YHANP--04-R-K20.ab1	NP_564781	expressed protein [Arabidopsis thaliana]	78.431	51	1.76E-18
YHANP--02-R-A10.ab1	NP_194153	expressed protein [Arabidopsis thaliana]	59.596	99	1.08E-25
YHANP--03-R-B20.ab1	NP_565384	expressed protein [Arabidopsis thaliana]	36.364	77	1.25243E-07
YHANP--02-R-H19.ab1	NP_197062	expressed protein [Arabidopsis thaliana]	35.294	119	1.24E-07
YHANP--03-R-O03.ab1	NP_850924	expressed protein [Arabidopsis thaliana]	46.835	79	2.40E-11
YHANP--04-R-N13.ab1	NP_564507	expressed protein [Arabidopsis thaliana]	42.718	103	3.77E-17
YHANP--02-R-G13.ab1	NP_189301	expressed protein [Arabidopsis thaliana]	89.286	28	9.32E-08
YHANP--01-R-J23.ab1	NP_564201	expressed protein [Arabidopsis thaliana]	41.379	87	5.28E-11
YHANP--02-R-J16.ab1	NP_178935	expressed protein [Arabidopsis thaliana]	60.494	81	1.23E-20
YHANP--04-R-O07.ab1	NP_683304	expressed protein [Arabidopsis thaliana]	53.333	120	4.29E-24
YHANP--04-R-A14.ab1	NP_196582	expressed protein [Arabidopsis thaliana]	95.105	143	7.75E-76
YHANP--02-R-E14.ab1	NP_191180	expressed protein [Arabidopsis thaliana]	70.588	153	7.60E-56
YHANP--02-R-E08.ab1	NP_196851	expressed protein [Arabidopsis thaliana]	49.618	131	1.35E-20
YHANP--03-R-J23.ab1	NP_190679	expressed protein [Arabidopsis thaliana]	66.234	77	3.3454E-25
YHANP--02-R-F12.ab1	NP_194660	expressed protein [Arabidopsis thaliana]	81.25	32	2.02913E-08
YHANP--02-R-G19.	NP_563929	expressed protein [Arabidopsis thaliana]	73.77	122	2.08E-37

IP : 14.49.138.138, 2017-11-03 13:30:33

ab1					
YHANP--02-R-M20.ab1	NP_565868	expressed protein [Arabidopsis thaliana]	71.141	149	5.05E-55
YHANP--04-R-M16.ab1	NP_565921	expressed protein [Arabidopsis thaliana]	45.833	120	3.20E-17
YHANP--03-R-B03.ab1	NP_194233	expressed protein [Arabidopsis thaliana]	76.471	102	4.75E-37
YHANP--02-R-E15.ab1	NP_850153	expressed protein [Arabidopsis thaliana]	78.351	97	3.19E-25
YHANP--01-R-J15.ab1	NP_566427	expressed protein [Arabidopsis thaliana]	82.857	105	9.21769E-49
YHANP--01-R-I01.ab1	NP_564082	expressed protein [Arabidopsis thaliana]	62.791	86	1.64E-13
YHANP--01-R-N24.ab1	NP_191227	expressed protein [Arabidopsis thaliana]	54.217	83	1.70E-18
YHANP--02-R-K20.ab1	NP_173046	expressed protein [Arabidopsis thaliana]	61.935	155	9.43E-49
YHANP--01-R-M20.ab1	NP_178346	expressed protein [Arabidopsis thaliana]	71.154	52	2.34E-15
YHANP--01-R-O22.ab1	NP_201239	expressed protein [Arabidopsis thaliana]	41.06	151	1.98503E-14
YHANP--02-R-E05.ab1	NP_188891	expressed protein [Arabidopsis thaliana]	35.821	67	7.56E-06
YHANP--03-R-N19.ab1	NP_177533	expressed protein [Arabidopsis thaliana]	78.981	157	1.31004E-66
YHANP--01-R-I23.ab1	NP_194505	expressed protein [Arabidopsis thaliana]	59.06	149	1.78E-39
YHANP--01-R-J24.ab1	NP_564480	expressed protein [Arabidopsis thaliana]	64.865	111	1.04E-34
YHANP--04-R-K11.ab1	NP_564344	expressed protein [Arabidopsis thaliana]	81.579	76	1.55E-30
YHANP--02-R-A05.ab1	NP_565383	expressed protein [Arabidopsis thaliana]	70.787	89	9.09E-23
YHANP--03-R-P22.ab1	NP_181016	expressed protein [Arabidopsis thaliana]	74.342	152	1.48478E-57
YHANP--04-R-O21.ab1	NP_565761	expressed protein [Arabidopsis thaliana]	88.811	143	1.33982E-66
YHANP--01-R-K08.ab1	NP_180718	expressed protein [Arabidopsis thaliana]	48.256	172	2.55E-33
YHANP--03-R-M02.ab1	NP_851134	expressed protein [Arabidopsis thaliana]	40	135	1.23E-11
YHANP--02-R-N24.ab1	NP_177770	expressed protein [Arabidopsis thaliana]	54.955	111	2.92E-29
YHANP--03-R-A11.ab1	NP_568600	expressed protein [Arabidopsis thaliana]	53.684	95	2.08E-14
YHANP--04-R-A11.ab1	NP_566131	expressed protein [Arabidopsis thaliana]	77.358	53	3.77E-08
YHANP--02-R-A22.ab1	NP_568287	expressed protein [Arabidopsis thaliana]	55.085	118	2.35E-26
YHANP--04-R-M06.ab1	NP_188110	expressed protein [Arabidopsis thaliana]	58.824	85	1.12E-16
YHANP--03-R-F14.ab1	AAS07181	expressed protein [Oryza sativa (japonica cultivar-group)]	65.152	66	9.19947E-20
YHANP--02-R-K03.ab1	AAM47507	extensin-like protein [Citrus junos]	74.51	51	8.82E-17
YHANP--01-R-M12.ab1	AAF79238	F10B6.23 [Arabidopsis thaliana]	91.736	121	1.06654E-47
YHANP--01-R-M24.ab1	C86268	F13B4.2 protein - Arabidopsis thaliana	50.515	97	3.73E-21
YHANP--01-R-C11.ab1	AAF79339	F14J16.7 [Arabidopsis thaliana]	64.189	148	8.17E-48
YHANP--01-R-I02.ab1	NP_568140	F1F0-ATPase inhibitor protein, putative [Arabidopsis thaliana]	51.613	62	1.08E-06
YHANP--01-R-O17.ab1	AAF19552	F23N19.4 [Arabidopsis thaliana]	39.241	158	1.11E-28
YHANP--04-R-J17.ab1	AAF19695	F2K11.3 [Arabidopsis thaliana]	44.545	110	1.61E-11
YHANP--02-R-M06.ab1	AAT37954	fasciclin-like AGP 11 [Populus alba x Populus tremula]	79.739	153	8.03E-63
YHANP--04-R-L04.ab1	AAK15070	fatty acid hydroperoxide lyase [Psidium guajava]	100	36	7.14E-16
YHANP--02-R-I20.ab1	NP_181023	fatty acid hydroxylase (FAH1) [Arabidopsis thaliana]	75.532	94	1.87E-40
YHANP--01-R-N08.ab1	NP_564350	F-box family protein [Arabidopsis thaliana]	39.437	142	2.02E-18
YHANP--03-R-K01.ab1	Q8H1T3	Ferritin 2, chloroplast precursor (NtFer2)	69.027	113	1.76119E-36
YHANP--01-R-M10.ab1	AAN77145	fiber protein Fb2 [Gossypium barbadense]	54.412	136	3.37E-30

IP : 14.49.138.138, 2017-11-03 13:30:33

YHANP--02-R-J02.ab1	AAQ84314	fiber protein Fb25 [Gossypium barbadense]	83.75	80	1.48E-36
YHANP--04-R-H06.ab1	AAR07599	fiber protein Fb37 [Gossypium barbadense]	81.356	59	2.41E-22
YHANP--02-R-O13.ab1	Q40284	Flavonol 3-O-glucosyltransferase 1 (UDP-glucose flavonoid 3-O-glucosyltransferase 1)	64.356	101	4.13354E-32
YHANP--01-R-M03.ab1	NP_567166	fringe-related protein [Arabidopsis thaliana]	41.333	75	5.00E-07
YHANP--02-R-G20.ab1	AAS67872	fructokinase [Citrus unshiu]	90.598	117	3.14999E-46
YHANP--03-R-I17.ab1	NP_178224	fructose-bisphosphate aldolase, putative [Arabidopsis thaliana]	78.723	141	5.97E-54
YHANP--03-R-H19.ab1	NP_567691	FtsH protease, putative [Arabidopsis thaliana]	82.192	146	1.17E-66
YHANP--02-R-P24.ab1	Q9M5Q1	Galactoside 2-alpha-L-fucosyltransferase (Xyloglucan alpha-(1,2)-fucosyltransferase) (PsFT1)	87.023	131	1.71E-58
YHANP--01-R-H12.ab1	NP_176215	gamma-adaptin, putative [Arabidopsis thaliana]	54.286	105	9.51306E-15
YHANP--04-R-M12.ab1	AAM53943	gamma-terpinene synthase [Citrus limon]	61.364	44	4.41279E-08
YHANP--01-R-O02.ab1	AAO24774	GCPE protein [Catharanthus roseus]	87.821	156	1.36E-76
YHANP--03-R-M18.ab1	AAK26637	GF14 kappa [Brassica napus]	83.019	106	2.71849E-43
YHANP--03-R-C05.ab1	AAB49334	GF14 mu [Arabidopsis thaliana]	88.333	60	9.29E-23
YHANP--04-R-P02.ab1	NP_564785	glucose-6-phosphate/phosphate translocator, putative [Arabidopsis thaliana]	91.275	149	3.94E-63
YHANP--03-R-G08.ab1	T06254	glucose-6-phosphate/phosphate-translocator precursor, plastid - garden pea	90.244	41	6.97752E-15
YHANP--02-R-I03.ab1	BAB88935	glucosyltransferase NTGT2 [Nicotiana tabacum]	58.333	144	2.62E-42
YHANP--02-R-A15.ab1	AAB61597	glutamine synthetase [Hevea brasiliensis]	100	30	8.09952E-11
YHANP--03-R-F21.ab1	AAB61597	glutamine synthetase [Hevea brasiliensis]	97.561	123	7.85E-67
YHANP--04-R-E15.ab1	P26518	Glyceraldehyde 3-phosphate dehydrogenase, cytosolic	94.737	114	5.45869E-59
YHANP--03-R-C12.ab1	BAA92155	glycine-rich protein [Citrus unshiu]	100	31	3.73732E-10
YHANP--04-R-G02.ab1	AAM97079	glycine--tRNA ligase precursor, chloroplast (edd1) [Arabidopsis thaliana]	57.692	156	3.28E-35
YHANP--03-R-E16.ab1	NP_565652	glycosyl hydrolase family 17 protein [Arabidopsis thaliana]	63.265	98	3.98E-31
YHANP--04-R-D21.ab1	NP_564059	glycosyl hydrolase family protein 17 [Arabidopsis thaliana]	63.38	71	6.26E-24
YHANP--02-R-O14.ab1	NP_190963	glyoxal oxidase-related [Arabidopsis thaliana]	79.268	82	5.53E-32
YHANP--03-R-P01.ab1	NP_563985	Golgi SNARE 11 protein [Arabidopsis thaliana]	84.247	146	8.79E-63
YHANP--01-R-K02.ab1	AAL49957	GTP cyclohydrolase I [Lycopersicon esculentum]	71.875	64	2.05E-18
YHANP--01-R-M01.ab1	NP_176029	GTP-binding protein (SAR1B) [Arabidopsis thaliana]	96.226	53	4.244E-22
YHANP--04-R-D18.ab1	AAK15703	GTP-binding protein [Oryza sativa]	97.143	105	9.58716E-53
YHANP--01-R-N13.ab1	S72515	GTP-binding protein RAB1 - garden petunia	98.519	135	5.93E-72
YHANP--01-R-E14.ab1	P93398	Guanine nucleotide-binding protein beta subunit 2	87.5	96	5.59E-46
YHANP--02-R-G05.ab1	Q39836	Guanine nucleotide-binding protein beta subunit-like protein	95	140	6.07E-72
YHANP--02-R-A08.ab1	NP_199109	GYF domain-containing protein [Arabidopsis thaliana]	60	110	2.21441E-18
YHANP--04-R-E04.ab1	BAA34919	heat shock protein 70 cognate [Salix gilgiana]	93.151	73	9.5942E-19
YHANP--03-R-O07.ab1	CAB52689	hexose transporter [Lycopersicon esculentum]	80	55	1.43E-19
YHANP--01-R-E05.ab1	NP_564276	histidine kinase (AHK3) [Arabidopsis thaliana]	70.079	127	1.47163E-46
YHANP--04-R-J21.ab1	NP_565424	histidine kinase 1 [Arabidopsis thaliana]	45.161	93	2.67174E-10
YHANP--01-R-F13.ab1	CAC20728	histidinol phosphate aminotransferase [Nicotiana plumbaginifolia]	84	100	1.22E-43
YHANP--02-R-M17.ab1	AAN37904	histone H1D [Nicotiana tabacum]	54.545	66	2.71E-08
YHANP--04-R-C21.ab1	AAL73044	histone H1-like protein [Zea mays]	52.866	157	1.23E-36
YHANP--02-R-P12.ab1	NP_175517	histone H2A, putative [Arabidopsis thaliana]	93.182	132	7.56E-43

IP : 14.49.138.138, 2017-11-03 13:30:33

YHANP--03-R-E22.ab1	NP_192234	homeobox-leucine zipper family protein [Arabidopsis thaliana]	71.667	60	5.96E-19
YHANP--01-R-D15.ab1	NP_849984	homogentisate phytylprenyltransferase family protein (HPT1) / tocopherol phytyltransferase family protein (TPT1) [Arabidopsis thaliana]	46.154	65	5.28E-12
YHANP--01-R-F05.ab1	Q9AR73	Hydroquinone glucosyltransferase (Arbutin synthase)	56.604	159	1.52E-43
YHANP--02-R-M22.ab1	NP_194559	hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana]	51.402	107	1.58E-18
YHANP--03-R-F23.ab1	AAN17455	hypersensitive-induced reaction protein 2 [Hordeum vulgare subsp. vulgare]	90.217	92	7.24E-41
YHANP--04-R-L15.ab1	AAF63769	hypothetical protein [Arabidopsis thaliana]	66.452	155	4.45E-64
YHANP--02-R-G24.ab1	AAF00640	hypothetical protein [Arabidopsis thaliana]	67.949	156	1.37E-39
YHANP--03-R-K20.ab1	AAO86843	hypothetical protein [Arabidopsis thaliana]	75	72	4.71E-24
YHANP--02-R-L21.ab1	CAA10123	hypothetical protein [Cicer arietinum]	58.209	67	4.59902E-10
YHANP--01-R-H01.ab1	BAB41197	hypothetical protein [Glycine max]	76.667	120	4.28178E-46
YHANP--02-R-C09.ab1	D86242	hypothetical protein [imported] - Arabidopsis thaliana	56.329	158	1.05E-44
YHANP--04-R-N05.ab1	B86191	hypothetical protein [imported] - Arabidopsis thaliana	68.59	156	7.72E-51
YHANP--01-R-P07.ab1	BAD06470	hypothetical protein [Nicotiana tabacum]	92.754	69	4.76E-29
YHANP--04-R-P16.ab1	S25786	hypothetical protein 3 - potato transposon Tst1	44.882	127	3.45E-24
YHANP--04-R-P19.ab1	S25786	hypothetical protein 3 - potato transposon Tst1	41.667	84	7.6285E-11
YHANP--02-R-M08.ab1	AAR99367	hypothetical protein At2g17705 [Arabidopsis thaliana]	68.8	125	3.58418E-48
YHANP--02-R-B12.ab1	E84710	hypothetical protein At2g30610 [imported] - Arabidopsis thaliana	75	72	1.35E-28
YHANP--01-R-D09.ab1	E84812	hypothetical protein At2g39050 [imported] - Arabidopsis thaliana	61.589	151	9.43E-49
YHANP--01-R-L06.ab1	E84813	hypothetical protein At2g39130 [imported] - Arabidopsis thaliana	83.333	138	1.13E-64
YHANP--02-R-C04.ab1	A84820	hypothetical protein At2g39670 [imported] - Arabidopsis thaliana	91.803	61	6.62E-45
YHANP--04-R-J08.ab1	A84823	hypothetical protein At2g39920 [imported] - Arabidopsis thaliana	39.241	79	1.14E-13
YHANP--04-R-G10.ab1	B85200	hypothetical protein AT4g17830 [imported] - Arabidopsis thaliana	85.567	97	6.29815E-44
YHANP--01-R-N07.ab1	E71422	hypothetical protein dl3905c - Arabidopsis thaliana	44.615	65	3.35E-09
YHANP--03-R-F02.ab1	C86159	hypothetical protein F22D16.11 - Arabidopsis thaliana	78.947	76	2.31E-28
YHANP--04-R-G18.ab1	A86146	hypothetical protein F22L4.8 - Arabidopsis thaliana	72.897	107	1.71378E-15
YHANP--04-R-I11.ab1	B96632	hypothetical protein F8A5.20 [imported] - Arabidopsis thaliana	70.492	61	3.86E-12
YHANP--04-R-M19.ab1	G96571	hypothetical protein F8L10.3 [imported] - Arabidopsis thaliana	57.616	151	1.28E-40
YHANP--03-R-N22.ab1	XP_389378	hypothetical protein FG09202.1 [Gibberella zeae PH-1]	44.444	45	6.99E-07
YHANP--04-R-O06.ab1	T48044	hypothetical protein T12C14.220 - Arabidopsis thaliana	56.667	150	1.07E-41
YHANP--01-R-B10.ab1	T01838	hypothetical protein T15F16.14 - Arabidopsis thaliana	45.806	155	7.90E-13
YHANP--02-R-M10.ab1	C86390	hypothetical protein T1K7.26 - Arabidopsis thaliana	59.756	82	3.05E-17
YHANP--02-R-P15.ab1	C96703	hypothetical protein T23K23.13 [imported] - Arabidopsis thaliana	81.333	75	8.83E-29
YHANP--04-R-C03.ab1	AAG51366	hypothetical protein; 78375-76401 [Arabidopsis thaliana]	53.125	128	8.51E-26
YHANP--02-R-C16.ab1	AAK38726	importin alpha 1 [Capsicum annuum]	86.429	140	8.53E-50
YHANP--04-R-K14.ab1	AAR83873	induced stolon tip protein NAP1Ps [Capsicum annuum]	49.425	87	4.37E-11
YHANP--01-R-G18.ab1	NP_196527	inorganic pyrophosphatase family protein [Arabidopsis thaliana]	86.667	75	1.34E-33
YHANP--04-R-L01.ab1	NP_191509	integral membrane HRF1 family protein [Arabidopsis thaliana]	79.339	121	6.74E-55
YHANP--02-R-G18.ab1	P52581	Isoflavone reductase homolog	80.892	157	6.43E-69
YHANP--02-R-G08.ab1	AAG43411	JAB [Lycopersicon esculentum]	81.25	144	1.66E-61
YHANP--01-R-I13.ab1	AAN62342	Jp18 [Poncirus trifoliata]	98.658	149	2.30E-79

IP : 14.49.138.138, 2017-11-03 13:30:33

YHANP--04-R-A18.ab1	CAA73905	JR3 protein [Arabidopsis thaliana]	57.317	82	9.55E-21
YHANP--01-R-F06.ab1	AAL87543	KAP-2 [Medicago truncatula]	68.182	132	1.04284E-47
YHANP--02-R-C08.ab1	AAP43505	katanin-like protein [Gossypium hirsutum]	96.341	82	1.07E-39
YHANP--03-R-C07.ab1	NP_851040	KH domain-containing protein [Arabidopsis thaliana]	66.225	151	1.87E-48
YHANP--01-R-F19.ab1	NP_564690	Kin17 DNA-binding protein-related [Arabidopsis thaliana]	83.846	130	4.51E-59
YHANP--04-R-E10.ab1	AAP51059	latex cyanogenic beta glucosidase [Hevea brasiliensis]	88.889	27	5.76E-08
YHANP--01-R-F20.ab1	AAG38522	lectin-related protein precursor [Citrus x paradisi]	98.182	55	1.09E-25
YHANP--01-R-I12.ab1	NP_565210	LEM3 (ligand-effect modulator 3) family protein / CDC50 family protein [Arabidopsis thaliana]	72.034	118	1.51E-46
YHANP--02-R-I23.ab1	NP_171929	lesion inducing protein-related [Arabidopsis thaliana]	70.093	107	9.81E-30
YHANP--03-R-I19.ab1	NP_197965	leucine-rich repeat family protein / protein kinase family protein [Arabidopsis thaliana]	65.789	152	4.37121E-54
YHANP--04-R-D17.ab1	AAG32022	LEUNIG [Arabidopsis thaliana]	89.333	75	3.18281E-33
YHANP--03-R-J11.ab1	Q9MB73	Limonoid UDP-glucosyltransferase (Limonoid glucosyltransferase) (Limonoid GTase) (LGTase)	98.765	162	2.33E-82
YHANP--01-R-L04.ab1	NP_973975	lipase class 3 family protein [Arabidopsis thaliana]	62	50	5.89E-11
YHANP--04-R-B12.ab1	AAM21292	lipid-transfer protein [Citrus sinensis]	70.455	88	1.06E-28
YHANP--01-R-E12.ab1	CAC08341	lipoic acid synthase-like protein [Arabidopsis thaliana]	68.235	85	5.15069E-26
YHANP--03-R-B11.ab1	BAB84352	lipoxygenase [Citrus jambhiri]	98.726	157	3.20E-89
YHANP--04-R-H02.ab1	BAA77218	LON protease homologue [Lithospermum erythrorhizon]	93.548	31	1.40233E-07
YHANP--02-R-K08.ab1	P53393	Low affinity sulphate transporter 3	63.333	90	2.73113E-27
YHANP--02-R-O24.ab1	AAO20104	mads-box transcription factor [Momordica charantia]	70.423	71	2.52774E-22
YHANP--03-R-O15.ab1	CAA96549	major allergen Cor a 1 [Corylus avellana]	52.482	141	8.77E-34
YHANP--01-R-H05.ab1	O24248	Major allergen Pru av 1 (Pru a 1)	52.252	111	1.50E-27
YHANP--01-R-F01.ab1	BAB85921	maturase K [Citrus maxima]	100	84	1.06E-58
YHANP--03-R-O24.ab1	AAS46232	methionine sulfoxide reductase A [Populus balsamifera subsp. trichocarpa x Populus deltoides]	81.579	114	1.13E-46
YHANP--04-R-N02.ab1	AAR01748	methylenetetrahydrofolate reductase, 3-partial [Oryza sativa (japonica cultivar-group)]	78.689	61	7.12E-23
YHANP--01-R-B21.ab1	AAL18925	mevalonate kinase [Hevea brasiliensis]	84.713	157	9.38841E-65
YHANP--03-R-N17.ab1	AAG38518	miraculin-like protein 2 [Citrus x paradisi]	99.213	127	5.81E-70
YHANP--01-R-L11.ab1	AAG38519	miraculin-like protein 3 [Citrus x paradisi]	98.529	68	4.57E-19
YHANP--01-R-L23.ab1	NP_567754	mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein [Arabidopsis thaliana]	65.714	105	4.25E-33
YHANP--03-R-N07.ab1	AAN65180	mitogen-activated protein kinase 4 [Petroselinum crispum]	87.387	111	4.83E-53
YHANP--03-R-D09.ab1	T14915	mitogen-activated protein kinase I (EC 2.7.1.-) - parsley	84.211	133	1.53E-62
YHANP--03-R-N12.ab1	NP_199799	mitotic checkpoint family protein [Arabidopsis thaliana]	60.759	158	4.95425E-45
YHANP--01-R-I24.ab1	NP_199565	Mo25 family protein [Arabidopsis thaliana]	89.809	157	1.71E-74
YHANP--02-R-L20.ab1	NP_196694	monooxygenase family protein [Arabidopsis thaliana]	50.467	107	1.14E-22
YHANP--04-R-J09.ab1	NP_196694	monooxygenase family protein [Arabidopsis thaliana]	61.404	57	9.43E-12
YHANP--02-R-H05.ab1	H84668	Mutator-like transposase [imported] - Arabidopsis thaliana	54.348	46	2.9879E-08
YHANP--01-R-E11.ab1	NP_189303	MutT/nudix family protein [Arabidopsis thaliana]	64.286	126	5.12685E-42
YHANP--01-R-L05.ab1	NP_200132	myb family transcription factor (TRIPTYCHON) [Arabidopsis thaliana]	67.47	83	3.48E-27
YHANP--03-R-B16.ab1	AAF97409	myo-inositol-1-phosphate synthase [Actinidia arguta]	98.101	158	2.25E-85
YHANP--04-R-C07.ab1	CAC18730	NADH glutamate dehydrogenase [Vitis vinifera]	92.208	77	1.67E-36
YHANP--04-R-G22.ab1	D84547	NAM (no apical meristem)-like protein [imported] - Arabidopsis thaliana	77.305	141	2.92E-66

IP : 14.49.138.138, 2017-11-03 13:30:33

YHANP--01-R-O03.ab1	AAP44393	nematode resistance-like protein [Solanum tuberosum]	46.087	115	4.66E-21
YHANP--03-R-A05.ab1	AAT36678	NHX1 [Poncirus trifoliata]	100	143	3.14281E-79
YHANP--04-R-B23.ab1	T14321	nuclear matrix constituent protein 1 - carrot	35.625	160	2.44832E-17
YHANP--01-R-B05.ab1	AAK52082	nuclease [Nicotiana tabacum]	77.612	67	3.33E-27
YHANP--04-R-I19.ab1	CAC69852	nucleic acid binding protein [Nicotiana tabacum]	69.643	56	1.74E-17
YHANP--01-R-E19.ab1	NP_190882	O-diphenol-O-methyl transferase, putative [Arabidopsis thaliana]	75.362	138	1.48478E-57
YHANP--02-R-M16.ab1	CAE03135	OJ000114_01.16 [Oryza sativa (japonica cultivar-group)]	51.923	52	1.7064E-09
YHANP--02-R-H20.ab1	AAN17502	omega-3 fatty acid desaturase [Betula pendula]	58.209	134	3.58E-31
YHANP--03-R-K17.ab1	CAE03433	OSJNBa0032F06.16 [Oryza sativa (japonica cultivar-group)]	80	65	1.81E-28
YHANP--01-R-K20.ab1	CAE03550	OSJNBa0060D06.16 [Oryza sativa (japonica cultivar-group)]	34.615	104	1.76E-07
YHANP--02-R-G10.ab1	CAD40734	OSJNBa0072D21.14 [Oryza sativa (japonica cultivar-group)]	73.718	156	3.49E-64
YHANP--03-R-I18.ab1	CAE03574	OSJNBa0085I10.19 [Oryza sativa (japonica cultivar-group)]	37.576	165	1.64E-19
YHANP--02-R-F11.ab1	CAE03557	OSJNBa0085I10.2 [Oryza sativa (japonica cultivar-group)]	97.619	42	4.97E-15
YHANP--01-R-H17.ab1	CAE03048	OSJNBa0089K21.2 [Oryza sativa (japonica cultivar-group)]	92.857	98	7.80E-47
YHANP--02-R-J03.ab1	CAD41638	OSJNBb0012E24.3 [Oryza sativa (japonica cultivar-group)]	80	20	2.02E-06
YHANP--03-R-C09.ab1	CAE05726	OSJNBb0017I01.6 [Oryza sativa (japonica cultivar-group)]	44.444	135	1.79123E-23
YHANP--03-R-M16.ab1	CAE05773	OSJNBb0020J19.2 [Oryza sativa (japonica cultivar-group)]	73.196	97	5.08479E-27
YHANP--01-R-P12.ab1	CAE04348	OSJNBb0038F03.12 [Oryza sativa (japonica cultivar-group)]	58	50	1.4549E-12
YHANP--04-R-J18.ab1	CAE03194	OSJNBb0060M15.6 [Oryza sativa (japonica cultivar-group)]	36.552	145	1.65E-12
YHANP--01-R-P11.ab1	CAE05949	OSJNBb0088C09.8 [Oryza sativa (japonica cultivar-group)]	58.442	77	5.89314E-22
YHANP--01-R-H08.ab1	NP_175482	OTU-like cysteine protease family protein [Arabidopsis thaliana]	85.437	103	5.24E-47
YHANP--02-R-J04.ab1	NP_173145	oxidoreductase, 2OG-Fe(II) oxygenase family protein [Arabidopsis thaliana]	57.143	126	5.93533E-35
YHANP--03-R-N06.ab1	NP_173145	oxidoreductase, 2OG-Fe(II) oxygenase family protein [Arabidopsis thaliana]	59.868	152	2.48E-49
YHANP--04-R-L22.ab1	NP_916598	P0456F08.26 [Oryza sativa (japonica cultivar-group)]	63.529	85	2.01E-26
YHANP--03-R-D11.ab1	NP_914258	P0483G10.15 [Oryza sativa (japonica cultivar-group)]	100	66	2.02E-30
YHANP--02-R-B05.ab1	NP_914471	P0489A01.9 [Oryza sativa (japonica cultivar-group)]	60.55	109	1.62386E-16
YHANP--04-R-K08.ab1	NP_917975	P0519E12.3 [Oryza sativa (japonica cultivar-group)]	88.732	71	1.83E-33
YHANP--03-R-H15.ab1	NP_918652	P0520B06.18 [Oryza sativa (japonica cultivar-group)]	75.926	54	1.33E-18
YHANP--04-R-A09.ab1	BAB90823	P0592G05.9 [Oryza sativa (japonica cultivar-group)]	76.471	102	2.73549E-57
YHANP--02-R-F10.ab1	AAK60517	P450 monooxygenase [Gossypium arboreum]	51.938	129	3.59E-37
YHANP--01-R-P08.ab1	AAF40414	papain-like cysteine proteinase isoform I [Ipomoea batatas]	96.053	76	2.15E-40
YHANP--03-R-F09.ab1	NP_567897	paramyosin-related [Arabidopsis thaliana]	46.377	138	1.68E-21
YHANP--01-R-J16.ab1	AAF98369	patatin-like protein 3 [Nicotiana tabacum]	62.42	157	7.14E-52
YHANP--04-R-D12.ab1	NP_191055	patatin-related [Arabidopsis thaliana]	53.125	96	2.96E-18
YHANP--02-R-N04.ab1	NP_566388	Paxneb protein-related [Arabidopsis thaliana]	53.247	154	3.51E-40
YHANP--03-R-K22.ab1	NP_197483	PBS lyase HEAT-like repeat-containing protein [Arabidopsis thaliana]	78.049	41	1.13E-09
YHANP--01-R-D06.ab1	NP_191074	pectate lyase family protein [Arabidopsis thaliana]	61.538	104	1.38E-34
YHANP--04-R-J10.ab1	S68805	pectin acetylesterase (EC 3.1.1.-) precursor - mung bean	70.968	31	5.56E-09
YHANP--01-R-M19.ab1	Q43062	Pectinesterase PPE8B precursor (Pectin methylesterase) (PE)	56.41	156	2.13E-37
YHANP--04-R-L11.ab1	AAM65650	pectinesterase, putative [Arabidopsis thaliana]	70.779	154	2.07E-53

IP : 14.49.138.138, 2017-11-03 13:30:33

YHANP--02-R-B01.ab1	NP_171855	pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana]	75.926	54	5.85E-26
YHANP--01-R-I10.ab1	NP_191713	peptidase family protein [Arabidopsis thaliana]	75.61	82	5.68E-33
YHANP--02-R-L11.ab1	NP_173104	Per1-like family protein [Arabidopsis thaliana]	74.483	145	3.5346E-63
YHANP--03-R-M05.ab1	NP_201094	permease, putative [Arabidopsis thaliana]	87.037	108	7.05774E-49
YHANP--03-R-L13.ab1	CAD67478	peroxidase [Asparagus officinalis]	66.667	156	1.22028E-43
YHANP--02-R-F22.ab1	AAD37374	peroxidase [Glycine max]	89.362	47	1.43534E-17
YHANP--04-R-O09.ab1	AAD11482	peroxidase precursor [Glycine max]	71.875	64	5.42E-19
YHANP--01-R-O09.ab1	BAB84550	peroxisomal ABC transporter [Arabidopsis thaliana]	77.941	68	7.63E-29
YHANP--03-R-F20.ab1	NP_189480	P-glycoprotein, putative [Arabidopsis thaliana]	83.099	71	1.74775E-25
YHANP--02-R-C11.ab1	Q04593	Phenylalanine ammonia-lyase 2	78.75	80	1.63205E-31
YHANP--03-R-F18.ab1	BAA33810	phi-1 [Nicotiana tabacum]	67.516	157	2.32E-47
YHANP--01-R-J08.ab1	NP_188044	phosphatidylinositol-4-phosphate 5-kinase family protein [Arabidopsis thaliana]	65.574	61	5.98E-19
YHANP--01-R-O16.ab1	BAB43909	phosphoenolpyruvate carboxykinase [Flaveria pringlei]	71.895	153	3.88E-45
YHANP--03-R-O11.ab1	NP_197506	phospholipase/carboxylesterase family protein [Arabidopsis thaliana]	77.869	122	4.72E-53
YHANP--03-R-L18.ab1	T09547	phosphoprotein phosphatase (EC 3.1.3.16) 1, catalytic gsmma chain - alfalfa	93.711	159	1.92E-89
YHANP--04-R-K02.ab1	NP_191061	phosphoribosylformylglycinamidine cyclo-ligase, chloroplast / phosphoribosyl-aminoimidazole synthetase / AIR synthase (PUR5) [Arabidopsis thaliana]	75	100	1.63E-37
YHANP--02-R-B21.ab1	P32869	Photosystem I reaction center subunit II, chloroplast precursor (Photosystem I 20 kDa subunit) (PSI-D) (PS I subunit 5)	97.647	85	2.35E-43
YHANP--01-R-L12.ab1	Q40519	Photosystem II 10 kDa polypeptide, chloroplast precursor (PII10)	85.263	95	1.53117E-37
YHANP--03-R-J04.ab1	Q41387	Photosystem II reaction center W protein, chloroplast precursor (PSII 6.1 kDa protein)	68.548	124	4.58E-30
YHANP--01-R-K12.ab1	AAC49301	phytochrome F [Lycopersicon esculentum]	69.697	33	2.12E-06
YHANP--04-R-F09.ab1	NP_199194	pinhead protein (PINHEAD) / zwille protein (ZWILLE) [Arabidopsis thaliana]	91.772	158	1.17E-78
YHANP--04-R-N12.ab1	JQ1670	polygalacturonase (EC 3.2.1.15) 1 beta chain precursor - tomato	77.5	120	8.61E-55
YHANP--04-R-P20.ab1	AAM66136	polyneuridine aldehyde esterase, putative [Arabidopsis thaliana]	67.213	61	2.12E-16
YHANP--02-R-H03.ab1	AAK53760	potassium transporter HAK3p [Mesembryanthemum crystallinum]	68.421	76	3.49E-32
YHANP--04-R-L23.ab1	AAR14273	predicted protein [Populus alba x Populus tremula]	69.474	95	8.14224E-31
YHANP--03-R-B06.ab1	NP_188887	prefoldin-related KE2 family protein [Arabidopsis thaliana]	75.824	91	2.06E-32
YHANP--04-R-O05.ab1	D84561	probable AAA-type ATPase [imported] - Arabidopsis thaliana	51.546	97	3.79534E-21
YHANP--02-R-P13.ab1	P93257	Probable mannitol dehydrogenase (NAD-dependent mannitol dehydrogenase)	80.292	137	9.39E-65
YHANP--02-R-C14.ab1	E84431	probable Na+/H+ antiporter [imported] - Arabidopsis thaliana	45.638	149	9.07E-25
YHANP--03-R-G22.ab1	Q06652	Probable phospholipid hydroperoxide glutathione peroxidase (PHGPx) (Salt-associated protein)	100	113	2.39E-60
YHANP--04-R-J15.ab1	T14735	probable serine/threonine kinase (EC 2.7.1.-) SNFL1 - sorghum	84.211	57	1.19616E-21
YHANP--04-R-D14.ab1	O82531	Proteasome subunit beta type 1 (20S proteasome alpha subunit F) (20S proteasome subunit beta-6)	90.164	122	5.61E-61
YHANP--01-R-K16.ab1	AAO26314	protein disulphide isomerase [Elaeis guineensis]	73.077	78	1.42E-28
YHANP--02-R-L12.ab1	Q01197	Protein E6	38.776	98	1.52E-08
YHANP--03-R-L24.ab1	D86478	protein F15O4.11 [imported] - Arabidopsis thaliana	58.427	89	3.27197E-17
YHANP--02-R-I14.ab1	AAA57119	protein kinase	75.949	79	1.09E-28
YHANP--03-R-C17.ab1	NP_197362	protein kinase family protein [Arabidopsis thaliana]	78.289	152	4.54646E-66
YHANP--04-R-M04.ab1	AAF40430	protein kinase MK5 [Mesembryanthemum crystallinum]	85	40	2.24E-13
YHANP--03-R-F24.ab1	BAB01182	protein kinase-like protein [Arabidopsis thaliana]	93.617	141	5.30639E-76
YHANP--03-R-P09.	NP_187278	protein phosphatase 2C, putative / PP2C, putative [Arabidopsis thaliana]	82.119	151	5.56E-68

IP : 14.49.138.138, 2017-11-03 13:30:33

ab1					
YHANP--04-R-O23.ab1	NP_190715	protein phosphatase 2C, putative / PP2C, putative [Arabidopsis thaliana]	83.929	56	1.44E-18
YHANP--03-R-K14.ab1	D86226	protein T31J12.5 [imported] - Arabidopsis thaliana	92.5	80	1.05E-37
YHANP--04-R-K03.ab1	O48650	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG	89.855	69	5.24E-31
YHANP--03-R-L06.ab1	NP_187366	protein transport protein Sec24, putative [Arabidopsis thaliana]	89.241	158	4.85992E-72
YHANP--04-R-E02.ab1	NP_180972	protein transport protein sec61, putative [Arabidopsis thaliana]	89.474	133	1.52E-64
YHANP--01-R-K11.ab1	NP_196844	proton-dependent oligopeptide transport (POT) family protein [Arabidopsis thaliana]	75.258	97	2.00E-25
YHANP--04-R-K22.ab1	CAC40032	P-type ATPase [Hordeum vulgare]	81.25	144	3.42E-66
YHANP--03-R-F16.ab1	BAC55155	purple acid phosphatase [Nicotiana tabacum]	65.455	55	1.00755E-13
YHANP--03-R-P03.ab1	AAN31781	Putataive glucan 1,3-beta-glucosidase precursor [Oryza sativa (japonica cultivar-group)]	59.627	161	6.80E-50
YHANP--02-R-B04.ab1	BAC84070	putative 2-oxoglutarate dehydrogenase, E1 subunit [Oryza sativa (japonica cultivar-group)]	70.588	68	5.26E-22
YHANP--03-R-B05.ab1	AAF23298	putative 40S ribosomal protein S23 [Arabidopsis thaliana]	100	65	5.62E-30
YHANP--01-R-C01.ab1	BAD21871	putative 40S ribosomal protein S8 [Oryza sativa (japonica cultivar-group)]	93.651	63	1.20E-27
YHANP--02-R-F01.ab1	AAD56335	putative 60S acidic ribosomal protein, 5' partial [Arabidopsis thaliana]	79.412	68	1.30E-25
YHANP--04-R-K10.ab1	BAD07825	putative 60S ribosomal protein L9 [Oryza sativa (japonica cultivar-group)]	85.714	91	1.21966E-37
YHANP--01-R-C19.ab1	AAG52466	putative ABC transporter; 73228-76244 [Arabidopsis thaliana]	55.963	109	1.71464E-21
YHANP--03-R-C08.ab1	BAD19899	putative ABI3-interacting protein 2 [Oryza sativa (japonica cultivar-group)]	53.782	119	8.22E-24
YHANP--02-R-A24.ab1	NP_912428	Putative apyrase [Oryza sativa (japonica cultivar-group)]	78.358	134	1.28E-55
YHANP--02-R-K24.ab1	AAO73272	putative ARP2/3 complex 20 kDa subunit, 3'-partial [Oryza sativa (japonica cultivar-group)]	92.174	115	1.33E-55
YHANP--03-R-K06.ab1	BAD10062	putative AT-hook DNA-binding protein [Oryza sativa (japonica cultivar-group)]	66.026	156	1.45E-20
YHANP--04-R-E12.ab1	BAD09626	putative Bet1/Sft1-related SNARE (AtBS14a) [Oryza sativa (japonica cultivar-group)]	88.889	27	3.02E-06
YHANP--02-R-H21.ab1	AAQ62586	putative beta-galactosidase [Glycine max]	67.213	61	3.80517E-17
YHANP--02-R-F23.ab1	AAQ62586	putative beta-galactosidase [Glycine max]	76.923	156	1.91E-70
YHANP--03-R-I13.ab1	NP_908347	putative C-8,7 sterol isomerase [Oryza sativa (japonica cultivar-group)]	53.333	150	1.46E-41
YHANP--02-R-O01.ab1	AAL31695	putative calcineurin B-like protein [Oryza sativa]	72	50	1.23E-13
YHANP--01-R-D22.ab1	NP_915149	putative calreticulin [Oryza sativa (japonica cultivar-group)]	86.842	152	2.92E-81
YHANP--01-R-F08.ab1	AAM63287	putative carboxymethylenebutenolidase [Arabidopsis thaliana]	66.667	45	1.43E-11
YHANP--01-R-A13.ab1	CAD38520	putative cation transporter [Beta procumbens]	59.524	84	3.09E-18
YHANP--04-R-P12.ab1	NP_918220	putative cdc21 protein [Oryza sativa (japonica cultivar-group)]	95.238	84	1.67736E-70
YHANP--01-R-G10.ab1	AAM64532	putative DNA binding protein [Arabidopsis thaliana]	81.667	60	6.96E-23
YHANP--03-R-B10.ab1	AAK59450	putative dolichyl-di-phosphooligosaccharide-protein glycotransferase [Arabidopsis thaliana]	69.014	142	2.26802E-53
YHANP--02-R-M09.ab1	AAL69493	putative H+-transporting ATP synthase [Arabidopsis thaliana]	53.125	96	5.75E-16
YHANP--03-R-P10.ab1	BAD07806	putative HECT ubiquitin-protein ligase 3 [Oryza sativa (japonica cultivar-group)]	55.782	147	1.09E-40
YHANP--02-R-N01.ab1	AAD55762	putative host factor [Nicotiana tabacum]	81.579	76	3.02E-31
YHANP--03-R-C18.ab1	NP_914996	putative hydroxymethyltransferase [Oryza sativa (japonica cultivar-group)]	69.388	49	8.34E-13
YHANP--04-R-I22.ab1	AAT39231	putative isovaleryl-CoA dehydrogenase [Oryza sativa (japonica cultivar-group)]	89.583	144	3.48E-66
YHANP--02-R-G06.ab1	NP_909832	putative leucine-rich repeat protein [Oryza sativa (japonica cultivar-group)]	70.093	107	1.09E-41
YHANP--03-R-E09.ab1	NP_909908	putative lipid acyl hydrolase [Oryza sativa]	58.491	53	2.57E-09
YHANP--03-R-E08.ab1	BAD15855	putative Mcsc-pending-prov protein [Oryza sativa (japonica cultivar-group)]	79.245	53	2.36891E-18
YHANP--01-R-E04.ab1	CAD12837	putative metallophosphatase [Lupinus luteus]	88.525	61	2.56E-26

IP : 14.49.138.138, 2017-11-03 13:30:33

YHANP--04-R-F18.ab1	AAP45162	putative Mob1/phocein family protein [Solanum bulbocastanum]	94.194	155	1.51E-83
YHANP--03-R-M21.ab1	AAC09468	putative NADPH-cytochrome P450 reductase [Pisum sativum]	82.667	150	3.16E-56
YHANP--04-R-O15.ab1	NP_916104	putative nitrate transporter [Oryza sativa (japonica cultivar-group)]	52.667	150	6.53E-36
YHANP--02-R-I17.ab1	NP_912363	putative peroxisomal Ca-dependent solute carrier protein [Oryza sativa (japonica cultivar-group)]	87.179	39	3.03E-12
YHANP--03-R-H20.ab1	BAC79968	putative phosphoglucomutase precursor, chloroplast [Oryza sativa (japonica cultivar-group)]	79.825	114	1.27E-36
YHANP--01-R-C14.ab1	BAD22406	putative PKG-Ib [Oryza sativa (japonica cultivar-group)]	58.125	160	5.30546E-39
YHANP--01-R-N11.ab1	NP_921503	putative polyprotein [Oryza sativa (japonica cultivar-group)]	76.119	134	1.78853E-57
YHANP--03-R-M22.ab1	AAM61395	putative P-protein: chorismate mutase, prephenate dehydratase [Arabidopsis thaliana]	84.314	51	8.96E-18
YHANP--01-R-D08.ab1	AAD34615	putative progesterone-binding protein homolog [Arabidopsis thaliana]	80.822	146	1.67E-60
YHANP--02-R-D04.ab1	CAB81548	putative proline-rich protein APG isolog [Cicer arietinum]	81.553	103	1.99E-35
YHANP--03-R-L05.ab1	CAB61995	putative protein (fragment) [Arabidopsis thaliana]	40.87	115	9.95E-17
YHANP--03-R-C19.ab1	NP_922818	putative protein kinase [Oryza sativa (japonica cultivar-group)]	83.871	155	1.21E-75
YHANP--04-R-F23.ab1	AAM65773	putative RING zinc finger protein [Arabidopsis thaliana]	56.028	141	9.66E-32
YHANP--03-R-I10.ab1	BAC79591	putative RING3 protein [Oryza sativa (japonica cultivar-group)]	60.8	125	2.89E-24
YHANP--01-R-A09.ab1	CAB85632	putative ripening-related bZIP protein [Vitis vinifera]	85.484	62	1.25451E-21
YHANP--03-R-A09.ab1	CAB85625	putative ripening-related protein [Vitis vinifera]	65.873	126	1.10E-44
YHANP--02-R-A14.ab1	AAF21191	putative RNA-binding protein [Arabidopsis thaliana]	64.901	151	2.1358E-52
YHANP--02-R-D10.ab1	NP_910037	putative RNA-binding protein [Oryza sativa (japonica cultivar-group)]	70.313	128	4.65E-34
YHANP--02-R-F09.ab1	BAC98582	putative RNA-binding region RNP-1 and Splicing factor PWI family member protein [Oryza sativa (japonica cultivar-group)]	70.115	87	6.63072E-30
YHANP--04-R-F22.ab1	BAB33422	putative senescence-associated protein [Pisum sativum]	76.623	77	8.83E-30
YHANP--02-R-L10.ab1	CAC19488	putative serine carboxypeptidase [Pisum sativum]	75.949	79	3.37E-32
YHANP--02-R-O21.ab1	AAM13204	putative serine protease-like protein [Arabidopsis thaliana]	79.487	78	2.334E-31
YHANP--02-R-J19.ab1	AAK84485	putative thermostable pectinesterase [Citrus sinensis]	100	125	2.33E-68
YHANP--04-R-C22.ab1	NP_921813	putative thiolase [Oryza sativa (japonica cultivar-group)]	86.957	115	8.43E-53
YHANP--01-R-H16.ab1	AAK25877	putative translation elongation factor eEF-1 alpha chain A4 [Arabidopsis thaliana]	100	134	5.49E-73
YHANP--03-R-D05.ab1	AAF02141	putative translation initiation factor EIF-2B beta subunit, 3' partial [Arabidopsis thaliana]	94.928	138	3.18899E-68
YHANP--02-R-L09.ab1	AAF26999	putative tRNA pseudouridine synthase [Arabidopsis thaliana]	64.865	74	1.85E-21
YHANP--02-R-P08.ab1	AAM64897	putative ubiquitin fusion-degradation protein [Arabidopsis thaliana]	78.981	157	6.95E-68
YHANP--01-R-F16.ab1	BAD22867	putative Vacuolar ATP synthase subunit F [Oryza sativa (japonica cultivar-group)]	86.667	45	5.89E-14
YHANP--02-R-H04.ab1	CAD27914	putative vacuolar ATPase subunit d [Mesembryanthemum crystallinum]	92.857	140	2.86E-73
YHANP--04-R-P10.ab1	AAO72382	putative vacuolar protein sorting-associated protein [Oryza sativa (japonica cultivar-group)]	87.898	157	4.31E-65
YHANP--04-R-F07.ab1	AAR92477	putative WRKY transcription factor 30 [Vitis aestivalis]	57.547	106	6.48E-23
YHANP--04-R-D11.ab1	BAD21477	putative X1 [Oryza sativa (japonica cultivar-group)]	47.059	85	8.71E-15
YHANP--02-R-O17.ab1	AAL33553	pyruvate decarboxylase [Cucumis melo]	81.148	122	7.54E-51
YHANP--02-R-M02.ab1	BAC23043	pyruvate decarboxylase [Solanum tuberosum]	91.083	157	2.63E-75
YHANP--02-R-C23.ab1	AAO72533	pyruvate decarboxylase 1 [Lotus corniculatus]	94.545	110	9.84488E-57
YHANP--03-R-H05.ab1	AAO22131	quinone oxidoreductase [Fragaria x ananassa]	75.796	157	8.04E-61
YHANP--02-R-K04.ab1	AAM18228	R1 [Citrus reticulata]	98.089	157	2.46E-81
YHANP--04-R-O02.ab1	NP_567008	Rab GTPase (ARA6) [Arabidopsis thaliana]	84.444	90	6.46E-36
YHANP--02-R-E18.ab1	NP_564606	Ran-binding protein 1 domain-containing protein / RanBP1 domain-containing protein [Arabidopsis thaliana]	66.667	78	8.06E-16

IP : 14.49.138.138, 2017-11-03 13:30:33

YHANP--01-R-B15.ab1	BAB84322	ras-related protein RAB8-1 [Nicotiana tabacum]	99.367	158	1.25E-72
YHANP--04-R-N14.ab1	AAD52097	receptor-like kinase CHRK1 [Nicotiana tabacum]	71.523	151	6.85E-59
YHANP--03-R-A12.ab1	NP_568913	riboflavin biosynthesis protein, putative [Arabidopsis thaliana]	54.082	98	2.76989E-16
YHANP--04-R-M11.ab1	NP_909841	ribosomal protein L15 [Oryza sativa (japonica cultivar-group)]	91.765	85	7.56E-43
YHANP--03-R-G10.ab1	NP_054972	ribosomal protein L16 [Spinacia oleracea]	93.333	120	1.15E-54
YHANP--04-R-C09.ab1	BAA96072	ribosomal protein L29 [Panax ginseng]	85.455	55	6.91674E-23
YHANP--03-R-H16.ab1	AAR17783	ribosomal protein L3 [Lycopersicon esculentum]	94.268	157	3.24E-84
YHANP--04-R-K04.ab1	JQ0772	ribosomal protein L3.e (clone ARP2), cytosolic - Arabidopsis thaliana	95.098	102	4.49E-46
YHANP--01-R-N12.ab1	JQ0772	ribosomal protein L3.e (clone ARP2), cytosolic - Arabidopsis thaliana	95.902	122	5.94E-61
YHANP--04-R-N19.ab1	NP_565109	ribosomal protein L31 family protein [Arabidopsis thaliana]	65.926	135	6.63E-46
YHANP--02-R-D22.ab1	AAK25760	ribosomal protein L33 [Castanea sativa]	92.857	112	2.05E-56
YHANP--01-R-G05.ab1	Q43843	Ribulose-phosphate 3-epimerase, chloroplast precursor (Pentose-5-phosphate 3-epimerase) (PPE) (RPE) (R5P3E)	91.549	71	8.87E-31
YHANP--01-R-B06.ab1	AAG49030	ripening regulated protein DDTFR8 [Lycopersicon esculentum]	66.423	137	6.61E-45
YHANP--03-R-F12.ab1	CAC01237	RNA Binding Protein 45 [Nicotiana plumbaginifolia]	70.149	134	3.82937E-50
YHANP--02-R-C22.ab1	CAA66825	RNA helicase [Arabidopsis thaliana]	86.364	66	1.85E-28
YHANP--04-R-F14.ab1	NP_196080	RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana]	70.297	101	1.28E-34
YHANP--03-R-E01.ab1	NP_851001	RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana]	83.871	93	2.46E-38
YHANP--03-R-H02.ab1	NP_188063	RNA-binding protein, putative [Arabidopsis thaliana]	82.353	85	4.61273E-34
YHANP--04-R-D03.ab1	BAA97146	RNA-binding protein-like [Arabidopsis thaliana]	50	92	1.16544E-28
YHANP--04-R-P23.ab1	AAQ23194	RPA 70kDa subunit [Pisum sativum]	72.289	83	4.87E-29
YHANP--01-R-K17.ab1	NP_187201	rubber elongation factor (REF) family protein [Arabidopsis thaliana]	67.48	123	5.79E-41
YHANP--04-R-P15.ab1	AAM62603	rubisco expression protein, putative [Arabidopsis thaliana]	81.395	43	2.61E-13
YHANP--01-R-F12.ab1	NP_175852	rubredoxin family protein [Arabidopsis thaliana]	87.143	70	1.24E-31
YHANP--01-R-A10.ab1	AAM44307	S-adenosylmethionine decarboxylase [x Citrofortunella mitis]	95.327	107	1.21E-55
YHANP--01-R-I09.ab1	AAK71233	S-adenosylmethionine synthetase [Brassica juncea]	96.063	127	2.39968E-67
YHANP--03-R-L11.ab1	NP_190741	saposin B domain-containing protein [Arabidopsis thaliana]	39.231	130	1.96E-17
YHANP--01-R-A02.ab1	BAB83081	Sec13p [Oryza sativa]	75.714	70	7.96E-27
YHANP--04-R-L17.ab1	AAF36688	secretory carrier membrane protein [Oryza sativa]	83.333	66	9.33E-26
YHANP--01-R-A16.ab1	NP_197570	senescence-associated protein-related [Arabidopsis thaliana]	43.713	167	1.37E-23
YHANP--02-R-N22.ab1	P55748	Serine carboxypeptidase II-2 precursor (CP-MII.2)	71.069	159	9.72E-62
YHANP--03-R-E10.ab1	P50433	SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE) (SHMT)	91.473	129	2.47E-65
YHANP--02-R-N10.ab1	O04856	Serine/threonine protein phosphatase PP1 isozyme 1	88.889	27	6.68E-07
YHANP--02-R-F15.ab1	AAL32440	SH3 domain-containing protein 3 [Arabidopsis thaliana]	76.389	72	5.04E-18
YHANP--02-R-E17.ab1	AAF04193	short-chain alcohol dehydrogenase [Pisum sativum]	61.538	156	1.13E-44
YHANP--04-R-B04.ab1	AAC64139	signal recognition particle 54 kDa subunit precursor [Arabidopsis thaliana]	88.816	152	2.56384E-69
YHANP--04-R-B02.ab1	AAK68820	similar to dihydroflavonol reductase [Arabidopsis thaliana]	83.146	89	1.79206E-38
YHANP--03-R-D08.ab1	AAK68820	similar to dihydroflavonol reductase [Arabidopsis thaliana]	94.304	158	3.51E-83
YHANP--02-R-E21.ab1	AAK58693	sinapyl alcohol dehydrogenase [Populus tremuloides]	84.906	106	6.77E-37
YHANP--01-R-G01.ab1	AAA80678	small GTP-binding protein	84.848	66	3.62E-26
YHANP--02-R-G11.	NP_178480	small nuclear ribonucleoprotein, putative / snRNP, putative / Sm protein, putative	94.048	84	1.13E-38

IP : 14.49.138.138, 2017-11-03 13:30:33

ab1		[Arabidopsis thaliana]			
YHANP--01-R-L08.ab1	AAO66433	small rubber particle protein [Hevea brasiliensis]	80	110	1.31E-37
YHANP--04-R-B21.ab1	NP_200010	sorbitol dehydrogenase, putative / L-iditol 2-dehydrogenase, putative [Arabidopsis thaliana]	84.615	156	3.80E-74
YHANP--03-R-O01.ab1	BAD10044	splicing factor 3B subunit 5-like protein [Oryza sativa (japonica cultivar-group)]	93.103	87	1.25E-43
YHANP--01-R-D07.ab1	NP_192918	SPX (SYG1/Pho81/XPR1) domain-containing protein [Arabidopsis thaliana]	83.951	81	2.11101E-32
YHANP--02-R-C20.ab1	T52602	squamosa promoter binding protein 1 [imported] - Arabidopsis thaliana	49.485	97	2.53E-28
YHANP--04-R-G17.ab1	NP_177523	Ssu72-like family protein [Arabidopsis thaliana]	86.905	84	2.57E-38
YHANP--01-R-C12.ab1	AAF15308	stearoyl-acyl-carrier-protein desaturase; stearoyl-ACP desaturase [Persea americana]	59.394	165	3.43093E-46
YHANP--04-R-I02.ab1	1VDC	Structure Of Nadph Dependent Thioredoxin Reductase	89.091	55	5.14E-22
YHANP--02-R-I21.ab1	NP_567972	subtilase family protein [Arabidopsis thaliana]	65.909	88	3.94E-40
YHANP--01-R-G11.ab1	NP_567972	subtilase family protein [Arabidopsis thaliana]	64.286	42	3.20258E-08
YHANP--03-R-P12.ab1	BAA89049	sucrose synthase [Citrus unshiu]	100	156	1.15E-89
YHANP--01-R-B16.ab1	NP_191029	sugar isomerase (SIS) domain-containing protein / CBS domain-containing protein [Arabidopsis thaliana]	68.531	143	1.55E-51
YHANP--02-R-B15.ab1	CAD58628	SUI1 protein [Coffea arabica]	92.857	28	5.70E-08
YHANP--01-R-I14.ab1	CAA73188	superoxide dismutase [Arabidopsis thaliana]	62.5	120	7.93E-35
YHANP--04-R-O13.ab1	P11796	Superoxide dismutase [Mn], mitochondrial precursor	72.794	136	5.07E-54
YHANP--01-R-E06.ab1	NP_173589	SWIRM domain-containing protein / DNA-binding family protein [Arabidopsis thaliana]	57.813	128	1.55E-30
YHANP--03-R-A02.ab1	BAB86893	syringolide-induced protein 1-3-1B [Glycine max]	53.03	66	8.67E-09
YHANP--01-R-H21.ab1	AAF79700	T1N15.14 [Arabidopsis thaliana]	93.548	31	5.82E-09
YHANP--03-R-J01.ab1	H86335	T20H2.2 protein - Arabidopsis thaliana	78.808	151	3.65714E-56
YHANP--04-R-P07.ab1	AAF17627	T23E18.7 [Arabidopsis thaliana]	68.59	156	3.16074E-57
YHANP--04-R-G03.ab1	AAF79733	T25N20.17 [Arabidopsis thaliana]	89.256	121	7.96E-56
YHANP--01-R-M09.ab1	A86366	T26J12.6 protein - Arabidopsis thaliana	54.545	77	3.46E-14
YHANP--02-R-I06.ab1	AAF79854	T7N9.11 [Arabidopsis thaliana]	48.75	80	5.47E-09
YHANP--02-R-L03.ab1	AAS79352	terpenoid synthase [Vitis vinifera]	49.275	69	8.36E-09
YHANP--04-R-P09.ab1	NP_194629	tesmin/TSO1-like CXC domain-containing protein [Arabidopsis thaliana]	41.509	159	1.33E-18
YHANP--04-R-G23.ab1	NP_197229	tetratricopeptide repeat (TPR)-containing protein [Arabidopsis thaliana]	92.857	56	6.82E-24
YHANP--03-R-I09.ab1	AAK84890	TGA-type basic leucine zipper protein TGA2.2 [Phaseolus vulgaris]	53.774	106	8.20002E-26
YHANP--04-R-B03.ab1	O23787	Thiazole biosynthetic enzyme, chloroplast precursor	90.476	42	1.06E-13
YHANP--02-R-P17.ab1	AAL09350	thiohydroximate S-glucosyltransferase [Brassica napus]	59.664	119	5.19E-39
YHANP--03-R-P02.ab1	NP_567831	thioredoxin family protein [Arabidopsis thaliana]	80	130	9.50675E-60
YHANP--01-R-J10.ab1	NP_194984	thioredoxin family protein [Arabidopsis thaliana]	80	85	2.27082E-37
YHANP--01-R-N14.ab1	AAN76509	thioredoxin h [Brassica rapa]	60.465	129	2.15853E-41
YHANP--02-R-B09.ab1	AAD33596	thioredoxin h [Hevea brasiliensis]	72.527	91	1.21E-34
YHANP--02-R-P09.ab1	Q43636	Thioredoxin H-type (TRX-H)	89.655	116	7.78517E-56
YHANP--02-R-C19.ab1	AAD54324	threonine dehydratase/deaminase [Arabidopsis thaliana]	86.957	69	3.62E-18
YHANP--04-R-N21.ab1	AAL57045	transcription factor AHAP2 [Malus x domestica]	50.943	106	8.69878E-21
YHANP--01-R-B13.ab1	NP_175816	transcription initiation factor IID (TFIID) 31 kDa subunit (TAFII-31) family protein [Arabidopsis thaliana]	63.81	105	1.10E-23
YHANP--04-R-C12.ab1	BAD13020	transducin / WD-40 repeat protein-like [Oryza sativa (japonica cultivar-group)]	70.588	68	1.65E-21
YHANP--01-R-N06.ab1	NP_182179	transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana]	75	108	4.96405E-45

IP : 14.49.138.138, 2017-11-03 13:30:33

YHANP--02-R-K13.ab1	NP_195154	transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana]	61.864	118	5.10E-28
YHANP--03-R-B17.ab1	NP_196473	transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana]	69.291	127	8.29E-61
YHANP--03-R-E05.ab1	NP_195741	transferase family protein [Arabidopsis thaliana]	64.516	155	9.13E-46
YHANP--02-R-P07.ab1	JC7299	transformer-2-like protein - liverwort (Marchantia polymorpha)	77	100	7.66E-38
YHANP--04-R-O22.ab1	NP_181006	transketolase family protein [Arabidopsis thaliana]	64.602	113	1.21E-24
YHANP--04-R-J22.ab1	NP_199959	trehalose-6-phosphate phosphatase (TPPA) [Arabidopsis thaliana]	50	72	2.55E-11
YHANP--03-R-G15.ab1	AAR29056	triacylglycerol/steryl ester lipase-like protein [Medicago truncatula]	78.378	111	2.74E-48
YHANP--03-R-E20.ab1	P12863	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)	87.075	147	2.76E-61
YHANP--01-R-J19.ab1	AAK01237	trithorax-like protein 1 [Arabidopsis thaliana]	88.889	153	5.92411E-74
YHANP--01-R-B11.ab1	AAM65526	tryptophan synthase alpha chain [Arabidopsis thaliana]	84.444	45	4.42E-14
YHANP--03-R-O12.ab1	AAG08961	tuber-specific and sucrose-responsive element binding factor [Solanum tuberosum]	50.847	59	6.47E-08
YHANP--04-R-D10.ab1	NP_171974	tubulin alpha-2/alpha-4 chain (TUA4) [Arabidopsis thaliana]	100	123	7.11931E-69
YHANP--04-R-B18.ab1	AAM62712	tubulin alpha-6 chain, putative [Arabidopsis thaliana]	90.625	32	9.90719E-10
YHANP--03-R-D14.ab1	BAA92699	type 2A protein phosphatase-3 [Vicia faba]	91.667	132	2.61E-62
YHANP--01-R-O04.ab1	NP_171993	tyrosine specific protein phosphatase family protein [Arabidopsis thaliana]	82.353	51	1.04E-18
YHANP--04-R-G05.ab1	CAA77136	U2 snRNP auxiliary factor, large subunit [Nicotiana plumbaginifolia]	71.084	83	8.49E-29
YHANP--01-R-M11.ab1	P51132	Ubiquinol-cytochrome c reductase iron-sulfur subunit 2, mitochondrial precursor (Rieske iron-sulfur protein 2) (RISP2)	64.789	142	1.34917E-42
YHANP--02-R-G14.ab1	NP_568288	ubiquinol-cytochrome C reductase iron-sulfur subunit, mitochondrial, putative / Rieske iron-sulfur protein, putative [Arabidopsis thaliana]	93.506	77	8.43E-41
YHANP--03-R-N16.ab1	NP_194200	ubiquitin-associated (UBA)/TS-N domain-containing protein / octicosapeptide/Phox/Bemp1 (PB1) domain-containing protein [Arabidopsis thaliana]	57.937	126	1.95E-41
YHANP--02-R-I08.ab1	AAR83898	ubiquitin-conjugating protein [Capsicum annuum]	98.131	107	2.23978E-58
YHANP--01-R-H03.ab1	NP_171649	UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana]	61.386	101	2.16E-26
YHANP--04-R-I05.ab1	NP_196793	UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana]	44.156	77	1.14E-11
YHANP--03-R-O14.ab1	NP_187742	UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana]	56.349	126	1.81E-34
YHANP--03-R-O17.ab1	NP_566885	UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana]	64.545	110	1.47E-36
YHANP--04-R-A12.ab1	NP_172738	UDP-glucose 4-epimerase / UDP-galactose 4-epimerase / Galactowaldenase [Arabidopsis thaliana]	74.286	140	7.21E-57
YHANP--03-R-B23.ab1	O65780	UDP-glucose 4-epimerase GEPI42 (Galactowaldenase) (UDP-galactose 4-epimerase)	77.66	94	3.18E-39
YHANP--02-R-D09.ab1	AAR84297	UDP-glucose dehydrogenase [Cinnamomum osmophloeum]	86.624	157	2.15E-77
YHANP--04-R-G14.ab1	AAF04455	UDP-glucose dehydrogenase [Populus tremula x Populus tremuloides]	90.968	155	1.86E-78
YHANP--03-R-D10.ab1	BAD20019	UDP-glucose glucosyltransferase-like protein [Oryza sativa (japonica cultivar-group)]	36.585	164	6.51563E-21
YHANP--01-R-L16.ab1	AAO48422	UDP-glucose pyrophosphorylase [Bambusa oldhamii]	83.607	61	9.09E-23
YHANP--03-R-F05.ab1	AAB71613	UDP-glucose pyrophosphorylase [Solanum tuberosum]	89.209	139	6.59892E-53
YHANP--02-R-O22.ab1	AAS00612	UDP-glucose-flavonoid-3-O-glucosyl transferase [Citrus sinensis]	93.21	162	5.48E-81
YHANP--01-R-C09.ab1	AAF86340	UMP synthase [Nicotiana plumbaginifolia]	77.778	72	6.43E-26
YHANP--02-R-D08.ab1	NP_191814	universal stress protein (USP) family protein [Arabidopsis thaliana]	58.333	108	4.65625E-21
YHANP--03-R-D06.ab1	AAH32196	Unknown (protein for MGC:38244) [Mus musculus]	92.908	141	5.07951E-74
YHANP--01-R-F11.ab1	AAM65976	unknown [Arabidopsis thaliana]	66.019	103	7.35E-35
YHANP--02-R-D15.ab1	AAM63626	unknown [Arabidopsis thaliana]	50	94	1.26E-15
YHANP--02-R-E10.ab1	AAM64721	unknown [Arabidopsis thaliana]	58.333	60	3.78E-12
YHANP--01-R-C22.ab1	AAM64606	unknown [Arabidopsis thaliana]	56.25	80	6.61E-10
YHANP--02-R-D24.ab1	AAN60317	unknown [Arabidopsis thaliana]	55.556	63	2.68E-11

IP : 14.49.138.138, 2017-11-03 13:30:33

YHANP--02-R-L18.ab1	AAM65519	unknown [Arabidopsis thaliana]	79.433	141	2.73161E-64
YHANP--03-R-D03.ab1	AAM61098	unknown [Arabidopsis thaliana]	43.411	129	3.74361E-13
YHANP--01-R-C05.ab1	AAM64770	unknown [Arabidopsis thaliana]	42.308	156	5.38E-28
YHANP--01-R-E08.ab1	AAM65222	unknown [Arabidopsis thaliana]	83.099	142	1.11E-49
YHANP--01-R-G16.ab1	AAM61300	unknown [Arabidopsis thaliana]	53.125	96	1.20149E-19
YHANP--01-R-O12.ab1	AAM66068	unknown [Arabidopsis thaliana]	76.543	81	3.23E-28
YHANP--03-R-B09.ab1	AAN60276	unknown [Arabidopsis thaliana]	51.429	140	3.08E-34
YHANP--03-R-I04.ab1	AAM66995	unknown [Arabidopsis thaliana]	63.235	68	9.00E-18
YHANP--04-R-E24.ab1	AAM65302	unknown [Arabidopsis thaliana]	93.617	47	7.21E-21
YHANP--04-R-D22.ab1	AAM60987	unknown [Arabidopsis thaliana]	60.656	61	2.85451E-12
YHANP--04-R-P24.ab1	AAK69274	unknown [Glycine max]	86.585	82	9.27E-37
YHANP--02-R-H12.ab1	AAF02418	unknown [Homo sapiens]	87.5	64	6.73E-25
YHANP--04-R-I04.ab1	AAO63778	unknown [Populus tremuloides]	44.554	101	7.17E-10
YHANP--01-R-D24.ab1	AAL26911	unknown [Prunus persica]	67.532	77	1.03E-23
YHANP--03-R-G21.ab1	BAC43076	unknown protein [Arabidopsis thaliana]	64.103	39	4.73E-08
YHANP--01-R-H20.ab1	AAK44087	unknown protein [Arabidopsis thaliana]	77.778	117	1.55E-51
YHANP--02-R-E13.ab1	AAK44165	unknown protein [Arabidopsis thaliana]	80.645	31	8.85E-07
YHANP--04-R-I01.ab1	AAO64172	unknown protein [Arabidopsis thaliana]	73.75	80	6.44E-34
YHANP--01-R-G19.ab1	BAC43034	unknown protein [Arabidopsis thaliana]	74.79	119	1.72E-31
YHANP--04-R-A20.ab1	AAK62450	Unknown protein [Arabidopsis thaliana]	76.699	103	4.08E-41
YHANP--02-R-D07.ab1	AAF14029	unknown protein [Arabidopsis thaliana]	59.459	37	3.85E-07
YHANP--02-R-D13.ab1	AAG51484	unknown protein [Arabidopsis thaliana]	42	100	1.83008E-09
YHANP--03-R-C20.ab1	AAM13092	unknown protein [Arabidopsis thaliana]	90.323	62	3.35E-26
YHANP--02-R-K19.ab1	AAF07837	unknown protein [Arabidopsis thaliana]	76.744	43	1.58E-10
YHANP--04-R-K07.ab1	BAC42883	unknown protein [Arabidopsis thaliana]	61.789	123	4.13E-35
YHANP--03-R-P06.ab1	BAC43565	unknown protein [Arabidopsis thaliana]	82.716	81	9.89E-35
YHANP--04-R-O12.ab1	AAO42272	unknown protein [Arabidopsis thaliana]	86.709	158	5.91956E-80
YHANP--02-R-A18.ab1	AAN13053	unknown protein [Arabidopsis thaliana]	76.433	157	4.36E-62
YHANP--02-R-G17.ab1	BAC42448	unknown protein [Arabidopsis thaliana]	52.252	111	6.56228E-34
YHANP--01-R-K07.ab1	AAM20412	unknown protein [Arabidopsis thaliana]	84.076	157	1.07E-76
YHANP--03-R-L19.ab1	AAN72190	Unknown protein [Arabidopsis thaliana]	72.785	158	4.77E-64
YHANP--03-R-M06.ab1	AAB88638	unknown protein [Arabidopsis thaliana]	62.308	130	9.37E-36
YHANP--01-R-M16.ab1	BAC42194	unknown protein [Arabidopsis thaliana]	78.571	56	1.54E-17
YHANP--03-R-K18.ab1	BAC43353	unknown protein [Arabidopsis thaliana]	90.141	71	1.42E-31
YHANP--03-R-M01.ab1	BAC43140	unknown protein [Arabidopsis thaliana]	70.313	64	2.85E-15
YHANP--03-R-K23.ab1	AAM53321	unknown protein [Arabidopsis thaliana]	94.565	92	1.94E-43
YHANP--01-R-H04.ab1	AAO00894	Unknown protein [Arabidopsis thaliana]	77.848	158	2.48E-57
YHANP--03-R-H11.ab1	C96797	unknown protein [imported] - Arabidopsis thaliana	59.167	120	7.84949E-30
YHANP--04-R-L13.ab1	BAC84582	unknown protein [Oryza sativa (japonica cultivar-group)]	65.625	64	6.44295E-18
YHANP--01-R-H23.ab1	AAT38077	unknown protein [Oryza sativa (japonica cultivar-group)]	64.706	34	2.77632E-08

IP : 14.49.138.138, 2017-11-03 13:30:33

YHANP--03-R-B21.ab1	BAD09002	unknown protein [Oryza sativa (japonica cultivar-group)]	45.588	68	2.13E-08
YHANP--03-R-I14.ab1	BAD01227	unknown protein [Oryza sativa (japonica cultivar-group)]	71.429	77	1.54366E-26
YHANP--02-R-N07.ab1	NP_912350	unknown protein [Oryza sativa (japonica cultivar-group)]	51.563	128	1.13E-29
YHANP--01-R-J14.ab1	BAC55691	unknown protein [Oryza sativa (japonica cultivar-group)]	76	75	7.59319E-27
YHANP--02-R-L01.ab1	AAP73840	unknown protein,3'-partial [Oryza sativa (japonica cultivar-group)]	62.857	70	1.73495E-18
YHANP--02-R-J23.ab1	BAB03124	unnamed protein product [Arabidopsis thaliana]	60.938	64	1.69E-20
YHANP--01-R-H06.ab1	BAB01236	unnamed protein product [Arabidopsis thaliana]	88.095	42	2.92E-15
YHANP--04-R-O14.ab1	BAB02713	unnamed protein product [Arabidopsis thaliana]	75.573	131	3.77388E-55
YHANP--04-R-M22.ab1	BAB09835	unnamed protein product [Arabidopsis thaliana]	91.089	101	4.88764E-50
YHANP--01-R-M05.ab1	BAB01723	unnamed protein product [Arabidopsis thaliana]	39.785	93	6.18E-08
YHANP--04-R-P03.ab1	BAB08350	unnamed protein product [Arabidopsis thaliana]	87.719	57	1.16E-22
YHANP--03-R-A03.ab1	BAB09194	unnamed protein product [Arabidopsis thaliana]	63.636	99	5.64E-20
YHANP--02-R-M03.ab1	NP_913508	unnamed protein product [Oryza sativa (japonica cultivar-group)]	87.705	122	3.02E-60
YHANP--04-R-C06.ab1	NP_908456	unnamed protein product [Oryza sativa (japonica cultivar-group)]	91.667	36	9.00E-14
YHANP--01-R-E18.ab1	NP_912975	unnamed protein product [Oryza sativa (japonica cultivar-group)]	80.128	156	8.39E-69
YHANP--03-R-P18.ab1	AAR20885	UV damaged DNA binding protein 1 [Lycopersicon esculentum]	92.453	159	1.27597E-80
YHANP--02-R-M15.ab1	P93231	Vacuolar assembly protein VPS41 homolog	91.925	161	1.4498E-84
YHANP--02-R-H11.ab1	P49043	Vacuolar processing enzyme precursor (VPE)	98.462	130	2.15E-71
YHANP--03-R-D01.ab1	P49043	Vacuolar processing enzyme precursor (VPE)	97.727	44	1.18E-18
YHANP--02-R-I19.ab1	NP_195251	vestitone reductase-related [Arabidopsis thaliana]	63.158	133	5.94E-35
YHANP--04-R-D08.ab1	NP_201533	WD-40 repeat family protein [Arabidopsis thaliana]	88.462	156	6.77E-82
YHANP--03-R-G20.ab1	NP_181613	WD-40 repeat protein family [Arabidopsis thaliana]	73.196	97	1.38E-36
YHANP--04-R-K12.ab1	AAT11860	xyloglucanendotransglycosylase [Mangifera indica]	81.955	133	4.49E-57
YHANP--03-R-G04.ab1	AAS10179	YABBY2-like transcription factor YAB2 [Antirrhinum majus]	75.758	66	8.69E-23
YHANP--02-R-L17.ab1	AAK51557	zeta-carotene desaturase precursor [Citrus x paradisi]	90.984	122	2.05E-56
YHANP--03-R-D13.ab1	NP_180326	zinc finger (AN1-like) family protein [Arabidopsis thaliana]	80.328	61	2.23E-25
YHANP--02-R-G03.ab1	NP_566182	zinc finger (C2H2 type) family protein [Arabidopsis thaliana]	70.526	95	1.42E-35
YHANP--03-R-P08.ab1	NP_179853	zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana]	41	100	7.22E-12
YHANP--02-R-P14.ab1	NP_850540	zinc finger (CCCH-type/C3HC4-type RING finger) family protein [Arabidopsis thaliana]	74.545	55	9.8288E-22
YHANP--02-R-B11.ab1	AAS13688	zinc finger protein LSD1 [Oryza sativa (japonica cultivar-group)]	93.333	75	2.37789E-27
YHANP--03-R-C04.ab1	AAK37761	zinc transporter protein ZIP1 [Glycine max]	66.667	156	5.64216E-57

Consensus Number	Accession No.	Definition of Putative homologue[Organism]	Matching %	Matching Length	E-value
1	AAB57670	pectinesterase [Citrus sinensis]	98.889	90	9.05E-48
2	No hits found				
3	C96755	Similar to acid beta-galactosidase [imported] - Arabidopsis thaliana	53.571	84	8.06E-16
4	No hits found				
5	No hits found				
6	No hits found				
7	1107298A	protein,small heat shock	75.46	163	1.17E-54

IP : 14.49.138.138, 2017-11-03 13:30:33

8	O22342	ADP,ATP carrier protein 1, mitochondrial precursor (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1)	88.35	309	3.48E-146
9	BAA31562	metallothionein-like protein [Citrus unshiu]	98.529	68	2.57236E-35
10	No hits found				
11	NP_195633	RER1A protein [Arabidopsis thaliana]	72.093	43	3.24E-12
12	No hits found				
13	No hits found				
14	NP_180871	synaptobrevin-related protein / vesicle-associated membrane protein 722 (VAMP722) (SAR1) [Arabidopsis thaliana]	81.9	221	3.70955E-92
15	CAA08758	BnMAP4K alpha2 [Brassica napus]	90.278	72	2.26591E-18
16	AAL06469	At2g16800/T24I21.21 [Arabidopsis thaliana]	78.481	158	3.42E-54
17	T10790	peroxidase (EC 1.11.1.7) - upland cotton	87.546	273	1.08E-143
18	No hits found				
19	No hits found				
20	AAB08874	malate dehydrogenase [Vitis vinifera]	87.755	294	1.7261E-140
21	BAA31561	metallothionein-like protein [Citrus unshiu]	100	40	5.04E-15
22	P41210	Caltractin (Centrin)	75.904	83	1.04E-30
23	NP_195174	glycosyl hydrolase family 17 protein [Arabidopsis thaliana]	87.805	82	1.02E-65
24	NP_567338	pollen Ole e 1 allergen and extensin family protein [Arabidopsis thaliana]	55.556	90	1.94674E-25
25	NP_566535	60S ribosomal protein L37 (RPL37C) [Arabidopsis thaliana]	92.771	83	8.55E-42
26	CAE22480	superoxide dismutase [Fe] [Lycopersicon esculentum]	61.818	110	5.78104E-33
27	AAB40608	glutamate decarboxylase	49.398	83	3.78E-12
28	NP_916025	P0638D12.10 [Oryza sativa (japonica cultivar-group)]	75	148	2.97E-70
29	NP_199687	60S ribosomal protein L13A (RPL13aD) [Arabidopsis thaliana]	93.333	120	3.07E-54
30	BAC20341	heat shock protein DnaJ [Glycine max]	72.727	44	4.04E-12
31	No hits found				
32	AAG38518	miraculin-like protein 2 [Citrus x paradisi]	46.119	219	6.41E-40
33	AAG38517	miraculin-like protein [Citrus x paradisi]	98.551	138	3.44127E-73
34	NP_175963	photosystem I reaction center subunit V, chloroplast, putative / PSI-G, putative (PSAG) [Arabidopsis thaliana]	63.393	112	3.68E-32
35	NP_194014	expressed protein [Arabidopsis thaliana]	87.5	88	6.40E-42
36	T10106	chitinase (EC 3.2.1.14) (class II, acidic) precursor - sweet orange	86.17	188	7.58E-96
37	F86339	protein F2D10.18 [imported] - Arabidopsis thaliana	71.324	136	2.10E-39
38	AAM53946	(+)-limonene synthase 2 [Citrus limon]	91.176	238	5.00E-116
39	AAS87371	zinc finger protein [Oryza sativa (japonica cultivar-group)]	58.621	58	5.22E-15
40	No hits found				
41	AAF76227	14-3-3 protein [Populus x canescens]	90.141	142	9.44E-68
42	NP_190560	60S ribosomal protein L26 (RPL26A) [Arabidopsis thaliana]	90.278	144	1.95E-52
43	T07844	BURP domain-containing protein - rape	43	100	9.27E-15
44	NP_194842	expressed protein [Arabidopsis thaliana]	76.271	177	1.38E-60
45	T08995	ribulose-1,5-bisphosphate carboxylase/oxygenase N-methyltransferase - spinach chloroplast	36.842	114	2.18496E-09
46	NP_566884	ubiquitin-conjugating enzyme 13 (UBC13) [Arabidopsis thaliana]	88.742	151	4.8612E-72
47	S28420	ubiquitin / ribosomal protein CEP52 - wood tobacco	97.656	128	4.69E-67

IP : 14.49.138.138, 2017-11-03 13:30:33

48	NP_198728	germin-like protein, putative [Arabidopsis thaliana]	68.844	199	3.39E-74
49	No hits found				
50	NP_564349	expressed protein [Arabidopsis thaliana]	49.438	89	4.34E-11
51	No hits found				
52	CAE06007	OSJNBa0016O02.17 [Oryza sativa (japonica cultivar-group)]	52.113	71	1.28666E-13
53	AAD32888	F14N23.26 [Arabidopsis thaliana]	80.909	110	2.62E-46
54	NP_187206	hypoxia-responsive family protein [Arabidopsis thaliana]	75.51	98	8.98E-26
55	AAD38925	OPDA-reductase homolog [Arabidopsis thaliana]	72.222	90	3.60E-32
56	NP_177658	integral membrane protein, putative [Arabidopsis thaliana]	75.294	85	1.11E-20
57	AAF74755	asparagine synthetase [Helianthus annuus]	93.023	172	3.21E-81
58	AAO49811	SEP3-related MADS-box protein; PTM6 [Populus tremuloides]	92.547	161	2.66E-79
59	No hits found				
60	AAG24642	J1P [Daucus carota]	88.235	68	4.25E-30
61	AAC24001	isoflavone reductase related protein [Pyrus communis]	83.803	142	3.85969E-61
62	NP_974629	hydrophobic protein, putative / low temperature and salt responsive protein, putative [Arabidopsis thaliana]	72.549	51	3.91E-14
63	1604470A	poly-ubiquitin	93.293	164	9.05E-78
64	AAA34123	hexameric polyubiquitin	100	85	7.24E-41
65	BAD11570	putative 70 kDa peptidylprolyl isomerase [Oryza sativa (japonica cultivar-group)]	62.59	139	9.13E-46
66	NP_199967	peptidase M3 family protein / thimet oligopeptidase family protein [Arabidopsis thaliana]	62.044	137	1.07E-46
67	AAF22246	ascorbate peroxidase [Pimpinella brachycarpa]	84.028	144	4.60639E-68
68	T08816	choline kinase (EC 2.7.1.32) CK2 - soybean	71.605	81	8.68E-29
69	AAK95687	transcription factor JERF1 [Lycopersicon esculentum]	63.934	61	3.27E-17
70	AAD41409	cytosolic class II low molecular weight heat shock protein [Prunus dulcis]	88.652	141	4.83427E-62
71	BAC20284	acidic class I chitinase [Citrus jambhiri]	92.754	138	4.14E-77
72	1604470A	poly-ubiquitin	100	191	6.60E-102
73	AAG49361	ACC oxidase [Citrus sinensis]	98.844	173	1.01E-79
74	AAD12055	DnaJ protein [Hevea brasiliensis]	93.151	146	1.24E-57
75	NP_200679	peptidyl-prolyl cis-trans isomerase, putative / cyclophilin, putative / rotamase, putative (ROC7) [Arabidopsis thaliana]	83.453	139	4.88252E-56
76	Q9FVI2	Actin-depolymerizing factor 1 (ADF 1)	88.489	139	2.11E-67
77	AAD48913	caffeate O-methyltransferase [Liquidambar styraciflua]	59.722	144	3.50E-47
78	AAO65874	putative leukotriene A-4 hydrolase [Oryza sativa (japonica cultivar-group)]	82.895	76	6.46E-31
79	NP_179347	high mobility group protein gamma (HMGgamma) / HMG protein gamma [Arabidopsis thaliana]	58.333	132	1.76E-34
80	AAM64815	unknown [Arabidopsis thaliana]	69.903	103	2.02E-38
81	Q9ZSW9	Translationally controlled tumor protein homolog (TCTP)	94.245	139	5.40E-59
82	NP_179354	phosphoserine aminotransferase, putative [Arabidopsis thaliana]	82.895	152	6.17E-70
83	Q40250	Ribulose bisphosphate carboxylase small chain, chloroplast precursor (RuBisCO small subunit)	77.095	179	1.78E-81
84	NP_179920	expressed protein [Arabidopsis thaliana]	73.958	96	4.39153E-38
85	NP_201564	DNA helicase, putative [Arabidopsis thaliana]	70.536	112	1.1753E-35
86	No hits found				
87	No hits found				

IP : 14.49.138.138, 2017-11-03 13:30:33

88	No hits found				
89	NP_173758	pyrrolidone-carboxylate peptidase family protein [Arabidopsis thaliana]	70.046	217	9.10E-89
90	AAM64931	unknown [Arabidopsis thaliana]	58.955	134	6.71E-35
91	AAM64554	unknown [Arabidopsis thaliana]	38.994	159	7.89E-21
92	No hits found				
93	AAL84319	putative pentatricopeptide repeat containing protein [Oryza sativa (japonica cultivar-group)]	63.636	88	2.00E-25
94	AAK62389	Unknown protein [Arabidopsis thaliana]	80.769	104	2.35E-42
95	AAD09518	NTGP4 [Nicotiana tabacum]	51.807	83	1.14E-12
96	AAK52077	dehydrin COR15 [Citrus x paradisi]	89.922	129	1.43271E-28
97	P31542	ATP-dependent clp protease ATP-binding subunit clpA homolog CD4B, chloroplast precursor	92.857	210	1.09E-107
98	P93629	Alcohol dehydrogenase class III (Glutathione-dependent formaldehyde dehydrogenase) (FDH) (FALDH) (GSH-FDH)	82.143	56	3.47733E-21
99	NP_683560	serine-rich protein-related [Arabidopsis thaliana]	45.714	70	9.19E-06
100	No hits found				
101	No hits found				
102	No hits found				
103	B86191	hypothetical protein [imported] - Arabidopsis thaliana	56.667	60	1.49E-12
104	BAB09801	unnamed protein product [Arabidopsis thaliana]	56.442	163	3.63E-43
105	CAA71892	putative pre-pro-cysteine proteinase [Nicotiana tabacum]	87.805	82	2.02E-39
106	BAC9992 9	unknown protein [Oryza sativa (japonica cultivar-group)]	70	60	3.22E-11
107	Q39644	Late embryogenesis abundant protein Lea5	97.938	97	3.10E-47
108	NP_196647	CBS domain-containing protein [Arabidopsis thaliana]	83.01	206	1.34E-92
109	AAF61436	lipid transfer protein precursor [Pisum sativum]	58.889	90	5.77044E-28
110	P51823	ADP-ribosylation factor	99.448	181	7.63E-100
111	NP_564828	ubiquitin-conjugating enzyme, putative [Arabidopsis thaliana]	97.297	148	1.74E-82
112	XP_393173	similar to Hypothetical protein CBG09037 [Apis mellifera]	63.107	103	1.82E-23
113	AAO24535	At5g58240 [Arabidopsis thaliana]	68.75	144	4.33E-49
114	BAD21657	putative LEUNIG [Oryza sativa (japonica cultivar-group)]	56.25	96	1.25E-15
115	D96745	hypothetical protein T9N14.9 [imported] - Arabidopsis thaliana	66.906	139	3.33E-42
116	BAA97361	Ca2+-transporting ATPase-like protein [Arabidopsis thaliana]	78.947	228	2.66E-100
117	AAM63747	mitochondrial heat shock 22 kd protein-like [Arabidopsis thaliana]	64.179	134	3.24E-38
118	NP_564305	dormancy-associated protein, putative (DRM1) [Arabidopsis thaliana]	65.833	120	1.16E-37
119	AAS68515	structural maintenance of chromosomes 1 protein [Arabidopsis thaliana]	62.963	216	1.63E-70
120	BAB08282	unnamed protein product [Arabidopsis thaliana]	68.345	139	2.97E-45
121	AAK71233	S-adenosylmethionine synthetase [Brassica juncea]	95.833	72	1.87E-35
122	No hits found				
123	NP_195713	histone H3.2 [Arabidopsis thaliana]	100	126	4.67E-65
124	No hits found				
125	AAL32644	fructose-bisphosphate aldolase-like protein [Arabidopsis thaliana]	89.333	150	1.19E-71
126	Q05047	Cytochrome P450 72A1 (CYPLXXII) (Secologanin synthase) (SLS)	65.957	141	3.53E-87
127	AAM75140	alkaline alpha galactosidase II [Cucumis melo]	88.085	235	2.81E-145

IP : 14.49.138.138, 2017-11-03 13:30:33

128	No hits found				
129	NP_177412	cinnamyl-alcohol dehydrogenase, putative [Arabidopsis thaliana]	70.833	72	4.92E-25
130	No hits found				
131	Q9ATF5	60S ribosomal protein L18a	95.775	142	2.86E-76
132	No hits found				
133	AAN60250	unknown [Arabidopsis thaliana]	94.118	85	2.31E-41
134	BAA92156	glycine-rich RNA-binding protein [Citrus unshiu]	97.753	89	1.32E-43
135	AAB57670	pectinesterase [Citrus sinensis]	100	144	8.70E-52

IP : 14.49.138.138, 2017-11-03 13:30:33

4) 한라봉 성숙과피

Clone No.	Accession No.	Definition of Putative homologue[Organism]	Matching %	Matching Length	E-value
HAN--02-F-A23	T10242	(S)-2-hydroxy-acid oxidase (EC 1.1.3.15)[Cucurbita cv. Kurokawa Amakuri]	85.714	112	8.50E-49
HAN--01-F-C03	AAQ20892	10-hydroxygeraniol oxidoreductase [Camptotheca acuminata]	78.182	110	2.02E-52
HAN--05-F-F20	P42856	14 KD ZINC-BINDING PROTEIN (PROTEIN KINASE C INHIBITOR) (PKCI) [Zea mays]	87.5	96	1.15E-50
HAN--04-F-A11	CAA65150	14-3-3 protein [Lycopersicon esculentum]	89.796	98	1.37E-42
HAN--02-F-L11	P02519	17.3 KD CLASS I HEAT SHOCK PROTEIN (HSP 17.3) [Glycine max]	84.27	89	4.93E-27
HAN--06-F-L07	P04793	17.5 KD CLASS I HEAT SHOCK PROTEIN (HSP 17.5-M) [Glycine max]	75.325	154	5.71E-55
HAN--01-F-M07	AAF20003	1-acyl-sn-glycerol-3-phosphate acyltransferase [Prunus dulcis]	69.118	68	5.84E-18
HAN--01-F-O15	AAF65154	1-deoxy-D-xylulose-5-phosphate reductoisomerase [Catharanthus roseus]	72.185	151	6.46E-56
HAN--02-F-O23	NP_194858	20S proteasome beta subunit A (PBA1) [Arabidopsis thaliana]	86.014	143	6.01E-68
HAN--03-F-I17	NP_568389	26S proteasome AAA-ATPase subunit RPT6a [Arabidopsis thaliana]	77.215	79	1.16E-26
HAN--01-F-E20	CAC48323	2-Cys peroxiredoxin [Pisum sativum]	84.848	33	4.38E-10
HAN--05-F-J10	P42055	34 kDa outer mitochondrial membrane protein porin (Voltage-dependent anion-selective channel protein) (VDAC) (POM 34) [Solanum tuberosum]	83.969	131	7.96E-63
HAN--01-F-F06	NP_188147	3-hydroxybutyryl-CoA dehydrogenase, putative [Arabidopsis thaliana]	63.636	44	5.99E-08
HAN--03-F-L09	NP_172256	40S ribosomal protein S15A (RPS15aA) [Arabidopsis thaliana]	97.692	130	1.55E-68
HAN--06-F-J04	CAC27136	40S ribosomal protein S2 [Picea abies]	84.536	97	1.02E-40
HAN--01-F-O19	NP_190321	40S ribosomal protein S20 (RPS20B) [Arabidopsis thaliana]	98.058	103	1.83E-51
HAN--02-F-J14	NP_180719	40S ribosomal protein S3 (RPS3A) [Arabidopsis thaliana]	96.269	134	3.82E-67
HAN--04-F-J17	Q9ZNS1	40S ribosomal protein S7 [Avicennia marina]	85.586	111	5.42E-50
HAN--03-F-M06	NP_198801	40S ribosomal protein S9 (RPS9C) [Arabidopsis thaliana]	90.541	148	1.69E-72
HAN--02-F-C04	NP_197636	60S ribosomal protein L10A (RPL10aC) [Arabidopsis thaliana]	97.273	110	2.62E-55
HAN--06-F-A23	NP_199687	60S ribosomal protein L13A (RPL13aD) [Arabidopsis thaliana]	93.793	145	9.28E-69
HAN--02-F-P21	AAG13986	60S ribosomal protein L24 [Prunus avium]	96.429	112	1.85E-56
HAN--04-F-F15	NP_173743	60S ribosomal protein L27A (RPL27aB) [Arabidopsis thaliana]	86.316	95	2.08E-70
HAN--04-F-J15	O49884	60S RIBOSOMAL PROTEIN L30 [Lupinus luteus]	90.909	110	2.03E-54
HAN--05-F-B08	Q9M573	60S ribosomal protein L31[Perilla frutescens]	91.089	101	1.30E-35
HAN--04-F-A02	P41098	60S RIBOSOMAL PROTEIN L34 [Nicotiana tabacum]	95.789	95	4.83E-47
HAN--05-F-C20	AAF34800	60S ribosomal protein L35 [Euphorbia esula]	96.739	92	1.58E-42
HAN--06-F-D04	NP_178190	60S ribosomal protein L7 (RPL7A) [Arabidopsis thaliana]	55.944	143	3.69E-35
HAN--03-F-I23	NP_186885	6-phosphogluconate dehydrogenase -related [Arabidopsis thaliana]	85.802	162	9.02E-75
HAN--05-F-K13	NP_195072	ABC transporter family protein [Arabidopsis thaliana]	69.725	109	1.11E-41
HAN--05-F-E18	O04866	Acetylornithine aminotransferase, mitochondrial precursor (ACOAT) (Acetylornithine transaminase) (AOTA) [Alnus glutinosa]	71.93	114	3.04E-40
HAN--03-F-J18	BAB01067	acetyltranferase-like protein [Arabidopsis thaliana]	42.331	163	1.73E-27
HAN--03-F-N11	BAB01067	acetyltranferase-like protein [Arabidopsis thaliana]	44.915	118	3.38E-23
HAN--03-F-J12	BAB82419	acid invertase [Citrus unshiu]	100	159	5.01E-88
HAN--03-F-L01	BAB82419	acid invertase [Citrus unshiu]	98.667	75	5.37E-53
HAN--05-F-F09	P49608	Aconitate hydratase, cytoplasmic (Citrate hydro-lyase) (Aconitase) [Cucurbita cv. Kurokawa Amakuri]	90	90	6.94E-42
HAN--04-F-N10	AAD23407	actin depolymerizing factor [Populus x canescens]	92.308	52	3.46E-21

IP : 14.49.138.138, 2017-11-03 13:30:33

HAN--02-F-E14	Q9FVI1	Actin-depolymerizing factor 2 (ADF 2) [Petunia x hybrida]	88.321	137	1.45E-66
HAN--04-F-H05	NP_201316	acyl-CoA oxidase (gb|AAC13497.1) [Arabidopsis thaliana]	93.939	132	1.03E-73
HAN--03-F-D24	AAL66290	adenosine 5'-phosphosulfate reductase [Glycine max]	63.71	124	3.16E-29
HAN--03-F-M11	NP_186831	adenylate kinase -related [Arabidopsis thaliana]	53.957	139	1.68E-22
HAN--01-F-I13	AAG51787	alanine aminotransferase, putative, 3' partial; 97582-98874 [Arabidopsis thaliana]	78.302	106	3.40E-44
HAN--04-F-N14	AAD48837	alanine:glyoxylate aminotransferase 2 homolog [Arabidopsis thaliana]	87.179	156	2.92E-77
HAN--04-F-K15	NP_181374	alanine--glyoxylate aminotransferase (beta-alanine-pyruvate aminotransferase/AGT), putative [Arabidopsis thaliana]	75.229	109	9.29E-44
HAN--06-F-I22	NP_199207	alcohol dehydrogenase class III (glutathione-dependent formaldehyde dehydrogenase) (GSH-FDH) (ADHIII) [Arabidopsis thaliana]	95.327	107	1.22E-56
HAN--05-F-F19	NP_175812	aldehyde dehydrogenase, putative (ALDH) [Arabidopsis thaliana]	90.244	82	1.77E-37
HAN--06-F-H23	AAM75140	alkaline alpha galactosidase II [Cucumis melo]	79.279	111	1.41E-67
HAN--02-F-A09	AAN32954	alkaline alpha-galactosidase seed imbibition protein [Lycopersicon esculentum]	64.407	59	1.27E-16
HAN--01-F-D22	NP_177004	Altered Response to Gravity (ARG1) protein [Arabidopsis thaliana]	68.354	158	5.80E-44
HAN--04-F-C01	AAK50814	aluminium induced protein [Avicennia marina]	74.419	86	1.71E-29
HAN--05-F-E10	NP_568597	amino acid transporter family [Arabidopsis thaliana]	83.019	106	1.15E-47
HAN--01-F-F12	NP_195035	aminopeptidase- like protein [Arabidopsis thaliana]	69.792	96	1.14E-44
HAN--05-F-H23	BAA94975	AMP-binding protein [Arabidopsis thaliana]	68.148	135	1.88E-47
HAN--05-F-J23	NP_188316	AMP-dependent synthetase and ligase family [Arabidopsis thaliana]	76.812	138	9.00E-56
HAN--06-F-O21	NP_197155	amylogenin; reversibly glycosylatable polypeptide [Arabidopsis thaliana]	63.265	98	1.58E-31
HAN--06-F-N15	AAG39222	anther ethylene-upregulated protein ER1 [Nicotiana tabacum]	62.5	40	2.29E-08
HAN--04-F-G07	NP_200995	AP2 domain transcription factor family [Arabidopsis thaliana]	43.678	87	4.69E-10
HAN--02-F-J20	AAK15006	arginase [Brassica napus]	92.063	63	1.66E-25
HAN--06-F-E21	AAN01361	ascorbate peroxidase [Capsicum annuum]	56.25	80	3.39E-15
HAN--02-F-H15	AAF22246	ascorbate peroxidase [Pimpinella brachycarpa]	84.507	142	1.03E-67
HAN--06-F-G11	AAF74755	asparagine synthetase [Helianthus annuus]	70.909	110	4.07E-42
HAN--05-F-M19	BAC16371	aspartic proteinase 5 [Glycine max]	76.136	88	3.48E-36
HAN--05-F-H11	NP_850499	ATP dependent RNA helicase GB:227525 [Arabidopsis thaliana]	73.718	156	5.58E-63
HAN--02-F-C16	S48643	ATP synthase - soybean [Glycine max]	71.875	128	2.72E-44
HAN--01-F-G12	Q01859	ATP synthase beta chain, mitochondrial precursor [Oryza sativa (japonica cultivar-group)]	95.062	162	2.06E-84
HAN--01-F-I24	P29685	ATP synthase beta chain, mitochondrial precursor [Hevea brasiliensis]	98.649	74	7.00E-35
HAN--03-F-G20	AAO16703	ATPase-like protein [Sorghum bicolor]	69.079	152	9.75E-55
HAN--01-F-B12	NP_180402	auxin response transcription factor [Arabidopsis thaliana]	69.892	93	1.57E-30
HAN--06-F-L18	NP_850063	auxin-regulated protein [Arabidopsis thaliana]	67.188	64	2.93E-14
HAN--01-F-H06	AAD22104	B12D protein [Ipomoea batatas]	73.864	88	1.24E-33
HAN--01-F-A20	AAG01129	BAC19.14 [Lycopersicon esculentum]	58.696	92	4.08E-24
HAN--06-F-F19	AAN09798	benzoyl coenzyme A: benzyl alcohol benzoyl transferase [Nicotiana tabacum]	64.336	143	2.97E-48
HAN--05-F-G12	AAK58515	beta-1,3-glucanase-like protein [Olea europaea]	69.231	78	1.48E-29
HAN--03-F-F15	AAG10793	beta-carotene hydroxylase [Citrus unshiu]	100	158	1.53E-79
HAN--01-F-A16	AAN86822	beta-cyanoalanine synthase [Betula pendula]	73.404	94	9.08E-34
HAN--03-F-E10	AAK31801	beta-galactosidase [Citrus sinensis]	93.333	30	4.74E-09

IP : 14.49.138.138, 2017-11-03 13:30:33

HAN--05-F-E04	NP_190400	betaine-aldehyde dehydrogenase, putative (BADH) [Arabidopsis thaliana]	84.783	92	1.99E-44
HAN--06-F-K15	AAB37271	beta-ketoacyl-ACP synthase II [Cuphea wrightii]	86.916	107	2.97E-48
HAN--01-F-O18	NP_187263	bHLH protein family [Arabidopsis thaliana]	74.737	95	3.53E-33
HAN--03-F-M20	O81395	BIFUNCTIONAL DIHYDROFOLATE REDUCTASE-THYMIDYLATE SYNTHASE (DHFR-TS) [INCLUDES: DIHYDROFOLATE REDUCTASE ; THYMIDYLATE SYNTHASE] [Zea mays]	89.744	39	5.10E-14
HAN--03-F-B18	AAN14410	bifunctional lysine-ketoglutarate reductase/saccharopine dehydrogenase [Gossypium hirsutum]	72.807	114	9.87E-42
HAN--06-F-H15	NP_563810	bZIP protein [Arabidopsis thaliana]	52.903	155	1.47E-26
HAN--06-F-C24	AAK19601	bZIP protein DPBF3 [Arabidopsis thaliana]	50	116	5.09E-22
HAN--02-F-P09	BAA97361	Ca2+-transporting ATPase-like protein [Arabidopsis thaliana]	79.012	162	1.53E-71
HAN--03-F-C05	AAF63200	caffeic acid O-3-methyltransferase [Populus tomentosa]	55.625	160	1.26E-41
HAN--05-F-K21	AAM91028	calcineurin B [Pisum sativum]	94.737	76	1.04E-35
HAN--02-F-J09	NP_198334	calcineurin-like phosphoesterase family [Arabidopsis thaliana]	85.714	84	3.51E-39
HAN--04-F-M05	AAL30818	calcium/calmodulin-dependent protein kinase CaMK1 [Nicotiana tabacum]	85.906	149	2.51E-72
HAN--01-F-N02	Q9M7R0	Calcium-binding allergen Ole e 8 (PCA18/PCA23) [Olea europaea]	57.516	153	8.01E-41
HAN--02-F-M03	NP_180804	calcium-binding EF-hand family protein [Arabidopsis thaliana]	95.96	99	1.52E-51
HAN--01-F-M18	NP_197446	calcium-dependent protein kinase 19 (CDPK19) [Arabidopsis thaliana]	87.931	58	4.78E-22
HAN--01-F-E03	NP_568281	calcium-dependent protein kinase 7 (CDPK)(CPK7) [Arabidopsis thaliana]	88.199	161	1.56E-79
HAN--01-F-K08	NP_187630	calmodulin, putative [Arabidopsis thaliana]	57.325	157	1.11E-39
HAN--02-F-I07	NP_201227	calmodulin-binding protein [Arabidopsis thaliana]	77.931	145	6.03E-60
HAN--06-F-O10	P41210	Caltractin (Centrin) [Atriplex nummularia]	75.61	82	6.63E-30
HAN--01-F-A04	Q9SEA0	Capsanthin/capsorubin synthase, chloroplast precursor [Citrus sinensis]	97.436	117	2.40E-53
HAN--02-F-M14	NP_197090	Carboxylesterase-related protein [Arabidopsis thaliana]	65.789	76	5.84E-20
HAN--03-F-F04	NP_180811	carboxymethylenebutenolidase -related [Arabidopsis thaliana]	90.299	134	1.64E-65
HAN--06-F-L24	AAM63923	carnitine racemase like protein [Arabidopsis thaliana]	72.603	146	1.36E-46
HAN--04-F-B11	BAC02726	casein kinase 2 catalytic subunit [Nicotiana tabacum]	91.429	140	1.08E-55
HAN--01-F-M21	NP_181477	cation efflux family protein [Arabidopsis thaliana]	91.818	110	2.73E-55
HAN--01-F-H21	NP_193194	CBL-interacting protein kinase 4 [Arabidopsis thaliana]	70.161	124	3.24E-40
HAN--01-F-G02	AAF62404	cell death associated protein [Nicotiana tabacum]	65.06	83	1.83E-22
HAN--02-F-O20	NP_193808	cell-cell signaling protein csgA - like [Arabidopsis thaliana]	84.211	76	3.76E-33
HAN--05-F-K11	AAO03579	cellulose synthase-like protein D4 [Populus tremuloides]	90.741	162	2.43E-85
HAN--03-F-I05	1FSI_A	Chain A, Crystal Structure Of Cyclic Nucleotide Phosphodiesterase Of Appr>p From Arabidopsis Thaliana [Arabidopsis thaliana]	61.667	120	8.47E-38
HAN--06-F-C18	NP_198008	chaperonin, putative [Arabidopsis thaliana]	93.496	123	2.24E-59
HAN--06-F-P22	NP_566466	chaperonin, putative [Arabidopsis thaliana]	72.165	97	4.81E-33
HAN--05-F-A03	T10106	chitinase (EC 3.2.1.14) (class II, acidic) precursor [Citrus sinensis]	93.252	163	5.46E-80
HAN--01-F-H18	AAC35981	chitinase CHI1 [Citrus sinensis]	97.938	97	1.70E-48
HAN--06-F-G24	NP_564534	chorismate synthase (5-enolpyruvylshikimate-3-phosphate phospholyase), putative [Arabidopsis thaliana]	75.758	66	3.11E-22
HAN--03-F-I08	BAB63262	CIG2 [Nicotiana tabacum]	79.845	129	5.93E-44
HAN--02-F-J05	AAK28509	cinnamyl alcohol dehydrogenase [Fragaria x ananassa]	81.481	54	2.04E-18
HAN--01-F-E02	AAL35901	clathrin assembly protein AP17-like protein [Oryza sativa]	98.182	110	1.21E-58
HAN--02-F	NP_191905	conserved hypothetical protein [Arabidopsis thaliana]	58.228	158	1.79E-32

IP : 14.49.138.138, 2017-11-03 13:30:33

-L10					
HAN--04-F-A17	NP_191905	conserved hypothetical protein [Arabidopsis thaliana]	73.451	113	1.98E-41
HAN--01-F-G10	BAB08274	contains similarity to chloroplast nucleoid DNA-binding protein~gene_id:MMG4.12 [Arabidopsis thaliana]	66.667	126	2.64E-41
HAN--04-F-I20	BAB10406	contains similarity to ribonucleoprotein F~gene_id:K2A18.8 [Arabidopsis thaliana]	68.966	58	4.78E-18
HAN--06-F-I15	BAA97328	contains similarity to small GTPase Ran binding protein 1~gene_id:MZN1.4 [Arabidopsis thaliana]	84.211	95	3.72E-38
HAN--06-F-G20	BAB09053	contains similarity to unknown protein~gene_id:MRH10.2~pir||T00959 [Arabidopsis thaliana]	53.279	122	1.22E-25
HAN--05-F-P03	NP_565206	copine-related [Arabidopsis thaliana]	37.895	95	2.10E-12
HAN--05-F-M21	NP_196946	copine-related [Arabidopsis thaliana]	54.839	93	4.23E-23
HAN--06-F-O05	NP_192597	copper chaperone (CCH)-related [Arabidopsis thaliana]	74.257	101	3.91E-25
HAN--06-F-M09	AAM77651	cp10-like protein [Gossypium hirsutum]	81.132	159	3.61E-70
HAN--03-F-H16	BAA83469	Csf-1 [Cucumis sativus]	82.353	136	1.72E-59
HAN--01-F-D20	AAL38532	CSLE1 [Oryza sativa]	34.437	151	5.47E-18
HAN--03-F-B21	AAN62336	CTV.2 [Poncirus trifoliata]	98.649	74	1.08E-35
HAN--03-F-J07	AAN62354	CTV.22 [Poncirus trifoliata]	93.919	148	1.50E-63
HAN--03-F-O05	NP_200679	cyclophilin ROC7 [Arabidopsis thaliana]	86.25	160	5.44E-69
HAN--04-F-A15	AAG38521	cystatin-like protein [Citrus x paradisi]	100	99	2.29E-52
HAN--01-F-O12	T12041	cysteine proteinase (EC 3.4.22.-) 3 precursor [Phaseolus vulgaris]	69.032	155	5.88E-58
HAN--05-F-D19	T07139	cysteine proteinase inhibitor [Glycine max]	76.667	90	1.55E-33
HAN--03-F-L07	BAB68079	cytochrome b245 beta chain homolog rbohA [Oryza sativa (japonica cultivar-group)]	97.368	38	1.26E-12
HAN--05-F-K04	AAL36459	cytochrome b5 reductase isoform II [Zea mays]	88.372	129	5.82E-63
HAN--06-F-E20	NP_192742	cytochrome c [Arabidopsis thaliana]	95.536	112	1.68E-59
HAN--06-F-E03	NP_200939	cytochrome c oxidase subunit - like [Arabidopsis thaliana]	83.636	55	2.58E-14
HAN--04-F-P12	Q05047	Cytochrome P450 72A1 (CYPLXXII) (Secologanin synthase) (SLS) [Catharanthus roseus]	51.304	115	2.23E-24
HAN--04-F-M11	NP_194925	cytochrome p450 family [Arabidopsis thaliana]	52.941	153	1.20E-38
HAN--03-F-G12	NP_189154	cytochrome P450 family [Arabidopsis thaliana]	55.357	112	6.00E-31
HAN--02-F-G23	NP_194922	cytochrome p450, putative [Arabidopsis thaliana]	63.975	161	1.52E-58
HAN--02-F-F09	BAB92709	cytokinesis regulating protein - like [Oryza sativa (japonica cultivar-group)]	31.298	131	2.66E-07
HAN--05-F-A16	AAO41731	cytoplasmic ribosomal protein S14 [Brassica napus]	92.701	137	3.05E-58
HAN--04-F-J22	NP_177360	cytosolic factor -related [Arabidopsis thaliana]	75	44	4.65E-13
HAN--05-F-F18	BAC07111	DEAD box protein-like [Oryza sativa (japonica cultivar-group)]	55.385	65	1.70E-12
HAN--03-F-G02	AAK50345	defense-related protein [Brassica carinata]	47.619	168	1.84E-35
HAN--06-F-E01	AAN87573	delta 12 oleic acid desaturase FAD2 [Vernicia fordii]	79.381	97	4.43E-45
HAN--02-F-H24	AAK73756	delta-1-pyrroline-5-carboxylate dehydrogenase precursor [Arabidopsis thaliana]	89.091	55	1.07E-25
HAN--06-F-I20	NP_565053	developmental protein DG1118 -related [Arabidopsis thaliana]	91.736	121	2.69E-41
HAN--04-F-E01	NP_190926	diaminopimelate epimerase - like protein [Arabidopsis thaliana]	72	25	1.84E-09
HAN--03-F-G05	AAF66242	dicyanin [Lycopersicon esculentum]	46.729	107	9.96E-10
HAN--02-F-D10	NP_195056	disease resistance protein (CC-NBS-LRR class), putative [Arabidopsis thaliana]	45	100	5.33E-20
HAN--03-F-O06	NP_197298	disease resistance protein (TIR-NBS-LRR class), putative [Arabidopsis thaliana]	44.966	149	1.56E-26
HAN--03-F-E18	T02434	DNA binding protein EREBP-4 [Nicotiana tabacum]	45.794	107	6.19E-09
HAN--06-F-J12	NP_179145	DNA-directed RNA polymerase II, third largest subunit [Arabidopsis thaliana]	82.667	150	1.45E-66

IP : 14.49.138.138, 2017-11-03 13:30:33

HAN--05-F-B18	BAB11387	DNA-directed RNA polymerase subunit [Arabidopsis thaliana]	82.734	139	3.65E-65
HAN--06-F-M07	NP_180257	DnaJ domain-containing protein [Arabidopsis thaliana]	71.311	122	1.50E-33
HAN--04-F-K17	AAD12055	DnaJ protein [Hevea brasiliensis]	93.421	152	1.07E-62
HAN--03-F-N21	NP_680194	DnaJ protein family [Arabidopsis thaliana]	87.5	64	1.20E-28
HAN--05-F-O08	NP_565163	DnaJ protein family [Arabidopsis thaliana]	69.182	159	6.38E-59
HAN--05-F-E17	CAB92142	DREPP1 protein [Nicotiana tabacum]	39.048	105	1.34E-11
HAN--04-F-H22	AAO43000	early tobacco anther 1 [Nicotiana tabacum]	51.852	108	1.07E-20
HAN--03-F-J02	CAA48027	Eli3-1 [Arabidopsis thaliana]	79.747	79	2.98E-30
HAN--01-F-E07	BAB16427	Elicitor inducible gene product Nt-SubE80 [Nicotiana tabacum]	68.367	98	5.03E-35
HAN--06-F-E24	AAK62346	elicitor-inducible cytochrome P450 [Nicotiana tabacum]	77.778	162	8.74E-70
HAN--01-F-L15	NP_181669	embryo-abundant protein -related [Arabidopsis thaliana]	56.897	58	3.97E-13
HAN--06-F-N08	NP_181669	embryo-abundant protein -related [Arabidopsis thaliana]	68.243	148	1.47E-55
HAN--01-F-B09	AAP42136	erg-1 [Solanum tuberosum]	78.846	104	5.90E-45
HAN--06-F-D08	AAP42136	erg-1 [Solanum tuberosum]	62.264	106	2.39E-34
HAN--05-F-O03	NP_566801	esterase/lipase/thioesterase family [Arabidopsis thaliana]	66.667	90	4.41E-31
HAN--02-F-A17	BAA92728	ESTs AU082419(E61744),AU031498(E61744) correspond to a region of the predicted gene.~Similar to Arabidopsis thaliana putative pathogenesis-related protein (U20347) [Oryza sativa (japonica cultivar-group)]	78.667	75	4.21E-29
HAN--05-F-M10	CAB76929	ethylene receptor (ETR-1 protein) [Citrus sinensis]	100	119	6.12E-59
HAN--02-F-D16	Q9ZWL6	Ethylene receptor (PE-ETR1) [Passiflora edulis]	96.855	159	2.01E-84
HAN--03-F-K16	CAC48386	ethylene receptor [Fragaria x ananassa]	74.419	129	6.40E-51
HAN--05-F-J04	BAA76734	ethylene responsive element binding factor [Nicotiana tabacum]	65.942	138	1.35E-25
HAN--03-F-E02	CAD21849	ethylene responsive element binding protein [Fagus sylvatica]	56.923	130	5.44E-24
HAN--04-F-I18	CAD21849	ethylene responsive element binding protein [Fagus sylvatica]	58.434	166	1.38E-46
HAN--06-F-A11	P56821	Eukaryotic translation initiation factor 3 subunit 9 (eIF-3 eta) (eIF3 p110) (eIF3b) [Nicotiana tabacum]	86.897	145	1.12E-71
HAN--01-F-D01	AAP86602	eukaryotic translation initiation factor 4E [Lactuca sativa]	78.906	128	1.06E-54
HAN--06-F-H03	P48724	Eukaryotic translation initiation factor 5 (eIF-5) [Phaseolus vulgaris]	71.429	84	3.34E-26
HAN--05-F-A15	AAQ08196	eukaryotic translation initiation factor 5A isoform 6 [Hevea brasiliensis]	97.297	148	8.24E-80
HAN--01-F-J18	AAP86603	eukaryotic translation initiation factor iso4E [Lactuca sativa]	84.507	142	3.08E-72
HAN--03-F-D20	NP_175851	exonuclease -related [Arabidopsis thaliana]	73.248	157	5.77E-60
HAN--02-F-J13	AAK48845	expansin [Prunus cerasus]	91.195	159	2.54E-87
HAN--05-F-A07	BAC66694	expansin [Vitis labrusca x Vitis vinifera]	86.777	121	2.96E-45
HAN--04-F-D09	NP_197204	exportin1 (XPO1) [Arabidopsis thaliana]	64.539	141	1.52E-32
HAN--01-F-D08	S54157	extensin-like protein [Vigna unguiculata]	36.283	113	3.14E-10
HAN--04-F-F16	NP_193816	FAD-linked oxidoreductase family [Arabidopsis thaliana]	77.108	83	5.41E-31
HAN--05-F-G17	NP_567108	F-box protein (lectin-related) [Arabidopsis thaliana]	68	100	8.07E-35
HAN--06-F-E11	AAM63110	F-box protein AtFBL5 [Arabidopsis thaliana]	69.697	33	8.94E-08
HAN--05-F-D02	NP_567343	F-box protein family, AtFBW2 [Arabidopsis thaliana]	72	75	4.92E-50
HAN--04-F-F03	P42044	Ferrochelatase II, chloroplast precursor (Protoheme ferro-lyase) (Heme synthetase) [Cucumis sativus]	76.087	138	4.86E-56
HAN--02-F-M16	AAP34362	fiber protein Fb15 [Gossypium barbadense]	71.91	89	1.27E-36
HAN--01-F	NP_193259	fringe-related protein [Arabidopsis thaliana]	38.75	80	2.71E-07

IP : 14.49.138.138, 2017-11-03 13:30:33

-N14					
HAN--03-F-J10	T07588	fructokinase (EC 2.7.1.4) 1 [Lycopersicon esculentum]	74.38	121	3.53E-33
HAN--04-F-P01	P37829	Fructokinase [Solanum tuberosum]	90.21	143	7.96E-65
HAN--05-F-P23	CAB41987	FtsZ-like protein [Nicotiana tabacum]	70.886	158	2.98E-30
HAN--05-F-E07	NP_172669	fumarylacetoacetate hydrolase-related protein [Arabidopsis thaliana]	74.126	143	2.27E-56
HAN--03-F-F06	AAD33959	G protein beta subunit [Pisum sativum]	83.333	30	2.50E-15
HAN--06-F-I24	AAK96841	G protein-coupled receptor-like protein [Arabidopsis thaliana]	57.534	73	1.98E-14
HAN--04-F-B05	NP_189474	galactinol synthase, putative [Arabidopsis thaliana]	82.105	95	1.53E-44
HAN--02-F-J23	NP_568791	galactosyltransferase family [Arabidopsis thaliana]	77.907	86	3.50E-38
HAN--04-F-G12	NP_566957	gamma response I protein [Arabidopsis thaliana]	81.034	58	1.18E-21
HAN--01-F-F15	AAO92257	gamma-aminobutyrate transaminase subunit precursor isozyme 3 [Lycopersicon esculentum]	64.394	132	8.45E-45
HAN--06-F-J22	AAK14790	G-box binding factor bZIP transcription factor [Catharanthus roseus]	79.787	94	2.07E-33
HAN--04-F-L06	NP_181435	GCN5-related N-acetyltransferase (GNAT) family [Arabidopsis thaliana]	63.303	109	6.69E-26
HAN--01-F-D07	AAO24774	GCPE protein [Catharanthus roseus]	94.175	103	4.13E-52
HAN--01-F-I09	T01782	GDP dissociation inhibitor [Nicotiana tabacum]	96.429	56	3.50E-24
HAN--03-F-C24	T02030	GDP dissociation inhibitor protein [Oryza sativa]	88.732	71	8.29E-33
HAN--02-F-C02	AAM49801	GFA2 [Arabidopsis thaliana]	76.471	68	1.29E-24
HAN--06-F-N04	T09154	glucose-6-phosphate isomerase (EC 5.3.1.9), cytosol [Spinacia oleracea]	80	120	1.29E-50
HAN--01-F-E13	P54234	Glucose-6-phosphate isomerase, cytosolic 1 (GPI) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI) [Clarkia arcuata]	81.102	127	7.46E-55
HAN--02-F-F18	AAB61597	glutamine synthetase [Hevea brasiliensis]	96.875	128	2.94E-70
HAN--05-F-M06	BAC21263	glutathione S-transferase [Cucurbita maxima]	44	75	4.79E-14
HAN--03-F-O01	NP_198937	glutathione transferase, putative [Arabidopsis thaliana]	76	150	5.51E-48
HAN--04-F-O24	AAM92008	glyceraldehyde 3-phosphate dehydrogenase [Solanum tuberosum]	96.825	63	1.47E-28
HAN--06-F-M10	AAM92008	glyceraldehyde 3-phosphate dehydrogenase [Solanum tuberosum]	94.805	77	4.92E-35
HAN--06-F-K04	NP_566891	glycerol-3-phosphate transporter (glycerol 3-phosphate permease), putative [Arabidopsis thaliana]	70.988	162	2.03E-60
HAN--05-F-L08	NP_567895	glycine hydroxymethyltransferase (EC 2.1.2.1) - like protein [Arabidopsis thaliana]	78.992	119	1.06E-46
HAN--02-F-P14	NP_195326	glycine-rich protein [Arabidopsis thaliana]	50.633	79	6.76E-11
HAN--01-F-A10	BAA92156	glycine-rich RNA-binding protein [Citrus unshiu]	100	85	8.74E-43
HAN--03-F-O09	BAA92156	glycine-rich RNA-binding protein [Citrus unshiu]	97.436	39	4.14E-15
HAN--02-F-D08	1803516A	glycolate oxidase [Lens culinaris]	92.424	132	4.68E-57
HAN--06-F-O01	CAA42103	glycolytic glyceraldehyde 3-phosphate dehydrogenase [Antirrhinum majus]	91.525	59	3.06E-24
HAN--01-F-B11	NP_680128	glycoside hydrolase family 2 [Arabidopsis thaliana]	72.868	129	2.65E-52
HAN--01-F-D12	NP_565652	glycosyl hydrolase family 17 [Arabidopsis thaliana]	61.538	91	1.73E-27
HAN--04-F-C10	NP_197525	glycosyl hydrolase family 36 [Arabidopsis thaliana]	87.333	150	2.13E-83
HAN--05-F-M16	NP_201416	glycosyl hydrolase family 38 (alpha-mannosidase) [Arabidopsis thaliana]	73.529	102	1.63E-35
HAN--03-F-E09	NP_187742	glycosyltransferase family [Arabidopsis thaliana]	44.937	158	4.93E-27
HAN--03-F-L10	NP_194487	glycosyltransferase family [Arabidopsis thaliana]	47.333	150	1.78E-40
HAN--05-F-A11	NP_177675	glycosyltransferase family 1 [Arabidopsis thaliana]	81.879	149	5.06E-56
HAN--05-F-G01	NP_175086	gr1 protein [Arabidopsis thaliana]	71.111	90	2.06E-34
HAN--05-F-I09	AAL14628	growth-on protein GRO11 [Euphorbia esula]	80.583	103	1.44E-45

IP : 14.49.138.138, 2017-11-03 13:30:33

HAN--01-F-P10	AAL65125	GT-2 factor [Glycine max]	63.542	96	2.34E-32
HAN--04-F-E18	T06410	GTP cyclohydrolase II (EC 3.5.4.25) / 3, 4-dihydroxy-2-butanone 4-phosphate synthase (EC 5.4.99.-) ribA [Lycopersicon esculentum]	38.095	105	3.00E-09
HAN--04-F-J02	AAB53256	GTP-binding protein [Arabidopsis thaliana]	92.593	108	9.67E-48
HAN--04-F-I12	AAM12880	GTP-binding protein [Helianthus annuus]	100	135	1.19E-78
HAN--04-F-O21	BAA02116	GTP-binding protein [Pisum sativum]	98.276	116	6.04E-62
HAN--01-F-G05	NP_200894	GTP-binding protein, putative [Arabidopsis thaliana]	90.323	31	5.36E-10
HAN--02-F-K20	CAA82710	guanine nucleotide regulatory protein [Vicia faba]	63.235	68	5.50E-11
HAN--05-F-I24	O24076	Guanine nucleotide-binding protein beta subunit-like protein [Medicago sativa]	82.022	89	2.07E-31
HAN--04-F-B17	T43789	H+-transporting two-sector ATPase (EC 3.6.3.14) chain B, vacuolar [imported] [Citrus unshiu]	100	159	1.65E-86
HAN--02-F-C24	NP_199286	haloacid dehalogenase-like hydrolase family [Arabidopsis thaliana]	85	100	3.74E-49
HAN--02-F-E09	AAF62403	harpin inducing protein [Nicotiana tabacum]	58.696	138	2.56E-26
HAN--02-F-P01	P37900	HEAT SHOCK 70 KD PROTEIN, MITOCHONDRIAL PRECURSOR [Pisum sativum]	81.013	79	8.68E-22
HAN--06-F-B24	P36181	HEAT SHOCK COGNATE PROTEIN 80 [Lycopersicon esculentum]	95.556	135	2.76E-71
HAN--04-F-D17	T02018	heat shock protein 26a, chloroplast [Nicotiana tabacum]	76.515	132	1.06E-46
HAN--01-F-B10	P33126	HEAT SHOCK PROTEIN 82 [Oryza sativa]	96.899	129	8.24E-64
HAN--04-F-H24	T10248	heat shock protein, 70K, chloroplast [Cucumis sativus]	65.789	76	1.26E-16
HAN--04-F-K13	AAF31705	heat-shock protein 80 [Euphorbia esula]	91.139	79	3.19E-27
HAN--01-F-I21	AAP91821	HECT ubiquitin-protein ligase 3 [Arabidopsis thaliana]	74.107	112	4.25E-54
HAN--03-F-D22	AAP91821	HECT ubiquitin-protein ligase 3 [Arabidopsis thaliana]	71.154	156	8.29E-40
HAN--05-F-P07	AAA34123	hexameric polyubiquitin [Nicotiana sylvestris]	100	97	2.97E-48
HAN--05-F-K01	CAB52689	hexose transporter [Lycopersicon esculentum]	79.167	72	2.56E-28
HAN--01-F-F16	CAC20728	histidinol phosphate aminotransferase [Nicotiana plumbaginifolia]	66.667	87	1.40E-26
HAN--02-F-L08	NP_175517	histone H2A, putative [Arabidopsis thaliana]	92.708	96	3.99E-32
HAN--05-F-N12	B38309	histone H3.2 [Medicago sativa]	96.667	30	6.72E-09
HAN--04-F-G05	1101277A	histone H4 [Triticum aestivum]	100	59	1.24E-26
HAN--06-F-N11	NP_179347	HMG protein -related [Arabidopsis thaliana]	48.551	138	2.71E-25
HAN--05-F-E03	O04136	Homeobox protein knotted-1 like 3 (KNAP3) [Malus x domestica]	65.217	92	1.76E-24
HAN--04-F-C24	NP_196886	H-protein promoter binding factor-1 (gb|AAC24592.1) [Arabidopsis thaliana]	50.318	157	1.58E-30
HAN--02-F-I19	AAL11446	HUA enhancer 2 [Arabidopsis thaliana]	89.873	158	6.14E-78
HAN--01-F-J23	NP_193740	hydantoin utilization protein-related [Arabidopsis thaliana]	71.074	121	4.43E-45
HAN--04-F-I10	NP_196726	hydrolase, alpha/beta fold family [Arabidopsis thaliana]	45.802	131	4.07E-18
HAN--03-F-A20	NP_194147	hydrolase, alpha/beta fold family [Arabidopsis thaliana]	90.426	94	1.97E-47
HAN--05-F-B22	NP_565629	hydroxymethylglutaryl-CoA lyase -related [Arabidopsis thaliana]	56.25	112	2.17E-27
HAN--05-F-H16	AAD25944	hypothetical EIF-2-Alpha [Arabidopsis thaliana]	98.113	106	1.77E-48
HAN--05-F-G03	NP_567717	immunophilin / FKBP-type peptidyl-prolyl cis-trans isomerase -related [Arabidopsis thaliana]	52.555	137	2.07E-34
HAN--02-F-L16	NP_201240	immunophilin / FKBP-type peptidyl-prolyl cis-trans isomerase, putative [Arabidopsis thaliana]	82.143	112	3.34E-53
HAN--04-F-M02	AAK38727	importin alpha 2 [Capsicum annuum]	80.255	157	3.09E-66
HAN--06-F-K14	P49249	IN2-2 protein [Zea mays]	85.714	154	1.39E-74
HAN--02-F-B09	AAC78101	inorganic pyrophosphatase [Oryza sativa]	77.273	44	1.10E-12
HAN--05-F	AAM20595	integral membrane protein, putative [Arabidopsis thaliana]	72.18	133	1.07E-40

IP : 14.49.138.138, 2017-11-03 13:30:33

-G06					
HAN--05-F-C12	NP_196963	isocitrate dehydrogenase [NADP+], putative [Arabidopsis thaliana]	79.825	114	5.54E-46
HAN--04-F-H17	CAB55554	Isovaleryl-CoA Dehydrogenase; auxin binding protein (ABP44) [Pisum sativum]	92.949	156	5.81E-81
HAN--06-F-N21	NP_566316	Kelch repeats protein family [Arabidopsis thaliana]	75	52	1.05E-17
HAN--03-F-N13	CAA48253	ketol-acid reductoisomerase [Arabidopsis thaliana]	67.308	156	1.44E-47
HAN--05-F-E09	NP_175569	KH domain protein [Arabidopsis thaliana]	71.875	64	8.86E-21
HAN--03-F-F20	NP_181395	KH domain protein [Arabidopsis thaliana]	77.5	40	3.11E-07
HAN--06-F-K12	BAC57956	laccase [Aster tripolium]	76.712	73	9.58E-29
HAN--03-F-P24	AAP23944	leucine-rich repeat protein [x Citrofortunella mitis]	93.333	75	6.14E-39
HAN--04-F-H11	Q9MB73	Limonoid UDP-glucosyltransferase (Limonoid glucosyltransferase) (Limonoid GTase) (LGTase) [Citrus unshiu]	98.582	141	6.37E-67
HAN--03-F-D10	AAG29777	lipid transfer protein 3 precursor [Gossypium hirsutum]	69.231	117	6.07E-36
HAN--03-F-M18	AAM21292	lipid-transfer protein [Citrus sinensis]	74.194	93	3.68E-33
HAN--06-F-I11	NP_179682	lipoic acid synthase (LIP1) [Arabidopsis thaliana]	77.5	40	4.20E-10
HAN--03-F-I11	BAB84352	lipoxygenase [Citrus jambhiri]	100	125	1.58E-68
HAN--03-F-K03	AAM28873	long chain acyl-CoA synthetase 6 [Arabidopsis thaliana]	86.145	166	1.67E-84
HAN--05-F-I03	NP_187777	lysyl-tRNA synthetase, putative [Arabidopsis thaliana]	73.718	156	3.36E-62
HAN--04-F-I03	AAK94426	LYTB-like protein 1 [Brassica rapa subsp. pekinensis]	85.629	167	2.54E-80
HAN--05-F-D10	CAA67969	MADS5 protein [Betula pendula]	87.879	132	3.83E-61
HAN--05-F-I20	AAM21344	MADS-box protein 4 [Vitis vinifera]	75.294	85	2.95E-31
HAN--03-F-D16	BAC77412	makorin ring-zinc-finger protein [Pisum sativum]	71.429	42	1.07E-13
HAN--06-F-F18	P19446	Malate dehydrogenase, glyoxysomal precursor [Citrullus lanatus]	86.364	66	1.22E-25
HAN--04-F-O05	BAB21610	mangrin [Bruguiera sexangula]	63.333	120	1.22E-29
HAN--02-F-K22	CAB61750	MAP kinase protein [Cicer arietinum]	86.667	120	1.28E-56
HAN--03-F-L16	NP_564656	membrane protein common family [Arabidopsis thaliana]	77.358	53	3.02E-18
HAN--01-F-N08	NP_172566	metal transporter, putative (ZIP4) [Arabidopsis thaliana]	85.915	71	3.94E-27
HAN--05-F-H03	AAD49573	methionine S-methyltransferase [Wollastonia biflora]	67.692	65	1.87E-22
HAN--01-F-A05	AAL73979	methionine synthase protein [Sorghum bicolor]	84.112	107	9.98E-47
HAN--06-F-H20	NP_176647	methionine/cystathionine gamma lyase -related [Arabidopsis thaliana]	78.261	92	1.36E-29
HAN--04-F-B06	E85437	methionyl aminopeptidase-like protein [imported][Arabidopsis thaliana]	86.957	69	4.56E-30
HAN--05-F-L19	AAD51733	methylenetetrahydrofolate reductase [Zea mays]	82.857	105	4.29E-47
HAN--03-F-H24	AAM62925	MFDX2 precursor [Arabidopsis thaliana]	82.979	47	9.69E-17
HAN--06-F-B08	NP_181459	middle domain of eukaryotic initiation factor 4G (MIF4G) domain-containing protein [Arabidopsis thaliana]	61.856	97	9.27E-24
HAN--01-F-O09	P42059	Minor allergen Cla h 5 (Cla h V) [Davidiella tassiana]	74.468	47	2.15E-22
HAN--02-F-N10	NP_194568	mitochondrial ADP,ATP carrier protein, putative [Arabidopsis thaliana]	66.897	145	2.01E-47
HAN--01-F-M22	NP_192019	mitochondrial carrier protein family [Arabidopsis thaliana]	82.353	68	9.73E-28
HAN--03-F-B15	S51590	mitochondrial processing peptidase (EC 3.4.24.64) alpha-II chain precursor [Solanum tuberosum]	60.377	106	2.24E-25
HAN--05-F-D18	P29677	Mitochondrial processing peptidase alpha subunit, mitochondrial precursor (Alpha-MPP) (Ubiquinol-cytochrome C reductase subunit II) [Solanum tuberosum]	75.524	143	1.50E-57
HAN--02-F-G20	AAK07827	mitochondrial processing peptidase beta subunit [Cucumis melo]	71.324	136	1.95E-42
HAN--03-F-O22	AAP20421	mitogen-activated protein kinase 3 [Lycopersicon esculentum]	83.696	92	1.95E-41

IP : 14.49.138.138, 2017-11-03 13:30:33

HAN--01-F-L16	NP_199799	mitotic checkpoint protein-related [Arabidopsis thaliana]	83.486	109	1.44E-47
HAN--04-F-M22	NP_200324	molybdenum cofactor synthesis protein 3 (molybdopterin synthase sulphurylase) [Arabidopsis thaliana]	81.111	90	4.16E-40
HAN--04-F-L24	NP_178391	mucin -related [Arabidopsis thaliana]	84.884	86	5.15E-37
HAN--05-F-F10	NP_197447	MutT/nudix family protein [Arabidopsis thaliana]	36.792	106	3.36E-07
HAN--02-F-J15	NP_189303	MutT/nudix family protein [Arabidopsis thaliana]	69.231	91	1.71E-30
HAN--05-F-E05	NP_568776	myb family transcription factor [Arabidopsis thaliana]	64.423	104	5.50E-29
HAN--06-F-L20	CAC19789	MYB-like DNA-binding protein [Catharanthus roseus]	83.333	66	1.37E-24
HAN--06-F-O23	T50498	myc-like protein [Arabidopsis thaliana]	44.318	176	3.74E-22
HAN--03-F-O17	NP_197549	myosin-related protein [Arabidopsis thaliana]	85.965	114	7.15E-45
HAN--02-F-F16	AAP35056	NAC-domain protein 485 [Brassica napus]	89.189	74	2.51E-34
HAN--02-F-G05	NP_196882	N-acetyltransferase, putative [Arabidopsis thaliana]	93.617	141	6.21E-73
HAN--05-F-I05	AAC49964	NAD+ dependent isocitrate dehydrogenase subunit 1 [Arabidopsis thaliana]	85.093	161	4.03E-74
HAN--06-F-P17	NP_191842	NAD-dependent epimerase/dehydratase family [Arabidopsis thaliana]	78.049	41	3.58E-12
HAN--02-F-E08	P37221	NAD-DEPENDENT MALIC ENZYME 62 KDA ISOFORM, MITOCHONDRIAL PRECURSOR (NAD-ME) [Solanum tuberosum]	78.523	149	5.46E-53
HAN--01-F-I07	P42027	NADH-ubiquinone oxidoreductase 20 kDa subunit, mitochondrial precursor (Complex I-20KD) (CI-20KD) [Brassica oleracea]	67.606	142	2.69E-41
HAN--05-F-D17	P51615	NADP-DEPENDENT MALIC ENZYME (NADP-ME) [Vitis vinifera]	86.869	99	1.22E-36
HAN--05-F-P18	AAM28891	NADPH oxidase [Nicotiana tabacum]	76.129	155	2.48E-60
HAN--02-F-K06	AAD51361	NADP-isocitrate dehydrogenase [Citrus limon]	98.529	68	2.58E-31
HAN--04-F-K11	AAD51361	NADP-isocitrate dehydrogenase [Citrus limon]	90.123	162	5.36E-83
HAN--01-F-A06	AAM34773	nam-like protein 10 [Petunia x hybrida]	95.041	121	2.01E-66
HAN--03-F-I18	NP_568251	Ndr family [Arabidopsis thaliana]	75	148	3.17E-58
HAN--03-F-C08	AAN15927	nitrate reductase [Tilia platyphyllos]	84.615	104	4.70E-41
HAN--03-F-C20	Q42965	Nitrilase 4 >gi|7435979|pir||T03736 nitrilase (EC 3.5.5.1) [Nicotiana tabacum]	77.551	49	6.03E-15
HAN--01-F-I19	NP_188170	No apical meristem (NAM) protein family [Arabidopsis thaliana]	53.535	99	1.64E-22
HAN--03-F-D12	AAD17804	nodule-enhanced protein phosphatase type 2C [Lotus japonicus]	50	62	1.26E-06
HAN--02-F-M12	NP_196821	nodulin MtN3 family protein [Arabidopsis thaliana]	66.964	112	5.41E-40
HAN--03-F-C23	NP_200396	NOI protein, nitrate-induced [Arabidopsis thaliana]	63.265	49	3.78E-09
HAN--06-F-H17	AAK07729	NTCP23-like cysteine proteinase [Nicotiana tabacum]	91.935	62	3.81E-30
HAN--04-F-M01	AAM63803	nuclear transport factor 2, putative [Arabidopsis thaliana]	90	80	1.91E-36
HAN--05-F-O09	AAL54888	obtusifoliol-14-demethylase [Nicotiana tabacum]	79.72	143	2.96E-64
HAN--02-F-L23	NP_569013	oligopeptidase A [Arabidopsis thaliana]	79.412	136	3.05E-59
HAN--06-F-M05	AAN17502	omega-3 fatty acid desaturase [Betula pendula]	61.538	143	7.84E-41
HAN--03-F-A22	BAB02242	organic anion transporter-like protein [Arabidopsis thaliana]	47.917	48	7.31E-06
HAN--06-F-E17	NP_567941	oxidoreductase, 2OG-Fe(II) oxygenase family [Arabidopsis thaliana]	87.037	54	4.51E-23
HAN--01-F-I06	NP_194260	oxidoreductase, 2OG-Fe(II) oxygenase family [Arabidopsis thaliana]	58.586	99	1.24E-22
HAN--05-F-D12	NP_566623	oxidoreductase, 2OG-Fe(II) oxygenase family [Arabidopsis thaliana]	52.201	159	8.88E-34
HAN--01-F-B21	NP_683525	p23 {Brassica napus} -related [Arabidopsis thaliana]	64.815	54	1.49E-15
HAN--06-F-C19	CAC16575	p23 co-chaperone [Arabidopsis thaliana]	70	100	4.51E-33
HAN--04-F-M20	AAF40414	papain-like cysteine proteinase isoform I [Ipomoea batatas]	97.03	101	4.10E-54

IP : 14.49.138.138, 2017-11-03 13:30:33

HAN--01-F-O17	NP_196024	patatin-related [Arabidopsis thaliana]	89.873	158	4.35E-79
HAN--06-F-J10	S23799	pathogenesis-related protein 4A [Nicotiana tabacum]	78.947	114	3.39E-52
HAN--04-F-M06	AAM21199	pathogenesis-related protein 5-1 [Helianthus annuus]	67.176	131	9.08E-51
HAN--06-F-O11	BAB89059	PDI-like protein [Oryza sativa (japonica cultivar-group)]	65.625	32	1.72E-08
HAN--02-F-A04	T10488	pectinesterase (EC 3.1.1.11) PECS1.2 [Citrus sinensis]	99.02	102	5.28E-56
HAN--04-F-K09	NP_195555	pectinesterase (pectin methylesterase), putative [Arabidopsis thaliana]	84.058	69	8.47E-31
HAN--01-F-G09	Q43111	Pectinesterase 3 precursor (Pectin methylesterase 3) (PE 3) [Phaseolus vulgaris]	60	60	3.53E-14
HAN--03-F-E11	NP_176276	pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana]	63.248	117	5.19E-40
HAN--01-F-D13	AAL90751	peroxiredoxin [Populus tremula x Populus tremuloides]	90	150	2.51E-72
HAN--04-F-I15	NP_568939	Peter Pan - like protein [Arabidopsis thaliana]	79.07	86	7.89E-26
HAN--03-F-H15	NP_195639	phenylalanyl-trna synthetase - like protein [Arabidopsis thaliana]	95.57	158	5.19E-85
HAN--06-F-K01	BAB43909	phosphoenolpyruvate carboxykinase [Flaveria pringlei]	89.241	158	1.46E-79
HAN--01-F-O01	AAM47007	phosphoenolpyruvate carboxylase [Citrus junos]	100	87	9.43E-43
HAN--05-F-O21	BAB02473	phosphoglycerate dehydrogenase [Arabidopsis thaliana]	85.556	90	2.09E-38
HAN--01-F-O04	Q42962	Phosphoglycerate kinase, cytosolic [Nicotiana tabacum]	96.629	89	3.32E-42
HAN--03-F-D11	AAD24857	phosphoglycerate mutase [Solanum tuberosum]	84.091	88	3.41E-36
HAN--05-F-G07	AAN05432	phospholipase D delta isoform 1b [Gossypium hirsutum]	70.056	177	1.23E-65
HAN--03-F-K09	AAB02913	phosphoribosylanthranilate transferase [Arabidopsis thaliana]	72.727	44	9.35E-10
HAN--06-F-C09	S63668	phragmoplastin 5 [Glycine max]	95.96	99	2.64E-41
HAN--02-F-O03	AAB35314	plasma membrane H(+)-ATPase precursor [Vicia faba]	100	27	4.27E-08
HAN--04-F-P16	BAB40143	plasma membrane intrinsic protein 2-2 [Pyrus communis]	85.345	116	1.66E-44
HAN--06-F-L23	NP_565730	poly(ADP-ribose) glycohydrolase -related [Arabidopsis thaliana]	74.468	94	1.18E-39
HAN--05-F-H22	BAA28763	polygalacturonase-inhibitor [Citrus jambhiri]	94.167	120	1.18E-57
HAN--02-F-M23	T17459	polyprotein [Lycopersicon esculentum]	68.323	161	6.80E-59
HAN--06-F-B21	T17459	polyprotein [Lycopersicon esculentum]	44.706	170	1.29E-22
HAN--06-F-B22	T17459	polyprotein [Lycopersicon esculentum]	69.595	148	1.86E-58
HAN--04-F-I13	T52377	pRIB5 protein [imported] [Ribes nigrum]	70.732	82	1.35E-25
HAN--02-F-H18	B84772	probable DnaJ protein [imported] [Arabidopsis thaliana]	78.102	137	5.11E-51
HAN--03-F-E22	T07944	probable long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) [Brassica napus]	73.846	130	4.33E-50
HAN--02-F-J10	A86427	probable serine/threonine kinase [imported] [Arabidopsis thaliana]	84.615	26	2.20E-06
HAN--04-F-G09	T03400	probable transcription factor SF3 [Nicotiana tabacum]	93.22	59	5.77E-27
HAN--06-F-D23	A96556	probable tRNA-guaninine transglycosylase [imported] [Arabidopsis thaliana]	91.304	69	8.16E-32
HAN--03-F-E20	T03964	probable ubiquitin-protein ligase (EC 6.3.2.19) [Nicotiana tabacum]	84.706	85	2.78E-39
HAN--04-F-C03	NP_192765	probable wound-induced protein [Arabidopsis thaliana]	55	80	7.07E-17
HAN--04-F-H14	NP_192765	probable wound-induced protein [Arabidopsis thaliana]	55.208	96	4.08E-14
HAN--06-F-O06	NP_192765	probable wound-induced protein [Arabidopsis thaliana]	56.667	90	8.07E-17
HAN--02-F-L14	Q8GT39	Profilin (Allergen Pru p 4.02) [Prunus persica]	91.129	124	1.36E-64
HAN--06-F-H04	NP_849837	protease inhibitor/seed storage/lipid transfer protein (LTP) family [Arabidopsis thaliana]	44.048	84	1.10E-08
HAN--06-F-C08	O82531	Proteasome subunit beta type 1 (20S proteasome alpha subunit F) (20S proteasome subunit beta-6) [Petunia x hybrida]	92.632	95	1.61E-50
HAN--05-F	F96604	protein F14G9.10 [imported] [Arabidopsis thaliana]	85.263	95	5.43E-42

IP : 14.49.138.138, 2017-11-03 13:30:33

-G18					
HAN--04-F-B08	D86379	protein F21J9.24 [imported] [Arabidopsis thaliana]	44.545	110	2.77E-10
HAN--03-F-L13	H86209	protein F22G5.10 [imported] [Arabidopsis thaliana]	93.671	158	7.75E-81
HAN--04-F-J07	H86209	protein F22G5.10 [imported] [Arabidopsis thaliana]	73.077	156	6.78E-42
HAN--05-F-L15	NP_190925	protein kinase (AME2/AFC1) [Arabidopsis thaliana]	62.963	108	3.30E-31
HAN--01-F-N13	BAB02184	protein kinase [Arabidopsis thaliana]	63.636	88	7.29E-22
HAN--04-F-P10	A55661	protein kinase ADK1 [Arabidopsis thaliana]	92.949	156	4.64E-83
HAN--06-F-H10	NP_191980	protein kinase family [Arabidopsis thaliana]	90.683	161	1.70E-83
HAN--03-F-I19	NP_192110	protein kinase family [Arabidopsis thaliana]	78	50	1.53E-07
HAN--01-F-G18	AAF40430	protein kinase MK5 [Mesembryanthemum crystallinum]	85.714	84	4.84E-36
HAN--05-F-J15	AAF40430	protein kinase MK5 [Mesembryanthemum crystallinum]	71.605	81	4.37E-28
HAN--05-F-G20	AAO92595	protein kinase Pti1 [Glycine max]	90	40	3.16E-11
HAN--04-F-N20	NP_180916	protein kinase -related [Arabidopsis thaliana]	54.14	157	8.97E-37
HAN--02-F-P02	NP_194179	protein kinase -related [Arabidopsis thaliana]	73.684	38	1.15E-10
HAN--04-F-L10	NP_567574	protein kinase, putative [Arabidopsis thaliana]	88.75	160	1.67E-83
HAN--02-F-B22	NP_563834	protein kinase, putative [Arabidopsis thaliana]	56.863	51	1.57E-10
HAN--01-F-K13	NP_566716	protein kinase, putative [Arabidopsis thaliana]	82.659	173	1.06E-79
HAN--05-F-F03	CAB90634	protein phosphatase 2C (PP2C) [Fagus sylvatica]	88.095	126	9.85E-53
HAN--05-F-H02	NP_191785	protein phosphatase 2C (PP2C), putative [Arabidopsis thaliana]	56.25	80	6.98E-19
HAN--06-F-L03	CAA05875	protein phosphatase 2C [Arabidopsis thaliana]	78.846	104	4.02E-45
HAN--03-F-M09	CAC10359	protein phosphatase 2C [Nicotiana tabacum]	70.886	79	2.42E-21
HAN--04-F-A21	T51100	protein phosphatase 2C homolog [imported] [Mesembryanthemum crystallinum]	84.127	63	6.74E-35
HAN--02-F-E18	CAB90633	protein phpsphatase 2C (PP2C) [Fagus sylvatica]	48.252	143	7.18E-29
HAN--06-F-G08	NP_172318	protein serine/threonine phosphatase alpha -related [Arabidopsis thaliana]	98.204	167	7.60E-93
HAN--02-F-G03	G96787	protein T4O12.9 [imported] [Arabidopsis thaliana]	93.827	81	2.87E-68
HAN--06-F-K23	NP_194480	proton pump interactor [Arabidopsis thaliana]	47.727	132	1.09E-21
HAN--01-F-F24	NP_568107	pseudo-response regulator, APRR7 (APRR1/TOC1 family) [Arabidopsis thaliana]	80.952	63	7.21E-23
HAN--05-F-H08	NP_568107	pseudo-response regulator, APRR7 (APRR1/TOC1 family) [Arabidopsis thaliana]	67.797	118	8.71E-24
HAN--02-F-P23	AAK98757	Putative translation initiation factor 2B beta subunit [Oryza sativa]	85	40	2.58E-13
HAN--02-F-B10	BAC20920	putative 40S ribosomal protein S12 [Oryza sativa (japonica cultivar-group)]	85.593	118	6.18E-54
HAN--03-F-H23	AAM92710	putative 40S ribosomal protein S3 [Triticum aestivum]	82.558	86	3.99E-34
HAN--06-F-E19	BAC75421	putative 70 kDa peptidylprolyl isomerase [Oryza sativa (japonica cultivar-group)]	69.565	69	1.00E-22
HAN--05-F-N02	AAG10141	putative activator subunit of SNF1-related protein kinase SNF4 [Arabidopsis thaliana]	79	100	4.53E-37
HAN--06-F-I18	AAL87174	putative apospory-associated protein C [Oryza sativa (japonica cultivar-group)]	83.505	97	9.90E-44
HAN--05-F-B15	AAM64665	putative ATP synthase [Arabidopsis thaliana]	74.468	47	3.97E-13
HAN--02-F-P13	AAL58201	putative ATP(GTP)-binding protein [Oryza sativa (japonica cultivar-group)]	77.143	70	6.29E-25
HAN--02-F-A11	AAF02825	putative ATPase [Arabidopsis thaliana]	68.966	116	8.11E-38
HAN--02-F-I11	BAB92346	putative casein kinase I [Oryza sativa (japonica cultivar-group)]	98.361	61	7.78E-28
HAN--04-F-L05	AAK98735	Putative cell death suppressor protein [Oryza sativa]	76.25	80	1.23E-22
HAN--03-F-C15	AAL15888	putative cysteine synthase [Castanea sativa]	89.011	91	1.00E-38

IP : 14.49.138.138, 2017-11-03 13:30:33

HAN--01-F-K09	AAB38779	putative cytoskeletal protein [Arabidopsis thaliana]	78.195	133	1.86E-51
HAN--02-F-L17	BAB90680	putative DEAD BOX RNA helicase [Oryza sativa (japonica cultivar-group)]	95.161	62	5.36E-27
HAN--03-F-D07	AAM67267	putative dihydrolipoamide succinyltransferase [Arabidopsis thaliana]	43.478	115	5.90E-15
HAN--06-F-E07	AAL76181	Putative disease resistance protein RPR1 [Oryza sativa]	26.207	145	1.66E-09
HAN--01-F-C01	AAM64532	putative DNA binding protein [Arabidopsis thaliana]	82.54	63	1.34E-24
HAN--04-F-P19	AAF91445	putative DNA binding protein [Atriplex hortensis]	81.982	111	2.06E-49
HAN--06-F-M17	AAM61627	putative ER lumen protein retaining receptor [Arabidopsis thaliana]	95.833	120	2.94E-53
HAN--05-F-O24	AAL87161	putative ethylene-responsive protein [Oryza sativa (japonica cultivar-group)]	91.803	61	6.05E-27
HAN--06-F-B04	AAK14423	putative exostoses [Oryza sativa]	67.925	159	8.61E-64
HAN--05-F-N07	AAK93667	putative glucan synthase [Arabidopsis thaliana]	89.189	37	3.35E-11
HAN--04-F-H03	AAO24914	putative glutamate carboxypeptidase [Oryza sativa (japonica cultivar-group)]	58.73	63	1.32E-14
HAN--05-F-G24	AAK92832	putative glycyl tRNA synthetase [Arabidopsis thaliana]	74.468	94	6.29E-35
HAN--06-F-F02	AAL38353	putative heat-shock protein [Arabidopsis thaliana]	88.372	129	3.39E-61
HAN--03-F-G22	CAB71135	putative imbibition protein [Cicer arietinum]	65.306	98	8.33E-31
HAN--02-F-M22	BAB86573	putative ketol-acid reductoisomerase [Oryza sativa (japonica cultivar-group)]	95	60	1.33E-26
HAN--06-F-E12	AAM65108	putative LEA protein [Arabidopsis thaliana]	58.491	53	7.34E-14
HAN--04-F-H16	AAO23085	putative leucine-rich repeat protein [Oryza sativa (japonica cultivar-group)]	70.548	146	2.31E-57
HAN--01-F-D15	BAC80040	putative microtubule associated protein [Oryza sativa (japonica cultivar-group)]	92.308	104	1.56E-48
HAN--02-F-I14	AAK71567	putative mitochondrial RNA helicase [Oryza sativa (japonica cultivar-group)]	77.333	75	5.57E-26
HAN--03-F-G10	BAB89723	putative nascent polypeptide associated complex alpha chain [Oryza sativa (japonica cultivar-group)]	80	75	2.53E-23
HAN--02-F-B06	BAB91740	putative nifU-like protein [Oryza sativa (japonica cultivar-group)]	100	29	3.71E-09
HAN--06-F-A05	AAP53971	putative phosphoglycerate kinase [Oryza sativa (japonica cultivar-group)]	40.217	92	1.17E-07
HAN--04-F-D07	AAO43306	putative polyubiquitin [Arabidopsis thaliana]	98.601	143	2.57E-73
HAN--03-F-G06	AAF23213	putative pre-rRNA processing protein, 5' partial [Arabidopsis thaliana]	82.963	135	4.17E-61
HAN--05-F-H01	AAM19130	Putative protein kinase [Oryza sativa (japonica cultivar-group)]	38.636	132	3.06E-19
HAN--05-F-O07	AAM19116	Putative protein kinase [Oryza sativa (japonica cultivar-group)]	30.822	146	2.14E-12
HAN--05-F-G04	AAK73157	putative protein kinase [Oryza sativa]	66.316	95	6.30E-27
HAN--02-F-A20	AAK13162	putative protein phosphatase 2A regulatory subunit [Oryza sativa (japonica cultivar-group)]	83.974	156	4.86E-76
HAN--04-F-D05	NP_180930	putative related to microbial divalent cation tolerance proteins [Arabidopsis thaliana]	61.438	153	7.02E-39
HAN--05-F-N11	AAP05800	putative ribosomal protein L19 [Oryza sativa (japonica cultivar-group)]	84.211	95	4.46E-28
HAN--02-F-H12	AAM61496	putative ribosomal-protein S6 kinase ATPK6 [Arabidopsis thaliana]	55.224	67	3.39E-15
HAN--05-F-C06	BAB85387	putative RIC1_ORYSA RAS-RELATED PROTEIN RIC1 [Oryza sativa (japonica cultivar-group)]	100	32	2.35E-10
HAN--01-F-P24	AAM19707	putative RING zinc finger protein-like protein [Thellungiella halophila]	63.636	55	9.88E-12
HAN--06-F-O03	CAB85635	putative ripening-related P-450 enzyme [Vitis vinifera]	48.052	154	2.36E-37
HAN--06-F-A18	AAM65608	putative senescence-associated protein 12 [Arabidopsis thaliana]	61.321	106	5.23E-31
HAN--01-F-P12	AAL67992	putative serine carboxypeptidase precursor [Gossypium hirsutum]	83.951	162	2.45E-80
HAN--03-F-E05	AAC69450	putative serine/threonine protein kinase [Nicotiana tabacum]	64.286	84	1.10E-24
HAN--03-F-E16	AAM44082	putative sorbitol transporter [Prunus cerasus]	55.455	110	6.16E-25
HAN--03-F-J01	AAM20703	putative splicing factor [Arabidopsis thaliana]	74.51	51	6.59E-21
HAN--04-F-C12	AAM00426	putative terpene synthase [Citrus x paradisi]	99.057	106	1.66E-55

IP : 14.49.138.138, 2017-11-03 13:30:33

HAN--06-F-O14	AAM00426	putative terpene synthase [Citrus x paradisi]	99.333	150	1.66E-81
HAN--05-F-C11	AAK18849	putative threonine dehydratase/deaminase [Oryza sativa]	84.962	133	3.47E-62
HAN--05-F-G14	AAP06839	putative transformer serine/arginine-rich ribonucleoprotein [Oryza sativa (japonica cultivar-group)]	83.333	48	6.31E-17
HAN--02-F-L24	AAO13361	putative transporter [Arabidopsis thaliana]	57.692	78	2.87E-14
HAN--01-F-F13	AAK59681	putative ubiquitin protein [Arabidopsis thaliana]	58.879	107	6.97E-26
HAN--02-F-O07	AAM22708	Putative ubiquitin protein [Oryza sativa (japonica cultivar-group)]	83.871	62	5.51E-21
HAN--01-F-K06	BAB90685	putative ubiquitin-specific protein [Oryza sativa (japonica cultivar-group)]	84.848	132	8.23E-62
HAN--06-F-D21	AAM63377	Putative UPF0183 protein [Arabidopsis thaliana]	83.333	42	1.41E-22
HAN--01-F-B24	AAL66955	putative UV-damaged DNA binding factor [Arabidopsis thaliana]	84.694	98	1.95E-42
HAN--03-F-N03	BAC20790	putative zinc finger POZ domain protein [Oryza sativa (japonica cultivar-group)]	73.75	160	9.04E-67
HAN--05-F-A18	AAC72193	pyruvate dehydrogenase E1 beta subunit isoform 2 [Zea mays]	93.548	31	7.57E-09
HAN--04-F-O02	AAG27431	QM-like protein [Elaeis guineensis]	96.667	150	1.84E-82
HAN--03-F-G17	CAA66447	RAB1A [Lotus corniculatus var. japonicus]	90.678	118	7.46E-55
HAN--06-F-K17	CAA98160	RAB1C [Lotus corniculatus var. japonicus]	84.337	83	7.11E-34
HAN--01-F-H17	NP_197131	RAD21-3 protein [Arabidopsis thaliana]	58.108	148	1.77E-37
HAN--01-F-D06	T14336	RAD23 protein, isoform I [Daucus carota]	73.864	88	1.31E-30
HAN--05-F-C17	NP_567869	receptor kinase -related [Arabidopsis thaliana]	70.423	71	4.56E-24
HAN--04-F-C20	AAK11255	regulator of gene silencing [Nicotiana tabacum]	37.719	114	3.10E-13
HAN--05-F-O12	NP_177871	replication factor C -related [Arabidopsis thaliana]	79.286	140	4.84E-56
HAN--05-F-J06	CAC82811	resistance gene-like [Solanum tuberosum subsp. andigena]	55.333	150	7.09E-42
HAN--06-F-I09	Q9S8P4	Rhicadhesin receptor precursor (Germin-like protein) [Pisum sativum]	79.661	118	4.59E-49
HAN--05-F-F04	NP_187445	RHO GDP-dissociation inhibitor 1 -related [Arabidopsis thaliana]	59.184	147	6.48E-38
HAN--05-F-M04	AAP80667	ribosomal Pr 117 [Triticum aestivum]	100	105	3.42E-55
HAN--01-F-N17	CAA44226	ribosomal protein L12-1a [Nicotiana tabacum]	92.857	70	9.38E-29
HAN--05-F-I02	BAB86520	ribosomal protein L28-like [Oryza sativa (japonica cultivar-group)]	81.818	66	1.21E-22
HAN--01-F-O21	JQ0771	ribosomal protein L3.e (clone ARP1), cytosolic [Arabidopsis thaliana]	79.605	152	7.40E-52
HAN--05-F-C19	1909359A	ribosomal protein S19 [Solanum tuberosum]	90.361	83	2.41E-37
HAN--06-F-M01	1909359A	ribosomal protein S19 [Solanum tuberosum]	94.595	37	3.90E-13
HAN--05-F-C13	AAM64753	ribosomal protein, putative [Arabidopsis thaliana]	87.821	156	4.77E-67
HAN--01-F-B23	AAL32040	ribosomal S15 protein [Retama raetam]	96.97	132	3.38E-68
HAN--05-F-P01	T06499	Rieske [2Fe-2S] iron-sulfur protein tic55 [Pisum sativum]	79.31	116	6.41E-43
HAN--03-F-J24	NP_173506	RING zinc finger protein -related [Arabidopsis thaliana]	59.813	107	1.83E-28
HAN--04-F-P05	AAG49034	ripening regulated protein DDTFR10 [Lycopersicon esculentum]	83.529	85	2.50E-26
HAN--01-F-E04	CAC01237	RNA Binding Protein 45 [Nicotiana plumbaginifolia]	80.882	68	3.70E-27
HAN--04-F-G22	CAA66825	RNA helicase [Arabidopsis thaliana]	89.172	157	2.97E-48
HAN--02-F-C05	AAM62793	RNA polymerase III subunit-like protein [Arabidopsis thaliana]	52.239	67	4.38E-10
HAN--01-F-A24	NP_565513	RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana]	76	50	1.74E-20
HAN--02-F-J17	AAK13589	rRNA intron-encoded homing endonuclease [Oryza sativa]	93.182	44	4.00E-16
HAN--01-F-P11	T07654	rudimentary enhancer [Glycine max]	88.889	36	2.37E-11
HAN--05-F-N18	BAB88939	Rurm1 [Oryza sativa]	76.25	80	1.82E-29

IP : 14.49.138.138, 2017-11-03 13:30:33

HAN--02-F-P20	CAB89082	S6 ribosomal protein kinase [Asparagus officinalis]	73.874	111	3.60E-41
HAN--01-F-H20	CAC85245	salt tolerance protein 4 [Beta vulgaris]	74.219	128	8.65E-48
HAN--03-F-E14	CAC85246	salt tolerance protein 6 [Beta vulgaris]	75	88	7.26E-34
HAN--03-F-O24	NP_181121	serine carboxypeptidase -related [Arabidopsis thaliana]	90.909	99	4.67E-65
HAN--05-F-K17	AAN84503	serine/threonine protein kinase [Oryza sativa (japonica cultivar-group)]	84.444	90	1.16E-39
HAN--04-F-K24	AAD10854	serine/threonine protein phosphatase 2A-3 catalytic subunit [Arabidopsis thaliana]	84	50	2.23E-12
HAN--04-F-N24	AAO17392	SET domain histone methyltransferase SUVH4 [Arabidopsis thaliana]	82.022	89	1.18E-39
HAN--04-F-E13	NP_191363	seven in absentia (sina) protein family [Arabidopsis thaliana]	87.234	94	6.41E-43
HAN--02-F-I18	AAB07879	similar to a E. coli hypothetical protein F402 encoded by GenBank Accession Number S47768 [Arabidopsis thaliana]	93.069	101	2.08E-43
HAN--02-F-C18	AAD49968	Similar to gb|X90982 phosphoenolpyruvate carboxylase (ppc1) from Solanum tuberosum. [Arabidopsis thaliana]	91.824	159	8.78E-72
HAN--02-F-I23	AAL32670	similar to homeobox protein [Arabidopsis thaliana]	81.356	59	1.87E-20
HAN--04-F-D21	B96671	similar to translational activator [imported] [Arabidopsis thaliana]	73.529	136	9.32E-53
HAN--03-F-A24	AAK58693	sinapyl alcohol dehydrogenase [Populus tremuloides]	84.277	159	4.77E-67
HAN--06-F-C17	AAL17678	S-locus glycoprotein [Raphanus sativus]	42.038	157	8.99E-29
HAN--02-F-M02	NP_176355	S-locus protein kinase, putative [Arabidopsis thaliana]	60.714	56	8.64E-11
HAN--04-F-E02	AAF28764	small GTP binding protein RACDP [Oryza sativa subsp. japonica]	100	79	2.19E-40
HAN--03-F-C12	AAA80678	small GTP-binding protein [Lycopersicon esculentum]	92	75	1.16E-32
HAN--04-F-I08	S59117	small nuclear ribonucleoprotein U1A [Solanum tuberosum]	76.101	159	8.06E-55
HAN--05-F-O04	AAM63846	small nuclear ribonucleoprotein, putative [Arabidopsis thaliana]	94.059	101	7.08E-50
HAN--02-F-F06	AAM63661	small nuclear ribonucleoprotein-like protein [Arabidopsis thaliana]	89.873	79	2.45E-39
HAN--06-F-N06	CAC44032	snakin-1 [Solanum tuberosum]	79.365	63	7.78E-28
HAN--02-F-O12	AAM62553	snap25a [Arabidopsis thaliana]	71.154	104	2.23E-30
HAN--06-F-B02	AAN64293	somatic embryogenesis receptor kinase 1 [Medicago truncatula]	74.359	78	1.41E-28
HAN--06-F-J01	AAM83095	SOS2-like protein kinase [Glycine max]	80	50	4.05E-14
HAN--06-F-A13	AAO31791	SP2G [Lycopersicon esculentum]	65.574	61	1.65E-18
HAN--06-F-N14	NP_174119	sphingosine-1-phosphate lyase -related [Arabidopsis thaliana]	84.375	96	3.13E-58
HAN--04-F-E05	NP_172503	splicing factor U2AF small subunit-related protein, putative [Arabidopsis thaliana]	48.855	131	5.94E-18
HAN--03-F-H12	AAL91182	splicing factor, putative [Arabidopsis thaliana]	75.532	94	2.34E-32
HAN--05-F-I18	BAC42769	SRG1 like protein [Arabidopsis thaliana]	57.426	101	1.38E-26
HAN--04-F-F04	CAC03675	SRPK1 [Arabidopsis thaliana]	91.304	23	1.12E-11
HAN--04-F-N02	AAM29154	starch phosphorylase type H [Citrus hybrid cultivar]	99.225	129	1.09E-58
HAN--01-F-A17	NP_176904	stress related protein -related [Arabidopsis thaliana]	61.491	161	3.62E-44
HAN--05-F-I08	NP_201477	succinate dehydrogenase [ubiquinone], putative [Arabidopsis thaliana]	90.385	156	2.83E-80
HAN--06-F-K02	S44267	sulfate adenylyltransferase (EC 2.7.7.4) met3-2 [Solanum tuberosum]	91.026	156	5.25E-82
HAN--05-F-J18	NP_190758	sulfate transporter ATST1 [Arabidopsis thaliana]	65.421	107	3.61E-35
HAN--01-F-G06	AAC24584	sulfite reductase [Prunus armeniaca]	83.636	55	4.03E-19
HAN--04-F-D19	CAE46442	sulphate transporter [Brassica napus]	81.646	158	2.05E-65
HAN--01-F-A13	F86356	T16E15.2 protein [Arabidopsis thaliana]	57.258	124	1.13E-39
HAN--06-F-H11	AAF63181	T5E21.1 [Arabidopsis thaliana]	83.721	43	1.29E-14

IP : 14.49.138.138, 2017-11-03 13:30:33

HAN--05-F-O16	AAD10237	TATA-box binding protein [Phaseolus vulgaris]	98.065	155	3.34E-81
HAN--05-F-L01	NP_172478	tat-binding protein -related [Arabidopsis thaliana]	60.526	114	6.65E-32
HAN--06-F-E22	BAB10803	tetrahydrofolylpolyglutamate synthase-like protein [Arabidopsis thaliana]	71.975	157	1.29E-51
HAN--04-F-F08	NP_197229	tetratricopeptide repeat (TPR)-containing protein [Arabidopsis thaliana]	54.902	51	1.41E-06
HAN--01-F-K16	CAA67368	TFIIA [Arabidopsis thaliana]	71.795	39	1.08E-10
HAN--03-F-F21	T12093	TGACG-motif binding protein [Vicia faba]	77.876	113	1.73E-35
HAN--02-F-L21	O24160	TGACG-sequence specific DNA-binding protein TGA-2.1 (TGA2.1) [Nicotiana tabacum]	91.549	71	6.95E-38
HAN--02-F-J21	AAD33943	Tha4 protein [Pisum sativum]	64.706	102	1.08E-26
HAN--02-F-M06	O80327	Thaumatin-like protein 1 precursor [Pyrus pyrifolia]	78.947	38	8.53E-14
HAN--06-F-P08	AAC36740	thaumatin-like protein precursor Mdtl1 [Malus x domestica]	70.803	137	5.71E-55
HAN--06-F-B16	O23787	Thiazole biosynthetic enzyme, chloroplast precursor [Citrus sinensis]	79.762	84	2.19E-30
HAN--01-F-P17	NP_567831	thioredoxin family [Arabidopsis thaliana]	43.846	130	3.83E-16
HAN--03-F-D09	AAN76509	thioredoxin h [Brassica rapa]	64.773	88	6.74E-29
HAN--01-F-B02	AAN63619	thioredoxin h-like protein [Nicotiana tabacum]	82.051	78	2.14E-31
HAN--06-F-C14	NP_849984	tocopherol polyprenyltransferase (homogentisate phytyltransferase) (tocopherol phytyltransferase) [Arabidopsis thaliana]	76.087	92	1.53E-36
HAN--03-F-I14	AAQ17460	transaldolase [Gossypium hirsutum]	81.72	93	1.28E-38
HAN--03-F-K08	AAQ17460	transaldolase [Gossypium hirsutum]	82.353	136	5.84E-55
HAN--01-F-K03	NP_563619	transcription co-activator (SYT2) -related [Arabidopsis thaliana]	56.522	161	1.11E-25
HAN--02-F-M15	T12113	transcription factor [Vicia faba]	82.759	58	2.64E-23
HAN--01-F-C12	AAL57045	transcription factor AHAP2 [Malus x domestica]	74.138	58	2.69E-06
HAN--02-F-P22	NP_177466	transcription factor BTF3 (RNA polymerase B transcription factor 3) -related [Arabidopsis thaliana]	76.923	52	4.13E-14
HAN--01-F-N04	NP_172371	transcription factor Hap5a, putative [Arabidopsis thaliana]	56.296	135	2.19E-22
HAN--03-F-O03	NP_194900	Transcription factor II homolog [Arabidopsis thaliana]	73.77	61	1.68E-14
HAN--03-F-A02	NP_563790	transcription factor IIA large subunit [Arabidopsis thaliana]	62.937	143	1.82E-40
HAN--03-F-B10	NP_849733	transcription factor -related [Arabidopsis thaliana]	53.125	128	3.00E-16
HAN--05-F-P10	P48513	Transcription initiation factor IIB (General transcription factor TFIIB) [Glycine max]	100	33	3.37E-13
HAN--06-F-A02	NP_190907	transducin / WD-40 repeat protein family [Arabidopsis thaliana]	80.255	157	5.01E-69
HAN--05-F-J24	NP_563703	transducin / WD-40 repeat protein family [Arabidopsis thaliana]	50	158	2.53E-24
HAN--06-F-J16	NP_178182	transducin / WD-40 repeat protein family [Arabidopsis thaliana]	92	50	1.13E-27
HAN--03-F-C19	NP_189600	transferase family [Arabidopsis thaliana]	45.89	146	4.26E-34
HAN--02-F-K15	AAM64468	transmembrane transport protein-like protein [Arabidopsis thaliana]	44.848	165	4.45E-26
HAN--06-F-L10	P48495	Triosephosphate isomerase, cytosolic (TIM) [Petunia x hybrida]	84.559	136	1.55E-60
HAN--02-F-P19	P21820	Triosephosphate isomerase, cytosolic (TIM) [Coptis japonica]	84.211	38	1.97E-12
HAN--05-F-L04	AAK92531	trithorax 3 [Arabidopsis thaliana]	69.286	140	9.13E-57
HAN--02-F-L02	NP_200155	trithorax 5 (TX5) -related [Arabidopsis thaliana]	58.824	170	1.27E-54
HAN--05-F-K24	AAG08959	tuber-specific and sucrose-responsive element binding factor [Solanum tuberosum]	90.909	110	7.64E-57
HAN--04-F-E16	AAN76363	type I proteinase inhibitor-like protein [Citrus x paradisi]	98.387	62	8.49E-47
HAN--03-F-B03	P49729	Ubiquinol-cytochrome C reductase iron-sulfur subunit 1, mitochondrial precursor (Rieske iron-sulfur protein 1) (RISP1) [Nicotiana tabacum]	82.955	88	1.06E-35
HAN--02-F-P15	T52334	ubiquitin extension protein [imported] [Solanum tuberosum]	100	156	7.90E-71

IP : 14.49.138.138, 2017-11-03 13:30:33

HAN--02-F-L22	NP_181079	ubiquitin family [Arabidopsis thaliana]	80	95	4.40E-41
HAN--03-F-O10	NP_565834	ubiquitin-conjugating enzyme family [Arabidopsis thaliana]	88.608	79	1.41E-37
HAN--03-F-P16	NP_564011	ubiquitin-conjugating enzyme, putative [Arabidopsis thaliana]	95.652	46	7.02E-19
HAN--02-F-K02	CAA67923	ubiquitin-like protein [Arabidopsis thaliana]	92.105	38	2.86E-12
HAN--06-F-C16	AAF36454	ubiquitin-protein ligase 1 [Arabidopsis thaliana]	78.846	52	2.65E-17
HAN--02-F-K08	NP_850783	ubiquitin-specific protease 12 (UBP12) [Arabidopsis thaliana]	80.672	119	1.17E-52
HAN--01-F-K10	O65781	UDP-glucose 4-epimerase GEPI48 (Galactowaldenase) (UDP-galactose 4-epimerase) [Cyamopsis tetragonoloba]	90.099	101	2.10E-49
HAN--02-F-I17	AAF61647	UDP-glucose:salicylic acid glucosyltransferase [Nicotiana tabacum]	53.472	144	2.02E-39
HAN--05-F-J01	AAF61647	UDP-glucose:salicylic acid glucosyltransferase [Nicotiana tabacum]	68.571	35	9.23E-09
HAN--06-F-P04	NP_181234	UDP-glycosyltransferase family [Arabidopsis thaliana]	57.282	103	3.45E-31
HAN--05-F-N24	NP_179907	UDP-glycosyltransferase family [Arabidopsis thaliana]	54.128	109	1.42E-29
HAN--03-F-K15	NP_172444	Ulp1 protease family [Arabidopsis thaliana]	74.775	111	4.46E-28
HAN--05-F-G02	NP_176228	Ulp1 protease family [Arabidopsis thaliana]	66.875	160	6.88E-64
HAN--04-F-O19	AAM19355	UOS1 [Pisum sativum]	85.915	142	5.43E-67
HAN--06-F-M03	Q43434	Vacuolar ATP synthase 16 kDa proteolipid subunit [Gossypium hirsutum]	100	65	6.87E-21
HAN--02-F-E17	Q9SM09	Vacuolar ATP synthase catalytic subunit A (V-ATPase A subunit) (Vacuolar proton pump alpha subunit) (V-ATPase 69 kDa subunit) [Citrus unshiu]	99.306	144	1.87E-82
HAN--01-F-N10	Q9SP55	Vacuolar ATP synthase subunit G (V-ATPase G subunit) (Vacuolar proton pump G subunit) [Citrus limon]	94.545	110	7.23E-35
HAN--01-F-L18	NP_565150	vacuolar protein sorting homolog [Arabidopsis thaliana]	89.172	157	2.58E-76
HAN--06-F-J19	NP_566004	VirF-interacting protein FIP1 [Arabidopsis thaliana]	54.615	130	1.87E-24
HAN--05-F-H15	T07720	VPS29-like phosphoesterase-related protein T23J7.140 [similarity] [Arabidopsis thaliana]	90	150	2.64E-78
HAN--02-F-I12	AAF24062	v-SNARE AtVTI1b [Arabidopsis thaliana]	74.286	105	5.08E-30
HAN--06-F-O02	BAB33037	VuP5CS [Vigna unguiculata]	89.308	159	1.83E-61
HAN--05-F-M07	AAK52092	WD-40 repeat protein [Lycopersicon esculentum]	91.071	56	1.92E-26
HAN--02-F-C22	AAM61064	WD-repeat protein-like [Arabidopsis thaliana]	87.654	81	9.75E-37
HAN--02-F-K16	Q09020	WOUND-INDUCED BASIC PROTEIN [Phaseolus vulgaris]	85.106	47	3.08E-17
HAN--02-F-I21	BAA89230	wts2L [Citrullus lanatus]	66.667	51	8.54E-07
HAN--03-F-A21	BAA89230	wts2L [Citrullus lanatus]	60.169	118	2.39E-24
HAN--05-F-G10	NP_179711	XAP-5 protein [Homo sapiens] -related [Arabidopsis thaliana]	98.305	59	2.05E-30
HAN--04-F-M13	AAM97085	X-Pro dipeptidase-like protein [Arabidopsis thaliana]	70.395	152	3.05E-59
HAN--01-F-B04	NP_199241	zinc finger (C3HC4-type RING finger) protein family [Arabidopsis thaliana]	86.25	80	1.92E-36
HAN--01-F-G20	NP_194477	zinc finger (C3HC4-type RING finger) protein family [Arabidopsis thaliana]	65.217	92	6.65E-32
HAN--06-F-H07	NP_568410	zinc finger (C3HC4-type RING finger) protein family [Arabidopsis thaliana]	80.556	108	1.97E-47
HAN--01-F-E22	BAB02957	zinc metalloprotease (insulinase family) [Arabidopsis thaliana]	82.143	140	3.46E-61
HAN--06-F-I19	AAD26942	zinc-finger protein 1 [Datisca glomerata]	57.031	128	4.13E-31
HAN--04-F-D04	NP_191783	zinc-finger protein -related [Arabidopsis thaliana]	79.452	73	7.33E-31
HAN--05-F-D23	AAL58923	At1g02780/T14P4_3 [Arabidopsis thaliana]	98.077	52	2.95E-20
HAN--03-F-N17	AAN72305	At1g28060/F13K9_16 [Arabidopsis thaliana]	75.63	119	1.84E-45
HAN--01-F-B13	AAL31216	At1g53450/T3F20_17 [Arabidopsis thaliana]	81.481	162	5.61E-74
HAN--01-F-M13	AAO42847	At1g58060 [Arabidopsis thaliana]	79.57	93	7.76E-36

IP : 14.49.138.138, 2017-11-03 13:30:33

HAN--01-F-H02	AAM98086	At1g73430/T9L24_16 [Arabidopsis thaliana]	78.992	119	2.32E-46
HAN--01-F-A01	AAM10397	At1g79730/F19K16_29 [Arabidopsis thaliana]	72.072	111	1.73E-58
HAN--01-F-M16	AAK74006	At2g14841 [Arabidopsis thaliana]	82.407	108	5.79E-52
HAN--05-F-G19	AAL90910	At2g30110/T27E13.15 [Arabidopsis thaliana]	80	95	3.25E-37
HAN--05-F-F06	AAL06505	At2g43970/F6E13.10 [Arabidopsis thaliana]	82.353	34	1.69E-08
HAN--06-F-P21	AAL16193	At2g47760/F17A22.15 [Arabidopsis thaliana]	78.125	96	2.34E-32
HAN--02-F-D17	AAL84973	AT3g05350/T12H1_32 [Arabidopsis thaliana]	76.842	95	1.54E-39
HAN--06-F-F11	AAG40030	AT3g28710 [Arabidopsis thaliana]	92	50	2.42E-21
HAN--02-F-F20	AAL91253	At3g51780/ORF3 [Arabidopsis thaliana]	64.103	117	5.37E-37
HAN--06-F-I17	AAK82549	AT3g54020/F5K20_320 [Arabidopsis thaliana]	79.487	156	7.04E-66
HAN--01-F-C23	AAL14392	AT3g55850/F27K19_30 [Arabidopsis thaliana]	72.917	96	2.39E-34
HAN--02-F-I09	AAL14388	AT4g15940/dl4011w [Arabidopsis thaliana]	83.333	162	6.12E-76
HAN--02-F-I15	AAP21181	At4g21470 [Arabidopsis thaliana]	76.471	34	1.56E-14
HAN--03-F-I21	AAL24198	AT4g26620/T15N24_70 [Arabidopsis thaliana]	80	45	1.06E-08
HAN--02-F-F03	AAM98083	AT4g31540/F3L17_110 [Arabidopsis thaliana]	63.83	47	2.40E-08
HAN--06-F-C21	AAM47465	AT5g09730/F17I14_80 [Arabidopsis thaliana]	84.615	65	4.99E-22
HAN--03-F-E17	AAN33204	At5g09860/MYH9_7 [Arabidopsis thaliana]	46	100	4.79E-14
HAN--03-F-J11	AAL67125	AT5g14200/MUA22_20 [Arabidopsis thaliana]	79.688	64	6.98E-34
HAN--06-F-J08	AAL09712	AT5g17920/MPI7_60 [Arabidopsis thaliana]	93.038	158	4.64E-81
HAN--01-F-O05	AAO24593	At5g49570 [Arabidopsis thaliana]	55.063	158	2.84E-36
HAN--06-F-F10	AAQ65193	At5g58760 [Arabidopsis thaliana]	82.895	76	3.40E-34
HAN--01-F-G07	NP_197408	expressed protein [Arabidopsis thaliana]	78.462	65	4.53E-17
HAN--01-F-H10	NP_172519	expressed protein [Arabidopsis thaliana]	82.209	163	3.36E-74
HAN--01-F-H19	NP_192575	expressed protein [Arabidopsis thaliana]	67.48	123	1.09E-40
HAN--01-F-K01	NP_195032	expressed protein [Arabidopsis thaliana]	56.322	174	1.62E-26
HAN--01-F-L17	NP_849715	expressed protein [Arabidopsis thaliana]	65.06	83	1.07E-13
HAN--02-F-D12	NP_197995	expressed protein [Arabidopsis thaliana]	52.427	103	1.38E-16
HAN--02-F-H08	NP_193063	expressed protein [Arabidopsis thaliana]	70.968	124	6.47E-46
HAN--04-F-C08	NP_189563	expressed protein [Arabidopsis thaliana]	68.992	129	2.41E-47
HAN--04-F-H01	NP_192795	expressed protein [Arabidopsis thaliana]	72.165	97	7.34E-39
HAN--04-F-H12	NP_191537	expressed protein [Arabidopsis thaliana]	70	80	5.04E-22
HAN--05-F-D15	NP_174223	expressed protein [Arabidopsis thaliana]	43.21	81	1.19E-09
HAN--05-F-L16	NP_564982	expressed protein [Arabidopsis thaliana]	57.5	80	3.62E-17
HAN--06-F-I06	NP_197484	expressed protein [Arabidopsis thaliana]	67.949	78	4.42E-23
HAN--06-F-L06	NP_194945	expressed protein [Arabidopsis thaliana]	89.796	49	2.89E-17
HAN--06-F-M13	NP_196806	expressed protein [Arabidopsis thaliana]	59.259	81	9.21E-21
HAN--06-F-N16	NP_173513	expressed protein [Arabidopsis thaliana]	60.748	107	2.86E-30
HAN--02-F-N15	NP_198681	expressed protein [Arabidopsis thaliana]	68.085	141	1.44E-53
HAN--04-F-B15	NP_197230	expressed protein [Arabidopsis thaliana]	88	25	5.13E-08
HAN--03-F-D21	NP_200056	expressed protein [Arabidopsis thaliana]	68.323	161	1.50E-55

IP : 14.49.138.138, 2017-11-03 13:30:33

HAN--03-F-M21	NP_569037	expressed protein [Arabidopsis thaliana]	79.141	163	4.70E-68
HAN--01-F-I14	NP_191352	expressed protein [Arabidopsis thaliana]	64.615	65	4.24E-15
HAN--02-F-J06	NP_197266	expressed protein [Arabidopsis thaliana]	61.644	73	6.31E-17
HAN--03-F-J04	NP_191832	expressed protein [Arabidopsis thaliana]	66.667	90	1.21E-12
HAN--06-F-C13	NP_191832	expressed protein [Arabidopsis thaliana]	69.182	159	1.47E-55
HAN--03-F-N24	NP_190679	expressed protein [Arabidopsis thaliana]	57.895	114	1.60E-30
HAN--06-F-M22	NP_191247	expressed protein [Arabidopsis thaliana]	40.58	138	2.04E-09
HAN--05-F-D05	NP_196716	expressed protein [Arabidopsis thaliana]	59.091	66	7.08E-14
HAN--06-F-G09	NP_196948	expressed protein [Arabidopsis thaliana]	72.269	119	9.56E-47
HAN--02-F-P08	NP_191295	expressed protein [Arabidopsis thaliana]	47.328	131	1.26E-23
HAN--05-F-K15	NP_195908	expressed protein [Arabidopsis thaliana]	61.438	153	1.63E-46
HAN--06-F-C23	NP_197048	expressed protein [Arabidopsis thaliana]	81.651	109	1.49E-52
HAN--01-F-N11	NP_196729	expressed protein [Arabidopsis thaliana]	83.065	124	2.17E-54
HAN--06-F-B07	NP_196344	expressed protein [Arabidopsis thaliana]	66.452	155	3.22E-47
HAN--02-F-N09	NP_566635	expressed protein [Arabidopsis thaliana]	66.412	131	6.44E-27
HAN--05-F-D24	NP_189118	expressed protein [Arabidopsis thaliana]	53.521	71	2.82E-15
HAN--04-F-C06	NP_565016	expressed protein [Arabidopsis thaliana]	42.609	115	5.86E-12
HAN--05-F-L18	NP_189513	expressed protein [Arabidopsis thaliana]	92.958	142	1.17E-73
HAN--04-F-G04	NP_198883	expressed protein [Arabidopsis thaliana]	71.839	174	2.12E-73
HAN--05-F-D21	NP_565612	expressed protein [Arabidopsis thaliana]	68.794	141	2.20E-51
HAN--03-F-N18	NP_564294	expressed protein [Arabidopsis thaliana]	56.338	71	2.54E-15
HAN--05-F-O22	NP_568150	expressed protein [Arabidopsis thaliana]	72.84	162	9.03E-50
HAN--06-F-C20	NP_849822	expressed protein [Arabidopsis thaliana]	59.42	138	7.61E-28
HAN--05-F-O23	NP_565314	expressed protein [Arabidopsis thaliana]	41.414	99	3.71E-11
HAN--01-F-P13	NP_567979	expressed protein [Arabidopsis thaliana]	82.927	41	1.97E-12
HAN--02-F-P17	NP_568123	expressed protein [Arabidopsis thaliana]	76.923	130	1.54E-55
HAN--02-F-B23	NP_563935	expressed protein [Arabidopsis thaliana]	70.755	106	4.74E-36
HAN--02-F-O08	NP_566443	expressed protein [Arabidopsis thaliana]	77.019	161	1.06E-72
HAN--04-F-N13	NP_568238	expressed protein [Arabidopsis thaliana]	63.095	84	6.75E-21
HAN--03-F-J14	NP_568247	expressed protein [Arabidopsis thaliana]	74.4	125	3.51E-49
HAN--02-F-B17	NP_567466	expressed protein [Arabidopsis thaliana]	78.125	32	3.61E-07
HAN--01-F-I18	NP_568607	expressed protein [Arabidopsis thaliana]	63.441	93	2.30E-16
HAN--01-F-H03	NP_563696	expressed protein [Arabidopsis thaliana]	85.246	122	8.95E-45
HAN--05-F-C02	NP_568985	expressed protein [Arabidopsis thaliana]	76.577	111	1.63E-39
HAN--06-F-J06	NP_568458	expressed protein [Arabidopsis thaliana]	70.886	158	8.54E-51
HAN--02-F-A01	NP_568526	expressed protein [Arabidopsis thaliana]	72.956	159	6.35E-65
HAN--04-F-I11	NP_683315	expressed protein [Arabidopsis thaliana]	71.795	39	8.37E-10
HAN--05-F-N13	NP_680720	expressed protein [Arabidopsis thaliana]	80.357	112	1.59E-62
HAN--03-F-J20	NP_195153	expressed protein [Arabidopsis thaliana]	77.778	90	1.49E-34
HAN--06-F-C05	NP_190931	expressed protein [Arabidopsis thaliana]	62.879	132	1.47E-26

IP : 14.49.138.138, 2017-11-03 13:30:33

HAN--06-F-N05	NP_199897	expressed protein [Arabidopsis thaliana]	72.131	61	2.30E-16
HAN--04-F-K07	NP_564362	expressed protein [Arabidopsis thaliana]	41.748	103	2.20E-10
HAN--02-F-K10	NP_188905	expressed protein [Arabidopsis thaliana]	54.206	107	2.30E-08
HAN--05-F-K20	NP_565055	expressed protein [Arabidopsis thaliana]	71.134	97	4.33E-39
HAN--02-F-F23	NP_566261	expressed protein [Arabidopsis thaliana]	63.462	104	3.30E-21
HAN--02-F-O13	NP_565868	expressed protein [Arabidopsis thaliana]	88.158	76	2.01E-37
HAN--04-F-A08	NP_190227	expressed protein [Arabidopsis thaliana]	70.909	55	1.61E-19
HAN--05-F-M11	NP_197949	expressed protein [Arabidopsis thaliana]	68.687	99	8.80E-29
HAN--01-F-M15	NP_566496	expressed protein [Arabidopsis thaliana]	49.107	112	3.70E-19
HAN--06-F-G19	NP_564506	expressed protein [Arabidopsis thaliana]	76.087	92	2.31E-35
HAN--04-F-E19	NP_564333	expressed protein [Arabidopsis thaliana]	71.515	165	7.27E-64
HAN--04-F-E08	NP_182061	expressed protein [Arabidopsis thaliana]	55.556	90	2.30E-17
HAN--02-F-B02	NP_173069	expressed protein [Arabidopsis thaliana]	92.233	103	1.19E-53
HAN--03-F-K02	NP_177318	expressed protein [Arabidopsis thaliana]	68.132	91	1.12E-16
HAN--04-F-K08	NP_174174	expressed protein [Arabidopsis thaliana]	91.139	158	6.13E-86
HAN--01-F-F04	NP_179959	expressed protein [Arabidopsis thaliana]	43.939	132	1.26E-14
HAN--02-F-O16	NP_195447	expressed protein [Arabidopsis thaliana]	50.943	106	4.99E-22
HAN--02-F-C03	NP_179621	expressed protein [Arabidopsis thaliana]	54.545	88	3.86E-27
HAN--02-F-N23	NP_564484	expressed protein [Arabidopsis thaliana]	79.874	159	2.55E-71
HAN--01-F-K14	NP_175488	expressed protein [Arabidopsis thaliana]	53.086	162	1.52E-42
HAN--06-F-H09	NP_177593	expressed protein [Arabidopsis thaliana]	64.474	76	1.80E-16
HAN--03-F-F16	NP_174061	expressed protein [Arabidopsis thaliana]	71.053	38	2.15E-10
HAN--02-F-G12	NP_176596	expressed protein [Arabidopsis thaliana]	68.254	126	8.45E-46
HAN--01-F-A15	NP_175906	expressed protein [Arabidopsis thaliana]	85.616	146	7.03E-74
HAN--02-F-G14	NP_563724	expressed protein [Arabidopsis thaliana]	67.586	145	8.78E-54
HAN--06-F-G13	NP_563777	expressed protein [Arabidopsis thaliana]	60.577	104	3.42E-28
HAN--03-F-I01	NP_180399	expressed protein [Arabidopsis thaliana]	87.952	83	1.88E-35
HAN--06-F-N22	NP_180455	expressed protein [Arabidopsis thaliana]	71.591	88	6.89E-29
HAN--03-F-H06	NP_565723	expressed protein [Arabidopsis thaliana]	64.189	148	3.76E-43
HAN--01-F-N24	NP_181336	expressed protein [Arabidopsis thaliana]	73.611	144	7.54E-60
HAN--01-F-N12	NP_565959	expressed protein [Arabidopsis thaliana]	58.036	112	6.28E-33
HAN--06-F-D17	NP_178872	expressed protein [Arabidopsis thaliana]	37.195	164	4.60E-23
HAN--01-F-J15	NP_850325	expressed protein [Arabidopsis thaliana]	66.055	109	1.65E-25
HAN--05-F-L14	NP_175105	expressed protein [Arabidopsis thaliana]	74.026	154	3.91E-61
HAN--02-F-N07	NP_567623	expressed protein [Arabidopsis thaliana]	80	105	2.51E-45
HAN--02-F-O02	NP_201355	expressed protein [Arabidopsis thaliana]	47.742	155	2.37E-22
HAN--05-F-G21	NP_173611	expressed protein [Arabidopsis thaliana]	79.688	64	2.17E-26
HAN--02-F-M24	NP_180592	expressed protein [Arabidopsis thaliana]	56.494	154	4.01E-43
HAN--04-F-L03	NP_567338	expressed protein [Arabidopsis thaliana]	63.441	93	2.31E-31
HAN--03-F-P02	NP_186856	expressed protein [Arabidopsis thaliana]	79.032	62	1.81E-22

IP : 14.49.138.138, 2017-11-03 13:30:33

HAN--03-F-P21	NP_566359	expressed protein [Arabidopsis thaliana]	68.852	61	6.03E-18
HAN--02-F-E24	NP_195655	expressed protein [Arabidopsis thaliana]	83.333	144	2.72E-54
HAN--01-F-O10	NP_181929	expressed protein [Arabidopsis thaliana]	44.737	114	4.69E-14
HAN--04-F-B22	NP_193524	expressed protein [Arabidopsis thaliana]	74.038	104	5.97E-37
HAN--04-F-O01	NP_194233	expressed protein [Arabidopsis thaliana]	72.727	110	1.18E-38
HAN--06-F-C10	NP_195118	expressed protein [Arabidopsis thaliana]	82.09	67	1.38E-27
HAN--02-F-D01	NP_194032	expressed protein [Arabidopsis thaliana]	85.393	89	1.02E-41
HAN--02-F-M13	NP_190390	expressed protein [Arabidopsis thaliana]	54.31	116	4.28E-18
HAN--03-F-C21	NP_565294	expressed protein [Arabidopsis thaliana]	71.622	74	2.44E-24
HAN--02-F-H14	NP_181375	expressed protein [Arabidopsis thaliana]	45.588	68	1.62E-07
HAN--06-F-J18	NP_193007	expressed protein [Arabidopsis thaliana]	70.37	162	2.66E-44
HAN--04-F-L21	NP_194153	expressed protein [Arabidopsis thaliana]	77.953	127	9.02E-58
HAN--04-F-N08	NP_194153	expressed protein [Arabidopsis thaliana]	70.068	147	4.73E-55
HAN--04-F-O12	NP_565968	expressed protein [Arabidopsis thaliana]	75.676	148	4.39E-49
HAN--01-F-C17	NP_194498	expressed protein [Arabidopsis thaliana]	60.377	53	7.91E-09
HAN--05-F-M05	NP_193468	expressed protein [Arabidopsis thaliana]	75.229	109	3.97E-45
HAN--05-F-A14	NP_564626	expressed protein [Arabidopsis thaliana]	61.94	134	6.69E-36
HAN--04-F-F11	NP_200072	expressed protein [Arabidopsis thaliana]	85.987	157	5.68E-81
HAN--03-F-L06	NP_566429	expressed protein [Arabidopsis thaliana]	55.758	165	6.75E-38
HAN--02-F-M05	NP_188401	expressed protein [Arabidopsis thaliana]	62.264	159	1.88E-45
HAN--06-F-E18	NP_199129	expressed protein [Arabidopsis thaliana]	48.684	76	9.65E-15
HAN--02-F-J08	NP_199015	expressed protein [Arabidopsis thaliana]	89.691	97	8.84E-48
HAN--05-F-N17	NP_199030	expressed protein [Arabidopsis thaliana]	51.748	143	1.49E-23
HAN--01-F-B07	NP_196244	expressed protein [Arabidopsis thaliana]	62.903	62	7.81E-16
HAN--06-F-G02	NP_568614	expressed protein [Arabidopsis thaliana]	71.605	81	1.42E-29
HAN--06-F-M21	NP_200428	expressed protein [Arabidopsis thaliana]	62.821	78	1.88E-23
HAN--03-F-N06	NP_197326	expressed protein [Arabidopsis thaliana]	73.958	96	6.35E-38
HAN--04-F-J19	NP_200265	expressed protein [Arabidopsis thaliana]	40.833	120	1.13E-12
HAN--04-F-N05	AAF79247	F10B6.11 [Arabidopsis thaliana]	61.417	127	1.38E-43
HAN--04-F-C13	F86160	F10O3.18 protein [Arabidopsis thaliana]	71.053	152	2.26E-53
HAN--04-F-F22	A86277	F14L17.5 protein [Arabidopsis thaliana]	71.242	153	2.69E-59
HAN--06-F-K19	AAF25987	F15H18.16 [Arabidopsis thaliana]	47.651	149	2.15E-14
HAN--01-F-F02	AAF79409	F16A14.27 [Arabidopsis thaliana]	49.495	99	3.61E-15
HAN--02-F-H10	AAF79522	F21D18.17 [Arabidopsis thaliana]	58.75	80	4.27E-26
HAN--06-F-E02	AAF69168	F27F5.22 [Arabidopsis thaliana]	72.115	104	2.51E-37
HAN--04-F-B04	AAF19695	F2K11.3 [Arabidopsis thaliana]	57.669	163	1.17E-37
HAN--03-F-D06	AAF79602	F5M15.3 [Arabidopsis thaliana]	96.429	28	3.71E-09
HAN--01-F-E10	BAB01942	gb|AAD15386.1~gene_id:MMP21.2~similar to unknown protein [Arabidopsis thaliana]	58.537	41	8.19E-06
HAN--01-F-F08	BAB01944	gb|AAF14829.1~gene_id:MMP21.4~similar to unknown protein [Arabidopsis thaliana]	71.429	70	2.57E-22
HAN--02-F-M18	BAB01075	gb|AAF35409.1~gene_id:MPE11.29~similar to unknown protein [Arabidopsis thaliana]	77.778	45	2.69E-14

IP : 14.49.138.138, 2017-11-03 13:30:33

HAN--06-F-G12	BAB10995	gene_id:K21L19.3~unknown protein [Arabidopsis thaliana]	52.795	161	1.35E-35
HAN--01-F-I01	BAB08817	gene_id:MLE2.15~pir||S76033~similar to unknown protein [Arabidopsis thaliana]	41.667	156	4.23E-23
HAN--02-F-D23	BAB01945	gene_id:MMP21.5~pir||C71413~strong similarity to unknown protein [Arabidopsis thaliana]	60.638	94	1.06E-19
HAN--04-F-A05	BAB01263	gene_id:MYA6.4~unknown protein [Arabidopsis thaliana]	63.014	73	8.17E-23
HAN--06-F-P06	BAB17025	gene_id:MYH9.23~unknown protein [Arabidopsis thaliana]	59.813	107	6.71E-35
HAN--03-F-C03	A71428	hypothetical protein [Arabidopsis thaliana]	70.408	98	2.34E-32
HAN--01-F-H09	NP_172530	hypothetical protein [Arabidopsis thaliana]	58.654	104	4.18E-26
HAN--02-F-E15	AAO37201	hypothetical protein [Arabidopsis thaliana]	35.862	145	1.02E-11
HAN--05-F-J11	NP_187930	hypothetical protein [Arabidopsis thaliana]	65.347	101	3.45E-33
HAN--06-F-P10	AAN85200	hypothetical protein [Arabidopsis thaliana]	73.333	45	9.62E-13
HAN--02-F-M21	NP_199000	hypothetical protein [Arabidopsis thaliana]	70.946	148	4.56E-55
HAN--03-F-H20	NP_196890	hypothetical protein [Arabidopsis thaliana]	42.373	118	2.56E-18
HAN--06-F-A19	NP_196570	hypothetical protein [Arabidopsis thaliana]	52.564	78	7.39E-15
HAN--05-F-I15	NP_172826	hypothetical protein [Arabidopsis thaliana]	50	150	4.33E-39
HAN--06-F-B03	NP_174310	hypothetical protein [Arabidopsis thaliana]	38.614	101	7.89E-07
HAN--06-F-K03	NP_175504	hypothetical protein [Arabidopsis thaliana]	47.692	65	1.71E-07
HAN--03-F-M24	NP_171626	hypothetical protein [Arabidopsis thaliana]	64.151	106	1.71E-32
HAN--06-F-J21	NP_178939	hypothetical protein [Arabidopsis thaliana]	63.918	97	4.18E-26
HAN--06-F-C22	NP_187206	hypothetical protein [Arabidopsis thaliana]	78.947	57	2.55E-07
HAN--01-F-G03	NP_176225	hypothetical protein [Arabidopsis thaliana]	48.366	153	1.99E-34
HAN--06-F-J03	NP_200114	hypothetical protein [Arabidopsis thaliana]	47.945	146	1.54E-13
HAN--06-F-B05	NP_201503	hypothetical protein [Arabidopsis thaliana]	45.455	99	5.84E-20
HAN--03-F-I12	CAA10123	hypothetical protein [Cicer arietinum]	61.667	60	1.15E-12
HAN--01-F-H13	CAB09799	hypothetical protein [Citrus x paradisi]	100	76	5.80E-37
HAN--02-F-P10	CAB09799	hypothetical protein [Citrus x paradisi]	98.571	140	4.62E-79
HAN--05-F-H13	NP_753525	Hypothetical protein [Escherichia coli CFT073]	90.741	54	4.80E-23
HAN--05-F-D11	E86177	hypothetical protein [imported] [Arabidopsis thaliana]	76.316	38	5.80E-09
HAN--05-F-B02	D86180	hypothetical protein [imported] [Arabidopsis thaliana]	88.679	53	1.78E-09
HAN--05-F-C21	E86193	hypothetical protein [imported] [Arabidopsis thaliana]	67.368	95	8.04E-29
HAN--01-F-J07	E86183	hypothetical protein [imported] [Arabidopsis thaliana]	59.813	107	1.69E-10
HAN--03-F-B12	BAC79160	hypothetical protein [Oryza sativa (japonica cultivar-group)]	33.094	139	1.38E-08
HAN--04-F-D23	C84511	hypothetical protein At2g13840 [imported] [Arabidopsis thaliana]	68.493	73	3.85E-17
HAN--06-F-L12	D84654	hypothetical protein At2g25920 [imported] [Arabidopsis thaliana]	55.238	105	2.32E-19
HAN--03-F-L03	D84706	hypothetical protein At2g30270 [imported] [Arabidopsis thaliana]	35.714	98	6.85E-08
HAN--04-F-L20	F84890	hypothetical protein At2g45450 [imported] [Arabidopsis thaliana]	51.852	54	1.56E-07
HAN--05-F-P14	H84899	hypothetical protein At2g46200 [imported] [Arabidopsis thaliana]	73.118	93	4.67E-20
HAN--04-F-H23	B84905	hypothetical protein At2g46620 [imported] [Arabidopsis thaliana]	54.945	91	1.01E-26
HAN--03-F-P14	B85063	hypothetical protein AT4g05020 [imported] [Arabidopsis thaliana]	77.181	149	1.66E-62
HAN--04-F-J09	E86463	hypothetical protein F12G12.20 [Arabidopsis thaliana]	69.565	69	6.24E-22
HAN--04-F-F01	G96586	hypothetical protein F20D21.30 [imported] [Arabidopsis thaliana]	81.988	161	1.85E-74

IP : 14.49.138.138, 2017-11-03 13:30:33

HAN--04-F-E21	T04543	hypothetical protein F28J12.130 [Arabidopsis thaliana]	60.938	64	3.63E-09
HAN--02-F-J03	B96818	hypothetical protein F9K20.8 [imported] [Arabidopsis thaliana]	92.727	55	6.84E-23
HAN--05-F-A23	T09559	hypothetical protein L73G19.50 [Arabidopsis thaliana]	61.538	52	2.32E-12
HAN--05-F-F24	Q8LHP0	Hypothetical protein P0519E12.3 [Oryza sativa (japonica cultivar-group)]	83.871	31	1.95E-08
HAN--05-F-N04	T00458	hypothetical protein T14N5.15 [Arabidopsis thaliana]	53.165	158	2.50E-34
HAN--01-F-J16	C86390	hypothetical protein T1K7.26 [Arabidopsis thaliana]	61.039	77	8.54E-16
HAN--05-F-P04	C86333	hypothetical protein T20H2.23 [Arabidopsis thaliana]	54.676	139	6.65E-32
HAN--02-F-G10	C86295	hypothetical protein T24D18.15 [Arabidopsis thaliana]	57.895	114	2.08E-53
HAN--01-F-E21	B86294	hypothetical protein T24D18.6 [imported] [Arabidopsis thaliana]	86.897	145	2.18E-64
HAN--03-F-F24	T47637	hypothetical protein T5N23.140 [Arabidopsis thaliana]	61.078	167	6.61E-49
HAN--03-F-K06	B96601	hypothetical protein T6H22.20 [imported] [Arabidopsis thaliana]	74.737	95	7.11E-34
HAN--05-F-F08	T05075	hypothetical protein T6K21.70 [Arabidopsis thaliana]	68.376	117	1.68E-40
HAN--01-F-C06	AAG52039	hypothetical protein; 29936-28688 [Arabidopsis thaliana]	84.314	51	1.54E-21
HAN--05-F-G09	BAC10750	OJ1116_H09.22 [Oryza sativa (japonica cultivar-group)]	91.667	36	6.36E-12
HAN--05-F-D07	CAA65335	ORF [Arabidopsis thaliana]	69.811	159	2.94E-45
HAN--04-F-O11	CAE04117	OSJNBa0009P12.2 [Oryza sativa (japonica cultivar-group)]	54.688	128	5.36E-27
HAN--01-F-J02	CAE03093	OSJNBa0017B10.8 [Oryza sativa (japonica cultivar-group)]	60	40	4.31E-07
HAN--04-F-M08	CAE01544	OSJNBa0033G05.15 [Oryza sativa (japonica cultivar-group)]	48.101	79	1.22E-10
HAN--04-F-I05	CAE05419	OSJNBa0035I04.7 [Oryza sativa (japonica cultivar-group)]	58.278	151	7.48E-49
HAN--05-F-F12	CAE02125	OSJNBa0035M09.5 [Oryza sativa (japonica cultivar-group)]	95.652	23	1.65E-06
HAN--01-F-D11	BAC24834	OSJNBa0038F22.13 [Oryza sativa (japonica cultivar-group)]	40.217	184	3.79E-28
HAN--06-F-H12	CAE05511	OSJNBa0038P21.4 [Oryza sativa (japonica cultivar-group)]	84.043	94	3.33E-34
HAN--03-F-B06	CAD41008	OSJNBa0042L16.14 [Oryza sativa (japonica cultivar-group)]	52.903	155	7.40E-42
HAN--06-F-I04	CAE05881	OSJNBa0044K18.23 [Oryza sativa (japonica cultivar-group)]	94.479	163	4.25E-72
HAN--02-F-K11	CAE03551	OSJNBa0060D06.17 [Oryza sativa (japonica cultivar-group)]	78.261	69	9.94E-18
HAN--06-F-L13	CAE03599	OSJNBb0004A17.1 [Oryza sativa (japonica cultivar-group)]	73.404	94	3.63E-62
HAN--01-F-K02	CAE04574	OSJNBb0039L24.13 [Oryza sativa (japonica cultivar-group)]	78.302	106	2.99E-33
HAN--03-F-N04	CAE01974	OSJNBb0051N19.3 [Oryza sativa (japonica cultivar-group)]	70	40	5.36E-11
HAN--02-F-P18	CAE05717	OSJNBb0065J09.13 [Oryza sativa (japonica cultivar-group)]	88.571	70	1.89E-31
HAN--04-F-M14	CAE02348	OSJNBb0072M01.9 [Oryza sativa (japonica cultivar-group)]	87.64	89	1.69E-39
HAN--02-F-O14	BAB64268	P0005H10.5 [Oryza sativa (japonica cultivar-group)]	62.025	79	3.08E-27
HAN--03-F-H05	BAB63796	P0423B08.5 [Oryza sativa (japonica cultivar-group)]	65.476	84	6.86E-27
HAN--03-F-O19	BAB55821	P0710A02.20 [Oryza sativa (japonica cultivar-group)]	77.165	127	3.31E-50
HAN--01-F-F10	AAM62578	unknown [Arabidopsis thaliana]	65.957	94	3.86E-27
HAN--01-F-G04	AAM61639	unknown [Arabidopsis thaliana]	91.304	92	3.39E-45
HAN--02-F-G06	AAM64357	unknown [Arabidopsis thaliana]	75.439	114	2.94E-43
HAN--02-F-H21	AAM61505	unknown [Arabidopsis thaliana]	40.132	152	1.59E-15
HAN--02-F-O22	AAM65494	unknown [Arabidopsis thaliana]	73.171	41	1.62E-07
HAN--03-F-K17	AAM60904	unknown [Arabidopsis thaliana]	78.049	41	5.17E-11
HAN--05-F-B07	AAM61083	unknown [Arabidopsis thaliana]	59.231	130	5.69E-38

IP : 14.49.138.138, 2017-11-03 13:30:33

HAN--06-F-F04	AAM67006	unknown [Arabidopsis thaliana]	81.132	53	1.08E-15
HAN--06-F-H22	AAM65519	unknown [Arabidopsis thaliana]	91.304	46	2.32E-31
HAN--02-F-G22	AAG00940	unknown [Glycine max]	85.417	96	3.28E-45
HAN--04-F-J12	AAK84475	unknown [Lycopersicon esculentum]	76.389	144	5.33E-54
HAN--01-F-J14	AAQ63971	unknown [Nicotiana benthamiana]	67.485	163	5.24E-53
HAN--01-F-O14	AAP30737	unknown [Vitis vinifera]	48.246	114	5.94E-18
HAN--01-F-H24	AAM91544	unknown protein [Arabidopsis thaliana]	72.381	105	1.27E-27
HAN--01-F-L02	AAK28636	unknown protein [Arabidopsis thaliana]	78.788	33	5.58E-08
HAN--02-F-D04	AAK59482	unknown protein [Arabidopsis thaliana]	71.287	101	1.77E-35
HAN--02-F-H22	AAO42141	unknown protein [Arabidopsis thaliana]	63.077	65	2.53E-18
HAN--02-F-J22	AAO64153	unknown protein [Arabidopsis thaliana]	63.415	164	8.05E-52
HAN--02-F-L01	BAC43150	unknown protein [Arabidopsis thaliana]	44.118	170	2.11E-23
HAN--02-F-M10	AAL36174	unknown protein [Arabidopsis thaliana]	68.254	63	5.90E-15
HAN--03-F-M05	AAL87328	unknown protein [Arabidopsis thaliana]	92.5	40	4.17E-16
HAN--04-F-A07	AAM53331	unknown protein [Arabidopsis thaliana]	84.524	84	1.58E-34
HAN--04-F-C07	BAC42742	unknown protein [Arabidopsis thaliana]	51.02	49	1.40E-06
HAN--04-F-H13	AAK93585	unknown protein [Arabidopsis thaliana]	57.143	105	9.97E-20
HAN--04-F-H21	AAF13075	unknown protein [Arabidopsis thaliana]	62.264	53	8.03E-14
HAN--04-F-K14	BAC42826	unknown protein [Arabidopsis thaliana]	67.677	99	1.62E-29
HAN--04-F-M04	BAC43564	unknown protein [Arabidopsis thaliana]	55.975	159	4.91E-43
HAN--05-F-B05	AAL32541	Unknown protein [Arabidopsis thaliana]	36.923	65	4.48E-13
HAN--05-F-B09	AAN72190	Unknown protein [Arabidopsis thaliana]	83.871	62	1.60E-24
HAN--05-F-C14	AAO00875	Unknown protein [Arabidopsis thaliana]	75	68	3.82E-22
HAN--05-F-E12	AAK64165	unknown protein [Arabidopsis thaliana]	75	48	1.90E-15
HAN--05-F-O15	AAM20131	unknown protein [Arabidopsis thaliana]	66.917	133	4.68E-39
HAN--06-F-B11	AAD55502	Unknown protein [Arabidopsis thaliana]	78.571	126	2.65E-50
HAN--06-F-B15	AAF02127	unknown protein [Arabidopsis thaliana]	78.947	57	1.79E-24
HAN--06-F-J24	AAN72190	Unknown protein [Arabidopsis thaliana]	65	100	2.11E-44
HAN--06-F-O20	BAC42598	unknown protein [Arabidopsis thaliana]	40.714	140	2.32E-21
HAN--06-F-P11	AAM13860	unknown protein [Arabidopsis thaliana]	78.344	157	5.76E-68
HAN--03-F-N23	AAK93644	unknown protein [Arabidopsis thaliana]	83.459	133	3.05E-67
HAN--06-F-F03	AAK68797	Unknown protein [Arabidopsis thaliana]	83.439	157	9.18E-74
HAN--05-F-K18	AAF02112	unknown protein [Arabidopsis thaliana]	74.603	63	3.96E-21
HAN--05-F-G08	AAL66981	unknown protein [Arabidopsis thaliana]	78.462	65	2.74E-22
HAN--02-F-K03	AAK68765	Unknown protein [Arabidopsis thaliana]	83.444	151	4.64E-63
HAN--05-F-D04	AAO00894	Unknown protein [Arabidopsis thaliana]	70.175	57	1.19E-14
HAN--02-F-G17	B96762	unknown protein [imported] [Arabidopsis thaliana]	62.245	98	5.77E-23
HAN--04-F-M10	AAP44748	unknown protein [Oryza sativa (japonica cultivar-group)]	52.113	71	9.73E-14
HAN--06-F-F07	BAC79672	unknown protein [Oryza sativa (japonica cultivar-group)]	40.252	159	4.80E-15
HAN--01-F-N03	AAK13159	unknown protein [Oryza sativa (japonica cultivar-group)]	88.136	118	6.72E-57

IP : 14.49.138.138, 2017-11-03 13:30:33

HAN--02-F-O11	AAK14411	unknown protein [Oryza sativa]	77.551	98	1.62E-33
HAN--01-F-B01	C96782	unknown protein F22H5.13 [imported] [Arabidopsis thaliana]	77.966	59	3.53E-23
HAN--05-F-A09	C96767	unknown protein F2P9.17 [imported] - Arabidopsis thaliana	70.27	148	4.93E-45
HAN--06-F-H08	AAF26168	unknown protin [Arabidopsis thaliana]	87.786	131	2.89E-64
HAN--03-F-J17	BAA94243	unnamed protein product [Oryza sativa (japonica cultivar-group)]	37.383	107	2.91E-11

Consensus Number	Accession No.	Definition of Putative homologue[Organism]	Matching %	Matching Length	E-value
1	Q39644	late-embryogenesis protein lea5 [Citrus sinensis]	98.182	55	3.90E-42
2	NP_173785	carbonic anhydrase -related [Arabidopsis thaliana]	65.217	92	4.35E-33
3	No hits found				
4	NP_564305	dormancy-associated protein -related [Arabidopsis thaliana]	55.67	97	3.88E-33
5	AAL24250	At1g19180/T29M8_5 [Arabidopsis thaliana]	45.714	105	1.65E-11
6	AAQ63461	calmodulin 4 [Daucus carota]	100	143	2.26E-76
7	No hits found				
8	AAF23543	alcohol dehydrogenase [Arabis hirsuta]	92.537	134	2.53E-71
9	AAG16981	transaldolase [Lycopersicon esculentum]	88.235	85	8.11E-37
10	NP_173259	calcium-binding protein, putative [Arabidopsis thaliana]	67.391	138	6.07E-48
11	CAE05157	OSJNBa0039C07.13 [Oryza sativa (japonica cultivar-group)]	61.667	120	2.11E-27
12	No hits found				
13	NP_194589	calmodulin-binding protein [Arabidopsis thaliana]	60.494	81	2.85E-20
14	AAO72533	pyruvate decarboxylase 1 [Lotus corniculatus]	91.228	57	1.05E-24
15	AAF19538	F23N19.10 [Arabidopsis thaliana]	62.759	290	2.99E-83
16	AAQ72788	hypersensitive-induced response protein [Cucumis sativus]	93.269	104	8.26E-48
17	AAO61853	glutathione S-transferase F1 [Malva pusilla]	77.778	45	6.65E-13
18	CAA08908	cytosolic class I small heat-shock protein HSP17.5 [Castanea sativa]	80.822	146	9.11E-51
19	Q43116	protein disulfide-isomerase (EC 5.3.4.1) [Ricinus communis (castor bean)]	69.565	69	1.28E-20
20	P35135	Ubiquitin-conjugating enzyme E2-17 kDa (Ubiquitin-protein ligase) (Ubiquitin carrier protein) [Lycopersicon esculentum (tomato)]	96.429	140	1.88E-77
21	AAQ08196	eukaryotic translation initiation factor 5A isoform 6 [Hevea brasiliensis]	93.711	159	4.73E-82
22	P19446	Malate dehydrogenase, glyoxysomal precursor [Citrullus lanatus (watermelon)]	84.028	144	2.00E-63
23	No hits found				
24	No hits found				
25	No hits found				
26	BAA31561	metallothionein-like protein [Citrus unshiu]	100	40	9.99E-15
27	AAN15459	26S proteasome AAA-ATPase subunit RPT5a [Arabidopsis thaliana]	97.842	139	1.29E-71
28	CAD40829	OSJNBa0086B14.1 [Oryza sativa (japonica cultivar-group)]	66.667	45	6.24E-15
29	BAA97184	contains similarity to embryo-specific protein 3~gene_id:MMI9.3 [Arabidopsis thaliana]	64.341	129	2.44E-44
30	No hits found				
31	BAA31562	metallothionein-like protein [Citrus unshiu]	98.529	68	1.15E-34
32	AAC50019	high mobility group protein 2 HMG2 [Ipomoea nil]	75.949	79	1.40E-21
33	Q9XF97	60S ribosomal protein L4 (L1) [Prunus armeniaca (apricot)]	96.032	126	1.38E-65
34	BAA95845	unnamed protein product [Oryza sativa (japonica cultivar-group)]	80.702	57	5.35E-21

IP : 14.49.138.138, 2017-11-03 13:30:33

35	AAM53946	(+)-limonene synthase 2 [Citrus limon]	91.034	145	3.65E-65
36	NP_567380	expressed protein [Arabidopsis thaliana]	82.857	35	5.22E-09
37	AAM60990	unknown [Arabidopsis thaliana]	85.987	157	1.81E-74
38	No hits found				
39	S62722	ferredoxin [2Fe-2S] fd1 precursor, non-photosynthetic [Citrus sinensis]	98	150	9.62E-80
40	No hits found				
41	AAF18611	hypothetical protein [Arabidopsis thaliana]	77.551	98	2.42E-33
42	No hits found				
43	BAB91740	putative nifU-like protein [Oryza sativa (japonica cultivar-group)]	90.789	76	1.28E-33
44	AAG38519	miraculin-like protein 3 [Citrus x paradisi]	100	154	4.67E-84
45	No hits found				
46	AAM29152	plastidic ATP/ADP transporter [Citrus hybrid cultivar]	100	58	2.77E-20
47	CAB64356	alternative oxidase [Populus tremula x Populus tremuloides]	88	75	3.05E-35
48	NP_566175	lateral organ boundaries (LOB) domain protein 41 (LBD41) [Arabidopsis thaliana]	55.319	235	1.64E-58
49	AAG01894	phosphoenolpyruvate carboxykinase [Lycopersicon esculentum]	63.636	66	3.55E-22
50	T10119	glucan endo-1,3-beta-D-glucosidase (EC 3.2.1.39) [Citrus sinensis]	86.228	167	3.98E-77
51	P25460	40S RIBOSOMAL PROTEIN S11 [Zea mays]	95.522	134	1.44E-70
52	BAA31562	metallothionein-like protein [Citrus unshiu]	98.529	68	3.55E-35
53	CAB87834	putative kinetochore protein [Vicia faba]	83.607	122	4.62E-52
54	No hits found				
55	P29685	ATP synthase beta chain, mitochondrial precursor [Hevea brasiliensis]	81.148	122	1.83E-43
56	NP_190877	expressed protein [Arabidopsis thaliana]	85.185	162	1.42E-75
57	AAG16758	putative glutathione S-transferase T3 [Lycopersicon esculentum]	66.364	220	4.85E-81
58	T10119	glucan endo-1,3-beta-D-glucosidase (EC 3.2.1.39) [Citrus sinensis]	88.679	106	7.89E-51
59	AAG33636	beta-carotene hydroxylase [Citrus unshiu]	99.153	118	2.66E-47
60	NP_188456	protease inhibitor/seed storage/lipid transfer protein (LTP) family [Arabidopsis thaliana]	58.571	70	1.08E-22
61	Q96551	S-adenosylmethionine synthetase 1 (Methionine adenosyltransferase 1) (AdoMet synthetase 1)[Catharanthus roseus]	95.93	172	4.17E-113
62	O23787	Thiazole biosynthetic enzyme, chloroplast precursor [Citrus sinensis]	100	111	1.69E-55
63	NP_085475	orf107a [Arabidopsis thaliana]	98.077	52	1.15E-24
64	AAN60276	unknown [Arabidopsis thaliana]	41.111	180	1.47E-35
65	P26518	Glyceraldehyde 3-phosphate dehydrogenase, cytosolic [Magnolia quinquepeta]	96.35	137	3.36E-62
66	Q43636	Thioredoxin H-type (TRX-H) [Ricinus communis]	88.793	116	3.36E-55
67	DAA00281	TPA: putative phytosulfokine peptide precursor [Glycine max]	54.098	61	6.45E-11
68	AAF72202	cysteine protease inhibitor [Manihot esculenta]	62.626	99	1.16E-25
69	AAM65672	4-coumarate-CoA ligase-like protein [Arabidopsis thaliana]	67.647	68	4.53E-17
70	NP_197016	expressed protein [Arabidopsis thaliana]	45.455	99	3.85E-20
71	NP_187644	transcription initiation factor IIB (TFIIB) [Arabidopsis thaliana]	93.519	108	1.92E-56
72	AAG27431	QM-like protein [Elaeis guineensis]	98.592	142	1.40E-79
73	F86339	protein F2D10.18 [imported][Arabidopsis thaliana]	71.304	115	4.46E-37
74	BAB40143	plasma membrane intrinsic protein 2-2 [Pyrus communis]	98.113	53	1.54E-24

IP : 14.49.138.138, 2017-11-03 13:30:33

75	P31542	ATP-dependent clp protease ATP-binding subunit clpA homolog CD4B, chloroplast precursor [Lycopersicon esculentum] (tomato)	92.179	179	1.97E-90
76	BAC78828	caffeic acid O-methyltransferase [Rosa chinensis var. spontanea]	50.98	153	1.15E-36
77	NP_683304	expressed protein [Arabidopsis thaliana]	46.231	199	5.50E-27
78	AAB64207	elongation factor 1-alpha [Zea mays]	100	139	8.61E-76
79	T07161	late-embryogenesis protein homolog[Lycopersicon esculentum] (tomato)	58.333	96	2.31E-19
80	No hits found				
81	NP_568988	2-nitropropane dioxygenase-related protein [Arabidopsis thaliana]	77.841	176	1.07E-78
82	P42896	Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) [Ricinus communis]	73.188	276	7.86E-105
83	AAM28891	NADPH oxidase [Nicotiana tabacum]	86.624	157	2.12E-74
84	NP_197300	anthranilate phosphoribosyltransferase [Arabidopsis thaliana]	75.342	219	1.19E-79
85	NP_564349	expressed protein [Arabidopsis thaliana]	45.238	126	8.92E-16
86	CAB85635	putative ripening-related P-450 enzyme [Vitis vinifera]	56.585	205	1.18E-65
87	Q96480	Delta 1-pyrroline-5-carboxylate synthetase (P5CS) [Includes: Glutamate 5-kinase (Gamma-glutamyl kinase) (GK); Gamma-glutamyl phosphate reductase (GPR) (Glutamate-5-semialdehyde dehydrogenase) (Glutamyl-gamma-semialdehyde dehydrogenase)] [Lycopersicon esculentum]	82.353	68	2.03E-17
88	AAK58599	ethylene-induced esterase [Citrus sinensis]	98.444	257	7.07E-147
89	BAB02396	cytochrome P450 [Arabidopsis thaliana]	70.313	128	7.20E-48
90	S30151	polyubiquitin 6 - parsley [Petroselinum crispum]	100	154	1.10E-80
91	No hits found				
92	S28420	ubiquitin / ribosomal protein CEP52 [Nicotiana sylvestris]	98.876	89	1.13E-45
93	BAA96794	cytosolic aldehyde dehydrogenase [Oryza sativa (japonica cultivar-group)]	69.863	146	2.85E-45
94	No hits found				
95	No hits found				
96	NP_172520	expressed protein [Arabidopsis thaliana]	67.47	166	2.78E-47
97	T05940	cytochrome P450 83D1p [Glycine max]	53.205	156	6.18E-44
98	No hits found				
99	AAF66066	cinnamate 4-hydroxylase CYP73 [Citrus sinensis]	99.306	144	1.21E-60
100	NP_196946	copine-related [Arabidopsis thaliana]	80.672	119	4.49E-51
101	No hits found				
102	BAB09825	gene_id:MYJ24.7~unknown protein [Arabidopsis thaliana]	62.288	236	1.89E-64
103	NP_850468	squamosa-promoter binding protein -related [Arabidopsis thaliana]	50.166	301	7.61E-76
104	NP_199284	expressed protein [Arabidopsis thaliana]	71.795	78	1.71E-27
105	EAA16547	hypothetical protein [Plasmodium yoelii yoelii]	44.715	123	3.74E-13
106	No hits found				
107	O23787	Thiazole biosynthetic enzyme, chloroplast precursor [Citrus sinensis]	99.225	258	6.82E-140
108	No hits found				
109	AAP33009	thioredoxin H [Citrus x paradisi]	98.23	113	1.71E-57
110	CAC80550	cyclophilin [Ricinus communis]	92.941	170	5.87E-83
111	NP_565634	expressed protein [Arabidopsis thaliana]	50	268	8.63E-60
112	P52178	Triose phosphate/phosphate translocator, non-green plastid, chloroplast precursor (CTPT) [Brassica oleracea]	84.091	88	1.81E-30
113	AAD02556	PGPD14 [Petunia x hybrida]	80.556	36	1.73E-12

IP : 14.49.138.138, 2017-11-03 13:30:33

114	NP_173391	plant defensin protein, putative (PDF1.4) [Arabidopsis thaliana]	52.632	57	1.80E-13
115	No hits found				
116	AAM63635	unknown [Arabidopsis thaliana]	62.712	59	8.67E-11
117	No hits found				
118	AAQ15287	synptobrevin-related protein [Pyrus pyrifolia]	91.473	129	5.98E-66
119	AAD46405	ethylene-responsive small GTP-binding protein [Lycopersicon esculentum]	97.101	69	3.84E-21
120	AAM61533	unknown [Arabidopsis thaliana]	56.667	150	4.49E-38
121	NP_188299	AP2 domain transcription factor RAP2.3 [Arabidopsis thaliana]	57.718	149	1.46E-32
122	CAA09804	1-deoxyxylulose 5-phosphate synthase [Catharanthus roseus]	68.085	141	4.96E-48
123	B84476	probable TPR repeat nuclear phosphoprotein [imported][Arabidopsis thaliana]	74.603	126	4.22E-34
124	NP_177852	hypothetical protein [Arabidopsis thaliana]	49.81	263	4.66E-62
125	NP_564417	60S ribosomal protein L9 (RPL90B) [Arabidopsis thaliana]	84.021	194	1.23E-89
126	O65731	40S RIBOSOMAL PROTEIN S5 [Cicer arietinum]	90.863	197	5.30E-97
127	P35493	2,3-bisphosphoglycerate-independent phosphoglycerate mutase (Phosphoglyceromutase) (BPG-independent PGAM) (PGAM-I) [Ricinus communis]	80.153	131	4.97E-60
128	P42896	Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) [Ricinus communis]	79.832	119	1.82E-48
129	Q06652	Probable phospholipid hydroperoxide glutathione peroxidase (PHGPx) (Salt-associated protein)[Citrus sinensis]	100	166	1.71E-91
130	P38661	PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR [Medicago sativa]	73.643	129	4.03E-48
131	No hits found				
132	No hits found				
133	AAO63774	3-phosphoglycerate kinase [Populus tremuloides]	92.701	137	5.41E-67
134	AAL33553	pyruvate decarboxylase [Cucumis melo]	81.89	127	1.15E-53
135	NP_200461	chaperonin, putative [Arabidopsis thaliana]	92.105	76	1.58E-34
136	NP_201373	NifS-related aminotranfserase [Arabidopsis thaliana]	67.89	109	1.28E-38
137	AAF61647	UDP-glucose:salicylic acid glucosyltransferase [Nicotiana tabacum]	61.538	117	1.48E-40
138	BAC84637	putative small nuclear ribonucleoprotein E [Oryza sativa (japonica cultivar-group)]	90	80	1.44E-35
139	NP_568375	elongation factor 1B alpha-subunit [Arabidopsis thaliana]	74.554	224	5.54E-67
140	No hits found				
141	CAA67923	ubiquitin-like protein [Arabidopsis thaliana]	92.135	89	9.50E-42
142	AAF05865	NAM-like protein (no apical meristem) [Arabidopsis thaliana]	80.272	147	2.56E-67
143	AAO41900	putative VAMP protein SEC22 [Arabidopsis thaliana]	66.667	54	9.74E-16
144	S18181	dnaK-type molecular chaperone Nthsp70 [Nicotiana tabacum]	86.611	239	8.14E-88
145	CAA07232	putative Pi starvation-induced protein [Cicer arietinum]	64.762	105	8.28E-31
146	BAB08587	beta-1,3-glucanase-like protein [Arabidopsis thaliana]	69.173	133	9.64E-50
147	BAA02729	cytoplasmic aldolase [Oryza sativa]	94.03	67	4.48E-29
148	P37707	B2 PROTEIN >gi|322726|pir||S32124 B2 protein[Daucus carota]	93.548	62	8.90E-28
149	Q9ZSW9	Translationally controlled tumor protein homolog (TCTP) [Hevea brasiliensis]	93.082	159	3.87E-71
150	Q9MB46	Vacuolar ATP synthase subunit E (V-ATPase E subunit) (Vacuolar proton pump E subunit) [Citrus unshiu]	100	97	1.30E-40
151	No hits found				
152	AAL47552	IAA-amino acid conjugate hydrolase-like protein [Arabidopsis thaliana]	75	60	6.65E-22
153	AAK52077	dehydrin COR15 [Citrus x paradisi]	100	25	2.12E-07

IP : 14.49.138.138, 2017-11-03 13:30:33

154	BAC42625	unknown protein [Arabidopsis thaliana]	39.091	110	5.67E-08
155	P16146	PPLZ02 PROTEIN [Lupinus polyphyllus]	69.474	95	1.30E-24
156	NP_193634	xyloglucan endotransglycosylase, putative [Arabidopsis thaliana]	73.267	101	4.15E-40
157	No hits found				
158	BAB93221	putative 60S RIBOSOMAL PROTEIN L36 [Oryza sativa (japonica cultivar-group)]	79.091	110	6.46E-45
159	AAD17933	catalase [Brassica juncea]	96.063	127	6.95E-69
160	T06407	monodehydroascorbate reductase (NADH2) (EC 1.6.5.4), cytosolic [Lycopersicon esculentum] (tomato)	88.485	165	2.33E-78
161	NP_563973	glyoxalase family protein (lactoylglutathione lyase family protein) [Arabidopsis thaliana]	80	65	6.26E-23
162	S62699	photoassimilate-responsive protein PAR-1b precursor [Nicotiana tabacum]	70.492	122	8.16E-49
163	No hits found				
164	No hits found				
165	No hits found				
166	AAL73489	repressor protein [Glycine max]	87.898	157	2.45E-57
167	NP_565682	small zinc finger-related protein (TIM10) [Arabidopsis thaliana]	86.076	79	1.14E-34
168	AAO49811	SEP3-related MADS-box protein; PTM6 [Populus tremuloides]	94.079	152	3.01E-75
169	AAL32574	putative protein phosphatase-2C (PP2C) [Arabidopsis thaliana]	54.167	72	1.67E-09
170	AAC24001	isoflavone reductase related protein [Pyrus communis]	80.583	309	1.88E-141
171	NP_200479	asparaginyl-tRNA synthetase, cytoplasmic 1 (asparagine-tRNA ligase 1) (SYNC1) [Arabidopsis thaliana]	92.035	113	6.24E-57
172	T03741	probable tyrosine-tRNA ligase (EC 6.1.1.1) [Nicotiana tabacum]	75.207	121	2.75E-49
173	BAB68552	zeta-carotene desaturase [Citrus unshiu]	96.996	233	9.80E-127
174	T08899	dnaK-type molecular chaperone HSC70-9, chloroplast [Spinacia oleracea]	73.529	102	3.53E-26
175	NP_173069	expressed protein [Arabidopsis thaliana]	80.851	94	3.73E-35
176	NP_174119	sphingosine-1-phosphate lyase -related [Arabidopsis thaliana]	77.483	151	7.81E-66
177	No hits found				
178	No hits found				
179	NP_190848	zinc finger - like protein [Arabidopsis thaliana]	63.529	170	2.64E-48
180	AAM28630	delta 1-pyrroline-5-carboxylate synthetase [Suaeda maritima subsp. salsa]	86.735	98	7.71E-45
181	AAP93138	unknown [Setaria italica]	46.018	113	3.45E-22
182	AAO22679	unknown protein [Arabidopsis thaliana]	38.365	159	2.68E-20
183	NP_200077	40S ribosomal protein S10 (RPS10C) [Arabidopsis thaliana]	86.458	96	6.71E-44
184	T09602	probable zinc finger protein SCOF-1, cold-inducible [Glycine max]	50.888	169	9.11E-29
185	AAF79313	F14J16.9 [Arabidopsis thaliana]	38.854	157	2.33E-25
186	No hits found				
187	AAG42754	ubiquitin-specific protease 12 [Arabidopsis thaliana]	85.507	69	1.78E-30
188	S39508	alcohol dehydrogenase homolog, ripening-related [Lycopersicon esculentum] (tomato)	72.611	157	3.13E-61
189	AAF86540	F21B7.3 [Arabidopsis thaliana]	62.766	94	2.20E-27
190	NP_188029	glycolate oxidase -related [Arabidopsis thaliana]	76.682	223	3.71E-95
191	AAD41409	cytosolic class II low molecular weight heat shock protein [Prunus dulcis]	89.041	146	1.71E-57
192	T09846	phosphoenolpyruvate carboxylase (EC 4.1.1.31) 1[Gossypium hirsutum]	91.089	101	9.65E-48
193	F84673	probable beta-1,3-glucanase [imported] - Arabidopsis thaliana	70.543	129	1.78E-33

IP : 14.49.138.138, 2017-11-03 13:30:33

194	CAA65455	methionine adenosyltransferase [Catharanthus roseus]	94.915	59	6.58E-27
195	NP_188081	cytochrome P450, putative [Arabidopsis thaliana]	45.313	64	9.33E-11
196	AAL04507	glutaredoxin [Tilia platyphyllos]	78.505	107	2.64E-44
197	NP_568363	expressed protein [Arabidopsis thaliana]	43.519	108	1.97E-21
198	AAN77300	Unknown protein [Oryza sativa (japonica cultivar-group)]	78.049	41	4.09E-12
199	NP_191308	40S ribosomal protein S2 (RPS2D) [Arabidopsis thaliana]	88.35	103	2.36E-46
200	AAO16559	mitogen-activated protein kinase [Triticum aestivum]	60.345	58	3.82E-10
201	P93257	Probable mannitol dehydrogenase (NAD-dependent mannitol dehydrogenase) [Mesembryanthemum crystallinum]	74.82	139	5.41E-58
202	NP_567952	CBS domain containing protein [Arabidopsis thaliana]	53.75	160	6.32E-36
203	P16064	Subtilisin inhibitor I (ASI-I) [Contains: Subtilisin inhibitor II (ASI-II)] [Vigna angularis]	57.692	78	1.61E-11
204	AAL32693	Unknown protein [Arabidopsis thaliana]	71.591	176	7.44E-57
205	NP_566623	oxidoreductase, 2OG-Fe(II) oxygenase family [Arabidopsis thaliana]	64.211	95	1.18E-31
206	O48920	ADP-ribosylation factor [Vigna unguiculata]	100	145	2.85E-77
207	BAC83073	putative succinyl-CoA ligase alpha subunit [Oryza sativa (japonica cultivar-group)]	88.636	44	2.81E-14
208	NP_567710	brefeldin A-sensitive Golgi protein - like [Arabidopsis thaliana]	70.93	86	2.57E-29
209	AAK73102	Bax inhibitor 1 [Nicotiana tabacum]	67.376	141	2.15E-49
210	No hits found				
211	AAF63704	phosphate/phosphoenolpyruvate translocator [Arabidopsis thaliana]	45.833	168	1.58E-26
212	AAN08216	ribosomal protein L15 [Oryza sativa (japonica cultivar-group)]	91.667	204	1.32E-95
213	No hits found				
214	NP_188871	DNA-directed RNA polymerase (RNA polymerase), putative [Arabidopsis thaliana]	73.684	95	1.24E-35
215	NP_195633	AtRer1A [Arabidopsis thaliana]	80.142	141	3.76E-48
216	NP_188923	early light-induced protein [Arabidopsis thaliana]	61.538	195	4.12E-54
217	NP_563916	vacuolar ATP synthase subunit C -related [Arabidopsis thaliana]	84.516	155	9.40E-66
218	AAG40371	AT4g27960 [Arabidopsis thaliana]	99	100	4.98E-54
219	No hits found				
220	AAF99780	F22O13.11 [Arabidopsis thaliana]	79.048	105	7.84E-31
221	NP_564555	expressed protein [Arabidopsis thaliana]	88.235	68	2.86E-52
222	BAB10068	emb|CAB80929.1~gene_id:MRO11.1~similar to unknown protein [Arabidopsis thaliana]	61.905	147	1.58E-42
223	AAQ22726	40S ribosomal protein S25 [Glycine max]	97.222	72	2.84E-31
224	NP_194934	calcium-binding EF-hand family protein [Arabidopsis thaliana]	50.862	116	2.16E-17
225	AAA34123	hexameric polyubiquitin [Nicotiana sylvestris]	100	94	3.19E-46
226	No hits found				
227	NP_566564	expressed protein [Arabidopsis thaliana]	71.069	159	1.12E-60
228	AAM64715	unknown [Arabidopsis thaliana]	67.027	185	3.89E-63
229	CAB85635	putative ripening-related P-450 enzyme [Vitis vinifera]	74.138	116	8.17E-48
230	NP_193677	pectinacetylesterase family [Arabidopsis thaliana]	64	100	3.05E-35
231	No hits found				
232	AAF73016	ubiquitin conjugating protein [Avicennia marina]	98.684	152	1.13E-85
233	No hits found				

IP : 14.49.138.138, 2017-11-03 13:30:33

234	A86345	F16F4.13 protein [Arabidopsis thaliana]	55.67	97	5.27E-22
235	NP_181466	expressed protein [Arabidopsis thaliana]	65.574	61	6.69E-20
236	NP_598197	mucin 10 [Rattus norvegicus]	34.459	148	5.04E-09
237	AAP80667	ribosomal Pr 117 [Triticum aestivum]	99.291	141	8.11E-76
238	A71421	hypothetical 15.5K protein [Arabidopsis thaliana]	56.164	73	1.01E-13
239	AAL26889	abscisic stress ripening-like protein [Prunus persica]	55	140	3.22E-07

5) 한라봉 흑변과피

Clone No.	Accession No.	Definition of Putative homologue[Organism]	Matching %	Matching Length	E-value
illhan--06-R-L10.ab1	AAL04426	14-3-3 family protein [Lycopersicon esculentum]	96.078	51	4.42E-21
illhan--03-R-G04.ab1	AAD27823	14-3-3 protein [Populus x canescens]	90.854	164	1.03E-70
illhan--07-R-N12.ab1	P02519	17.3 KD CLASS I HEAT SHOCK PROTEIN (HSP 17.3) [Glycine max]	74.242	132	2.17515E-36
illhan--02-R-I07.ab1	AAM13010	20S proteasome beta subunit PBB2 [Arabidopsis thaliana]	80.882	68	3.43E-25
illhan--06-R-A11.ab1	AAF22521	26S proteasome AAA-ATPase subunit RPT1a [Arabidopsis thaliana]	98.765	81	2.48E-40
illhan--02-R-B02.ab1	NP_200637	26S proteasome AAA-ATPase subunit RPT3 [Arabidopsis thaliana]	83.803	142	1.79E-57
illhan--04-R-E04.ab1	AAN15459	26S proteasome AAA-ATPase subunit RPT5a [Arabidopsis thaliana]	100	31	3.51E-10
illhan--05-R-F01.ab1	BAB78487	26S proteasome regulatory particle non-ATPase subunit8 [Oryza sativa (japonica cultivar-group)]	86.154	65	2.67E-18
illhan--03-R-E16.ab1	NP_176633	26S proteasome regulatory subunit (RPN12), putative [Arabidopsis thaliana]	79.032	62	1.27E-21
illhan--06-R-C09.ab1	AAL32634	26S proteasome regulatory subunit [Arabidopsis thaliana]	75.152	165	1.96E-69
illhan--07-R-P10.ab1	A84591	26S proteasome regulatory subunit S2 [imported] [Arabidopsis thaliana]	81.132	106	2.49447E-24
illhan--03-R-D18.ab1	BAB09205	26S proteasome subunit-like protein [Arabidopsis thaliana]	84.906	159	5.76E-74
illhan--03-R-O15.ab1	NP_192418	3(2),5-BISPHOSPHATE NUCLEOTIDASE -related protein [Arabidopsis thaliana]	65.972	144	1.32E-49
illhan--03-R-C16.ab1	CAA47926	3-ketoacyl-CoA thiolase; acetyl-CoA acyltransferase [Cucumis sativus]	78.231	147	1.04325E-54
illhan--06-R-H19.ab1	AAO63774	3-phosphoglycerate kinase [Populus tremuloides]	91.2	125	5.24E-59
illhan--05-R-H18.ab1	AAF34799	40S ribosomal protein S16 [Euphorbia esula]	98.333	120	1.35E-62
illhan--07-R-P16.ab1	NP_186857	40S ribosomal protein S19 (RPS19A) [Arabidopsis thaliana]	86.792	106	1.89671E-48
illhan--03-R-D11.ab1	AAF26742	40s ribosomal protein S23 [Euphorbia esula]	100	105	1.15E-53
illhan--06-R-O07.ab1	AAQ22726	40S ribosomal protein S25 [Glycine max]	91.667	72	2.34E-30
illhan--04-R-D13.ab1	CAA09042	40S ribosomal protein S6 [Cicer arietinum]	94.444	108	4.99E-38
illhan--04-R-O23.ab1	Q08069	40S ribosomal protein S8 [Zea mays]	91.549	71	2.76E-31
illhan--04-R-D05.ab1	Q08069	40S ribosomal protein S8 [Zea mays]	91.228	57	3.57E-24
illhan--02-R-O13.ab1	P50346	60S ACIDIC RIBOSOMAL PROTEIN P0 [Glycine max]	81.197	117	6.81E-30
illhan--04-R-A17.ab1	P41129	60S RIBOSOMAL PROTEIN L13-2 (COLD INDUCED PROTEIN C24B) [Brassica napus]	93.662	142	1.86E-64
illhan--02-R-P18.ab1	NP_193053	60S ribosomal protein L13A (RPL13aC) [Arabidopsis thaliana]	86.792	106	4.25E-48
illhan--02-R-L18.ab1	O82528	60S RIBOSOMAL PROTEIN L15 [Petunia x hybrida]	95.833	144	1.25E-60
illhan--04-R-F02.ab1	Q9M573	60S ribosomal protein L31 [Perilla frutescens]	86.777	121	9.30355E-43
illhan--05-R-I07.ab1	P40590	60S RIBOSOMAL PROTEIN L34 [Pisum sativum]	96.842	95	2.75178E-47
illhan--04-R-A18.ab1	NP_175640	60S ribosomal protein L37 (RPL37B) [Arabidopsis thaliana]	92.405	79	2.70188E-39

IP : 14.49.138.138, 2017-11-03 13:30:33

illhan--03-R-M17.ab1	Q9XHE4	60S RIBOSOMAL PROTEIN L37A [Gossypium hirsutum]	98.901	91	2.86E-46
illhan--05-R-G09.ab1	Q9XF97	60S ribosomal protein L4 (L1) [Prunus armeniaca]	86.667	30	2.03E-06
illhan--04-R-N05.ab1	AAM63366	6-phosphogluconolactonase-like protein [Arabidopsis thaliana]	87.5	40	2.46E-32
illhan--05-R-F17.ab1	NP_190362	ABC transporter family protein [Arabidopsis thaliana]	75.862	87	8.42E-33
illhan--06-R-H17.ab1	NP_190362	ABC transporter family protein [Arabidopsis thaliana]	86.957	161	2.93E-75
illhan--02-R-C09.ab1	CAB56614	acetolactate synthase small subunit [Nicotiana plumbaginifolia]	86.452	155	2.37E-72
illhan--05-R-A10.ab1	S72532	acetyl-CoA C-acyltransferase (EC 2.3.1.16) precursor [Cucurbita cv. Kurokawa Amakuri]	88.889	63	6.9028E-27
illhan--06-R-E22.ab1	AAQ88109	actin 1 [Physcomitrella patens]	98.913	92	1.05E-46
illhan--03-R-F08.ab1	AAM53244	actin-related protein 4 [Arabidopsis thaliana]	75.949	158	2.942E-59
illhan--06-R-M13.ab1	AAM62469	acyl carrier protein, putative [Arabidopsis thaliana]	79.2	125	3.25E-48
illhan--05-R-B21.ab1	CAA05979	adenine nucleotide translocator [Lupinus albus]	98.718	78	3.17E-30
illhan--05-R-A05.ab1	NP_191320	adenylosuccinate synthetase [Arabidopsis thaliana]	65.409	159	3.97E-46
illhan--02-R-G10.ab1	NP_197208	ADP-ribosylation factor, putative [Arabidopsis thaliana]	96.61	118	2.56367E-61
illhan--04-R-O15.ab1	BAC98491	AG-motif binding protein-1 [Nicotiana tabacum]	58.889	90	7.15E-19
illhan--07-R-G07.ab1	CAB64719	AKIN beta2 [Arabidopsis thaliana]	81.132	106	1.15613E-45
illhan--07-R-O24.ab1	AAQ74889	Al-induced protein [Gossypium hirsutum]	90.566	53	1.90477E-21
illhan--02-R-O15.ab1	BAA89423	allyl alcohol dehydrogenase [Nicotiana tabacum]	76.991	113	1.25E-44
illhan--07-R-A05.ab1	NP_197201	allyl alcohol dehydrogenase, putative [Arabidopsis thaliana]	55.882	34	5.50E-06
illhan--03-R-I04.ab1	NP_187203	alpha subunit of F-actin capping protein [Arabidopsis thaliana]	87.805	41	6.69E-15
illhan--02-R-E21.ab1	NP_195214	amidase - like protein [Arabidopsis thaliana]	64.626	147	1.43E-48
illhan--05-R-E07.ab1	AAF20002	amino acid/peptide transporter [Prunus dulcis]	88.415	164	6.07E-79
illhan--07-R-E16.ab1	BAB87832	ammonium transporter [Oryza sativa]	84.848	33	4.08136E-10
illhan--05-R-N03.ab1	NP_565886	AMP deaminase -related [Arabidopsis thaliana]	46.032	63	2.28E-09
illhan--07-R-A08.ab1	NP_197155	amylogenin; reversibly glycosylatable polypeptide [Arabidopsis thaliana]	56.757	111	5.72E-37
illhan--07-R-D22.ab1	AAK49036	ania-6a type cyclin [Arabidopsis thaliana]	87.662	154	5.32084E-75
illhan--05-R-L21.ab1	AAB71830	annexin [Lavatera thuringiaca]	77.528	89	6.45E-33
illhan--03-R-I19.ab1	BAA89009	anthocyanin 5-O-glucosyltransferase [Petunia x hybrida]	66.412	131	7.24154E-48
illhan--03-R-B22.ab1	AAM61215	anthranilate N-benzoyltransferase [Arabidopsis thaliana]	52.5	80	1.20E-18
illhan--04-R-A08.ab1	NP_196837	AP2 domain transcription factor family [Arabidopsis thaliana]	41.284	109	2.01775E-10
illhan--03-R-D09.ab1	BAC43101	ap2 SCARECROW-like protein [Arabidopsis thaliana]	43.636	165	2.25E-22
illhan--05-R-E05.ab1	NP_199475	AP47/50p (gb|AAB88283.1) [Arabidopsis thaliana]	96.694	121	1.34E-49
illhan--06-R-E24.ab1	CAE53882	aquaporin [Ricinus communis]	95.745	94	5.43E-48
illhan--03-R-G08.ab1	NP_199487	ARF GTPase-activating domain-containing protein [Arabidopsis thaliana]	84.962	133	2.74E-63
illhan--02-R-K22.ab1	NP_191045	armadillo repeat containing protein [Arabidopsis thaliana]	79.141	163	1.62E-68
illhan--04-R-H10.ab1	NP_180654	aspartate aminotransferase, mitochondrial (transaminase A/Asp1) [Arabidopsis thaliana]	90.769	65	6.67E-30
illhan--04-R-B10.ab1	JC5125	aspartate transaminase (EC 2.6.1.1) precursor, mitochondrial [Oryza sativa (japonica cultivar-group)]	87.654	81	1.50079E-35
illhan--05-R-P04.ab1	AAD09510	ATFP6 [Arabidopsis thaliana]	77.551	98	5.64427E-40
illhan--01-R-D02.ab1	P14862	ATP synthase A chain (Protein 6) [Cochliobolus heterostrophus]	89.209	139	3.12E-48
illhan--02-R-E04.ab1	NP_199514	ATP synthase delta chain, mitochondrial precursor (sp|Q96252) [Arabidopsis thaliana]	69.565	69	7.38E-19
illhan--03-R-J12.	NP_197752	ATPase, E1-E2 type family [Arabidopsis thaliana]	75.342	73	6.61518E-27

IP : 14.49.138.138, 2017-11-03 13:30:33

ab1					
illhan--05-R-B01.ab1	NP_568746	ATP-dependent Clp protease ATP-binding subunit (ClpC1) [Arabidopsis thaliana]	96.61	59	8.93E-26
illhan--03-R-A02.ab1	NP_568792	ATP-dependent Clp protease ATP-binding subunit ClpX1 [Arabidopsis thaliana]	96.154	52	2.84E-30
illhan--06-R-D09.ab1	NP_564560	ATP-dependent Clp protease proteolytic subunit (ClpR1) [Arabidopsis thaliana]	60.714	56	5.42E-11
illhan--04-R-I23.ab1	NP_563907	ATP-dependent Clp protease proteolytic subunit (ClpR2) [Arabidopsis thaliana]	78.571	70	5.94945E-27
illhan--03-R-H02.ab1	AAP80272	ATP-dependent Clp protease proteolytic subunit [Malus x domestica]	79.612	103	7.75E-42
illhan--03-R-P11.ab1	NP_179754	AtRer1B [Arabidopsis thaliana]	76.829	82	1.08462E-35
illhan--05-R-O15.ab1	NP_568652	autophagy 7 (APG7) [Arabidopsis thaliana]	73.214	112	3.13E-40
illhan--05-R-B15.ab1	NP_565417	auxin efflux carrier protein family [Arabidopsis thaliana]	48.466	163	2.77E-23
illhan--03-R-F04.ab1	NP_850063	auxin-regulated protein [Arabidopsis thaliana]	67.188	64	3.06E-14
illhan--05-R-C02.ab1	NP_850005	auxin-regulated protein [Arabidopsis thaliana]	59.722	72	3.56003E-18
illhan--05-R-P22.ab1	NP_200019	BAG domain containing protein [Arabidopsis thaliana]	50.962	104	6.14E-23
illhan--01-R-P02.ab1	AAK73102	Bax inhibitor 1 [Nicotiana tabacum]	68.276	145	1.46E-51
illhan--04-R-F13.ab1	AAM64718	BCS1 protein-like protein [Arabidopsis thaliana]	41.758	91	1.38E-14
illhan--03-R-H06.ab1	AAK96884	beta tubulin [Arabidopsis thaliana] >gi|20148289|gb|AAM10035.1| beta tubulin [Arabidopsis thaliana]	100	87	2.57559E-45
illhan--04-R-C06.ab1	BAB08587	beta-1,3-glucanase-like protein [Arabidopsis thaliana]	69.565	138	1.41E-51
illhan--04-R-L03.ab1	AAM66982	beta-1,3-glucanase-like protein [Arabidopsis thaliana]	59.722	144	8.5337E-41
illhan--05-R-A16.ab1	AAQ92665	beta-tubulin 5 [Gossypium hirsutum]	98.78	82	4.92E-41
illhan--02-R-D24.ab1	AAQ92666	beta-tubulin 6 [Gossypium hirsutum]	97.546	163	1.57E-90
illhan--01-R-L06.ab1	NP_200279	bHLH protein [Arabidopsis thaliana]	77.083	96	2.49166E-28
illhan--04-R-H07.ab1	NP_563839	bHLH protein [Arabidopsis thaliana]	66	50	3.74E-12
illhan--05-R-I19.ab1	NP_193829	bHLH protein family [Arabidopsis thaliana]	32.653	98	7.79E-10
illhan--03-R-N15.ab1	AAN14410	bifunctional lysine-ketoglutarate reductase/saccharopine dehydrogenase [Gossypium hirsutum]	73.394	109	4.26E-40
illhan--05-R-E15.ab1	NP_565946	bZIP family transcription factor [Arabidopsis thaliana]	59.375	128	8.07726E-40
illhan--03-R-F01.ab1	AAL27150	bZIP transcription factor [Nicotiana tabacum]	84.932	146	1.1848E-47
illhan--04-R-K15.ab1	Q43047	Caffeic acid 3-O-methyltransferase 3 (S-adenosysl-L-methionine:caffeic acid 3-O-methyltransferase 1) (COMT-3) (CAOMT-3) [Populus kitakamiensis]	53.289	152	9.21E-37
illhan--02-R-P12.ab1	BAB39213	caffeine synthase [Coffea arabica]	43.363	113	5.30E-25
illhan--03-R-G01.ab1	Q8H9B6	Caffeoyl-CoA O-methyltransferase (Trans-caffeoyl-CoA 3-O-methyltransferase) (CCoAMT) (CCoAOMT) [Solanum tuberosum]	75.652	115	2.18E-47
illhan--04-R-J17.ab1	P43187	Calcium-binding allergen Bet v 3 (Bet v III) [Betula pendula]	63.83	141	5.26083E-43
illhan--04-R-A14.ab1	NP_198235	calcium-binding EF-hand family protein [Arabidopsis thaliana]	55.245	143	5.83E-34
illhan--06-R-J15.ab1	NP_173499	calcium-binding EF-hand family protein [Arabidopsis thaliana]	62.105	95	2.75796E-23
illhan--07-R-I11.ab1	NP_568568	calcium-binding EF-hand family protein [Arabidopsis thaliana]	40.645	155	6.19394E-18
illhan--07-R-H21.ab1	NP_850178	callose synthase (1,3-beta-glucan synthase) family [Arabidopsis thaliana]	92.793	111	1.18802E-50
illhan--06-R-O03.ab1	AAB86496	calmodulin [Zea mays]	100	53	6.14E-23
illhan--06-R-P20.ab1	AAM20498	calmodulin-like protein [Arabidopsis thaliana]	60.177	113	5.23E-22
illhan--03-R-L16.ab1	P41210	Caltractin (Centrin) [Atriplex nummularia]	75	80	9.43E-29
illhan--04-R-H19.ab1	NP_195802	CBL-interacting protein kinase 14 [Arabidopsis thaliana]	76.866	134	1.62E-56
illhan--05-R-K23.ab1	NP_196301	CDK5 activator-binding protein-related [Arabidopsis thaliana]	79.389	131	8.53E-57
illhan--02-R-M1	AAB63624	cellulose synthase isolog [Arabidopsis thaliana]	42	150	1.01753E-25

IP : 14.49.138.138, 2017-11-03 13:30:33

8.ab1					
illhan--06-R-C24.ab1	AAC68501	chaperonin 60 alpha subunit [Canavalia lineata]	85.95	121	4.38278E-37
illhan--07-R-B23.ab1	AAC68501	chaperonin 60 alpha subunit [Canavalia lineata]	92.063	63	5.03E-25
illhan--07-R-C11.ab1	Q05046	CHAPERONIN CPN60-2, MITOCHONDRIAL PRECURSOR (HSP60-2) [Cucurbita maxima]	84.906	53	1.32E-16
illhan--03-R-G03.ab1	NP_200461	chaperonin, putative [Arabidopsis thaliana]	94.444	36	4.90E-12
illhan--07-R-L12.ab1	CAA09110	chitinase [Hevea brasiliensis]	66.667	99	8.41855E-33
illhan--02-R-C11.ab1	T08816	choline kinase (EC 2.7.1.32) CK2 [Glycine max]	73.256	86	2.81E-32
illhan--04-R-N24.ab1	AAD48923	chorimate mutase [Lycopersicon esculentum]	66.071	56	4.43424E-13
illhan--03-R-I15.ab1	P49299	Citrate synthase, glyoxysomal precursor (GCS) [Cucurbita maxima]	87.302	126	2.39952E-59
illhan--06-R-K15.ab1	BAB62040	CjMDR1 [Coptis japonica]	48.447	161	1.02E-25
illhan--06-R-G21.ab1	AAG25709	class III acidic chitinase [Malus x domestica]	79.167	144	9.76E-53
illhan--02-R-N11.ab1	NP_179569	clathrin assembly protein -related [Arabidopsis thaliana]	72.848	151	4.86062E-54
illhan--05-R-J17.ab1	T04143	CLB1 protein [Lycopersicon esculentum]	78.378	37	8.65E-09
illhan--05-R-F22.ab1	AAD29679	CLC-Nt2 protein [Nicotiana tabacum]	81.553	103	2.18E-44
illhan--03-R-F16.ab1	BAB10643	cleavage stimulation factor subunit 1-like protein [Arabidopsis thaliana]	74.138	58	2.15E-20
illhan--07-R-A23.ab1	AAC99310	CONSTANS-like protein 2 [Malus x domestica]	80	140	1.90E-56
illhan--02-R-K11.ab1	BAB02567	contains similarity to 26S proteasome subunit 4~gene_id:F4B12.4 [Arabidopsis thaliana]	87.975	158	1.40E-77
illhan--07-R-P13.ab1	NP_567233	contains similarity to a protein kinase domain (Pfam: pkinase.hmm, score: 166.20) and to legume lectins beta domain (Pfam: lectin_legB.hmm, score: 139.32) [Arabidopsis thaliana]	53.03	66	1.32883E-09
illhan--07-R-J10.ab1	BAA97184	contains similarity to embryo-specific protein 3~gene_id:MMI9.3 [Arabidopsis thaliana]	64.341	129	7.34088E-45
illhan--05-R-K21.ab1	BAB10406	contains similarity to ribonucleoprotein F~gene_id:K2A18.8 [Arabidopsis thaliana]	66.667	81	1.08714E-27
illhan--06-R-O19.ab1	AAF75817	Contains similarity to transcriptional activator CBF1 from Arabidopsis thaliana gb|U77378 and contains an AP2 PF|00847 domain. This gene may be cut off [Arabidopsis thaliana]	81.159	69	1.22E-20
illhan--06-R-I04.ab1	BAB08843	contains similarity to unknown protein~dbj|BAA89593.1~gene_id:MJH22.6 [Arabidopsis thaliana]	64.444	45	8.51E-08
illhan--07-R-I14.ab1	BAA97320	contains similarity to zinc finger protein~gene_id:MYN8.4 [Arabidopsis thaliana]	92.857	28	2.05978E-10
illhan--05-R-N21.ab1	NP_179573	copia-related retroelement pol polyprotein [Arabidopsis thaliana]	81.818	88	1.24468E-33
illhan--04-R-C08.ab1	NP_196946	copine-related [Arabidopsis thaliana]	85.35	157	5.73469E-73
illhan--06-R-J03.ab1	NP_201202	copine-related [Arabidopsis thaliana]	80.851	47	8.30E-20
illhan--03-R-N19.ab1	NP_849973	copper chaperone (CCH)-related [Arabidopsis thaliana]	77.586	116	4.51E-50
illhan--04-R-L09.ab1	NP_195680	copper chaperone (CCH)-related [Arabidopsis thaliana]	67.123	73	3.6383E-17
illhan--02-R-D10.ab1	NP_200711	copper transport protein [Arabidopsis thaliana]	59.756	82	1.26E-12
illhan--03-R-I20.ab1	AAL38527	CSLC7 [Oryza sativa]	81.633	147	2.39952E-59
illhan--03-R-E04.ab1	AAK40361	CTR1-like protein kinase [Rosa hybrid cultivar]	59.006	161	1.37E-46
illhan--05-R-G11.ab1	AAK01931	Cu/Zn-superoxide dismutase copper chaperone precursor [Glycine max]	78.906	128	1.04E-54
illhan--03-R-J19.ab1	NP_199675	cyclin family [Arabidopsis thaliana]	72	50	1.69006E-14
illhan--03-R-J15.ab1	AAM63088	cyclophilin [Arabidopsis thaliana]	79.661	59	6.12745E-20
illhan--03-R-F02.ab1	NP_200679	cyclophilin ROC7 [Arabidopsis thaliana]	83.688	141	2.37E-57
illhan--06-R-E12.ab1	AAQ20042	CYP81E8 [Medicago truncatula]	61.739	115	5.54E-32
illhan--03-R-A08.ab1	AAG38521	cystatin-like protein [Citrus x paradisi]	100	118	9.83722E-64
illhan--07-R-N17.ab1	NP_567983	cysteine protease XCP1 [Arabidopsis thaliana]	85.294	102	6.51889E-49
illhan--04-R-F21.ab1	NP_179417	cytidylyltransferase domain-containing protein [Arabidopsis thaliana]	84.956	113	2.77E-51

IP : 14.49.138.138, 2017-11-03 13:30:33

illhan--01-R-I04.ab1	NP_198679	cytochrome b-561 (gb|AAD45585.1) [Arabidopsis thaliana]	78.462	65	4.06E-23
illhan--06-R-O05.ab1	P05642	Cytochrome b6 [Zea mays]	99.029	103	9.57E-53
illhan--03-R-P08.ab1	BAB02396	cytochrome P450 [Arabidopsis thaliana]	72.549	51	1.53E-15
illhan--03-R-A12.ab1	Q43147	Cytochrome P450 85 (Dwarf protein) [Lycopersicon esculentum]	81.132	53	1.17329E-31
illhan--07-R-P11.ab1	Q42798	Cytochrome P450 93A1 >gi|2129824|pir||S62899 cytochrome P450 (CYP93 A1) [Glycine max]	53.659	164	4.22542E-48
illhan--05-R-P15.ab1	AAA69928	cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]	91.566	83	2.7452E-39
illhan--06-R-K08.ab1	AAB96833	cytosolic cyclophilin [Arabidopsis thaliana]	80.769	78	1.47E-32
illhan--07-R-P06.ab1	BAB02860	dbj|BAA20807.2~gene_id:MFJ20.13~similar to unknown protein [Arabidopsis thaliana]	69.014	142	7.47646E-53
illhan--07-R-C24.ab1	NP_181602	DEAD/DEAH box helicase, putative [Arabidopsis thaliana]	82.639	144	1.78072E-64
illhan--07-R-J02.ab1	AAO13360	dehydration-responsive element binding protein 3 [Lycopersicon esculentum]	64.865	148	2.32934E-30
illhan--05-R-M24.ab1	AAP56259	dehydrin [Citrus sinensis]	100	21	5.06E-07
illhan--02-R-G14.ab1	BAA74736	dehydrin [Citrus unshiu]	97.297	37	1.12389E-15
illhan--03-R-I16.ab1	AAN78125	dehydrin [Citrus x paradisi]	100	31	1.78246E-10
illhan--07-R-L03.ab1	NP_182144	delta-8 sphingolipid desaturase, putative [Arabidopsis thaliana]	81.333	75	5.54423E-32
illhan--01-R-M04.ab1	AAL32062	deoxy-D-xylulose-5-phosphate synthase [Morinda citrifolia]	87.013	77	4.63E-33
illhan--04-R-J05.ab1	F96520	dihydrolipoamide dehydrogenase (EC 1.8.1.4) [similarity] [Arabidopsis thaliana]	98.182	55	1.42387E-24
illhan--02-R-M12.ab1	NP_173703	disease resistance response protein-related [Arabidopsis thaliana]	43.284	67	1.13E-08
illhan--04-R-G05.ab1	NP_173703	disease resistance response protein-related [Arabidopsis thaliana]	55.385	130	7.28E-32
illhan--02-R-L06.ab1	AAQ18645	division protein; ARC6 [Arabidopsis thaliana]	65.323	124	2.21028E-41
illhan--07-R-C18.ab1	NP_850847	DNA-dependent ATPase, putative [Arabidopsis thaliana]	88.462	78	4.71565E-31
illhan--05-R-N23.ab1	NP_188871	DNA-directed RNA polymerase (RNA polymerase), putative [Arabidopsis thaliana]	93.548	93	1.07701E-43
illhan--04-R-P19.ab1	NP_190777	DNA-directed RNA polymerase II 13.6K chain [Arabidopsis thaliana]	87.069	116	1.50645E-53
illhan--02-R-A11.ab1	NP_179145	DNA-directed RNA polymerase II, third largest subunit [Arabidopsis thaliana]	80.795	151	1.13962E-66
illhan--07-R-L22.ab1	AAD12055	DnaJ protein [Hevea brasiliensis]	77.778	117	1.66945E-44
illhan--02-R-L08.ab1	NP_181633	DnaJ protein family [Arabidopsis thaliana]	67.123	73	2.30E-22
illhan--05-R-J10.ab1	NP_564717	DnaJ protein family [Arabidopsis thaliana]	84.211	95	2.26E-41
illhan--07-R-N22.ab1	AAM63624	DnaJ protein, putative [Arabidopsis thaliana]	55.556	117	4.69347E-31
illhan--06-R-F17.ab1	JC4786	dnaK-type molecular chaperone hsc70-3 [Lycopersicon esculentum]	100	71	1.81E-35
illhan--05-R-F24.ab1	NP_177574	dolichyl-phosphate mannosyltransferase polypeptide 2 -related [Arabidopsis thaliana]	57.407	54	4.41E-13
illhan--05-R-H11.ab1	BAA23657	EF-1 alpha [Oryza sativa]	98.077	52	1.32E-22
illhan--05-R-I05.ab1	AAK62346	elicitor-inducible cytochrome P450 [Nicotiana tabacum]	69.565	92	1.1224E-32
illhan--06-R-M01.ab1	NP_568375	elongation factor 1B alpha-subunit [Arabidopsis thaliana]	70	150	2.29259E-30
illhan--07-R-E14.ab1	NP_181669	embryo-abundant protein -related [Arabidopsis thaliana]	64.706	51	9.47524E-13
illhan--03-R-H05.ab1	NP_176075	emp24/gp25L/p24 family [Arabidopsis thaliana]	78.409	88	3.09E-35
illhan--04-R-N12.ab1	NP_178306	endomembrane protein 70, putative [Arabidopsis thaliana]	97.647	85	2.33E-38
illhan--05-R-F06.ab1	NP_178306	endomembrane protein 70, putative [Arabidopsis thaliana]	91.463	164	2.49E-74
illhan--05-R-O21.ab1	CAB65283	Enod93 protein [Medicago sativa subsp. x varia]	65.934	91	1.89E-27
illhan--07-R-A20.ab1	NP_191610	enoyl-CoA hydratase/isomerase family [Arabidopsis thaliana]	69.444	36	2.22E-08
illhan--05-R-D10.ab1	NP_199142	enoyl-CoA hydratase/isomerase family [Arabidopsis thaliana]	67.949	156	1.61E-55
illhan--06-R-O20.ab1	NP_175576	epsilon subunit of mitochondrial F1-ATPase [Arabidopsis thaliana]	88.71	62	2.86089E-28

IP : 14.49.138.138, 2017-11-03 13:30:33

illhan--03-R-M05.ab1	A85196	EREBP-2 protein [imported] [Arabidopsis thaliana]	50.617	81	1.66E-08
illhan--02-R-F01.ab1	BAD01556	ERF-like protein [Cucumis melo]	60.656	122	6.58015E-33
illhan--06-R-G20.ab1	BAD01556	ERF-like protein [Cucumis melo]	66.667	54	2.38E-11
illhan--07-R-O02.ab1	AAP42136	erg-1 [Solanum tuberosum]	73.973	73	2.37246E-27
illhan--06-R-L14.ab1	CAD21849	ethylene responsive element binding protein [Fagus sylvatica]	49.153	118	2.0832E-15
illhan--04-R-P17.ab1	BAA97123	ethylene-responsive element binding factor [Nicotiana sylvestris]	78.161	87	2.51E-24
illhan--07-R-A03.ab1	AAN17444	eukaryotic initiation factor 4, eIF4-like protein [Arabidopsis thaliana]	62	50	7.16E-09
illhan--05-R-M03.ab1	Q94HF1	Eukaryotic translation initiation factor 3 subunit 11 (eIF-3 p25) (eIF3k) [Oryza sativa]	78.313	166	1.52E-69
illhan--02-R-G16.ab1	AAQ08191	eukaryotic translation initiation factor 5A isoform I [Hevea brasiliensis]	92.391	92	1.85E-43
illhan--07-R-N15.ab1	Q9AXQ5	Eukaryotic translation initiation factor 5A-2 (eIF-5A 2) [Lycopersicon esculentum]	93.836	146	2.80808E-76
illhan--01-R-A04.ab1	NP_193436	expansin- related [Arabidopsis thaliana]	59.211	152	1.01E-49
illhan--01-R-B03.ab1	CAC13114	F-1-ATP synthase [Elymus sibiricus]	82.353	34	1.27E-06
illhan--06-R-N09.ab1	NP_193816	FAD-linked oxidoreductase family [Arabidopsis thaliana]	71.698	106	1.36E-38
illhan--04-R-B03.ab1	NP_192993	F-box protein family [Arabidopsis thaliana]	57.927	164	3.36382E-45
illhan--05-R-F18.ab1	NP_564150	F-box protein family [Arabidopsis thaliana]	80.667	150	1.68E-73
illhan--05-R-N08.ab1	NP_567343	F-box protein family, AtFBW2 [Arabidopsis thaliana]	69.853	136	6.52E-49
illhan--03-R-A16.ab1	S60307	fbp6 protein [Petunia x hybrida]	60	50	4.93E-06
illhan--07-R-N01.ab1	O22101	Ferrochelatase II, chloroplast precursor (Protoheme ferro-lyase) (Heme synthetase) [Oryza sativa]	85.965	57	1.28112E-20
illhan--06-R-P15.ab1	AAN77144	fiber protein Fb1 [Gossypium barbadense]	83.784	37	2.43315E-11
illhan--04-R-P04.ab1	JQ2272	formate dehydrogenase (EC 1.2.1.2) precursor, mitochondrial [Solanum tuberosum]	93.333	105	2.31E-54
illhan--07-R-L08.ab1	AAO60427	FPh1 [Gossypium hirsutum]	73.529	34	2.23633E-14
illhan--03-R-I23.ab1	NP_181187	fructose-bisphosphate aldolase, putative [Arabidopsis thaliana]	92.857	84	4.78E-39
illhan--07-R-D23.ab1	AAM97352	G protein alpha II subunit [Pisum sativum]	92.982	57	1.03149E-22
illhan--02-R-I17.ab1	AAD49742	G protein beta subunit [Pisum sativum]	88.8	125	8.63E-62
illhan--05-R-K15.ab1	AAM13196	galactosidase, putative [Arabidopsis thaliana]	83.871	62	8.62E-28
illhan--07-R-E13.ab1	Q9M5Q1	Galactoside 2-alpha-L-fucosyltransferase (Xyloglucan alpha-(1,2)-fucosyltransferase) (PsFT1) [Pisum sativum]	71.569	102	1.32278E-41
illhan--06-R-M23.ab1	AAK14790	G-box binding factor bZIP transcription factor [Catharanthus roseus]	71.212	66	1.17E-17
illhan--04-R-E12.ab1	AAD42937	G-box binding protein 1 [Catharanthus roseus]	67.5	40	3.64E-07
illhan--04-R-M23.ab1	T01782	GDP dissociation inhibitor [Nicotiana tabacum]	94.203	138	1.60E-71
illhan--04-R-D03.ab1	CAB45241	GEG protein [Gerbera hybrid cultivar]	67.925	53	1.33E-17
illhan--06-R-H05.ab1	AAF00023	GIGANTEA [Arabidopsis thaliana]	70.861	151	2.43E-56
illhan--04-R-E20.ab1	T06254	glucose-6-phosphate/phosphate-translocator precursor, plastid [Pisum sativum]	45.455	132	6.92E-19
illhan--05-R-C17.ab1	NP_178310	glutamate decarboxylase [Arabidopsis thaliana]	93.007	143	2.68E-71
illhan--04-R-P16.ab1	AAK62421	glutamate dehydrogenase 2 [Arabidopsis thaliana]	92.366	131	1.13962E-66
illhan--02-R-G24.ab1	AAL04507	glutaredoxin [Tilia platyphyllos]	77.57	107	8.583E-44
illhan--04-R-G17.ab1	NP_174170	glutaredoxin protein family [Arabidopsis thaliana]	72.5	40	1.39733E-11
illhan--02-R-J02.ab1	AAM65800	glutaredoxin-like protein [Arabidopsis thaliana]	71.631	141	2.99E-49
illhan--01-R-O03.ab1	Q43621	Glutathione reductase, cytosolic (GR) (GRase) (GOR2) [Pisum sativum]	88.485	165	2.59E-77
illhan--03-R-A10.ab1	AAN39918	glutathione S-transferase [Capsicum annuum]	80	25	9.93E-08

IP : 14.49.138.138, 2017-11-03 13:30:33

illhan--06-R-D17.ab1	BAC21263	glutathione S-transferase [Cucurbita maxima]	83.333	60	6.88236E-22
illhan--04-R-P22.ab1	AAG34803	glutathione S-transferase GST 13 [Glycine max]	63.975	161	5.72E-53
illhan--05-R-K01.ab1	AAG34808	glutathione S-transferase GST 18 [Glycine max]	52.174	92	1.80E-22
illhan--02-R-E18.ab1	AAM92008	glyceraldehyde 3-phosphate dehydrogenase [Solanum tuberosum]	97.26	73	5.83003E-34
illhan--04-R-K03.ab1	P26518	Glyceraldehyde 3-phosphate dehydrogenase, cytosolic [Magnolia quinquepeta]	91.743	109	1.15E-53
illhan--07-R-L17.ab1	NP_193893	glycine-rich protein [Arabidopsis thaliana]	80.357	56	2.25527E-14
illhan--02-R-G08.ab1	NP_188029	glycolate oxidase -related [Arabidopsis thaliana]	69.93	143	1.96749E-53
illhan--04-R-J08.ab1	NP_188029	glycolate oxidase -related [Arabidopsis thaliana]	80.531	113	3.18E-48
illhan--03-R-F13.ab1	NP_195174	glycosyl hydrolase family 17 [Arabidopsis thaliana]	82.927	123	1.48E-53
illhan--06-R-K16.ab1	NP_191010	glycosyl hydrolase family 19 (class IV chitinase) [Arabidopsis thaliana]	80.368	163	4.35272E-77
illhan--03-R-M14.ab1	NP_197525	glycosyl hydrolase family 36 [Arabidopsis thaliana]	69.565	138	1.40E-52
illhan--07-R-I02.ab1	AAB17995	glyoxalase II [Arabidopsis thaliana]	83.962	106	1.89671E-48
illhan--06-R-D07.ab1	BAA34247	GPI-anchored protein [Vigna radiata]	64.286	56	5.79E-13
illhan--05-R-D16.ab1	NP_196824	GRAM domain-containing protein [Arabidopsis thaliana]	66.279	86	5.91E-31
illhan--02-R-B16.ab1	T06251	GTP binding protein [Pisum sativum]	88	50	1.31E-11
illhan--06-R-M07.ab1	AAL49957	GTP cyclohydrolase I [Lycopersicon esculentum]	70.69	58	2.13E-15
illhan--05-R-C24.ab1	AAM12880	GTP-binding protein [Helianthus annuus]	97.143	70	3.27E-24
illhan--03-R-N24.ab1	NP_192117	GTP-binding protein SAR1A [Arabidopsis thaliana]	87.5	56	2.44313E-23
illhan--06-R-O13.ab1	NP_175638	GTP-binding protein, putative [Arabidopsis thaliana]	90.123	81	5.20E-38
illhan--07-R-L24.ab1	NP_195311	GTP-binding protein, putative [Arabidopsis thaliana]	82.243	107	2.23444E-46
illhan--06-R-J12.ab1	NP_567051	guanylate kinase-related protein [Arabidopsis thaliana]	48.039	102	1.86E-19
illhan--03-R-M03.ab1	T43789	H+-transporting two-sector ATPase (EC 3.6.3.14) chain B, vacuolar [imported] [Citrus unshiu]	100	56	9.97E-26
illhan--02-R-F24.ab1	AAO34666	HASTY [Arabidopsis thaliana]	54.601	163	2.32E-46
illhan--07-R-I04.ab1	NP_175627	HD-Zip transcription factor [Arabidopsis thaliana]	86.111	108	3.24659E-45
illhan--02-R-N19.ab1	BAA83710	heat shock factor [Nicotiana tabacum]	83.333	48	2.98E-19
illhan--06-R-C10.ab1	P22335	HEAT SHOCK FACTOR PROTEIN HSF24 (HEAT SHOCK TRANSCRIPTION FACTOR 24) (HSTF 24) (HEAT STRESS TRANSCRIPTION FACTOR) [Lycopersicon peruvianum]	42.478	113	6.40302E-12
illhan--02-R-G23.ab1	AAQ08597	heat shock protein [Hevea brasiliensis]	86.585	82	1.64E-28
illhan--05-R-G21.ab1	CAA47948	heat shock protein 70 [Oryza sativa (indica cultivar-group)]	83.065	124	2.66E-50
illhan--06-R-A08.ab1	NP_180184	heat shock transcription factor family [Arabidopsis thaliana]	70.968	124	2.36E-43
illhan--02-R-B24.ab1	BAB71737	heat stress transcription factor Spl7 [Oryza sativa (japonica cultivar-group)]	69.697	132	1.24E-50
illhan--06-R-F18.ab1	AAP91821	HECT ubiquitin-protein ligase 3 [Arabidopsis thaliana]	79.866	149	9.11E-61
illhan--07-R-I18.ab1	NP_567206	helicase domain-containing protein [Arabidopsis thaliana]	67.045	88	3.09029E-42
illhan--06-R-L22.ab1	AAA34123	hexameric polyubiquitin [Nicotiana sylvestris]	100	89	2.41E-43
illhan--07-R-B09.ab1	AAF34134	high molecular weight heat shock protein [Malus x domestica]	88.75	160	3.01E-78
illhan--02-R-F10.ab1	CAD89802	histidine amino acid transporter [Oryza sativa (indica cultivar-group)]	78.049	41	3.68E-12
illhan--02-R-J09.ab1	0912198A	histone H4 [Physarum polycephalum]	100	39	4.73758E-15
illhan--05-R-G01.ab1	P26585	HMG1/2-like protein (SB11 protein) [Glycine max]	65.385	52	1.38E-09
illhan--05-R-G04.ab1	AAL33650	HMG-like nucleosome/chromatin assembly factor D [Zea mays]	71.111	45	5.15E-09
illhan--07-R-J14.ab1	NP_182191	homeobox-leucine zipper protein ATHB-7 (HD-ZIP protein ATHB-7) [Arabidopsis thaliana]	57.143	49	8.78699E-08
illhan--05-R-C20	NP_189219	homocysteine S-methyltransferase AtHMT-1 [Arabidopsis thaliana]	78.082	73	3.38E-29

IP : 14.49.138.138, 2017-11-03 13:30:33

.ab1					
illhan--06-R-D05.ab1	AAM61538	homoserine dehydrogenase-like protein [Arabidopsis thaliana]	76.106	113	1.85E-35
illhan--04-R-L20.ab1	AAN17424	HSP100/ClpB, putative [Arabidopsis thaliana]	73.077	104	2.03E-31
illhan--01-R-E06.ab1	AAB99745	HSP70 [Triticum aestivum]	95.062	162	2.01E-71
illhan--03-R-B12.ab1	AAL60450	HUELLENLOS-like protein [Oryza sativa]	73.684	76	2.18E-17
illhan--05-R-N12.ab1	NP_194147	hydrolase, alpha/beta fold family [Arabidopsis thaliana]	81.25	64	3.27E-24
illhan--02-R-P10.ab1	T12197	immunophilin [Vicia faba]	84.314	102	6.5497E-49
illhan--02-R-O24.ab1	NP_197178	Inositol 1,3,4-Trisphosphate 5/6 kinase [Arabidopsis thaliana]	63.699	146	2.09705E-47
illhan--06-R-G17.ab1	AAM20595	integral membrane protein, putative [Arabidopsis thaliana]	69.421	121	1.32E-33
illhan--02-R-E24.ab1	AAC24001	isoflavone reductase related protein [Pyrus communis]	82.558	86	3.65E-36
illhan--01-R-C05.ab1	NP_568763	K+ efflux antiporter, putative (KEA5) [Arabidopsis thaliana]	72.222	36	7.03E-08
illhan--07-R-A14.ab1	NP_200865	Kelch repeat containing F-box protein family [Arabidopsis thaliana]	70.27	74	5.29E-27
illhan--07-R-M02.ab1	NP_191420	ketol-acid reductoisomerase [Arabidopsis thaliana]	92.135	89	1.91009E-40
illhan--06-R-I14.ab1	NP_200118	KH domain protein [Arabidopsis thaliana]	69.355	62	1.92E-16
illhan--02-R-A15.ab1	NP_197779	kinesin-related protein [Arabidopsis thaliana]	70.27	74	1.32E-22
illhan--07-R-E04.ab1	CAB51835	l1332.6 [Oryza sativa (indica cultivar-group)]	66.949	118	2.73901E-40
illhan--06-R-I18.ab1	NP_187533	laccase (diphenol oxidase) family [Arabidopsis thaliana]	68.182	110	3.57E-44
illhan--07-R-M03.ab1	NP_187533	laccase (diphenol oxidase) family [Arabidopsis thaliana]	70.186	161	1.47229E-61
illhan--03-R-O05.ab1	P46518	Late embryogenesis abundant protein Lea14-A [Gossypium hirsutum]	78.788	132	9.0507E-56
illhan--04-R-P20.ab1	AAC36318	leucine-rich receptor-like protein kinase [Malus x domestica]	85.976	164	3.22804E-72
illhan--02-R-O18.ab1	BAB08479	leucine-rich repeat disease resistance protein-like [Arabidopsis thaliana]	89.506	162	1.76E-70
illhan--06-R-O24.ab1	NP_188919	leucine-rich repeat extensin family [Arabidopsis thaliana]	71.053	114	5.27E-46
illhan--02-R-F17.ab1	BAC87845	leucine-rich repeat receptor-like protein kinase 1 [Populus nigra]	43.59	117	6.61E-17
illhan--06-R-G16.ab1	Q9MB73	Limonoid UDP-glucosyltransferase (Limonoid glucosyltransferase) (Limonoid GTase) (LGTase) [Citrus unshiu]	95.614	114	3.80E-54
illhan--05-R-K04.ab1	AAM62634	lipid transfer protein, putative [Arabidopsis thaliana]	68.085	47	1.09E-11
illhan--04-R-L04.ab1	NP_179682	lipoic acid synthase (LIP1) [Arabidopsis thaliana]	75.926	108	2.69E-40
illhan--05-R-A23.ab1	CAC08341	lipoic acid synthase-like protein [Arabidopsis thaliana]	60.909	110	8.69E-27
illhan--02-R-D09.ab1	AAC39360	LMW heat shock protein [Fragaria x ananassa]	85.882	85	1.90E-29
illhan--07-R-C02.ab1	NP_194116	long-chain-fatty-acid--CoA ligase (acyl-CoA synthetase) [Arabidopsis thaliana]	78.916	166	5.32641E-78
illhan--05-R-E20.ab1	AAK20740	LRK33 [Triticum aestivum]	51.961	102	3.55E-25
illhan--06-R-D19.ab1	Q03685	Luminal binding protein 5 precursor (BiP 5) (78 kDa glucose-regulated protein homolog 5) (GRP 78-5) [Nicotiana tabacum]	97.531	162	5.11551E-67
illhan--03-R-L20.ab1	NP_195785	Macrophage migration inhibitory factor (MIF) family [Arabidopsis thaliana]	90.816	98	1.08E-43
illhan--07-R-L05.ab1	AAM21344	MADS-box protein 4 [Vitis vinifera]	73.611	72	6.5644E-25
illhan--02-R-J23.ab1	CAC12826	malate dehydrogenase [Nicotiana tabacum]	95.833	144	6.37154E-73
illhan--06-R-H08.ab1	P17783	Malate dehydrogenase, mitochondrial precursor [Citrullus lanatus]	91.667	72	4.23446E-31
illhan--02-R-G19.ab1	AAD28760	membrane related protein CP5 [Arabidopsis thaliana]	71.698	53	9.35E-16
illhan--05-R-A24.ab1	NP_172566	metal transporter, putative (ZIP4) [Arabidopsis thaliana]	87.879	66	1.66E-25
illhan--07-R-K12.ab1	CAA65455	methionine adenosyltransferase [Catharanthus roseus]	96.429	56	4.56748E-26
illhan--07-R-H17.ab1	NP_176647	methionine/cystathionine gamma lyase -related [Arabidopsis thaliana]	76.238	101	2.26157E-33
illhan--02-R-I14.	AAL18927	mevalonate disphosphate decarboxylase [Hevea brasiliensis]	88.333	120	6.85494E-51

IP : 14.49.138.138, 2017-11-03 13:30:33

ab1					
illhan--04-R-A20.ab1	AAM62925	MFDX2 precursor [Arabidopsis thaliana]	83.673	49	4.30E-18
illhan--02-R-P02.ab1	CAD33929	microtubule associated protein [Cicer arietinum]	96.226	106	1.80E-51
illhan--04-R-D12.ab1	CAD33929	microtubule associated protein [Cicer arietinum]	93.162	117	3.04E-46
illhan--05-R-N10.ab1	P92792	Mitochondrial import receptor subunit TOM20 (Translocase of outer membrane 20 kDa subunit) [Solanum tuberosum]	62.987	154	1.0796E-51
illhan--04-R-K11.ab1	NP_196908	mitochondrial phosphate transporter [Arabidopsis thaliana]	61.719	128	4.04E-35
illhan--04-R-G04.ab1	BAB83689	mitochondrial phosphate transporter [Lotus corniculatus var. japonicus]	86.667	90	4.6826E-39
illhan--03-R-C22.ab1	S51590	mitochondrial processing peptidase (EC 3.4.24.64) alpha-II chain precursor [Solanum tuberosum]	65	140	1.64E-28
illhan--05-R-K14.ab1	AAK07827	mitochondrial processing peptidase beta subunit [Cucumis melo]	89.024	164	1.00E-65
illhan--07-R-H24.ab1	AAK07827	mitochondrial processing peptidase beta subunit [Cucumis melo]	95.89	73	2.87215E-40
illhan--06-R-O14.ab1	AAN75065	mitogen-activated protein kinase [Malus micromalus]	88.496	113	1.50E-53
illhan--05-R-G15.ab1	CAC82727	monodehydroascorbate reductase [Mesembryanthemum crystallinum]	81.651	109	1.28E-46
illhan--02-R-H01.ab1	BAB63925	monodehydroascorbate reductase [Spinacia oleracea]	91.304	46	2.7569E-24
illhan--04-R-K20.ab1	NP_566428	MutT/nudix family protein [Arabidopsis thaliana]	68.085	94	6.31157E-33
illhan--06-R-O02.ab1	NP_567384	MutT/nudix family protein [Arabidopsis thaliana]	72.222	90	2.49E-32
illhan--05-R-E03.ab1	NP_190248	myb family transcription factor [Arabidopsis thaliana]	78.873	71	2.75796E-23
illhan--07-R-P03.ab1	BAC53938	Myb-like protein [Nicotiana tabacum]	77.778	54	1.33202E-17
illhan--06-R-M03.ab1	AAN28270	myb-like transcription factor 1 [Gossypium hirsutum]	94.309	123	2.34511E-67
illhan--07-R-J09.ab1	AAN28270	myb-like transcription factor 1 [Gossypium hirsutum]	94.03	134	2.58681E-74
illhan--03-R-D17.ab1	AAB63650	Myb-related transcription activator (MybSt1) isolog [Arabidopsis thaliana]	55.625	160	1.12E-40
illhan--03-R-A03.ab1	NP_191192	N2,N2-dimethylguanosine tRNA methyltransferases-related protein [Arabidopsis thaliana]	59.06	149	9.85725E-40
illhan--07-R-A12.ab1	CAC83608	Na+/H+ antiporter, isoform 2 [Lycopersicon esculentum]	61.333	75	9.22453E-19
illhan--04-R-M21.ab1	AAM08407	Na+/H+ exchanger 6 [Arabidopsis thaliana]	85.714	56	1.16E-20
illhan--04-R-A03.ab1	AAK84884	NAC domain protein NAC2 [Phaseolus vulgaris]	84.314	102	1.29E-49
illhan--02-R-D07.ab1	BAD02267	NAD synthetase [Nicotiana tabacum]	87.671	146	7.37E-74
illhan--03-R-B23.ab1	NP_193779	NAD-dependent epimerase/dehydratase family [Arabidopsis thaliana]	79.762	84	2.04E-34
illhan--07-R-M17.ab1	NP_188097	NAD-dependent epimerase/dehydratase family [Arabidopsis thaliana]	86.957	46	5.48212E-16
illhan--04-R-K17.ab1	AAL11502	NAD-dependent malate dehydrogenase [Prunus persica]	92.537	67	2.93184E-30
illhan--02-R-K07.ab1	NP_568550	NADH dehydrogenase (ubiquinone), mitochondrial, putative [Arabidopsis thaliana]	73.239	71	1.37E-23
illhan--04-R-L14.ab1	AAF73006	NADP-dependent malic protein [Ricinus communis]	88.406	69	1.28E-28
illhan--05-R-L17.ab1	AAM28891	NADPH oxidase [Nicotiana tabacum]	87.407	135	4.43E-68
illhan--05-R-N17.ab1	AAD51361	NADP-isocitrate dehydrogenase [Citrus limon]	100	115	9.74E-61
illhan--02-R-M07.ab1	AAM34773	nam-like protein 10 [Petunia x hybrida]	86.992	123	2.72513E-61
illhan--05-R-G17.ab1	AAM34766	nam-like protein 3 [Petunia x hybrida]	61.29	31	4.52E-06
illhan--04-R-F15.ab1	AAN62348	NBS-LRR type disease resistance protein [Poncirus trifoliata]	66.129	62	1.92343E-16
illhan--03-R-N01.ab1	AAR19095	NBS-LRR type disease resistance protein RPG1-B [Glycine max]	38.318	107	2.41E-12
illhan--06-R-L07.ab1	AAP30841	nectarin 5 [Nicotiana langsdorffii x Nicotiana sanderae]	70.909	55	8.93E-14
illhan--06-R-B10.ab1	BAB19757	nitrate transporter NRT1-2 [Glycine max]	63.81	105	7.28E-32
illhan--02-R-M16.ab1	NP_567773	No apical meristem (NAM) protein family [Arabidopsis thaliana]	90.647	139	2.92E-73
illhan--04-R-C16	NP_196822	No apical meristem (NAM) protein family [Arabidopsis thaliana]	92.857	28	6.2552E-10

IP : 14.49.138.138, 2017-11-03 13:30:33

.ab1					
illhan--04-R-C07.ab1	NP_181454	nodulin-related protein [Arabidopsis thaliana]	79.032	62	3.03E-22
illhan--07-R-G19.ab1	AAN86274	non-cell-autonomous heat shock cognate protein 70 [Cucurbita maxima]	96.491	57	6.59543E-25
illhan--06-R-M24.ab1	BAA93004	nonclathrin coat protein zeta2-COP [Glycine max]	90.541	74	9.86E-21
illhan--04-R-G01.ab1	Q947C5	Non-symbiotic hemoglobin 1 (Hb1) (GOShi GLB1) [Gossypium hirsutum]	87.919	149	5.34E-70
illhan--07-R-C09.ab1	BAB16427	NtEIG-E80 [Nicotiana tabacum]	68.182	66	3.11E-19
illhan--04-R-B22.ab1	NP_199209	NTF2-containing RNA-binding protein, putative [Arabidopsis thaliana]	67.073	82	1.13E-24
illhan--05-R-E23.ab1	B96804	nucellin-like protein, 27671-25467 [imported] [Arabidopsis thaliana]	80	35	2.77E-11
illhan--04-R-O21.ab1	AAF14582	nucleotide excision repair protein XP-D homolog [Arabidopsis thaliana]	76.364	55	1.38E-16
illhan--05-R-L16.ab1	AAD13527	omega-3 fatty acid desaturase precursor [Vernicia fordii]	86.667	30	4.29E-08
illhan--04-R-E24.ab1	AAD38925	OPDA-reductase homolog [Arabidopsis thaliana]	48.387	93	2.82E-12
illhan--07-R-E06.ab1	AAF13707	osmotin-like protein [Fragaria x ananassa]	76.224	143	1.20441E-63
illhan--06-R-N16.ab1	T12288	O-succinylhomoserine (thiol)-lyase (EC 4.2.99.9) [Mesembryanthemum crystallinum]	83.908	87	8.08457E-70
illhan--05-R-F09.ab1	NP_192203	oxidoreductase, 2OG-Fe(II) oxygenase family [Arabidopsis thaliana]	55.372	121	6.37E-28
illhan--06-R-B21.ab1	NP_566600	oxidoreductase, 2OG-Fe(II) oxygenase family [Arabidopsis thaliana]	70.94	117	3.86E-43
illhan--06-R-C08.ab1	NP_566623	oxidoreductase, 2OG-Fe(II) oxygenase family [Arabidopsis thaliana]	62.353	85	1.78E-27
illhan--06-R-F04.ab1	NP_187728	oxidoreductase, 2OG-Fe(II) oxygenase family [Arabidopsis thaliana]	37.037	108	1.40E-11
illhan--06-R-N14.ab1	NP_174442	oxidoreductase, 2OG-Fe(II) oxygenase family [Arabidopsis thaliana]	56.688	157	2.12E-41
illhan--03-R-P14.ab1	AAD28476	papain-like cysteine protease [Sandersonia aurantiaca]	77.333	75	8.81E-35
illhan--05-R-P20.ab1	AAB94051	PAP-specific phosphatase; HAL2-like protein [Arabidopsis thaliana]	65.591	93	2.77E-23
illhan--05-R-P10.ab1	NP_176378	patatin family [Arabidopsis thaliana]	56.805	169	1.36E-46
illhan--06-R-O08.ab1	CAD59566	PDR-like ABC transporter [Oryza sativa (japonica cultivar-group)]	88.889	108	1.538E-47
illhan--04-R-F14.ab1	NP_192976	pectinesterase - related [Arabidopsis thaliana]	74.026	77	4.19E-24
illhan--03-R-N14.ab1	AAB57670	pectinesterase [Citrus sinensis]	100	152	2.38176E-56
illhan--05-R-D06.ab1	NP_178295	pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana]	61.224	49	6.59E-12
illhan--05-R-G23.ab1	NP_173907	pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana]	56.329	158	2.38729E-48
illhan--06-R-H11.ab1	NP_171699	pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana]	65.263	95	6.80939E-30
illhan--06-R-K13.ab1	CAC84116	peptidylprolyl isomerase (cyclophilin) [Betula pendula]	92.5	80	3.60E-39
illhan--04-R-E07.ab1	AAM65904	peptidylprolyl isomerase-like protein [Arabidopsis thaliana]	86.792	106	1.06E-51
illhan--05-R-F08.ab1	NP_201094	permease 1 - like protein [Arabidopsis thaliana]	86.325	117	7.47646E-53
illhan--07-R-O13.ab1	AAL90751	peroxiredoxin [Populus tremula x Populus tremuloides]	90.278	144	1.49243E-69
illhan--02-R-D03.ab1	BAB84550	peroxisomal ABC transporter [Arabidopsis thaliana]	85.714	35	3.11293E-11
illhan--03-R-B07.ab1	NP_568939	Peter Pan - like protein [Arabidopsis thaliana]	74.286	35	5.88E-08
illhan--06-R-A04.ab1	AAM28274	PFE18 protein [Ananas comosus]	30.625	160	5.87074E-10
illhan--05-R-O24.ab1	NP_567816	pfkB type carbohydrate kinase protein family [Arabidopsis thaliana]	73.913	69	4.70E-23
illhan--04-R-I19.ab1	BAC84952	PHCLF3 [Petunia x hybrida]	92.308	104	4.75E-52
illhan--01-R-G05.ab1	NP_195639	phenylalanyl-trna synthetase - like protein [Arabidopsis thaliana]	94.203	69	1.08E-32
illhan--04-R-E08.ab1	BAA33810	phi-1 [Nicotiana tabacum]	63.717	113	1.08E-24
illhan--04-R-N06.ab1	NP_201231	phi-1-related protein [Arabidopsis thaliana]	82.895	76	1.4659E-32
illhan--06-R-O15.ab1	AAN59904	phosphate transporter [Medicago sativa]	85.714	49	3.50532E-18

IP : 14.49.138.138, 2017-11-03 13:30:33

illhan--05-R-P03.ab1	NP_177043	phosphoenolpyruvate carboxylase -related [Arabidopsis thaliana]	73.881	134	2.66E-50
illhan--06-R-I05.ab1	AAG38144	phosphoglycerate mutase-like protein [Glycine max]	75.342	73	1.26E-28
illhan--02-R-I03.ab1	NP_568146	phospholipid-transporting ATPase 1 (aminophospholipid flippase 1) (magnesium-ATPase) [Arabidopsis thaliana]	59.091	88	5.29E-27
illhan--01-R-D03.ab1	T52337	phosphoprotein phosphatase (EC 3.1.3.16) 2C [imported] [Mesembryanthemum crystallinum]	77.711	166	1.73837E-73
illhan--03-R-F21.ab1	CAB43599	phosphoribosyl pyrophosphate synthase [Spinacia oleracea]	91.86	86	4.25525E-40
illhan--05-R-I23.ab1	CAC35703	photoperiod responsive protein [Solanum tuberosum subsp. andigena]	45.588	68	4.17E-12
illhan--03-R-H23.ab1	AAP03873	photosystem I reaction center subunit X psaK [Nicotiana tabacum]	100	47	8.44E-30
illhan--06-R-A07.ab1	NP_190811	phytoalexin-deficient 4 protein (pad4) [Arabidopsis thaliana]	47.368	133	4.13E-27
illhan--02-R-C06.ab1	NP_174245	plasma membrane associated protein -related [Arabidopsis thaliana]	69.444	36	4.65E-07
illhan--02-R-I01.ab1	BAB40143	plasma membrane intrinsic protein 2-2 [Pyrus communis]	94.175	103	4.86E-51
illhan--02-R-A14.ab1	T03678	plasma membrane protein [Nicotiana tabacum]	74.242	132	9.59E-45
illhan--05-R-H06.ab1	NP_173866	polcalcin (calcium-binding pollen allergen), putative [Arabidopsis thaliana]	39.024	82	1.21E-12
illhan--05-R-L10.ab1	AAF82809	polyadenylation cleavage/specificity factor 100 kDa subunit [Arabidopsis thaliana]	86.885	61	9.52378E-24
illhan--02-R-G09.ab1	BAA31841	polygalacturonase inhibitor (PGIP) [Citrus unshiu]	100	160	5.83E-79
illhan--07-R-H15.ab1	NP_115454	polyprotein [Maize rayado fino virus]	55.769	104	4.47427E-26
illhan--06-R-H21.ab1	NP_175010	polypyrimidine tract-binding protein 1 (PTB) (heterogeneous nuclear ribonucleoprotein I) (hnRNP I), putative [Arabidopsis thaliana]	90.164	122	2.15E-57
illhan--06-R-A09.ab1	AAC16012	polyubiquitin [Elaeagnus umbellata]	100	26	1.66E-07
illhan--07-R-F15.ab1	BAA11024	possible aldehyde decarbonylase [Arabidopsis thaliana]	67.722	158	1.21758E-68
illhan--05-R-J12.ab1	NP_567404	potassium transporter, putative (HAK5/POT5) [Arabidopsis thaliana]	62.162	111	3.59E-31
illhan--04-R-I16.ab1	AAL49994	PR10 protein [Pinus monticola]	38.824	85	2.64E-10
illhan--06-R-K01.ab1	AAL49995	PR10 protein [Pinus monticola]	50	74	1.62062E-15
illhan--03-R-K12.ab1	NP_196724	predicted protein [Arabidopsis thaliana]	82.609	46	4.34E-13
illhan--07-R-H08.ab1	NP_172644	prephenate dehydratase family [Arabidopsis thaliana]	69.027	113	1.23226E-39
illhan--05-R-G16.ab1	Q41062	Preprotein translocase secA subunit, chloroplast precursor [Pisum sativum]	80.488	41	1.86299E-11
illhan--06-R-C17.ab1	F84673	probable beta-1,3-glucanase [imported] [Arabidopsis thaliana]	71.069	159	7.57902E-50
illhan--05-R-H12.ab1	A96836	probable DNA repair protein, 81467-82519 [imported] [Arabidopsis thaliana]	55.263	114	5.24E-24
illhan--02-R-D14.ab1	NP_191174	PROBABLE EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 8 [Arabidopsis thaliana]	54.455	101	9.37E-08
illhan--07-R-C06.ab1	T07944	probable long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) [Brassica napus]	81.159	138	3.27E-64
illhan--03-R-M13.ab1	G86203	probable N-arginine dibasic convertase [imported] [Arabidopsis thaliana]	71.613	155	2.81349E-57
illhan--06-R-A15.ab1	F84435	probable phloem-specific lectin [imported] - Arabidopsis thaliana	51.02	98	1.08E-19
illhan--02-R-L07.ab1	T07857	probable phosphoenolpyruvate carboxykinase (ATP) (EC 4.1.1.49) - rape (fragment) [Brassica napus]	79.646	113	7.09E-48
illhan--02-R-O05.ab1	T03644	probable protein disulfide-isomerase (EC 5.3.4.1) precursor [Nicotiana tabacum]	90.099	101	1.95149E-49
illhan--05-R-D04.ab1	D84727	probable RAD50 DNA repair protein [imported] [Arabidopsis thaliana]	69.182	159	4.79909E-57
illhan--04-R-I05.ab1	T10449	probable serine/threonine-specific protein kinase (EC 2.7.1.-) [Cucumis sativus]	93.22	59	6.06E-15
illhan--05-R-L15.ab1	T03400	probable transcription factor SF3 [Nicotiana tabacum]	94.521	73	4.66991E-36
illhan--07-R-B20.ab1	A96556	probable tRNA-guaninine transglycosylase [imported] [Arabidopsis thaliana]	87.805	82	3.98E-38
illhan--04-R-G11.ab1	H84920	probable Tub family protein [imported] [Arabidopsis thaliana]	93.75	96	1.58032E-47
illhan--04-R-L05.ab1	T03741	probable tyrosine-tRNA ligase (EC 6.1.1.1) [Nicotiana tabacum]	68.056	72	2.11E-23

IP : 14.49.138.138, 2017-11-03 13:30:33

illhan--04-R-E16.ab1	Q9M7N0	Profilin 3 (Pollen allergen Hev b 8.0201) [Hevea brasiliensis]	91.603	131	4.34E-60
illhan--05-R-A03.ab1	AAM64845	prohibitin, putative [Arabidopsis thaliana]	80.303	66	9.86E-21
illhan--07-R-N18.ab1	AAM61502	prolylcarboxypeptidase-like protein [Arabidopsis thaliana]	53.378	148	6.76166E-38
illhan--02-R-L01.ab1	BAB10606	protease-like protein [Arabidopsis thaliana]	74.706	170	2.70E-69
illhan--01-R-B05.ab1	Q04903	Protein farnesyltransferase beta subunit (CAAX farnesyltransferase beta subunit) (RAS proteins prenyltransferase beta) (FTase-beta) [Pisum sativum]	72.449	98	2.02566E-39
illhan--05-R-C06.ab1	NP_172889	protein kinase (APK2a) [Arabidopsis thaliana]	63.636	110	1.02058E-27
illhan--03-R-H07.ab1	AAQ54539	protein kinase [Malus x domestica]	70.27	74	5.98E-18
illhan--03-R-G21.ab1	NP_190047	protein kinase family [Arabidopsis thaliana]	91.228	57	8.99E-26
illhan--03-R-E20.ab1	NP_179344	protein kinase family [Arabidopsis thaliana]	86.42	81	2.77E-35
illhan--05-R-E11.ab1	NP_200643	protein kinase family [Arabidopsis thaliana]	49.565	115	5.12E-22
illhan--04-R-L16.ab1	T04125	protein kinase PK12 (EC 2.7.1.-), ethylene-induced [Nicotiana tabacum]	63.462	104	1.21564E-31
illhan--02-R-P23.ab1	NP_180916	protein kinase -related [Arabidopsis thaliana]	67.925	53	6.70E-14
illhan--07-R-F16.ab1	NP_567945	protein kinase, putative [Arabidopsis thaliana]	97.561	164	2.8083E-92
illhan--05-R-N18.ab1	NP_200515	protein phosphatase 2C, ABI2 [Arabidopsis thaliana]	51.923	156	9.40955E-37
illhan--05-R-F02.ab1	AAO72543	protein tyrosine phosphatase-like protein [Oryza sativa (japonica cultivar-group)]	74.324	74	3.22E-28
illhan--06-R-A19.ab1	AAF64547	purine permease [Arabidopsis thaliana]	63.333	90	4.21E-27
illhan--07-R-J22.ab1	NP_909855	putative cytochrome c oxidase subunit VIa precursor [Oryza sativa (japonica cultivar-group)]	74.074	81	1.28804E-30
illhan--06-R-P19.ab1	AAM92710	putative 40S ribosomal protein S3 [Triticum aestivum]	81.395	86	4.94E-33
illhan--04-R-L01.ab1	BAC42016	putative acyl CoA thioesterase [Arabidopsis thaliana]	54.237	118	4.21652E-30
illhan--07-R-F07.ab1	CAD31841	putative adenosine kinase [Cicer arietinum]	86.842	76	2.26157E-33
illhan--05-R-L08.ab1	AAK59591	putative alanine aminotransferase [Arabidopsis thaliana]	87.629	97	1.72E-41
illhan--04-R-B12.ab1	BAB86175	putative alpha-glucosidase 1 [Oryza sativa (japonica cultivar-group)]	72.727	66	2.77099E-23
illhan--03-R-M16.ab1	AAG52429	putative aminopeptidase; 4537-10989 [Arabidopsis thaliana]	69.159	107	2.83314E-33
illhan--07-R-A22.ab1	AAG52429	putative aminopeptidase; 4537-10989 [Arabidopsis thaliana]	90.991	111	7.44129E-53
illhan--02-R-F19.ab1	AAM67247	putative aminotransferase [Arabidopsis thaliana]	78	100	2.95E-41
illhan--03-R-P05.ab1	AAG24944	putative ammonium transporter AMT1;1 [Lotus japonicus]	74.39	82	3.15E-27
illhan--07-R-C21.ab1	AAL08212	putative ammonium transporter AMT2 [Lotus japonicus]	73.077	130	2.11E-47
illhan--02-R-P21.ab1	AAL69511	putative AMP-binding protein [Arabidopsis thaliana]	72.455	167	2.18E-55
illhan--02-R-I08.ab1	AAL36326	putative arginine methyltransferase pam1 [Arabidopsis thaliana]	79.787	94	5.44E-40
illhan--06-R-P17.ab1	AAF02825	putative ATPase [Arabidopsis thaliana]	82.759	29	3.66E-14
illhan--03-R-K09.ab1	NP_915073	putative ATP-dependent Clp protease regulatory subunit CLPX [Oryza sativa (japonica cultivar-group)]	60.294	136	1.24E-39
illhan--03-R-P04.ab1	AAM63287	putative carboxymethylenebutenolidase [Arabidopsis thaliana]	76.667	90	1.97191E-29
illhan--02-R-G03.ab1	AAK25754	putative chaperon P13.9 [Castanea sativa]	76.531	98	4.51365E-41
illhan--06-R-O01.ab1	AAM61312	putative chaperonin [Arabidopsis thaliana]	96.319	163	1.39E-83
illhan--07-R-D05.ab1	NP_922868	putative cinnamoyl-CoA reductase [Oryza sativa (japonica cultivar-group)]	46.465	99	2.76E-15
illhan--03-R-O01.ab1	NP_913038	putative coatmer beta subunit (beta-coat protein) (beta-COP) [Oryza sativa (japonica cultivar-group)]	85.207	169	1.08E-81
illhan--05-R-D11.ab1	AAN40022	putative cytidine deaminase [Zea mays]	90.351	114	2.83425E-44
illhan--07-R-E12.ab1	NP_914759	putative cytochrome c oxidase subunit 6b-1 [Oryza sativa (japonica cultivar-group)]	92.727	55	6.34341E-28
illhan--04-R-C24	AAM62810	putative diacylglycerol kinase [Arabidopsis thaliana]	57.895	57	3.8053E-09

IP : 14.49.138.138, 2017-11-03 13:30:33

.ab1					
illhan--03-R-M07.ab1	NP_916401	putative diacylglycerol kinase [Oryza sativa (japonica cultivar-group)]	60.976	82	3.21E-16
illhan--03-R-L02.ab1	AAP85544	putative DIM-like protein [Glycine max]	98.165	109	4.43295E-58
illhan--03-R-G14.ab1	NP_910169	putative disulfide-isomerase precursor [Oryza sativa]	79.412	34	2.04E-07
illhan--02-R-F16.ab1	AAL86003	putative E2, ubiquitin-conjugating enzyme UBC7 [Arabidopsis thaliana]	87.586	145	6.59E-70
illhan--04-R-A22.ab1	BAC83252	putative eukaryotic peptide chain release factor subunit 1-3 (eRF1-3) [Oryza sativa (japonica cultivar-group)]	91.176	68	3.46E-31
illhan--06-R-G05.ab1	AAN05494	Putative F-box protein [Oryza sativa (japonica cultivar-group)]	64.22	109	2.19E-36
illhan--03-R-H18.ab1	AAK76701	putative fibrillarin 2 protein AtFib2 [Arabidopsis thaliana]	93.939	99	1.00E-46
illhan--04-R-E15.ab1	NP_921092	putative Glucan 1,3-beta-glucosidase precursor [Oryza sativa (japonica cultivar-group)]	66.667	138	2.55E-50
illhan--07-R-F10.ab1	AAO42218	putative G-protein beta subunit [Arabidopsis thaliana]	84	125	5.88243E-58
illhan--06-R-A01.ab1	AAF21204	putative GTPase activating protein [Arabidopsis thaliana]	81.667	120	5.24864E-51
illhan--05-R-E22.ab1	AAQ72787	putative GTP-binding protein [Cucumis sativus]	97.546	163	5.86E-90
illhan--07-R-M08.ab1	AAM64677	putative HesB-like protein [Arabidopsis thaliana]	97.619	42	1.73149E-17
illhan--07-R-G06.ab1	NP_912583	Putative leucine-rich repeat transmembrane protein kinase [Oryza sativa (japonica cultivar-group)]	87.037	54	1.48006E-20
illhan--06-R-H09.ab1	AAM62848	putative membrane-associated salt-inducible protein [Arabidopsis thaliana]	53.125	96	3.71E-21
illhan--04-R-F10.ab1	AAK43892	putative methylenetetrahydrofolate reductase [Arabidopsis thaliana]	82.456	57	6.69E-22
illhan--06-R-K18.ab1	NP_915208	putative MRP-like ABC transporter [Oryza sativa (japonica cultivar-group)]	72.785	158	5.8529E-63
illhan--02-R-I05.ab1	AAF23291	putative MYB-related protein [Arabidopsis thaliana]	82.222	45	6.57E-16
illhan--01-R-G06.ab1	BAD03666	putative Na+/K+/Cl-cotransport protein [Oryza sativa (japonica cultivar-group)]	90.683	161	4.31E-82
illhan--01-R-A01.ab1	AAF02110	putative NADPH-ferrihemoprotein reductase [Arabidopsis thaliana]	64.706	51	5.62E-11
illhan--04-R-I09.ab1	NP_917385	putative nifU-like protein [Oryza sativa (japonica cultivar-group)]	73.885	157	2.08169E-60
illhan--07-R-G22.ab1	NP_916104	putative nitrate transporter [Oryza sativa (japonica cultivar-group)]	55.814	43	6.35564E-09
illhan--04-R-B14.ab1	AAL73534	putative nucleolar protein [Sorghum bicolor]	70.297	101	5.35758E-35
illhan--02-R-D01.ab1	NP_920923	putative nucleosid phosphatase [Oryza sativa (japonica cultivar-group)]	59.406	101	1.21E-10
illhan--06-R-A06.ab1	BAD03784	putative p23 co-chaperone [Oryza sativa (japonica cultivar-group)]	80	100	2.75817E-39
illhan--05-R-M21.ab1	NP_916676	putative PGPD14 protein (pollen germination related protein) [Oryza sativa (japonica cultivar-group)]	61.224	98	1.07659E-32
illhan--03-R-E12.ab1	AAN77002	putative phosphatidylcholine acyltransferase [Medicago truncatula]	80.303	132	8.63E-62
illhan--03-R-G02.ab1	AAP21414	putative polyprotein [Oryza sativa (japonica cultivar-group)]	56.604	106	9.78648E-29
illhan--07-R-H22.ab1	BAB90375	putative polyprotein [Oryza sativa (japonica cultivar-group)]	39.024	123	3.61903E-23
illhan--03-R-F05.ab1	AAL32574	putative protein phosphatase-2C (PP2C) [Arabidopsis thaliana]	65.812	117	8.60E-36
illhan--06-R-M12.ab1	NP_504775	putative protein, with 4 coiled coil-4 domains (5H491) [Caenorhabditis elegans]	33.636	110	2.09E-07
illhan--04-R-O07.ab1	AAP45176	putative receptor protein kinase [Solanum bulbocastanum]	52.381	42	1.75805E-06
illhan--07-R-K09.ab1	NP_919913	putative receptor-like protein kinase [Oryza sativa (japonica cultivar-group)]	35.455	110	5.02049E-13
illhan--02-R-N24.ab1	AAR01683	putative ribosomal protein L13a [Oryza sativa (japonica cultivar-group)]	87.963	108	1.32E-49
illhan--07-R-K08.ab1	AAP05800	putative ribosomal protein L19 [Oryza sativa (japonica cultivar-group)]	86.325	117	2.32934E-30
illhan--03-R-P02.ab1	NP_918377	putative RIC1_ORYSA RAS-RELATED PROTEIN RIC1 [Oryza sativa (japonica cultivar-group)]	99.16	119	2.32E-62
illhan--06-R-G10.ab1	AAF30307	putative RING zinc finger protein [Arabidopsis thaliana]	71.795	117	6.78E-46
illhan--02-R-N03.ab1	AAM19707	putative RING zinc finger protein-like protein [Thellungiella halophila]	63.38	71	9.52E-24
illhan--05-R-H16.ab1	BAD03017	putative RNA recognition motif (RRM)-containing protein [Oryza sativa (japonica cultivar-group)]	70.455	44	6.14E-12

IP : 14.49.138.138, 2017-11-03 13:30:33

illhan--05-R-G06.ab1	AAM63845	putative signal sequence receptor, alpha subunit (SSR-alpha) [Arabidopsis thaliana]	57.746	142	4.41372E-29
illhan--02-R-H10.ab1	NP_916320	putative transcription initiation factor [Oryza sativa (japonica cultivar-group)]	54	100	6.92E-19
illhan--02-R-J16.ab1	BAC22427	putative translation elongation factor eEF-1 beta' chain [Oryza sativa (japonica cultivar-group)]	94.253	87	1.40E-40
illhan--04-R-J23.ab1	AAL87276	putative translation initiation factor IF-2 [Arabidopsis thaliana]	73.529	34	1.08411E-08
illhan--02-R-B21.ab1	AAP40643	putative triose-phosphate isomerase [Gossypium barbadense]	88.889	90	5.00E-41
illhan--04-R-O24.ab1	BAA11389	putative ubiquitin extension protein [Brassica rapa]	98.246	57	3.10E-27
illhan--04-R-L22.ab1	AAM64897	putative ubiquitin fusion-degradation protein [Arabidopsis thaliana]	89.655	29	1.31E-09
illhan--02-R-B04.ab1	AAK16194	putative UDP-glucose dehydrogenase [Oryza sativa (japonica cultivar-group)]	87.719	57	1.69E-23
illhan--02-R-E06.ab1	AAL85977	putative uridine kinase [Arabidopsis thaliana]	89.362	94	1.41E-43
illhan--06-R-E01.ab1	AAO38447	putative zinc binding protein [Oryza sativa (japonica cultivar-group)]	75.862	58	6.51E-21
illhan--03-R-C13.ab1	BAC42445	putative zinc finger protein [Arabidopsis thaliana]	65.278	72	1.57E-26
illhan--05-R-O01.ab1	BAC23043	pyruvate decarboxylase [Solanum tuberosum]	89.873	158	2.87E-76
illhan--06-R-P04.ab1	NP_171617	pyruvate dehydrogenase E1 alpha subunit [Arabidopsis thaliana]	94.872	39	3.61E-15
illhan--07-R-O12.ab1	NP_566976	pyruvate kinase, putative [Arabidopsis thaliana]	84.564	149	4.80098E-68
illhan--05-R-G13.ab1	AAO38223	RCa12 [Manihot esculenta]	67.5	40	8.65E-09
illhan--07-R-F23.ab1	NP_188224	receptor kinase -related [Arabidopsis thaliana]	54.688	128	2.56757E-31
illhan--06-R-F22.ab1	BAB02287	receptor protein-like [Arabidopsis thaliana]	74.627	67	8.4381E-25
illhan--05-R-J18.ab1	BAC07504	receptor-like protein kinase [Nicotiana tabacum]	87.879	99	1.52E-46
illhan--04-R-O10.ab1	AAK28315	receptor-like protein kinase 4 [Arabidopsis thaliana]	59.292	113	2.00E-34
illhan--03-R-M06.ab1	NP_197965	receptor-related protein kinase - like [Arabidopsis thaliana]	45.714	70	1.21E-10
illhan--03-R-P24.ab1	NP_197965	receptor-related protein kinase - like [Arabidopsis thaliana]	70.303	165	1.19E-61
illhan--04-R-D18.ab1	NP_179503	receptor-related protein kinase [Arabidopsis thaliana]	56.738	141	3.14091E-35
illhan--05-R-K12.ab1	NP_849928	receptor-related protein kinase [Arabidopsis thaliana]	70.769	65	3.38731E-21
illhan--07-R-A18.ab1	BAB69675	replication factor C 40kDa subunit [Oryza sativa (japonica cultivar-group)]	87.805	164	1.34672E-78
illhan--06-R-B13.ab1	AAC02202	resistance protein candidate [Lactuca sativa]	37.5	128	2.46E-16
illhan--02-R-O01.ab1	AAP80667	ribosomal Pr 117 [Triticum aestivum]	100	94	2.51E-49
illhan--06-R-K12.ab1	NP_904140	ribosomal protein L2 [Amborella trichopoda]	51.923	52	8.06E-07
illhan--06-R-O11.ab1	AAM64816	Ribosomal protein L7Ae-like [Arabidopsis thaliana]	97.802	91	2.00E-34
illhan--04-R-F20.ab1	NP_568396	ring-box protein - like [Arabidopsis thaliana]	89.655	58	2.14E-19
illhan--04-R-I11.ab1	AAG49034	ripening regulated protein DDTFR10 [Lycopersicon esculentum]	83.529	85	2.51E-26
illhan--03-R-D04.ab1	NP_196604	ripening regulated protein, putative [Arabidopsis thaliana]	64.035	114	1.04E-35
illhan--06-R-D18.ab1	BAB08363	RNA and export factor binding protein 2-I-like protein [Arabidopsis thaliana]	57.143	147	2.49E-32
illhan--02-R-J14.ab1	CAC01237	RNA Binding Protein 45 [Nicotiana plumbaginifolia]	76.471	34	4.50E-10
illhan--03-R-F03.ab1	NP_567192	RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana]	69.231	65	2.0398E-15
illhan--04-R-P10.ab1	NP_568011	RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana]	64.706	68	1.18E-18
illhan--07-R-N02.ab1	NP_182201	RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana]	82.609	46	9.35107E-16
illhan--02-R-A22.ab1	CAD22099	RNase Z [Arabidopsis thaliana]	84.444	45	5.58E-15
illhan--06-R-C12.ab1	AAF19827	RUB1 conjugating enzyme [Arabidopsis thaliana]	83.553	152	2.19E-73
illhan--07-R-F03.ab1	C96597	Rubisco subunit binding-protein beta subunit [imported] [Arabidopsis thaliana]	50	92	8.47733E-09
illhan--01-R-B01	AAK43840	S18.A ribosomal protein [Arabidopsis thaliana]	98.734	79	6.12E-32

IP : 14.49.138.138, 2017-11-03 13:30:33

.ab1					
illhan--04-R-M04.ab1	CAB89082	S6 ribosomal protein kinase [Asparagus officinalis]	73.451	113	5.69535E-42
illhan--06-R-B16.ab1	AAM44307	S-adenosylmethionine decarboxylase [x Citrofortunella mitis]	96.364	110	1.71E-57
illhan--04-R-M16.ab1	AAP13994	S-adenosylmethionine synthetase [Litchi chinensis]	92.105	76	1.02E-37
illhan--02-R-E13.ab1	AAF36688	secretory carrier membrane protein [Oryza sativa]	84.615	65	9.97E-26
illhan--05-R-A15.ab1	NP_174485	secretory carrier membrane protein -related [Arabidopsis thaliana]	86.885	61	4.28E-24
illhan--07-R-I21.ab1	NP_174485	secretory carrier membrane protein -related [Arabidopsis thaliana]	69.281	153	2.02646E-50
illhan--06-R-D03.ab1	AAD51625	seed maturation protein PM37 [Glycine max]	87.407	135	1.00E-65
illhan--01-R-J01.ab1	F85430	serine C-palmitoyltransferase like protein [imported] [Arabidopsis thaliana]	71.084	83	3.87E-25
illhan--02-R-M10.ab1	AAL23677	Serine/threonine Kinase [Persea americana]	82.051	78	2.56669E-45
illhan--02-R-F11.ab1	AAM65833	serine/threonine protein kinase [Arabidopsis thaliana]	77.193	57	6.63E-19
illhan--02-R-P16.ab1	AAO48744	serine/threonine protein kinase [Oryza sativa (japonica cultivar-group)]	97.727	44	1.74E-17
illhan--04-R-E03.ab1	AAN84503	serine/threonine protein kinase [Oryza sativa (japonica cultivar-group)]	90.854	164	1.54E-82
illhan--06-R-G03.ab1	NP_191781	serine/threonine protein kinase, putative [Arabidopsis thaliana]	87.654	81	7.28E-32
illhan--02-R-C22.ab1	AAO59488	ser-thr protein kinase [Gossypium hirsutum]	64.646	99	3.70019E-33
illhan--07-R-A11.ab1	NP_198095	signal peptidase [Arabidopsis thaliana]	88.596	114	6.09E-55
illhan--05-R-K19.ab1	NP_175669	signal peptidase subunit -related [Arabidopsis thaliana]	81.25	80	9.50E-32
illhan--05-R-O08.ab1	P49964	SIGNAL RECOGNITION PARTICLE 19 KD PROTEIN (SRP19) [Oryza sativa]	72.152	79	5.76449E-29
illhan--03-R-N21.ab1	BAA90501	similar to a putative RING zinc finger protein of Arabidopsis thaliana (AC003672) [Oryza sativa]	58.559	111	1.56E-34
illhan--04-R-A09.ab1	F84552	similar to Mlo proteins from H. vulgare [imported] [Arabidopsis thaliana]	88.636	44	3.08E-28
illhan--06-R-J22.ab1	AAF02840	Similar to serine/threonine kinases [Arabidopsis thaliana]	68.421	57	1.62828E-15
illhan--04-R-G19.ab1	AAN03473	small GTP-binding protein [Glycine max]	81.915	94	1.01E-38
illhan--07-R-K23.ab1	NP_179464	small nuclear ribonucleo protein E -related [Arabidopsis thaliana]	95.455	66	5.73738E-29
illhan--02-R-B10.ab1	NP_181909	small nuclear ribonucleo protein polypeptide F -related [Arabidopsis thaliana]	88.679	53	7.55E-21
illhan--07-R-G24.ab1	NP_177812	Sm-related protein [Arabidopsis thaliana]	88.66	97	1.08827E-30
illhan--05-R-L04.ab1	NP_179466	SNF2domain/helicase domain-containing protein [Arabidopsis thaliana]	64.557	158	5.50E-45
illhan--04-R-M18.ab1	AAK27314	sodium/proton exchanger [Citrus x paradisi]	72.973	37	6.63E-09
illhan--05-R-B04.ab1	NP_199759	sodium-inducible calcium-binding protein [Arabidopsis thaliana]	78.873	71	3.13967E-24
illhan--05-R-L13.ab1	AAC17971	soluble starch synthase [Chlamydomonas reinhardtii]	53.226	62	1.74E-09
illhan--02-R-G02.ab1	NP_177188	spermidine synthase -related [Arabidopsis thaliana]	63.953	86	3.55E-23
illhan--07-R-E15.ab1	NP_850468	squamosa-promoter binding protein -related [Arabidopsis thaliana]	58.282	163	3.14844E-43
illhan--03-R-E13.ab1	NP_195990	S-receptor kinase - like protein [Arabidopsis thaliana]	43.966	116	3.17E-19
illhan--06-R-M08.ab1	CAB40749	starch branching enzyme II [Solanum tuberosum]	47.009	117	1.46182E-13
illhan--06-R-K24.ab1	AAG01535	stellacyanin-like protein CASLP1 precursor [Capsicum annuum]	62.264	53	4.15E-14
illhan--01-R-N04.ab1	AAF97824	Strong similarity to EF-1-alpha-related GTP-binding protein (SUP1) from Nicotiana tabacum gb|L38828 and is a member of the elongation factor Tu PF|00009 family. ESTs gb|W43190, gb|W43332, gb|A1995372, gb|AV563399, gb|AV549134, gb|AV554843, gb|AV527836 come from this gene. [Arabidopsis thaliana]	57.862	159	3.57562E-36
illhan--04-R-M15.ab1	AAO12871	submergence induced protein 2-like [Vitis vinifera]	75.342	73	6.11E-28
illhan--02-R-K15.ab1	AAM65047	succinate dehydrogenase iron-protein subunit-like [Arabidopsis thaliana]	94.186	86	2.58E-45
illhan--02-R-O07.ab1	AAK77126	succinate dehydrogenase subunit 3 [Lycopersicon esculentum]	83.333	108	6.43E-41

IP : 14.49.138.138, 2017-11-03 13:30:33

illhan--05-R-N01.ab1	AAN86619	succinyl-CoA ligase alpha subunit [Lycopersicon esculentum]	91.228	114	1.32E-44
illhan--02-R-F06.ab1	AAM65450	succinyl-CoA synthetase, alpha subunit [Arabidopsis thaliana]	74.312	109	2.02E-32
illhan--04-R-G16.ab1	BAA88905	sucrose synthase [Citrus unshiu]	61.688	154	7.28E-42
illhan--06-R-B05.ab1	AAN86062	sugar transporter [Citrus unshiu]	100	38	1.16E-13
illhan--02-R-C16.ab1	CAA73188	superoxide dismutase [Arabidopsis thaliana]	69.792	96	3.61065E-31
illhan--05-R-E02.ab1	NP_173859	T-complex protein 1, epsilon subunit/chaperonin [Arabidopsis thaliana]	94.792	96	7.16E-83
illhan--07-R-K17.ab1	AAN39330	telomere binding protein TBP1 [Nicotiana glutinosa]	52.747	91	1.63206E-07
illhan--05-R-J22.ab1	NP_567663	tetratricopeptide repeat (TPR)-containing protein [Arabidopsis thaliana]	65.359	153	4.57E-26
illhan--02-R-H21.ab1	NP_180524	thiamin biosynthesis protein -related [Arabidopsis thaliana]	53.247	77	9.69E-13
illhan--03-R-A23.ab1	O23787	Thiazole biosynthetic enzyme, chloroplast precursor [Citrus sinensis]	100	39	1.80E-14
illhan--07-R-N09.ab1	O23787	Thiazole biosynthetic enzyme, chloroplast precursor [Citrus sinensis]	99.291	141	4.63936E-71
illhan--01-R-C03.ab1	NP_199648	thioesterase family [Arabidopsis thaliana]	77.6	125	9.36936E-48
illhan--02-R-M15.ab1	NP_196046	thioredoxin family [Arabidopsis thaliana]	76.316	38	3.30E-11
illhan--02-R-M17.ab1	AAD33596	thioredoxin h [Hevea brasiliensis]	70.833	72	3.47E-23
illhan--03-R-B11.ab1	AAO12855	thioredoxin h [Pisum sativum]	66.667	105	6.65E-38
illhan--04-R-F06.ab1	DAA00874	TPA: PDR6 ABC transporter [Arabidopsis thaliana]	76.398	161	2.15506E-68
illhan--02-R-B05.ab1	NP_566519	transducin / WD-40 repeat protein family [Arabidopsis thaliana]	71.91	89	1.01E-30
illhan--05-R-C16.ab1	NP_566620	transducin / WD-40 repeat protein family [Arabidopsis thaliana]	72.222	36	1.80446E-06
illhan--06-R-N17.ab1	NP_566620	transducin / WD-40 repeat protein family [Arabidopsis thaliana]	73.469	147	3.28E-61
illhan--07-R-D18.ab1	NP_563675	transducin / WD-40 repeat protein family [Arabidopsis thaliana]	57.6	125	1.37E-30
illhan--03-R-B16.ab1	Q9ZSW9	Translationally controlled tumor protein homolog (TCTP) [Hevea brasiliensis]	97.701	87	1.05E-32
illhan--05-R-M12.ab1	NP_568535	transmembrane protein FT27/PFT27-related [Arabidopsis thaliana]	90.09	111	2.53E-37
illhan--01-R-O05.ab1	NP_179250	TRAP protein -related [Arabidopsis thaliana]	72.222	36	6.82E-09
illhan--05-R-B02.ab1	AAO62728	truncated NBS-LRR resistance-like protein isoform JA88 [Phaseolus vulgaris]	41.304	138	9.47524E-13
illhan--03-R-A20.ab1	AAM65526	tryptophan synthase alpha chain [Arabidopsis thaliana]	81.707	82	9.11E-32
illhan--06-R-I20.ab1	AAG08959	tuber-specific and sucrose-responsive element binding factor [Solanum tuberosum]	89.216	102	2.77E-51
illhan--07-R-P15.ab1	NP_197478	tubulin alpha-3/alpha-5 chain (TUA3) [Arabidopsis thaliana]	94.958	119	5.97743E-63
illhan--06-R-D06.ab1	BAA92699	type 2A protein phosphatase-3 [Vicia faba]	100	28	5.87E-10
illhan--06-R-J21.ab1	NP_190636	U1 small nuclear ribonucleoprotein 70 (U1-70k) [Arabidopsis thaliana]	82.353	51	2.12095E-16
illhan--04-R-A23.ab1	NP_176564	U3 small nucleolar ribonucleo proteinprotein -related [Arabidopsis thaliana]	82.759	29	9.18E-08
illhan--05-R-M10.ab1	S28420	ubiquitin / ribosomal protein CEP52 [Nicotiana sylvestris]	98.305	118	8.63E-62
illhan--06-R-J17.ab1	S57619	ubiquitin conjugating enzyme [Lycopersicon esculentum]	78.378	74	4.78E-28
illhan--02-R-E12.ab1	AAF73016	ubiquitin conjugating protein [Avicennia marina]	97.037	135	8.71E-75
illhan--07-R-H02.ab1	AAF73016	ubiquitin conjugating protein [Avicennia marina]	98.374	123	5.78697E-69
illhan--01-R-M02.ab1	AAG42754	ubiquitin-specific protease 12 [Arabidopsis thaliana]	34.737	95	1.24E-06
illhan--07-R-D19.ab1	AAG42757	ubiquitin-specific protease 16 [Arabidopsis thaliana]	72.561	164	5.71126E-61
illhan--06-R-N11.ab1	BAB40967	UDP-D-glucuronate carboxy-lyase [Pisum sativum]	89.796	98	1.06E-35
illhan--07-R-P07.ab1	Q96558	UDP-glucose 6-dehydrogenase (UDP-Glc dehydrogenase) (UDP-GlcDH) (UDPGDH) [Glycine max]	88.506	87	6.43093E-41
illhan--04-R-H09.ab1	NP_197053	UDP-glucose dehydrogenase-related protein [Arabidopsis thaliana]	95.536	112	7.40E-58
illhan--03-R-I13.	AAL32657	UDP-glucose glucosyltransferase [Arabidopsis thaliana]	69.421	121	1.5374E-47

IP : 14.49.138.138, 2017-11-03 13:30:33

ab1					
illhan--06-R-B09.ab1	AAL33919	UDP-glucose pyrophosphorylase [Amorpha fruticosa]	73.913	46	4.90262E-12
illhan--04-R-G03.ab1	AAF61647	UDP-glucose:salicylic acid glucosyltransferase [Nicotiana tabacum]	50.407	123	1.51E-26
illhan--04-R-O16.ab1	AAF61647	UDP-glucose:salicylic acid glucosyltransferase [Nicotiana tabacum]	56.338	71	4.48E-18
illhan--06-R-J10.ab1	NP_196793	UDP-glycosyltransferase family [Arabidopsis thaliana]	58.333	120	3.1324E-32
illhan--04-R-G15.ab1	NP_189355	uracil phosphoribosyltransferase -related [Arabidopsis thaliana]	56.061	66	4.03E-08
illhan--07-R-K04.ab1	NP_180994	urease accessory protein -related [Arabidopsis thaliana]	95.385	65	3.28725E-58
illhan--07-R-F13.ab1	Q9SM09	Vacuolar ATP synthase catalytic subunit A (V-ATPase A subunit) (Vacuolar proton pump alpha subunit) (V-ATPase 69 kDa subunit) [Citrus unshiu]	100	145	3.71201E-84
illhan--04-R-D01.ab1	Q9MB46	Vacuolar ATP synthase subunit E (V-ATPase E subunit) (Vacuolar proton pump E subunit) [Citrus unshiu]	100	46	4.56E-18
illhan--02-R-C21.ab1	BAA75516	vacuolar H+-ATPase c subunit [Citrus unshiu]	100	125	2.26E-44
illhan--02-R-P24.ab1	T00044	vacuolar sorting receptor protein homolog PV72 [Cucurbita cv. Kurokawa Amakuri]	70.588	153	1.08E-54
illhan--03-R-O10.ab1	AAQ04608	valencene synthase [Citrus sinensis]	100	120	2.42681E-64
illhan--02-R-O08.ab1	NP_199529	VAMP (vesicle-associated membrane protein)-associated protein family [Arabidopsis thaliana]	84.211	95	2.61E-42
illhan--03-R-L04.ab1	AAB61590	VVTL1 [Vitis vinifera]	61.017	59	5.47E-14
illhan--03-R-B14.ab1	BAA89230	wts2L [Citrullus lanatus]	40.58	138	1.69E-14
illhan--02-R-N05.ab1	NP_179069	xyloglucan endotransglycosylase, putative [Arabidopsis thaliana]	71.812	149	5.89654E-66
illhan--03-R-A13.ab1	NP_568404	zinc finger (C3HC4-type RING finger) protein family [Arabidopsis thaliana]	51.563	64	1.51275E-10
illhan--06-R-L15.ab1	NP_178396	zinc finger (C3HC4-type RING finger) protein family [Arabidopsis thaliana]	73.438	64	2.04534E-18
illhan--02-R-D04.ab1	NP_189461	zinc finger protein (PMZ) -related [Arabidopsis thaliana]	53.774	106	4.78E-28
illhan--05-R-E12.ab1	NP_566877	zinc finger protein [Arabidopsis thaliana]	85.256	156	3.87E-70
illhan--02-R-E14.ab1	AAK37761	zinc transporter protein ZIP1 [Glycine max]	79.348	92	1.68E-30
illhan--02-R-G11.ab1	AAN12917	At1g15130/F9L1_7 [Arabidopsis thaliana]	77.381	84	2.88238E-54
illhan--06-R-E07.ab1	AAL24250	At1g19180/T29M8_5 [Arabidopsis thaliana]	43.902	82	1.24963E-07
illhan--06-R-F03.ab1	AAM19821	At1g24050/T23E23_11 [Arabidopsis thaliana]	55.319	141	3.23E-37
illhan--06-R-L09.ab1	AAL31904	At1g53570/F22G10_18 [Arabidopsis thaliana]	60.465	86	1.61E-22
illhan--02-R-N12.ab1	AAO42832	At2g03440 [Arabidopsis thaliana]	51.613	93	6.44E-06
illhan--06-R-E13.ab1	AAO64812	At2g03510 [Arabidopsis thaliana]	83.974	156	7.42E-77
illhan--07-R-E23.ab1	AAM19795	At2g04030/F3C11.14 [Arabidopsis thaliana]	64.844	128	1.09238E-30
illhan--02-R-N06.ab1	AAK63974	At2g16900/F12A24.8 [Arabidopsis thaliana]	41.25	80	1.02226E-09
illhan--07-R-G08.ab1	AAO42809	At2g18100 [Arabidopsis thaliana]	42.308	78	4.72624E-07
illhan--02-R-I09.ab1	AAK73974	At2g42220/T24P15.13 [Arabidopsis thaliana]	71.812	149	4.34E-58
illhan--02-R-O21.ab1	AAK60318	AT3g03980/T11I18_9 [Arabidopsis thaliana]	74.713	87	7.13E-32
illhan--03-R-M21.ab1	AAL50082	AT3g22845/MWI23_22 [Arabidopsis thaliana]	88.35	103	1.51E-47
illhan--07-R-A19.ab1	AAL24175	AT3g27570/MMJ24_12 [Arabidopsis thaliana]	54.887	133	8.69E-38
illhan--02-R-K13.ab1	AAG40343	AT4g13930 [Arabidopsis thaliana]	84.884	86	3.57562E-36
illhan--02-R-N01.ab1	AAL07001	AT4g15470/dl3775w [Arabidopsis thaliana]	68.125	160	3.83E-41
illhan--03-R-B15.ab1	AAL77705	AT4g18710/F28A21_120 [Arabidopsis thaliana]	93.878	49	8.85E-19
illhan--02-R-I18.ab1	AAL57648	AT4g23460/F16G20_160 [Arabidopsis thaliana]	71.605	81	1.36559E-30
illhan--07-R-J11.ab1	AAK91357	AT5g40810/MHK7_4 [Arabidopsis thaliana]	80.159	126	2.56962E-53
illhan--04-R-J10.	AAK83629	AT5g41970/MJC20_7 [Arabidopsis thaliana]	81.579	76	5.57E-32

IP : 14.49.138.138, 2017-11-03 13:30:33

ab1					
illhan--06-R-E05.ab1	AAK32788	AT5g46190/MCL19_25 [Arabidopsis thaliana]	51.471	136	5.84357E-26
illhan--06-R-M17.ab1	AAL31256	AT5g51140/MWD22_8 [Arabidopsis thaliana]	71.875	32	7.83E-10
illhan--04-R-M19.ab1	AAL57666	AT5g53140/MFH8_8 [Arabidopsis thaliana]	63.265	49	1.30786E-09
illhan--04-R-H23.ab1	AAG01126	BAC19.11 [Lycopersicon esculentum]	83.704	135	9.19E-70
illhan--02-R-C14.ab1	AAG01117	BAC19.2 [Lycopersicon esculentum]	33.333	96	5.04E-06
illhan--07-R-B10.ab1	NP_915121	B1078G07.14 [Oryza sativa (japonica cultivar-group)]	60	145	1.41E-43
illhan--04-R-M20.ab1	NP_608835	CG15438-PA [Drosophila melanogaster]	42.105	57	8.40713E-06
illhan--04-R-A11.ab1	NP_910543	EST AU065533(C2174) corresponds to a region of the predicted gene.~Similar to Homo sapiens splicing factor Prp8 mRNA, complete cds.(AF092565) [Oryza sativa (japonica cultivar-group)]	85.057	87	7.60E-42
illhan--03-R-P19.ab1	BAA82391	ESTs C99174(E10437),D22295(C10709) correspond to a region of the predicted gene.~Similar to Arabidopsis thaliana BAC genomic sequence. (AC005314) [Oryza sativa (japonica cultivar-group)]	58.904	146	1.24E-39
illhan--01-R-C01.ab1	NP_566048	expressed protein [Arabidopsis thaliana]	52.143	140	2.66E-23
illhan--02-R-C13.ab1	NP_188550	expressed protein [Arabidopsis thaliana]	64.567	127	4.66E-44
illhan--02-R-D06.ab1	NP_849979	expressed protein [Arabidopsis thaliana]	52.439	82	8.04E-15
illhan--02-R-G01.ab1	NP_566574	expressed protein [Arabidopsis thaliana]	73.504	117	2.04E-41
illhan--02-R-J15.ab1	NP_567918	expressed protein [Arabidopsis thaliana]	79.121	91	1.20E-34
illhan--02-R-J21.ab1	NP_178872	expressed protein [Arabidopsis thaliana]	73.846	65	3.22626E-19
illhan--02-R-P05.ab1	NP_176566	expressed protein [Arabidopsis thaliana]	56.78	118	9.20E-27
illhan--03-R-C24.ab1	NP_201385	expressed protein [Arabidopsis thaliana]	59.06	149	2.70692E-42
illhan--03-R-G17.ab1	NP_192395	expressed protein [Arabidopsis thaliana]	80.556	72	6.24E-28
illhan--03-R-L11.ab1	NP_850432	expressed protein [Arabidopsis thaliana]	69.048	42	8.63E-08
illhan--04-R-A05.ab1	NP_173069	expressed protein [Arabidopsis thaliana]	79.817	109	5.56E-40
illhan--04-R-G12.ab1	NP_175542	expressed protein [Arabidopsis thaliana]	62.025	79	5.78E-21
illhan--04-R-I01.ab1	NP_186920	expressed protein [Arabidopsis thaliana]	81.707	82	4.7025E-26
illhan--04-R-J01.ab1	AAO29946	expressed protein [Arabidopsis thaliana]	52	100	8.89E-20
illhan--04-R-M08.ab1	NP_197954	expressed protein [Arabidopsis thaliana]	52.273	44	5.14302E-06
illhan--04-R-O04.ab1	NP_196665	expressed protein [Arabidopsis thaliana]	70.303	165	6.50E-57
illhan--05-R-H10.ab1	NP_683424	expressed protein [Arabidopsis thaliana]	54.93	71	9.48E-13
illhan--05-R-H23.ab1	AAB87596	expressed protein [Arabidopsis thaliana]	72.973	74	3.79475E-28
illhan--05-R-M13.ab1	NP_568659	expressed protein [Arabidopsis thaliana]	55.769	52	4.59E-10
illhan--06-R-L03.ab1	NP_564863	expressed protein [Arabidopsis thaliana]	44.172	163	2.22E-25
illhan--06-R-O09.ab1	NP_196112	expressed protein [Arabidopsis thaliana]	67.059	85	5.96531E-26
illhan--07-R-D20.ab1	NP_198128	expressed protein [Arabidopsis thaliana]	72.222	54	1.30483E-17
illhan--07-R-F24.ab1	NP_564113	expressed protein [Arabidopsis thaliana]	66.667	87	1.96657E-26
illhan--07-R-J04.ab1	NP_201247	expressed protein [Arabidopsis thaliana]	51.923	104	3.60201E-23
illhan--07-R-J12.ab1	NP_172074	expressed protein [Arabidopsis thaliana]	80.392	51	9.12053E-19
illhan--07-R-K01.ab1	NP_850886	expressed protein [Arabidopsis thaliana]	57.303	89	2.25615E-25
illhan--07-R-L01.ab1	NP_567146	expressed protein [Arabidopsis thaliana]	56.028	141	4.26959E-35
illhan--07-R-P14.ab1	NP_194549	expressed protein [Arabidopsis thaliana]	60	130	1.1198E-40
illhan--01-R-F05	NP_566048	expressed protein [Arabidopsis thaliana]	83.333	66	7.46E-41

IP : 14.49.138.138, 2017-11-03 13:30:33

.ab1					
illhan--01-R-K04.ab1	NP_171807	expressed protein [Arabidopsis thaliana]	55.056	89	5.79735E-16
illhan--01-R-M03.ab1	NP_567356	expressed protein [Arabidopsis thaliana]	46.341	82	6.67655E-07
illhan--02-R-D16.ab1	NP_195447	expressed protein [Arabidopsis thaliana]	50.794	63	6.63E-09
illhan--02-R-E20.ab1	NP_199210	expressed protein [Arabidopsis thaliana]	66.667	81	3.84E-22
illhan--02-R-H11.ab1	NP_564781	expressed protein [Arabidopsis thaliana]	78.462	130	4.68E-55
illhan--02-R-H13.ab1	NP_195318	expressed protein [Arabidopsis thaliana]	40.462	173	1.24E-23
illhan--02-R-I24.ab1	NP_197021	expressed protein [Arabidopsis thaliana]	75.497	151	3.17E-54
illhan--02-R-K06.ab1	NP_563633	expressed protein [Arabidopsis thaliana]	72.581	62	7.06E-19
illhan--02-R-L11.ab1	NP_564346	expressed protein [Arabidopsis thaliana]	70.588	119	1.67445E-46
illhan--02-R-L21.ab1	NP_683304	expressed protein [Arabidopsis thaliana]	53.623	138	7.14E-24
illhan--02-R-M05.ab1	NP_566150	expressed protein [Arabidopsis thaliana]	82.09	67	2.80E-28
illhan--02-R-M11.ab1	NP_568867	expressed protein [Arabidopsis thaliana]	89.474	76	8.03E-39
illhan--02-R-M19.ab1	NP_567210	expressed protein [Arabidopsis thaliana]	66.25	160	1.02671E-38
illhan--02-R-M22.ab1	NP_566827	expressed protein [Arabidopsis thaliana]	54.286	35	2.36E-06
illhan--02-R-N10.ab1	NP_680215	expressed protein [Arabidopsis thaliana]	68.831	77	4.94688E-25
illhan--02-R-O11.ab1	NP_563822	expressed protein [Arabidopsis thaliana]	51.724	58	1.09E-11
illhan--02-R-O19.ab1	NP_565723	expressed protein [Arabidopsis thaliana]	64.189	148	4.09E-43
illhan--02-R-O22.ab1	NP_187400	expressed protein [Arabidopsis thaliana]	66.071	56	6.27E-12
illhan--03-R-A04.ab1	NP_172583	expressed protein [Arabidopsis thaliana]	58.824	85	3.92E-22
illhan--03-R-A14.ab1	NP_174405	expressed protein [Arabidopsis thaliana]	49.697	165	8.62E-35
illhan--03-R-B09.ab1	NP_567830	expressed protein [Arabidopsis thaliana]	64.706	34	1.0014E-09
illhan--03-R-C12.ab1	NP_567466	expressed protein [Arabidopsis thaliana]	84.058	69	1.74E-27
illhan--03-R-D02.ab1	NP_178027	expressed protein [Arabidopsis thaliana]	54.762	84	1.12624E-13
illhan--03-R-D08.ab1	NP_177175	expressed protein [Arabidopsis thaliana]	55.046	109	6.40733E-22
illhan--03-R-D22.ab1	NP_190467	expressed protein [Arabidopsis thaliana]	79.032	62	2.33E-26
illhan--03-R-F20.ab1	NP_565759	expressed protein [Arabidopsis thaliana]	62.143	140	8.15E-38
illhan--03-R-G23.ab1	NP_179627	expressed protein [Arabidopsis thaliana]	48.571	105	2.42E-19
illhan--03-R-I22.ab1	NP_175278	expressed protein [Arabidopsis thaliana]	93.103	29	6.58E-09
illhan--03-R-J05.ab1	NP_190227	expressed protein [Arabidopsis thaliana]	72.727	55	1.27251E-18
illhan--03-R-J23.ab1	NP_172369	expressed protein [Arabidopsis thaliana]	66.165	133	3.52E-47
illhan--03-R-K03.ab1	NP_564610	expressed protein [Arabidopsis thaliana]	56.818	44	6.20183E-07
illhan--03-R-K17.ab1	NP_177536	expressed protein [Arabidopsis thaliana]	61.458	96	4.44E-23
illhan--03-R-L17.ab1	NP_187436	expressed protein [Arabidopsis thaliana]	64.356	101	8.76E-26
illhan--03-R-N05.ab1	NP_178872	expressed protein [Arabidopsis thaliana]	64.103	117	7.51E-37
illhan--03-R-O08.ab1	NP_565706	expressed protein [Arabidopsis thaliana]	49.524	105	2.06E-18
illhan--03-R-P17.ab1	NP_568238	expressed protein [Arabidopsis thaliana]	84.615	156	1.32E-67
illhan--03-R-P18.ab1	NP_564545	expressed protein [Arabidopsis thaliana]	77.5	40	1.50E-12
illhan--04-R-A13.ab1	NP_178546	expressed protein [Arabidopsis thaliana]	71.795	39	3.8053E-09
illhan--04-R-B06.ab1	NP_172077	expressed protein [Arabidopsis thaliana]	51.145	131	1.33E-25

IP : 14.49.138.138, 2017-11-03 13:30:33

illhan--04-R-B23.ab1	NP_181804	expressed protein [Arabidopsis thaliana]	47.727	132	1.88E-24
illhan--04-R-C21.ab1	NP_568280	expressed protein [Arabidopsis thaliana]	69.93	143	7.24E-54
illhan--04-R-D17.ab1	NP_191650	expressed protein [Arabidopsis thaliana]	63.333	90	9.97E-57
illhan--04-R-D19.ab1	NP_196665	expressed protein [Arabidopsis thaliana]	80.435	46	1.80E-14
illhan--04-R-D23.ab1	NP_199956	expressed protein [Arabidopsis thaliana]	80.303	132	1.18E-55
illhan--04-R-E01.ab1	NP_566667	expressed protein [Arabidopsis thaliana]	71.642	67	1.0908E-22
illhan--04-R-F01.ab1	NP_197620	expressed protein [Arabidopsis thaliana]	67.327	101	2.54538E-24
illhan--04-R-G10.ab1	NP_194885	expressed protein [Arabidopsis thaliana]	47.399	173	2.66E-23
illhan--04-R-H08.ab1	NP_200128	expressed protein [Arabidopsis thaliana]	89.474	38	7.4093E-13
illhan--04-R-J21.ab1	NP_568234	expressed protein [Arabidopsis thaliana]	60	65	1.33E-20
illhan--04-R-K08.ab1	NP_194941	expressed protein [Arabidopsis thaliana]	80.702	57	9.39E-35
illhan--04-R-K12.ab1	NP_680449	expressed protein [Arabidopsis thaliana]	68.657	67	4.7266E-23
illhan--04-R-K14.ab1	NP_201479	expressed protein [Arabidopsis thaliana]	64.356	101	7.75E-26
illhan--04-R-L19.ab1	NP_564755	expressed protein [Arabidopsis thaliana]	88.66	97	5.83E-44
illhan--04-R-M24.ab1	NP_567044	expressed protein [Arabidopsis thaliana]	71.141	149	3.52E-58
illhan--04-R-P18.ab1	NP_850928	expressed protein [Arabidopsis thaliana]	62.5	96	1.01745E-09
illhan--05-R-F04.ab1	NP_566943	expressed protein [Arabidopsis thaliana]	82.857	35	6.59E-09
illhan--05-R-F20.ab1	NP_173611	expressed protein [Arabidopsis thaliana]	66.667	48	8.5079E-10
illhan--05-R-I03.ab1	NP_199030	expressed protein [Arabidopsis thaliana]	83.562	73	1.30E-28
illhan--05-R-J08.ab1	NP_177593	expressed protein [Arabidopsis thaliana]	68.085	94	2.26682E-25
illhan--05-R-K10.ab1	NP_197440	expressed protein [Arabidopsis thaliana]	87.654	81	2.62306E-26
illhan--05-R-O14.ab1	NP_199284	expressed protein [Arabidopsis thaliana]	72.603	73	7.75E-26
illhan--05-R-P05.ab1	NP_564163	expressed protein [Arabidopsis thaliana]	71.028	107	1.72748E-25
illhan--05-R-P16.ab1	NP_197366	expressed protein [Arabidopsis thaliana]	88	50	2.07E-22
illhan--06-R-A22.ab1	NP_196825	expressed protein [Arabidopsis thaliana]	63.057	157	2.16E-49
illhan--06-R-D23.ab1	NP_179959	expressed protein [Arabidopsis thaliana]	45.455	132	9.35E-16
illhan--06-R-E21.ab1	NP_565951	expressed protein [Arabidopsis thaliana]	80	55	1.09E-19
illhan--06-R-F05.ab1	NP_566496	expressed protein [Arabidopsis thaliana]	56.291	151	1.04E-35
illhan--06-R-F19.ab1	NP_568280	expressed protein [Arabidopsis thaliana]	86.207	87	3.96406E-38
illhan--06-R-H02.ab1	NP_564606	expressed protein [Arabidopsis thaliana]	66.667	78	7.27465E-16
illhan--06-R-H04.ab1	NP_565648	expressed protein [Arabidopsis thaliana]	81.148	122	1.50645E-53
illhan--06-R-I24.ab1	NP_565612	expressed protein [Arabidopsis thaliana]	82.857	70	5.74E-29
illhan--06-R-J16.ab1	NP_190880	expressed protein [Arabidopsis thaliana]	62.893	159	7.49E-45
illhan--06-R-K11.ab1	NP_564050	expressed protein [Arabidopsis thaliana]	66.667	99	9.55E-16
illhan--06-R-P03.ab1	NP_172526	expressed protein [Arabidopsis thaliana]	54.14	157	1.52E-29
illhan--07-R-A10.ab1	NP_565199	expressed protein [Arabidopsis thaliana]	67.5	160	4.85E-55
illhan--07-R-A24.ab1	NP_564301	expressed protein [Arabidopsis thaliana]	77.049	61	1.33844E-20
illhan--07-R-D01.ab1	NP_566014	expressed protein [Arabidopsis thaliana]	72.581	62	1.56606E-18
illhan--07-R-D08.ab1	NP_568286	expressed protein [Arabidopsis thaliana]	72.388	134	5.88243E-58
illhan--07-R-D14.ab1	NP_564307	expressed protein [Arabidopsis thaliana]	63.69	168	2.48E-48

IP : 14.49.138.138, 2017-11-03 13:30:33

illhan--07-R-E10.ab1	NP_181495	expressed protein [Arabidopsis thaliana]	77.778	45	1.17857E-12
illhan--07-R-H04.ab1	NP_196257	expressed protein [Arabidopsis thaliana]	95.652	46	2.42751E-19
illhan--07-R-H09.ab1	NP_191316	expressed protein [Arabidopsis thaliana]	62.745	51	2.38349E-11
illhan--07-R-H20.ab1	NP_566055	expressed protein [Arabidopsis thaliana]	90.566	159	3.00018E-78
illhan--07-R-J17.ab1	NP_566017	expressed protein [Arabidopsis thaliana]	68	125	2.94003E-49
illhan--07-R-K21.ab1	NP_565283	expressed protein [Arabidopsis thaliana]	64.493	138	2.37083E-37
illhan--07-R-L19.ab1	NP_564069	expressed protein [Arabidopsis thaliana]	48.78	41	3.55394E-06
illhan--07-R-N06.ab1	NP_193963	expressed protein [Arabidopsis thaliana]	58.14	129	5.3954E-27
illhan--07-R-N10.ab1	NP_567059	expressed protein [Arabidopsis thaliana]	84.211	38	4.41338E-13
illhan--07-R-N23.ab1	NP_196799	expressed protein [Arabidopsis thaliana]	52.542	118	4.12962E-32
illhan--04-R-D08.ab1	AAR01643	expressed protein [Oryza sativa (japonica cultivar-group)]	73.171	82	4.13E-27
illhan--04-R-O08.ab1	AAF79247	F10B6.11 [Arabidopsis thaliana]	47.312	93	1.42E-19
illhan--04-R-H18.ab1	AAF79294	F14D16.26 [Arabidopsis thaliana]	71.97	132	1.54E-55
illhan--07-R-F12.ab1	AAG00242	F1N21.17 [Arabidopsis thaliana]	78.571	84	1.73337E-36
illhan--06-R-H20.ab1	AAF68108	F20B17.11 [Arabidopsis thaliana]	69.663	89	9.83E-29
illhan--04-R-K13.ab1	AAF79503	F20N2.15 [Arabidopsis thaliana]	82.353	34	6.49E-09
illhan--01-R-D01.ab1	AAF24571	F22C12.25 [Arabidopsis thaliana]	61.404	57	2.09E-10
illhan--03-R-K18.ab1	A86315	F2H15.19 protein [Arabidopsis thaliana]	59.756	82	5.01363E-24
illhan--02-R-E10.ab1	AAF27066	F4N2.17 [Arabidopsis thaliana]	73.611	72	1.95E-21
illhan--03-R-H24.ab1	AAF79653	F5O11.17 [Arabidopsis thaliana]	75.362	69	1.51E-26
illhan--03-R-N04.ab1	AAF79641	F5O11.22 [Arabidopsis thaliana]	64.22	109	2.67151E-34
illhan--02-R-B08.ab1	E86350	F8K7.14 protein [Arabidopsis thaliana]	83.81	105	3.36382E-45
illhan--04-R-B05.ab1	BAB08870	gb|AAD25584.1~gene_id:MTI20.26~similar to unknown protein [Arabidopsis thaliana]	57.955	88	6.60E-25
illhan--04-R-P08.ab1	BAB01179	gb|AAD55299.1~gene_id:MIE15.8~similar to unknown protein [Arabidopsis thaliana]	76.744	86	2.17515E-36
illhan--02-R-J12.ab1	BAB09687	gb|AAF00669.1~gene_id:MBL20.10~strong similarity to unknown protein [Arabidopsis thaliana]	60.465	43	1.48E-08
illhan--03-R-H01.ab1	BAB10164	gb|AAF50025.1~gene_id:MTG10.5~similar to unknown protein [Arabidopsis thaliana]	58.696	92	1.84994E-19
illhan--05-R-A11.ab1	BAB08771	gene_id:MBG8.19~pir||T04822~strong similarity to unknown protein [Arabidopsis thaliana]	46.667	90	7.33E-08
illhan--03-R-L23.ab1	BAB09766	gene_id:MNC17.12~unknown protein [Arabidopsis thaliana]	89.063	64	5.21E-14
illhan--04-R-O05.ab1	BAB01074	gene_id:MPE11.28~unknown protein [Arabidopsis thaliana]	58.654	104	2.21E-26
illhan--06-R-D04.ab1	BAA97221	gene_id:MSD23.5~pir||C71447~similar to unknown protein [Arabidopsis thaliana]	70.968	93	4.39E-29
illhan--05-R-E04.ab1	BAB10188	gene_id:MTG13.5~unknown protein [Arabidopsis thaliana]	60.714	56	1.26E-10
illhan--03-R-G09.ab1	BAB09523	gene_id:MTH16.10~unknown protein [Arabidopsis thaliana]	57.407	108	3.29E-29
illhan--07-R-F04.ab1	BAB08282	gene_id:MUA22.2~similar to unknown protein~sp|P23438 [Arabidopsis thaliana]	68.613	137	9.58749E-45
illhan--05-R-O04.ab1	T09841	hypothetical protein [Gossypium hirsutum]	47.778	90	1.13E-08
illhan--03-R-E14.ab1	T03812	hypothetical protein (clone NF22) [Nicotiana tabacum]	76.224	143	1.65709E-41
illhan--01-R-E03.ab1	NP_191276	hypothetical protein [Arabidopsis thaliana]	50	66	2.26E-14
illhan--02-R-A12.ab1	B71431	hypothetical protein [Arabidopsis thaliana]	57.955	88	1.90E-17
illhan--02-R-A19.ab1	AAO37147	hypothetical protein [Arabidopsis thaliana]	42.553	141	4.42396E-21
illhan--03-R-D19.ab1	AAF26078	hypothetical protein [Arabidopsis thaliana]	85.106	47	1.47E-16
illhan--03-R-E03	NP_199047	hypothetical protein [Arabidopsis thaliana]	75	68	1.00E-22

IP : 14.49.138.138, 2017-11-03 13:30:33

.ab1					
illhan--04-R-I12.ab1	AAF14032	hypothetical protein [Arabidopsis thaliana]	67.778	90	5.84357E-26
illhan--05-R-M17.ab1	AAF76371	hypothetical protein [Arabidopsis thaliana]	47.2	125	3.55E-15
illhan--06-R-N18.ab1	AAD25934	hypothetical protein [Arabidopsis thaliana]	64.516	186	5.35E-59
illhan--07-R-E01.ab1	NP_195157	hypothetical protein [Arabidopsis thaliana]	82.051	39	6.63745E-11
illhan--07-R-L14.ab1	NP_187206	hypothetical protein [Arabidopsis thaliana]	79.661	59	2.51791E-08
illhan--03-R-D16.ab1	NP_176225	hypothetical protein [Arabidopsis thaliana]	38.235	102	4.80E-12
illhan--03-R-I12.ab1	NP_188488	hypothetical protein [Arabidopsis thaliana]	69.892	93	5.83E-34
illhan--03-R-N22.ab1	NP_195400	hypothetical protein [Arabidopsis thaliana]	70.833	48	3.30E-15
illhan--06-R-B12.ab1	NP_192178	hypothetical protein [Arabidopsis thaliana]	69.466	131	2.17011E-44
illhan--06-R-E09.ab1	NP_199075	hypothetical protein [Arabidopsis thaliana]	61.429	70	4.06E-19
illhan--06-R-I17.ab1	NP_187080	hypothetical protein [Arabidopsis thaliana]	77.143	70	3.36E-29
illhan--06-R-J07.ab1	NP_173662	hypothetical protein [Arabidopsis thaliana]	71.951	164	3.44E-66
illhan--04-R-O01.ab1	CAA10129	hypothetical protein [Cicer arietinum]	89.744	78	5.14E-36
illhan--02-R-L20.ab1	E86183	hypothetical protein [imported] [Arabidopsis thaliana]	63.855	83	1.58E-10
illhan--06-R-L23.ab1	D86254	hypothetical protein [imported] [Arabidopsis thaliana]	70	40	2.28E-09
illhan--01-R-D06.ab1	H86206	hypothetical protein [imported] [Arabidopsis thaliana]	79.245	106	1.04E-43
illhan--06-R-G06.ab1	BAC92446	hypothetical protein [Oryza sativa (japonica cultivar-group)]	68.421	57	1.47E-16
illhan--07-R-D21.ab1	AAL34122	hypothetical protein [Oryza sativa (japonica cultivar-group)]	63.889	36	6.82468E-06
illhan--07-R-B24.ab1	AAO14624	hypothetical protein [Prunus persica]	61.35	163	2.03E-50
illhan--02-R-G12.ab1	AAL73530	hypothetical protein [Sorghum bicolor]	45.614	114	2.85E-17
illhan--04-R-N03.ab1	S68989	hypothetical protein 1 [Catharanthus roseus]	94.444	36	5.79E-13
illhan--06-R-L08.ab1	S25786	hypothetical protein 3 - potato transposon Tst1 [Solanum tuberosum]	49.689	161	2.11E-39
illhan--07-R-O16.ab1	AAK73103	hypothetical protein 4 [Zea mays]	40	145	3.06369E-22
illhan--03-R-C01.ab1	A84449	hypothetical protein At2g03480 [imported] [Arabidopsis thaliana]	84.848	165	1.82E-83
illhan--07-R-G09.ab1	H84551	hypothetical protein At2g17410 [imported] [Arabidopsis thaliana]	87.755	98	5.73781E-45
illhan--03-R-O11.ab1	H84607	hypothetical protein At2g22010 [imported] [Arabidopsis thaliana]	60	85	2.12E-23
illhan--06-R-G08.ab1	F84610	hypothetical protein At2g22260 [imported] - Arabidopsis thaliana	75.41	61	1.86E-19
illhan--05-R-B22.ab1	D84644	hypothetical protein At2g25110 [imported] [Arabidopsis thaliana]	84.314	51	9.81E-21
illhan--02-R-A17.ab1	A84652	hypothetical protein At2g25730 [imported] [Arabidopsis thaliana]	76.687	163	2.64684E-66
illhan--04-R-P24.ab1	A84690	hypothetical protein At2g28880 [imported] [Arabidopsis thaliana]	82.278	79	7.24E-23
illhan--03-R-E05.ab1	B84698	hypothetical protein At2g29590 [imported] [Arabidopsis thaliana]	74.39	82	5.76E-29
illhan--05-R-D14.ab1	D84706	hypothetical protein At2g30270 [imported] [Arabidopsis thaliana]	43.077	130	1.97649E-21
illhan--02-R-O03.ab1	B84746	hypothetical protein At2g33490 [imported] - Arabidopsis thaliana >gi|2459431|gb|AAB80666.1| unknown protein [Arabidopsis thaliana]	77.778	54	5.238E-14
illhan--03-R-F22.ab1	G84809	hypothetical protein At2g38820 [imported] [Arabidopsis thaliana]	61.364	44	2.05E-10
illhan--07-R-O17.ab1	E85429	hypothetical protein AT4g36390 [imported] [Arabidopsis thaliana]	66.418	134	6.98101E-43
illhan--05-R-F12.ab1	B96832	hypothetical protein F18B13.15 [imported] [Arabidopsis thaliana]	90.062	161	4.08E-85
illhan--07-R-M07.ab1	F86347	hypothetical protein F24J8.9 [Arabidopsis thaliana]	69.014	71	1.6811E-20
illhan--06-R-A12.ab1	H96753	hypothetical protein F3N23.8 [imported] [Arabidopsis thaliana]	77.698	139	2.32E-38
illhan--04-R-G07.ab1	A86298	hypothetical protein F3O9.10 [Arabidopsis thaliana]	95.556	45	1.74E-17

IP : 14.49.138.138, 2017-11-03 13:30:33

illhan--06-R-N23.ab1	A86297	hypothetical protein F3O9.2 [Arabidopsis thaliana]	69.663	89	2.63E-21
illhan--05-R-F16.ab1	G86329	hypothetical protein F6F9.26 [imported] [Arabidopsis thaliana]	58.333	120	4.54E-34
illhan--06-R-J24.ab1	D86349	hypothetical protein F8K7.5 [Arabidopsis thaliana]	94.444	108	2.75E-57
illhan--02-R-O10.ab1	T00458	hypothetical protein T14N5.15 [Arabidopsis thaliana]	59.375	64	3.32589E-13
illhan--03-R-A18.ab1	F86156	hypothetical protein T14P4.6 [Arabidopsis thaliana]	47.887	71	1.45E-10
illhan--02-R-I21.ab1	AAG52039	hypothetical protein; 29936-28688 [Arabidopsis thaliana]	85.417	48	3.67E-20
illhan--01-R-D05.ab1	AAG52180	hypothetical protein; 45807-49650 [Arabidopsis thaliana]	46.154	130	1.08E-16
illhan--06-R-N06.ab1	CAE03124	OJ000114_01.5 [Oryza sativa (japonica cultivar-group)]	59.259	81	3.40E-13
illhan--02-R-I02.ab1	NP_909441	OJ1276_B06.30 [Oryza sativa (japonica cultivar-group)]	68.75	80	1.23E-21
illhan--03-R-O19.ab1	CAE02043	OJ990528_30.1 [Oryza sativa (japonica cultivar-group)]	93.056	72	1.50E-34
illhan--05-R-I22.ab1	NP_085475	orf107a [Arabidopsis thaliana]	97.826	46	1.40E-20
illhan--07-R-L06.ab1	NP_085585	orf107h [Arabidopsis thaliana]	75.728	103	1.62451E-23
illhan--04-R-I06.ab1	CAE03090	OSJNBa0017B10.5 [Oryza sativa (japonica cultivar-group)]	45.679	81	5.238E-14
illhan--06-R-G19.ab1	CAD39568	OSJNBa0019G23.12 [Oryza sativa (japonica cultivar-group)]	35.156	128	3.28E-16
illhan--04-R-F18.ab1	CAE05156	OSJNBa0039C07.12 [Oryza sativa (japonica cultivar-group)]	94.118	68	6.23E-36
illhan--06-R-C23.ab1	CAE03008	OSJNBa0043L09.27 [Oryza sativa (japonica cultivar-group)]	92.157	51	9.86E-21
illhan--07-R-E24.ab1	CAE05696	OSJNBa0083D01.10 [Oryza sativa (japonica cultivar-group)]	83.051	59	3.59225E-20
illhan--06-R-P23.ab1	CAE03572	OSJNBa0085I10.17 [Oryza sativa (japonica cultivar-group)]	50.485	103	1.41619E-10
illhan--01-R-E04.ab1	CAD40829	OSJNBa0086B14.1 [Oryza sativa (japonica cultivar-group)]	66.667	45	5.93E-15
illhan--05-R-F07.ab1	NP_913582	OSJNBa0086P08.14 [Oryza sativa (japonica cultivar-group)]	67.826	115	7.03029E-35
illhan--03-R-H15.ab1	CAE03446	OSJNBa0088H09.4 [Oryza sativa (japonica cultivar-group)]	70.769	65	7.55E-21
illhan--02-R-K14.ab1	CAE03052	OSJNBa0089K21.6 [Oryza sativa (japonica cultivar-group)]	55.462	119	1.2988E-33
illhan--04-R-G20.ab1	CAE03930	OSJNBa0093F12.4 [Oryza sativa (japonica cultivar-group)]	85.556	90	5.52E-39
illhan--07-R-P12.ab1	CAE05725	OSJNBb0017I01.5 [Oryza sativa (japonica cultivar-group)]	57.857	140	9.4314E-29
illhan--02-R-G15.ab1	CAD41421	OSJNBb0032E06.4 [Oryza sativa (japonica cultivar-group)]	42.105	114	8.17E-20
illhan--07-R-B06.ab1	CAE02348	OSJNBb0072M01.9 [Oryza sativa (japonica cultivar-group)]	87.313	134	5.59E-61
illhan--04-R-K18.ab1	NP_915490	P0005H10.15 [Oryza sativa (japonica cultivar-group)]	75.61	164	5.98E-63
illhan--04-R-F11.ab1	NP_909237	P0434B04.3 [Oryza sativa (japonica cultivar-group)]	85.714	42	1.98108E-13
illhan--04-R-I18.ab1	NP_916147	P0435B05.20 [Oryza sativa (japonica cultivar-group)]	83.607	61	3.14696E-16
illhan--02-R-C19.ab1	NP_908397	P0482C06.20 [Oryza sativa (japonica cultivar-group)]	40.833	120	1.60E-15
illhan--07-R-G15.ab1	NP_908806	P0487E11.18 [Oryza sativa (japonica cultivar-group)]	82.857	105	2.89143E-43
illhan--04-R-M06.ab1	NP_917975	P0519E12.3 [Oryza sativa (japonica cultivar-group)]	88.732	71	2.94E-33
illhan--03-R-J18.ab1	NP_913363	P0665D10.14 [Oryza sativa (japonica cultivar-group)]	79.675	123	3.80E-54
illhan--07-R-H05.ab1	NP_914457	P0666G04.16 [Oryza sativa (japonica cultivar-group)]	48.936	141	3.25788E-24
illhan--02-R-P19.ab1	NP_915014	P0698A10.29 [Oryza sativa (japonica cultivar-group)]	70.652	92	2.26E-33
illhan--06-R-D02.ab1	F86200	protein F12K11.17 [imported] [Arabidopsis thaliana]	63.158	57	1.87E-15
illhan--02-R-C10.ab1	D86182	protein F13M7.11 [imported] [Arabidopsis thaliana]	74.194	93	9.53E-36
illhan--06-R-J11.ab1	D86318	protein F15H18.6 [imported] [Arabidopsis thaliana]	80.741	135	4.81E-60
illhan--07-R-K24.ab1	A86327	protein F18O14.11 [imported] [Arabidopsis thaliana]	72.727	165	9.07528E-59
illhan--06-R-E06.ab1	A86470	protein F21H2.12 [imported] [Arabidopsis thaliana]	85.714	49	1.74E-17

IP : 14.49.138.138, 2017-11-03 13:30:33

illhan--02-R-E02.ab1	D96665	protein F22C12.18 [imported] [Arabidopsis thaliana]	95.146	103	3.00081E-52
illhan--07-R-P17.ab1	B86260	protein T12C24.18 [imported] [Arabidopsis thaliana]	74	50	7.30903E-16
illhan--07-R-F21.ab1	E96525	protein T1N15.21 [imported] [Arabidopsis thaliana]	72.519	131	1.07452E-51
illhan--04-R-O18.ab1	F86214	protein T6D22.2 [imported] [Arabidopsis thaliana]	58.871	124	4.25E-24
illhan--05-R-G19.ab1	CAC08345	putative protein [Arabidopsis thaliana]	84.211	76	2.67E-34
illhan--06-R-K19.ab1	AAM20496	putative protein [Arabidopsis thaliana]	69.62	79	3.16E-27
illhan--05-R-O19.ab1	AAM97006	putative protein [Arabidopsis thaliana]	68.595	121	4.37E-45
illhan--04-R-P14.ab1	AAP40475	putative protein kinase [Arabidopsis thaliana]	51.974	152	1.79E-38
illhan--03-R-I21.ab1	AAF79729	T25N20.22 [Arabidopsis thaliana]	100	52	1.79E-22
illhan--02-R-L13.ab1	AAK32797	T3B23.2/T3B23.2 [Arabidopsis thaliana]	75.758	66	2.49E-32
illhan--05-R-O03.ab1	AAF63166	T5E21.6 [Arabidopsis thaliana]	75	88	3.50E-32
illhan--01-R-H06.ab1	AAM63041	unknown [Arabidopsis thaliana]	71.622	74	7.98416E-28
illhan--01-R-K02.ab1	AAM61439	unknown [Arabidopsis thaliana]	74.561	114	1.04E-43
illhan--02-R-B12.ab1	AAM64456	unknown [Arabidopsis thaliana]	61.111	72	4.79144E-20
illhan--02-R-C03.ab1	AAM64972	unknown [Arabidopsis thaliana]	70.13	77	9.96762E-26
illhan--03-R-E08.ab1	AAM61533	unknown [Arabidopsis thaliana]	55.862	145	1.77E-35
illhan--03-R-K13.ab1	AAM64712	unknown [Arabidopsis thaliana]	80.488	41	1.14E-13
illhan--03-R-M15.ab1	AAM64310	unknown [Arabidopsis thaliana]	89.286	56	6.85E-24
illhan--03-R-P10.ab1	AAM63698	unknown [Arabidopsis thaliana]	64.865	111	7.86E-29
illhan--04-R-E17.ab1	AAM65302	unknown [Arabidopsis thaliana]	86.364	44	1.56E-15
illhan--04-R-G14.ab1	AAM63790	unknown [Arabidopsis thaliana]	67.593	108	8.89E-30
illhan--04-R-H04.ab1	AAN60309	unknown [Arabidopsis thaliana]	79.577	142	6.30E-52
illhan--04-R-J12.ab1	AAM67062	unknown [Arabidopsis thaliana]	40.187	107	3.92875E-14
illhan--04-R-L02.ab1	AAM62979	unknown [Arabidopsis thaliana]	92.793	111	7.72E-58
illhan--04-R-P07.ab1	AAM63612	unknown [Arabidopsis thaliana]	52.727	110	2.33475E-22
illhan--05-R-E06.ab1	AAM64669	unknown [Arabidopsis thaliana]	53.731	134	5.05334E-35
illhan--05-R-E21.ab1	AAM65849	unknown [Arabidopsis thaliana]	68.868	106	2.48E-37
illhan--05-R-J06.ab1	AAM65675	unknown [Arabidopsis thaliana]	95.652	46	1.20E-18
illhan--05-R-K08.ab1	AAM61043	unknown [Arabidopsis thaliana]	39.024	164	3.51E-10
illhan--05-R-M01.ab1	AAM65278	unknown [Arabidopsis thaliana]	80.702	114	1.43201E-51
illhan--05-R-N09.ab1	AAM60987	unknown [Arabidopsis thaliana]	67.021	94	7.49E-29
illhan--05-R-P17.ab1	AAM63888	unknown [Arabidopsis thaliana]	71.93	57	8.17E-20
illhan--06-R-G11.ab1	AAM65026	unknown [Arabidopsis thaliana]	67.647	68	5.41E-19
illhan--06-R-H03.ab1	AAM61485	unknown [Arabidopsis thaliana]	47.541	61	9.18E-08
illhan--06-R-J18.ab1	AAM64554	unknown [Arabidopsis thaliana]	64.865	37	0.000004001
illhan--06-R-K02.ab1	AAM61570	unknown [Arabidopsis thaliana]	64.815	54	3.88458E-09
illhan--06-R-M16.ab1	AAM63875	unknown [Arabidopsis thaliana]	53.642	151	3.36E-45
illhan--07-R-K05.ab1	AAM65976	unknown [Arabidopsis thaliana]	67.778	90	2.63974E-29
illhan--07-R-P05.ab1	AAM61228	unknown [Arabidopsis thaliana]	82.27	141	5.6844E-61
illhan--07-R-P18.ab1	AAM62501	unknown [Arabidopsis thaliana]	43.75	80	1.85423E-11

IP : 14.49.138.138, 2017-11-03 13:30:33

illhan--04-R-G13.ab1	AAK84476	unknown [Lycopersicon esculentum]	58.947	95	5.66E-21
illhan--05-R-A19.ab1	AAF27920	unknown [Malus x domestica]	96.454	141	3.64856E-82
illhan--04-R-G09.ab1	AAP93138	unknown [Setaria italica]	46.018	113	2.34579E-22
illhan--01-R-J06.ab1	BAC42585	unknown protein [Arabidopsis thaliana]	76.577	111	3.15E-52
illhan--02-R-B23.ab1	BAC42194	unknown protein [Arabidopsis thaliana]	80.769	52	1.60E-15
illhan--02-R-N09.ab1	BAC42039	unknown protein [Arabidopsis thaliana]	83.333	96	2.88671E-41
illhan--04-R-J03.ab1	BAC42946	unknown protein [Arabidopsis thaliana]	71.622	74	8.64E-27
illhan--05-R-C23.ab1	BAC42366	unknown protein [Arabidopsis thaliana]	78.261	46	1.06949E-13
illhan--05-R-D22.ab1	BAC43410	unknown protein [Arabidopsis thaliana]	54.795	73	5.57E-07
illhan--05-R-M04.ab1	BAC42598	unknown protein [Arabidopsis thaliana]	40.476	168	2.35E-22
illhan--07-R-A21.ab1	AAL07108	unknown protein [Arabidopsis thaliana]	77.778	36	5.07E-09
illhan--07-R-G14.ab1	AAL87284	unknown protein [Arabidopsis thaliana]	69.006	171	1.36569E-46
illhan--07-R-K03.ab1	AAG50527	unknown protein [Arabidopsis thaliana]	64.706	68	2.61632E-17
illhan--07-R-L02.ab1	AAG28819	unknown protein [Arabidopsis thaliana]	47.273	55	4.2747E-08
illhan--07-R-L21.ab1	AAL91153	unknown protein [Arabidopsis thaliana]	56.897	58	1.14765E-10
illhan--02-R-O04.ab1	AAM13089	unknown protein [Arabidopsis thaliana]	67.626	139	2.79E-37
illhan--03-R-B05.ab1	BAC43037	unknown protein [Arabidopsis thaliana]	58.824	51	4.80E-12
illhan--03-R-F14.ab1	AAM13020	unknown protein [Arabidopsis thaliana]	52.273	88	2.38E-21
illhan--03-R-P15.ab1	AAO42078	unknown protein [Arabidopsis thaliana]	68.868	106	5.3829E-35
illhan--04-R-J16.ab1	AAM15212	unknown protein [Arabidopsis thaliana]	26.667	120	1.76763E-06
illhan--04-R-O03.ab1	NP_921429	unknown protein [Oryza sativa (japonica cultivar-group)]	57.377	61	9.88E-13
illhan--06-R-B23.ab1	NP_922766	unknown protein [Oryza sativa (japonica cultivar-group)]	71.166	163	9.41E-64
illhan--07-R-C03.ab1	BAD01347	unknown protein [Oryza sativa (japonica cultivar-group)]	61.062	113	3.04E-30
illhan--03-R-N11.ab1	AAK50128	unknown protein [Oryza sativa]	43	100	6.70143E-14
illhan--05-R-N15.ab1	AAG52505	unknown protein; 30607-27264 [Arabidopsis thaliana]	92.208	77	4.28E-27
illhan--06-R-C15.ab1	AAG51438	unknown protein; 72859-71336 [Arabidopsis thaliana]	91	100	2.66E-50
illhan--01-R-M01.ab1	NP_912984	unnamed protein product [Oryza sativa (japonica cultivar-group)]	83.784	111	6.74E-71
illhan--06-R-A10.ab1	NP_913023	unnamed protein product [Oryza sativa (japonica cultivar-group)]	51.181	127	1.78E-30
illhan--06-R-C14.ab1	NP_912909	unnamed protein product [Oryza sativa (japonica cultivar-group)]	95.082	122	5.90E-50

Consensus Number	Accession No.	Definition of Putative homologue[Organism]	Matching %	Matching Length	E-value
1	NP_175482	expressed protein [Arabidopsis thaliana]	41.463	123	6.07E-18
2	No hits found				
3	NP_915506	P0529H11.12 [Oryza sativa (japonica cultivar-group)]	49.296	71	4.62E-14
4	AAF66823	poly(A)-binding protein [Nicotiana tabacum]	89.13	92	2.53E-37
5	No hits found				
6	AAM63610	unknown [Arabidopsis thaliana]	87.097	31	2.61344E-07
7	NP_181874	60S ribosomal protein L38 (RPL38A) [Arabidopsis thaliana]	94.203	69	3.46327E-31
8	NP_908456	unnamed protein product [Oryza sativa (japonica cultivar-group)]	80.702	57	6.41278E-21
9	No hits				

IP : 14.49.138.138, 2017-11-03 13:30:33

	found				
10	AAP33009	thioredoxin H [Citrus x paradisi]	97.619	84	4.62E-53
11	P93768	Probable 26S proteasome non-ATPase regulatory subunit 3 (26S proteasome subunit S3) (Nuclear antigen 21D7) [Nicotiana tabacum]	98.276	58	2.54E-14
12	Q9FUM1	Elongation factor 1-gamma (EF-1-gamma) (eEF-1B gamma) [Prunus avium]	85.714	98	2.97586E-45
13	No hits found				
14	NP_195626	DnaJ protein family [Arabidopsis thaliana]	79.747	79	3.89E-25
15	NP_189290	expressed protein [Arabidopsis thaliana]	71.014	69	1.62E-23
16	AAQ22726	40S ribosomal protein S25 [Glycine max]	97.222	72	2.75E-31
17	NP_199015	expressed protein [Arabidopsis thaliana]	88.776	98	7.50E-48
18	NP_913448	P0492F05.25 [Oryza sativa (japonica cultivar-group)]	76.364	55	1.34E-17
19	BAC41328	similar to S-receptor kinase [Lotus corniculatus var. japonicus]	38.095	147	1.24384E-23
20	P35493	2,3-bisphosphoglycerate-independent phosphoglycerate mutase (Phosphoglyceromutase) (BPG-independent PGAM) (PGAM-I) [Ricinus communis]	81.429	140	2.97E-65
21	AAO41731	cytoplasmic ribosomal protein S14 [Brassica napus]	95.27	148	4.08E-67
22	No hits found				
23	P42754	Mannitol dehydrogenase (NAD-dependent mannitol dehydrogenase) [Petroselinum crispum]	81.707	82	7.08E-33
24	No hits found				
25	Q96558	UDP-glucose 6-dehydrogenase (UDP-Glc dehydrogenase) (UDP-GlcDH) (UDPGDH) [Glycine max]	97.26	146	2.47E-75
26	NP_565652	glycosyl hydrolase family 17 [Arabidopsis thaliana]	63.636	99	2.17E-31
27	BAB41205	kinase-like protein [Oryza sativa]	43.81	105	3.21E-12
28	NP_196946	copine-related [Arabidopsis thaliana]	57.5	80	1.18E-19
29	No hits found				
30	T09781	glutathione transferase (EC 2.5.1.18) [Carica papaya]	80.263	152	7.08E-65
31	NP_191801	bZIP family transcription factor [Arabidopsis thaliana]	70	60	9.16E-15
32	NP_921899	60S ribosomal protein L21 [Oryza sativa (japonica cultivar-group)]	95.455	110	1.68E-56
33	AAM14957	hypothetical protein [Arabidopsis thaliana]	65.556	90	3.55E-23
34	NP_176355	S-locus protein kinase, putative [Arabidopsis thaliana]	50.495	101	7.47E-26
35	AAQ72789	60S ribosomal protein L5 [Cucumis sativus]	78.667	75	4.62E-27
36	No hits found				
37	NP_566231	expressed protein [Arabidopsis thaliana]	69.295	241	2.20E-79
38	NP_568152	expressed protein [Arabidopsis thaliana]	51.049	143	1.18E-33
39	AAP06757	copper chaperone [Lycopersicon esculentum]	83.544	79	6.23511E-30
40	No hits found				
41	No hits found				
42	AAN86822	beta-cyanoalanine synthase [Betula pendula]	91.525	59	4.33E-28
43	No hits found				
44	AAQ84334	zinc-finger protein [Oryza sativa (indica cultivar-group)]	71.345	171	3.65E-60
45	P42056	36 kDa outer mitochondrial membrane protein porin (Voltage-dependent anion-selective channel protein) (VDAC) (POM 36) >gi|515360|emb|CAA56600.1| 36kDA porin II [Solanum tuberosum]	86.957	161	6.38E-71
46	BAC20920	putative 40S ribosomal protein S12 [Oryza sativa (japonica cultivar-group)]	88.312	77	1.61E-35
47	No hits found				
48	AAG34804	glutathione S-transferase GST 14 [Glycine max]	61.905	84	4.47E-25

IP : 14.49.138.138, 2017-11-03 13:30:33

49	BAB02396	cytochrome P450 [Arabidopsis thaliana]	70.229	131	2.01E-49
50	AAA79700	GF14 Kappa isoform [Arabidopsis thaliana]	97.26	73	2.53E-33
51	NP_198728	germin-like protein, putative [Arabidopsis thaliana]	70.5	200	3.56E-77
52	AAK50091	At1g78070/F28K19_28 [Arabidopsis thaliana]	85.714	126	2.79E-59
53	AAQ63461	calmodulin 4 [Daucus carota]	100	149	1.12742E-79
54	No hits found				
55	NP_909832	putative leucine-rich repeat protein [Oryza sativa (japonica cultivar-group)]	68.837	215	1.67E-82
56	No hits found				
57	NP_178163	expressed protein [Arabidopsis thaliana]	87.755	98	1.66E-44
58	Q9M4T8	Proteasome subunit alpha type 5 (20S proteasome alpha subunit E) (20S proteasome subunit alpha-5)[Glycine max]	94.737	76	9.58543E-34
59	NP_415718	putative dihydroxyacetone kinase [Escherichia coli K12]	100	93	3.25E-48
60	AAA86689	ascorbate peroxidase [Nicotiana tabacum]	94.382	89	4.56E-34
61	AAM64427	acidic ribosomal protein, putative [Arabidopsis thaliana]	80	40	2.64E-10
62	BAB33421	putative senescence-associated protein [Pisum sativum]	94.737	114	8.08E-60
63	H96563	hypothetical protein F19K6.5 [imported] [Arabidopsis thaliana]	63.636	55	1.98E-13
64	AAL25130	cellulose synthase-like protein OsCslE2 [Oryza sativa]	31.731	104	7.79E-10
65	No hits found				
66	T07161	late-embryogenesis protein homolog [Lycopersicon esculentum]	58.333	96	2.19003E-19
67	AAG34808	glutathione S-transferase GST 18 [Glycine max]	55.814	86	6.99446E-24
68	AAM61561	cyclophilin-like protein [Arabidopsis thaliana]	84.314	51	3.87558E-17
69	AAM65544	unknown [Arabidopsis thaliana]	46.988	83	2.33467E-06
70	BAB82980	polygalacturonase-inhibitor protein [Citrus sp. cv. Sainumphung]	100	102	1.73535E-54
71	No hits found				
72	NP_190750	chlorophyll synthetase, putative [Arabidopsis thaliana]	41.667	84	1.76763E-06
73	DAA00281	TPA: putative phytosulfokine peptide precursor [Glycine max]	54.098	61	8.89623E-11
74	NP_850015	auxin-regulated protein [Arabidopsis thaliana]	63.934	183	2.15999E-62
75	No hits found				
76	Q05045	CHAPERONIN CPN60-1, MITOCHONDRIAL PRECURSOR (HSP60-1) [Cucurbita maxima]	42.029	138	5.05187E-21
77	AAM28873	long chain acyl-CoA synthetase 6 [Arabidopsis thaliana]	83.01	206	8.3031E-99
78	CAC43238	calcium binding protein [Sesbania rostrata]	69.608	102	8.95391E-35
79	No hits found				
80	NP_188087	cytochrome P450, putative [Arabidopsis thaliana]	49.669	151	1.46689E-42
81	No hits found				
82	AAC36740	thaumatin-like protein precursor Mdtl1 [Malus x domestica]	70.455	132	3.69307E-52
83	No hits found				
84	NP_563758	expressed protein [Arabidopsis thaliana]	67.647	34	1.79318E-07
85	NP_921503	putative polyprotein [Oryza sativa (japonica cultivar-group)]	61.111	126	1.75457E-41
86	No hits found				
87	AAD34458	Skp1 [Medicago sativa]	86.538	156	4.7582E-67
88	No hits found				

IP : 14.49.138.138, 2017-11-03 13:30:33

89	BAC76894	protein kinase [Raphanus sativus]	65.079	63	7.11676E-17
90	No hits found				
91	NP_567338	expressed protein [Arabidopsis thaliana]	60	140	7.38121E-48
92	NP_568988	2-nitropropane dioxygenase-related protein [Arabidopsis thaliana]	74.783	115	2.73884E-47
93	No hits found				
94	No hits found				
95	No hits found				
96	No hits found				
97	NP_196150	expressed protein [Arabidopsis thaliana]	77.049	122	2.46913E-49
98	NP_922615	hypothetical protein [Oryza sativa (japonica cultivar-group)]	67.619	105	2.61699E-34
99	AAG49361	ACC oxidase [Citrus sinensis]	99.123	114	2.62457E-59
100	B84772	probable DnaJ protein [imported] [Arabidopsis thaliana]	89.535	86	7.25835E-40
101	NP_915424	putative 60S RIBOSOMAL PROTEIN L36 [Oryza sativa (japonica cultivar-group)]	79.091	110	7.30E-45
102	BAC76729	alpha-amylase [Vigna angularis]	75.806	124	4.29E-53
103	T09602	probable zinc finger protein SCOF-1, cold-inducible [Glycine max]	55.376	186	2.22E-40
104	NP_566110	expressed protein [Arabidopsis thaliana]	52	125	8.00585E-31
105	AAQ20892	10-hydroxygeraniol oxidoreductase [Camptotheca acuminata]	76.216	185	3.87E-85
106	NP_914258	P0483G10.15 [Oryza sativa (japonica cultivar-group)]	100	61	8.15E-28
107	1803516A	glycolate oxidase [Lens culinaris]	91.613	155	5.97E-69
108	NP_566727	expressed protein [Arabidopsis thaliana]	91.954	87	1.30E-42
109	No hits found				
110	CAB77243	fructose-bisphosphate aldolase [Persea americana]	88.816	152	8.08E-71
111	O80327	Thaumatin-like protein 1 precursor [Pyrus pyrifolia]	78.947	38	1.07E-13
112	No hits found				
113	NP_196824	GRAM domain-containing protein [Arabidopsis thaliana]	66.667	81	4.46E-30
114	NP_187006	hypothetical protein [Arabidopsis thaliana]	30.075	133	5.25E-06
115	No hits found				
116	NP_192742	cytochrome c [Arabidopsis thaliana]	94.737	38	3.79E-15
117	CAE02979	OSJNBa0086B14.21 [Oryza sativa (japonica cultivar-group)]	88.889	54	2.59E-27
118	AAA56991	formerly called HAT24; synaptobrevin-related protein [Arabidopsis thaliana]	92.708	96	6.51E-34
119	NP_910018	putative phospholipase [Oryza sativa]	77.5	80	4.32364E-29
120	NP_192742	cytochrome c [Arabidopsis thaliana]	95.536	112	1.82861E-59
121	BAA31562	metallothionein-like protein [Citrus unshiu]	98.529	68	3.15E-35
122	BAB90653	B1033B05.3 [Oryza sativa (japonica cultivar-group)]	66.038	53	2.57E-20
123	NP_200611	SPP30 - like protein [Arabidopsis thaliana]	95.05	101	6.38E-50
124	AAG10793	beta-carotene hydroxylase [Citrus unshiu]	100	111	6.19E-48
125	NP_199243	auxin-repressed protein-related [Arabidopsis thaliana]	84.375	32	6.90592E-10
126	BAC24799	alpha tubulin [Physcomitrella patens]	100	74	1.13E-36
127	AAP86603	eukaryotic translation initiation factor iso4E [Lactuca sativa]	85.333	75	1.46E-32
128	AAN72051	cell cycle control crn (crooked neck) protein-like [Arabidopsis thaliana]	75	76	5.94E-26

IP : 14.49.138.138, 2017-11-03 13:30:33

129	S51529	SPF1 protein [Ipomoea batatas]	63.793	58	3.55E-11
130	T50842	phospholipase C2 [imported] [Nicotiana tabacum]	73.256	86	3.31E-46
131	NP_173712	copper chaperone (CCH)-related [Arabidopsis thaliana]	63.816	152	6.25E-50
132	NP_680687	hypothetical protein [Arabidopsis thaliana]	30.952	84	8.65394E-09
133	P46416	Glutathione synthetase, chloroplast precursor (Glutathione synthase) (GSH synthetase) (GSH-S) [Arabidopsis thaliana]	58.763	97	2.18E-28
134	AAO49811	SEP3-related MADS-box protein; PTM6 [Populus tremuloides]	91.975	162	3.65926E-79
135	AAK52077	dehydrin COR15 [Citrus x paradisi]	98.039	51	1.35E-06
136	AAK97760	endo-beta-mannanase [Lycopersicon esculentum]	58.571	140	4.11199E-43
137	T06404	resistance complex protein I2C-2 [Lycopersicon esculentum]	35.537	121	2.67E-11
138	BAC41811	unknown protein [Arabidopsis thaliana]	78.667	75	3.54E-29
139	AAL33553	pyruvate decarboxylase [Cucumis melo]	83.333	138	2.83447E-60
140	No hits found				
141	NP_565875	expressed protein [Arabidopsis thaliana]	71.831	71	4.46E-19
142	NP_850867	predicted protein [Arabidopsis thaliana]	92	100	1.64E-47
143	NP_568614	expressed protein [Arabidopsis thaliana]	70.476	105	9.64E-41
144	P35007	Adenosylhomocysteinase (S-adenosyl-L-homocysteine hydrolase) (AdoHcyase) [Catharanthus roseus]	89.474	57	1.01E-15
145	Q9ATF5	60S ribosomal protein L18a [Castanea sativa]	96.35	137	4.41E-74
146	AAM14957	hypothetical protein [Arabidopsis thaliana]	73.239	142	5.02E-52
147	NP_916550	putative vesicle transport v-SNARE protein [Oryza sativa (japonica cultivar-group)]	77.711	166	1.2892E-68
148	AAK82489	AT5g56360/MCD7_9 [Arabidopsis thaliana]	60.976	41	5.04E-06
149	No hits found				
150	BAA21921	ZPT2-12 [Petunia x hybrida]	52.326	172	2.48E-29
151	AAM62669	unknown [Arabidopsis thaliana]	78.862	123	1.66E-52
152	BAC84089	putative transducin / WD-40 repeat protein [Oryza sativa (japonica cultivar-group)]	90.789	76	2.70E-37
153	Q40578	Alternative oxidase 2, mitochondrial precursor [Nicotiana tabacum]	61.616	99	8.32E-28
154	BAC66615	L-asparaginase [Glycine max]	92.857	154	6.05E-76
155	No hits found				
156	NP_177275	expressed protein [Arabidopsis thaliana]	63.333	90	2.87E-25
157	NP_198801	40S ribosomal protein S9 (RPS9C) [Arabidopsis thaliana]	92.701	137	1.37E-68
158	NP_568715	expressed protein [Arabidopsis thaliana]	69.068	236	8.95E-79
159	NP_916467	OSJNBa0089K24.4 [Oryza sativa (japonica cultivar-group)]	78.431	102	4.09E-37
160	BAB86890	syringolide-induced protein 19-1-5 [Glycine max]	90.435	115	7.40E-58
161	AAB02913	phosphoribosylanthranilate transferase [Arabidopsis thaliana]	76.389	72	3.83E-15
162	BAC45212	putative eukaryotic translation initiation factor 6 [Oryza sativa (japonica cultivar-group)]	90.816	98	1.20E-45
163	AAM19356	embryo-abundant protein EMB [Pisum sativum]	59.615	156	3.23E-50
164	AAP42136	erg-1 [Solanum tuberosum]	80.769	130	1.35E-61
165	BAA36556	homolog to defender against apoptotic death 1 [Citrus unshiu]	100	87	2.39E-53
166	NP_187201	stress related protein -related [Arabidopsis thaliana]	71.053	228	1.85E-83
167	NP_190500	expressed protein [Arabidopsis thaliana]	68.75	48	3.49E-12
168	No hits found				

IP : 14.49.138.138, 2017-11-03 13:30:33

169	CAD29823	putative ubiquitin-conjugating enzyme [Populus euramericana]	94.375	160	6.77E-90
170	NP_567581	cytochrome P450 family [Arabidopsis thaliana]	81.651	109	1.04448E-50
171	NP_199957	heat shock protein, putative [Arabidopsis thaliana]	52.288	153	3.12E-26
172	AAA18550	putative. proteolipid subunit of vacuolar H+ ATPase [Zea mays]	100	49	9.53E-12
173	NP_173391	plant defensin protein, putative (PDF1.4) [Arabidopsis thaliana]	52.632	57	2.95E-13
174	O22493	Glutamate--cysteine ligase, chloroplast precursor (Gamma-glutamylcysteine synthetase) (Gamma-ECS) (GCS) [Lycopersicon esculentum]	85	120	1.11E-55
175	No hits found				
176	NP_567533	calcineurin B-like protein 1 (CBL1) [Arabidopsis thaliana]	86.508	126	9.88E-58
177	BAB33422	putative senescence-associated protein [Pisum sativum]	75.641	78	5.19E-30
178	BAC42872	unknown protein [Arabidopsis thaliana]	81.159	69	8.89E-30
179	No hits found				
180	NP_200058	MATE efflux protein - related [Arabidopsis thaliana]	68.421	76	2.52834E-26
181	NP_187531	60S acidic ribosomal protein P0 (RPP0B) [Arabidopsis thaliana]	84.536	97	1.82E-41
182	T47996	hypothetical protein F21F14.210 [Arabidopsis thaliana]	78.417	139	8.26E-63
183	No hits found				
184	CAB85635	putative ripening-related P-450 enzyme [Vitis vinifera]	76.667	90	3.19522E-49
185	NP_189303	MutT/nudix family protein [Arabidopsis thaliana]	69.136	81	7.05E-26
186	AAG16758	putative glutathione S-transferase T3 [Lycopersicon esculentum]	66.368	223	2.38E-82
187	CAB99493	protein kinase-like protein [Arabidopsis thaliana]	93.75	48	2.71194E-19
188	S68805	pectin acetylesterase (EC 3.1.1.-) precursor [Vigna radiata var. radiata]	62.821	156	5.29E-54
189	Q39242	Thioredoxin reductase 2 (NADPH-dependent thioredoxin reductase 2) (NTR 2) [Arabidopsis thaliana]	77.869	122	1.82E-44
190	No hits found				
191	BAB10068	emb|CAB80929.1~gene_id:MRO11.1~similar to unknown protein [Arabidopsis thaliana]	61.905	147	1.99E-42
192	AAL12626	leucine-rich repeat receptor-like kinase F21M12.36 [Arabidopsis thaliana]	61.538	78	3.37E-21
193	AAL84973	AT3g05350/T12H1_32 [Arabidopsis thaliana]	83.621	116	2.21E-51
194	AAK43709	ribosomal protein L32 [Mercurialis annua]	93.233	133	3.13698E-56
195	NP_192787	oxidoreductase, 2OG-Fe(II) oxygenase family [Arabidopsis thaliana]	68.605	86	4.96E-28
196	AAM00426	putative terpene synthase [Citrus x paradisi]	99.346	153	2.37168E-83
197	AAM63846	small nuclear ribonucleoprotein, putative [Arabidopsis thaliana]	94.059	101	1.57E-49
198	AAD22104	B12D protein [Ipomoea batatas]	73.864	88	1.64E-33
199	AAK84459	putative serine peptidase [Oryza sativa (japonica cultivar-group)]	73.81	84	6.00E-29
200	CAA80380	mitochondrial tRNA-Ala synthetase [Arabidopsis thaliana]	77.381	84	8.30E-20
201	T07139	cysteine proteinase inhibitor [Glycine max]	78.431	102	4.28135E-40
202	CAC85245	salt tolerance protein 4 [Beta vulgaris]	72.078	154	1.17E-57
203	AAD13305	SC0A [Lycopersicon esculentum]	40.299	67	8.03736E-07
204	AAF26098	unknown protein [Arabidopsis thaliana]	64.532	203	2.24E-64
205	BAA89423	allyl alcohol dehydrogenase [Nicotiana tabacum]	67.742	155	2.10E-55
206	AAF75749	dehydration-induced protein ERD15 [Lycopersicon esculentum]	41.509	106	5.51E-13
207	AAF65767	glutathione S-transferase [Euphorbia esula]	70.755	212	3.54E-79
208	NP_200349	long-chain-alcohol O-fatty-acyltransferase (wax synthase) family [Arabidopsis thaliana]	42.857	154	5.65E-18

IP : 14.49.138.138, 2017-11-03 13:30:33

209	AAD24857	phosphoglycerate mutase [Solanum tuberosum]	83.871	93	6.37E-39
210	AAM63013	unknown [Arabidopsis thaliana]	45.455	165	1.06E-35
211	P35135	Ubiquitin-conjugating enzyme E2-17 kDa (Ubiquitin-protein ligase) (Ubiquitin carrier protein) [Lycopersicon esculentum]	95.868	121	1.10E-65
212	Q39644	Late embryogenesis abundant protein Lea5 [Citrus sinensis]	97.938	97	3.22E-47
213	No hits found				
214	AAD02556	PGPD14 [Petunia x hybrida]	80.556	36	3.38E-12
215	P37707	B2 PROTEIN >gi|322726|pir||S32124 B2 protein [Daucus carota]	94.203	69	2.74E-32
216	AAM64870	putative microtubule-associated protein [Arabidopsis thaliana]	90.826	109	1.21943E-50
217	NP_200615	outer membrane lipo protein - like [Arabidopsis thaliana]	75.806	186	7.34008E-73
218	AAF72202	cysteine protease inhibitor [Manihot esculenta]	62.626	99	2.27E-25
219	CAA67923	ubiquitin-like protein [Arabidopsis thaliana]	88.298	94	1.23E-41
220	AAC16012	polyubiquitin [Elaeagnus umbellata]	99.167	120	1.29E-61
221	AAG49361	ACC oxidase [Citrus sinensis]	100	114	1.53E-61
222	No hits found				
223	No hits found				
224	P51823	ADP-ribosylation factor [Oryza sativa]	99.448	181	6.4987E-100
225	AAD38148	beta-amylase [Prunus armeniaca]	76.371	237	5.86E-106
226	AAK07610	prohibitin 1-like protein [Brassica napus]	87.719	114	2.88E-47
227	BAA31561	metallothionein-like protein [Citrus unshiu]	100	40	2.48E-14
228	P27608	Phospho-2-dehydro-3-deoxyheptonate aldolase 1, chloroplast precursor (Phospho-2-keto-3-deoxyheptonate aldolase 1) (DAHP synthetase 1) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase 1) [Nicotiana tabacum]	98.958	96	2.39E-50
229	AAP45162	putative Mob1/phocein family protein [Solanum bulbocastanum]	95.349	215	3.37E-119
230	P56821	Eukaryotic translation initiation factor 3 subunit 9 (eIF-3 eta) (eIF3 p110) (eIF3b) [Nicotiana tabacum]	88.406	138	5.67E-69
231	AAF73006	NADP-dependent malic protein [Ricinus communis]	89.873	79	9.78E-22
232	CAA10129	hypothetical protein [Cicer arietinum]	84.615	78	8.95E-35
233	AAN74634	heat shock protein [Pisum sativum]	79.63	162	1.41E-58
234	1E09_A	Chain A, Solution Structure Of The Major Cherry Allergen Pru Av 1 [Prunus avium]	49.558	113	2.67898E-27
235	BAB43909	phosphoenolpyruvate carboxykinase [Flaveria pringlei]	63.441	93	1.97E-25
236	CAC44032	snakin-1 [Solanum tuberosum]	82.54	63	2.98E-29
237	NP_182192	auxin-induced (indole-3-acetic acid induced) protein family [Arabidopsis thaliana]	72.881	59	6.83E-22
238	P49198	40S RIBOSOMAL PROTEIN S3A >gi|7441118|pir||T09301 ribosomal protein S3a [Helianthus annuus]	85.088	114	1.13E-47
239	No hits found				
240	AAO20063	putative aspartate kinase [Oryza sativa (japonica cultivar-group)]	85.567	97	3.57E-40
241	CAA66447	RAB1A [Lotus corniculatus var. japonicus]	89.313	131	4.06E-60
242	AAM21199	pathogenesis-related protein 5-1 [Helianthus annuus]	70.352	199	1.34E-88
243	AAG30576	nitrate reductase [Ricinus communis]	88	100	1.37E-37
244	F86214	protein T6D22.2 [imported] [Arabidopsis thaliana]	62.914	151	3.83E-40
245	NP_569012	14-3-3 protein GF14 kappa (grf8) [Arabidopsis thaliana]	82.781	151	2.84944E-66
246	BAA96072	ribosomal protein L29 [Panax ginseng]	86.667	60	2.14037E-25
247	AAF80591	xyloglucan endotransglycosylase XET2 [Asparagus officinalis]	73.554	121	1.31065E-46

IP : 14.49.138.138, 2017-11-03 13:30:33

248	AAO16703	ATPase-like protein [Sorghum bicolor]	69.079	152	3.20E-54
249	AAF76226	14-3-3 protein [Populus x canescens]	93.243	74	1.17E-30
250	CAC37356	putative membrane protein [Solanum tuberosum]	66.216	74	2.67E-22
251	Q43636	Thioredoxin H-type (TRX-H) >gi|7430846|pir||T10170 thioredoxin [Ricinus communis]	89.655	116	1.55E-55
252	NP_197108	UVB-resistance protein-related [Arabidopsis thaliana]	82.927	123	5.53E-56
253	NP_191788	ADP-ribosylation factor [Arabidopsis thaliana]	98.913	92	3.39E-47
254	NP_192117	GTP-binding protein SAR1A [Arabidopsis thaliana]	94.03	67	3.09E-31
255	Q9ZSW9	Translationally controlled tumor protein homolog (TCTP) [Hevea brasiliensis]	91.525	59	3.63E-23
256	NP_186962	ADP-ribosylation factor, putative [Arabidopsis thaliana]	87.179	78	1.61E-34
257	AAR10854	putative ribosomal protein [Oryza sativa (japonica cultivar-group)]	87.097	93	1.94E-40
258	AAM13860	unknown protein [Arabidopsis thaliana]	71.111	225	1.39191E-93
259	No hits found				
260	NP_180326	zinc finger protein -related [Arabidopsis thaliana]	60.366	164	1.02E-49
261	Q9SPB3	60S ribosomal protein L10 (QM protein homolog) [Vitis riparia]	92.727	220	2.61E-121
262	No hits found				
263	NP_175482	expressed protein [Arabidopsis thaliana]	82.022	89	3.90E-37
264	CAC27136	40S ribosomal protein S2 [Picea abies]	85.294	102	8.93E-44
265	No hits found				
266	No hits found				
267	AAF29773	glutathione S-transferase [Gossypium hirsutum]	70.909	55	8.11E-17
268	NP_195713	histone H3.2 [Arabidopsis thaliana]	99.206	126	7.25E-64
269	CAE54083	zinc finger protein [Fagus sylvatica]	79.348	92	1.73E-40
270	No hits found				
271	AAN76363	type I proteinase inhibitor-like protein [Citrus x paradisi]	97.087	103	5.86E-52
272	T10242	(S)-2-hydroxy-acid oxidase (EC 1.1.3.15) [Cucurbita cv. Kurokawa Amakuri]	85.047	107	5.17E-46
273	Q06652	Probable phospholipid hydroperoxide glutathione peroxidase (PHGPx) (Salt-associated protein) [Citrus sinensis]	100	166	1.45E-91
274	NP_180417	lateral organ boundaries (LOB) domain family [Arabidopsis thaliana]	89.247	93	2.26E-43
275	NP_564069	expressed protein [Arabidopsis thaliana]	50	84	3.19E-17
276	P42896	Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) [Ricinus communis]	97.802	91	4.31E-44

6) 진귤 미숙과실

Clone No.	Accession No.	Definition of Putative homologue[Organism]	Matching %	Matching Length	E-value
CT--07-F-L02.ab1	1909359A	ribosomal protein S19 [Solanum tuberosum]	93.9394	33	5.97E-11
CT--07-F-L04.ab1	1909359A	ribosomal protein S19 [Solanum tuberosum]	95.4545	66	9.36E-31
CT--04-F-L09.ab1	1909359B	ribosomal protein L7 [Solanum tuberosum]	92.3077	39	1.83E-07
CT--02-F-M20.ab1	1APX_A	Chain A, Crystal Structure Of Recombinant Ascorbate Peroxidase	95.2381	63	1.68E-17
CT--02-F-M03.ab1	2114378A	aminolevulinate dehydratase [Lycopersicon esculentum]	94.6237	93	3.20E-44
CT--07-F-N15.ab1	A46304	homeotic protein HAT4 - Arabidopsis thaliana	56	100	7.43E-20
CT--02-F-H02.ab1	A47557	S-like ribonuclease RNS2 - Arabidopsis thaliana	55.8824	34	0.0048848

IP : 14.49.138.138, 2017-11-03 13:30:33

CT--04-F-G06.ab1	A57478	serine O-acetyltransferase - watermelon	88.8889	99	1.16E-44
CT--01-F-F21.ab1	A60671	tubulin alpha chain - sea urchin	100	25	2.99E-07
CT--01-F-C14.ab1	AAA18550	putative, proteolipid subunit of vacuolar H+ ATPase [Zea mays]	100	28	3.52E-07
CT--04-F-B04.ab1	AAA56908	homeobox protein [Arabidopsis thaliana]	42.1488	121	7.84E-09
CT--04-F-C08.ab1	AAA80678	small GTP-binding protein [Lycopersicon esculentum]	83.5821	67	1.23E-26
CT--06-F-E03.ab1	AAA96253	GF14omega isoform [Arabidopsis thaliana]	87.5	40	4.28E-14
CT--03-F-N24.ab1	AAA99934	vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]	95.0495	101	5.67E-27
CT--04-F-G15.ab1	AAB05871	PAPS-reductase-like protein [Catharanthus roseus]	88.8889	45	3.38E-16
CT--06-F-B17.ab1	AAB17193	laccase [Liriodendron tulipifera]	86.747	83	2.90E-42
CT--02-F-G17.ab1	AAB62892	catalase-1 [Nicotiana glutinosa]	83.7209	43	3.66E-16
CT--07-F-O06.ab1	AAB62947	LTCOR11 [Lavatera thuringiaca]	69.3548	62	3.87E-24
CT--01-F-H05.ab1	AAB64207	elongation factor 1-alpha [Zea mays]	98.4496	129	3.23E-69
CT--07-F-B06.ab1	AAB65494	hypothetical protein; 51018-49636 [Arabidopsis thaliana]	71.4286	77	6.96E-27
CT--05-F-A15.ab1	AAB70426	Strong similarity to 60S ribosomal protein L17 . EST gb|AA042332 comes from this gene. [Arabidopsis thaliana]	100	33	2.06E-12
CT--07-F-A08.ab1	AAB70433	Similar to Babesia aldo-keto reductase . [Arabidopsis thaliana]	58.4158	101	2.99E-26
CT--04-F-L02.ab1	AAB80624	Strong similarity to Arabidopsis ATHSAR1 . ESTs gb|T44122,gb|N65276,gb|AA041135 come from this gene. [Arabidopsis thaliana]	69.8113	53	4.48E-08
CT--05-F-O01.ab1	AAB86513	putative ribosomal protein S4 [Arabidopsis thaliana]	92	75	6.37E-35
CT--06-F-P02.ab1	AAB97312	salt stress inducible small GTP binding protein Ran1 homolog [Arabidopsis thaliana]	100	36	0.000221
CT--01-F-P09.ab1	AAC09388	xyloglucan endotransglycosylase precursor [Actinidia deliciosa]	80.2469	81	3.03E-39
CT--02-F-D16.ab1	AAC09388	xyloglucan endotransglycosylase precursor [Actinidia deliciosa]	84.4262	122	2.10E-64
CT--03-F-L05.ab1	AAC12797	adenosine triphosphatase; c-subunit of V-ATPase [Vigna radiata]	100	65	4.01E-21
CT--02-F-C24.ab1	AAC15992	chlorophyll a/b binding protein [Oryza sativa]	95.8904	73	5.08E-36
CT--04-F-J16.ab1	AAC16012	polyubiquitin [Elaeagnus umbellata]	98.1818	110	3.19E-55
CT--05-F-A11.ab1	AAC24588	late embryogenesis-like protein [Prunus armeniaca]	86.2069	29	2.52E-07
CT--07-F-P21.ab1	AAC32121	probable 40S ribosomal protein S15 [Picea mariana]	100	67	6.29E-33
CT--07-F-E14.ab1	AAC32140	probable ubiquitin activating enzyme 2 [Picea mariana]	54.5455	33	2.88E-06
CT--07-F-F02.ab1	AAC34983	light harvesting chlorophyll A/B binding protein [Prunus persica]	76.7442	129	8.85E-50
CT--02-F-A18.ab1	AAC36058	calmodulin [Oryza sativa]	100	59	8.34E-27
CT--05-F-H01.ab1	AAC72543	unknown [Oryza sativa] [Oryza sativa]	52.4272	103	9.62E-24
CT--01-F-D04.ab1	AAD03486	MADS1 [Corylus avellana]	77.5	40	8.16E-12
CT--03-F-K12.ab1	AAD09518	NTGP4 [Nicotiana tabacum]	72.1649	97	4.84E-29
CT--02-F-E22.ab1	AAD24540	vacuole-associated annexin VCaB42 [Nicotiana tabacum]	82.1782	101	1.30E-41
CT--01-F-G23.ab1	AAD25793	Belongs to PF|00583 Acetyltransfersase family. [Arabidopsis thaliana]	94.2857	35	7.70E-13
CT--01-F-B21.ab1	AAD27590	elongation factor 1-alpha 1; EF-1-alpha1 [Lilium longiflorum]	100	29	3.23E-09
CT--06-F-L04.ab1	AAD27878	chlorophyll a/b binding protein CP29 [Vigna radiata]	72.2222	72	8.74E-19
CT--04-F-N10.ab1	AAD27882	chlorophyll a/b-binding protein CP24 precursor [Vigna radiata]	90.7563	119	8.82E-61
CT--07-F-A11.ab1	AAD33072	secretory peroxidase [Nicotiana tabacum]	55.8824	34	0.0049208
CT--01-F-N04.ab1	AAD39034	MADS-box protein MADS3 [Nicotiana sylvestris]	95.7746	142	9.41E-71
CT--03-F-D11.ab1	AAD43150	Unknown Protein [Arabidopsis thaliana]	54.902	51	1.40E-10
CT--05-F-E12.ab1	AAD50034	Very similar to SRG1 [Arabidopsis thaliana]	36.9565	46	0.0014945

IP : 14.49.138.138, 2017-11-03 13:30:33

CT--01-F-G17.ab1	AAF13094	unknown protein [Arabidopsis thaliana]	96.2264	53	6.02E-23
CT--04-F-A18.ab1	AAF13094	unknown protein [Arabidopsis thaliana]	95.3488	43	4.51E-17
CT--05-F-P10.ab1	AAF16753	F3M18.15 [Arabidopsis thaliana]	42.0455	88	2.35E-09
CT--06-F-H23.ab1	AAF17236	adenosine-5'-phosphosulfate kinase [Zea mays]	86.2069	29	2.78E-12
CT--01-F-K10.ab1	AAF21428	suppressor of K+ transport growth defect-like protein [Mesembryanthemum crystallinum]	74.4681	47	2.83E-13
CT--01-F-G14.ab1	AAF24583	F22C12.2 [Arabidopsis thaliana]	96	50	3.20E-22
CT--05-F-C10.ab1	AAF27917	nascent polypeptide associated complex alpha chain [Pinus taeda]	88.6364	44	1.65E-14
CT--03-F-L20.ab1	AAF34800	60S ribosomal protein L35 [Euphorbia esula]	96.1538	78	8.41E-35
CT--04-F-I23.ab1	AAF37726	LMW heat shock protein [Euphorbia esula]	60.4938	81	1.18E-18
CT--03-F-H09.ab1	AAF40462	ESTs gb|T76891 and gb|T21582 come from this gene. [Arabidopsis thaliana]	55	60	1.27E-08
CT--04-F-L04.ab1	AAF48120	nbA gene product [Drosophila melanogaster]	50	32	0.0416569
CT--02-F-F15.ab1	AAF60293	chaperonin 21 precursor [Lycopersicon esculentum]	80	70	8.60E-28
CT--06-F-K03.ab1	AAF61440	papain-like cysteine proteinase isoform I [Ipomoea batatas]	97.2603	73	6.90E-39
CT--07-F-D21.ab1	AAF63200	caffeic acid O-3-methyltransferase [Populus tomentosa]	41.7722	158	7.56E-20
CT--07-F-E10.ab1	AAF63824	hypothetical protein [Arabidopsis thaliana]	77.3585	53	2.24E-12
CT--07-F-E12.ab1	AAF63824	hypothetical protein [Arabidopsis thaliana]	76.087	46	1.02E-08
CT--07-F-P01.ab1	AAF64170	plastid ribosomal protein S9 precursor [Spinacia oleracea]	69.2982	114	2.59E-36
CT--03-F-B20.ab1	AAF64457	ribosomal protein L18 [Oreochromis niloticus]	100	15	0.0949927
CT--06-F-B01.ab1	AAF65155	2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase [Catharanthus roseus]	45.283	106	2.46E-11
CT--04-F-A14.ab1	AAF71695	phospholipid transfer protein [Aerides japonica]	70.2703	37	6.21E-08
CT--04-F-L03.ab1	AAF73016	ubiquitin conjugating protein [Avicennia marina]	97.9452	146	4.00E-82
CT--06-F-P15.ab1	AAF78279	Contains similarity to unknown protein F27F5.5 gi|7767655 from Arabidopsis thaliana F27F5 gb|AC007915 and contains a DedA PF|00597 domain. EST gb|T44906 comes from this gene	44.8276	58	2.93E-06
CT--02-F-G19.ab1	AAF78382	T10O22.21 [Arabidopsis thaliana]	71.831	71	3.27E-27
CT--06-F-D02.ab1	AAF79239	F10B6.22 [Arabidopsis thaliana]	72.9412	85	3.74E-30
CT--05-F-A05.ab1	AAF79517	F21D18.7 [Arabidopsis thaliana]	57.1429	77	7.82E-17
CT--07-F-H18.ab1	AAF80655	It is a member of an Uncharacterised protein family PF|01894. ESTs gb|T43915, gb|AA395185 and gb|AI997079 come from this gene. [Arabidopsis thaliana]	87.7193	57	5.97E-25
CT--04-F-O24.ab1	AAF82212	Contains similarity to an unknown protein F7A7_100 gi|7327817 from Arabidopsis thaliana BAC F7A7 gb|AL161946. ESTs gb|N65842, gb|F19836 and gb|AI993679 come from this gene	60.6897	145	5.55E-47
CT--06-F-I20.ab1	AAF82212	Contains similarity to an unknown protein F7A7_100 gi|7327817 from Arabidopsis thaliana BAC F7A7 gb|AL161946. ESTs gb|N65842, gb|F19836 and gb|AI993679 come from this gene	87.1795	39	1.06E-15
CT--02-F-A11.ab1	AAF97276	Contains similarity to RING-H2 finger protein RHG1a from Arabidopsis thaliana gb|AF079183 and contains a Zinc finger PF|00097 domain. EST gb|AV522036 comes from this gene	67.3077	52	1.65E-18
CT--07-F-M23.ab1	AAF98369	patatin-like protein 3 [Nicotiana tabacum]	55.8824	68	2.92E-16
CT--02-F-O10.ab1	AAF99846	Unknown protein [Arabidopsis thaliana]	64	50	0.0006555
CT--03-F-G06.ab1	AAG09086	Unknown Protein [Arabidopsis thaliana]	100	28	5.88E-09
CT--01-F-E24.ab1	AAG10600	MYB-related transcription factor PHAN1 [Pisum sativum]	75.2294	109	9.47E-44
CT--02-F-P12.ab1	AAG13068	Similar to cytokinin oxidase [Arabidopsis thaliana]	69.8413	126	1.16E-44
CT--07-F-F05.ab1	AAG23847	RUB1 conjugating enzyme [Lycopersicon esculentum]	85.7143	49	1.49E-19
CT--07-F-E24.ab1	AAG27431	QM-like protein [Elaeis guineensis]	79.0123	81	3.56E-30
CT--02-F-E02.ab1	AAG34813	glutathione S-transferase GST 23 [Glycine max]	69.697	33	1.14E-07
CT--02-F-F23.ab1	AAG34872	In2-1 protein [Glycine max]	76.8595	121	3.52E-53
CT--02-F-O06.ab1	AAG38522	lectin-related protein precursor [Citrus x paradisi]	44.6154	130	1.23E-20

IP : 14.49.138.138, 2017-11-03 13:30:33

CT--07-F-L24.ab1	AAG38522	lectin-related protein precursor [Citrus x paradisi]	100	61	3.38E-28
CT--01-F-O11.ab1	AAG40371	AT4g27960 [Arabidopsis thaliana]	97.8947	95	1.67E-51
CT--02-F-P11.ab1	AAG40386	AT5g02160 [Arabidopsis thaliana]	87.2727	55	1.38E-21
CT--06-F-N11.ab1	AAG52341	hypothetical protein; 86186-84430 [Arabidopsis thaliana]	59.7826	92	4.14E-23
CT--07-F-A13.ab1	AAG59894	phosphoethanolamine N-methyltransferase [Lycopersicon esculentum]	77.7778	36	2.23E-11
CT--06-F-J12.ab1	AAK00965	putative ubiquitin-conjugating enzyme E2 [Oryza sativa]	100	23	1.74E-06
CT--06-F-P04.ab1	AAK01235	minor allergen hazelnut profilin [Corylus avellana]	95.4545	44	3.85E-18
CT--04-F-E10.ab1	AAK16172	putative glucosyltransferase [Oryza sativa]	52.1277	94	1.47E-23
CT--02-F-C23.ab1	AAK25760	ribosomal protein L33 [Castanea sativa]	91.4894	94	3.60E-46
CT--05-F-N09.ab1	AAK25904	unknown protein [Arabidopsis thaliana]	82.1429	28	2.91E-07
CT--01-F-O10.ab1	AAK27801	60S ribosomal protein L21 [Oryza sativa]	100	28	2.06E-09
CT--01-F-K15.ab1	AAK31146	unknown [Arabidopsis thaliana]	55.814	43	0.0005452
CT--04-F-I24.ab1	AAK38665	stem secoisolariciresinol dehydrogenase [Forsythia x intermedia]	67.8261	115	5.47E-38
CT--04-F-M06.ab1	AAK43709	ribosomal protein L32 [Mercurialis annua]	77.907	86	7.29E-31
CT--02-F-L04.ab1	AAK48956	Unknown protein [Arabidopsis thaliana]	83.7209	43	3.42E-17
CT--03-F-B24.ab1	AAK49947	TGF-beta receptor-interacting protein 1 [Phaseolus vulgaris]	95.6522	115	3.20E-60
CT--01-F-L10.ab1	AAK52587	Putative NADPH-dependent oxidoreductase [Oryza sativa]	54.7945	73	1.72E-20
CT--07-F-D11.ab1	AAK52587	Putative NADPH-dependent oxidoreductase [Oryza sativa]	61.6071	112	2.95E-37
CT--01-F-P14.ab1	AAK55776	Putative small nuclear ribonucleoprotein G [Oryza sativa]	86.2069	29	1.26E-06
CT--03-F-N11.ab1	AAK55776	Putative small nuclear ribonucleoprotein G [Oryza sativa]	84.6154	26	8.82E-05
CT--01-F-F11.ab1	AAK58693	sinapyl alcohol dehydrogenase [Populus tremuloides]	59.4203	69	8.01E-14
CT--04-F-H06.ab1	AAK62446	putative fructokinase [Arabidopsis thaliana]	76.1905	105	2.67E-41
CT--06-F-O21.ab1	AAK68809	similar to GTP-binding protein [Arabidopsis thaliana]	64.0625	64	1.13E-15
CT--02-F-I18.ab1	AAK93649	unknown protein [Arabidopsis thaliana]	72.3077	65	1.76E-24
CT--07-F-I18.ab1	AAK93649	unknown protein [Arabidopsis thaliana]	70	30	6.73E-07
CT--06-F-N10.ab1	AAK94781	gamma hydroxybutyrate dehydrogenase [Arabidopsis thaliana]	77.1429	70	5.24E-16
CT--05-F-F14.ab1	AAK95282	AT4g03280/F4C21_21 [Arabidopsis thaliana]	72.3077	130	7.63E-51
CT--01-F-F17.ab1	AAK95517	cyclase [Nicotiana tabacum]	57.1429	105	4.73E-27
CT--04-F-E05.ab1	AAL06348	submergence induced protein-like protein [Musa acuminata]	53.8462	26	0.0010175
CT--03-F-E06.ab1	AAL09401	ribosomal protein [Petunia x hybrida]	82.6923	52	8.16E-12
CT--03-F-C22.ab1	AAL14412	At1g12410/F5O11_7 [Arabidopsis thaliana]	68.0851	47	1.25E-13
CT--05-F-O11.ab1	AAL14412	At1g12410/F5O11_7 [Arabidopsis thaliana]	59.0909	88	7.13E-31
CT--02-F-O19.ab1	AAL16282	At1g18030/T10F20_3 [Arabidopsis thaliana]	53.3784	148	6.03E-27
CT--03-F-F05.ab1	AAL24258	At1g47530/F16N3_20 [Arabidopsis thaliana]	65.625	32	9.72E-05
CT--05-F-D11.ab1	AAL24269	AT5g51550/K17N15_10 [Arabidopsis thaliana]	87.7358	106	1.85E-42
CT--02-F-H21.ab1	AAL32441	Fe-superoxide dismutase precursor [Medicago sativa]	81.3953	43	1.36E-15
CT--01-F-F03.ab1	AAL35979	extensin-like protein [Cucumis sativus]	72.7273	22	0.0040386
CT--02-F-D06.ab1	AAL38267	unknown protein [Arabidopsis thaliana]	77.9221	77	8.62E-23
CT--01-F-I18.ab1	AAL38757	unknown protein [Arabidopsis thaliana]	66.1538	130	1.42E-34
CT--02-F-J16.ab1	AAL38841	unknown protein [Arabidopsis thaliana]	81.25	32	3.26E-09

IP : 14.49.138.138, 2017-11-03 13:30:33

CT--06-F-F21.ab1	AAL38852	unknown protein [Arabidopsis thaliana]	42.6087	115	4.74E-12
CT--06-F-G17.ab1	AAL49750	aquaporin-like protein [Petunia x hybrida]	96.8254	63	5.17E-31
CT--05-F-P20.ab1	AAL62421	ADP-RIBOSYLATION FACTOR -like protein [Arabidopsis thaliana]	97.2973	74	1.64E-35
CT--01-F-J23.ab1	AAL79831	cystatin [Sandersonia aurantiaca]	85.7143	63	7.18E-25
CT--01-F-M11.ab1	AAL86003	putative E2, ubiquitin-conjugating enzyme UBC7 [Arabidopsis thaliana]	86.4286	140	3.46E-65
CT--07-F-D23.ab1	AAL86003	putative E2, ubiquitin-conjugating enzyme UBC7 [Arabidopsis thaliana]	90	50	2.09E-19
CT--01-F-G24.ab1	AAL91164	unknown protein [Arabidopsis thaliana]	78.125	32	1.25E-06
CT--01-F-F19.ab1	AAL91176	eukaryotic translation initiation factor [Arabidopsis thaliana]	97.561	41	2.87E-16
CT--02-F-L14.ab1	AAL93042	hypothetical protein [Dictyostelium discoideum]	38.0952	63	0.0099139
CT--01-F-B16.ab1	AAM10318	MFL8.1/MFL8.1 [Arabidopsis thaliana]	70	40	4.20E-11
CT--02-F-O21.ab1	AAM12880	GTP-binding protein [Helianthus annuus]	99.2188	128	3.12E-74
CT--06-F-N04.ab1	AAM12880	GTP-binding protein [Helianthus annuus]	100	18	0.0045588
CT--05-F-O06.ab1	BAA23657	EF-1 alpha [Oryza sativa]	95.122	41	2.15E-23
CT--04-F-O16.ab1	BAA31561	metallothionein-like protein [Citrus unshiu]	100	39	7.20E-15
CT--07-F-F17.ab1	BAA81870	ESTD24835 corresponds to a region of the predicted gene.~Similar to Arabidopsis thaliana chromosome II BAC T06D20 genomic sequence, complete sequence. [Oryza sativa]	59.322	59	2.42E-14
CT--04-F-E21.ab1	BAA87043	N-hydroxycinnamoyl/benzoyltransferase [Ipomoea batatas]	61.1511	139	3.11E-46
CT--02-F-C22.ab1	BAA88636	elicitor-inducible LRR receptor-like protein EILP [Nicotiana tabacum]	52.459	61	3.63E-11
CT--05-F-P12.ab1	BAA89230	wts2L [Citrullus lanatus]	37.3913	115	1.71E-07
CT--06-F-B04.ab1	BAA90806	ESTs C26000,AU082130 correspond to a region of the predicted gene.~Similar to mRNA for zinc-finger protein [Oryza sativa]	49.0909	55	2.97E-11
CT--02-F-P09.ab1	BAA92699	type 2A protein phosphatase-3 [Vicia faba]	91.7293	133	3.13E-63
CT--01-F-I01.ab1	BAA96453	F1-ATPase [Pyrus pyrifolia]	90.9091	44	2.15E-14
CT--04-F-G04.ab1	BAA97477	gb|AAF17201.1~gene_id:F2O15.9~similar to unknown protein [Arabidopsis thaliana]	69.1176	68	2.09E-17
CT--07-F-M24.ab1	BAB01889	ER lumen protein-retaining receptor-like protein [Arabidopsis thaliana]	85.1064	47	6.94E-15
CT--03-F-L11.ab1	BAB02761	cytochrome c oxidoreductase-like [Arabidopsis thaliana]	48.1481	54	0.0003408
CT--06-F-L18.ab1	BAB02809	contains similarity to EH domain containing proteins~gene_id:MQC12.3 [Arabidopsis thaliana]	77.2152	79	2.18E-31
CT--01-F-A19.ab1	BAB09444	gene_id:MSI17.3~unknown protein [Arabidopsis thaliana]	54.5455	44	0.0236219
CT--04-F-L06.ab1	BAB09970	contains similarity to chalcone-flavonone isomerase ~gene_id:K18I23.7 [Arabidopsis thaliana]	69.1489	94	1.29E-27
CT--04-F-K02.ab1	BAB10495	gene_id:K21I16.3~unknown protein [Arabidopsis thaliana]	68.9655	29	0.0002152
CT--04-F-N06.ab1	BAB10495	gene_id:K21I16.3~unknown protein [Arabidopsis thaliana]	63.5294	85	3.34E-20
CT--07-F-K07.ab1	BAB10643	cleavage stimulation factor subunit 1-like protein [Arabidopsis thaliana]	82.7586	29	8.37E-06
CT--03-F-M14.ab1	BAB11028	gene_id:MUL8.23~pir||S77152~similar to unknown protein [Arabidopsis thaliana]	70.3704	27	0.0032184
CT--03-F-I01.ab1	BAB11233	6-phosphogluconolactonase-like protein [Arabidopsis thaliana]	60.2564	78	5.37E-20
CT--07-F-P22.ab1	BAB11233	6-phosphogluconolactonase-like protein [Arabidopsis thaliana]	57.971	69	3.89E-24
CT--01-F-A18.ab1	BAB11565	14-3-3 protein GF14 [Arabidopsis thaliana]	84.058	138	2.52E-61
CT--03-F-J04.ab1	BAB17821	vf14-3-3c protein [Vicia faba]	96.1538	52	4.07E-22
CT--07-F-G16.ab1	BAB20580	response regulator 5 [Zea mays]	88.3721	43	7.69E-14
CT--04-F-D05.ab1	BAB32723	contains ESTs AU030293,AU030294~similar to Arabidopsis thaliana chromosome 4, F9D16.100~unknown protein [Oryza sativa]	75.6098	82	1.10E-30
CT--02-F-P10.ab1	BAB32914	contains ESTs AU029632,AU162277~similar to Arabidopsis thaliana chromosome 3 T6K12.29~unknown protein [Oryza sativa]	76.2712	59	1.92E-23
CT--02-F-L02.ab1	BAB40128	hypothetical protein~similar to Arabidopsis thaliana F13M22.18 [Oryza sativa]	80.7692	26	4.10E-05
CT--02-F-I02.ab1	BAB40142	plasma membrane intrinsic protein 1-1 [Pyrus communis]	67.2414	58	1.44E-19

IP : 14.49.138.138, 2017-11-03 13:30:33

CT--07-F-B18.ab1	BAB40143	plasma membrane intrinsic protein 2-2 [Pyrus communis]	83.1169	77	3.66E-23
CT--02-F-N05.ab1	BAB59136	casein kinase II alpha [Triticum aestivum]	88.8889	18	0.063632
CT--01-F-J14.ab1	BAB60678	geranylgeranyl diphosphate synthase [Hevea brasiliensis]	43.5644	101	4.97E-15
CT--07-F-H16.ab1	BAB63491	contains ESTs AU100716,AU029967,C26395~hypothetical protein~similar to Arabidopsis thaliana chromosome 2, At2g25910 [Oryza sativa]	85.7143	35	1.84E-10
CT--02-F-B16.ab1	BAB64099	putative photosystem II subunit precursor [Oryza sativa]	87.3684	95	7.59E-44
CT--04-F-D13.ab1	BAB67953	putative auxin-induced protein [Oryza sativa]	61.0169	59	6.05E-13
CT--04-F-N07.ab1	BAB67953	putative auxin-induced protein [Oryza sativa]	47.7612	67	5.30E-06
CT--05-F-B04.ab1	BAB67953	putative auxin-induced protein [Oryza sativa]	55.9322	59	3.75E-11
CT--04-F-D03.ab1	BAB78597	copper/zinc superoxide dismutase [Bruguiera gymnorrhiza]	89.0244	82	3.38E-31
CT--07-F-F13.ab1	BAB88934	glucosyltransferase NTGT3 [Nicotiana tabacum]	50	126	8.33E-25
CT--07-F-M10.ab1	BAB88939	Rurm1 [Oryza sativa]	72.5275	91	2.67E-31
CT--03-F-H24.ab1	BAB89352	1-aminocyclopropane-1-carboxylate oxidase [Diospyros kaki]	93.1818	44	1.20E-25
CT--03-F-K13.ab1	CAA09042	40S ribosomal protein S6 [Cicer arietinum]	90	60	4.11E-12
CT--03-F-I08.ab1	CAA09603	20S proteasome beta subunit [Cicer arietinum]	87.1795	39	1.40E-14
CT--07-F-O15.ab1	CAA11553	2-oxoglutarate dehydrogenase E2 subunit [Arabidopsis thaliana]	90.4762	42	2.14E-16
CT--02-F-C09.ab1	CAA12199	caffeoyl-CoA 3-O-methyltransferase [Populus balsamifera subsp. trichocarpa]	85.2459	61	1.27E-24
CT--05-F-I15.ab1	CAA18194	putative protein [Arabidopsis thaliana]	87.5	56	1.50E-08
CT--02-F-P20.ab1	CAA63107	ribosomal protein L23 [Spinacia oleracea]	98.5507	69	2.26E-20
CT--07-F-B01.ab1	CAA66034	peroxidase [Populus balsamifera subsp. trichocarpa]	55.5556	36	0.011075
CT--02-F-M10.ab1	CAA67969	MADS5 protein [Betula pendula]	75	28	0.000175
CT--07-F-I22.ab1	CAA75386	3-deoxy-D-arabino-heptulosonate 7-phosphate synthase; 2-dehydro-3-deoxyphosphoheptonate aldolase [Morinda citrifolia]	87.8788	33	4.07E-10
CT--02-F-H10.ab1	CAB09799	hypothetical protein [Citrus x paradisi]	97.2973	37	8.77E-15
CT--06-F-A01.ab1	CAB42658	iron sulfur subunit of succinate dehydrogenase and ribosomal protein S14 [Zea mays]	72.3404	94	5.86E-33
CT--02-F-I12.ab1	CAB45387	NAD-malate dehydrogenase [Nicotiana tabacum]	86.8421	38	3.76E-11
CT--02-F-G20.ab1	CAB72130	heat shock protein 70 [Cucumis sativus]	87.234	47	1.00E-07
CT--02-F-K20.ab1	CAB85625	putative ripening-related protein [Vitis vinifera]	70.4225	71	4.24E-25
CT--03-F-O11.ab1	CAB90214	putative elongation factor 1 beta [Hordeum vulgare subsp. vulgare]	85.5072	69	4.35E-28
CT--04-F-B13.ab1	CAB90214	putative elongation factor 1 beta [Hordeum vulgare subsp. vulgare]	84.7222	72	9.28E-30
CT--02-F-P05.ab1	CAC12882	O-linked GlcNAc transferase like [Nicotiana tabacum]	85	40	5.00E-12
CT--02-F-L10.ab1	CAC34489	putative protein [Arabidopsis thaliana]	66.2162	74	1.83E-17
CT--01-F-L21.ab1	CAC39061	putative protein [Oryza sativa]	87.0968	31	2.14E-08
CT--03-F-O04.ab1	CAC39071	DnaJ-like protein [Oryza sativa]	64.5161	62	8.21E-12
CT--05-F-C09.ab1	CAC83750	reversibly glycosylated polypeptide [Gossypium hirsutum]	74.4681	47	2.98E-13
CT--03-F-H15.ab1	CAC84489	putative translation factor [Pinus pinaster]	88.4956	113	3.85E-48
CT--04-F-E23.ab1	CAC84547	dicarboxylate/tricarboxylate carrier [Nicotiana tabacum]	94.5946	37	4.43E-15
CT--04-F-G01.ab1	CAC86996	ATP citrate lyase b-subunit [Lupinus albus]	83.8983	118	7.11E-52
CT--03-F-N04.ab1	CAD21142	ribosome-associated protein [Neurospora crassa]	49.1803	122	7.16E-31
CT--02-F-A06.ab1	H71409	hypothetical protein - Arabidopsis thaliana	41.5094	159	6.63E-18
CT--02-F-L06.ab1	JC2511	beta-tubulin R2242 - rice	100	42	1.03E-18
CT--02-F-H14.ab1	NP_027545	expressed protein [Arabidopsis thaliana]	86.6667	45	2.58E-23

IP : 14.49.138.138, 2017-11-03 13:30:33

CT--02-F-N15.ab1	NP_084540	hypothetical protein MGC6623 [Mus musculus]	91.5663	83	6.69E-41
CT--04-F-F17.ab1	NP_171963	putative K+ channel, beta subunit [Arabidopsis thaliana]	86.6667	75	8.61E-31
CT--02-F-N14.ab1	NP_172094	salt-tolerance protein [Arabidopsis thaliana]	54.6512	86	1.05E-17
CT--04-F-G08.ab1	NP_172638	Avr9 elicitor response-like protein [Arabidopsis thaliana]	41.4286	70	5.17E-05
CT--02-F-B17.ab1	NP_172893	DNA-binding protein p24, putative [Arabidopsis thaliana]	69.2308	52	1.77E-18
CT--04-F-D14.ab1	NP_173079	hypothetical protein [Arabidopsis thaliana]	72.7273	55	6.58E-33
CT--04-F-M03.ab1	NP_173114	NADH:ubiquinone oxidoreductase, putative [Arabidopsis thaliana]	100	17	0.0134538
CT--02-F-A02.ab1	NP_173261	pathogenesis-related group 5 protein, putative [Arabidopsis thaliana]	66.6667	72	2.36E-24
CT--02-F-G12.ab1	NP_173387	GSH-dependent dehydroascorbate reductase 1, putative [Arabidopsis thaliana]	75.8621	87	1.53E-34
CT--03-F-F17.ab1	NP_173923	transmembrane protein, putative [Arabidopsis thaliana]	79.0323	62	4.11E-22
CT--03-F-J18.ab1	NP_174108	hypothetical protein [Arabidopsis thaliana]	36.7347	49	0.0928019
CT--02-F-F20.ab1	NP_174210	19S proteosome subunit 9, putative [Arabidopsis thaliana]	91.1111	90	8.81E-41
CT--06-F-D04.ab1	NP_174351	coatomer-like protein, epsilon subunit [Arabidopsis thaliana]	84.375	96	1.85E-34
CT--01-F-I08.ab1	NP_174376	hypothetical protein [Arabidopsis thaliana]	60	55	5.86E-12
CT--05-F-L01.ab1	NP_175482	unknown protein [Arabidopsis thaliana]	90.9091	44	2.98E-18
CT--07-F-I24.ab1	NP_175517	histone H2A, putative [Arabidopsis thaliana]	100	76	6.65E-26
CT--03-F-L18.ab1	NP_175576	epsilon subunit of mitochondrial F1-ATPase [Arabidopsis thaliana]	89.8551	69	5.05E-32
CT--03-F-B09.ab1	NP_175641	protein kinase, putative [Arabidopsis thaliana]	87.8049	41	3.20E-14
CT--01-F-B12.ab1	NP_175669	signal peptidase subunit, putative [Arabidopsis thaliana]	94.9153	59	3.63E-26
CT--07-F-D12.ab1	NP_175963	photosystem I subunit V precursor, putative [Arabidopsis thaliana]	94.5946	37	6.17E-28
CT--01-F-E12.ab1	NP_176075	integral membrane protein, putative [Arabidopsis thaliana]	80	70	3.33E-27
CT--01-F-E20.ab1	NP_176291	ferrodoxin precursor [Arabidopsis thaliana]	89.2857	28	2.01E-08
CT--01-F-C23.ab1	NP_176395	symbiosis-related protein, putative [Arabidopsis thaliana]	92.0354	113	2.07E-54
CT--02-F-P07.ab1	NP_176568	unknown protein [Arabidopsis thaliana]	57.2414	145	1.16E-42
CT--04-F-G18.ab1	NP_178073	phosphoglycerate kinase, putative [Arabidopsis thaliana]	94.5652	92	1.23E-43
CT--02-F-D13.ab1	NP_178163	hypothetical protein [Arabidopsis thaliana]	84.9057	53	6.54E-21
CT--02-F-J06.ab1	NP_178204	unknown protein [Arabidopsis thaliana]	68.1818	22	6.19E-05
CT--03-F-L06.ab1	NP_178453	putative esterase [Arabidopsis thaliana]	42.8571	49	3.18E-05
CT--03-F-K02.ab1	NP_179558	copia-like retroelement pol polyprotein [Arabidopsis thaliana]	100	31	1.30E-12
CT--05-F-A24.ab1	NP_179646	putative heat shock protein [Arabidopsis thaliana]	65.3846	52	1.37E-14
CT--05-F-C23.ab1	NP_179713	putative triosephosphate isomerase [Arabidopsis thaliana]	100	18	0.0231644
CT--04-F-P09.ab1	NP_179822	putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	37.6623	77	1.19E-09
CT--01-F-N06.ab1	NP_180719	40S ribosomal protein; contains C-terminal domain [Arabidopsis thaliana]	94.4444	126	2.88E-61
CT--05-F-H17.ab1	NP_180831	putative cytochrome b5 [Arabidopsis thaliana]	86.6667	45	2.98E-31
CT--02-F-J24.ab1	NP_180879	mitochondrial chaperonin [Arabidopsis thaliana]	68.1818	44	1.06E-10
CT--05-F-J21.ab1	NP_180909	hypothetical protein [Arabidopsis thaliana]	52.2727	88	7.20E-17
CT--04-F-J21.ab1	NP_181046	putative thioredoxin [Arabidopsis thaliana]	60.8696	46	3.48E-09
CT--05-F-K22.ab1	NP_181057	glycine decarboxylase complex H-protein [Arabidopsis thaliana]	80.5755	139	6.01E-60
CT--01-F-I16.ab1	NP_181187	putative fructose bisphosphate aldolase [Arabidopsis thaliana]	89.7959	49	5.92E-18
CT--04-F-F12.ab1	NP_181196	putative receptor-like protein kinase [Arabidopsis thaliana]	75.8621	29	2.26E-06

IP : 14.49.138.138, 2017-11-03 13:30:33

CT--01-F-N23.ab1	NP_181277	putative protein translocase [Arabidopsis thaliana]	70	30	0.0009915
CT--06-F-H04.ab1	NP_181674	ERD15 protein [Arabidopsis thaliana]	76.9231	65	2.20E-26
CT--03-F-I23.ab1	NP_181827	putative APG isolog protein [Arabidopsis thaliana]	44.8598	107	7.29E-26
CT--04-F-D01.ab1	NP_181874	60S ribosomal protein L38 [Arabidopsis thaliana]	94.2029	69	1.05E-31
CT--01-F-I04.ab1	NP_182109	putative AT-hook DNA-binding protein [Arabidopsis thaliana]	42.3913	92	1.79E-06
CT--02-F-K09.ab1	NP_186983	unknown protein [Arabidopsis thaliana]	72	25	0.0112211
CT--02-F-M07.ab1	NP_187142	putative mitogen activated protein kinase kinase [Arabidopsis thaliana]	45.5224	134	1.02E-22
CT--06-F-B05.ab1	NP_187420	putative P-protein: chorismate mutase, prephenate dehydratase [Arabidopsis thaliana]	91.3043	23	5.26E-05
CT--07-F-P13.ab1	NP_187780	hypothetical protein [Arabidopsis thaliana]	69.6429	56	1.01E-15
CT--01-F-B19.ab1	NP_187865	unknown protein [Arabidopsis thaliana]	73.1707	41	3.86E-10
CT--06-F-N03.ab1	NP_188422	hypothetical protein [Arabidopsis thaliana]	41.1765	102	2.74E-06
CT--01-F-K22.ab1	NP_189339	hypothetical protein [Arabidopsis thaliana]	66.6667	66	3.46E-21
CT--02-F-C04.ab1	NP_189421	50S ribosomal protein L12-A [Arabidopsis thaliana]	57.5758	66	1.63E-11
CT--02-F-N09.ab1	NP_189984	ribosomal S29 -like protein [Arabidopsis thaliana]	87.5	56	4.77E-26
CT--04-F-L22.ab1	NP_189996	putative protein [Arabidopsis thaliana]	53.8462	130	7.78E-33
CT--03-F-O24.ab1	NP_190278	dUTP pyrophosphatase-like protein [Arabidopsis thaliana]	79.3103	29	9.28E-06
CT--03-F-H16.ab1	NP_190735	putative protein [Arabidopsis thaliana]	60.4651	43	4.76E-06
CT--04-F-O05.ab1	NP_191007	putative protein [Arabidopsis thaliana]	80.2469	81	1.68E-27
CT--03-F-J08.ab1	NP_191507	fructokinase-like protein [Arabidopsis thaliana]	81.0526	95	3.67E-39
CT--01-F-C10.ab1	NP_191681	putative protein [Arabidopsis thaliana]	61.6438	73	5.87E-19
CT--02-F-F12.ab1	NP_191705	RING finger protein [Arabidopsis thaliana]	57.9832	119	4.72E-29
CT--02-F-I05.ab1	NP_191721	exonuclease RRP41 [Arabidopsis thaliana]	80	25	0.0011311
CT--01-F-L22.ab1	NP_192056	putative water channel protein [Arabidopsis thaliana]	82.7586	87	4.55E-39
CT--03-F-E07.ab1	NP_192170	tryptophan synthase alpha 1-like protein [Arabidopsis thaliana]	84.6154	39	3.42E-11
CT--01-F-O21.ab1	NP_192230	putative xyloglucan endotransglycosylase [Arabidopsis thaliana]	64.5833	96	5.84E-34
CT--07-F-O24.ab1	NP_192634	putative phi-1-like phosphate-induced protein [Arabidopsis thaliana]	67.1875	64	4.80E-21
CT--01-F-H18.ab1	NP_193202	RNA polymerase II fifth largest subunit like protein [Arabidopsis thaliana]	66.3793	116	9.60E-45
CT--04-F-J11.ab1	NP_193313	SYBL1 like protein [Arabidopsis thaliana]	65.3543	127	4.05E-37
CT--04-F-N24.ab1	NP_193718	putative protein [Arabidopsis thaliana]	56.1404	171	4.48E-41
CT--04-F-L14.ab1	NP_194071	water channel - like protein [Arabidopsis thaliana]	97.1429	35	1.22E-14
CT--03-F-J22.ab1	NP_194296	putative protein [Arabidopsis thaliana]	46.3415	41	0.0025492
CT--06-F-E04.ab1	NP_194319	putative acidic ribosomal protein [Arabidopsis thaliana]	86.9565	46	2.13E-14
CT--07-F-L13.ab1	NP_194377	putative protein [Arabidopsis thaliana]	57.5	40	8.41E-08
CT--07-F-N14.ab1	NP_194791	putative protein [Arabidopsis thaliana]	71.9298	57	5.04E-13
CT--04-F-N12.ab1	NP_194842	putative protein [Arabidopsis thaliana]	78.8732	71	1.38E-21
CT--01-F-L12.ab1	NP_195013	putative protein [Arabidopsis thaliana]	44.1176	34	0.0073313
CT--03-F-P16.ab1	NP_195072	putative protein [Arabidopsis thaliana]	61.1111	144	1.33E-32
CT--02-F-L22.ab1	NP_195662	GTP-binding - like protein [Arabidopsis thaliana]	93.1034	29	5.80E-09
CT--03-F-I16.ab1	NP_195825	putative protein [Arabidopsis thaliana]	45.4545	132	4.97E-17
CT--07-F-J01.ab1	NP_195891	putative protein [Arabidopsis thaliana]	73.6111	72	2.37E-33

IP : 14.49.138.138, 2017-11-03 13:30:33

CT--01-F-O02.ab1	NP_196069	putative protein [Arabidopsis thaliana]	74.0741	54	2.86E-16
CT--01-F-I17.ab1	NP_196082	8-amino-7-oxononanoate synthase - like protein [Arabidopsis thaliana]	64.7059	102	2.44E-34
CT--01-F-O14.ab1	NP_196578	-hydroxymyristoyl- dehydratase -like protein [Arabidopsis thaliana]	94.9153	59	4.26E-25
CT--02-F-P08.ab1	NP_196652	putative protein [Arabidopsis thaliana]	46.25	80	8.10E-11
CT--06-F-G11.ab1	NP_196822	NAM-like protein [Arabidopsis thaliana]	37.9747	79	6.51E-07
CT--07-F-A23.ab1	NP_196845	putative protein [Arabidopsis thaliana]	87.8049	41	1.06E-23
CT--02-F-E08.ab1	NP_197406	putative protein [Arabidopsis thaliana]	70.4	125	1.86E-36
CT--01-F-H24.ab1	NP_197430	phospholipase - like protein [Arabidopsis thaliana]	75	116	1.64E-51
CT--01-F-O06.ab1	NP_197483	putative protein [Arabidopsis thaliana]	86.6667	30	6.11E-06
CT--01-F-L08.ab1	NP_198197	PS I antenna protein Lhca2 fragment [Arabidopsis thaliana]	94.1176	85	1.05E-44
CT--05-F-F12.ab1	NP_198418	putative protein [Arabidopsis thaliana]	95.7447	47	5.37E-19
CT--01-F-A20.ab1	NP_198627	anti-silencing factor 1-like protein [Arabidopsis thaliana]	90	60	1.52E-28
CT--06-F-A16.ab1	NP_198790	ribosomal protein L5 - like [Arabidopsis thaliana]	89.2857	112	6.60E-58
CT--07-F-G05.ab1	NP_198824	putative protein [Arabidopsis thaliana]	73.5294	34	1.75E-14
CT--02-F-N04.ab1	NP_199196	aluminum-induced protein-like [Arabidopsis thaliana]	78.125	64	8.25E-23
CT--06-F-C22.ab1	NP_199326	ras-related GTP-binding protein RHA1 [Arabidopsis thaliana]	94.8052	77	2.12E-35
CT--03-F-F16.ab1	NP_199373	putative protein [Arabidopsis thaliana]	78	50	4.06E-16
CT--01-F-N10.ab1	NP_199544	palmitoyl-protein thioesterase precursor-like [Arabidopsis thaliana]	50	46	2.72E-06
CT--04-F-C17.ab1	NP_199598	putative protein [Arabidopsis thaliana]	81.5789	76	7.78E-33
CT--01-F-F16.ab1	NP_199683	putative protein [Arabidopsis thaliana]	59.8214	112	3.44E-33
CT--05-F-I09.ab1	NP_199687	60S ribosomal protein L13a [Arabidopsis thaliana]	75	40	2.71E-10
CT--04-F-A05.ab1	NP_200119	putative protein [Arabidopsis thaliana]	82.7586	29	3.12E-15
CT--03-F-E12.ab1	NP_200265	putative protein [Arabidopsis thaliana]	28.9855	69	0.0367528
CT--04-F-K09.ab1	NP_200311	FH protein interacting protein FIP2 [Arabidopsis thaliana]	83.7209	86	1.44E-36
CT--04-F-A04.ab1	NP_200560	CCHH finger protein 2-like protein [Arabidopsis thaliana]	74.4186	86	1.74E-24
CT--03-F-O08.ab1	NP_200632	bis-triphosphatase-like; also similar to fragile histidine triad [Arabidopsis thaliana]	75	44	2.24E-12
CT--04-F-K21.ab1	NP_200632	bis-triphosphatase-like; also similar to fragile histidine triad [Arabidopsis thaliana]	78.3784	111	7.02E-46
CT--05-F-C11.ab1	NP_200632	bis-triphosphatase-like; also similar to fragile histidine triad [Arabidopsis thaliana]	54.5455	33	0.0416569
CT--01-F-A02.ab1	NP_201035	putative protein [Arabidopsis thaliana]	58.9286	56	5.80E-11
CT--04-F-G23.ab1	NP_201231	phi-1-like protein [Arabidopsis thaliana]	80	90	7.03E-39
CT--06-F-B24.ab1	NP_201242	beta-ureidopropionase [Arabidopsis thaliana]	83.6957	92	8.30E-43
CT--02-F-O23.ab1	NP_229486	conserved hypothetical protein [Thermotoga maritima]	48.7179	39	0.0409626
CT--04-F-H24.ab1	NP_249984	hypothetical protein [Pseudomonas aeruginosa]	31.25	96	0.0002064
CT--04-F-K12.ab1	NP_310552	putative transport protein [Escherichia coli O157:H7]	100	171	1.86E-82
CT--01-F-G12.ab1	NP_502933	Y7A9C.3.p [Caenorhabditis elegans]	31.8841	69	0.0371207
CT--07-F-F21.ab1	NP_563698	expressed protein [Arabidopsis thaliana]	51.4563	103	1.45E-19
CT--01-F-F18.ab1	NP_563780	expressed protein [Arabidopsis thaliana]	90.9091	55	2.68E-25
CT--02-F-H12.ab1	NP_563823	expressed protein [Arabidopsis thaliana]	67.1053	76	8.70E-24
CT--03-F-D18.ab1	NP_564150	expressed protein [Arabidopsis thaliana]	79.2208	77	1.72E-31
CT--06-F-H02.ab1	NP_564308	Expressed protein [Arabidopsis thaliana]	62.8866	97	9.30E-27

IP : 14.49.138.138, 2017-11-03 13:30:33

CT--01-F-K02.ab1	NP_564334	expressed protein [Arabidopsis thaliana]	35.4545	110	2.34E-07
CT--01-F-P18.ab1	NP_564482	expressed protein [Arabidopsis thaliana]	51.7857	56	1.60E-07
CT--03-F-J23.ab1	NP_564507	expressed protein [Arabidopsis thaliana]	66.6667	48	2.21E-27
CT--02-F-O18.ab1	NP_564748	expressed protein [Arabidopsis thaliana]	40.5797	69	4.16E-05
CT--01-F-D14.ab1	NP_564819	expressed protein [Arabidopsis thaliana]	96.1538	26	1.41E-06
CT--03-F-E17.ab1	NP_564933	Expressed protein [Arabidopsis thaliana]	41.1765	51	0.0014697
CT--02-F-F06.ab1	NP_564974	expressed protein [Arabidopsis thaliana]	60.7143	84	7.95E-18
CT--03-F-M08.ab1	NP_565029	expressed protein [Arabidopsis thaliana]	70	70	4.91E-21
CT--01-F-D16.ab1	NP_565057	Expressed protein [Arabidopsis thaliana]	74.6032	63	2.52E-07
CT--06-F-I11.ab1	NP_565076	expressed protein [Arabidopsis thaliana]	41.2371	97	1.34E-11
CT--06-F-N15.ab1	NP_565206	expressed protein [Arabidopsis thaliana]	43.6364	55	3.19E-07
CT--01-F-O17.ab1	NP_565284	NAM -like protein [Arabidopsis thaliana]	87.931	116	4.83E-57
CT--03-F-F14.ab1	NP_565294	expressed protein [Arabidopsis thaliana]	84.8485	66	1.50E-18
CT--06-F-E01.ab1	NP_565336	expressed protein [Arabidopsis thaliana]	83.3333	90	1.74E-21
CT--01-F-N03.ab1	NP_565409	expressed protein [Arabidopsis thaliana]	65.8537	41	1.16E-11
CT--07-F-B11.ab1	NP_565561	expressed protein [Arabidopsis thaliana]	88.3721	43	7.10E-14
CT--06-F-I22.ab1	NP_565834	E2, ubiquitin-conjugating enzyme, putative [Arabidopsis thaliana]	88.7324	71	5.96E-33
CT--03-F-J16.ab1	NP_565836	ubiquitin extension protein [Arabidopsis thaliana]	100	34	9.32E-15
CT--01-F-L05.ab1	NP_566014	expressed protein [Arabidopsis thaliana]	68.9655	58	4.65E-15
CT--07-F-O04.ab1	NP_566526	expressed protein [Arabidopsis thaliana]	64.4444	90	1.86E-26
CT--06-F-C04.ab1	NP_566535	putative ribosomal protein [Arabidopsis thaliana]	92.7711	83	5.29E-42
CT--03-F-P22.ab1	NP_566677	expressed protein [Arabidopsis thaliana]	75	44	5.23E-12
CT--07-F-C06.ab1	NP_566691	expressed protein [Arabidopsis thaliana]	44.2623	61	3.98E-07
CT--05-F-K11.ab1	NP_566715	putative selenocysteine methyltransferase [Arabidopsis thaliana]	80.5556	36	7.10E-10
CT--06-F-J03.ab1	NP_566858	expressed protein [Arabidopsis thaliana]	43.4343	99	9.18E-23
CT--04-F-O02.ab1	NP_567154	putative YABBY3 axial regulator [Arabidopsis thaliana]	51.6779	149	1.02E-31
CT--02-F-E23.ab1	NP_567663	HSP associated protein like [Arabidopsis thaliana]	87.8049	41	2.93E-14
CT--01-F-P13.ab1	NP_567726	expressed protein [Arabidopsis thaliana]	48.8889	45	0.0081138
CT--04-F-G22.ab1	NP_567832	Expressed protein [Arabidopsis thaliana]	76.7857	56	1.76E-16
CT--03-F-P04.ab1	NP_567835	mRNA cleavage factor subunit - like protein [Arabidopsis thaliana]	71.831	71	4.14E-26
CT--04-F-N18.ab1	NP_567871	predicted protein [Arabidopsis thaliana]	52	75	3.18E-10
CT--07-F-O08.ab1	NP_567872	predicted protein [Arabidopsis thaliana]	73.7705	61	1.11E-20
CT--01-F-N16.ab1	NP_567979	putative protein [Arabidopsis thaliana]	81.8182	44	1.28E-13
CT--07-F-G23.ab1	NP_567984	putative protein [Arabidopsis thaliana]	100	23	7.06E-15
CT--01-F-P17.ab1	NP_568013	putative protein [Arabidopsis thaliana]	70	40	1.72E-08
CT--05-F-O12.ab1	NP_568040	expressed protein [Arabidopsis thaliana]	74.6667	75	2.15E-36
CT--01-F-A12.ab1	NP_568046	putative thaumatin-like protein [Arabidopsis thaliana]	67.8571	112	1.01E-40
CT--04-F-P03.ab1	NP_568103	putative protein [Arabidopsis thaliana]	55.2632	38	0.0013165
CT--04-F-I18.ab1	NP_568115	Expressed protein [Arabidopsis thaliana]	71.4286	63	3.12E-21
CT--02-F-G18.ab1	NP_568331	Expressed protein [Arabidopsis thaliana]	51.6484	91	1.38E-21

IP : 14.49.138.138, 2017-11-03 13:30:33

CT--01-F-H06.ab1	NP_568392	expressed protein [Arabidopsis thaliana]	79.5455	44	2.11E-21
CT--06-F-L24.ab1	NP_568699	Expressed protein [Arabidopsis thaliana]	53.5714	56	1.40E-10
CT--01-F-O24.ab1	NP_568727	Expressed protein [Arabidopsis thaliana]	80	40	2.67E-11
CT--07-F-P10.ab1	NP_568906	putative protein [Arabidopsis thaliana]	70.2128	47	4.98E-13
CT--07-F-P12.ab1	NP_568906	putative protein [Arabidopsis thaliana]	75.7576	33	4.07E-07
CT--07-F-A10.ab1	NP_568976	expressed protein [Arabidopsis thaliana]	88.4058	69	2.53E-32
CT--06-F-D22.ab1	NP_596201	hypothetical F-box domain protein [Schizosaccharomyces pombe]	28.9474	114	8.09E-10
CT--07-F-J11.ab1	O04885	LACTOYLGLUTATHIONE LYASE	85.7143	49	1.80E-21
CT--01-F-M24.ab1	O23787	Thiazole biosynthetic enzyme, chloroplast precursor	100	44	1.73E-18
CT--06-F-G23.ab1	O48922	CYTOCHROME P450 98A2	81.0127	79	1.51E-34
CT--07-F-B16.ab1	O49884	60S RIBOSOMAL PROTEIN L30	91.0891	101	3.85E-50
CT--03-F-A19.ab1	O50003	60S RIBOSOMAL PROTEIN L12	91.4894	47	5.24E-18
CT--07-F-F23.ab1	O81263	Thymidine kinase	86.6667	30	2.03E-05
CT--01-F-K23.ab1	O81363	40S ribosomal protein S4	81.1594	69	3.43E-26
CT--04-F-P16.ab1	O81363	40S ribosomal protein S4	92.1053	76	2.72E-62
CT--05-F-I20.ab1	P26518	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC	88.7097	124	1.42E-59
CT--02-F-B05.ab1	P28643	3-oxoacyl-[acyl-carrier protein] reductase, chloroplast precursor	81.25	32	2.20E-08
CT--06-F-B02.ab1	P34091	60S RIBOSOMAL PROTEIN L6	82.9268	41	4.63E-13
CT--03-F-F04.ab1	P35694	Brassinosteroid-regulated protein BRU1 precursor	69.697	99	1.73E-32
CT--04-F-L11.ab1	P42056	36 kDa outer mitochondrial membrane protein porin	94.3662	71	6.18E-32
CT--03-F-K18.ab1	P42553	DNA BINDING PROTEIN S1FA	67.5676	74	0.0143173
CT--05-F-M12.ab1	P42896	ENOLASE	82.1782	101	3.67E-42
CT--03-F-H21.ab1	P46277	G2/mitotic-specific cyclin 1	68.8172	93	1.12E-31
CT--03-F-H12.ab1	P48495	Triosephosphate isomerase, cytosolic	85.3659	82	5.39E-34
CT--04-F-D22.ab1	P49198	40S RIBOSOMAL PROTEIN S3A	88.4615	78	1.65E-31
CT--01-F-L15.ab1	P52424	Phosphoribosylformylglycinamidine cyclo-ligase, chloroplast precursor	76.6667	30	1.92E-08
CT--04-F-E12.ab1	P93847	60S RIBOSOMAL PROTEIN L10	87.0968	62	6.24E-26
CT--03-F-C09.ab1	Q03666	PROBABLE GLUTATHIONE S-TRANSFERASE	70.9677	62	1.02E-21
CT--04-F-H04.ab1	Q08069	40S ribosomal protein S8	92.7273	55	8.00E-24
CT--07-F-C05.ab1	Q40519	Photosystem II 10 kDa polypeptide, chloroplast precursor	88.2353	68	1.13E-23
CT--05-F-E11.ab1	Q41387	Photosystem II reaction center W protein, chloroplast precursor	59.1837	98	4.73E-19
CT--05-F-K23.ab1	Q42463	DCL PROTEIN, CHLOROPLAST PRECURSOR	89.5522	67	8.13E-31
CT--02-F-G03.ab1	Q43019	NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR	69.0476	42	3.63E-11
CT--06-F-I19.ab1	Q43019	NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR	69.6429	56	6.72E-18
CT--07-F-N19.ab1	Q43814	Ornithine carbamoyltransferase, chloroplast precursor	53.5211	71	1.03E-12
CT--02-F-L12.ab1	Q43843	Ribulose-phosphate 3-epimerase, chloroplast precursor	91.6667	72	1.92E-31
CT--02-F-P18.ab1	Q96499	60S RIBOSOMAL PROTEIN L44	100	105	2.25E-58
CT--01-F-A15.ab1	Q9SLQ8	Oxygen-evolving enhancer protein 2, chloroplast precursor	81.4433	97	7.46E-38
CT--03-F-P13.ab1	Q9SP55	Vacuolar ATP synthase subunit G	94.8276	58	1.26E-23
CT--05-F-C12.ab1	Q9XF97	60S ribosomal protein L4	88.3721	43	2.69E-09

IP : 14.49.138.138, 2017-11-03 13:30:33

CT--02-F-O22.ab1	Q9ZT05	Photosystem I reaction center subunit X, chloroplast precursor	95.7447	47	4.89E-27
CT--03-F-I21.ab1	Q9ZWQ9	Flavonol synthase	97.619	126	1.34E-65
CT--01-F-M03.ab1	S22522	chlorophyll a/b-binding protein precursor - Japanese black pine	78.7234	141	3.14E-55
CT--05-F-G06.ab1	S28827	chlorophyll a/b-binding protein type I - common tobacco	87.5	56	1.83E-22
CT--07-F-L22.ab1	S65062	fiber protein E6 - upland cotton	50.8197	61	9.27E-07
CT--07-F-J05.ab1	T01782	GDP dissociation inhibitor - common tobacco	89.7436	78	3.65E-62
CT--04-F-M02.ab1	T04077	probable ribosomal protein L9 - rice	88.6792	53	5.03E-20
CT--07-F-E02.ab1	T05707	phosphate transport protein G7, mitochondrial - soybean	88.7324	71	1.58E-23
CT--02-F-L08.ab1	T07086	acid phosphatase - soybean	43.3962	106	3.02E-18
CT--06-F-M02.ab1	T07780	remorin - potato	89.2308	65	2.72E-26
CT--03-F-M11.ab1	T09399	caffeoyl-CoA O-methyltransferase - alfalfa	80	75	1.39E-25
CT--02-F-B06.ab1	T09541	transketolase TKT1 precursor, chloroplast [validated] - pepper	92.1053	38	1.44E-12
CT--01-F-B03.ab1	T09704	probable arginine/serine-rich splicing factor - alfalfa	77.6119	134	6.30E-55
CT--03-F-M23.ab1	T10106	chitinase precursor - sweet orange	68.932	103	1.83E-30
CT--02-F-J08.ab1	T10106	chitinase precursor - sweet orange	100	50	2.10E-24
CT--03-F-G10.ab1	T10173	24-sterol C-methyltransferase - castor bean	91.8919	37	1.02E-12
CT--03-F-H22.ab1	T10174	hypothetical protein - castor bean	72.7273	121	1.97E-44
CT--04-F-C14.ab1	T10790	peroxidase - upland cotton	91.3462	104	1.82E-51
CT--01-F-C01.ab1	T31611	hypothetical protein Y50E8A.g - Caenorhabditis elegans	33.3333	69	0.0018955
CT--01-F-H04.ab1	T50847	hypothetical protein 110K5.11 [imported] - sorghum	85.7143	28	9.40E-06
CT--04-F-C20.ab1	T51098	hypothetical protein p85RF [imported] - Prunus armeniaca	68.4211	76	1.25E-19
CT--04-F-H21.ab1	XP_064564	similar to mucin [Homo sapiens]	27.3585	106	0.0416569

Consensus Number	Accession No.	Definition of Putative homologue[Organism]	Matching %	Matching Length	E-value
1	gi|62183960|gb|AAX73301.1|	putative ribosomal-protein S6 kinase-like protein [Lycopersicon esculentum]	44.444	99	1.17E-12
2	gi|2501497|sp|Q43716|UFOG_PETHY	Flavonol 3-O-glucosyltransferase (UDP-glucose flavonoid 3-O-glucosyltransferase) (Anthocyanin rhamnosyl transferase)	73.109	119	4.90E-45
3	gi|15235982|ref|NP_195678.1|	DNA binding [Arabidopsis thaliana]	43.636	55	3.9511E-06
4	gi|15232607|ref|NP_187533.1|	copper ion binding [Arabidopsis thaliana]	68.468	111	6.374E-45
5	gi|15237656|ref|NP_201231.1|	MSJ1.10 [Arabidopsis thaliana]	69.748	119	4.2465E-38
6	gi|18417514|ref|NP_567839.1|	peptidase/ subtilase [Arabidopsis thaliana]	75.949	79	4.7598E-28
7	No hits found				
8	No hits found				
9	gi|10637893|emb|CAC10555.1|	ammonium transporter (AMT1.1) [Lotus corniculatus var. japonicus]	65.217	138	3.1227E-43
10	gi|587562|emb|CAA56520.1|	mitochondrial processing peptidase [Solanum tuberosum]	59.494	79	9.44E-18
11	No hits found				
12	gi|396589|emb|CAA52461.1|	catechol O-methyltransferase [Nicotiana tabacum]	57.093	289	3.2934E-94
13	No hits found				
14	gi|18390623|ref|NP_563761.1|	unknown protein [Arabidopsis thaliana]	40.909	132	7.0994E-16
15	gi|6969575|gb|AAF33823.1|	phospholipase C1 [Nicotiana tabacum]	64.848	165	1.33E-57
16	gi|23496445|dbj|BAC20284.1|	acidic class I chitinase [Citrus jambhiri]	92.308	117	2.33E-63

IP : 14.49.138.138, 2017-11-03 13:30:33

17	gi|30909057|gb|AAP37470.1|	ENSP-like protein [Hevea brasiliensis]	61.417	127	1.86E-38
18	gi|9794870|gb|AAF98369.1|	patatin-like protein 3 [Nicotiana tabacum]	60.465	129	6.16E-38
19	gi|19566|emb|CAA42905.1|	glyceraldehyde 3-phosphate dehydrogenase [Magnolia quinquepeta]	85.507	138	6.6574E-63
20	No hits found				
21	No hits found				
22	gi|33330870|gb|AAQ10678.1|	type-B response regulator [Catharanthus roseus]	86	50	8.52E-18
23	gi|15234551|ref|NP_192979.1|	SKU5; copper ion binding [Arabidopsis thaliana]	68.657	67	1.7279E-19
24	gi|23496447|dbj|BAC20285.1|	acidic class II chitinase [Citrus jambhiri]	87.218	133	5.4739E-64
25	gi|2225993|emb|CAA74359.1|	ferredoxin--NADP(+) reductase [Nicotiana tabacum]	67.01	97	9.539E-30
26	gi|6136119|sp|Q96558|UGDH_SOYBN	UDP-glucose 6-dehydrogenase (UDP-Glc dehydrogenase) (UDP-GlcDH) (UDPGDH)	96.386	83	7.6231E-39
27	gi|18406799|ref|NP_566043.1|	FLA8 [Arabidopsis thaliana]	81.106	217	2.0747E-92
28	gi|15237721|ref|NP_200670.1|	transcription factor [Arabidopsis thaliana]	67.442	86	5.4825E-27
29	gi|12802327|gb|AAK07827.1|	mitochondrial processing peptidase beta subunit [Cucumis melo]	68.421	152	1.4758E-50
30	No hits found				
31	gi|71000469|dbj|BAE07181.1|	methionine synthase [Beta vulgaris]	81.728	301	9.297E-140
32	gi|26452988|dbj|BAC43570.1|	putative ankyrin [Arabidopsis thaliana]	54.545	66	1.713E-12
33	gi|15235280|ref|NP_194568.1|	AAC3 (ADP/ATP CARRIER 3); ATP:ADP antiporter/ binding [Arabidopsis thaliana]	64.748	139	2.5889E-42
34	No hits found				
35	gi|24461866|gb|AAN62353.1|	NBS-LRR type disease resistance protein [Poncirus trifoliata]	40.94	149	1.1618E-19
36	gi|18141289|gb|AAL60582.1|	senescence-associated cysteine protease [Brassica oleracea]	63.571	140	1.4732E-43
37	gi|1171966|sp|P42348|PI3K2_SOYBN	Phosphatidylinositol 3-kinase, nodule isoform (PI3-kinase) (PtdIns-3-kinase) (PI3K) (SPI3K-1)	71.277	94	5.8012E-32
38	gi|1279654|emb|CAA66037.1|	peroxidase [Populus trichocarpa]	75.2	125	3.9989E-49
39	No hits found				
40	gi|602565|emb|CAA83565.1|	INO1 [Citrus x paradisi]	97.727	176	2.3982E-96
41	gi|12322574|gb|AAG51288.1|	protein kinase, putative [Arabidopsis thaliana]	44	75	8.8883E-10
42	gi|10834552|gb|AAG23721.1|	seed imbibition protein [Arabidopsis thaliana]	83.439	157	3.1713E-75
43	gi|59896064|gb|AAX11392.1|	bZIP transcription factor [Malus x domestica]	65.766	111	4.4871E-29
44	gi|1185390|gb|AAA87731.1|	alphacpn60 precursor [Pisum sativum]	91.753	97	6.7828E-43
45	gi|15238952|ref|NP_199054.1|	metalloendopeptidase [Arabidopsis thaliana]	64.815	108	1.1216E-32
46	gi|15236577|ref|NP_194917.1|	unknown protein [Arabidopsis thaliana]	48.837	129	7.1804E-20
47	gi|18390392|ref|NP_563706.1|	unknown protein [Arabidopsis thaliana]	76.364	55	3.3956E-16
48	No hits found				
49	gi|4519264|dbj|BAA75517.1|	vacuolar H+-ATPase B subunit [Citrus unshiu]	100	88	3.2008E-43
50	No hits found				
51	gi|50902072|ref|XP_463469.1|	secretory carrier membrane protein [Oryza sativa (japonica cultivar-group)]	44.715	123	4.6072E-21
52	No hits found				
53	gi|22218300|gb|AAM94622.1|	myb/SANT domain protein [Arabidopsis thaliana]	73.418	79	1.1587E-26
54	gi|32478660|gb|AAP83582.1|	phosphoethanolamine N-methyltransferase [Brassica napus]	80.851	94	9.9003E-38
55	gi|15239022|ref|NP_196694.1|	oxidoreductase [Arabidopsis thaliana]	52.288	153	4.7053E-42
56	gi|18399877|ref|NP_565525.1|	RNA binding / nucleic acid binding [Arabidopsis thaliana]	55.882	68	1.7765E-15

IP : 14.49.138.138, 2017-11-03 13:30:33

57	gi|2369714|emb|CAB09900.1|	elongation factor 2 [Beta vulgaris subsp. vulgaris]	94.815	135	9.1253E-66
58	gi|73624747|gb|AAZ79231.1|	cellulose synthase-like protein CslG [Nicotiana tabacum]	42.767	159	9.3717E-30
59	gi|12321686|gb|AAG50888.1|	hypothetical protein [Arabidopsis thaliana]	71.605	81	7.3296E-27
60	gi|30693541|ref|NP_190751.2|	ATG5; phosphoinositide 5-phosphatase [Arabidopsis thaliana]	72.139	201	2.9671E-82
61	gi|38230504|gb|AAR14273.1|	predicted protein [Populus alba x Populus tremula]	95.082	61	1.4197E-24
62	gi|62526575|gb|AAX84673.1|	cysteine protease CP1 [Manihot esculenta]	74.83	147	1.0295E-55
63	gi|30027167|gb|AAP06759.1|	auxin response factor-like protein [Mangifera indica]	75.316	158	7.6778E-61
64	gi|18403810|ref|NP_566730.1|	ALF5 (ABERRANT LATERAL ROOT FORMATION 5); antiporter/ drug transporter/ transporter [Arabidopsis thaliana]	55.147	136	2.0643E-35
65	gi|18415982|ref|NP_567663.1|	unknown protein [Arabidopsis thaliana]	52.555	137	7.8406E-29
66	No hits found				
67	gi|1841468|emb|CAA71881.1|	Tyrosyl-tRNA synthetase [Nicotiana tabacum]	75.61	123	1.0604E-50
68	gi|34903256|ref|NP_912975.1|	unnamed protein product [Oryza sativa (japonica cultivar-group)]	74.194	217	5.5663E-91
69	No hits found				
70	gi|67003905|gb|AAN04496.2|	endo-1,4-beta-glucanase [Gossypium hirsutum]	97.333	75	2.0585E-37
71	gi|3914394|sp|Q42908|PMGI_MESCR	2,3-bisphosphoglycerate-independent phosphoglycerate mutase (Phosphoglyceromutase) (BPG-independent PGAM) (PGAM-I)	79.832	119	1.3545E-46
72	gi|14009640|gb|AAK51690.1|	cytosolic 6-phosphogluconate dehydrogenase [Spinacia oleracea]	94.175	103	7.1458E-49
73	gi|30680274|ref|NP_849972.1|	ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding [Arabidopsis thaliana]	46.512	129	2.0363E-28
74	gi|30685276|ref|NP_197031.3|	nucleic acid binding [Arabidopsis thaliana]	73.77	61	3.7145E-20
75	gi|1204096|emb|CAA40325.1|	hexaubiquitin protein [Helianthus annuus]	100	146	6.3868E-76
76	gi|15237274|ref|NP_197719.1|	transcription factor [Arabidopsis thaliana]	66.379	116	9.1631E-33
77	gi|18411520|ref|NP_567094.1|	ADL4 (DYNAMIN-LIKE PROTEIN 4); GTP binding / GTPase [Arabidopsis thaliana]	71.963	107	6.6221E-36
78	gi|24461849|gb|AAN62336.1|	CTV.2 [Poncirus trifoliata]	100	89	5.276E-46
79	gi|37529496|gb|AAQ92666.1|	beta-tubulin 6 [Gossypium hirsutum]	89.34	197	6.759E-101
80	gi|8843866|dbj|BAA97392.1|	unnamed protein product [Arabidopsis thaliana]	49.398	166	4.2923E-35
81	gi|37625031|gb|AAQ96339.1|	putative ankyrin-repeat protein [Vitis aestivalis]	66.667	135	3.9242E-38
82	gi|7528270|gb|AAF63202.1|	poly(A)-binding protein [Cucumis sativus]	75.2	125	7.2071E-47
83	gi|18409740|ref|NP_566976.1|	pyruvate kinase [Arabidopsis thaliana]	86.25	80	1.1073E-34
84	No hits found				
85	gi|16226319|gb|AAL16133.1|	At2g28840/F8N16.13 [Arabidopsis thaliana]	61.458	96	7.2374E-28
86	gi|1107526|emb|CAA61158.1|	SIEP1L protein [Beta vulgaris subsp. vulgaris]	69.504	141	9.0437E-53
87	No hits found				
88	gi|15229038|ref|NP_190452.1|	RNA binding / nucleic acid binding / nucleotidyltransferase/ polynucleotide adenylyltransferase [Arabidopsis thaliana]	58.594	128	1.2501E-32
89	gi|11691594|emb|CAA09804.2|	1-deoxyxylulose 5-phosphate synthase [Catharanthus roseus]	66.912	136	1.0022E-43
90	gi|15223707|ref|NP_172882.1|	unknown protein [Arabidopsis thaliana]	71.163	215	9.1242E-83
91	gi|464981|sp|P35135|UBC4_LYCES	Ubiquitin-conjugating enzyme E2-17 kDa (Ubiquitin-protein ligase) (Ubiquitin carrier protein)	96.403	139	1.4582E-75
92	gi|14517410|gb|AAK62595.1|	At1g30970/F17F8_14 [Arabidopsis thaliana]	87.755	98	1.0553E-47
93	gi|79318100|ref|NP_001031061.1|	PGDH; phosphoglycerate dehydrogenase [Arabidopsis thaliana]	52.778	108	1.4049E-20
94	gi|1255951|emb|CAA65634.1|	PS60 [Nicotiana tabacum]	81.905	105	1.7435E-42
95	gi|15229656|ref|NP_188478.1|	pepsin A [Arabidopsis thaliana]	37.984	129	1.7409E-14
96	gi|22329488|ref|NP_172583.2|	unknown protein [Arabidopsis thaliana]	52.041	98	2.2487E-17

IP : 14.49.138.138, 2017-11-03 13:30:33

97	gi|1946222|emb|CAA96512.1|	knotted1-like homeobox protein [Malus x domestica]	45.033	151	1.6799E-20
98	gi|15237391|ref|NP_199429.1|	unknown protein [Arabidopsis thaliana]	80	60	2.9863E-20
99	No hits found				
100	gi|2463569|dbj|BAA22559.1|	squalene synthase [Glycine max]	91.045	134	1.90E-68
101	gi|18643341|gb|AAL76272.1|	transcription factor EIL1 [Vigna radiata]	57.5	40	2.21E-06
102	gi|8071626|gb|AAF71819.1|	putative aquaporin PIP1-3 [Vitis berlandieri x Vitis rupestris]	90.37	135	2.42E-68
103	gi|37549278|gb|AAQ93077.1|	putative TIR-NBS type R protein 11 [Malus x domestica]	46.951	164	1.29E-37
104	No hits found				
105	gi|18401506|ref|NP_566577.1|	organic anion transporter [Arabidopsis thaliana]	79.006	181	6.53E-74
106	No hits found				
107	gi|15231092|ref|NP_191420.1|	ketol-acid reductoisomerase [Arabidopsis thaliana]	75.333	300	4.27E-118
108	gi|38567956|emb|CAD39696.3|	OSJNBb0115I21.12 [Oryza sativa (japonica cultivar-group)]	88.679	53	1.86E-16
109	gi|71535031|gb|AAZ32913.1|	beta-mannosidase [Medicago sativa]	73.684	133	2.22E-50
110	gi|18406468|ref|NP_566011.1|	MTHFR2; methylenetetrahydrofolate reductase (NADPH) [Arabidopsis thaliana]	83.06	183	1.1092E-87
111	gi|18395874|ref|NP_565315.1|	N-acetyltransferase [Arabidopsis thaliana]	73.529	136	3.7466E-54
112	gi|20322|emb|CAA34356.1|	unnamed protein product [Oryza sativa (indica cultivar-group)]	100	127	1.87E-70
113	gi|79481791|ref|NP_193944.2|	ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein-tyrosine kinase [Arabidopsis thaliana]	63.158	76	8.72E-22
114	gi|15919089|emb|CAC86996.1|	ATP citrate lyase b-subunit [Lupinus albus]	80.723	83	8.8755E-32
115	gi|12231178|dbj|BAB20972.1|	aspartic proteinase 4 [Nepenthes alata]	55.102	147	8.16E-39
116	gi|1213629|emb|CAA65237.1|	pectinesterase [Prunus persica]	68.033	122	2.9656E-44
117	gi|4559292|gb|AAD22970.1|	trehalase 1 GMTRE1 [Glycine max]	64.423	104	3.00E-33
118	gi|15220533|ref|NP_176352.1|	ARP2/RPL3B; structural constituent of ribosome [Arabidopsis thaliana]	97.59	83	3.88E-43
119	gi|29838631|gb|AAM75140.1|	alkaline alpha galactosidase II [Cucumis melo]	78.182	110	1.99E-46
120	gi|2739002|gb|AAB94589.1|	CYP83D1p [Glycine max]	47.791	249	9.26E-64
121	No hits found				
122	gi|50939903|ref|XP_479479.1|	putative pre-mRNA splicing factor SF2 [Oryza sativa (japonica cultivar-group)]	58.48	171	3.87E-44
123	gi|22329097|ref|NP_194968.2|	peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana]	76.296	135	3.38E-56
124	gi|15218227|ref|NP_177935.1|	unknown protein [Arabidopsis thaliana]	47.368	114	1.96E-17
125	gi|18411520|ref|NP_567094.1|	ADL4 (DYNAMIN-LIKE PROTEIN 4); GTP binding / GTPase [Arabidopsis thaliana]	61.194	67	5.84E-14
126	gi|16944811|emb|CAC82811.1|	resistance gene-like [Solanum tuberosum subsp. andigena]	63.636	99	1.3949E-31
127	No hits found				
128	gi|15233478|ref|NP_192344.1|	EMB2369; ATP binding / leucine-tRNA ligase/ tRNA ligase [Arabidopsis thaliana]	78.409	88	4.2465E-38
129	gi|167367|gb|AAA99868.1|	peroxidase	89.764	127	1.31E-62
130	gi|59800341|gb|AAX07458.1|	ethylene-responsive element binding protein ERF2 [Gossypium hirsutum]	47.445	137	9.92E-24
131	gi|15237609|ref|NP_201211.1|	ANAC103; transcription factor [Arabidopsis thaliana]	85.714	28	2.33E-07
132	gi|18400044|ref|NP_566457.1|	unknown protein [Arabidopsis thaliana]	71.515	165	4.18E-64
133	gi|1321656|dbj|BAA08249.1|	alpha subunit of tlanslation elongation factor 1 [Zea mays]	100	147	5.58E-80
134	gi|11596180|gb|AAG38518.1|	miraculin-like protein 2 [Citrus x paradisi]	51.333	150	1.95E-29
135	gi|11762130|gb|AAG40343.1|	AT4g13930 [Arabidopsis thaliana]	87.654	162	3.96E-79
136	gi|18406841|ref|NP_566048.1|	nucleotidyltransferase [Arabidopsis thaliana]	38.76	129	5.56E-08

IP : 14.49.138.138, 2017-11-03 13:30:33

137	gi|15234508|ref|NP_195392.1|	DNA binding / transcription factor [Arabidopsis thaliana]	57.692	130	3.21E-31
138	gi|15218021|ref|NP_173499.1|	calcium ion binding [Arabidopsis thaliana]	71.429	63	4.15E-18
139	No hits found				
140	No hits found				
141	No hits found				
142	gi|30690476|ref|NP_174175.2|	unknown protein [Arabidopsis thaliana]	46.296	108	2.26E-19
143	gi|1480670|gb|AAB67875.1|	delta 1-pyrroline-5-carboxylate synthetase [Lycopersicon esculentum]	68.831	77	8.31E-22
144	No hits found				
145	gi|49659437|dbj|BAD27257.1|	d-limonene synthase [Citrus unshiu]	91.156	147	3.9844E-72
146	No hits found				
147	gi|30679158|ref|NP_567238.2|	ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding [Arabidopsis thaliana]	66.242	157	1.03E-48
148	gi|62526583|gb|AAX84677.1|	auxin-repressed protein-like protein ARP1 [Manihot esculenta]	65	120	1.09E-38
149	gi|15220329|ref|NP_171974.1|	Tubulin alpha-2/alpha-4 chain [Arabidopsis thaliana]	100	133	7.58E-75
150	gi|42571987|ref|NP_974084.1|	rhodopsin-like receptor [Arabidopsis thaliana]	77.419	93	1.03E-41
151	gi|15277529|gb|AAK93948.1|	TatC [Pisum sativum]	37.634	93	1.82E-09
152	gi|1345571|emb|CAA56320.1|	starch branching enzyme II [Pisum sativum]	51.572	159	3.49E-37
153	gi|20465634|gb|AAM20148.1|	unknown protein [Arabidopsis thaliana]	74.359	117	2.3249E-48
154	gi|45331333|gb|AAS57921.1|	hydroxylase-like cytochrome P450 CASS [Camptotheca acuminata]	59.006	161	1.34E-45
155	No hits found				
156	gi|18076679|emb|CAC84774.1|	P70 protein [Nicotiana tabacum]	51.412	177	2.01E-41
157	No hits found				
158	gi|12002865|gb|AAG43411.1|	JAB [Lycopersicon esculentum]	80	140	1.73E-58
159	gi|18025321|gb|AAK20170.1|	caffeic acid O-methyltransferase [Catharanthus roseus]	47.712	153	2.666E-32
160	gi|15229784|ref|NP_189967.1|	CAM7 (CALMODULIN 7); calcium ion binding [Arabidopsis thaliana]	100	149	7.70E-80
161	gi|30695777|ref|NP_199801.2|	unknown protein [Arabidopsis thaliana]	65.217	138	8.3778E-46
162	gi|15238313|ref|NP_201300.1|	unknown protein [Arabidopsis thaliana]	41.667	120	1.13E-19
163	gi|18417054|ref|NP_567786.1|	unknown protein [Arabidopsis thaliana]	87.324	142	2.15E-68
164	gi|6683114|dbj|BAA89049.1|	sucrose synthase [Citrus unshiu]	95.339	236	1.34E-124
165	gi|18420724|ref|NP_568437.1|	TUB8 [Arabidopsis thaliana]	90.576	191	3.37E-98
166	gi|18405537|ref|NP_564700.1|	unknown protein [Arabidopsis thaliana]	61.905	147	1.9501E-47
167	gi|15234316|ref|NP_192086.1|	unknown protein [Arabidopsis thaliana]	64.151	53	4.52E-12
168	gi|15241404|ref|NP_196949.1|	carboxylic ester hydrolase/ hydrolase, acting on ester bonds [Arabidopsis thaliana]	68.212	151	2.80E-53
169	gi|15223133|ref|NP_177194.1|	polygalacturonase [Arabidopsis thaliana]	57.983	119	8.50E-35
170	gi|68164987|gb|AAY87459.1|	omega-6 fatty acid desaturase [Hevea brasiliensis]	81.065	169	8.01E-84
171	No hits found				
172	No hits found				
173	No hits found				
174	gi|2098711|gb|AAB57670.1|	pectinesterase [Citrus sinensis]	100	100	2.6718E-51
175	gi|4808128|emb|CAB42794.1|	phenylalanine-ammonia lyase [Citrus clementina x Citrus reticulata]	100	116	9.904E-61
176	gi|9864189|gb|AAG01339.1|	terpene synthase [Citrus junos]	90.726	248	5.23E-124

IP : 14.49.138.138, 2017-11-03 13:30:33

177	gi|42567286|ref|NP_567862.3|	transcription factor [Arabidopsis thaliana]	42.763	152	4.91E-24
178	gi|53792876|dbj|BAD54053.1|	GCIP-interacting family protein-like [Oryza sativa (japonica cultivar-group)]	38.462	91	3.55E-12
179	gi|10334503|emb|CAC10213.1|	GTP-binding protein [Cicer arietinum]	99.275	138	2.32E-79
180	gi|15236265|ref|NP_192230.1|	XTH9 (XYLOGLUCAN ENDOTRANSGLUCOSYLASE/HYDROLASE 9); hydrolase, acting on glycosyl bonds [Arabidopsis thaliana]	82.243	107	7.94E-47
181	gi|11131745|sp|P93508|CRTC_RICCO	Calreticulin precursor	93.893	131	2.57E-72
182	gi|15226955|ref|NP_178345.1|	cinnamoyl-CoA reductase [Arabidopsis thaliana]	67.568	148	5.21E-57
183	gi|30697395|ref|NP_851233.1|	CLB4 (CHLOROPLAST BIOGENESIS 4); 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase [Arabidopsis thaliana]	75.714	140	8.72E-55
184	gi|15233123|ref|NP_188804.1|	transporter [Arabidopsis thaliana]	70.513	156	1.11E-54
185	gi|20269051|emb|CAC84706.1|	aux/IAA protein [Populus tremula x Populus tremuloides]	56.557	122	1.1865E-27
186	gi|77549198|gb|ABA91995.1|	G-protein alpha subunit, putative [Oryza sativa (japonica cultivar-group)]	55.056	89	3.08E-21
187	gi|22331666|ref|NP_190402.2|	ATM (ATAXIA-TELANGIECTASIA MUTATED) [Arabidopsis thaliana]	62.252	151	8.2292E-46
188	gi|50942111|ref|XP_480583.1|	putative Receptor-like serine/threonine kinase(RFK1) [Oryza sativa (japonica cultivar-group)]	43.878	98	6.67E-12
189	No hits found				
190	gi|11994548|dbj|BAB02735.1|	unnamed protein product [Arabidopsis thaliana]	37.109	256	1.83E-34
191	gi|15240215|ref|NP_196311.1|	kinase [Arabidopsis thaliana]	58.025	81	5.89E-18
192	gi|16118856|gb|AAL14629.1|	growth-on protein GRO10 [Euphorbia esula]	81.818	209	1.48E-95
193	gi|575605|dbj|BAA07664.1|	cationic peroxidase isozyme 40K precursor [Nicotiana tabacum]	55.556	144	6.14E-39
194	gi|3493172|gb|AAC33305.1|	fiber annexin [Gossypium hirsutum]	83.2	125	1.81E-54
195	gi|28204810|gb|AAO37147.1|	hypothetical protein [Arabidopsis thaliana]	35.032	157	7.88E-19
196	gi|18418598|ref|NP_567979.1|	unknown protein [Arabidopsis thaliana]	67.797	118	2.66E-42
197	gi|21553837|gb|AAM62930.1|	phytochelatin synthetase-like protein [Arabidopsis thaliana]	72.174	115	2.1135E-46
198	gi|34906226|ref|NP_914460.1|	gigantea-like protein [Oryza sativa (japonica cultivar-group)]	70.968	31	2.17E-07
199	gi|37529492|gb|AAQ92664.1|	beta-tubulin 3 [Gossypium hirsutum]	99.254	134	4.65E-76
200	gi|77999255|gb|ABB16974.1|	unknown [Solanum tuberosum]	94.262	122	1.55E-60
201	gi|50947327|ref|XP_483191.1|	heat shock protein 82 [Oryza sativa (japonica cultivar-group)]	96.748	123	6.42E-60
202	gi|30678225|ref|NP_178637.2|	hydrolase, hydrolyzing O-glycosyl compounds [Arabidopsis thaliana]	78.082	146	3.34E-63
203	No hits found				
204	gi|14289169|dbj|BAB59066.1|	pectate lyase [Salix gilgiana]	89.683	126	5.88E-64
205	gi|71999169|gb|AAZ57444.1|	lipoxygenase LOX1 [Populus deltoides]	38.636	132	4.14E-13
206	gi|13508844|emb|CAC35167.1|	arbutin synthase [Rauvolfia serpentina]	57.037	135	5.35E-36
207	gi|34902854|ref|NP_912774.1|	unnamed protein product [Oryza sativa (japonica cultivar-group)]	92.308	104	6.66E-49
208	gi|30697468|ref|NP_176888.2|	unknown protein [Arabidopsis thaliana]	65.116	86	8.76E-25
209	gi|18405560|ref|NP_565947.1|	nucleic acid binding [Arabidopsis thaliana]	93.617	47	3.83E-19
210	gi|12229614|sp|Q9XJ57|CHS2_CITSI	Chalcone synthase 2 (Naringenin-chalcone synthase 2)	99.355	155	1.19E-84
211	gi|13676413|dbj|BAB41197.1|	hypothetical protein [Glycine max]	81.553	103	2.53E-42
212	No hits found				
213	gi|886434|emb|CAA89858.1|	ARP protein [Arabidopsis thaliana]	69.274	179	1.47E-62
214	No hits found				
215	No hits found				
216	gi|34910658|ref|NP_916676.1|	putative PGPD14 protein (pollen germination related protein) [Oryza sativa	65.6	125	6.49E-48

IP : 14.49.138.138, 2017-11-03 13:30:33

		(japonica cultivar-group)]			
217	gi|15233984|ref|NP_193606.1|	BIN2 (BRASSINOSTEROID-INSENSITIVE 2); kinase [Arabidopsis thaliana]	94.595	111	5.55E-54
218	gi|457756|emb|CAA82995.1|	cysteine proteinase [Vicia sativa]	77.206	136	3.74E-55
219	gi|15242959|ref|NP_197666.1|	ATCSLA02; transferase, transferring glycosyl groups [Arabidopsis thaliana]	63.462	52	4.98E-12
220	No hits found				
221	gi|18403383|ref|NP_566709.1|	unknown protein [Arabidopsis thaliana]	65.487	113	2.5324E-34
222	gi|15221283|ref|NP_172076.1|	ELP (ECTOPIC DEPOSITION OF LIGNIN IN PITH); chitinase [Arabidopsis thaliana]	81.461	178	2.734E-90
223	No hits found				
224	gi|6094228|sp|P93253|SAHH_MESCR	Adenosylhomocysteinase (S-adenosyl-L-homocysteine hydrolase) (AdoHcyase)	82.787	122	2.478E-54
225	gi|28630973|gb|AAO45885.1|	chlorophyll a/b-binding protein precursor [Citrus limon]	100	141	4.2741E-80
226	gi|51535987|dbj|BAD38067.1|	putative elicitor-inducible cytochrome P450 [Oryza sativa (japonica cultivar-group)]	53.846	104	1.9312E-27
227	gi|26449973|dbj|BAC42107.1|	putative protein kinase [Arabidopsis thaliana]	51.913	183	8.6245E-45
228	gi|15240970|ref|NP_195760.1|	unknown protein [Arabidopsis thaliana]	46.914	162	1.2908E-25
229	gi|1199467|dbj|BAA11024.1|	possible aldehyde decarbonylase [Arabidopsis thaliana]	60	225	2.6793E-79
230	gi|18396075|ref|NP_564265.1|	unknown protein [Arabidopsis thaliana]	78.75	80	4.3966E-31
231	gi|30679912|ref|NP_195935.2|	nucleic acid binding / transcription factor/ zinc ion binding [Arabidopsis thaliana]	60.317	126	1.7682E-36
232	gi|11993471|gb|AAG42754.1|	ubiquitin-specific protease 12 [Arabidopsis thaliana]	73.282	131	1.2479E-52
233	gi|30682927|ref|NP_850072.1|	catalytic/ hydrolase [Arabidopsis thaliana]	48.571	140	3.1996E-20
234	gi|10178116|dbj|BAB11409.1|	ubiquitin carboxyl-terminal hydrolase [Arabidopsis thaliana]	84.393	173	2.3523E-84
235	gi|15225846|ref|NP_180277.1|	unknown protein [Arabidopsis thaliana]	58.779	131	2.1268E-32
236	gi|15226618|ref|NP_182273.1|	FUM1 (FUMARASE 1); catalytic/ fumarate hydratase [Arabidopsis thaliana]	79.208	101	4.4526E-39
237	gi|14210375|gb|AAK57011.1|	cinnamate 4-hydroxylase [Citrus x paradisi]	89.394	132	9.8317E-62
238	gi|18423534|ref|NP_568795.1|	unknown protein [Arabidopsis thaliana]	58.462	65	1.0978E-08
239	No hits found				
240	gi|11596180|gb|AAG38518.1|	miraculin-like protein 2 [Citrus x paradisi]	87.075	147	3.2304E-69
241	gi|14600068|gb|AAK71233.1|	S-adenosylmethionine synthetase [Brassica juncea]	97.059	136	1.1643E-73
242	gi|30696383|ref|NP_200196.2|	hydrolase [Arabidopsis thaliana]	70.94	117	3.2008E-43
243	No hits found				
244	No hits found				
245	gi|461753|sp|P35100|CLPA_PEA	ATP-dependent Clp protease ATP-binding subunit clpA homolog, chloroplast precursor	54.032	124	2.3607E-25
246	gi|30684227|ref|NP_196807.2|	unknown protein [Arabidopsis thaliana]	54.61	141	3.7187E-33
247	No hits found				
248	gi|3097056|emb|CAA05895.1|	dihydrofolate reductase-thymidylate synthetase precursor [Daucus carota]	69.318	88	4.5602E-31
249	gi|42795470|gb|AAS46245.1|	HMG-CoA synthase 2 [Hevea brasiliensis]	89.216	102	5.276E-46

IP : 14.49.138.138, 2017-11-03 13:30:33

7) 진귤성숙과실

Clone No.	Accession No.	Definition of Putative homologue[Organism]	Matching %	Matching Length	E-value
Mjin_1A_T_A01.ab1	gi|30693378|ref|NP_190662.2|	AAA-type ATPase family protein [Arabidopsis thaliana] >gi|18086343|gb|AAL57634.1| AT3g50930/F18B3_210 [Arabidopsis thaliana] >gi|27363216|gb|AAO11527.1| At3g50930/F18B3_210 [Arabidopsis thaliana]	52.42	227	8.0E-62
Mjin_1A_T_A05.ab1	gi|157337924|emb|CAO38968.1|	unnamed protein product [Vitis vinifera]	76.92	195	8.0E-83
Mjin_1A_T_A06.ab1	gi|10567808|gb|AAG16758.1|	putative glutathione S-transferase T3 [Lycopersicon esculentum]	51.25	80	7.0E-17
Mjin_1A_T_A12.ab1	gi|50400859|sp|Q42711|MDARS_CUCSA	RecName: Full=Monodehydroascorbate reductase, seedling isozyme; Short=MDAR seedling; AltName: Full=Ascorbate free radical reductase seedling; Short=AFR reductase seedling >gi|452165|dbj|BAA05408.1| monodehydroascorbate reductase [Cucumis sativus]	81.03	58	2.0E-20
Mjin_1A_T_B05.ab1	gi|157339018|emb|CAO42369.1|	unnamed protein product [Vitis vinifera]	74.03	154	5.0E-61
Mjin_1A_T_B06.ab1	gi|157342562|emb|CAO65274.1|	unnamed protein product [Vitis vinifera]	85.96	57	1.0E-21
Mjin_1A_T_B07.ab1	gi|157344156|emb|CAO69089.1|	unnamed protein product [Vitis vinifera]	62.24	98	3.0E-14
Mjin_1A_T_B11.ab1	gi|157340781|emb|CAO47586.1|	unnamed protein product [Vitis vinifera]	83.48	115	8.0E-48
Mjin_1A_T_C10.ab1	gi|147799857|emb|CAN66057.1|	hypothetical protein [Vitis vinifera]	50.82	61	5.0E-13
Mjin_1A_T_D01.ab1	gi|118196907|gb|ABK78670.1|	plastid phosphoenolpyruvate/phosphate translocator [Brassica napus] >gi|187940348|gb|ACD39395.1| plastid phosphoenolpyruvate/phosphate translocator [Brassica napus]	90.12	81	9.0E-28
Mjin_1A_T_D05.ab1	gi|40317278|gb|AAR84297.1|	UDP-glucose dehydrogenase [Cinnamomum osmophloeum]	83.33	90	2.0E-37
Mjin_1A_T_E08.ab1	gi|76446335|gb|ABA42952.1|	RING-H2 finger protein [Poncirus trifoliata]	100	56	2.0E-29
Mjin_1A_T_E09.ab1	gi|1061408|gb|AAB52963.1|	citrin	96.97	66	2.0E-29
Mjin_1A_T_E11.ab1	gi|118484264|gb|ABK94012.1|	unknown [Populus trichocarpa]	80.73	218	4.0E-100
Mjin_1A_T_E12.ab1	gi|118489079|gb|ABK96346.1|	unknown [Populus trichocarpa x Populus deltoides]	56.79	162	1.0E-37
Mjin_1A_T_F01.ab1	gi|157338655|emb|CAO42006.1|	unnamed protein product [Vitis vinifera]	83.58	67	2.0E-27
Mjin_1A_T_F02.ab1	gi|15225760|ref|NP_180854.1|	COP1 (CONSTITUTIVE PHOTOMORPHOGENIC 1) [Arabidopsis thaliana] >gi|20141387|sp|P43254|COP1_ARATH E3 ubiquitin-protein ligase COP1 (Constitutive photomorphogenesis protein 1) >gi|2702280|gb|AAB91983.1| COP1 regulatory protein [Arabidopsis thaliana] >gi|95147316|gb|ABF57293.1| At2g32950 [Arabidopsis thaliana]	93.44	122	1.0E-63
Mjin_1A_T_F06.ab1	gi|89276295|gb|ABD66504.1|	actin depolymerizing factor 8 [Gossypium hirsutum] >gi|119388970|gb|AAY88048.2| actin depolymerizing factor [Gossypium hirsutum]	94.74	114	4.0E-56
Mjin_1A_T_F10.ab1	gi|157353438|emb|CAO45377.1|	unnamed protein product [Vitis vinifera]	78.57	126	1.0E-48
Mjin_1A_T_G03.ab1	gi|157358195|emb|CAO65832.1|	unnamed protein product [Vitis vinifera]	57.89	95	2.0E-22
Mjin_1A_T_G07.ab1	gi|157339586|emb|CAO44127.1|	unnamed protein product [Vitis vinifera]	61.47	231	6.0E-75
Mjin_1A_T_G09.ab1	gi|15238960|ref|NP_199059.1|	protein kinase family protein [Arabidopsis thaliana] >gi|9759480|dbj|BAB10485.1| serine/threonine protein kinase-like protein [Arabidopsis thaliana] >gi|38638690|gb|AAR25639.1| At5g42440 [Arabidopsis thaliana]	60.71	112	9.0E-29
Mjin_1A_T_H01.ab1	gi|15233571|ref|NP_194672.1|	RPS15AE (ribosomal protein S15A E); structural constituent of ribosome [Arabidopsis thaliana] >gi|75311751|sp|Q9M0E0|R15A5_ARATH RecName: Full=40S ribosomal protein S15a-5 >gi|7269842|emb|CAB79701.1| ribosomal protein S15a homolog [Arabidopsis thaliana] >gi|21553914|gb|AAM62997.1| ribosomal protein S15a homolog [Arabidopsis thaliana] >gi|110737866|dbj|BAF00871.1| ribosomal protein S15a homolog [Arabidopsis thaliana] >gi|111074474|gb|ABH04610.1| At4g29430 [Arabidopsis thaliana]	81.4	129	2E-56
Mjin_1A_T_H05.ab1	gi|147778506|emb|CAN76103.1|	hypothetical protein [Vitis vinifera]	44.19	215	3E-35
Mjin_1A_T_H06.ab1	gi|157339291|emb|CAO43832.1|	unnamed protein product [Vitis vinifera]	66.42	134	2E-40
Mjin_1A_T_H12.ab1	gi|118483487|gb|ABK93642.1|	unknown [Populus trichocarpa] >gi|118483908|gb|ABK93844.1| unknown [Populus trichocarpa]	65.06	83	5E-12
Mjin_1B_T_A05.ab1	gi|157360102|emb|CAO69285.1|	unnamed protein product [Vitis vinifera]	67	203	8E-69
Mjin_1B_T_A06.ab1	gi|197726026|gb|ACH73166.1|	CONSTANS-like protein [Prunus persica]	70.94	234	9E-81

IP : 14.49.138.138, 2017-11-03 13:30:33

Mjin_1B_T_A07.ab1	gi|147856360|emb|CAN79636.1|	hypothetical protein [Vitis vinifera]	90.38	208	4E-107
Mjin_1B_T_A09.ab1	gi|147841749|emb|CAN77737.1|	hypothetical protein [Vitis vinifera]	64.1	117	3E-33
Mjin_1B_T_A11.ab1	gi|157346253|emb|CAO15950.1|	unnamed protein product [Vitis vinifera]	79.59	147	4E-64
Mjin_1B_T_B01.ab1	gi|118486538|gb|ABK95108.1|	unknown [Populus trichocarpa]	81.48	108	8E-44
Mjin_1B_T_B02.ab1	gi|26000725|gb|AAN75219.1|	chloroplast protein translocon component Tic40 precursor [Pisum sativum]	47.11	225	4E-21
Mjin_1B_T_B04.ab1	gi|118483169|gb|ABK93489.1|	unknown [Populus trichocarpa]	93.25	163	3E-85
Mjin_1B_T_B06.ab1	gi|157344339|emb|CAO69722.1|	unnamed protein product [Vitis vinifera]	76.67	60	1E-20
Mjin_1B_T_B08.ab1	gi|118489924|gb|ABK96759.1|	unknown [Populus trichocarpa x Populus deltoides]	90.07	151	4E-74
Mjin_1B_T_C01.ab1	gi|7573600|dbj|BAA94511.1|	ABC transporter homolog [Populus nigra]	85.94	64	1E-21
Mjin_1B_T_C03.ab1	gi|118482805|gb|ABK93319.1|	unknown [Populus trichocarpa]	88.33	60	1E-24
Mjin_1B_T_C05.ab1	gi|1711512|sp|P49972|SR542_SOLLC	RecName: Full=Signal recognition particle 54 kDa protein 2; Short=SRP54 >gi|556902|emb|CAA84288.1| 54-kD signal recognition particle (SRP) specific protein [Solanum lycopersicum]	93.83	81	2E-40
Mjin_1B_T_C10.ab1	gi|157357744|emb|CAO64738.1|	unnamed protein product [Vitis vinifera]	73.51	185	3E-69
Mjin_1B_T_C12.ab1	gi|27450532|gb|AAO14627.1|AF467900_4	hypothetical protein [Prunus persica]	86.36	198	1E-94
Mjin_1B_T_D06.ab1	gi|157349919|emb|CAO39775.1|	unnamed protein product [Vitis vinifera]	81.63	49	6E-19
Mjin_1B_T_D11.ab1	gi|183211890|gb|ACC59195.1|	cellulose synthase [Betula platyphylla]	97.7	87	3E-37
Mjin_1B_T_E02.ab1	gi|118484045|gb|ABK93908.1|	unknown [Populus trichocarpa]	93.22	59	3E-25
Mjin_1B_T_E03.ab1	gi|118430824|gb|ABK91948.1|	proline dehydrogenase [Actinidia deliciosa]	77.78	144	9E-59
Mjin_1B_T_E05.ab1	gi|147798263|emb|CAN63457.1|	hypothetical protein [Vitis vinifera]	93.65	63	1E-27
Mjin_1B_T_E06.ab1	gi|164564733|dbj|BAF98215.1|	CM0216.310.nc [Lotus japonicus]	81.48	54	2E-21
Mjin_1B_T_E09.ab1	gi|116787512|gb|ABK24536.1|	unknown [Picea sitchensis]	74.68	79	2E-17
Mjin_1B_T_E12.ab1	gi|14532772|gb|AAK64167.1|	putative methionine synthase [Arabidopsis thaliana]	90.24	41	3E-13
Mjin_1B_T_F04.ab1	gi|195642944|gb|ACG40940.1|	unknown [Zea mays]	97.22	36	2E-13
Mjin_1B_T_F05.ab1	gi|18404892|ref|NP_565897.1|	hydrophobic protein, putative / low temperature and salt responsive protein, putative [Arabidopsis thaliana] >gi|15529214|gb|AAK97701.1| unknown protein [Arabidopsis thaliana] >gi|16974383|gb|AAL31117.1| At2g38901/At2g38901 [Arabidopsis thaliana] >gi|20197443|gb|AAM15078.1| Expressed protein [Arabidopsis thaliana]	96.3	54	1E-23
Mjin_1B_T_F07.ab1	gi|147790699|emb|CAN61017.1|	hypothetical protein [Vitis vinifera] >gi|157359448|emb|CAO67619.1| unnamed protein product [Vitis vinifera]	94.74	114	1E-56
Mjin_1B_T_G02.ab1	gi|157341491|emb|CAO62046.1|	unnamed protein product [Vitis vinifera]	79.17	72	5E-24
Mjin_1B_T_G03.ab1	gi|157335752|emb|CAO61582.1|	unnamed protein product [Vitis vinifera]	59.84	127	6E-20
Mjin_1B_T_G04.ab1	gi|116782603|gb|ABK22569.1|	unknown [Picea sitchensis] >gi|116782987|gb|ABK22751.1| unknown [Picea sitchensis]	97.89	142	2E-77
Mjin_1B_T_G12.ab1	gi|157328180|emb|CAO17291.1|	unnamed protein product [Vitis vinifera]	77.97	227	1E-91
Mjin_1B_T_H05.ab1	gi|28371827|gb|AAO37754.1|	delta-12 oleate desaturase [Punica granatum]	86.24	189	6E-99
Mjin_1B_T_H06.ab1	gi|157339115|emb|CAO42466.1|	unnamed protein product [Vitis vinifera]	90.34	207	4E-101
Mjin_1B_T_H09.ab1	gi|158518695|gb|AAB67829.2|	developmentally regulated GTP binding protein [Pisum sativum]	97.57	206	3E-105
Mjin_1C_T_A04.ab1	gi|147798814|emb|CAN74239.1|	hypothetical protein [Vitis vinifera]	78.46	65	2E-25
Mjin_1C_T_A08.ab1	gi|388896|gb|AAA50160.1|	aspartate aminotransferase P1	81.82	143	2E-62
Mjin_1C_T_A10.ab1	gi|30679736|ref|NP_17214 4.2|	PDS1 (PHYTOENE DESATURATION 1) [Arabidopsis thaliana] >gi|6692679|gb|AAF24813.1|AC007592_6 F12K11.9 [Arabidopsis thaliana]	75	220	4E-93
Mjin_1C_T_B02.ab1	gi|91694293|gb|ABE41798.1|	gamma-tocopherol methyltransferase [Gossypium hirsutum]	80	105	1E-46
Mjin_1C_T_B04.ab1	gi|157346313|emb|CAO16010.1|	unnamed protein product [Vitis vinifera]	82.28	79	5E-25
Mjin_1C_T_B07.ab1	gi|15218281|ref|NP_173022.1|	ATPC2 (ATP synthase gamma chain 2) [Arabidopsis thaliana] >gi|461551|sp|Q01909|ATPG2_ARATH RecName: Full=ATP synthase	84.71	85	7E-32

IP : 14.49.138.138, 2017-11-03 13:30:33

		gamma chain 2, chloroplastic; AltName: Full=F-ATPase gamma subunit 2; Flags: Precursor >gi|8927649|gb|AAF82140.1|AC034256_4 Identical to ATP sythase gamma subunit (atpC2) from Arabidopsis thaliana gb|M61742 and contains an ATP synthase PF|00231 domain >gi|166788|gb|AAA32833.1| ATP synthase gamma-subunit >gi|17529042|gb|AAL38731.1| putative ATP synthase gamma-subunit [Arabidopsis thaliana] >gi|21436197|gb|AAM51386.1| putative ATP synthase gamma-subunit [Arabidopsis thaliana]			
Mjin_1C_T_B10.ab1	gi|32364696|gb|AAP80385.1|	ABC transporter [Gossypium hirsutum]	94.68	94	1E-46
Mjin_1C_T_C03.ab1	gi|157356856|emb|CAO63058.1|	unnamed protein product [Vitis vinifera]	86.6	97	2E-46
Mjin_1C_T_C05.ab1	gi|4102690|gb|AAD01540.1|	24 kDa seed maturation protein [Glycine max]	51.35	74	6E-14
Mjin_1C_T_C07.ab1	gi|147791077|emb|CAN68018.1|	hypothetical protein [Vitis vinifera]	64.91	114	7E-34
Mjin_1C_T_C09.ab1	gi|8099682|gb|AAF72202.1|AF265551_1	cysteine protease inhibitor [Manihot esculenta]	61.62	99	2E-24
Mjin_1C_T_C10.ab1	gi|147779866|emb|CAN74784.1|	hypothetical protein [Vitis vinifera]	82.61	46	5E-17
Mjin_1C_T_D07.ab1	gi|6651272|gb|AAF22246.1|	ascorbate peroxidase [Pimpinella brachycarpa]	85.45	110	1E-49
Mjin_1C_T_D08.ab1	gi|30575686|gb|AAP33009.1|	thioredoxin H [Citrus x paradisi]	97.59	83	4E-39
Mjin_1C_T_D10.ab1	gi|624674|gb|AAA82742.1|	heat shock protein	91.78	73	2E-30
Mjin_1C_T_E01.ab1	gi|157339996|emb|CAO45673.1|	unnamed protein product [Vitis vinifera]	86.32	95	3E-40
Mjin_1C_T_E02.ab1	gi|86156028|gb|ABC86745.1|	pollen-specific protein [Vitis pseudoreticulata]	74.63	67	5E-23
Mjin_1C_T_E03.ab1	gi|118487420|gb|ABK95538.1|	unknown [Populus trichocarpa]	94.74	38	4E-13
Mjin_1C_T_E06.ab1	gi|147864472|emb|CAN82640.1|	hypothetical protein [Vitis vinifera]	68.6	86	6E-21
Mjin_1C_T_E07.ab1	gi|147819809|emb|CAN60740.1|	hypothetical protein [Vitis vinifera]	72.03	143	1E-59
Mjin_1C_T_E08.ab1	gi|118483861|gb|ABK93821.1|	unknown [Populus trichocarpa]	85	40	1E-12
Mjin_1C_T_E10.ab1	gi|147797981|emb|CAN65009.1|	hypothetical protein [Vitis vinifera]	72.73	66	7E-16
Mjin_1C_T_E12.ab1	gi|147792571|emb|CAN71032.1|	hypothetical protein [Vitis vinifera]	91.35	185	8E-94
Mjin_1C_T_F02.ab1	gi|147768778|emb|CAN60458.1|	hypothetical protein [Vitis vinifera]	97.16	141	6E-78
Mjin_1C_T_F05.ab1	gi|157349815|emb|CAO39671.1|	unnamed protein product [Vitis vinifera]	54.22	83	2E-17
Mjin_1C_T_G02.ab1	gi|157347106|emb|CAO17488.1|	unnamed protein product [Vitis vinifera]	73.96	96	2E-29
Mjin_1C_T_G07.ab1	gi|146772370|gb|ABQ45487.1|	unknown [Solanum lycopersicum]	51.85	216	5E-37
Mjin_1C_T_G09.ab1	gi|115488784|ref|NP_001066879.1|	Os12g0514100 [Oryza sativa (japonica cultivar-group)] >gi|113649386|dbj|BAF29898.1| Os12g0514100 [Oryza sativa (japonica cultivar-group)] >gi|125536811|gb|EAY83299.1| hypothetical protein OsI_037258 [Oryza sativa (indica cultivar-group)]	76.47	68	4E-15
Mjin_1C_T_H01.ab1	gi|157341397|emb|CAO49304.1|	unnamed protein product [Vitis vinifera]	97.13	174	9E-89
Mjin_1C_T_H04.ab1	gi|82568695|dbj|BAE48661.1|	Pm27 [Prunus mume]	60.76	79	2E-17
Mjin_1C_T_H05.ab1	gi|145323752|ref|NP_001077465.1|	unknown protein [Arabidopsis thaliana]	48	125	2E-23
Mjin_1C_T_H08.ab1	gi|157341161|emb|CAO49068.1|	unnamed protein product [Vitis vinifera]	66.95	233	5E-91
Mjin_1C_T_H10.ab1	gi|147836228|emb|CAN68775.1|	hypothetical protein [Vitis vinifera]	51.24	201	1E-47
Mjin_1C_T_H11.ab1	gi|157358875|emb|CAO66763.1|	unnamed protein product [Vitis vinifera]	73.49	166	5E-55
Mjin_1D_T_A01.ab1	gi|147863931|emb|CAN81112.1|	hypothetical protein [Vitis vinifera]	73.62	235	1E-95
Mjin_1D_T_A02.ab1	gi|84514139|gb|ABC59078.1|	cytochrome P450 monooxygenase CYP72A59 [Medicago truncatula]	64.47	228	4E-84
Mjin_1D_T_A06.ab1	gi|157354134|emb|CAO46701.1|	unnamed protein product [Vitis vinifera]	69.2	224	2E-90
Mjin_1D_T_A08.ab1	gi|11596182|gb|AAG38519.1|AF283534_1	miraculin-like protein 3 [Citrus x paradisi]	100	110	2E-45
Mjin_1D_T_A12.ab1	gi|157358736|emb|CAO66421.1|	unnamed protein product [Vitis vinifera]	46.85	222	2E-37
Mjin_1D_T_B08.ab1	gi|147779866|emb|CAN74784.1|	hypothetical protein [Vitis vinifera]	85.38	130	5E-57
Mjin_1D_T_B10.ab1	gi|157358183|emb|CAO65820.1|	unnamed protein product [Vitis vinifera]	74.77	222	6E-90

IP : 14.49.138.138, 2017-11-03 13:30:33

Mjin_1D_T_B11.ab1	gi|157341176|emb|CAO49083.1|	unnamed protein product [Vitis vinifera]	90.78	141	3E-62
Mjin_1D_T_C04.ab1	gi|118487322|gb|ABK95489.1|	unknown [Populus trichocarpa]	76.88	160	3E-60
Mjin_1D_T_C05.ab1	gi|1061408|gb|AAB52963.1|	citrin	98.25	57	3E-16
Mjin_1D_T_C06.ab1	gi|157346255|emb|CAO15952.1|	unnamed protein product [Vitis vinifera]	95.81	167	7E-95
Mjin_1D_T_D03.ab1	gi|30696056|ref|NP_849818.1|	LOS1 (Low expression of osmotically responsive genes 1); translation elongation factor/ translation factor, nucleic acid binding [Arabidopsis thaliana] >gi|13605865|gb|AAK32918.1|AF367331_1 At1g56070/T6H22_13 [Arabidopsis thaliana] >gi|15450763|gb|AAK96653.1| elongation factor EF-2 [Arabidopsis thaliana] >gi|23397045|gb|AAN31808.1| putative elongation factor [Arabidopsis thaliana] >gi|23397162|gb|AAN31864.1| putative elongation factor [Arabidopsis thaliana] >gi|27363422|gb|AAO11630.1| At1g56070/T6H22_13 [Arabidopsis thaliana]	80.95	42	3E-11
Mjin_1D_T_D05.ab1	gi|157342804|emb|CAO65516.1|	unnamed protein product [Vitis vinifera]	59.64	223	3E-69
Mjin_1D_T_D06.ab1	gi|15235569|ref|NP_193953.1|	ISU1 (Iron-sulfur cluster assembly complex protein) [Arabidopsis thaliana] >gi|13605507|gb|AAK32747.1|AF361579_1 AT4g22220/T10I14_50 [Arabidopsis thaliana] >gi|2832672|emb|CAA16772.1| nifU-like protein [Arabidopsis thaliana] >gi|7269067|emb|CAB79177.1| nifU-like protein [Arabidopsis thaliana] >gi|19548021|gb|AAL87374.1| AT4g22220/T10I14_50 [Arabidopsis thaliana] >gi|82937831|emb|CAI29442.1| Fe-S scaffold protein 1 [Arabidopsis thaliana]	90.24	41	3E-15
Mjin_1D_T_D07.ab1	gi|6007781|gb|AAF01037.1|	NADH ubiquinone oxidoreductase PSST subunit [Lupinus luteus]	89.33	75	3E-33
Mjin_1D_T_D08.ab1	gi|147833564|emb|CAN63848.1|	hypothetical protein [Vitis vinifera] >gi|157352507|emb|CAO43613.1| unnamed protein product [Vitis vinifera]	90.91	110	1E-53
Mjin_1D_T_E03.ab1	gi|6136119|sp|Q96558|UGDH_SOYBN	RecName: Full=UDP-glucose 6-dehydrogenase; Short=UDP-Glc dehydrogenase; Short=UDP-GlcDH; Short=UDPGDH >gi|1518540|gb|AAB58398.1| UDP-glucose dehydrogenase [Glycine max]	95	40	6E-15
Mjin_1D_T_E05.ab1	gi|1351408|sp|P49043|VPE_CITSI	Vacuolar-processing enzyme precursor (VPE) >gi|633185|emb|CAA87720.1| cystein proteinase (by similarity) [Citrus sinensis] >gi|1588548|prf||2208463A vascular processing protease	100	32	9E-11
Mjin_1D_T_E06.ab1	gi|1351408|sp|P49043|VPE_CITSI	Vacuolar-processing enzyme precursor (VPE) >gi|633185|emb|CAA87720.1| cystein proteinase (by similarity) [Citrus sinensis] >gi|1588548|prf||2208463A vascular processing protease	100	55	4E-27
Mjin_1D_T_E08.ab1	gi|157348573|emb|CAO23465.1|	unnamed protein product [Vitis vinifera]	97.56	82	6E-37
Mjin_1D_T_E12.ab1	gi|118486812|gb|ABK95241.1|	unknown [Populus trichocarpa]	79.01	81	4E-34
Mjin_1D_T_F12.ab1	gi|157355295|emb|CAO48682.1|	unnamed protein product [Vitis vinifera]	73.05	167	2E-44
Mjin_1D_T_G02.ab1	gi|156001070|gb|ABU42022.1|	11S globulin [Pistacia vera]	57.5	80	3E-13
Mjin_1D_T_G08.ab1	gi|118483106|gb|ABK93462.1|	unknown [Populus trichocarpa] >gi|118483497|gb|ABK93647.1| unknown [Populus trichocarpa] >gi|118488634|gb|ABK96129.1| unknown [Populus trichocarpa]	94.37	71	1E-31
Mjin_1D_T_G10.ab1	gi|147842499|emb|CAN65219.1|	hypothetical protein [Vitis vinifera]	59.38	192	2E-55
Mjin_1D_T_G11.ab1	gi|157346589|emb|CAO16658.1|	unnamed protein product [Vitis vinifera]	89	200	1E-96
Mjin_1D_T_G12.ab1	gi|147799457|emb|CAN65949.1|	hypothetical protein [Vitis vinifera] >gi|157353747|emb|CAO46279.1| unnamed protein product [Vitis vinifera]	84	100	2E-38
Mjin_1D_T_H01.ab1	gi|147789691|emb|CAN74060.1|	hypothetical protein [Vitis vinifera] >gi|157349781|emb|CAO39637.1| unnamed protein product [Vitis vinifera]	90.76	184	5E-83
Mjin_1D_T_H05.ab1	gi|118486589|gb|ABK95133.1|	unknown [Populus trichocarpa]	91.95	87	4E-40
Mjin_1D_T_H06.ab1	gi|147778498|emb|CAN67205.1|	hypothetical protein [Vitis vinifera]	78.24	193	6E-88
Mjin_1D_T_H08.ab1	gi|15235263|ref|NP_193735.1|	unknown protein [Arabidopsis thaliana] >gi|2827656|emb|CAA16610.1| DAG-like protein [Arabidopsis thaliana] >gi|7268797|emb|CAB79002.1| DAG-like protein [Arabidopsis thaliana] >gi|27754272|gb|AAO22589.1| putative DAG protein [Arabidopsis thaliana]	78.63	131	4E-56
Mjin_1D_T_H11.ab1	gi|18400436|ref|NP_565561.1|	unknown protein [Arabidopsis thaliana] >gi|15081684|gb|AAK82497.1| At2g24020/T29E15.22 [Arabidopsis thaliana] >gi|20147169|gb|AAM10301.1| At2g24020/T29E15.22 [Arabidopsis thaliana] >gi|20197299|gb|AAC63670.2| expressed protein [Arabidopsis thaliana]	80.26	152	3E-59
Mjin_1D_T_H12.ab1	gi|118484462|gb|ABK94107.1|	unknown [Populus trichocarpa] >gi|118487969|gb|ABK95806.1| unknown [Populus trichocarpa]	78.43	51	2E-17

IP : 14.49.138.138, 2017-11-03 13:30:33

Mjin_2A_T_A02.ab1	gi|147805324|emb|CAN63089.1|	hypothetical protein [Vitis vinifera]	94.12	187	1E-101
Mjin_2A_T_A0.ab1	gi|1061408|gb|AAB52963.1|	citrin	100	87	4E-42
Mjin_2A_T_A05.ab1	gi|18412023|ref|NP_565182.1|	bile acid:sodium symporter family protein [Arabidopsis thaliana] >gi|16648877|gb|AAL24290.1| Unknown protein [Arabidopsis thaliana] >gi|21593677|gb|AAM65644.1| unknown [Arabidopsis thaliana] >gi|23197632|gb|AAN15343.1| Unknown protein [Arabidopsis thaliana]	82.35	51	6E-17
Mjin_2A_T_A12.ab1	gi|157343123|emb|CAO66612.1|	unnamed protein product [Vitis vinifera]	69.41	170	6E-57
Mjin_2A_T_B01.ab1	gi|157359322|emb|CAO67479.1|	unnamed protein product [Vitis vinifera]	90.24	82	3E-26
Mjin_2A_T_B04.ab1	gi|147855202|emb|CAN83835.1|	hypothetical protein [Vitis vinifera]	56.1	123	5E-27
Mjin_2A_T_B05.ab1	gi|157332350|emb|CAO70185.1|	unnamed protein product [Vitis vinifera]	85.53	76	7E-27
Mjin_2A_T_C01.ab1	gi|1061408|gb|AAB52963.1|	citrin	100	85	2E-41
Mjin_2A_T_C03.ab1	gi|157339774|emb|CAO44315.1|	unnamed protein product [Vitis vinifera]	61.94	134	3E-38
Mjin_2A_T_C04.ab1	gi|12585316|sp|Q9M4G4|PGMC_SOLTU	RecName: Full=Phosphoglucomutase, cytoplasmic; Short=PGM; AltName: Full=Glucose phosphomutase >gi|8250624|emb|CAB93681.1| cytosolic phosphoglucomutase [Solanum tuberosum]	88.51	148	2E-71
Mjin_2A_T_C05.ab1	gi|15186732|dbj|BAB62890.1|	aspartic proteinase 1 [Glycine max]	84.93	219	2E-102
Mjin_2A_T_C08.ab1	gi|147787378|emb|CAN60092.1|	hypothetical protein [Vitis vinifera] >gi|157339072|emb|CAO42423.1| unnamed protein product [Vitis vinifera]	92.54	67	5E-30
Mjin_2A_T_C12.ab1	gi|4519262|dbj|BAA75516.1|	vacuolar H+-ATPase c subunit [Citrus unshiu] >gi|6721531|dbj|BAA89596.1| vacuolar H+-ATPase c subunit [Citrus unshiu]	100	166	4E-57
Mjin_2A_T_D04.ab1	gi|186493687|ref|NP_683478.2|	binding [Arabidopsis thaliana]	73.56	87	1E-32
Mjin_2A_T_D07.ab1	gi|24473800|gb|AAL91665.1|	2s albumin [Anacardium occidentale]	52.07	121	6E-19
Mjin_2A_T_E02.ab1	gi|157342533|emb|CAO65245.1|	unnamed protein product [Vitis vinifera]	64.58	96	1E-30
Mjin_2A_T_E06.ab1	gi|157338314|emb|CAO39358.1|	unnamed protein product [Vitis vinifera]	86.09	115	2E-58
Mjin_2A_T_E09.ab1	gi|118488579|gb|ABK96102.1|	unknown [Populus trichocarpa]	91.58	95	8E-37
Mjin_2A_T_E12.ab1	gi|157338698|emb|CAO42049.1|	unnamed protein product [Vitis vinifera]	78.46	65	5E-13
Mjin_2A_T_F05.ab1	gi|18400426|ref|NP_565560.1|	ATCNGC6 (CYCLIC NUCLEOTIDE GATED CHANNEL 6); calmodulin binding [Arabidopsis thaliana] >gi|38502863|sp|O82226|CNGC6_ARATH RecName: Full=Probable cyclic nucleotide-gated ion channel 6; Short=AtCNGC6; AltName: Full=Cyclic nucleotide- and calmodulin-regulated ion channel 6 >gi|4581207|emb|CAB40131.1| cyclic nucleotide and calmodulin-regulated ion channel [Arabidopsis thaliana] >gi|20197298|gb|AAC63666.2| cyclic nucleotide and calmodulin-regulated ion channel [Arabidopsis thaliana]	71.96	107	8E-27
Mjin_2A_T_F10.ab1	gi|115438725|ref|NP_001043642.1|	Os01g0629900 [Oryza sativa (japonica cultivar-group)] >gi|108860801|sp|Q5ZCI1|MPK10_ORYSJ Mitogen-activated protein kinase 10 (MAP kinase 10) >gi|54291541|dbj|BAD61401.1| mitogen-activated protein kinase 7-like [Oryza sativa Japonica Group] >gi|113533173|dbj|BAF05556.1| Os01g0629900 [Oryza sativa (japonica cultivar-group)]	93.89	131	1E-56
Mjin_2A_T_F11.ab1	gi|147833549|emb|CAN63850.1|	hypothetical protein [Vitis vinifera]	59.3	86	2E-16
Mjin_2A_T_G02.ab1	gi|147861754|emb|CAN83169.1|	hypothetical protein [Vitis vinifera]	86.89	244	7E-115
Mjin_2A_T_G06.ab1	gi|1061408|gb|AAB52963.1|	citrin	100	64	1E-28
Mjin_2A_T_G07.ab1	gi|15230124|ref|NP_189092.1|	transcription factor [Arabidopsis thaliana] >gi|9294038|dbj|BAB01995.1| unnamed protein product [Arabidopsis thaliana]	64.81	108	6E-27
Mjin_2A_T_G09.ab1	gi|68138959|gb|AAY86033.1|	alcohol dehydrogenase [Citrus x paradisi]	98.95	95	1E-48
Mjin_2A_T_G10.ab1	gi|115483602|ref|NP_001065471.1|	Os10g0573700 [Oryza sativa (japonica cultivar-group)] >gi|12643054|gb|AAK00443.1|AC060755_13 putative carnitine/acylcarnitine translocase [Oryza sativa] >gi|31433632|gb|AAP55124.1| Mitochondrial carnitine/acylcarnitine carrier, putative, expressed [Oryza sativa (japonica cultivar-group)] >gi|110289630|gb|ABG66285.1| Mitochondrial carnitine/acylcarnitine carrier, putative, expressed [Oryza sativa (japonica cultivar-group)] >gi|113640003|dbj|BAF27308.1| Os10g0573700 [Oryza sativa (japonica cultivar-group)]	86.75	83	2E-35
Mjin_2A_T_G12.ab	gi|157349815|emb|CAO	unnamed protein product [Vitis vinifera]	62.16	222	6E-70

IP : 14.49.138.138, 2017-11-03 13:30:33

1	39671.1|				
Mjin_2A_T_H02.ab 1	gi|157344316|emb|CAO 69249.1|	unnamed protein product [Vitis vinifera]	60.65	155	3E-28
Mjin_2A_T_H05.ab 1	gi|118482084|gb|ABK92 973.1|	unknown [Populus trichocarpa] >gi|118483879|gb|ABK93830.1| unknown [Populus trichocarpa] >gi|118486451|gb|ABK95065.1| unknown [Populus trichocarpa]	79.88	164	2E-74
Mjin_2A_T_H06.ab 1	gi|33325127|gb|AAQ081 96.1|	eukaryotic translation initiation factor 5A isoform VI [Hevea brasiliensis]	97.48	159	2E-85
Mjin_2A_T_H07.ab 1	gi|157336333|emb|CAO 71018.1|	unnamed protein product [Vitis vinifera]	60.16	123	2E-30
Mjin_2A_T_H08.ab 1	gi|118489959|gb|ABK96 776.1|	unknown [Populus trichocarpa x Populus deltoides]	84.69	196	6E-93
Mjin_2A_T_H11.ab 1	gi|147798057|emb|CAN 60703.1|	hypothetical protein [Vitis vinifera]	87.25	149	9E-72
Mjin_2B_T_A05.ab 1	gi|33340236|gb|AAQ145 91.1|	copper/zinc superoxide dismutase [Citrus limon]	96	50	4E-20
Mjin_2B_T_B11.ab 1	gi|157354841|emb|CAO 48187.1|	unnamed protein product [Vitis vinifera]	95.48	177	3E-91
Mjin_2B_T_B12.ab 1	gi|157360948|emb|CAO 70777.1|	unnamed protein product [Vitis vinifera]	98.48	132	8E-71
Mjin_2B_T_C03.ab 1	gi|1061408|gb|AAB5296 3.1|	citrin	97.27	110	1E-54
Mjin_2B_T_E08	gi|147846707|emb|CAN 80637.1|	hypothetical protein [Vitis vinifera]	95.83	48	5E-18
Mjin_2B_T_E09.ab 1	gi|116778782|gb|ABK20 993.1|	unknown [Picea sitchensis] >gi|116781861|gb|ABK22272.1| unknown [Picea sitchensis]	92.31	39	2E-13
Mjin_2B_T_E11.ab 1	gi|157350059|emb|CAO 39997.1|	unnamed protein product [Vitis vinifera]	93.2	103	1E-50
Mjin_2B_T_F05.ab 1	gi|50199132|emb|CAH0 3799.1|	lipid transfer protein [Citrus sinensis]	70.59	51	1E-13
Mjin_2B_T_F11.ab 1	gi|118481641|gb|ABK92 762.1|	unknown [Populus trichocarpa]	48.62	181	5E-33
Mjin_2B_T_H03.ab 1	gi|77997745|gb|ABB163 53.1|	seed maturation protein [Medicago truncatula]	75.73	103	7E-36
Mjin_2C_T_A08.ab 1	gi|157328215|emb|CAO 17688.1|	unnamed protein product [Vitis vinifera]	65.65	131	6E-39
Mjin_2C_T_A09.ab 1	gi|157359175|emb|CAO 67097.1|	unnamed protein product [Vitis vinifera]	71.88	128	7E-49
Mjin_2C_T_A10.ab 1	gi|157344348|emb|CAO 69731.1|	unnamed protein product [Vitis vinifera]	67.33	150	2E-53
Mjin_2C_T_B01.ab 1	gi|13111324|dbj|BAB327 93.1|	110 kDa 4SNc-Tudor domain protein [Pisum sativum]	65.55	119	7E-29
Mjin_2C_T_B07.ab 1	gi|157340248|emb|CAO 45925.1|	unnamed protein product [Vitis vinifera]	72.45	98	2E-20
Mjin_2C_T_B12.ab 1	gi|157344200|emb|CAO 69133.1|	unnamed protein product [Vitis vinifera]	71.94	139	2E-58
Mjin_2C_T_C01.ab 1	gi|147768434|emb|CAN 69262.1|	hypothetical protein [Vitis vinifera]	88.73	142	2E-66
Mjin_2C_T_C08.ab 1	gi|12229948|sp|Q9XG77| PSA6_TOBAC	RecName: Full=Proteasome subunit alpha type-6; AltName: Full=20S proteasome alpha subunit A; AltName: Full=20S proteasome subunit alpha-1 >gi|4539545|emb|CAB39975.1| PRCI [Nicotiana tabacum]	93.33	210	4E-109
Mjin_2C_T_C09.ab 1	gi|147838442|emb|CAN 63258.1|	hypothetical protein [Vitis vinifera]	60.27	219	1E-65
Mjin_2C_T_D01.ab 1	gi|147862660|emb|CAN 83594.1|	hypothetical protein [Vitis vinifera] >gi|157336300|emb|CAO70985.1| unnamed protein product [Vitis vinifera]	87.93	58	1E-23
Mjin_2C_T_D02.ab 1	gi|124360985|gb|ABN08 957.1|	H+-transporting two-sector ATPase, C (AC39) subunit [Medicago truncatula]	97.73	176	2E-97
Mjin_2C_T_D03.ab 1	gi|33347413|gb|AAQ152 89.1|	aspartic protease [Pyrus pyrifolia]	87.82	156	4E-79
Mjin_2C_T_D05.ab 1	gi|4928460|gb|AAD3359 6.1|AF133127_1	thioredoxin h [Hevea brasiliensis]	81.97	122	7E-43
Mjin_2C_T_D06.ab 1	gi|157354370|emb|CAO 46985.1|	unnamed protein product [Vitis vinifera]	77.97	227	5E-84
Mjin_2C_T_D07.ab 1	gi|102655942|gb|AAY33 920.2|	polyubiquitin [Euphorbia characias]	100	78	4E-36
Mjin_2C_T_D08.ab 1	gi|157343805|emb|CAO 68311.1|	unnamed protein product [Vitis vinifera]	86.89	61	3E-23
Mjin_2C_T_D09.ab 1	gi|157347567|emb|CAO 18204.1|	unnamed protein product [Vitis vinifera]	78.06	196	2E-78
Mjin_2C_T_D11.ab 1	gi|118489666|gb|ABK96 634.1|	unknown [Populus trichocarpa x Populus deltoides]	77.63	219	4E-93
Mjin_2C_T_E11.ab 1	gi|115453537|ref|NP_00 1050369.1|	Os03g0416500 [Oryza sativa (japonica cultivar-group)] >gi|75226378|sp|Q75IV7|6PGL1_ORYSJ Probable 6-phosphogluconolactonase 1 (6PGL 1) >gi|41469141|gb|AAS07092.1| putative 6-phosphogluconolactonase (with alternative splicing) [Oryza sativa (japonica cultivar-group)] >gi|108708828|gb|ABF96623.1| 6-phosphogluconolactonase family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|108708829|gb|ABF96624.1| 6-phosphogluconolactonase family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113548840|dbj|BAF12283.1| Os03g0416500 [Oryza sativa (japonica cultivar-group)]	46.09	243	2E-52

IP : 14.49.138.138, 2017-11-03 13:30:33

Mjin_2C_T_F01.ab1	gi|157351530|emb|CAO41755.1|	unnamed protein product [Vitis vinifera]	70.91	55	2E-17
Mjin_2C_T_F02.ab1	gi|147795076|emb|CAN60856.1|	hypothetical protein [Vitis vinifera]	69.62	79	4E-23
Mjin_2C_T_F03.ab1	gi|157335576|emb|CAO61406.1|	unnamed protein product [Vitis vinifera]	76.11	180	5E-67
Mjin_2C_T_F05.ab1	gi|157345907|emb|CAO15422.1|	unnamed protein product [Vitis vinifera]	89.08	174	3E-71
Mjin_2C_T_F06.ab1	gi|147826465|emb|CAN71094.1|	hypothetical protein [Vitis vinifera]	92.07	164	2E-85
Mjin_2C_T_F08.ab1	gi|162568912|gb|ABY19382.1|	putative staygreen protein [Nicotiana tabacum]	63.73	102	5E-31
Mjin_2C_T_F12.ab1	gi|113367192|gb|ABI34653.1|	bZIP transcription factor bZIP78 [Glycine max]	72.9	107	8E-44
Mjin_2C_T_G03.ab1	gi|4927284|gb|AAD33072.1|AF149251_1	secretory peroxidase [Nicotiana tabacum]	90.67	75	8E-34
Mjin_2C_T_G07.ab1	gi|157335203|emb|CAO61033.1|	unnamed protein product [Vitis vinifera]	86.52	178	9E-90
Mjin_2C_T_G08.ab1	gi|118481419|gb|ABK92652.1|	unknown [Populus trichocarpa]	98.46	130	4E-57
Mjin_2C_T_G09.ab1	gi|118484991|gb|ABK94360.1|	unknown [Populus trichocarpa]	79.06	191	3E-83
Mjin_2C_T_H04.ab1	gi|154269428|gb|ABS72341.1|	rapid alkalinization factor precursor [Litchi chinensis]	75.25	101	2E-36
Mjin_2C_T_H07.ab1	gi|157358395|emb|CAO66055.1|	unnamed protein product [Vitis vinifera]	61.74	149	7E-46
Mjin_2D_T_A03.ab1	gi|147803594|emb|CAN64280.1|	hypothetical protein [Vitis vinifera]	65.91	88	1E-20
Mjin_2D_T_A06.ab1	gi|118487894|gb|ABK95769.1|	unknown [Populus trichocarpa]	82.2	236	3E-99
Mjin_2D_T_A07.ab1	gi|147790518|emb|CAN69766.1|	hypothetical protein [Vitis vinifera]	71.03	214	4E-72
Mjin_2D_T_B01.ab1	gi|147807640|emb|CAN68846.1|	hypothetical protein [Vitis vinifera] >gi|157360261|emb|CAO69472.1| unnamed protein product [Vitis vinifera]	77.78	54	2E-19
Mjin_2D_T_B04.ab1	gi|89276295|gb|ABD66504.1|	actin depolymerizing factor 8 [Gossypium hirsutum] >gi|119388970|gb|AAY88048.2| actin depolymerizing factor [Gossypium hirsutum]	92.81	139	5E-68
Mjin_2D_T_B05.ab1	gi|152962682|dbj|BAF73931.1|	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase [Citrus jambhiri]	97.88	236	7E-108
Mjin_2D_T_B09.ab1	gi|23194453|gb|AAN15183.1|	MADS box protein GHMADS-2 [Gossypium hirsutum] >gi|122938397|gb|ABM69044.1| MADS-box protein MADS6 [Gossypium hirsutum] >gi|207298817|gb|ACI23560.1| agamous-like protein 1 [Gossypium barbadense]	91.93	223	6E-106
Mjin_2D_T_B10.ab1	gi|10177870|dbj|BAB11240.1|	potassium/proton antiporter-like protein [Arabidopsis thaliana]	73.44	64	4E-13
Mjin_2D_T_B11.ab1	gi|157347419|emb|CAO18056.1|	unnamed protein product [Vitis vinifera]	77.35	234	2E-101
Mjin_2D_T_B12.ab1	gi|147776901|emb|CAN65723.1|	hypothetical protein [Vitis vinifera]	69.85	136	7E-47
Mjin_2D_T_C03.ab1	gi|147765852|emb|CAN62430.1|	hypothetical protein [Vitis vinifera]	77.05	61	3E-18
Mjin_2D_T_C06.ab1	gi|116831052|gb|ABK28481.1|	unknown [Arabidopsis thaliana]	90.57	53	2E-12
Mjin_2D_T_C09.ab1	gi|157335235|emb|CAO61065.1|	unnamed protein product [Vitis vinifera]	64.04	114	3E-33
Mjin_2D_T_C10.ab1	gi|118482114|gb|ABK92988.1|	unknown [Populus trichocarpa]	84.31	51	5E-18
Mjin_2D_T_C11.ab1	gi|13094202|dbj|BAB32735.1|	ubiquitin [Eustoma grandiflorum]	100	69	1E-31
Mjin_2D_T_C12.ab1	gi|118487224|gb|ABK95440.1|	unknown [Populus trichocarpa]	48.51	101	8E-15
Mjin_2D_T_D11.ab1	gi|30685928|ref|NP_188714.2|	ATTOP6B (BRASSINOSTEROID INSENSITIVE 3, ROOT HAIRLESS 3) [Arabidopsis thaliana] >gi|75169001|sp|Q9C5V6|TOP6B_ARATH RecName: Full=DNA topoisomerase 6 subunit B; Short=AtTOP6B; AltName: Full=Protein BRASSINOSTEROID INSENSITIVE 3; AltName: Full=Protein ROOT HAIRLESS 3; AltName: Full=Protein ELONGATED HYPOCOTYL 6 >gi|12331188|emb|CAC24690.1| topoisomerase 6 subunit B [Arabidopsis thaliana]	92.31	91	2E-40
Mjin_2D_T_D12.ab1	gi|157344046|emb|CAO68979.1|	unnamed protein product [Vitis vinifera]	72.22	90	4E-29
Mjin_2D_T_E01.ab1	gi|1061408|gb|AAB52963.1|	citrin	100	58	5E-25
Mjin_2D_T_E08.ab1	gi|118488288|gb|ABK95963.1|	unknown [Populus trichocarpa]	87.31	134	3E-60
Mjin_2D_T_E09.ab1	gi|18420844|ref|NP_568458.1|	ABC1 family protein [Arabidopsis thaliana] >gi|16649083|gb|AAL24393.1| Unknown protein [Arabidopsis thaliana] >gi|33589758|gb|AAQ22645.1| At5g24810/F6A4.20 [Arabidopsis thaliana]	61.96	92	5E-25

IP : 14.49.138.138, 2017-11-03 13:30:33

Mjin_2D_T_E10.ab1	gi|118487336|gb|ABK95496.1|	unknown [Populus trichocarpa]	65.53	206	2E-72
Mjin_2D_T_F01.ab1	gi|192910686|gb|ACF06451.1|	QM-like protein [Elaeis guineensis]	73.81	42	7E-11
Mjin_2D_T_F03.ab1	gi|18408929|ref|NP_564919.1|	FKF1 (FLAVIN-BINDING KELCH DOMAIN F BOX PROTEIN); ubiquitin-protein ligase [Arabidopsis thaliana] >gi|75169796|sp|Q9C9W9|ADO3_ARATH RecName: Full=Adagio protein 3; AltName: Full=Flavin-binding kelch repeat F-box protein 1; AltName: Full=F-box only protein 2a; Short=FBX2a >gi|12324066|gb|AAG51994.1|AC012563_4 unknown protein; 35653-33693 [Arabidopsis thaliana] >gi|18086374|gb|AAL57647.1| At1g68050/T23K23_10 [Arabidopsis thaliana] >gi|21360443|gb|AAM47337.1| At1g68050/T23K23_10 [Arabidopsis thaliana]	85.63	167	2E-72
Mjin_2D_T_F07.ab1	gi|1143388|emb|CAA57973.1|	class III ADH, glutathione-dependent formaldehyde dehydrogenase. [Arabidopsis thaliana]	93.75	192	1E-104
Mjin_2D_T_F10.ab1	gi|118482567|gb|ABK93204.1|	unknown [Populus trichocarpa]	88.24	119	1E-54
Mjin_2D_T_F12.ab1	gi|15223416|ref|NP_171656.1|	heavy-metal-associated domain-containing protein [Arabidopsis thaliana] >gi|79316252|ref|NP_001030928.1| heavy-metal-associated domain-containing protein [Arabidopsis thaliana] >gi|1922242|emb|CAA71173.1| hypothetical protein [Arabidopsis thaliana] >gi|17380662|gb|AAL36161.1| unknown protein [Arabidopsis thaliana] >gi|20258999|gb|AAM14215.1| unknown protein [Arabidopsis thaliana]	91.67	48	4E-17
Mjin_2D_T_G03.ab1	gi|147772246|emb|CAN67174.1|	hypothetical protein [Vitis vinifera] >gi|157327253|emb|CAO14548.1| unnamed protein product [Vitis vinifera]	92.98	114	2E-55
Mjin_2D_T_G05.ab1	gi|14486705|gb|AAK63247.1|AF367433_1	phosphatidylinositol transfer-like protein III [Lotus japonicus]	88.89	45	4E-16
Mjin_2D_T_G07.ab1	gi|157340849|emb|CAO47654.1|	unnamed protein product [Vitis vinifera]	58.14	86	8E-16
Mjin_2D_T_G09.ab1	gi|157357917|emb|CAO64929.1|	unnamed protein product [Vitis vinifera]	67.2	186	3E-62
Mjin_2D_T_G12.ab1	gi|118489971|gb|ABK96782.1|	unknown [Populus trichocarpa x Populus deltoides]	94.12	102	8E-53
Mjin_2D_T_H02.ab1	gi|118482684|gb|ABK93261.1|	unknown [Populus trichocarpa]	89.83	59	1E-23
Mjin_2D_T_H03.ab1	gi|18396008|ref|NP_564255.1|	ATVTI12/VTI12/VTI1B (VESICAL TRANSPORT V-SNARE 12); SNARE binding / receptor/ soluble NSF attachment protein [Arabidopsis thaliana] >gi|83305646|sp|Q9SEL5|VTI12_ARATH RecName: Full=Vesicle transport v-SNARE 12; Short=AtVTI12; AltName: Full=Vesicle transport v-SNARE protein VTI1b; AltName: Full=Vesicle soluble NSF attachment protein receptor VTI1b; Short=AtVTI1b >gi|9295720|gb|AAF87026.1|AC006535_4 T24P13.5 [Arabidopsis thaliana]	73.87	222	3E-80
Mjin_2D_T_H12.ab1	gi|27728729|gb|AAO18638.1|	cystatin [Malus x domestica]	57.94	107	2E-25
Mjin_3A_T_A01.ab1	gi|157330427|emb|CAO46591.1|	unnamed protein product [Vitis vinifera]	67.86	224	3E-89
Mjin_3A_T_A03.ab1	gi|12830830|gb|AAK08208.1|AF320905_1	metallothionein-like protein [Citrus unshiu] >gi|12830832|gb|AAK08209.1|AF320906_1 metallothionein-like protein [Citrus unshiu] >gi|3308982|dbj|BAA31562.1| metallothionein-like protein [Citrus unshiu] >gi|158936952|dbj|BAF91493.1| metallothionein type 3 [Citrus unshiu]	100	68	3E-35
Mjin_3A_T_A06.ab1	gi|157349947|emb|CAO39846.1|	unnamed protein product [Vitis vinifera]	77.18	241	3E-96
Mjin_3A_T_A08.ab1	gi|110741806|dbj|BAE98846.1|	hypothetical protein [Arabidopsis thaliana]	84.91	212	1E-92
Mjin_3A_T_A10.ab1	gi|122894106|gb|ABM67699.1|	NAC domain protein [Citrus sinensis]	99.47	187	8E-110
Mjin_3A_T_A12.ab1	gi|47680455|gb|AAT37172.1|	caffeoyl-CoA-O-methyltransferase [Broussonetia papyrifera]	77.38	221	6E-95
Mjin_3A_T_B01.ab1	gi|15221746|ref|NP_173852.1|	transferase family protein [Arabidopsis thaliana] >gi|124300996|gb|ABN04750.1| At1g24430 [Arabidopsis thaliana]	38.89	234	2E-39
Mjin_3A_T_B03.ab1	gi|157342896|emb|CAO65608.1|	unnamed protein product [Vitis vinifera]	92.77	166	6E-89
Mjin_3A_T_C01.ab1	gi|157344409|emb|CAO69792.1|	unnamed protein product [Vitis vinifera]	92.05	176	3E-77
Mjin_3A_T_C06.ab1	gi|118486249|gb|ABK94966.1|	unknown [Populus trichocarpa]	87.18	39	8E-12
Mjin_3A_T_C07.ab1	gi|147866674|emb|CAN83681.1|	hypothetical protein [Vitis vinifera]	88.1	42	2E-13
Mjin_3A_T_C08.ab1	gi|1061408|gb|AAB52963.1|	citrin	93.94	66	8E-21
Mjin_3A_T_C10.ab1	gi|157359353|emb|CAO67510.1|	unnamed protein product [Vitis vinifera]	95	60	3E-25
Mjin_3A_T_C11.ab1	gi|157336927|emb|CAO21273.1|	unnamed protein product [Vitis vinifera]	93.75	128	1E-60
Mjin_3A_T_D03.ab1	gi|37625037|gb|AAQ96342.1|	putative ethylene response factor ERF3b [Vitis aestivalis]	87.14	70	9E-19

IP : 14.49.138.138, 2017-11-03 13:30:33

Mjin_3A_T_E01.ab1	gi|147856839|emb|CAN83475.1|	hypothetical protein [Vitis vinifera]	44.58	166	1E-22
Mjin_3A_T_E03.ab1	gi|118488145|gb|ABK95892.1|	unknown [Populus trichocarpa]	45.12	164	5E-24
Mjin_3A_T_E04.ab1	gi|7768151|emb|CAB90633.1|	protein phpsphatase 2C (PP2C) [Fagus sylvatica]	75.89	112	1E-37
Mjin_3A_T_E05.ab1	gi|86156028|gb|ABC86745.1|	pollen-specific protein [Vitis pseudoreticulata]	77.27	66	6E-24
Mjin_3A_T_E08.ab1	gi|157343560|emb|CAO68066.1|	unnamed protein product [Vitis vinifera]	68.85	61	5E-14
Mjin_3A_T_E10.ab1	gi|118488125|gb|ABK95882.1|	unknown [Populus trichocarpa]	76.64	107	3E-35
Mjin_3A_T_E11.ab1	gi|118488480|gb|ABK96054.1|	unknown [Populus trichocarpa]	62.77	188	1E-51
Mjin_3A_T_F02.ab1	gi|10798892|gb|AAG23129.1|AF198259_1	diacylglycerol kinase [Lycopersicon esculentum]	75	100	6E-39
Mjin_3A_T_F06.ab1	gi|157343779|emb|CAO68285.1|	unnamed protein product [Vitis vinifera]	82.61	230	5E-65
Mjin_3A_T_F08.ab1	gi|1061408|gb|AAB52963.1|	citrin	100	38	9E-15
Mjin_3A_T_F09.ab1	gi|183447473|gb|ACC62519.1|	Bax inhibitor [Capsicum annuum]	68.67	83	1E-25
Mjin_3A_T_F10.ab1	gi|18401736|ref|NP_029430.1|	unknown protein [Arabidopsis thaliana] >gi|4432834|gb|AAD20683.1| expressed protein [Arabidopsis thaliana] >gi|16648716|gb|AAL25550.1| At2g28430/T1B3.5 [Arabidopsis thaliana] >gi|20334920|gb|AAM16216.1| At2g28430/T1B3.5 [Arabidopsis thaliana]	60	65	3E-14
Mjin_3A_T_G01.ab1	gi|118488973|gb|ABK96294.1|	unknown [Populus trichocarpa x Populus deltoides] >gi|118488989|gb|ABK96302.1| unknown [Populus trichocarpa x Populus deltoides]	67.5	120	2E-36
Mjin_3A_T_G03.ab1	gi|147858623|emb|CAN83091.1|	hypothetical protein [Vitis vinifera]	84.17	240	2E-98
Mjin_3A_T_G04.ab1	gi|88193285|gb|AAV34889.2|	osmotin-like [Theobroma cacao]	80.21	192	2E-96
Mjin_3A_T_G05.ab1	gi|37524017|gb|AAQ92310.1|	COR15 [Citrus clementina x Citrus reticulata]	98.55	69	4E-23
Mjin_3A_T_G09.ab1	gi|75213086|sp|Q9SWB4|PARP3_SOYBN	RecName: Full=Poly [ADP-ribose] polymerase 3; Short=PARP-3; AltName: Full=ADPRT 3; AltName: Full=NAD(+) ADP-ribosyltransferase 3; AltName: Full=Poly[ADP-ribose] synthetase 3 >gi|5802246|gb|AAD51626.1|AF169023_1 seed maturation protein PM38 [Glycine max]	67.92	240	7E-90
Mjin_3A_T_G10.ab1	gi|60459234|gb|AAX20004.1|	putative cytochrome c1 precursor protein [Ornithogalum virens]	92.86	84	9E-38
Mjin_3A_T_G11.ab1	gi|118482262|gb|ABK93058.1|	unknown [Populus trichocarpa]	91.67	156	7E-73
Mjin_3A_T_H03.ab1	gi|195650895|gb|ACG44915.1|	unknown [Zea mays] >gi|195659223|gb|ACG49079.1| unknown [Zea mays]	80	45	2E-12
Mjin_3A_T_H04.ab1	gi|157342153|emb|CAO64266.1|	unnamed protein product [Vitis vinifera]	81.31	107	9E-44
Mjin_3A_T_H05.ab1	gi|192911946|gb|ACF06581.1|	translational initiation factor eIF1 [Elaeis guineensis]	84.96	113	9E-44
Mjin_3A_T_H07.ab1	gi|157356530|emb|CAO62717.1|	unnamed protein product [Vitis vinifera]	64.98	257	2E-88
Mjin_3A_T_H08.ab1	gi|157354198|emb|CAO46779.1|	unnamed protein product [Vitis vinifera]	80.7	171	4E-78
Mjin_3A_T_H10.ab1	gi|147790138|emb|CAN70124.1|	hypothetical protein [Vitis vinifera]	87.67	73	1E-19
Mjin_3A_T_H11.ab1	gi|157344148|emb|CAO69081.1|	unnamed protein product [Vitis vinifera]	59.36	251	2E-84
Mjin_3A_T_H12.ab1	gi|147860060|emb|CAN83123.1|	hypothetical protein [Vitis vinifera]	63.29	207	2E-57
Mjin_3B_T_A02.ab1	gi|157344375|emb|CAO69758.1|	unnamed protein product [Vitis vinifera]	64.07	231	1E-75
Mjin_3B_T_A03.ab1	gi|157341137|emb|CAO49044.1|	unnamed protein product [Vitis vinifera]	55	80	1E-11
Mjin_3B_T_A10.ab1	gi|6706333|emb|CAB66003.1|	NADP-dependent malate dehydrogenase (decarboxylating) [Apium graveolens]	97.56	41	4E-16
Mjin_3B_T_A12.ab1	gi|13936812|gb|AAK49947.1|AF335551_1	TGF-beta receptor-interacting protein 1 [Phaseolus vulgaris]	94.57	129	4E-66
Mjin_3B_T_B01.ab1	gi|147774978|emb|CAN59912.1|	hypothetical protein [Vitis vinifera]	67.16	204	2E-63
Mjin_3B_T_B04.ab1	gi|9587329|gb|AAF89266.1|AF285991_1	granule-bound starch synthase [Prunus virginiana]	84.62	247	2E-126
Mjin_3B_T_B05.ab1	gi|157345934|emb|CAO15631.1|	unnamed protein product [Vitis vinifera]	88.82	152	3E-74
Mjin_3B_T_B06.ab1	gi|1061408|gb|AAB52963.1|	citrin	96.36	110	2E-47
Mjin_3B_T_B07.ab1	gi|1170506|sp|P41379|IF4A2_NICPL	RecName: Full=Eukaryotic initiation factor 4A-2; Short=eIF-4A-2; AltName: Full=ATP-dependent RNA helicase eIF4A-2 >gi|19697|emb|CAA43513.1| nicotiana eukaryotic translation initiation factor	96	50	4E-20

IP : 14.49.138.138, 2017-11-03 13:30:33

		4A [Nicotiana plumbaginifolia]			
Mjin_3B_T_C01.ab1	gi|157338378|emb|CAO39422.1|	unnamed protein product [Vitis vinifera]	96.71	213	9E-113
Mjin_3B_T_C02.ab1	gi|15224063|ref|NP_179959.1|	unknown protein [Arabidopsis thaliana] >gi|3152605|gb|AAC17084.1| hypothetical protein [Arabidopsis thaliana]	63.43	134	8E-45
Mjin_3B_T_C03.ab1	gi|157341169|emb|CAO49076.1|	unnamed protein product [Vitis vinifera]	65.33	225	7E-77
Mjin_3B_T_C07.ab1	gi|147802534|emb|CAN62144.1|	hypothetical protein [Vitis vinifera]	59.65	57	1E-12
Mjin_3B_T_C10.ab1	gi|157338008|emb|CAO39052.1|	unnamed protein product [Vitis vinifera]	90.45	157	3E-65
Mjin_3B_T_D12.ab1	gi|157345722|emb|CAO15020.1|	unnamed protein product [Vitis vinifera]	88.24	153	1E-75
Mjin_3B_T_E01.ab1	gi|147818712|emb|CAN65041.1|	hypothetical protein [Vitis vinifera]	76.55	226	2E-83
Mjin_3B_T_E02.ab1	gi|147767048|emb|CAN67679.1|	hypothetical protein [Vitis vinifera]	91.84	49	2E-18
Mjin_3B_T_E03.ab1	gi|162460933|ref|NP_001105032.1|	tonoplast membrane integral protein ZmTIP3-1 [Zea mays] >gi|75308062|sp|Q9ATL7|TIP31_MAIZE Aquaporin TIP3-1 (Tonoplast intrinsic protein 3-1) (ZmTIP3-1) (ZmTIP3;1) >gi|13447827|gb|AAK26771.1| tonoplast membrane integral protein ZmTIP3-1 [Zea mays]	60.18	221	2E-73
Mjin_3B_T_E04.ab1	gi|157350499|emb|CAO40548.1|	unnamed protein product [Vitis vinifera]	72.15	79	5E-24
Mjin_3B_T_E08.ab1	gi|157346114|emb|CAO15811.1|	unnamed protein product [Vitis vinifera]	70.39	152	2E-62
Mjin_3B_T_E09.ab1	gi|147844251|emb|CAN82123.1|	hypothetical protein [Vitis vinifera]	87.8	82	1E-40
Mjin_3B_T_E10.ab1	gi|147821566|emb|CAN70031.1|	hypothetical protein [Vitis vinifera] >gi|157345595|emb|CAO14893.1| unnamed protein product [Vitis vinifera]	74.31	109	2E-40
Mjin_3B_T_E12.ab1	gi|118488935|gb|ABK96276.1|	unknown [Populus trichocarpa x Populus deltoides]	75.42	118	9E-45
Mjin_3B_T_F09.ab1	gi|147775541|emb|CAN62879.1|	hypothetical protein [Vitis vinifera]	80.49	82	5E-21
Mjin_3B_T_G03.ab1	gi|14194119|gb|AAK56254.1|AF367265_1	At1g01540/F22L4_6 [Arabidopsis thaliana] >gi|20334728|gb|AAM16225.1| At1g01540/F22L4_6 [Arabidopsis thaliana]	80.1	191	5E-59
Mjin_3B_T_G10.ab1	gi|59668642|emb|CAI53675.1|	pyruvate kinase [Glycine max]	90.52	116	5E-53
Mjin_3B_T_H01.ab1	gi|106879589|emb|CAJ38378.1|	glyceraldehyde-3-phosphate dehydrogenase [Plantago major]	74.39	82	7E-19
Mjin_3B_T_H02.ab1	gi|147794105|emb|CAN62361.1|	hypothetical protein [Vitis vinifera] >gi|157327992|emb|CAO16962.1| unnamed protein product [Vitis vinifera]	78.72	47	2E-14
Mjin_3B_T_H03.ab1	gi|157342231|emb|CAO64344.1|	unnamed protein product [Vitis vinifera]	84.5	129	2E-58
Mjin_3B_T_H04.ab1	gi|15229584|ref|NP_188436.1|	glycosyl hydrolase family 1 protein [Arabidopsis thaliana] >gi|9294063|dbj|BAB02020.1| beta-glucosidase [Arabidopsis thaliana] >gi|21537086|gb|AAM61427.1| beta-glucosidase, putative [Arabidopsis thaliana]	89.08	119	2E-58
Mjin_3B_T_H06.ab1	gi|30690823|ref|NP_850481.1|	AtTLP3 (TUBBY LIKE PROTEIN 3); phosphoric diester hydrolase/ transcription factor [Arabidopsis thaliana] >gi|79324947|ref|NP_001031558.1| AtTLP3 (TUBBY LIKE PROTEIN 3); phosphoric diester hydrolase/ transcription factor [Arabidopsis thaliana] >gi|75248467|sp|Q8VY21|TLP3_ARATH RecName: Full=Tubby-like F-box protein 3; Short=AtTLP3 >gi|18377640|gb|AAL66970.1| putative tubby protein [Arabidopsis thaliana] >gi|20465543|gb|AAM20254.1| putative tubby protein [Arabidopsis thaliana] >gi|27372514|gb|AAK98802.1| tubby-like protein 3 [Arabidopsis thaliana]	80.65	248	1E-112
Mjin_3B_T_H08.ab1	gi|11994739|dbj|BAB03068.1|	aminotransferase-like protein [Arabidopsis thaliana]	91.11	135	3E-67
Mjin_3B_T_H10.ab1	gi|157346733|emb|CAO16802.1|	unnamed protein product [Vitis vinifera]	53.06	245	1E-65
Mjin_3B_T_H12.ab1	gi|118485149|gb|ABK94437.1|	unknown [Populus trichocarpa]	72.84	81	2E-26
Mjin_3C_T_A01.ab1	gi|1061408|gb|AAB52963.1|	citrin	98	100	1E-48
Mjin_3C_T_A03.ab1	gi|213268485|gb|ACJ45013.1|	NPR1-1 protein [Glycine max]	58.57	140	1E-28
Mjin_3C_T_A06.ab1	gi|118482397|gb|ABK93121.1|	unknown [Populus trichocarpa] >gi|118486743|gb|ABK95207.1| unknown [Populus trichocarpa]	87.67	73	1E-28
Mjin_3C_T_A09.ab1	gi|118484748|gb|ABK94243.1|	unknown [Populus trichocarpa] >gi|118485182|gb|ABK94452.1| unknown [Populus trichocarpa] >gi|118488047|gb|ABK95844.1| unknown [Populus trichocarpa]	93.55	155	3E-74
Mjin_3C_T_A12.ab1	gi|30689156|ref|NP_189474.2|	GATL10 (Galacturonosyltransferase-like 10); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring hexosyl groups [Arabidopsis thaliana] >gi|11994580|dbj|BAB02626.1| glycosyl transferase-like protein [Arabidopsis thaliana] >gi|44917577|gb|AAS49113.1| At3g28340 [Arabidopsis thaliana] >gi|51971391|dbj|BAD44360.1| unknown	66.08	227	1E-79

IP : 14.49.138.138, 2017-11-03 13:30:33

		protein [Arabidopsis thaliana]			
Mjin_3C_T_B01.ab1	gi|3308980|dbj|BAA31561.1|	metallothionein-like protein [Citrus unshiu]	100	39	7E-14
Mjin_3C_T_B05.ab1	gi|157356742|emb|CAO62937.1|	unnamed protein product [Vitis vinifera]	83.2	125	3E-56
Mjin_3C_T_B08.ab1	gi|3377822|gb|AAC28195.1|	contains similarity to Caenorhabditis elegans MEL-26 (GB:U67737) [Arabidopsis thaliana]	60.58	241	3E-57
Mjin_3C_T_B11.ab1	gi|157340781|emb|CAO47586.1|	unnamed protein product [Vitis vinifera]	57.55	106	6E-20
Mjin_3C_T_C04.ab1	gi|147810057|emb|CAN78280.1|	hypothetical protein [Vitis vinifera]	73.68	247	1E-96
Mjin_3C_T_C06.ab1	gi|1174867|sp|P46269|QCR8_SOLTU	RecName: Full=Cytochrome b-c1 complex subunit 8; AltName: Full=Ubiquinol-cytochrome c reductase complex ubiquinone-binding protein QP-C; AltName: Full=Ubiquinol-cytochrome c reductase complex 8.2 kDa protein; AltName: Full=Complex III subunit VII; AltName: Full=Complex III subunit 8 >gi|633687|emb|CAA55862.1| ubiquinol--cytochrome c reductase [Solanum tuberosum] >gi|1094912|prf||2107179A cytochrome c oxidase:SUBUNIT=8.2kD	85.71	49	6E-18
Mjin_3C_T_C09.ab1	gi|157341635|emb|CAO62190.1|	unnamed protein product [Vitis vinifera]	81.37	102	2E-43
Mjin_3C_T_C12.ab1	gi|15233746|ref|NP_194716.1|	unknown protein [Arabidopsis thaliana] >gi|4914411|emb|CAB43662.1| putative protein [Arabidopsis thaliana] >gi|7269886|emb|CAB79745.1| putative protein [Arabidopsis thaliana] >gi|21618273|gb|AAM67323.1| unknown [Arabidopsis thaliana] >gi|194708824|gb|ACF88496.1| At4g29870 [Arabidopsis thaliana]	86.75	151	5E-63
Mjin_3C_T_D04.ab1	gi|157350889|emb|CAO41004.1|	unnamed protein product [Vitis vinifera]	69.05	84	1E-25
Mjin_3C_T_D05.ab1	gi|3308980|dbj|BAA31561.1|	metallothionein-like protein [Citrus unshiu]	90	50	2E-17
Mjin_3C_T_D07.ab1	gi|116831573|gb|ABK28739.1|	unknown [Arabidopsis thaliana]	70.79	89	1E-29
Mjin_3C_T_D09.ab1	gi|1061408|gb|AAB52963.1|	citrin	82.26	62	1E-23
Mjin_3C_T_D12.ab1	gi|157327057|emb|CAO72016.1|	unnamed protein product [Vitis vinifera]	76.92	182	1E-60
Mjin_3C_T_E05.ab1	gi|9794870|gb|AAF98369.1|AF158253_1	patatin-like protein 3 [Nicotiana tabacum]	70.53	190	1E-65
Mjin_3C_T_E07.ab1	gi|157346726|emb|CAO16795.1|	unnamed protein product [Vitis vinifera]	86.01	143	4E-46
Mjin_3C_T_E08.ab1	gi|159459822|gb|ABW96308.1|	heat shock protein 90 [Vitis pseudoreticulata]	94.19	86	4E-41
Mjin_3C_T_E11.ab1	gi|15237175|ref|NP_197686.1|	VPS24.1 [Arabidopsis thaliana] >gi|10177242|dbj|BAB10616.1| unnamed protein product [Arabidopsis thaliana] >gi|15451068|gb|AAK96805.1| Unknown protein [Arabidopsis thaliana] >gi|22136128|gb|AAM91142.1| unknown protein [Arabidopsis thaliana]	85.19	81	3E-32
Mjin_3C_T_F02.ab1	gi|133874242|dbj|BAF49324.1|	flavonoid 3'-hydroxylase [Lobelia erinus]	79.45	146	4E-64
Mjin_3C_T_F03.ab1	gi|113967811|gb|ABI49160.1|	SM10 [Nicotiana tabacum]	87.18	39	8E-13
Mjin_3C_T_G03.ab1	gi|108711707|gb|ABF99502.1|	ADP-ribosylation factor, putative, expressed [Oryza sativa (japonica cultivar-group)]	100	103	3E-53
Mjin_3C_T_G04.ab1	gi|147818338|emb|CAN75840.1|	hypothetical protein [Vitis vinifera]	76.67	180	4E-64
Mjin_3C_T_G05.ab1	gi|147783308|emb|CAN64127.1|	hypothetical protein [Vitis vinifera]	92.86	112	2E-54
Mjin_3C_T_G08.ab1	gi|147815273|emb|CAN70022.1|	hypothetical protein [Vitis vinifera]	90.32	155	1E-76
Mjin_3C_T_G10.ab1	gi|157335309|emb|CAO61139.1|	unnamed protein product [Vitis vinifera]	80.59	170	6E-68
Mjin_3C_T_H01.ab1	gi|157349804|emb|CAO39660.1|	unnamed protein product [Vitis vinifera]	93.41	167	1E-86
Mjin_3C_T_H02.ab1	gi|157360536|emb|CAO70099.1|	unnamed protein product [Vitis vinifera]	97.24	145	2E-71
Mjin_3C_T_H11.ab1	gi|83628266|gb|ABC26013.1|	9-cis-epoxycarotenoid dioxygenase 3 [Citrus clementina]	98.89	180	2E-60
Mjin_3D_T_A03.ab1	gi|157337417|emb|CAO21763.1|	unnamed protein product [Vitis vinifera]	62.25	151	7E-44
Mjin_3D_T_A07.ab1	gi|13359451|dbj|BAB33421.1|	putative senescence-associated protein [Pisum sativum]	77.72	193	9E-80
Mjin_3D_T_A08.ab1	gi|157350711|emb|CAO40802.1|	unnamed protein product [Vitis vinifera]	81.25	224	2E-105
Mjin_3D_T_B03.ab1	gi|157352714|emb|CAO44529.1|	unnamed protein product [Vitis vinifera]	67.5	120	1E-25
Mjin_3D_T_B05.ab1	gi|157358177|emb|CAO65814.1|	unnamed protein product [Vitis vinifera]	70	200	6E-65
Mjin_3D_T_B07.ab1	gi|18402129|ref|NP_566626.1|	unknown protein [Arabidopsis thaliana] >gi|9294613|dbj|BAB02952.1| unnamed protein product [Arabidopsis thaliana]	86.99	123	1E-58

IP : 14.49.138.138, 2017-11-03 13:30:33

		>gi|17979471|gb|AAL50072.1| AT3g19120/MVI11_3 [Arabidopsis thaliana] >gi|23506151|gb|AAN31087.1| At3g19120/MVI11_3 [Arabidopsis thaliana]			
Mjin_3D_T_B10.ab1	gi|118340979|gb|ABK80758.1|	7S globulin precursor [Ficus pumila var. awkeotsang]	64.29	196	2E-62
Mjin_3D_T_B11.ab1	gi|157327143|emb|CAO14415.1|	unnamed protein product [Vitis vinifera]	82.14	112	4E-44
Mjin_3D_T_B12.ab1	gi|147837828|emb|CAN73791.1|	hypothetical protein [Vitis vinifera]	79.17	168	1E-76
Mjin_3D_T_C01.ab1	gi|6682841|dbj|BAA88904.1|	sucrose synthase [Citrus unshiu]	100	36	3E-11
Mjin_3D_T_C02.ab1	gi|147867156|emb|CAN80504.1|	hypothetical protein [Vitis vinifera] >gi|157343453|emb|CAO67959.1| unnamed protein product [Vitis vinifera]	84.08	157	3E-69
Mjin_3D_T_C03.ab1	gi|1864017|dbj|BAA09709.1|	elongation factor-1 alpha [Nicotiana tabacum]	99.57	232	2E-132
Mjin_3D_T_C07.ab1	gi|117607067|gb|ABK42077.1|	ubiquitin extension protein [Capsicum annuum]	95.71	163	7E-70
Mjin_3D_T_C09.ab1	gi|1061408|gb|AAB52963.1|	citrin	94.67	75	2E-25
Mjin_3D_T_C12.ab1	gi|1061408|gb|AAB52963.1|	citrin	98.85	87	6E-42
Mjin_3D_T_D02.ab1	gi|118488222|gb|ABK95930.1|	unknown [Populus trichocarpa]	56.52	69	9E-11
Mjin_3D_T_D07.ab1	gi|157344228|emb|CAO69161.1|	unnamed protein product [Vitis vinifera]	58.59	99	2E-24
Mjin_3D_T_D08.ab1	gi|157352776|emb|CAO44591.1|	unnamed protein product [Vitis vinifera]	73.68	76	4E-23
Mjin_3D_T_E04.ab1	gi|157351336|emb|CAO41523.1|	unnamed protein product [Vitis vinifera]	47.4	154	3E-25
Mjin_3D_T_E06.ab1	gi|15221429|ref|NP_177018.1|	LBD42 (LOB DOMAIN-CONTAINING PROTEIN 42) [Arabidopsis thaliana] >gi|29427986|sp|Q9CA30|LBD42_ARATH LOB domain-containing protein 42 (ASYMMETRIC LEAVES 2-like protein 36) (AS2-like protein 36) >gi|12324879|gb|AAG52389.1|AC011915_3 hypothetical protein; 48379-49350 [Arabidopsis thaliana] >gi|17227174|gb|AAL38041.1|AF447896_1 LOB DOMAIN 42 [Arabidopsis thaliana]	72	50	9E-14
Mjin_3D_T_E12.ab1	gi|12830830|gb|AAK08208.1|AF320905_1	metallothionein-like protein [Citrus unshiu] >gi|12830832|gb|AAK08209.1|AF320906_1 metallothionein-like protein [Citrus unshiu] >gi|3308982|dbj|BAA31562.1| metallothionein-like protein [Citrus unshiu] >gi|158936952|dbj|BAF91493.1| metallothionein type 3 [Citrus unshiu]	100	52	3E-23
Mjin_3D_T_F05.ab1	gi|23345021|gb|AAN17502.1|	omega-3 fatty acid desaturase [Betula pendula]	74.03	231	6E-81
Mjin_3D_T_F07.ab1	gi|26453171|dbj|BAC43661.1|	unknown protein [Arabidopsis thaliana] >gi|28416759|gb|AAO42910.1| At4g15810 [Arabidopsis thaliana]	88.89	54	1E-19
Mjin_3D_T_F08.ab1	gi|161377377|gb|ABX71676.1|	60S ribosomal protein L6-like protein [Panax quinquefolius]	82.67	75	1E-23
Mjin_3D_T_G02.ab1	gi|147838167|emb|CAN60915.1|	hypothetical protein [Vitis vinifera]	88.94	199	3E-98
Mjin_3D_T_G03.ab1	gi|157346435|emb|CAO16318.1|	unnamed protein product [Vitis vinifera]	44.67	244	6E-37
Mjin_3D_T_G04.ab1	gi|29786399|emb|CAD29822.2|	putative serine protease [Populus x canadensis]	76.21	206	2E-88
Mjin_3D_T_G05.ab1	gi|118482479|gb|ABK93162.1|	unknown [Populus trichocarpa]	60.23	171	9E-41
Mjin_3D_T_G06.ab1	gi|22653808|sp|Q39644|LEA5_CITSI	Late embryogenesis abundant protein Lea5 >gi|599726|emb|CAA86851.1| Lea5 protein [Citrus sinensis]	98.97	97	2E-47
Mjin_3D_T_G07.ab1	gi|157358382|emb|CAO66042.1|	unnamed protein product [Vitis vinifera]	82	150	9E-50
Mjin_3D_T_G09.ab1	gi|157355254|emb|CAO48630.1|	unnamed protein product [Vitis vinifera]	93.98	83	3E-37
Mjin_3D_T_H01.ab1	gi|147855753|emb|CAN83442.1|	hypothetical protein [Vitis vinifera] >gi|157355613|emb|CAO49430.1| unnamed protein product [Vitis vinifera]	82.28	158	1E-59
Mjin_3D_T_H02.ab1	gi|1061408|gb|AAB52963.1|	citrin	100	36	5E-13
Mjin_3D_T_H05.ab1	gi|197726070|gb|ACH73186.1|	coat protein [Dweet mottle virus]	87.65	243	4E-117
Mjin_3D_T_H06.ab1	gi|15238947|ref|NP_196670.1|	serine-rich protein-related [Arabidopsis thaliana] >gi|9795161|emb|CAC03457.1| putative protein [Arabidopsis thaliana] >gi|21592828|gb|AAM64778.1| serine-rich protein [Arabidopsis thaliana] >gi|28466931|gb|AAO44074.1| At5g11090 [Arabidopsis thaliana] >gi|110743766|dbj|BAE99719.1| hypothetical protein [Arabidopsis thaliana]	69.35	62	1E-16
Mjin_3D_T_H07.ab1	gi|118481849|gb|ABK92861.1|	unknown [Populus trichocarpa]	61.93	197	5E-49
Mjin_3D_T_H08.ab1	gi|157359150|emb|CAO67072.1|	unnamed protein product [Vitis vinifera]	74.89	223	3E-91
Mjin_3D_T_H09.ab1	gi|1061408|gb|AAB52963.1|	citrin	97.06	68	3E-30
Mjin_3D_T_H11.ab	gi|12325096|gb|AAG525	unknown protein; 30607-27264 [Arabidopsis thaliana]	88.51	87	7E-30

IP : 14.49.138.138, 2017-11-03 13:30:33

1	05.1|AC018364_23				
Mjin_3D_T_H12.ab 1	gi|147772470|emb|CAN 65104.1|	hypothetical protein [Vitis vinifera]	69	100	1E-26
Mjin_4A_T_A01.ab 1	gi|84453224|dbj|BAE712 09.1|	putative importin alpha [Trifolium pratense]	85.19	216	1E-89
Mjin_4A_T_B03.ab 1	gi|157338804|emb|CAO 42155.1|	unnamed protein product [Vitis vinifera]	62.32	138	2E-36
Mjin_4A_T_B05.ab 1	gi|147843005|emb|CAN 83318.1|	hypothetical protein [Vitis vinifera] >gi|157353605|emb|CAO46122.1| unnamed protein product [Vitis vinifera]	80.82	73	2E-20
Mjin_4A_T_B08.ab 1	gi|136057|sp|P21820|TP IS_COPJA	RecName: Full=Triosephosphate isomerase, cytosolic; Short=TIM; Short=Triose-phosphate isomerase >gi|556171|gb|AAB62730.1| triosephosphate isomerase [Coptis japonica]	90.51	137	2E-53
Mjin_4A_T_B09.ab 1	gi|118488012|gb|ABK95 827.1|	unknown [Populus trichocarpa]	78.71	155	1E-61
Mjin_4A_T_C02.ab 1	gi|157342999|emb|CAO 65711.1|	unnamed protein product [Vitis vinifera]	85.14	148	2E-71
Mjin_4A_T_C11.ab 1	gi|110748606|gb|ABG89 856.1|	cystatin [Amaranthus hypochondriacus]	74.83	151	2E-54
Mjin_4A_T_D04.ab 1	gi|157346124|emb|CAO 15821.1|	unnamed protein product [Vitis vinifera]	89.92	119	3E-55
Mjin_4A_T_D06.ab 1	gi|118486583|gb|ABK95 130.1|	unknown [Populus trichocarpa]	89.13	46	3E-17
Mjin_4A_T_D07.ab 1	gi|157341170|emb|CAO 49077.1|	unnamed protein product [Vitis vinifera]	60.71	112	3E-16
Mjin_4A_T_D10.ab 1	gi|18700701|gb|AAL786 74.1|AF458699_1	ankyrin-kinase [Medicago truncatula]	84.55	123	4E-52
Mjin_4A_T_D11.ab 1	gi|157338928|emb|CAO 42279.1|	unnamed protein product [Vitis vinifera]	50.74	136	2E-27
Mjin_4A_T_D12.ab 1	gi|147806249|emb|CAN 72198.1|	hypothetical protein [Vitis vinifera]	78.12	128	6E-54
Mjin_4A_T_E09.ab 1	gi|147856146|emb|CAN 82436.1|	hypothetical protein [Vitis vinifera]	94.16	154	9E-73
Mjin_4A_T_E10.ab 1	gi|118484844|gb|ABK94 289.1|	unknown [Populus trichocarpa] >gi|118487240|gb|ABK95448.1| unknown [Populus trichocarpa]	99.19	124	8E-69
Mjin_4A_T_F02.ab 1	gi|3023858|sp|Q39836|G BLP_SOYBN	Guanine nucleotide-binding protein subunit beta-like protein >gi|1256608|gb|AAB05941.1| G beta-like protein [Glycine max]	93.55	155	5E-80
Mjin_4A_T_F06.ab 1	gi|147784332|emb|CAN 70587.1|	hypothetical protein [Vitis vinifera]	88.82	170	4E-72
Mjin_4A_T_F07.ab 1	gi|33340517|gb|AAQ148 54.1|AF321140_1	S-adenosylmethionine synthase [Nicotiana tabacum]	96.88	64	5E-30
Mjin_4A_T_F08.ab 1	gi|118485842|gb|ABK94 768.1|	unknown [Populus trichocarpa]	79.39	131	1E-58
Mjin_4A_T_F09.ab 1	gi|118486297|gb|ABK94 990.1|	unknown [Populus trichocarpa]	69.7	99	1E-20
Mjin_4A_T_G02.ab 1	gi|147818792|emb|CAN 67280.1|	hypothetical protein [Vitis vinifera] >gi|157339239|emb|CAO43780.1| unnamed protein product [Vitis vinifera]	86.81	91	3E-36
Mjin_4A_T_G07.ab 1	gi|157348345|emb|CAO 23132.1|	unnamed protein product [Vitis vinifera]	68.83	247	1E-83
Mjin_4A_T_G08.ab 1	gi|24461860|gb|AAN623 47.1|AF506028_14	CTV.20 [Poncirus trifoliata]	79.09	110	1E-39
Mjin_4A_T_G10.ab 1	gi|157345676|emb|CAO 14974.1|	unnamed protein product [Vitis vinifera]	72.08	154	6E-64
Mjin_4A_T_G12.ab 1	gi|157345987|emb|CAO 15684.1|	unnamed protein product [Vitis vinifera]	85.9	156	2E-74
Mjin_4A_T_H05.ab 1	gi|157336135|emb|CAO 61965.1|	unnamed protein product [Vitis vinifera]	70.21	47	7E-12
Mjin_4A_T_H08.ab 1	gi|110740505|dbj|BAE98 358.1|	hypothetical protein [Arabidopsis thaliana]	73.28	131	7E-46
Mjin_4A_T_H10.ab 1	gi|157353131|emb|CAO 45041.1|	unnamed protein product [Vitis vinifera]	87.78	90	5E-34
Mjin_4B_T_A01.ab 1	gi|147794687|emb|CAN 69148.1|	hypothetical protein [Vitis vinifera] >gi|157336587|emb|CAO71272.1| unnamed protein product [Vitis vinifera]	80.85	188	2E-76
Mjin_4B_T_A04.ab 1	gi|157351628|emb|CAO 42587.1|	unnamed protein product [Vitis vinifera]	69.51	246	4E-78
Mjin_4B_T_A05.ab 1	gi|119367477|gb|ABL67 654.1|	putative H-type thioredoxin [Citrus cv. Shiranuhi]	97.5	40	2E-13
Mjin_4B_T_A08.ab 1	gi|73665916|gb|AAZ796 55.1|	putative arginine decarboxylase [Fagus sylvatica]	59.76	82	7E-19
Mjin_4B_T_A11.ab 1	gi|118489858|gb|ABK96 728.1|	unknown [Populus trichocarpa x Populus deltoides]	83.87	62	1E-23
Mjin_4B_T_B01.ab 1	gi|102655942|gb|AAY33 920.2|	polyubiquitin [Euphorbia characias]	100	114	7E-57
Mjin_4B_T_B03.ab 1	gi|138559|sp|P27078|VI NT_BP434	RecName: Full=Integrase >gi|215353|gb|AAA67900.1| integrase [Phage 434]	100	71	1E-35
Mjin_4B_T_B04.ab 1	gi|108706254|gb|ABF94 049.1|	40S ribosomal protein S9, putative, expressed [Oryza sativa (japonica cultivar-group)]	97.62	42	3E-17
Mjin_4B_T_B10.ab 1	gi|118481612|gb|ABK92 748.1|	unknown [Populus trichocarpa]	89.11	202	1E-95
Mjin_4B_T_C05.ab 1	gi|15220378|ref|NP_171 991.1|	unknown protein [Arabidopsis thaliana] >gi|27754677|gb|AAO22782.1| unknown protein [Arabidopsis thaliana] >gi|28393999|gb|AAO42407.1|	68.12	160	2E-40

IP : 14.49.138.138, 2017-11-03 13:30:33

		unknown [Arabidopsis thaliana]			
Mjin_4B_T_C07.ab1	gi|11036950|gb|AAG27431.1|	QM-like protein [Elaeis guineensis]	98.47	131	2E-72
Mjin_4B_T_C10.ab1	gi|76261993|gb|ABA41273.1|	NPR1-like protein [Prunus laurocerasus]	60	150	3E-38
Mjin_4B_T_C12.ab1	gi|19570344|dbj|BAB86292.1|	nucleoside diphosphate kinase 1 [Brassica rapa] >gi|19744165|dbj|BAB86841.1| NDPK I [Brassica rapa]	84.46	148	1E-68
Mjin_4B_T_D10.ab1	gi|147772924|emb|CAN67177.1|	hypothetical protein [Vitis vinifera]	58.23	158	9E-38
Mjin_4B_T_E06.ab1	gi|18424166|ref|NP_568892.1|	FTSH9 (FtsH protease 9); ATP-dependent peptidase/ ATPase/ metallopeptidase [Arabidopsis thaliana] >gi|75170859|sp|Q9FIM2|FTSH9_ARATH Cell division protease ftsH homolog 9, chloroplast precursor (AtFtsH9) >gi|9759220|dbj|BAB09632.1| cell division protein FtsH [Arabidopsis thaliana] >gi|16648973|gb|AAL24338.1| cell division protein FtsH [Arabidopsis thaliana]	74.32	148	3E-59
Mjin_4B_T_E08.ab1	gi|147862203|emb|CAN80473.1|	hypothetical protein [Vitis vinifera]	75	64	2E-18
Mjin_4B_T_E11.ab1	gi|15220188|ref|NP_172538.1|	PGP10 (P-GLYCOPROTEIN 10); ATPase, coupled to transmembrane movement of substances [Arabidopsis thaliana]	84.21	114	2E-49
Mjin_4B_T_F02.ab1	gi|1170936|sp|P43280|METK1_SOLLC	RecName: Full=S-adenosylmethionine synthetase 1; Short=AdoMet synthetase 1; AltName: Full=Methionine adenosyltransferase 1; Short=MAT 1 >gi|429104|emb|CAA80865.1| S-adenosyl-L-methionine synthetase [Solanum lycopersicum]	100	35	1E-12
Mjin_4B_T_F04.ab1	gi|157358624|emb|CAO66300.1|	unnamed protein product [Vitis vinifera]	63.41	164	2E-35
Mjin_4B_T_F06.ab1	gi|10176767|dbj|BAB09881.1|	pyrophosphate-dependent phosphofructo-1-kinase-like protein [Arabidopsis thaliana]	75.76	66	6E-24
Mjin_4B_T_F07.ab1	gi|126770|sp|P17432|MASY_GOSHI	RecName: Full=Malate synthase, glyoxysomal >gi|18507|emb|CAA36546.1| unnamed protein product [Gossypium hirsutum]	76.92	65	3E-20
Mjin_4B_T_F09.ab1	gi|157345827|emb|CAO15342.1|	unnamed protein product [Vitis vinifera]	85.57	201	9E-89
Mjin_4B_T_F11.ab1	gi|115440899|ref|NP_001044729.1|	Os01g0835900 [Oryza sativa (japonica cultivar-group)] >gi|113534260|dbj|BAF06643.1| Os01g0835900 [Oryza sativa (japonica cultivar-group)]	100	62	1E-26
Mjin_4B_T_G06.ab1	gi|157346269|emb|CAO15966.1|	unnamed protein product [Vitis vinifera]	82.76	203	1E-94
Mjin_4B_T_G07.ab1	gi|157347909|emb|CAO22496.1|	unnamed protein product [Vitis vinifera]	68.21	173	2E-66
Mjin_4B_T_H01.ab1	gi|118483011|gb|ABK93417.1|	unknown [Populus trichocarpa]	75.33	150	2E-64
Mjin_4B_T_H04.ab1	gi|5802248|gb|AAD51627.1|	seed maturation protein PM39 [Glycine max]	44.58	166	3E-26
Mjin_4B_T_H05.ab1	gi|157358714|emb|CAO66399.1|	unnamed protein product [Vitis vinifera]	79.07	43	1E-11
Mjin_4B_T_H07.ab1	gi|157327804|emb|CAO16493.1|	unnamed protein product [Vitis vinifera]	88.8	125	2E-49
Mjin_4B_T_H09.ab1	gi|129771323|gb|ABO31374.1|	unknown [Gossypium hirsutum]	66.27	169	7E-25
Mjin_4B_T_H11.ab1	gi|147791679|emb|CAN72862.1|	hypothetical protein [Vitis vinifera] >gi|157353260|emb|CAO45183.1| unnamed protein product [Vitis vinifera]	93.3	179	1E-88
Mjin_4C_T_A02.ab1	gi|118481984|gb|ABK92923.1|	unknown [Populus trichocarpa] >gi|118485253|gb|ABK94486.1| unknown [Populus trichocarpa] >gi|118487184|gb|ABK95420.1| unknown [Populus trichocarpa]	88.59	184	2E-91
Mjin_4C_T_A04.ab1	gi|19878|emb|CAA44820.1|	heat shock protein 70 [Nicotiana tabacum]	95.61	228	6E-121
Mjin_4C_T_A05.ab1	gi|157329323|emb|CAO39803.1|	unnamed protein product [Vitis vinifera]	76.09	184	2E-76
Mjin_4C_T_A07.ab1	gi|147805324|emb|CAN63089.1|	hypothetical protein [Vitis vinifera]	94.7	151	2E-80
Mjin_4C_T_A09.ab1	gi|8886726|gb|AAF80560.1|AF192486_1	omega-6 fatty acid desaturase [Sesamum indicum] >gi|59896214|gb|AAX11454.1| microsomal oleic acid desaturase [Sesamum indicum]	90.76	119	7E-63
Mjin_4C_T_B07.ab1	gi|147805324|emb|CAN63089.1|	hypothetical protein [Vitis vinifera]	94.12	187	1E-101
Mjin_4C_T_B08.ab1	gi|157346196|emb|CAO15893.1|	unnamed protein product [Vitis vinifera]	93.75	80	8E-36
Mjin_4C_T_B10.ab1	gi|157346832|emb|CAO17071.1|	unnamed protein product [Vitis vinifera]	58.95	95	1E-22
Mjin_4C_T_C02.ab1	gi|157352531|emb|CAO43637.1|	unnamed protein product [Vitis vinifera]	93.48	92	4E-44
Mjin_4C_T_C03.ab1	gi|157340224|emb|CAO45901.1|	unnamed protein product [Vitis vinifera]	81.67	120	1E-41
Mjin_4C_T_C04.ab1	gi|147802763|emb|CAN66303.1|	hypothetical protein [Vitis vinifera]	70.23	131	4E-30
Mjin_4C_T_C06.ab1	gi|157345069|emb|CAO71797.1|	unnamed protein product [Vitis vinifera]	85	40	3E-11

IP : 14.49.138.138, 2017-11-03 13:30:33

Mjin_4C_T_C07.ab1	gi|147858134|emb|CAN83936.1|	hypothetical protein [Vitis vinifera] >gi|157330198|emb|CAO44703.1| unnamed protein product [Vitis vinifera]	97.62	42	1E-16
Mjin_4C_T_C08.ab1	gi|15219837|ref|NP_176291.1|	FED A (FERREDOXIN 2); 2 iron, 2 sulfur cluster binding / electron carrier/ iron-sulfur cluster binding [Arabidopsis thaliana] >gi|119975|sp|P16972|FER2_ARATH Ferredoxin-2, chloroplast precursor (AtFd2) >gi|11692908|gb|AAG40057.1|AF324706_1 At1g60950 [Arabidopsis thaliana] >gi|11908076|gb|AAG41467.1|AF326885_1 putative ferrodoxin precursor protein [Arabidopsis thaliana] >gi|12323344|gb|AAG51652.1|AC018908_18 ferrodoxin precursor; 39650-40096 [Arabidopsis thaliana] >gi|12642890|gb|AAK00387.1|AF339705_1 putative ferrodoxin precursor protein [Arabidopsis thaliana] >gi|16437|emb|CAA35754.1| ferredoxin precursor [Arabidopsis thaliana] >gi|166698|gb|AAA32790.1| ferrodoxin A >gi|20260270|gb|AAM13033.1| ferrodoxin precursor [Arabidopsis thaliana] >gi|22136516|gb|AAM91336.1| ferrodoxin precursor [Arabidopsis thaliana] >gi|110740859|dbj|BAE98526.1| ferrodoxin precursor [Arabidopsis thaliana]	72.28	101	2E-34
Mjin_4C_T_C09.ab1	gi|147863191|emb|CAN82624.1|	hypothetical protein [Vitis vinifera]	82.52	143	2E-57
Mjin_4C_T_C12.ab1	gi|118488282|gb|ABK95960.1|	unknown [Populus trichocarpa]	73.38	154	2E-64
Mjin_4C_T_D02.ab1	gi|157344149|emb|CAO69082.1|	unnamed protein product [Vitis vinifera]	62.3	61	2E-14
Mjin_4C_T_D06.ab1	gi|115463137|ref|NP_001055168.1|	Os05g0314100 [Oryza sativa (japonica cultivar-group)] >gi|113578719|dbj|BAF17082.1| Os05g0314100 [Oryza sativa (japonica cultivar-group)]	98.41	63	3E-29
Mjin_4C_T_D07.ab1	gi|49659437|dbj|BAD27257.1|	d-limonene synthase [Citrus unshiu]	98.72	156	3E-76
Mjin_4C_T_D08.ab1	gi|157356693|emb|CAO62888.1|	unnamed protein product [Vitis vinifera]	79.37	63	3E-27
Mjin_4C_T_D11.ab1	gi|157357748|emb|CAO64742.1|	unnamed protein product [Vitis vinifera]	81.06	132	1E-46
Mjin_4C_T_E02.ab1	gi|157340863|emb|CAO47668.1|	unnamed protein product [Vitis vinifera]	75.53	237	6E-87
Mjin_4C_T_E04.ab1	gi|544437|sp|Q06652|GPX4_CITSI	RecName: Full=Probable phospholipid hydroperoxide glutathione peroxidase; Short=PHGPx; AltName: Full=Salt-associated protein >gi|296358|emb|CAA47018.1| CIT-SAP [Citrus sinensis] >gi|119367482|gb|ABL67656.1| putative phospholipid hydroperoxide glutathione peroxidase [Citrus cv. Shiranuhi]	100	66	9E-30
Mjin_4C_T_E09.ab1	gi|157352198|emb|CAO43226.1|	unnamed protein product [Vitis vinifera]	69.49	59	1E-17
Mjin_4C_T_F02.ab1	gi|157327792|emb|CAO16481.1|	unnamed protein product [Vitis vinifera]	91.86	86	7E-40
Mjin_4C_T_F03.ab1	gi|157348060|emb|CAO22647.1|	unnamed protein product [Vitis vinifera]	96.08	51	6E-19
Mjin_4C_T_F05.ab1	gi|157339484|emb|CAO44025.1|	unnamed protein product [Vitis vinifera]	75.29	174	7E-73
Mjin_4C_T_F07.ab1	gi|118488644|gb|ABK96134.1|	unknown [Populus trichocarpa]	95.79	95	4E-45
Mjin_4C_T_F09.ab1	gi|147786913|emb|CAN68895.1|	hypothetical protein [Vitis vinifera]	59.66	233	1E-70
Mjin_4C_T_F10.ab1	gi|157336280|emb|CAO70965.1|	unnamed protein product [Vitis vinifera]	74.86	175	4E-77
Mjin_4C_T_G03.ab1	gi|118486353|gb|ABK95017.1|	unknown [Populus trichocarpa]	93.61	219	4E-105
Mjin_4C_T_G05.ab1	gi|192912980|gb|ACF06598.1|	translation initiation factor [Elaeis guineensis]	91.95	87	3E-39
Mjin_4C_T_G08.ab1	gi|118484726|gb|ABK94232.1|	unknown [Populus trichocarpa]	50.71	211	8E-47
Mjin_4C_T_G11.ab1	gi|134038586|gb|ABO48361.1|	DRE-binding protein 2 [Populus trichocarpa]	77.5	120	1E-39
Mjin_4C_T_H03.ab1	gi|21616053|emb|CAC86004.1|	aspartic proteinase [Theobroma cacao]	85.25	61	3E-16
Mjin_4C_T_H05.ab1	gi|157418810|gb|ABV55108.1|	catalase 2 [Musa acuminata]	82.93	205	2E-102
Mjin_4C_T_H06.ab1	gi|157335048|emb|CAO60878.1|	unnamed protein product [Vitis vinifera]	88.41	69	2E-26
Mjin_4C_T_H12.ab1	gi|15241564|ref|NP_199286.1|	haloacid dehalogenase-like hydrolase family protein [Arabidopsis thaliana] >gi|42573575|ref|NP_974884.1| haloacid dehalogenase-like hydrolase family protein [Arabidopsis thaliana] >gi|2660676|gb|AAC79147.1| Dreg-2 like protein [Arabidopsis thaliana] >gi|9758377|dbj|BAB08826.1| Dreg-2 like protein [Arabidopsis thaliana] >gi|106879171|gb|ABF82615.1| At5g44730 [Arabidopsis thaliana]	81.25	176	1E-85
Mjin_4D_T_A03.ab1	gi|157355861|emb|CAO49718.1|	unnamed protein product [Vitis vinifera]	69.08	152	3E-51
Mjin_4D_T_A05.ab1	gi|157344731|emb|CAO70486.1|	unnamed protein product [Vitis vinifera]	88	125	1E-44

IP : 14.49.138.138, 2017-11-03 13:30:33

Mjin_4D_T_A09.ab1	gi|157344802|emb|CAO70557.1|	unnamed protein product [Vitis vinifera]	51.53	196	1E-35
Mjin_4D_T_A10.ab1	gi|118482534|gb|ABK93188.1|	unknown [Populus trichocarpa]	93.62	141	6E-69
Mjin_4D_T_B01.ab1	gi|40287480|gb|AAR83854.1|	induced stolon tip protein [Capsicum annuum]	86.84	38	4E-13
Mjin_4D_T_B02.ab1	gi|118483222|gb|ABK93514.1|	unknown [Populus trichocarpa] >gi|118487214|gb|ABK95435.1| unknown [Populus trichocarpa]	98.75	80	2E-36
Mjin_4D_T_B07.ab1	gi|28881455|emb|CAD46560.1|	profilin [Malus x domestica]	92.42	66	6E-31
Mjin_4D_T_B08.ab1	gi|82621166|gb|ABB86271.1|	adenine phosphoribosyltransferase-like [Solanum tuberosum]	89.56	182	6E-85
Mjin_4D_T_B09.ab1	gi|187369229|dbj|BAG31375.1|	topoisomerase I [Ophiorrhiza japonica]	93.33	75	6E-34
Mjin_4D_T_B10.ab1	gi|158635126|gb|ABW76425.1|	branched-chain aminotransferase [Nicotiana benthamiana]	72.97	148	2E-54
Mjin_4D_T_C01.ab1	gi|1061408|gb|AAB52963.1|	citrin	74.53	106	2E-38
Mjin_4D_T_C03.ab1	gi|157339679|emb|CAO44220.1|	unnamed protein product [Vitis vinifera]	89.02	82	9E-36
Mjin_4D_T_C05.ab1	gi|118485407|gb|ABK94560.1|	unknown [Populus trichocarpa]	80.68	88	6E-35
Mjin_4D_T_C08.ab1	gi|115466174|ref|NP_001056686.1|	Os06g0130000 [Oryza sativa (japonica cultivar-group)] >gi|52075628|dbj|BAD44799.1| putative spastin protein orthologue [Oryza sativa Japonica Group] >gi|113594726|dbj|BAF18600.1| Os06g0130000 [Oryza sativa (japonica cultivar-group)] >gi|124361604|gb|ABN09244.1| putative spastin-like protein [Oryza sativa (japonica cultivar-group)]	79.07	43	1E-13
Mjin_4D_T_C09.ab1	gi|110931850|gb|ABH02924.1|	MYB transcription factor MYB131 [Glycine max]	84.81	79	6E-33
Mjin_4D_T_D04.ab1	gi|157360856|emb|CAO70671.1|	unnamed protein product [Vitis vinifera]	87.5	144	9E-70
Mjin_4D_T_D09.ab1	gi|118487432|gb|ABK95544.1|	unknown [Populus trichocarpa]	88.46	52	3E-18
Mjin_4D_T_D11.ab1	gi|15240163|ref|NP_200929.1|	SNAP33 (synaptosomal-associated protein 33); SNAP receptor [Arabidopsis thaliana] >gi|27805727|sp|Q9S7P9|SNP33_ARATH SNAP25 homologous protein SNAP33 (AtSNAP33) (Synaptosomal-associated protein SNAP25-like 1) (SNAP-25-like protein 1) (Snap25a) >gi|5731763|emb|CAB52582.1| SNAP33 protein [Arabidopsis thaliana] >gi|5731764|emb|CAB52583.1| SNAP33B protein [Arabidopsis thaliana] >gi|9759467|dbj|BAB10383.1| SNAP25A protein [Arabidopsis thaliana] >gi|16323047|gb|AAL15258.1| AT5g61210/maf19_210 [Arabidopsis thaliana] >gi|18072736|emb|CAC79615.1| SNAP-25 like protein [Arabidopsis thaliana] >gi|22655332|gb|AAM98258.1| At5g61210/maf19_210 [Arabidopsis thaliana]	71.31	122	2E-37
Mjin_4D_T_E05.ab1	gi|157327185|emb|CAO14466.1|	unnamed protein product [Vitis vinifera]	78.95	57	3E-20
Mjin_4D_T_E07.ab1	gi|118482536|gb|ABK93189.1|	unknown [Populus trichocarpa]	62.37	93	2E-14
Mjin_4D_T_F01.ab1	gi|37993504|gb|AAR06858.1|	putative calcium-dependent protein kinase CPK1 adapter protein 2 [Mesembryanthemum crystallinum]	63.78	127	7E-42
Mjin_4D_T_F04.ab1	gi|147797356|emb|CAN76005.1|	hypothetical protein [Vitis vinifera]	50.65	77	9E-14
Mjin_4D_T_F05.ab1	gi|147772450|emb|CAN63002.1|	hypothetical protein [Vitis vinifera]	58.11	74	6E-17
Mjin_4D_T_F06.ab1	gi|157329208|emb|CAO38679.1|	unnamed protein product [Vitis vinifera]	81.98	111	1E-49
Mjin_4D_T_F09	gi|147806197|emb|CAN65479.1|	hypothetical protein [Vitis vinifera]	63.21	106	6E-27
Mjin_4D_T_G01.ab1	gi|118488661|gb|ABK96142.1|	unknown [Populus trichocarpa]	64.55	189	4E-36
Mjin_4D_T_G02.ab1	gi|147857366|emb|CAN80795.1|	hypothetical protein [Vitis vinifera]	73.26	86	1E-27
Mjin_4D_T_G06.ab1	gi|106879589|emb|CAJ38378.1|	glyceraldehyde-3-phosphate dehydrogenase [Plantago major]	93.48	46	8E-18
Mjin_4D_T_G08.ab1	gi|154269428|gb|ABS72341.1|	rapid alkalinization factor precursor [Litchi chinensis]	62.03	79	2E-13
Mjin_4D_T_H12.ab1	gi|157329812|emb|CAO42642.1|	unnamed protein product [Vitis vinifera]	61.82	220	1E-68
Mjin_5A_T_A07.ab1	gi|10177007|dbj|BAB10195.1|	unnamed protein product [Arabidopsis thaliana]	49.01	151	4E-23
Mjin_5A_T_A10.ab1	gi|118486650|gb|ABK95162.1|	unknown [Populus trichocarpa]	48.53	136	7E-22
Mjin_5A_T_A11.ab1	gi|1504063|emb|CAA68872.1|	shaggy-like kinase kappa [Arabidopsis thaliana]	90	40	1E-14
Mjin_5A_T_A12.ab1	gi|195649473|gb|ACG44204.1|	unknown [Zea mays]	86.15	231	1E-115
Mjin_5A_T_B08.ab1	gi|13491752|gb|AAK27969.1|AF242373_1	cysteine protease [Ipomoea batatas]	94.17	103	6E-53

IP : 14.49.138.138, 2017-11-03 13:30:33

Mjin_5A_T_B09.ab1	gi|118481523|gb|ABK92704.1|	unknown [Populus trichocarpa]	65.79	114	1E-37
Mjin_5A_T_C01.ab1	gi|145332395|ref|NP_001078154.1|	(S)-2-hydroxy-acid oxidase, peroxisomal, putative / glycolate oxidase, putative / short chain alpha-hydroxy acid oxidase, putative [Arabidopsis thaliana]	84.21	171	5E-77
Mjin_5A_T_C02.ab1	gi|20340233|gb|AAM19703.1|AF499716_1	ethylene responsive element binding factor 4-like protein [Thellungiella halophila]	84.81	79	7E-20
Mjin_5A_T_C04.ab1	gi|157336328|emb|CAO71013.1|	unnamed protein product [Vitis vinifera]	94.08	169	6E-89
Mjin_5A_T_C05.ab1	gi|1061408|gb|AAB52963.1|	citrin	77.33	75	5E-20
Mjin_5A_T_C07.ab1	gi|147802843|emb|CAN75153.1|	hypothetical protein [Vitis vinifera]	69.8	149	9E-38
Mjin_5A_T_C11.ab1	gi|157343312|emb|CAO67363.1|	unnamed protein product [Vitis vinifera]	53.68	231	2E-49
Mjin_5A_T_D01.ab1	gi|147855132|emb|CAN83842.1|	hypothetical protein [Vitis vinifera]	78.86	175	3E-73
Mjin_5A_T_D02.ab1	gi|118488628|gb|ABK96126.1|	unknown [Populus trichocarpa]	82.61	46	1E-12
Mjin_5A_T_D06.ab1	gi|118487840|gb|ABK95743.1|	unknown [Populus trichocarpa]	93.55	62	1E-25
Mjin_5A_T_D07.ab1	gi|157337511|emb|CAO21857.1|	unnamed protein product [Vitis vinifera]	50	172	1E-30
Mjin_5A_T_D10.ab1	gi|157336358|emb|CAO71043.1|	unnamed protein product [Vitis vinifera]	85.94	64	6E-27
Mjin_5A_T_D11.ab1	gi|147773643|emb|CAN76464.1|	hypothetical protein [Vitis vinifera] >gi|157335552|emb|CAO61382.1| unnamed protein product [Vitis vinifera]	85.84	233	4E-110
Mjin_5A_T_E02.ab1	gi|118487990|gb|ABK95816.1|	unknown [Populus trichocarpa]	96.32	136	7E-59
Mjin_5A_T_E03.ab1	gi|1061408|gb|AAB52963.1|	citrin	100	61	4E-26
Mjin_5A_T_E05.ab1	gi|147865395|emb|CAN79815.1|	hypothetical protein [Vitis vinifera]	90.91	88	3E-43
Mjin_5A_T_E09.ab1	gi|118481907|gb|ABK92888.1|	unknown [Populus trichocarpa]	62.11	95	1E-28
Mjin_5A_T_F02.ab1	gi|157358494|emb|CAO66161.1|	unnamed protein product [Vitis vinifera]	62.81	121	1E-32
Mjin_5A_T_F05.ab1	gi|157341495|emb|CAO62050.1|	unnamed protein product [Vitis vinifera]	90.87	219	5E-108
Mjin_5A_T_F08.ab1	gi|119367477|gb|ABL67654.1|	putative H-type thioredoxin [Citrus cv. Shiranuhi]	96.92	65	1E-30
Mjin_5A_T_F10.ab1	gi|1351408|sp|P49043|VPE_CITSI	Vacuolar-processing enzyme precursor (VPE) >gi|633185|emb|CAA87720.1| cystein proteinase (by similarity) [Citrus sinensis] >gi|1588548|prf||2208463A vascular processing protease	96.67	60	2E-27
Mjin_5A_T_F11.ab1	gi|21063921|gb|AAM29150.1|	citrus sucrose transporter 1 [Citrus sinensis]	99.29	141	1E-70
Mjin_5A_T_G01.ab1	gi|11385443|gb|AAG34804.1|AF243369_1	glutathione S-transferase GST 14 [Glycine max]	57.84	204	3E-60
Mjin_5A_T_G03.ab1	gi|147790480|emb|CAN72172.1|	hypothetical protein [Vitis vinifera]	60.65	155	6E-39
Mjin_5A_T_G05.ab1	gi|1707657|emb|CAA96305.1|	DnaJ homologue [Pisum sativum]	68.66	134	2E-43
Mjin_5A_T_G09.ab1	gi|147838876|emb|CAN61572.1|	hypothetical protein [Vitis vinifera]	69.51	82	7E-22
Mjin_5A_T_G12.ab1	gi|147853333|emb|CAN82327.1|	hypothetical protein [Vitis vinifera] >gi|157350404|emb|CAO40384.1| unnamed protein product [Vitis vinifera]	65.24	210	3E-59
Mjin_5A_T_H02.ab1	gi|157344732|emb|CAO70487.1|	unnamed protein product [Vitis vinifera]	97.78	225	3E-115
Mjin_5A_T_H06.ab1	gi|116078101|dbj|BAF34914.1|	MADS-box protein [Citrus unshiu]	100	208	8E-102
Mjin_5A_T_H08.ab1	gi|157345980|emb|CAO15677.1|	unnamed protein product [Vitis vinifera]	68.28	145	7E-46
Mjin_5A_T_H11.ab1	gi|147814811|emb|CAN72342.1|	hypothetical protein [Vitis vinifera]	83.56	73	3E-29
Mjin_5B_T_A02.ab1	gi|24461867|gb|AAN62354.1|AF506028_23	CTV.22 [Poncirus trifoliata]	100	69	9E-32
Mjin_5B_T_A03.ab1	gi|164430467|gb|ABY55551.1|	calcium-dependent protein kinase [Swainsona canescens]	96.15	234	1E-128
Mjin_5B_T_A09.ab1	gi|20385449|gb|AAM21292.1|AF369931_1	lipid-transfer protein [Citrus sinensis]	97.5	80	6E-39
Mjin_5B_T_A10.ab1	gi|209168551|gb|ACI42271.1|	glutathione S-transferase Tau2 [Citrus sinensis]	88.79	116	6E-56
Mjin_5B_T_A11.ab1	gi|147860904|emb|CAN80873.1|	hypothetical protein [Vitis vinifera]	86.11	108	6E-45
Mjin_5B_T_B01.ab1	gi|157337815|emb|CAO38859.1|	unnamed protein product [Vitis vinifera]	72.26	155	5E-57
Mjin_5B_T_B04.ab1	gi|157353528|emb|CAO45484.1|	unnamed protein product [Vitis vinifera]	89.13	138	6E-64

IP : 14.49.138.138, 2017-11-03 13:30:33

Mjin_5B_T_B05.ab1	gi|157328698|emb|CAO22716.1|	unnamed protein product [Vitis vinifera]	78.7	108	3E-43
Mjin_5B_T_B06.ab1	gi|147783628|emb|CAN68149.1|	hypothetical protein [Vitis vinifera] >gi|157353814|emb|CAO46346.1| unnamed protein product [Vitis vinifera]	75	188	2E-78
Mjin_5B_T_B07.ab1	gi|147857777|emb|CAN80801.1|	hypothetical protein [Vitis vinifera]	84.62	39	4E-12
Mjin_5B_T_B12.ab1	gi|116791648|gb|ABK26055.1|	unknown [Picea sitchensis]	49.3	71	2E-11
Mjin_5B_T_C03.ab1	gi|157357944|emb|CAO64956.1|	unnamed protein product [Vitis vinifera]	81.36	118	2E-41
Mjin_5B_T_C04.ab1	gi|147791112|emb|CAN70271.1|	hypothetical protein [Vitis vinifera]	73.68	152	1E-51
Mjin_5B_T_C05.ab1	gi|157338493|emb|CAO41844.1|	unnamed protein product [Vitis vinifera]	73.98	123	6E-49
Mjin_5B_T_C07.ab1	gi|118487434|gb|ABK95545.1|	unknown [Populus trichocarpa]	78.95	76	2E-30
Mjin_5B_T_C09.ab1	gi|157336067|emb|CAO61897.1|	unnamed protein product [Vitis vinifera]	78.7	108	1E-42
Mjin_5B_T_C11.ab1	gi|122894098|gb|ABM67695.1|	cinnamyl alcohol dehydrogenase [Citrus sinensis]	100	94	5E-46
Mjin_5B_T_C12.ab1	gi|157355058|emb|CAO48419.1|	unnamed protein product [Vitis vinifera]	80.49	123	4E-52
Mjin_5B_T_D01.ab1	gi|6478218|gb|AAF13743.1|AF109921_1	caleosin [Sesamum indicum]	84	50	1E-19
Mjin_5B_T_D06.ab1	gi|18417474|ref|NP_567835.1|	ATCFIM-25/CFIM-25 (ARABIDOPSIS HOMOLOG OF CFIM-25) [Arabidopsis thaliana] >gi|15081674|gb|AAK82492.1| AT4g29820/F27B13_60 [Arabidopsis thaliana] >gi|20147173|gb|AAM10303.1| AT4g29820/F27B13_60 [Arabidopsis thaliana] >gi|21554114|gb|AAM63194.1| mRNA cleavage factor subunit-like protein [Arabidopsis thaliana]	83.33	90	1E-36
Mjin_5B_T_D09.ab1	gi|1170745|sp|P46518|LEA14_GOSHI	Late embryogenesis abundant protein Lea14-A >gi|167326|gb|AAA18542.1| Group 4 late embryogenesis-abundant protein >gi|167328|gb|AAA18543.1| Group 4 late embryogenesis-abundant protein	76.39	144	9E-59
Mjin_5B_T_D12.ab1	gi|15234910|ref|NP_192742.1|	CYTC-2 (CYTOCHROME C-2); electron carrier [Arabidopsis thaliana] >gi|27734261|sp|Q9T0G2|CYC3_ARATH RecName: Full=Probable cytochrome c At4g10040 >gi|4539007|emb|CAB39628.1| cytochrome c [Arabidopsis thaliana] >gi|7267700|emb|CAB78127.1| cytochrome c [Arabidopsis thaliana] >gi|15028283|gb|AAK76618.1| putative cytochrome c protein [Arabidopsis thaliana] >gi|19310747|gb|AAL85104.1| putative cytochrome c protein [Arabidopsis thaliana] >gi|21592668|gb|AAM64617.1| cytochrome c [Arabidopsis thaliana]	97.5	40	8E-16
Mjin_5B_T_E06.ab1	gi|7387726|sp|O22582|H2B_GOSHI	Histone H2B >gi|2558962|gb|AAB97163.1| histone H2B1 [Gossypium hirsutum]	95	80	3E-30
Mjin_5B_T_E07.ab1	gi|9622153|gb|AAF89645.1|AF169018_1	seed maturation protein PM34 [Glycine max]	76.83	82	3E-30
Mjin_5B_T_E09.ab1	gi|118483644|gb|ABK93716.1|	unknown [Populus trichocarpa]	65.35	127	8E-29
Mjin_5B_T_E12.ab1	gi|119367470|gb|ABL67651.1|	putative auxin-repressed/dormancy-associated protein [Citrus cv. Shiranuhi]	95.77	71	8E-18
Mjin_5B_T_F04.ab1	gi|157349164|emb|CAO24310.1|	unnamed protein product [Vitis vinifera]	85.81	155	4E-73
Mjin_5B_T_F10.ab1	gi|118486164|gb|ABK94925.1|	unknown [Populus trichocarpa]	97.04	135	1E-69
Mjin_5B_T_F11.ab1	gi|4519264|dbj|BAA75517.1|	vacuolar H+-ATPase B subunit [Citrus unshiu]	100	56	4E-24
Mjin_5B_T_G01.ab1	gi|157351151|emb|CAO41338.1|	unnamed protein product [Vitis vinifera]	97.47	79	8E-37
Mjin_5B_T_G02	gi|157339699|emb|CAO44240.1|	unnamed protein product [Vitis vinifera]	56.14	114	8E-30
Mjin_5B_T_G04.ab1	gi|157327749|emb|CAO16179.1|	unnamed protein product [Vitis vinifera]	88	100	2E-36
Mjin_5B_T_G05.ab1	gi|147780466|emb|CAN62547.1|	hypothetical protein [Vitis vinifera]	77.33	75	1E-22
Mjin_5B_T_G06.ab1	gi|118486764|gb|ABK95217.1|	unknown [Populus trichocarpa]	79.52	83	2E-31
Mjin_5B_T_G07.ab1	gi|12830830|gb|AAK08208.1|AF320905_1	metallothionein-like protein [Citrus unshiu] >gi|12830832|gb|AAK08209.1|AF320906_1 metallothionein-like protein [Citrus unshiu] >gi|3308982|dbj|BAA31562.1| metallothionein-like protein [Citrus unshiu] >gi|158936952|dbj|BAF91493.1| metallothionein type 3 [Citrus unshiu]	100	35	2E-14
Mjin_5B_T_H03.ab1	gi|147860006|emb|CAN81047.1|	hypothetical protein [Vitis vinifera]	91.91	173	2E-91
Mjin_5C_T_A03.ab1	gi|147804684|emb|CAN71441.1|	hypothetical protein [Vitis vinifera]	66.94	124	4E-44
Mjin_5C_T_A07.ab1	gi|157329481|emb|CAO40455.1|	unnamed protein product [Vitis vinifera]	66.83	205	2E-78
Mjin_5C_T_A08.ab1	gi|157345322|emb|CAO14620.1|	unnamed protein product [Vitis vinifera]	89.08	229	7E-114

IP : 14.49.138.138, 2017-11-03 13:30:33

Mjin_5C_T_B03.ab1	gi|147852275|emb|CAN82235.1|	hypothetical protein [Vitis vinifera]	82.93	205	2E-92
Mjin_5C_T_B06.ab1	gi|157335692|emb|CAO61522.1|	unnamed protein product [Vitis vinifera]	65.22	184	1E-53
Mjin_5C_T_B07.ab1	gi|157345201|emb|CAO71929.1|	unnamed protein product [Vitis vinifera]	56.7	97	2E-20
Mjin_5C_T_B11.ab1	gi|15219028|ref|NP_175665.1|	26.5 kDa class I small heat shock protein-like (HSP26.5-P) [Arabidopsis thaliana] >gi|5903049|gb|AAD55608.1|AC008016_18 Similar to gb|X07187 heat shock protein 21 precursor from Pisum sativum and is a member of the PF|00011 HSP20/alpha crystallin family. [Arabidopsis thaliana] >gi|38566632|gb|AAR24206.1| At1g52560 [Arabidopsis thaliana] >gi|40824092|gb|AAR92344.1| At1g52560 [Arabidopsis thaliana]	54.42	226	3E-48
Mjin_5C_T_B12.ab1	gi|13899067|gb|AAK48955.1|AF370528_1	ATP-dependent Clp protease; nClpP3 [Arabidopsis thaliana] >gi|18377550|gb|AAL66941.1| ATP-dependent Clp protease (nClpP3) [Arabidopsis thaliana]	77.08	192	2E-79
Mjin_5C_T_C02.ab1	gi|157345021|emb|CAO71749.1|	unnamed protein product [Vitis vinifera]	91.43	70	2E-29
Mjin_5C_T_C03.ab1	gi|157335517|emb|CAO61347.1|	unnamed protein product [Vitis vinifera]	81.56	141	1E-49
Mjin_5C_T_C06.ab1	gi|157348673|emb|CAO23565.1|	unnamed protein product [Vitis vinifera]	95.56	90	9E-46
Mjin_5C_T_C07.ab1	gi|147794108|emb|CAN62364.1|	hypothetical protein [Vitis vinifera]	90.22	92	1E-38
Mjin_5C_T_C08.ab1	gi|152002268|gb|ABS19535.1|	CT114 [Solanum chilense]	92.39	92	1E-42
Mjin_5C_T_D03.ab1	gi|177536014|gb|ACB72861.1|	flowering locus C variant 2 [Poncirus trifoliata]	96.15	78	4E-34
Mjin_5C_T_D05.ab1	gi|147774374|emb|CAN72399.1|	hypothetical protein [Vitis vinifera]	78.57	70	1E-15
Mjin_5C_T_D07.ab1	gi|157352236|emb|CAO43264.1|	unnamed protein product [Vitis vinifera]	75.97	154	3E-64
Mjin_5C_T_D10.ab1	gi|15242242|ref|NP_200011.1|	WD-40 repeat family protein / zfwd2 protein (ZFWD2), putative [Arabidopsis thaliana] >gi|10177733|dbj|BAB11046.1| unnamed protein product [Arabidopsis thaliana]	77.3	163	9E-75
Mjin_5C_T_D11.ab1	gi|1351408|sp|P49043|VPE_CITSI	Vacuolar-processing enzyme precursor (VPE) >gi|633185|emb|CAA87720.1| cystein proteinase (by similarity) [Citrus sinensis] >gi|1588548|prf||2208463A vascular processing protease	100	76	9E-38
Mjin_5C_T_D12.ab1	gi|6094476|sp|O23787|THI4_CITSI	RecName: Full=Thiazole biosynthetic enzyme, chloroplastic; Flags: Precursor >gi|2582665|emb|CAB05370.1| thi [Citrus sinensis]	100	83	2E-39
Mjin_5C_T_E01.ab1	gi|194698770|gb|ACF83469.1|	unknown [Zea mays]	86.05	43	3E-14
Mjin_5C_T_E08.ab1	gi|37524017|gb|AAQ92310.1|	COR15 [Citrus clementina x Citrus reticulata]	98.41	63	1E-19
Mjin_5C_T_E09.ab1	gi|118488785|gb|ABK96203.1|	unknown [Populus trichocarpa]	75.33	150	1E-56
Mjin_5C_T_E11.ab1	gi|118486538|gb|ABK95108.1|	unknown [Populus trichocarpa]	81.48	108	8E-44
Mjin_5C_T_F03.ab1	gi|157336860|emb|CAO71545.1|	unnamed protein product [Vitis vinifera]	75.51	49	4E-14
Mjin_5C_T_F05.ab1	gi|157342096|emb|CAO64209.1|	unnamed protein product [Vitis vinifera]	79.17	48	5E-13
Mjin_5C_T_F07.ab1	gi|147800246|emb|CAN68708.1|	hypothetical protein [Vitis vinifera]	85.57	97	4E-41
Mjin_5C_T_F08.ab1	gi|118486870|gb|ABK95269.1|	unknown [Populus trichocarpa]	82.98	47	1E-17
Mjin_5C_T_F09.ab1	gi|157336132|emb|CAO61962.1|	unnamed protein product [Vitis vinifera]	85.71	70	2E-32
Mjin_5C_T_G03.ab1	gi|22653808|sp|Q39644|LEA5_CITSI	Late embryogenesis abundant protein Lea5 >gi|599726|emb|CAA86851.1| Lea5 protein [Citrus sinensis]	98.97	97	2E-47
Mjin_5C_T_G04.ab1	gi|157336286|emb|CAO70971.1|	unnamed protein product [Vitis vinifera]	99.42	171	4E-92
Mjin_5C_T_G07.ab1	gi|20385508|gb|AAM21317.1|AF373100_1	auxin-regulated protein [Populus tremula x Populus tremuloides]	65.48	197	6E-57
Mjin_5C_T_G12.ab1	gi|145361384|ref|NP_849541.2|	transport protein, putative [Arabidopsis thaliana]	79.57	230	1E-96
Mjin_5C_T_H01.ab1	gi|147810112|emb|CAN75832.1|	hypothetical protein [Vitis vinifera]	60.23	171	2E-45
Mjin_5C_T_H02.ab1	gi|90657614|gb|ABD96913.1|	hypothetical protein [Cleome spinosa]	83.87	93	3E-40
Mjin_5C_T_H09.ab1	gi|18416872|ref|NP_568281.1|	CPK7 (CALMODULIN-DOMAIN PROTEIN KINASE 7); calmodulin-dependent protein kinase/ kinase [Arabidopsis thaliana] >gi|75319419|sp|Q38873|CDPK7_ARATH RecName: Full=Calcium-dependent protein kinase 7 >gi|13605617|gb|AAK32802.1|AF361634_1 AT5g19450/F7K24_200 [Arabidopsis thaliana] >gi|1399277|gb|AAB03247.1| calmodulin-domain protein kinase CDPK isoform 7 [Arabidopsis thaliana] >gi|14586378|emb|CAC42909.1| calcium-dependent protein kinase-like protein [Arabidopsis thaliana]	71.71	152	3E-59

IP : 14.49.138.138, 2017-11-03 13:30:33

Mjin_5C_T_H10.ab1	gi|157329331|emb|CAO39810.1|	unnamed protein product [Vitis vinifera]	83.33	54	1E-19
Mjin_5D_T_A02.ab1	gi|118481698|gb|ABK92789.1|	unknown [Populus trichocarpa] >gi|118483656|gb|ABK93722.1| unknown [Populus trichocarpa] >gi|118487386|gb|ABK95521.1| unknown [Populus trichocarpa]	97.93	145	3E-76
Mjin_5D_T_A03.ab1	gi|157357469|emb|CAO64003.1|	unnamed protein product [Vitis vinifera]	81.31	198	4E-84
Mjin_5D_T_A06.ab1	gi|157337231|emb|CAO21577.1|	unnamed protein product [Vitis vinifera]	68.63	102	5E-31
Mjin_5D_T_A07.ab1	gi|147784740|emb|CAN74796.1|	hypothetical protein [Vitis vinifera]	96.1	231	9E-122
Mjin_5D_T_A08.ab1	gi|147787358|emb|CAN64632.1|	hypothetical protein [Vitis vinifera]	81.86	215	2E-85
Mjin_5D_T_A09.ab1	gi|157330142|emb|CAO44599.1|	unnamed protein product [Vitis vinifera]	73.3	206	5E-85
Mjin_5D_T_B08.ab1	gi|18397852|ref|NP_566299.1|	GPI transamidase component Gpi16 subunit family protein [Arabidopsis thaliana] >gi|15292901|gb|AAK92821.1| unknown protein [Arabidopsis thaliana] >gi|22136838|gb|AAM91763.1| unknown protein [Arabidopsis thaliana]	68.85	183	2E-65
Mjin_5D_T_B11.ab1	gi|76160982|gb|ABA40454.1|	proteasome alpha subunit-like protein [Solanum tuberosum]	98.42	190	3E-95
Mjin_5D_T_B12.ab1	gi|157351144|emb|CAO41331.1|	unnamed protein product [Vitis vinifera]	81.14	175	7E-74
Mjin_5D_T_C02.ab1	gi|57013900|ref|YP_173374.1|	hypothetical protein NitaMp027 [Nicotiana tabacum] >gi|57014030|ref|YP_173501.1| hypothetical protein NitaMp164 [Nicotiana tabacum] >gi|56806536|dbj|BAD83437.1| hypothetical protein [Nicotiana tabacum] >gi|56806666|dbj|BAD83567.1| hypothetical protein [Nicotiana tabacum]	97.33	75	5E-36
Mjin_5D_T_C04.ab1	gi|157349838|emb|CAO39694.1|	unnamed protein product [Vitis vinifera]	77.78	54	3E-18
Mjin_5D_T_C06.ab1	gi|147795418|emb|CAN77104.1|	hypothetical protein [Vitis vinifera] >gi|157345456|emb|CAO14754.1| unnamed protein product [Vitis vinifera]	92.59	81	2E-36
Mjin_5D_T_C08.ab1	gi|231586|sp|P29685|ATPBM_HEVBR	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor >gi|18831|emb|CAA41401.1| mitochondrial ATP synthase beta-subunit [Hevea brasiliensis]	97.56	123	4E-63
Mjin_5D_T_D06.ab1	gi|37524017|gb|AAQ92310.1|	COR15 [Citrus clementina x Citrus reticulata]	100	49	2E-12
Mjin_5D_T_D08.ab1	gi|186498546|ref|NP_178253.3|	ATP-dependent helicase [Arabidopsis thaliana]	87.07	147	1E-57
Mjin_5D_T_D09.ab1	gi|118484677|gb|ABK94209.1|	unknown [Populus trichocarpa]	90.78	141	8E-67
Mjin_5D_T_E01.ab1	gi|18378999|ref|NP_563661.1|	unknown protein [Arabidopsis thaliana] >gi|9972373|gb|AAG10623.1|AC022521_1 Unknown protein [Arabidopsis thaliana] >gi|15810579|gb|AAL07177.1| unknown protein [Arabidopsis thaliana] >gi|20259577|gb|AAM14131.1| unknown protein [Arabidopsis thaliana]	59.73	149	4E-43
Mjin_5D_T_E02.ab1	gi|151934217|gb|ABS18446.1|	WRKY50 [Glycine max]	87.16	109	8E-53
Mjin_5D_T_E03.ab1	gi|157355496|emb|CAO48886.1|	unnamed protein product [Vitis vinifera]	83.48	224	2E-107
Mjin_5D_T_E06.ab1	gi|157342907|emb|CAO65619.1|	unnamed protein product [Vitis vinifera]	73.91	69	9E-25
Mjin_5D_T_F01.ab1	gi|125524676|gb|EAY72790.1|	hypothetical protein OsI_000637 [Oryza sativa (indica cultivar-group)]	85.47	117	3E-52
Mjin_5D_T_F02.ab1	gi|90820120|gb|ABD98820.1|	UDP-glucose pyrophosphorylase [Cucumis melo]	94.44	54	1E-22
Mjin_5D_T_F05.ab1	gi|157346563|emb|CAO16446.1|	unnamed protein product [Vitis vinifera]	33.33	162	6E-12
Mjin_5D_T_F07.ab1	gi|147814792|emb|CAN74415.1|	hypothetical protein [Vitis vinifera]	88.59	149	4E-70
Mjin_5D_T_F10.ab1	gi|157338571|emb|CAO41922.1|	unnamed protein product [Vitis vinifera]	84.21	76	2E-29
Mjin_5D_T_G02.ab1	gi|25992545|gb|AAN77152.1|	fiber protein Fb13 [Gossypium barbadense]	81.82	55	3E-11
Mjin_5D_T_G03.ab1	gi|147784893|emb|CAN70824.1|	hypothetical protein [Vitis vinifera]	82.04	167	3E-75
Mjin_5D_T_G05.ab1	gi|157328061|emb|CAO17045.1|	unnamed protein product [Vitis vinifera]	56.52	115	2E-21
Mjin_5D_T_G07.ab1	gi|157349921|emb|CAO39777.1|	unnamed protein product [Vitis vinifera]	51.32	152	3E-33
Mjin_5D_T_G12.ab1	gi|157338278|emb|CAO39322.1|	unnamed protein product [Vitis vinifera]	74.23	97	2E-31
Mjin_5D_T_H02.ab1	gi|118488759|gb|ABK96190.1|	unknown [Populus trichocarpa]	56.9	116	6E-18
Mjin_5D_T_H11.ab1	gi|114682|sp|P22778|ATPO_IPOBA	RecName: Full=ATP synthase subunit O, mitochondrial; AltName: Full=Oligomycin sensitivity conferral protein; Short=OSCP; Flags: Precursor >gi|168270|gb|AAA33388.1| F-1-ATPase delta subunit precursor (EC 3.6.1.3)	61.4	171	5E-48
Mjin_6A_T_A01.ab1	gi|118488238|gb|ABK95938.1|	unknown [Populus trichocarpa]	93.06	216	8E-114

IP : 14.49.138.138, 2017-11-03 13:30:33

Mjin_6A_T_A02.ab1	gi|118482989|gb|ABK93406.1|	unknown [Populus trichocarpa]	77.73	220	1E-82
Mjin_6A_T_A03.ab1	gi|54043095|gb|AAV28535.1|	glycolate oxidase [Brassica napus]	92.24	116	1E-48
Mjin_6A_T_A04.ab1	gi|118482280|gb|ABK93067.1|	unknown [Populus trichocarpa]	58.86	158	1E-30
Mjin_6A_T_A05.ab1	gi|157350210|emb|CAO40148.1|	unnamed protein product [Vitis vinifera]	65	100	9E-14
Mjin_6A_T_A06.ab1	gi|116078095|dbj|BAF34911.1|	MADS-box protein [Citrus unshiu]	97.35	189	2E-97
Mjin_6A_T_A08.ab1	gi|157329805|emb|CAO42636.1|	unnamed protein product [Vitis vinifera]	78.38	148	2E-59
Mjin_6A_T_A09.ab1	gi|118483982|gb|ABK93878.1|	unknown [Populus trichocarpa]	96	75	4E-37
Mjin_6A_T_B03.ab1	gi|1351408|sp|P49043|VPE_CITSI	Vacuolar-processing enzyme precursor (VPE) >gi|633185|emb|CAA87720.1| cystein proteinase (by similarity) [Citrus sinensis] >gi|1588548|prf||2208463A vascular processing protease	100	69	8E-34
Mjin_6A_T_B06.ab1	gi|157341122|emb|CAO49029.1|	unnamed protein product [Vitis vinifera]	82.61	46	1E-14
Mjin_6A_T_C01.ab1	gi|118488632|gb|ABK96128.1|	unknown [Populus trichocarpa]	82.35	68	5E-26
Mjin_6A_T_C04.ab1	gi|116784108|gb|ABK23217.1|	unknown [Picea sitchensis]	92.54	67	1E-30
Mjin_6A_T_C09.ab1	gi|16604641|gb|AAL24113.1|	unknown protein [Arabidopsis thaliana]	85.63	167	3E-75
Mjin_6A_T_D04.ab1	gi|157359175|emb|CAO67097.1|	unnamed protein product [Vitis vinifera]	69.37	111	2E-29
Mjin_6A_T_E01.ab1	gi|115455427|ref|NP_001051314.1|	Os03g0756000 [Oryza sativa (japonica cultivar-group)] >gi|37718812|gb|AAR01683.1| putative ribosomal protein L13a [Oryza sativa (japonica cultivar-group)] >gi|108711156|gb|ABF98951.1| 60S ribosomal protein L13a-2, putative, expressed [Oryza sativa (japonica cultivar-group)] >gi|113549785|dbj|BAF13228.1| Os03g0756000 [Oryza sativa (japonica cultivar-group)] >gi|125545767|gb|EAY91906.1| hypothetical protein OsI_013139 [Oryza sativa (indica cultivar-group)] >gi|125587965|gb|EAZ28629.1| hypothetical protein OsJ_012112 [Oryza sativa (japonica cultivar-group)]	89.25	186	1E-86
Mjin_6A_T_E04.ab1	gi|76782194|gb|ABA54867.1|	putative 3-dehydroquinate dehydratase/shikimate dehydrogenase [Fagus sylvatica]	66.97	109	3E-35
Mjin_6A_T_E08.ab1	gi|145334227|ref|NP_001078494.1|	unknown protein [Arabidopsis thaliana]	56.84	95	2E-17
Mjin_6A_T_E12.ab1	gi|157359079|emb|CAO66991.1|	unnamed protein product [Vitis vinifera]	75.86	58	1E-17
Mjin_6A_T_F02.ab1	gi|147818517|emb|CAN67470.1|	hypothetical protein [Vitis vinifera]	65.43	81	2E-21
Mjin_6A_T_F03.ab1	gi|157335435|emb|CAO61265.1|	unnamed protein product [Vitis vinifera]	67.35	49	5E-13
Mjin_6A_T_F05.ab1	gi|157342273|emb|CAO64386.1|	unnamed protein product [Vitis vinifera]	89.01	182	9E-94
Mjin_6A_T_F09.ab1	gi|157358159|emb|CAO65789.1|	unnamed protein product [Vitis vinifera]	81.82	99	4E-44
Mjin_6A_T_F10.ab1	gi|157358270|emb|CAO65907.1|	unnamed protein product [Vitis vinifera]	87.5	88	2E-41
Mjin_6A_T_F11.ab1	gi|147833195|emb|CAN68644.1|	hypothetical protein [Vitis vinifera] >gi|157360452|emb|CAO69675.1| unnamed protein product [Vitis vinifera]	94.05	84	5E-44
Mjin_6A_T_G01.ab1	gi|157340566|emb|CAO47371.1|	unnamed protein product [Vitis vinifera]	95.24	126	6E-63
Mjin_6A_T_G02.ab1	gi|118484704|gb|ABK94222.1|	unknown [Populus trichocarpa]	90.62	64	7E-20
Mjin_6A_T_G03.ab1	gi|147804843|emb|CAN66875.1|	hypothetical protein [Vitis vinifera]	94.12	51	9E-20
Mjin_6A_T_G04.ab1	gi|147816093|emb|CAN72892.1|	hypothetical protein [Vitis vinifera] >gi|157328427|emb|CAO21128.1| unnamed protein product [Vitis vinifera]	88.46	52	2E-19
Mjin_6A_T_G10.ab1	gi|118488403|gb|ABK96018.1|	unknown [Populus trichocarpa]	95.95	74	7E-36
Mjin_6A_T_G11.ab1	gi|118485751|gb|ABK94725.1|	unknown [Populus trichocarpa]	94.39	196	6E-103
Mjin_6A_T_H06.ab1	gi|30696637|ref|NP_176382.2|	unknown protein [Arabidopsis thaliana] >gi|75150628|sp|Q8GUI4|UGPI6_ARATH RecName: Full=Uncharacterized GPI-anchored protein At1g61900; Flags: Precursor >gi|27311769|gb|AAO00850.1| Unknown protein [Arabidopsis thaliana] >gi|30387511|gb|AAP31921.1| At1g61900 [Arabidopsis thaliana] >gi|110740384|dbj|BAF02087.1| predicted GPI-anchored protein [Arabidopsis thaliana]	64.73	241	7E-85
Mjin_6A_T_H08.ab1	gi|157341951|emb|CAO63407.1|	unnamed protein product [Vitis vinifera]	80.18	227	2E-87
Mjin_6A_T_H10.ab1	gi|118487854|gb|ABK95750.1|	unknown [Populus trichocarpa]	85.16	128	3E-58

IP : 14.49.138.138, 2017-11-03 13:30:33

Mjin_6A_T_H12.ab1	gi|157360082|emb|CAO69265.1|	unnamed protein product [Vitis vinifera]	71.94	139	2E-55
Mjin_6B_T_A02.ab1	gi|157344639|emb|CAO70022.1|	unnamed protein product [Vitis vinifera]	94.74	38	3E-14
Mjin_6B_T_A04.ab1	gi|157335758|emb|CAO61588.1|	unnamed protein product [Vitis vinifera]	56.72	134	3E-27
Mjin_6B_T_A06.ab1	gi|118482646|gb|ABK93242.1|	unknown [Populus trichocarpa]	77.03	74	9E-22
Mjin_6B_T_B07.ab1	gi|147775474|emb|CAN62882.1|	hypothetical protein [Vitis vinifera]	77.78	144	1E-56
Mjin_6B_T_B08.ab1	gi|157335199|emb|CAO61029.1|	unnamed protein product [Vitis vinifera]	69.78	139	4E-52
Mjin_6B_T_B11.ab1	gi|147805693|emb|CAN76154.1|	hypothetical protein [Vitis vinifera]	83.33	54	9E-19
Mjin_6B_T_C02.ab1	gi|117607067|gb|ABK42077.1|	ubiquitin extension protein [Capsicum annuum]	95.71	163	7E-70
Mjin_6B_T_C06.ab1	gi|195976673|dbj|BAG68575.1|	arginine decarboxylase [Prunus persica]	74.9	251	2E-94
Mjin_6B_T_C07.ab1	gi|147819065|emb|CAN64891.1|	hypothetical protein [Vitis vinifera]	76.39	72	2E-12
Mjin_6B_T_C09.ab1	gi|6225817|sp|Q96480|P5CS_SOLLC	RecName: Full=Delta-1-pyrroline-5-carboxylate synthetase; Short=P5CS; Includes: RecName: Full=Glutamate 5-kinase; Short=GK; AltName: Full=Gamma-glutamyl kinase; Includes: RecName: Full=Gamma-glutamyl phosphate reductase; Short=GPR; AltName: Full=Glutamate-5-semialdehyde dehydrogenase; AltName: Full=Glutamyl-gamma-semialdehyde dehydrogenase >gi|1480670|gb|AAB67875.1| delta 1-pyrroline-5-carboxylate synthetase [Lycopersicon esculentum]	82.8	157	6E-51
Mjin_6B_T_D04.ab1	gi|157345730|emb|CAO15028.1|	unnamed protein product [Vitis vinifera]	77.59	116	6E-35
Mjin_6B_T_D05.ab1	gi|124109187|gb|ABM91069.1|	xyloglucan endotransglycosylase/hydrolase precursor XTH-27 [Populus trichocarpa]	82.35	102	1E-44
Mjin_6B_T_D11.ab1	gi|157336549|emb|CAO71234.1|	unnamed protein product [Vitis vinifera]	76.81	69	6E-24
Mjin_6B_T_D12.ab1	gi|157335088|emb|CAO60918.1|	unnamed protein product [Vitis vinifera]	87.3	63	1E-23
Mjin_6B_T_F02.ab1	gi|118485533|gb|ABK94619.1|	unknown [Populus trichocarpa]	92.44	119	2E-59
Mjin_6B_T_F07.ab1	gi|115455495|ref|NP_001051348.1|	Os03g0760800 [Oryza sativa (japonica cultivar-group)] >gi|14488366|gb|AAK63933.1|AC084282_14 putative protein of gibberellin-stimulated transcript [Oryza sativa (japonica cultivar-group)] >gi|55167448|dbj|BAD67542.1| Gibberellin stimulated transcript related protein 1 [Oryza sativa Japonica Group] >gi|108711207|gb|ABF99002.1| Gibberellin-regulated protein 2 precursor, putative, expressed [Oryza sativa (japonica cultivar-group)] >gi|113549819|dbj|BAF13262.1| Os03g0760800 [Oryza sativa (japonica cultivar-group)] >gi|125545799|gb|EAY91938.1| hypothetical protein OsI_013171 [Oryza sativa (indica cultivar-group)] >gi|125587999|gb|EAZ28663.1| hypothetical protein OsJ_012146 [Oryza sativa (japonica cultivar-group)]	80	35	6E-11
Mjin_6B_T_G01.ab1	gi|147835114|emb|CAN67946.1|	hypothetical protein [Vitis vinifera] >gi|157356264|emb|CAO62399.1| unnamed protein product [Vitis vinifera]	89.15	129	8E-57
Mjin_6B_T_G03.ab1	gi|147806280|emb|CAN72193.1|	hypothetical protein [Vitis vinifera]	55.88	136	4E-33
Mjin_6B_T_G05.ab1	gi|147774807|emb|CAN71367.1|	hypothetical protein [Vitis vinifera]	57.72	246	8E-71
Mjin_6B_T_G06.ab1	gi|116643152|gb|ABK06393.1|	stress-related protein [Citrus sinensis]	96.27	161	3E-84
Mjin_6B_T_G08.ab1	gi|147771517|emb|CAN66748.1|	hypothetical protein [Vitis vinifera] >gi|157349198|emb|CAO24344.1| unnamed protein product [Vitis vinifera]	88.16	76	4E-30
Mjin_6B_T_G11.ab1	gi|157343704|emb|CAO68210.1|	unnamed protein product [Vitis vinifera]	88.39	224	6E-105
Mjin_6B_T_G12.ab1	gi|157327131|emb|CAO14403.1|	unnamed protein product [Vitis vinifera]	68.84	199	7E-73
Mjin_6B_T_H01.ab1	gi|126572488|gb|ABO21639.1|	importin alpha-like protein [Brassica napus] >gi|126572504|gb|ABO21640.1| importin alpha-like protein [Brassica napus]	86	50	3E-16
Mjin_6B_T_H02.ab1	gi|157340137|emb|CAO45814.1|	unnamed protein product [Vitis vinifera]	82.68	231	9E-109
Mjin_6C_T_A02.ab1	gi|110740035|dbj|BAF01921.1|	putative cAMP-dependent protein kinase [Arabidopsis thaliana]	72.06	247	1E-95
Mjin_6C_T_A03.ab1	gi|147862427|emb|CAN79750.1|	hypothetical protein [Vitis vinifera]	68.66	201	1E-70
Mjin_6C_T_A04.ab1	gi|147815462|emb|CAN66086.1|	hypothetical protein [Vitis vinifera]	43.94	198	1E-35
Mjin_6C_T_A08.ab1	gi|123335|sp|P29057|HMDH1_HEVBR	RecName: Full=3-hydroxy-3-methylglutaryl-coenzyme A reductase 1; Short=HMG-CoA reductase 1 >gi|16417954|gb|AAL18929.1|AF429388_1 hydroxymethylglutaryl coenzyme A reductase [Hevea brasiliensis] >gi|18833|emb|CAA38467.1| hydroxymethylglutaryl-CoA reductase [Hevea brasiliensis] >gi|18835|emb|CAA38469.1| hydroxymethylglutaryl-CoA reductase [Hevea brasiliensis] >gi|34223773|gb|AAQ63055.1|	94.06	101	5E-45

IP : 14.49.138.138, 2017-11-03 13:30:33

		3-hydroxy-3-methylglutaryl-coenzyme A reductase [Hevea brasiliensis]			
Mjin_6C_T_A12.ab1	gi|157347813|emb|CAO22400.1|	unnamed protein product [Vitis vinifera]	78.32	226	6E-95
Mjin_6C_T_B04.ab1	gi|147802535|emb|CAN62145.1|	hypothetical protein [Vitis vinifera]	46.55	116	9E-17
Mjin_6C_T_B05.ab1	gi|207059702|dbj|BAG71891.1|	caffeoyl CoA O-methyltransferase [Carthamus tinctorius]	76.55	145	6E-62
Mjin_6C_T_B06.ab1	gi|15222481|ref|NP_177142.1|	band 7 family protein [Arabidopsis thaliana] >gi|30697929|ref|NP_849870.1| band 7 family protein [Arabidopsis thaliana] >gi|42572051|ref|NP_974116.1| band 7 family protein [Arabidopsis thaliana] >gi|42572053|ref|NP_974117.1| band 7 family protein [Arabidopsis thaliana] >gi|145327201|ref|NP_001077802.1| band 7 family protein [Arabidopsis thaliana] >gi|145327203|ref|NP_001077803.1| band 7 family protein [Arabidopsis thaliana] >gi|12325226|gb|AAG52556.1|AC010675_4 unknown protein; 58197-59415 [Arabidopsis thaliana] >gi|20466748|gb|AAM20691.1| unknown protein [Arabidopsis thaliana] >gi|23198256|gb|AAN15655.1| unknown protein [Arabidopsis thaliana]	85.49	193	2E-77
Mjin_6C_T_B07.ab1	gi|157352448|emb|CAO43528.1|	unnamed protein product [Vitis vinifera]	82.88	222	4E-93
Mjin_6C_T_B08.ab1	gi|157350851|emb|CAO40966.1|	unnamed protein product [Vitis vinifera]	53.85	78	5E-17
Mjin_6C_T_B09.ab1	gi|126506746|gb|ABO14801.1|	acetyl CoA carboxylase [Camellia sinensis]	83.61	61	4E-23
Mjin_6C_T_C01.ab1	gi|147838425|emb|CAN76587.1|	hypothetical protein [Vitis vinifera]	84.91	53	5E-21
Mjin_6C_T_C02.ab1	gi|118487561|gb|ABK95607.1|	unknown [Populus trichocarpa]	82.86	105	5E-45
Mjin_6C_T_C03.ab1	gi|108706480|gb|ABF94275.1|	Elongation factor 1-alpha, putative, expressed [Oryza sativa (japonica cultivar-group)]	91.67	60	4E-24
Mjin_6C_T_C08.ab1	gi|544437|sp|Q06652|GPX4_CITSI	RecName: Full=Probable phospholipid hydroperoxide glutathione peroxidase; Short=PHGPx; AltName: Full=Salt-associated protein >gi|296358|emb|CAA47018.1| CIT-SAP [Citrus sinensis] >gi|119367482|gb|ABL67656.1| putative phospholipid hydroperoxide glutathione peroxidase [Citrus cv. Shiranuhi]	100	157	3E-86
Mjin_6C_T_C09.ab1	gi|118482544|gb|ABK93193.1|	unknown [Populus trichocarpa]	77.63	76	1E-30
Mjin_6C_T_C11.ab1	gi|157345301|emb|CAO14599.1|	unnamed protein product [Vitis vinifera]	87.04	247	6E-120
Mjin_6C_T_C12.ab1	gi|13016808|emb|CAC29436.1|	P-type H+-ATPase [Vicia faba]	89.62	212	2E-97
Mjin_6C_T_D01.ab1	gi|683553|emb|CAA88360.1|	oleosin-like protein [Citrus sinensis] >gi|1582679|prf||2119230A oleosin homolog	96.77	62	7E-19
Mjin_6C_T_D04.ab1	gi|118487186|gb|ABK95421.1|	unknown [Populus trichocarpa]	73.01	163	7E-62
Mjin_6C_T_D06.ab1	gi|157344081|emb|CAO69014.1|	unnamed protein product [Vitis vinifera]	58.2	189	3E-48
Mjin_6C_T_D08.ab1	gi|118487330|gb|ABK95493.1|	unknown [Populus trichocarpa]	84.78	46	1E-16
Mjin_6C_T_D12.ab1	gi|29124969|gb|AAO63774.1|	3-phosphoglycerate kinase [Populus tremuloides]	91.67	96	2E-43
Mjin_6C_T_E01.ab1	gi|18390521|ref|NP_563738.1|	unknown protein [Arabidopsis thaliana] >gi|18086400|gb|AAL57658.1| At1g05410/T25N20_5 [Arabidopsis thaliana] >gi|18491167|gb|AAL69486.1| unknown protein [Arabidopsis thaliana] >gi|20465537|gb|AAM20251.1| unknown protein [Arabidopsis thaliana] >gi|22655430|gb|AAM98307.1| At1g05410/T25N20_5 [Arabidopsis thaliana]	61.18	85	5E-24
Mjin_6C_T_F01.ab1	gi|157337600|emb|CAO21946.1|	unnamed protein product [Vitis vinifera]	69.87	156	5E-58
Mjin_6C_T_F03.ab1	gi|157347664|emb|CAO18301.1|	unnamed protein product [Vitis vinifera]	89.71	68	6E-27
Mjin_6C_T_F05.ab1	gi|118485828|gb|ABK94761.1|	unknown [Populus trichocarpa]	83.78	222	2E-102
Mjin_6C_T_F07.ab1	gi|144905184|dbj|BAF56241.1|	cytochrome P450 enzyme [Pisum sativum]	71.31	244	1E-96
Mjin_6C_T_F11.ab1	gi|118487382|gb|ABK95519.1|	unknown [Populus trichocarpa]	91.6	131	1E-61
Mjin_6C_T_G01.ab1	gi|147846526|emb|CAN81650.1|	hypothetical protein [Vitis vinifera]	84.44	135	3E-54
Mjin_6C_T_G02.ab1	gi|1061408|gb|AAB52963.1|	citrin	100	88	3E-46
Mjin_6C_T_G03.ab1	gi|15224105|ref|NP_180001.1|	potassium channel tetramerisation domain-containing protein [Arabidopsis thaliana] >gi|4115384|gb|AAD03385.1| unknown protein [Arabidopsis thaliana] >gi|56236038|gb|AAV84475.1| At2g24240 [Arabidopsis thaliana] >gi|56790194|gb|AAW30014.1| At2g24240 [Arabidopsis thaliana] >gi|110738282|dbj|BAF01070.1| hypothetical protein [Arabidopsis thaliana]	92.68	41	1E-15

IP : 14.49.138.138, 2017-11-03 13:30:33

Mjin_6C_T_G04.ab1	gi|195626372|gb|ACG35016.1|	unknown [Zea mays]	91.5	153	7E-67
Mjin_6C_T_G05.ab1	gi|49333397|gb|AAT64036.1|	putative serine-threonine kinase [Gossypium hirsutum]	86.56	253	1E-119
Mjin_6C_T_G06.ab1	gi|157357247|emb|CAO63749.1|	unnamed protein product [Vitis vinifera]	78.89	90	3E-34
Mjin_6C_T_G07.ab1	gi|157341162|emb|CAO49069.1|	unnamed protein product [Vitis vinifera]	77.33	150	2E-61
Mjin_6C_T_G08.ab1	gi|15824408|gb|AAL09328.1|AF302806_1	steroleosin [Sesamum indicum] >gi|16033752|gb|AAL13315.1|AF421889_1 steroleosin [Sesamum indicum]	70.11	87	1E-22
Mjin_6C_T_G09.ab1	gi|6683114|dbj|BAA89049.1|	sucrose synthase [Citrus unshiu]	99.6	249	3E-137
Mjin_6C_T_G10.ab1	gi|157353332|emb|CAO45258.1|	unnamed protein product [Vitis vinifera]	67.81	233	2E-88
Mjin_6C_T_G11.ab1	gi|157345558|emb|CAO14856.1|	unnamed protein product [Vitis vinifera]	80.25	81	6E-32
Mjin_6C_T_H06.ab1	gi|18406507|ref|NP_566015.1|	calcium-binding EF hand family protein [Arabidopsis thaliana] >gi|3128177|gb|AAC16081.1| expressed protein [Arabidopsis thaliana] >gi|18252875|gb|AAL62364.1| unknown protein [Arabidopsis thaliana] >gi|21387065|gb|AAM47936.1| unknown protein [Arabidopsis thaliana] >gi|21554910|gb|AAM63727.1| unknown [Arabidopsis thaliana]	80.88	136	2E-56
Mjin_6C_T_H07.ab1	gi|157350908|emb|CAO41023.1|	unnamed protein product [Vitis vinifera]	63.33	90	2E-24
Mjin_6C_T_H09.ab1	gi|157339896|emb|CAO45573.1|	unnamed protein product [Vitis vinifera]	78.4	125	3E-41
Mjin_6C_T_H11.ab1	gi|118487902|gb|ABK95773.1|	unknown [Populus trichocarpa]	68.97	87	7E-26
Mjin_6D_T_A01.ab1	gi|157328425|emb|CAO21126.1|	unnamed protein product [Vitis vinifera]	80.97	247	4E-114
Mjin_6D_T_A05.ab1	gi|147852748|emb|CAN79523.1|	hypothetical protein [Vitis vinifera]	62.5	56	4E-11
Mjin_6D_T_A06.ab1	gi|148615629|gb|ABQ96643.1|	NAC domain protein [Citrus sinensis]	99.37	159	2E-91
Mjin_6D_T_A08.ab1	gi|157336829|emb|CAO71514.1|	unnamed protein product [Vitis vinifera]	60.21	191	2E-58
Mjin_6D_T_A10.ab1	gi|147792835|emb|CAN77748.1|	hypothetical protein [Vitis vinifera] >gi|157328614|emb|CAO22312.1| unnamed protein product [Vitis vinifera]	79.65	231	4E-91
Mjin_6D_T_B04.ab1	gi|38198152|emb|CAE53882.1|	aquaporin [Ricinus communis]	91.23	114	6E-55
Mjin_6D_T_B08.ab1	gi|157355069|emb|CAO48430.1|	unnamed protein product [Vitis vinifera]	76.16	151	2E-57
Mjin_6D_T_B09.ab1	gi|157353117|emb|CAO45027.1|	unnamed protein product [Vitis vinifera]	79.31	174	2E-74
Mjin_6D_T_B10.ab1	gi|157342826|emb|CAO65538.1|	unnamed protein product [Vitis vinifera]	86.29	175	4E-76
Mjin_6D_T_C02.ab1	gi|11245486|gb|AAG33636.1|AF315289_1	beta-carotene hydroxylase [Citrus unshiu]	98.97	97	1E-36
Mjin_6D_T_C04.ab1	gi|157355188|emb|CAO48564.1|	unnamed protein product [Vitis vinifera]	59.09	176	2E-52
Mjin_6D_T_C05.ab1	gi|147784318|emb|CAN61810.1|	hypothetical protein [Vitis vinifera]	92.2	141	2E-61
Mjin_6D_T_C06.ab1	gi|147780246|emb|CAN65739.1|	hypothetical protein [Vitis vinifera]	89.74	117	4E-54
Mjin_6D_T_C07.ab1	gi|15238277|ref|NP_199024.1|	unknown protein [Arabidopsis thaliana] >gi|9757954|dbj|BAB08442.1| unnamed protein product [Arabidopsis thaliana] >gi|16648953|gb|AAL24328.1| Unknown protein [Arabidopsis thaliana] >gi|20259830|gb|AAM13262.1| unknown protein [Arabidopsis thaliana]	82.4	125	4E-50
Mjin_6D_T_C08.ab1	gi|112292929|emb|CAL35827.1|	alpha-2 tubulin [Plantago major]	100	79	2E-39
Mjin_6D_T_C11.ab1	gi|157350991|emb|CAO41148.1|	unnamed protein product [Vitis vinifera]	62.99	127	1E-39
Mjin_6D_T_D04.ab1	gi|157353375|emb|CAO45301.1|	unnamed protein product [Vitis vinifera]	82.28	158	7E-80
Mjin_6D_T_D06.ab1	gi|157335068|emb|CAO60898.1|	unnamed protein product [Vitis vinifera]	78.15	119	2E-39
Mjin_6D_T_D07.ab1	gi|46410175|gb|AAS93947.1|	disease resistance protein RPP13 variant [Arabidopsis thaliana]	57.34	143	5E-41
Mjin_6D_T_D10.ab1	gi|118488671|gb|ABK96147.1|	unknown [Populus trichocarpa]	62.42	149	1E-33
Mjin_6D_T_D12.ab1	gi|147783369|emb|CAN72961.1|	hypothetical protein [Vitis vinifera]	49	100	1E-15
Mjin_6D_T_E02.ab1	gi|12802327|gb|AAK07827.1|AF297643_1	mitochondrial processing peptidase beta subunit [Cucumis melo]	71.53	137	4E-42
Mjin_6D_T_E03.ab1	gi|116293737|gb|ABJ98060.1|	glucose 6-Pi/Pi transporter [Thellungiella halophila]	97.37	76	2E-26
Mjin_6D_T_E04.ab1	gi|3608477|gb|AAC35981.1|	chitinase CHI1 [Citrus sinensis]	68.21	151	2E-57

IP : 14.49.138.138, 2017-11-03 13:30:33

Mjin_6D_T_E05.ab1	gi|157336299|emb|CAO70984.1|	unnamed protein product [Vitis vinifera]	65.96	188	3E-61
Mjin_6D_T_E09.ab1	gi|147856520|emb|CAN82835.1|	hypothetical protein [Vitis vinifera]	83.95	81	7E-32
Mjin_6D_T_E10.ab1	gi|102655942|gb|AAY33920.2|	polyubiquitin [Euphorbia characias]	100	75	1E-34
Mjin_6D_T_E11.ab1	gi|15241190|ref|NP_200446.1|	pyruvate kinase, putative [Arabidopsis thaliana] >gi|10177833|dbj|BAB11262.1| pyruvate kinase [Arabidopsis thaliana] >gi|15450942|gb|AAK96742.1| pyruvate kinase [Arabidopsis thaliana] >gi|17978781|gb|AAL47384.1| pyruvate kinase [Arabidopsis thaliana] >gi|21592702|gb|AAM64651.1| pyruvate kinase [Arabidopsis thaliana]	98.61	72	1E-32
Mjin_6D_T_F02.ab1	gi|15237699|ref|NP_196061.1|	NAC2 (Arabidopsis NAC domain containing protein 78); transcription factor [Arabidopsis thaliana] >gi|51316421|sp|Q84K00|NAC78_ARATH RecName: Full=NAC domain-containing protein 78; AltName: Full=ANAC078 >gi|7406445|emb|CAB85547.1| putative protein [Arabidopsis thaliana] >gi|20466286|gb|AAM20460.1| putative protein [Arabidopsis thaliana] >gi|22136362|gb|AAM91259.1| putative protein [Arabidopsis thaliana]	82.11	95	1E-40
Mjin_6D_T_F04.ab1	gi|18404099|ref|NP_565843.1|	inosine-uridine preferring nucleoside hydrolase family protein [Arabidopsis thaliana] >gi|15809830|gb|AAL06843.1| At2g36310/F2H17.8 [Arabidopsis thaliana] >gi|17978871|gb|AAL47407.1| At2g36310/F2H17.8 [Arabidopsis thaliana] >gi|20197937|gb|AAD21435.2| expressed protein [Arabidopsis thaliana] >gi|21554564|gb|AAM63615.1| unknown [Arabidopsis thaliana]	86.84	76	1E-35
Mjin_6D_T_F06.ab1	gi|7484767|pir||T10443	probable major protein body membrane protein MP27 / major protein body protein MP32 precursor - cucurbit >gi|691752|dbj|BAA06186.1| preproMP27-MP32 [Cucurbita cv. Kurokawa Amakuri]	70.87	103	2E-37
Mjin_6D_T_F08.ab1	gi|151347490|gb|ABS01354.1|	translation initiation factor [Carica papaya]	92.22	90	2E-40
Mjin_6D_T_F09.ab1	gi|157849754|gb|ABV89660.1|	chitinase [Brassica rapa]	83.48	115	1E-54
Mjin_6D_T_F10.ab1	gi|147865994|emb|CAN83050.1|	hypothetical protein [Vitis vinifera]	91.51	106	1E-51
Mjin_6D_T_F11.ab1	gi|18395537|ref|NP_565300.1|	unknown protein [Arabidopsis thaliana] >gi|4335763|gb|AAD17440.1| expressed protein [Arabidopsis thaliana] >gi|29028804|gb|AAO64781.1| At2g03350 [Arabidopsis thaliana] >gi|110736354|dbj|BAF00146.1| hypothetical protein [Arabidopsis thaliana]	82.76	116	1E-48
Mjin_6D_T_F12.ab1	gi|157338314|emb|CAO39358.1|	unnamed protein product [Vitis vinifera]	83.04	230	2E-112
Mjin_6D_T_G02.ab1	gi|157356879|emb|CAO63081.1|	unnamed protein product [Vitis vinifera]	75.51	98	1E-37
Mjin_6D_T_G04.ab1	gi|118489526|gb|ABK96565.1|	unknown [Populus trichocarpa x Populus deltoides]	82.83	99	1E-44
Mjin_6D_T_G05.ab1	gi|189543218|ref|XP_001922358.1|	PREDICTED: similar to cysteine conjugate-beta lyase 2, partial [Danio rerio]	93.18	44	2E-16
Mjin_6D_T_G06.ab1	gi|147775461|emb|CAN60659.1|	hypothetical protein [Vitis vinifera]	96.77	93	3E-46
Mjin_6D_T_H11.ab1	gi|13877755|gb|AAK43955.1|AF370140_1	unknown protein [Arabidopsis thaliana]	67.53	77	8E-16
Mjin_7A_T_A03.ab1	gi|118487731|gb|ABK95689.1|	unknown [Populus trichocarpa]	66.94	121	2E-39
Mjin_7A_T_A05.ab1	gi|147865388|emb|CAN79814.1|	hypothetical protein [Vitis vinifera]	49.43	176	1E-34
Mjin_7A_T_A08.ab1	gi|157359826|emb|CAO68550.1|	unnamed protein product [Vitis vinifera]	50.98	102	5E-20
Mjin_7A_T_A10.ab1	gi|55375985|gb|AAV50005.1|	14-3-3 family protein [Malus x domestica]	97.52	202	1E-105
Mjin_7A_T_A12.ab1	gi|157354064|emb|CAO46631.1|	unnamed protein product [Vitis vinifera]	89.32	234	3E-109
Mjin_7A_T_B05.ab1	gi|157343948|emb|CAO68881.1|	unnamed protein product [Vitis vinifera]	70.75	106	5E-28
Mjin_7A_T_B06.ab1	gi|157345169|emb|CAO71897.1|	unnamed protein product [Vitis vinifera]	73.38	154	8E-57
Mjin_7A_T_B07.ab1	gi|18394706|ref|NP_564075.1|	JAZ1/TIFY10A (JASMONATE-ZIM-DOMAIN PROTEIN 1); protein binding [Arabidopsis thaliana] >gi|75174736|sp|Q9LMA8|TI10A_ARATH RecName: Full=Protein TIFY 10A; AltName: Full=Jasmonate ZIM domain-containing protein 1 >gi|8954056|gb|AAF82229.1|AC069143_5 Contains similarity to an unknown protein T10D10.8 gi|6730756 from Arabidopsis thaliana BAC T10D10 gb|AC016529. ESTs gb|T14209, gb|BE038503, gb|AA650871, gb|AA597384, gb|H76606, gb|AI996806, gb|AI100291 come from this gene >gi|12083250|gb|AAG48784.1|AF332421_1 unknown protein [Arabidopsis thaliana] >gi|14532540|gb|AAK63998.1| At1g19180/T29M8_5 [Arabidopsis thaliana] >gi|17473768|gb|AAL38322.1| unknown protein [Arabidopsis thaliana] >gi|19548055|gb|AAL87391.1| At1g19180/T29M8_5 [Arabidopsis thaliana] >gi|20148609|gb|AAM10195.1| unknown protein [Arabidopsis thaliana]	35.65	216	4E-24

IP : 14.49.138.138, 2017-11-03 13:30:33

Mjin_7A_T_B08.ab1	gi|18396484|ref|NP_564295.1|	ACA1 (autoinhibited Ca2+ -ATPase 1); calmodulin binding [Arabidopsis thaliana]	82.71	133	2E-55
Mjin_7A_T_B11.ab1	gi|157344926|emb|CAO71654.1|	unnamed protein product [Vitis vinifera]	75	56	2E-18
Mjin_7A_T_C04.ab1	gi|118488898|gb|ABK96258.1|	unknown [Populus trichocarpa x Populus deltoides]	91.8	61	1E-25
Mjin_7A_T_C05.ab1	gi|16226454|gb|AAL16172.1|AF428404_1	AT3g01400/T13O15_4 [Arabidopsis thaliana] >gi|21928049|gb|AAM78053.1| AT3g01400/T13O15_4 [Arabidopsis thaliana]	86	50	3E-16
Mjin_7A_T_C10.ab1	gi|118486747|gb|ABK95209.1|	unknown [Populus trichocarpa]	95.05	101	1E-47
Mjin_7A_T_D05	gi|12641853|dbj|BAB21545.1|	phosphate transporter [Nicotiana tabacum]	94.87	78	3E-35
Mjin_7A_T_D06.ab1	gi|118481753|gb|ABK92816.1|	unknown [Populus trichocarpa]	85.87	92	4E-39
Mjin_7A_T_D09.ab1	gi|89276797|gb|ABD66597.1|	iron-binding protein [Pyrus pyrifolia]	84.21	95	1E-39
Mjin_7A_T_D12.ab1	gi|18418346|ref|NP_567947.1|	unknown protein [Arabidopsis thaliana] >gi|110736175|dbj|BAF00059.1| hypothetical protein [Arabidopsis thaliana]	66.18	136	9E-39
Mjin_7A_T_E05.ab1	gi|15028035|gb|AAK76548.1|	unknown protein [Arabidopsis thaliana]	74.29	70	2E-23
Mjin_7A_T_E11.ab1	gi|118481637|gb|ABK92760.1|	unknown [Populus trichocarpa]	91.79	207	6E-103
Mjin_7A_T_E12.ab1	gi|118487026|gb|ABK95344.1|	unknown [Populus trichocarpa]	55.24	143	8E-32
Mjin_7A_T_F01.ab1	gi|157350858|emb|CAO40973.1|	unnamed protein product [Vitis vinifera]	76.06	213	2E-86
Mjin_7A_T_F06.ab1	gi|10178872|emb|CAC08442.1|	(1-4)-beta-mannan endohydrolase [Coffea arabica]	70	100	2E-38
Mjin_7A_T_F12.ab1	gi|157360438|emb|CAO69661.1|	unnamed protein product [Vitis vinifera]	68.67	83	2E-23
Mjin_7A_T_G02.ab1	gi|147814901|emb|CAN61534.1|	hypothetical protein [Vitis vinifera]	66.25	80	5E-25
Mjin_7A_T_G07.ab1	gi|147833057|emb|CAN70546.1|	hypothetical protein [Vitis vinifera]	65.95	232	4E-84
Mjin_7A_T_G08.ab1	gi|83628260|gb|ABC26010.1|	9-cis-epoxycarotenoid dioxygenase 5 [Citrus clementina]	99.52	209	2E-109
Mjin_7A_T_G09.ab1	gi|157335798|emb|CAO61628.1|	unnamed protein product [Vitis vinifera]	72.26	137	1E-50
Mjin_7A_T_G10.ab1	gi|1061408|gb|AAB52963.1|	citrin	70.67	75	3E-18
Mjin_7A_T_G11.ab1	gi|157335073|emb|CAO60903.1|	unnamed protein product [Vitis vinifera]	63.96	111	1E-12
Mjin_7A_T_H02.ab1	gi|147866332|emb|CAN79917.1|	hypothetical protein [Vitis vinifera]	92.04	201	7E-88
Mjin_7A_T_H03.ab1	gi|152926165|gb|ABS32236.1|	phosphoglucosamine mutase [Carica papaya]	67.18	195	4E-61
Mjin_7A_T_H04.ab1	gi|6685536|sp|P56821|EIF3B_TOBAC	Eukaryotic translation initiation factor 3 subunit B (eIF3b) (eIF-3-eta) (eIF3 p110) >gi|5911685|emb|CAA72721.1| PRT1 protein [Nicotiana tabacum]	85.71	70	2E-27
Mjin_7A_T_H05.ab1	gi|15231789|ref|NP_188029.1|	(S)-2-hydroxy-acid oxidase, peroxisomal, putative / glycolate oxidase, putative / short chain alpha-hydroxy acid oxidase, putative [Arabidopsis thaliana] >gi|9294638|dbj|BAB02977.1| glycolate oxidase [Arabidopsis thaliana] >gi|27754229|gb|AAO22568.1| putative glycolate oxidase [Arabidopsis thaliana]	80.22	91	8E-37
Mjin_7A_T_H06.ab1	gi|157352122|emb|CAO43129.1|	unnamed protein product [Vitis vinifera]	51.6	219	2E-54
Mjin_7A_T_H07.ab1	gi|157348980|emb|CAO24058.1|	unnamed protein product [Vitis vinifera]	95.56	90	6E-43
Mjin_7A_T_H10.ab1	gi|15224204|ref|NP_181830.1|	ATPAO2 (POLYAMINE OXIDASE 2); amine oxidase [Arabidopsis thaliana] >gi|75206576|sp|Q9SKX5|PAO2_ARATH RecName: Full=Probable polyamine oxidase 2; Short=AtPAO2; AltName: Full=Amine oxidase 1 >gi|29468124|gb|AAO85404.1|AF364952_1 putative amine oxidase 1 [Arabidopsis thaliana] >gi|4531444|gb|AAD22129.1| putative amine oxidase [Arabidopsis thaliana] >gi|115311507|gb|ABI93934.1| At2g43020 [Arabidopsis thaliana]	89.02	82	4E-35
Mjin_7A_T_H11.ab1	gi|157339236|emb|CAO43777.1|	unnamed protein product [Vitis vinifera]	70.35	199	7E-81
Mjin_7B_T_A06.ab1	gi|145105398|gb|ABP35583.1|	CBL-interacting protein kinase [Gossypium hirsutum]	87.35	166	8E-67
Mjin_7B_T_A07.ab1	gi|147771279|emb|CAN76254.1|	hypothetical protein [Vitis vinifera]	51.72	87	4E-12
Mjin_7B_T_A08.ab1	gi|157335160|emb|CAO60990.1|	unnamed protein product [Vitis vinifera]	71.43	77	9E-30
Mjin_7B_T_B06.ab1	gi|157355167|emb|CAO48543.1|	unnamed protein product [Vitis vinifera]	68.28	145	1E-46
Mjin_7B_T_B09.ab1	gi|158518418|sp|P83326|PMEI_ACTDE	RecName: Full=Pectinesterase inhibitor; AltName: Full=Pectin methylesterase inhibitor; AltName: Full=AdPMEI; Short=PMEI; Flags:	32.41	145	4E-15

IP : 14.49.138.138, 2017-11-03 13:30:33

		Precursor >gi|27544452|dbj|BAC54964.1| pectinmethylesterase inhibitor [Actinidia deliciosa]			
Mjin_7B_T_B11.ab1	gi|24473800|gb|AAL91665.1|	2s albumin [Anacardium occidentale]	52.9	138	2E-24
Mjin_7B_T_C08.ab1	gi|22653808|sp|Q39644|LEA5_CITSI	Late embryogenesis abundant protein Lea5 >gi|599726|emb|CAA86851.1| Lea5 protein [Citrus sinensis]	69.75	119	4E-34
Mjin_7B_T_D04.ab1	gi|157329624|emb|CAO41063.1|	unnamed protein product [Vitis vinifera]	93.7	127	9E-65
Mjin_7B_T_D05.ab1	gi|157347550|emb|CAO18187.1|	unnamed protein product [Vitis vinifera]	93.33	120	1E-58
Mjin_7B_T_E05.ab1	gi|157343051|emb|CAO66540.1|	unnamed protein product [Vitis vinifera]	90.08	121	2E-54
Mjin_7B_T_E06.ab1	gi|194705234|gb|ACF86701.1|	unknown [Zea mays]	96.12	103	1E-49
Mjin_7B_T_E11.ab1	gi|15232357|ref|NP_191613.1|	sec61beta family protein [Arabidopsis thaliana] >gi|42572743|ref|NP_974467.1| sec61beta family protein [Arabidopsis thaliana] >gi|7288002|emb|CAB81840.1| transport protein subunit-like [Arabidopsis thaliana]	89.13	46	3E-16
Mjin_7B_T_E12.ab1	gi|157349176|emb|CAO24322.1|	unnamed protein product [Vitis vinifera]	65.67	134	2E-38
Mjin_7B_T_F08.ab1	gi|157329547|emb|CAO40658.1|	unnamed protein product [Vitis vinifera]	86.67	45	1E-14
Mjin_7B_T_F09.ab1	gi|3913711|sp|P81406|GAPN_PEA	RecName: Full=NADP-dependent glyceraldehyde-3-phosphate dehydrogenase; AltName: Full=Non-phosphorylating glyceraldehyde 3-phosphate dehydrogenase; AltName: Full=Glyceraldehyde-3-phosphate dehydrogenase [NADP+]; AltName: Full=Triosephosphate dehydrogenase >gi|4379384|emb|CAA53076.1| glyceraldehyde-3-phosphate dehydrogenase (nonphosphorylating,NADP+) [Pisum sativum] >gi|2827680|gb|AAO38512.1| non-phosphorylating glyceraldehyde-3-phosphate dehydrogenase [Pisum sativum]	75.29	85	4E-30
Mjin_7B_T_F11.ab1	gi|118486443|gb|ABK95061.1|	unknown [Populus trichocarpa]	85.37	41	2E-12
Mjin_7B_T_F12.ab1	gi|118485599|gb|ABK94650.1|	unknown [Populus trichocarpa]	95.65	46	3E-18
Mjin_7B_T_G08.ab1	gi|147863949|emb|CAN83214.1|	hypothetical protein [Vitis vinifera]	87.05	193	4E-97
Mjin_7B_T_G12.ab1	gi|147833400|emb|CAN64099.1|	hypothetical protein [Vitis vinifera]	85.53	76	1E-31
Mjin_7B_T_H01.ab1	gi|118489780|gb|ABK96690.1|	unknown [Populus trichocarpa x Populus deltoides]	55.8	138	7E-29
Mjin_7B_T_H04.ab1	gi|157359791|emb|CAO68513.1|	unnamed protein product [Vitis vinifera]	82.25	169	1E-68
Mjin_7B_T_H08.ab1	gi|147800964|emb|CAN75567.1|	hypothetical protein [Vitis vinifera]	42.36	203	1E-18
Mjin_7B_T_H10.ab1	gi|147815277|emb|CAN70026.1|	hypothetical protein [Vitis vinifera] >gi|157359873|emb|CAO68602.1| unnamed protein product [Vitis vinifera]	97.62	126	5E-50
Mjin_7B_T_H11.ab1	gi|15234170|ref|NP_192049.1|	pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|7267637|emb|CAB80949.1| hypothetical protein [Arabidopsis thaliana]	80.62	129	1E-51
Mjin_7C_T_A04.ab1	gi|118489791|gb|ABK96695.1|	unknown [Populus trichocarpa x Populus deltoides]	46.12	219	1E-24
Mjin_7C_T_A05.ab1	gi|157347049|emb|CAO17431.1|	unnamed protein product [Vitis vinifera]	72.37	152	1E-42
Mjin_7C_T_A06.ab1	gi|157350391|emb|CAO40371.1|	unnamed protein product [Vitis vinifera]	75.42	236	2E-99
Mjin_7C_T_A09.ab1	gi|15229845|ref|NP_187143.1|	40S ribosomal protein S24 (RPS24A) [Arabidopsis thaliana] >gi|11134742|sp|Q9SS17|RS241_ARATH 40S ribosomal protein S24-1 >gi|12322851|gb|AAG51413.1|AC009465_13 putative ribosomal protein s19 or s24; 43956-42880 [Arabidopsis thaliana] >gi|15215672|gb|AAK91381.1| AT3g04920/T9J14_13 [Arabidopsis thaliana] >gi|17065190|gb|AAL32749.1| putative ribosomal protein [Arabidopsis thaliana] >gi|20259968|gb|AAM13331.1| putative ribosomal protein s19 or s24 [Arabidopsis thaliana] >gi|20334888|gb|AAM16200.1| AT3g04920/T9J14_13 [Arabidopsis thaliana] >gi|21554374|gb|AAM63481.1| putative ribosomal protein s19 or s24 [Arabidopsis thaliana]	93.44	122	1E-59
Mjin_7C_T_A10.ab1	gi|157340260|emb|CAO45937.1|	unnamed protein product [Vitis vinifera]	45.54	112	1E-17
Mjin_7C_T_A11.ab1	gi|11385443|gb|AAG34804.1|AF243369_1	glutathione S-transferase GST 14 [Glycine max]	61.67	180	4E-65
Mjin_7C_T_B05.ab1	gi|157350057|emb|CAO39995.1|	unnamed protein product [Vitis vinifera]	86.99	123	7E-47
Mjin_7C_T_B08.ab1	gi|1009712|gb|AAA80652.1|	calreticulin	95.28	106	2E-54
Mjin_7C_T_B11.ab1	gi|157356287|emb|CAO62439.1|	unnamed protein product [Vitis vinifera]	88.03	117	1E-55
Mjin_7C_T_B12.ab1	gi|18399596|ref|NP_566423.1|	ATELC/ELC; ubiquitin binding [Arabidopsis thaliana] >gi|12321968|gb|AAG51025.1|AC069474_24 unknown protein; 81998-83194 [Arabidopsis thaliana] >gi|15795159|dbj|BAB03147.1| mouse and human tumor susceptibility gene-like protein [Arabidopsis thaliana] >gi|15810489|gb|AAL07132.1| unknown protein [Arabidopsis thaliana]	83.44	151	7E-73

IP : 14.49.138.138, 2017-11-03 13:30:33

		>gi|21593369|gb|AAM65318.1| unknown [Arabidopsis thaliana] >gi|22136968|gb|AAM91713.1| unknown protein [Arabidopsis thaliana]			
Mjin_7C_T_C04.ab1	gi|157342800|emb|CAO65512.1|	unnamed protein product [Vitis vinifera]	92.72	206	3E-109
Mjin_7C_T_C08.ab1	gi|118483685|gb|ABK93736.1|	unknown [Populus trichocarpa]	94.53	128	7E-53
Mjin_7C_T_C09.ab1	gi|157346166|emb|CAO15863.1|	unnamed protein product [Vitis vinifera]	67.29	214	6E-67
Mjin_7C_T_C10.ab1	gi|147821099|emb|CAN70962.1|	hypothetical protein [Vitis vinifera]	80.5	241	5E-109
Mjin_7C_T_D05.ab1	gi|10177661|dbj|BAB11123.1|	unnamed protein product [Arabidopsis thaliana]	43.88	98	1E-16
Mjin_7C_T_D07.ab1	gi|192338748|gb|ACF04279.1|	UDP-D-glucuronate carboxy-lyase [Eucalyptus grandis]	96.24	133	2E-70
Mjin_7C_T_D08.ab1	gi|15237269|ref|NP_200093.1|	ornithine cyclodeaminase/mu-crystallin family protein [Arabidopsis thaliana] >gi|10177095|dbj|BAB10429.1| unnamed protein product [Arabidopsis thaliana] >gi|57610643|gb|AAW52557.1| At5g52810 [Arabidopsis thaliana] >gi|63003756|gb|AAY25407.1| At5g52810 [Arabidopsis thaliana]	78.69	122	5E-36
Mjin_7C_T_D09.ab1	gi|147821626|emb|CAN70316.1|	hypothetical protein [Vitis vinifera] >gi|157358483|emb|CAO66150.1| unnamed protein product [Vitis vinifera]	94.39	107	6E-53
Mjin_7C_T_D11.ab1	gi|60752251|gb|AAX36074.1|	non-intrinsic ABC protein [Nicotiana benthamiana]	100	40	1E-14
Mjin_7C_T_F01.ab1	gi|157352185|emb|CAO43213.1|	unnamed protein product [Vitis vinifera]	84.86	185	2E-88
Mjin_7C_T_F02.ab1	gi|147804847|emb|CAN78056.1|	hypothetical protein [Vitis vinifera] >gi|157352071|emb|CAO43061.1| unnamed protein product [Vitis vinifera]	64.49	245	2E-63
Mjin_7C_T_F05.ab1	gi|157349806|emb|CAO39662.1|	unnamed protein product [Vitis vinifera]	60	125	2E-34
Mjin_7C_T_F07.ab1	gi|157357947|emb|CAO64959.1|	unnamed protein product [Vitis vinifera]	85.61	132	3E-61
Mjin_7C_T_F11.ab1	gi|14548096|sp|Q9LW96|INO1_TOBAC	RecName: Full=Inositol-3-phosphate synthase; AltName: Full=Myo-inositol-1-phosphate synthase; Short=MI-1-P synthase; Short=IPS >gi|8096266|dbj|BAA95788.1| myo-inositol 1-phosphate synthase [Nicotiana tabacum]	98.41	189	3E-101
Mjin_7C_T_G04.ab1	gi|147841887|emb|CAN65217.1|	hypothetical protein [Vitis vinifera]	62.5	88	3E-24
Mjin_7C_T_G05.ab1	gi|157337229|emb|CAO21575.1|	unnamed protein product [Vitis vinifera]	87.1	93	4E-30
Mjin_7C_T_G06.ab1	gi|157343104|emb|CAO66593.1|	unnamed protein product [Vitis vinifera]	38.64	176	5E-19
Mjin_7C_T_G11.ab1	gi|37524017|gb|AAQ92310.1|	COR15 [Citrus clementina x Citrus reticulata]	100	101	2E-27
Mjin_7C_T_G12.ab1	gi|157348406|emb|CAO23193.1|	unnamed protein product [Vitis vinifera]	81.58	38	2E-11
Mjin_7C_T_H01.ab1	gi|157346844|emb|CAO17083.1|	unnamed protein product [Vitis vinifera]	62.42	165	4E-39
Mjin_7C_T_H02.ab1	gi|164605000|dbj|BAF98296.1|	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase [Hevea brasiliensis]	94.55	220	5E-117
Mjin_7C_T_H04.ab1	gi|147866525|emb|CAN83700.1|	hypothetical protein [Vitis vinifera]	60.22	186	4E-63
Mjin_7C_T_H05.ab1	gi|22328262|ref|NP_192211.2|	transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana] >gi|20466538|gb|AAM20586.1| putative WD-repeat protein [Arabidopsis thaliana] >gi|23198298|gb|AAN15676.1| putative WD-repeat protein [Arabidopsis thaliana]	86.54	104	7E-45
Mjin_7D_T_A04.ab1	gi|115454983|ref|NP_001051092.1|	Os03g0719100 [Oryza sativa (japonica cultivar-group)] >gi|50540681|gb|AAT77838.1| putative zinc finger protein [Oryza sativa (japonica cultivar-group)] >gi|10871078|gb|ABF98573.1| Sumoylation ligase E3, putative, expressed [Oryza sativa (japonica cultivar-group)] >gi|113549563|dbj|BAF13006.1| Os03g0719100 [Oryza sativa (japonica cultivar-group)]	70.09	117	1E-47
Mjin_7D_T_A05.ab1	gi|152206074|gb|ABS30422.1|	acyl-ACP thioesterase FatA [Ricinus communis]	90.8	163	1E-83
Mjin_7D_T_A06.ab1	gi|115444401|ref|NP_001045980.1|	Os02g0161900 [Oryza sativa (japonica cultivar-group)] >gi|115469558|ref|NP_001058378.1| Os06g0681400 [Oryza sativa (japonica cultivar-group)] >gi|6013289|gb|AAF01315.1|AF184279_1 polyubiquitin [Oryza sativa] >gi|6013291|gb|AAF01316.1|AF184280_1 polyubiquitin [Oryza sativa] >gi|416038|emb|CAA53665.1| polyubiquitin [Oryza sativa (indica cultivar-group)] >gi|1574944|gb|AAC49806.1| polyubiquitin >gi|49389251|dbj|BAD25213.1| polyubiquitin 6 [Oryza sativa Japonica Group] >gi|113535511|dbj|BAF07894.1| Os02g0161900 [Oryza sativa (japonica cultivar-group)] >gi|113596418|dbj|BAF20292.1| Os06g0681400 [Oryza sativa (japonica cultivar-group)]	99.54	217	5E-116
Mjin_7D_T_A10.ab1	gi|118485648|gb|ABK94674.1|	unknown [Populus trichocarpa]	77.99	159	5E-65
Mjin_7D_T_A11.ab1	gi|118480991|gb|ABK92449.1|	unknown [Populus trichocarpa]	59.56	136	2E-35

IP : 14.49.138.138, 2017-11-03 13:30:33

Mjin_7D_T_B06.ab1	gi|157328019|emb|CAO16989.1|	unnamed protein product [Vitis vinifera]	55.08	236	2E-51
Mjin_7D_T_B09.ab1	gi|121720665|ref|YP_001001585.1|	photosystem I subunit VII [Nuphar advena] >gi|170784794|ref|YP_001718710.1| photosystem I subunit VII [Trachelium caeruleum] >gi|69217720|gb|AAZ04107.1| photosystem I subunit VII [Nuphar advena] >gi|84682256|gb|ABC60510.1| photosystem I subunit VII [Nuphar advena] >gi|156598849|gb|ABU85677.1| photosystem I subunit VII [Trachelium caeruleum] >gi|157267542|gb|ABV26535.1| photosystem I subunit VII [Trachelium caeruleum]	98.77	81	1E-43
Mjin_7D_T_B12.ab1	gi|157348973|emb|CAO24051.1|	unnamed protein product [Vitis vinifera]	76	100	1E-38
Mjin_7D_T_C07.ab1	gi|156446279|gb|ABU63401.1|	heat shock protein [Corchorus olitorius]	78.69	61	4E-23
Mjin_7D_T_C08.ab1	gi|118489609|gb|ABK96606.1|	unknown [Populus trichocarpa x Populus deltoides]	91.2	125	1E-59
Mjin_7D_T_C10.ab1	gi|3540182|gb|AAC34332.1|	Unknown protein [Arabidopsis thaliana]	64.37	87	3E-24
Mjin_7D_T_C12.ab1	gi|18395162|ref|NP_564181.1|	unknown protein [Arabidopsis thaliana] >gi|79318389|ref|NP_001031081.1| unknown protein [Arabidopsis thaliana] >gi|21618018|gb|AAM67068.1| unknown [Arabidopsis thaliana] >gi|27754683|gb|AAO22785.1| unknown protein [Arabidopsis thaliana] >gi|28394087|gb|AAO42451.1| unknown protein [Arabidopsis thaliana]	43.05	151	8E-23
Mjin_7D_T_D04.ab1	gi|108864390|gb|ABG22487.1|	40S ribosomal protein S5, putative, expressed [Oryza sativa (japonica cultivar-group)]	100	42	4E-15
Mjin_7D_T_D10.ab1	gi|118488653|gb|ABK96138.1|	unknown [Populus trichocarpa]	77.59	58	6E-19
Mjin_7D_T_D12.ab1	gi|147773026|emb|CAN67181.1|	hypothetical protein [Vitis vinifera] >gi|157336556|emb|CAO71241.1| unnamed protein product [Vitis vinifera]	59.63	109	2E-26
Mjin_7D_T_E04.ab1	gi|147818815|emb|CAN60726.1|	hypothetical protein [Vitis vinifera] >gi|157344057|emb|CAO68990.1| unnamed protein product [Vitis vinifera]	88.89	63	2E-26
Mjin_7D_T_E05.ab1	gi|10834829|gb|AAG23841.1|AF302808_1	metallothionein-like protein [Sesamum indicum] >gi|40732882|gb|AAR88997.1| seed-specific metallothionein-like protein [Sesamum indicum]	67.27	55	5E-20
Mjin_7D_T_E06.ab1	gi|18420313|ref|NP_568401.1|	unknown protein [Arabidopsis thaliana]	39.89	183	7E-23
Mjin_7D_T_F07.ab1	gi|15233990|ref|NP_192705.1|	oxidoreductase family protein [Arabidopsis thaliana] >gi|73921136|sp|Q9SZ83|Y4967_ARATH RecName: Full=Uncharacterized oxidoreductase At4g09670 >gi|4538897|emb|CAB39634.1| AX110P-like protein [Arabidopsis thaliana] >gi|7267662|emb|CAB78090.1| AX110P-like protein [Arabidopsis thaliana] >gi|21554042|gb|AAM63123.1| AX110P-like protein [Arabidopsis thaliana] >gi|26983872|gb|AAN86188.1| putative AX110P protein [Arabidopsis thaliana]	73.81	126	3E-41
Mjin_7D_T_F10.ab1	gi|157343944|emb|CAO68877.1|	unnamed protein product [Vitis vinifera]	56.21	153	9E-37
Mjin_7D_T_G04.ab1	gi|157338371|emb|CAO39415.1|	unnamed protein product [Vitis vinifera]	58.7	92	3E-32
Mjin_7D_T_G11.ab1	gi|6682841|dbj|BAA88904.1|	sucrose synthase [Citrus unshiu]	100	43	7E-17
Mjin_7D_T_G12.ab1	gi|157340494|emb|CAO47299.1|	unnamed protein product [Vitis vinifera]	63.39	112	4E-31
Mjin_7D_T_H03.ab1	gi|147783622|emb|CAN68143.1|	hypothetical protein [Vitis vinifera] >gi|157353821|emb|CAO46353.1| unnamed protein product [Vitis vinifera]	88.5	113	3E-54
Mjin_7D_T_H08.ab1	gi|157342810|emb|CAO65522.1|	unnamed protein product [Vitis vinifera]	94.74	76	4E-35
Mjin_7D_T_H09.ab1	gi|157335309|emb|CAO61139.1|	unnamed protein product [Vitis vinifera]	82.99	194	4E-85
Mjin_7D_T_H12.ab1	gi|157351115|emb|CAO41272.1|	unnamed protein product [Vitis vinifera]	64.39	205	3E-70
Mjin_8A_T_A01	gi|2661460|emb|CAA05921.1|	ABI3 [Populus trichocarpa]	53.85	208	1E-27
Mjin_8A_T_A05.ab1	gi|157360273|emb|CAO69484.1|	unnamed protein product [Vitis vinifera]	90.6	234	7E-117
Mjin_8A_T_A06.ab1	gi|147816024|emb|CAN61543.1|	hypothetical protein [Vitis vinifera]	58.88	107	2E-24
Mjin_8A_T_A11.ab1	gi|156754275|gb|ABU94631.1|	putative aquaporin PIP2;3 [Phaseolus vulgaris]	93.38	151	2E-77
Mjin_8A_T_A12.ab1	gi|15231104|ref|NP_191426.1|	unknown protein [Arabidopsis thaliana] >gi|145332889|ref|NP_001078310.1| unknown protein [Arabidopsis thaliana] >gi|7630062|emb|CAB88284.1| putative protein [Arabidopsis thaliana] >gi|15293013|gb|AAK93617.1| unknown protein [Arabidopsis thaliana] >gi|21536892|gb|AAM61224.1| unknown [Arabidopsis thaliana] >gi|23296434|gb|AAN13116.1| unknown protein [Arabidopsis thaliana]	78.07	187	7E-83
Mjin_8A_T_B02.ab1	gi|118486025|gb|ABK94856.1|	unknown [Populus trichocarpa]	72.56	164	5E-57
Mjin_8A_T_B04.ab1	gi|118483198|gb|ABK93503.1|	unknown [Populus trichocarpa]	95.83	96	2E-33

IP : 14.49.138.138, 2017-11-03 13:30:33

Mjin_8A_T_B05.ab1	gi|157335805|emb|CAO61635.1|	unnamed protein product [Vitis vinifera]	77.19	57	5E-23
Mjin_8A_T_B07.ab1	gi|18396344|ref|NP_564284.1|	APT1; adenine phosphoribosyltransferase [Arabidopsis thaliana] >gi|38503396|sp|P31166|APT1_ARATH RecName: Full=Adenine phosphoribosyltransferase 1; Short=APRT 1 >gi|21536559|gb|AAM60891.1| adenine phosphoribosyltransferase 1, APRT [Arabidopsis thaliana]	71.19	59	8E-15
Mjin_8A_T_B08.ab1	gi|147782859|emb|CAN70098.1|	hypothetical protein [Vitis vinifera]	75.34	146	5E-53
Mjin_8A_T_B10.ab1	gi|209967439|gb|ACJ02348.1|	60s ribosome protein L19 [Vernicia fordii]	82.98	94	6E-18
Mjin_8A_T_C07.ab1	gi|8134299|sp|P93110|ACEA_CUCMA	RecName: Full=Isocitrate lyase; Short=ICL; Short=Isocitratase; Short=Isocitrase >gi|1695645|dbj|BAA11320.1| Isocitrate Lyase [Cucurbita cv. Kurokawa Amakuri]	96.97	132	3E-52
Mjin_8A_T_C08.ab1	gi|147853780|emb|CAN83822.1|	hypothetical protein [Vitis vinifera]	63.01	73	2E-20
Mjin_8A_T_C12.ab1	gi|38679311|gb|AAR26477.1|	harpin binding protein 1 [Citrus x paradisi]	96.94	98	2E-18
Mjin_8A_T_D01.ab1	gi|118722670|gb|ABL10073.1|	17.7 KD class I small heat-shock protein [Ageratina adenophora]	81.93	83	2E-28
Mjin_8A_T_D02.ab1	gi|157335421|emb|CAO61251.1|	unnamed protein product [Vitis vinifera]	63.64	88	6E-29
Mjin_8A_T_D06.ab1	gi|4928460|gb|AAD33596.1|AF133127_1	thioredoxin h [Hevea brasiliensis]	81.74	115	4E-40
Mjin_8A_T_D08.ab1	gi|15233740|ref|NP_194150.1|	SHD (SHEPHERD); ATP binding [Arabidopsis thaliana] >gi|75337653|sp|Q9STX5|ENPL_ARATH RecName: Full=Endoplasmin homolog; AltName: Full=GRP94 homolog; AltName: Full=Protein SHEPHERD; AltName: Full=HSP90-like protein 7; Flags: Precursor >gi|5051761|emb|CAB45054.1| HSP90-like protein [Arabidopsis thaliana] >gi|7269269|emb|CAB79329.1| HSP90-like protein [Arabidopsis thaliana] >gi|14532542|gb|AAK63999.1| AT4g24190/T22A6_20 [Arabidopsis thaliana] >gi|19570872|dbj|BAB86369.1| SHEPHERD [Arabidopsis thaliana] >gi|28416485|gb|AAO42773.1| At4g24190/T22A6_20 [Arabidopsis thaliana]	92.67	150	3E-77
Mjin_8A_T_D12.ab1	gi|157328757|emb|CAO22793.1|	unnamed protein product [Vitis vinifera]	57.69	104	7E-22
Mjin_8A_T_E01.ab1	gi|1061408|gb|AAB52963.1|	citrin	98.08	52	2E-20
Mjin_8A_T_E03.ab1	gi|118481891|gb|ABK92881.1|	unknown [Populus trichocarpa]	90.4	125	4E-64
Mjin_8A_T_E11.ab1	gi|157344046|emb|CAO68979.1|	unnamed protein product [Vitis vinifera]	75.61	82	1E-27
Mjin_8A_T_F02.ab1	gi|157351275|emb|CAO41462.1|	unnamed protein product [Vitis vinifera]	81.82	44	6E-13
Mjin_8A_T_F06.ab1	gi|124360347|gb|ABN08360.1|	Cation transporting ATPase, C-terminal [Medicago truncatula]	69.11	123	5E-46
Mjin_8A_T_F08.ab1	gi|22331783|ref|NP_680128.1|	glycoside hydrolase family 2 protein [Arabidopsis thaliana] >gi|20147224|gb|AAM10327.1| At3g54435 [Arabidopsis thaliana]	83.43	169	9E-85
Mjin_8A_T_F10.ab1	gi|147777809|emb|CAN64607.1|	hypothetical protein [Vitis vinifera]	75.95	79	4E-24
Mjin_8A_T_G05.ab1	gi|118486538|gb|ABK95108.1|	unknown [Populus trichocarpa]	81.48	108	9E-44
Mjin_8A_T_G10.ab1	gi|157347192|emb|CAO17574.1|	unnamed protein product [Vitis vinifera]	71.23	146	1E-45
Mjin_8A_T_H01.ab1	gi|1061408|gb|AAB52963.1|	citrin	98.39	62	2E-27
Mjin_8A_T_H04.ab1	gi|157337063|emb|CAO21409.1|	unnamed protein product [Vitis vinifera]	93.15	219	2E-117
Mjin_8A_T_H09.ab1	gi|157349969|emb|CAO39868.1|	unnamed protein product [Vitis vinifera]	79.71	138	2E-52
Mjin_8A_T_H11.ab1	gi|14916566|sp|Q9ZWQ9|FLS_CITUN	RecName: Full=Flavonol synthase/flavanone 3-hydroxylase; AltName: Full=CitFLS; Short=FLS >gi|4126403|dbj|BAA36554.1| flavonol synthase [Citrus unshiu]	96.59	88	6E-42
Mjin_8A_T_H12.ab1	gi|116643152|gb|ABK06393.1|	stress-related protein [Citrus sinensis]	98.61	72	1E-33
Mjin_8B_T_A02.ab1	gi|118485751|gb|ABK94725.1|	unknown [Populus trichocarpa]	98.29	175	1E-92
Mjin_8B_T_A04.ab1	gi|157337914|emb|CAO38958.1|	unnamed protein product [Vitis vinifera]	80.54	149	9E-61
Mjin_8B_T_A07.ab1	gi|147768913|emb|CAN75887.1|	hypothetical protein [Vitis vinifera]	45	260	7E-41
Mjin_8B_T_B10.ab1	gi|21615419|emb|CAD33929.1|	microtubule associated protein [Cicer arietinum]	97.85	93	3E-45
Mjin_8B_T_B11.ab1	gi|12830830|gb|AAK08208.1|AF320905_1	metallothionein-like protein [Citrus unshiu] >gi|12830832|gb|AAK08209.1|AF320906_1 metallothionein-like protein [Citrus unshiu] >gi|3308982|dbj|BAA31562.1| metallothionein-like protein [Citrus unshiu] >gi|158936952|dbj|BAF91493.1| metallothionein type 3 [Citrus unshiu]	100	49	8E-21
Mjin_8B_T_C01.ab	gi|24461855|gb|AAN623	Jp18 [Poncirus trifoliata]	98.28	58	9E-16

IP : 14.49.138.138, 2017-11-03 13:30:33

1	42.1|AF506028_9				
Mjin_8B_T_C03.ab 1	gi|157329387|emb|CAO 39963.1|	unnamed protein product [Vitis vinifera]	89.93	149	1E-76
Mjin_8B_T_C04.ab 1	gi|119367461|gb|ABL67 648.1|	putative metallothionein-like protein [Citrus cv. Shiranuhi]	100	46	4E-19
Mjin_8B_T_C05.ab 1	gi|84453228|dbj|BAE712 11.1|	putative DNA ligase [Trifolium pratense]	82.31	130	1E-58
Mjin_8B_T_C11.ab 1	gi|157336327|emb|CAO 71012.1|	unnamed protein product [Vitis vinifera]	96.82	157	3E-85
Mjin_8B_T_D05.ab 1	gi|147778418|emb|CAN 60810.1|	hypothetical protein [Vitis vinifera]	92.98	57	3E-23
Mjin_8B_T_D06.ab 1	gi|157357900|emb|CAO 64912.1|	unnamed protein product [Vitis vinifera]	86.62	157	3E-64
Mjin_8B_T_D08.ab 1	gi|151547430|gb|ABS12 459.1|	cysteine protease Cp [Citrus sinensis]	100	88	6E-45
Mjin_8B_T_D12.ab 1	gi|147810266|emb|CAN 71449.1|	hypothetical protein [Vitis vinifera]	80.25	81	2E-31
Mjin_8B_T_E03.ab 1	gi|157328084|emb|CAO 17184.1|	unnamed protein product [Vitis vinifera]	62.86	70	4E-14
Mjin_8B_T_E04.ab 1	gi|133902320|gb|ABO41 848.1|	putative calcium-binding protein [Gossypium hirsutum]	78.12	64	6E-23
Mjin_8B_T_F02.ab 1	gi|157354141|emb|CAO 46708.1|	unnamed protein product [Vitis vinifera]	69.7	66	2E-17
Mjin_8B_T_F03.ab 1	gi|147780497|emb|CAN 67050.1|	hypothetical protein [Vitis vinifera]	72.22	90	8E-21
Mjin_8B_T_F06.ab 1	gi|10732644|gb|AAG224 88.1|AF195868_1	pyruvate decarboxylase 1 [Vitis vinifera]	90.77	195	1E-102
Mjin_8B_T_F10.ab 1	gi|157348530|emb|CAO 23422.1|	unnamed protein product [Vitis vinifera]	63.58	151	6E-48
Mjin_8B_T_F11.ab 1	gi|15241978|ref|NP_198 242.1|	calcium-binding EF hand family protein [Arabidopsis thaliana] >gi|17380962|gb|AAL36293.1| putative protein phosphatase 2A regulatory subunit B [Arabidopsis thaliana] >gi|20465395|gb|AAM20122.1| putative phosphatase 2A regulatory subunit B protein [Arabidopsis thaliana]	86.67	60	5E-25
Mjin_8B_T_G02.ab 1	gi|40645459|dbj|BAD06 575.1|	LEDI-5c protein [Lithospermum erythrorhizon]	82.76	58	1E-21
Mjin_8B_T_G03.ab 1	gi|14589309|emb|CAC43 237.1|	lipoxygenase [Sesbania rostrata]	81.11	90	4E-31
Mjin_8B_T_G04.ab 1	gi|157353706|emb|CAO 46238.1|	unnamed protein product [Vitis vinifera]	94.12	153	2E-82
Mjin_8B_T_G05.ab 1	gi|147833364|emb|CAN 72935.1|	hypothetical protein [Vitis vinifera] >gi|157345655|emb|CAO14953.1| unnamed protein product [Vitis vinifera]	95.06	81	1E-37
Mjin_8B_T_G06.ab 1	gi|1061408|gb|AAB5296 3.1|	citrin	98.67	75	3E-35
Mjin_8B_T_G09.ab 1	gi|147865194|emb|CAN 81960.1|	hypothetical protein [Vitis vinifera]	79.05	210	2E-87
Mjin_8B_T_H01.ab 1	gi|147779004|emb|CAN 75753.1|	hypothetical protein [Vitis vinifera]	74.07	54	2E-18
Mjin_8B_T_H02.ab 1	gi|1061408|gb|AAB5296 3.1|	citrin	96.67	60	2E-26
Mjin_8B_T_H06.ab 1	gi|1061408|gb|AAB5296 3.1|	citrin	100	88	7E-43
Mjin_8B_T_H07.ab 1	gi|117557146|gb|ABK35 750.1|	sulfate transporter [Populus alba x Populus tremula]	79.83	119	2E-38
Mjin_8B_T_H08.ab 1	gi|157345381|emb|CAO 14679.1|	unnamed protein product [Vitis vinifera]	63.86	166	1E-43
Mjin_8C_T_A03.ab 1	gi|157349886|emb|CAO 39742.1|	unnamed protein product [Vitis vinifera]	63.1	187	4E-57
Mjin_8C_T_A06.ab 1	gi|145334873|ref|NP_00 1078782.1|	permease, putative [Arabidopsis thaliana]	82.02	228	9E-99
Mjin_8C_T_A10.ab 1	gi|157347868|emb|CAO 22455.1|	unnamed protein product [Vitis vinifera]	65.1	192	8E-71
Mjin_8C_T_B01.ab 1	gi|118481158|gb|ABK92 531.1|	unknown [Populus trichocarpa]	90.57	53	6E-19
Mjin_8C_T_B02.ab 1	gi|115460714|ref|NP_00 1053957.1|	Os04g0628100 [Oryza sativa (japonica cultivar-group)] >gi|113565528|dbj|BAF15871.1| Os04g0628100 [Oryza sativa (japonica cultivar-group)]	94.41	161	2E-78
Mjin_8C_T_B04.ab 1	gi|157340001|emb|CAO 45678.1|	unnamed protein product [Vitis vinifera]	77.27	110	2E-42
Mjin_8C_T_B05.ab 1	gi|90017355|emb|CAI68 019.1|	endo-beta-1,4-glucanase [Prunus persica]	61.64	159	2E-45
Mjin_8C_T_C01.ab 1	gi|157356489|emb|CAO 62669.1|	unnamed protein product [Vitis vinifera]	83.44	151	2E-65
Mjin_8C_T_C02.ab 1	gi|147785090|emb|CAN 68791.1|	hypothetical protein [Vitis vinifera]	77.59	58	2E-18
Mjin_8C_T_C09.ab 1	gi|115487294|ref|NP_00 1066134.1|	Os12g0143100 [Oryza sativa (japonica cultivar-group)] >gi|77553656|gb|ABA96452.1| GRF zinc finger family protein [Oryza sativa (japonica cultivar-group)] >gi|113648641|dbj|BAF29153.1| Os12g0143100 [Oryza sativa (japonica cultivar-group)]	88.75	80	1E-35

IP : 14.49.138.138, 2017-11-03 13:30:33

Mjin_8C_T_D02.ab1	gi|121308296|dbj|BAF43572.1|	pectate lyase [Prunus persica]	95.28	106	1E-57
Mjin_8C_T_D04.ab1	gi|4102690|gb|AAD01540.1|	24 kDa seed maturation protein [Glycine max]	52.99	134	4E-35
Mjin_8C_T_D05.ab1	gi|157328082|emb|CAO17182.1|	unnamed protein product [Vitis vinifera]	69.23	65	1E-21
Mjin_8C_T_D12.ab1	gi|12585490|sp|Q9SM09|VATA_CITUN	RecName: Full=V-type proton ATPase catalytic subunit A; Short=V-ATPase subunit A; AltName: Full=Vacuolar proton pump subunit alpha; AltName: Full=V-ATPase 69 kDa subunit >gi|6518112|dbj|BAA87891.1| H+-ATPase catalytic subunit [Citrus unshiu]	100	114	1E-60
Mjin_8C_T_F04.ab1	gi|117549810|gb|ABK35086.1|	EIL2 [Prunus persica]	60.98	82	2E-20
Mjin_8C_T_F05.ab1	gi|115467132|ref|NP_001057165.1|	Os06g0219800 [Oryza sativa (japonica cultivar-group)] >gi|51535369|dbj|BAD37240.1| putative phosphotyrosyl phosphatase activator [Oryza sativa Japonica Group] >gi|113595205|dbj|BAF19079.1| Os06g0219800 [Oryza sativa (japonica cultivar-group)]	91.3	46	8E-18
Mjin_8C_T_F11.ab1	gi|157329640|emb|CAO41075.1|	unnamed protein product [Vitis vinifera]	71.79	195	1E-75
Mjin_8C_T_F12.ab1	gi|115463395|ref|NP_001055297.1|	Os05g0357600 [Oryza sativa (japonica cultivar-group)] >gi|55167981|gb|AAV43849.1| putative GTP binding protein [Oryza sativa (japonica cultivar-group)] >gi|113578848|dbj|BAF17211.1| Os05g0357600 [Oryza sativa (japonica cultivar-group)]	94.8	173	7E-79
Mjin_8C_T_G01.ab1	gi|157356700|emb|CAO62895.1|	unnamed protein product [Vitis vinifera]	75.12	213	2E-93
Mjin_8C_T_G07.ab1	gi|157345300|emb|CAO14598.1|	unnamed protein product [Vitis vinifera]	89.02	173	1E-84
Mjin_8C_T_G08.ab1	gi|157346008|emb|CAO15705.1|	unnamed protein product [Vitis vinifera]	83.8	216	1E-106
Mjin_8C_T_G09.ab1	gi|194239854|emb|CAP58016.1|	putative stay green protein [Citrus sinensis]	98.31	59	3E-23
Mjin_8C_T_H02.ab1	gi|157342853|emb|CAO65565.1|	unnamed protein product [Vitis vinifera]	55.17	174	1E-43
Mjin_8C_T_H06.ab1	gi|52783264|sp|Q9FUL4|RL24_PRUAV	60S ribosomal protein L24 >gi|10180025|gb|AAG13986.1|AF298827_1 60S ribosomal protein L24 [Prunus avium]	93.57	140	3E-60
Mjin_8C_T_H07.ab1	gi|77416945|gb|ABA81868.1|	unknown [Solanum tuberosum]	64.62	195	8E-58
Mjin_8C_T_H10.ab1	gi|118484294|gb|ABK94026.1|	unknown [Populus trichocarpa]	67.59	108	7E-32
Mjin_8C_T_H11.ab1	gi|15231899|ref|NP_188082.1|	CYP72A10 (cytochrome P450, family 72, subfamily A, polypeptide 10); oxygen binding [Arabidopsis thaliana]	67.97	128	2E-45
Mjin_8D_T_A01.ab1	gi|15230180|ref|NP_191259.1|	nucleolar essential protein-related [Arabidopsis thaliana] >gi|6911870|emb|CAB72170.1| putative protein [Arabidopsis thaliana] >gi|28466945|gb|AAO44081.1| At3g57000 [Arabidopsis thaliana] >gi|110735698|dbj|BAE99829.1| hypothetical protein [Arabidopsis thaliana]	66.07	168	2E-54
Mjin_8D_T_A02.ab1	gi|157350049|emb|CAO39987.1|	unnamed protein product [Vitis vinifera]	82.02	89	9E-35
Mjin_8D_T_A07.ab1	gi|18411611|ref|NP_565158.1|	glucose-6-phosphate/phosphate translocator-related [Arabidopsis thaliana] >gi|12323396|gb|AAG51677.1|AC010704_21 unknown protein; 76010-78007 [Arabidopsis thaliana] >gi|13430498|gb|AAK25871.1|AF360161_1 unknown protein [Arabidopsis thaliana] >gi|21281058|gb|AAM44935.1| unknown protein [Arabidopsis thaliana] >gi|46934764|emb|CAG18176.1| UDP-galactose transporter [Arabidopsis thaliana]	100	53	4E-24
Mjin_8D_T_A08.ab1	gi|8131905|gb|AAF73132.1|AF149017_1	homogentisate 1,2-dioxygenase [Lycopersicon esculentum]	87.72	57	1E-22
Mjin_8D_T_A09.ab1	gi|157340561|emb|CAO47366.1|	unnamed protein product [Vitis vinifera]	70.94	203	2E-82
Mjin_8D_T_A11.ab1	gi|118488342|gb|ABK95989.1|	unknown [Populus trichocarpa]	87.14	210	2E-100
Mjin_8D_T_B02.ab1	gi|1061408|gb|AAB52963.1|	citrin	94.85	97	2E-38
Mjin_8D_T_B04.ab1	gi|118489325|gb|ABK96467.1|	unknown [Populus trichocarpa x Populus deltoides]	85.26	156	2E-77
Mjin_8D_T_B05.ab1	gi|157337388|emb|CAO21734.1|	unnamed protein product [Vitis vinifera]	70	150	5E-58
Mjin_8D_T_B11.ab1	gi|147838249|emb|CAN76598.1|	hypothetical protein [Vitis vinifera] >gi|157345819|emb|CAO15334.1| unnamed protein product [Vitis vinifera]	75.58	217	3E-79
Mjin_8D_T_C04.ab1	gi|114329680|ref|YP_740501.1|	clp protease proteolytic subunit [Citrus sinensis] >gi|122166158|sp|Q09MF2|CLPP_CITSI RecName: Full=ATP-dependent Clp protease proteolytic subunit; AltName: Full=Endopeptidase Clp >gi|113952646|gb|ABI49044.1| clp protease proteolytic subunit [Citrus sinensis]	100	121	1E-64
Mjin_8D_T_C06.ab1	gi|118484032|gb|ABK93902.1|	unknown [Populus trichocarpa]	86.76	68	1E-27
Mjin_8D_T_C09.ab1	gi|31321942|gb|AAM54365.1|	2S albumin seed storage protein [Juglans nigra]	56.67	90	3E-15
Mjin_8D_T_C12.ab	gi|157355344|emb|CAO	unnamed protein product [Vitis vinifera]	64.1	117	1E-33

IP : 14.49.138.138, 2017-11-03 13:30:33

1	48731.1|				
Mjin_8D_T_D01.ab 1	gi|192764525|gb|ACF05 806.1|	PAE [Litchi chinensis]	88.24	119	6E-58
Mjin_8D_T_D04.ab 1	gi|157343901|emb|CAO 68407.1|	unnamed protein product [Vitis vinifera]	52.99	117	2E-23
Mjin_8D_T_D12.ab 1	gi|147864472|emb|CAN 82640.1|	hypothetical protein [Vitis vinifera]	76.07	117	7E-38
Mjin_8D_T_E07.ab 1	gi|157337780|emb|CAO 22126.1|	unnamed protein product [Vitis vinifera]	78.12	64	4E-19
Mjin_8D_T_F02.ab 1	gi|109390302|gb|ABG33 750.1|	cysteine protease [Hevea brasiliensis]	76.7	103	7E-41
Mjin_8D_T_F03.ab 1	gi|1808656|emb|CAA71 762.1|	Ubiquitin activating enzyme E1 [Nicotiana tabacum]	84.91	106	9E-52
Mjin_8D_T_F04.ab 1	gi|17385640|dbj|BAA87 070.2|	TAT-binding protein homolog [Matricaria chamomilla]	93.14	102	4E-39
Mjin_8D_T_F05.ab 1	gi|157353782|emb|CAO 46314.1|	unnamed protein product [Vitis vinifera]	93.1	58	2E-23
Mjin_8D_T_F08.ab 1	gi|157350461|emb|CAO 40510.1|	unnamed protein product [Vitis vinifera]	69.57	115	2E-42
Mjin_8D_T_F10.ab 1	gi|1710807|sp|P08926|R UBA_PEA	RecName: Full=RuBisCO large subunit-binding protein subunit alpha, chloroplastic; AltName: Full=60 kDa chaperonin subunit alpha; AltName: Full=CPN-60 alpha; Flags: Precursor >gi|1185390|gb|AAA87731.1| alphacpn60 precursor [Pisum sativum]	90.54	74	2E-30
Mjin_8D_T_G04.ab 1	gi|118485987|gb|ABK94 838.1|	unknown [Populus trichocarpa]	56.58	152	1E-37
Mjin_8D_T_G11.ab 1	gi|110289420|gb|ABB47 893.2|	Major Facilitator Superfamily protein, expressed [Oryza sativa (japonica cultivar-group)]	97.83	46	7E-19
Mjin_8D_T_H09.ab 1	gi|157345390|emb|CAO 14688.1|	unnamed protein product [Vitis vinifera]	88.24	119	2E-47
Mjin_8D_T_H12.ab 1	gi|118482816|gb|ABK93 324.1|	unknown [Populus trichocarpa]	79.55	44	1E-13
Mjin_9A_T_A03.ab 1	gi|147794656|emb|CAN 73508.1|	hypothetical protein [Vitis vinifera] >gi|157354939|emb|CAO48285.1| unnamed protein product [Vitis vinifera]	66.03	156	6E-26
Mjin_9A_T_A04.ab 1	gi|157349049|emb|CAO 24127.1|	unnamed protein product [Vitis vinifera]	90.08	121	6E-65
Mjin_9A_T_A10.ab 1	gi|71999169|gb|AAZ574 44.1|	lipoxygenase LOX1 [Populus deltoides]	53.62	235	2E-55
Mjin_9A_T_B04.ab 1	gi|157340751|emb|CAO 47556.1|	unnamed protein product [Vitis vinifera]	80.68	176	9E-82
Mjin_9A_T_B06.ab 1	gi|1061408|gb|AAB5296 3.1|	citrin	97.26	73	1E-25
Mjin_9A_T_B09.ab 1	gi|118486136|gb|ABK94 911.1|	unknown [Populus trichocarpa]	71.11	135	4E-50
Mjin_9A_T_C01.ab 1	gi|106879601|emb|CAJ3 8384.1|	actin-depolymerizing factor [Plantago major]	94.74	38	2E-12
Mjin_9A_T_C06.ab 1	gi|1061408|gb|AAB5296 3.1|	citrin	94.44	36	8E-13
Mjin_9A_T_C11.ab 1	gi|118484475|gb|ABK94 113.1|	unknown [Populus trichocarpa]	98.18	55	2E-23
Mjin_9A_T_D03.ab 1	gi|147805843|emb|CAN 62787.1|	hypothetical protein [Vitis vinifera] >gi|157350349|emb|CAO40329.1| unnamed protein product [Vitis vinifera]	60.63	127	1E-28
Mjin_9A_T_D04.ab 1	gi|147856360|emb|CAN 79636.1|	hypothetical protein [Vitis vinifera]	96.47	85	1E-39
Mjin_9A_T_D09.ab 1	gi|125564704|gb|EAZ10 084.1|	hypothetical protein OsI_031316 [Oryza sativa (indica cultivar-group)]	36.69	139	4E-15
Mjin_9A_T_E01.ab 1	gi|147820654|emb|CAN 65362.1|	hypothetical protein [Vitis vinifera]	76	200	3E-72
Mjin_9A_T_E05.ab 1	gi|147790682|emb|CAN 61026.1|	hypothetical protein [Vitis vinifera]	79.25	106	2E-44
Mjin_9A_T_E10.ab 1	gi|118482551|gb|ABK93 196.1|	unknown [Populus trichocarpa]	87.14	70	3E-32
Mjin_9A_T_E11.ab 1	gi|1061408|gb|AAB5296 3.1|	citrin	72.58	62	9E-12
Mjin_9A_T_F01.ab 1	gi|147858113|emb|CAN 81413.1|	hypothetical protein [Vitis vinifera] >gi|157359533|emb|CAO67734.1| unnamed protein product [Vitis vinifera]	92.31	234	2E-120
Mjin_9A_T_F05.ab 1	gi|157359785|emb|CAO 68507.1|	unnamed protein product [Vitis vinifera]	31.14	228	2E-19
Mjin_9A_T_F11.ab 1	gi|157351040|emb|CAO 41197.1|	unnamed protein product [Vitis vinifera]	98.78	82	2E-41
Mjin_9A_T_F12.ab 1	gi|157341740|emb|CAO 62295.1|	unnamed protein product [Vitis vinifera]	91.14	79	1E-38
Mjin_9A_T_G04.ab 1	gi|118486780|gb|ABK95 225.1|	unknown [Populus trichocarpa]	86.67	105	1E-48
Mjin_9A_T_G07.ab 1	gi|147858691|emb|CAN 78879.1|	hypothetical protein [Vitis vinifera]	89.74	39	1E-12
Mjin_9A_T_G10.ab 1	gi|18412508|ref|NP_567 133.1|	complex 1 family protein / LVR family protein [Arabidopsis thaliana] >gi|7362761|emb|CAB83131.1| hypothetical protein [Arabidopsis thaliana] >gi|21554092|gb|AAM63173.1| unknown [Arabidopsis thaliana] >gi|28466831|gb|AAO44024.1| At3g62810 [Arabidopsis thaliana] >gi|110743822|dbj|BAE99746.1| hypothetical protein [Arabidopsis thaliana]	74.49	98	1E-33

IP : 14.49.138.138, 2017-11-03 13:30:33

Mjin_9A_T_G12.ab1	gi|157335108|emb|CAO60938.1|	unnamed protein product [Vitis vinifera]	51.43	245	1E-46
Mjin_9A_T_H01.ab1	gi|157358580|emb|CAO66256.1|	unnamed protein product [Vitis vinifera]	80.92	131	5E-57
Mjin_9A_T_H02.ab1	gi|157339429|emb|CAO43970.1|	unnamed protein product [Vitis vinifera]	86.34	161	1E-80
Mjin_9A_T_H03.ab1	gi|157341915|emb|CAO63371.1|	unnamed protein product [Vitis vinifera]	75	168	3E-63
Mjin_9A_T_H06.ab1	gi|157356722|emb|CAO62917.1|	unnamed protein product [Vitis vinifera]	87.34	158	8E-68
Mjin_9A_T_H09.ab1	gi|157336285|emb|CAO70970.1|	unnamed protein product [Vitis vinifera]	67.63	207	1E-80
Mjin_9A_T_H10.ab1	gi|1061408|gb|AAB52963.1|	citrin	100	84	7E-41
Mjin_9A_T_H11.ab1	gi|157341869|emb|CAO63325.1|	unnamed protein product [Vitis vinifera]	58.88	107	1E-18
Mjin_9A_T_H12.ab1	gi|157360716|emb|CAO70315.1|	unnamed protein product [Vitis vinifera]	79.49	78	4E-29

Consensus Number	Accession No.	Definition of Putative homologue[Organism]	Matching %	Matching Length	E-value
Consensus10	gi|15485720|emb|CAC67501.1|	selenium binding protein [Medicago sativa]	84.56	136	2.0E-62
Consensus102	gi|147858960|emb|CAN80825.1|	hypothetical protein [Vitis vinifera]	76.07	163	2.0E-67
Consensus103	gi|118483621|gb|ABK93705.1|	unknown [Populus trichocarpa]	87.18	39	6E-13
Consensus104	gi|147775314|emb|CAN72509.1|	hypothetical protein [Vitis vinifera]	94.12	51	1E-19
Consensus105	gi|37932221|gb|AAP72960.1|	putative ribosomal protein L31 [Lactuca sativa]	90.91	121	1E-43
Consensus106	gi|119367477|gb|ABL67654.1|	putative H-type thioredoxin [Citrus cv. Shiranuhi]	100	119	1E-61
Consensus107	gi|15229784|ref|NP_189967.1|	CAM7 (CALMODULIN 7); calcium ion binding [Arabidopsis thaliana] >gi|27805429|sp|P59220|CALM7_ARATH RecName: Full=Calmodulin-7; Short=CaM-7 >gi|49037479|sp|P62199|CALM1_PETHY Calmodulin-1 (CaM-1) >gi|49037480|sp|P62200|CALM1_DAUCA Calmodulin-1/11/16 (CaM-1/11/16) >gi|49037481|sp|P62201|CALM_LILLO Calmodulin (CaM) >gi|49037482|sp|P62202|CALM_BRYDI Calmodulin (CaM) (BC329) >gi|62286560|sp|Q7Y052|CALM_EUPCH Calmodulin (CaM) >gi|5825598|gb|AAD53313.1|AF178073_1 calmodulin 7 [Arabidopsis thaliana] >gi|9992891|gb|AAG11418.1|AF292108_1 calmodulin [Prunus avium] >gi|21913285|gb|AAM81202.1|AF494219_1 calmodulin 1 [Medicago truncatula] >gi|18326|emb|CAA42423.1| calmodulin [Daucus carota] >gi|19447|emb|CAA78301.1| calmodulin [Lilium longiflorum] >gi|169207|gb|AAA33706.1| calmodulin >gi|308900|gb|AAA33397.1| calmodulin >gi|505154|emb|CAA43143.1| Calmodulin [Malus x domestica] >gi|535444|gb|AAA92681.1| calmodulin >gi|7362781|emb|CAB83153.1| calmodulin 7 [Arabidopsis thaliana] >gi|11036952|gb|AAG27432.1| calmodulin [Elaeis guineensis] >gi|14625405|dbj|BAB61909.1| calmodulin NtCaM3 [Nicotiana tabacum] >gi|14625407|dbj|BAB61910.1| calmodulin NtCaM4 [Nicotiana tabacum] >gi|14625409|dbj|BAB61911.1| calmodulin NtCaM5 [Nicotiana tabacum] >gi|14625411|dbj|BAB61912.1| calmodulin NtCaM6 [Nicotiana tabacum] >gi|14625413|dbj|BAB61913.1| calmodulin NtCaM7 [Nicotiana tabacum] >gi|14625415|dbj|BAB61914.1| calmodulin NtCaM8 [Nicotiana tabacum] >gi|14625421|dbj|BAB61917.1| calmodulin NtCaM11 [Nicotiana tabacum] >gi|14625423|dbj|BAB61918.1| calmodulin NtCaM12 [Nicotiana tabacum] >gi|21594484|gb|AAM66013.1| calmodulin 7 [Arabidopsis thaliana] >gi|40365136|gb|AAP55717.2| calmodulin [Euphorbia characias] >gi|45181612|gb|AAS55460.1| calmodulin cam-11 [Daucus carota] >gi|45181614|gb|AAS55461.1| calmodulin cam-16 [Daucus carota] >gi|50299503|gb|AAT73615.1| calmodulin cam-202 [Daucus carota] >gi|50299507|gb|AAT73617.1| calmodulin cam-204 [Daucus carota] >gi|50299515|gb|AAT73621.1| calmodulin cam-208 [Daucus carota] >gi|50299517|gb|AAT73622.1| calmodulin cam-209 [Daucus carota] >gi|52851162|emb|CAH58629.1| calmodulin [Plantago major] >gi|52851164|emb|CAH58630.1| calmodulin [Plantago major] >gi|60729719|emb|CAH57707.1| calmodulin [Quercus petraea] >gi|62125396|gb|AAX63770.1| calmodulin [Populus tomentosa] >gi|75756242|gb|ABA27138.1| calmodulin 2 [Catharanthus roseus] >gi|9896891|gb|ABF58929.1| At3g43810 [Arabidopsis thaliana] >gi|110742424|dbj|BAE99131.1| calmodulin 7 [Arabidopsis thaliana] >gi|118136471|gb|ABK62856.1| calmodulin [Scoparia dulcis] >gi|118481324|gb|ABK92605.1| unknown [Populus trichocarpa] >gi|118481354|gb|ABK92620.1| unknown [Populus trichocarpa] >gi|118481535|gb|ABK92710.1| unknown [Populus trichocarpa] >gi|118482590|gb|ABK93215.1| unknown [Populus trichocarpa] >gi|118483779|gb|ABK93782.1| unknown [Populus trichocarpa] >gi|118484140|gb|ABK93953.1| unknown [Populus trichocarpa] >gi|118484730|gb|ABK94234.1| unknown [Populus trichocarpa] >gi|118484977|gb|ABK94353.1| unknown [Populus trichocarpa] >gi|118485441|gb|ABK94577.1| unknown [Populus trichocarpa] >gi|118485636|gb|ABK94668.1| unknown [Populus trichocarpa] >gi|118485771|gb|ABK94734.1| unknown [Populus trichocarpa] >gi|118485950|gb|ABK94820.1| unknown [Populus trichocarpa] >gi|146403792|gb|ABQ32302.1| putative calmodulin [Artemisia annua] >gi|147837821|emb|CAN63123.1| hypothetical protein [Vitis vinifera] >gi|151500327|gb|ABS12105.1| calmodulin 1 [Morus nigra] >gi|157343285|emb|CAO67336.1| unnamed protein product [Vitis vinifera] >gi|189031544|gb|ACD74910.1| calmodulin [Vitis quinquangularis] >gi|192910746|gb|ACF06481.1| calmodulin 8 [Elaeis guineensis] >gi|192910748|gb|ACF06482.1| calmodulin 8 [Elaeis guineensis] >gi|192910750|gb|ACF06483.1| calmodulin 8 [Elaeis guineensis] >gi|192910752|gb|ACF06484.1| calmodulin 8 [Elaeis guineensis] >gi|197312869|gb|ACH63215.1| calmodulin [Rheum australe] >gi|445602|prf||1909349A calmodulin	100	149	3E-79

IP : 14.49.138.138, 2017-11-03 13:30:33

Consensus108	gi|118483548|gb|ABK93672.1|	unknown [Populus trichocarpa]	90.36	83	2E-36
Consensus109	gi|157344312|emb|CAO69245.1|	unnamed protein product [Vitis vinifera]	98.77	163	3E-73
Consensus110	gi|157358588|emb|CAO66264.1|	unnamed protein product [Vitis vinifera]	66.11	180	7.0E-42
Consensus111	gi|157335706|emb|CAO61536.1|	unnamed protein product [Vitis vinifera]	88.46	52	3.0E-20
Consensus112	gi|157343933|emb|CAO68866.1|	unnamed protein product [Vitis vinifera]	47.67	172	2.0E-31
Consensus113	gi|9626264|ref|NP_040600.1|	tail:host specificity protein [Enterobacteria phage lambda] >gi|138412|sp|P03749|VHSJ_LAMBD RecName: Full=Host specificity protein J >gi|215125|gb|AAA96553.1| J (tail:host specificity;1132) [Enterobacteria phage lambda]	100	255	1.0E-147
Consensus114	gi|118485826|gb|ABK94760.1|	unknown [Populus trichocarpa] >gi|118487675|gb|ABK95662.1| unknown [Populus trichocarpa] >gi|118489562|gb|ABK96583.1| unknown [Populus trichocarpa x Populus deltoides]	81.9	105	2.0E-44
Consensus115	gi|14596167|gb|AAK68811.1|	zinc finger-like protein [Arabidopsis thaliana] >gi|18377546|gb|AAL66939.1| zinc finger-like protein [Arabidopsis thaliana]	61.03	136	3.0E-30
Consensus116	gi|21063925|gb|AAM29152.1|	plastidic ATP/ADP transporter [Citrus hybrid cultivar]	100	57	2.0E-17
Consensus117	gi|186694325|gb|ACC86142.1|	heat shock protein 17.5 [Malus x domestica]	87.82	156	7.0E-57
Consensus118	gi|157355224|emb|CAO48600.1|	unnamed protein product [Vitis vinifera]	82.09	134	3.0E-50
Consensus119	gi|157336792|emb|CAO71477.1|	unnamed protein product [Vitis vinifera]	55.43	175	7.0E-45
Consensus12	gi|118488585|gb|ABK96105.1|	unknown [Populus trichocarpa]	91.95	149	1.0E-67
Consensus120	gi|147794105|emb|CAN62361.1|	hypothetical protein [Vitis vinifera] >gi|157327992|emb|CAO16962.1| unnamed protein product [Vitis vinifera]	74.45	227	3.0E-94
Consensus121	gi|157336956|emb|CAO21302.1|	unnamed protein product [Vitis vinifera]	82.8	186	2.0E-74
Consensus122	gi|147816254|emb|CAN77545.1|	hypothetical protein [Vitis vinifera]	86.03	179	4.0E-72
Consensus123	gi|147827198|emb|CAN70975.1|	hypothetical protein [Vitis vinifera]	71.07	121	3.0E-48
Consensus124	gi|99646724|emb|CAK22419.1|	B12D-like protein [Beta vulgaris]	87.95	83	2.0E-37
Consensus125	gi|186701247|gb|ACC91273.1|	putative beta-adaptin [Capsella rubella]	76.51	166	8.0E-72
Consensus127	gi|1351408|sp|P49043|VPE_CITSI	Vacuolar-processing enzyme precursor (VPE) >gi|633185|emb|CAA87720.1| cystein proteinase (by similarity) [Citrus sinensis] >gi|1588548|prf||2208463A vascular processing protease	99.6	494	0
Consensus128	gi|157355464|emb|CAO48854.1|	unnamed protein product [Vitis vinifera]	64.71	187	1E-55
Consensus129	gi|118481204|gb|ABK92553.1|	unknown [Populus trichocarpa] >gi|118482913|gb|ABK93370.1| unknown [Populus trichocarpa] >gi|133925835|gb|ABO43670.1| actin [Populus trichocarpa]	99.43	176	2E-95
Consensus130	gi|24473800|gb|AAL91665.1|	2s albumin [Anacardium occidentale]	51.45	138	4E-18
Consensus131	gi|15219950|ref|NP_173692.1|	PFL (POINTED FIRST LEAVES); structural constituent of ribosome [Arabidopsis thaliana] >gi|15234790|ref|NP_192718.1| RPS18C (S18 RIBOSOMAL PROTEIN); structural constituent of ribosome [Arabidopsis thaliana] >gi|18399100|ref|NP_564434.1| 40S ribosomal protein S18 (RPS18B) [Arabidopsis thaliana] >gi|464707|sp|P34788|RS18_ARATH RecName: Full=40S ribosomal protein S18 >gi|3287678|gb|AAC25506.1|AAC25506 Match to ribosomal S18 gene mRNA gb|Z28701, DNA gb|Z23165 from A. thaliana. ESTs gb|T21121, gb|Z17755, gb|R64776 and gb|R30430 come from this gene. [Arabidopsis thaliana] >gi|10086474|gb|AAG12534.1|AC015446_15 ribosomal protein S18 [Arabidopsis thaliana] >gi|10092450|gb|AAG12853.1|AC079286_10 40S ribosomal protein S18; 25853-24673 [Arabidopsis thaliana] >gi|14423408|gb|AAK62386.1|AF386941_1 S18.A ribosomal protein [Arabidopsis thaliana] >gi|15724158|gb|AAL06471.1|AF411781_1 At1g22780/T22J18_5 [Arabidopsis thaliana] >gi|405613|emb|CAA80684.1| ribosomal protein S18A [Arabidopsis thaliana] >gi|434343|emb|CAA82273.1| S18 ribosomal protein [Arabidopsis thaliana] >gi|434345|emb|CAA82274.1| S18 ribosomal protein [Arabidopsis thaliana] >gi|434906|emb|CAA82275.1| S18 ribosomal protein [Arabidopsis thaliana] >gi|2505871|emb|CAA72909.1| ribosomal protein S18A [Arabidopsis thaliana] >gi|4538910|emb|CAB39647.1| S18.A ribosomal protein [Arabidopsis thaliana] >gi|7267675|emb|CAB78103.1| S18.A ribosomal protein [Arabidopsis thaliana] >gi|14334584|gb|AAK59471.1| putative ribosomal protein S18 [Arabidopsis thaliana] >gi|17979113|gb|AAL47500.1| putative ribosomal protein S18 [Arabidopsis thaliana] >gi|21555397|gb|AAM63849.1| ribosomal protein S18, putative [Arabidopsis thaliana] >gi|21592452|gb|AAM64403.1| ribosomal protein S18, putative [Arabidopsis thaliana] >gi|21593027|gb|AAM64976.1| ribosomal protein S18, putative [Arabidopsis thaliana] >gi|30102858|gb|AAP21347.1| At4g09800 [Arabidopsis thaliana] >gi|56236126|gb|AAV84519.1| At1g22780 [Arabidopsis thaliana] >gi|98961089|gb|ABF59028.1| At1g22780 [Arabidopsis thaliana] >gi|145713244|gb|ABP96570.1| pointed first leaf [Arabidopsis thaliana] >gi|145713246|gb|ABP96571.1| pointed first leaf [Arabidopsis thaliana] >gi|145713248|gb|ABP96572.1| pointed first leaf [Arabidopsis thaliana] >gi|145713250|gb|ABP96573.1| pointed first leaf [Arabidopsis thaliana] >gi|145713252|gb|ABP96574.1| pointed first leaf [Arabidopsis thaliana] >gi|145713254|gb|ABP96575.1| pointed first leaf [Arabidopsis thaliana] >gi|145713256|gb|ABP96576.1| pointed first leaf [Arabidopsis thaliana] >gi|145713258|gb|ABP96577.1| pointed first leaf [Arabidopsis thaliana] >gi|145713260|gb|ABP96578.1| pointed first leaf [Arabidopsis thaliana] >gi|145713262|gb|ABP96579.1| pointed first leaf [Arabidopsis thaliana] >gi|145713264|gb|ABP96580.1| pointed first leaf [Arabidopsis thaliana] >gi|145713266|gb|ABP96581.1| pointed first leaf [Arabidopsis thaliana] >gi|145713268|gb|ABP96582.1| pointed first leaf [Arabidopsis thaliana] >gi|145713270|gb|ABP96583.1| pointed first leaf [Arabidopsis thaliana] >gi|145713272|gb|ABP96584.1| pointed first leaf [Arabidopsis thaliana] >gi|145713274|gb|ABP96585.1| pointed first leaf [Arabidopsis thaliana]	97.37	152	3E-71

IP : 14.49.138.138, 2017-11-03 13:30:33

		>gi|145713276|gb|ABP96586.1| pointed first leaf [Arabidopsis thaliana] >gi|145713278|gb|ABP96587.1| pointed first leaf [Arabidopsis thaliana] >gi|145713280|gb|ABP96588.1| pointed first leaf [Arabidopsis thaliana] >gi|145713282|gb|ABP96589.1| pointed first leaf [Arabidopsis thaliana] >gi|145713284|gb|ABP96590.1| pointed first leaf [Arabidopsis thaliana]			
Consensus132	gi|157359387|emb|CAO67548.1|	unnamed protein product [Vitis vinifera]	81.48	54	7E-19
Consensus133	gi|157344526|emb|CAO69909.1|	unnamed protein product [Vitis vinifera]	49.03	155	4E-36
Consensus134	gi|157346234|emb|CAO15931.1|	unnamed protein product [Vitis vinifera]	59.01	161	7E-46
Consensus135	gi|147816930|emb|CAN64392.1|	hypothetical protein [Vitis vinifera]	70.73	205	2E-73
Consensus136	gi|42565467|gb|AAS21001.1|	diadenosine tetraphosphate hydrolase [Hyacinthus orientalis]	74.26	136	3E-53
Consensus137	gi|115482580|ref|NP_001064883.1|	Os10g0483000 [Oryza sativa (japonica cultivar-group)] >gi|22094348|gb|AAM91875.1| putative transcription factor [Oryza sativa (japonica cultivar-group)] >gi|31432723|gb|AAP54321.1| Transcription factor BTF3, putative, expressed [Oryza sativa (japonica cultivar-group)] >gi|78708822|gb|ABB47797.1| Transcription factor BTF3, putative, expressed [Oryza sativa (japonica cultivar-group)] >gi|113639492|dbj|BAF26797.1| Os10g0483000 [Oryza sativa (japonica cultivar-group)]	91.27	126	1E-59
Consensus138	gi|2501850|gb|AAB80717.1|	GDP dissociation inhibitor [Nicotiana tabacum]	94.21	363	0
Consensus139	gi|147787459|emb|CAN60089.1|	hypothetical protein [Vitis vinifera]	61.69	154	2E-44
Consensus14	gi|147843797|emb|CAN79460.1|	hypothetical protein [Vitis vinifera]	79.05	105	2E-36
Consensus140	gi|118489566|gb|ABK96585.1|	unknown [Populus trichocarpa x Populus deltoides]	82.72	301	3E-137
Consensus141	gi|147838250|emb|CAN72267.1|	hypothetical protein [Vitis vinifera]	94	150	8E-82
Consensus142	gi|147865705|emb|CAN83263.1|	hypothetical protein [Vitis vinifera]	73.53	102	6E-40
Consensus143	gi|147839203|emb|CAN76920.1|	hypothetical protein [Vitis vinifera]	81.15	191	2E-83
Consensus144	gi|21311553|gb|AAM46777.1|AF466102_1	16.9 kDa oleosin [Theobroma cacao]	61.87	139	2E-28
Consensus146	gi|158564576|gb|ABW74476.1|	unknown [Paeonia suffruticosa]	57.89	190	3E-32
Consensus147	gi|115446173|ref|NP_001046866.1|	Os02g0489400 [Oryza sativa (japonica cultivar-group)] >gi|109940162|sp|P49199|RS8_ORYSJ RecName: Full=40S ribosomal protein S8 >gi|47848087|dbj|BAD21871.1| putative 40S ribosomal protein S8 [Oryza sativa Japonica Group] >gi|47848093|dbj|BAD21876.1| putative 40S ribosomal protein S8 [Oryza sativa Japonica Group] >gi|113536397|dbj|BAF08780.1| Os02g0489400 [Oryza sativa (japonica cultivar-group)]	94.59	74	2E-22
Consensus148	gi|157344080|emb|CAO69013.1|	unnamed protein product [Vitis vinifera]	81.46	151	2E-63
Consensus149	gi|118482922|gb|ABK93374.1|	unknown [Populus trichocarpa] >gi|118484750|gb|ABK94244.1| unknown [Populus trichocarpa]	92.62	122	2E-53
Consensus150	gi|118481723|gb|ABK92801.1|	unknown [Populus trichocarpa]	66.07	56	5E-13
Consensus151	gi|118482762|gb|ABK93299.1|	unknown [Populus trichocarpa] >gi|118483053|gb|ABK93436.1| unknown [Populus trichocarpa] >gi|118483119|gb|ABK93468.1| unknown [Populus trichocarpa] >gi|118483283|gb|ABK93544.1| unknown [Populus trichocarpa] >gi|118489714|gb|ABK96658.1| unknown [Populus trichocarpa x Populus deltoides]	95.73	164	5E-78
Consensus153	gi|4008159|dbj|BAA35121.1|	DnaJ homolog [Salix gilgiana]	92.94	170	5E-89
Consensus154	gi|48210049|gb|AAT40548.1|	Putative vicilin, identical [Solanum demissum]	65.22	184	1E-59
Consensus155	gi|157336132|emb|CAO61962.1|	unnamed protein product [Vitis vinifera]	71.98	182	6E-64
Consensus156	gi|115450713|ref|NP_001048957.1|	Os03g0146300 [Oryza sativa (japonica cultivar-group)] >gi|75127295|sp|Q6PS57|CKS1_ORYSJ RecName: Full=Cyclin-dependent kinases regulatory subunit 1 >gi|158512867|sp|A2XCH8|CKS1_ORYSI RecName: Full=Cyclin-dependent kinases regulatory subunit 1 >gi|15451612|gb|AAK98736.1|AC090485_15 Putative cyclin-dependent kinase regulatory subunit [Oryza sativa] >gi|46487749|gb|AAS99236.1| cyclin-dependent kinase subunit [Oryza sativa (japonica cultivar-group)] >gi|108706167|gb|ABF93962.1| cyclin-dependent kinases regulatory subunit, putative, expressed [Oryza sativa (japonica cultivar-group)] >gi|113547428|dbj|BAF10871.1| Os03g0146300 [Oryza sativa (japonica cultivar-group)] >gi|125542399|gb|EAY88538.1| hypothetical protein OsI_009771 [Oryza sativa (indica cultivar-group)] >gi|125584911|gb|EAZ25575.1| hypothetical protein OsJ_009058 [Oryza sativa (japonica cultivar-group)]	97.18	71	6E-35
Consensus157	gi|76559894|tpe|CAI56334.1|	TPA: isoflavone reductase-like protein 5 [Vitis vinifera]	85.35	157	2E-75
Consensus158	gi|157357936|emb|CAO64948.1|	unnamed protein product [Vitis vinifera]	80.62	227	6E-105
Consensus159	gi|147790060|emb|CAN75982.1|	hypothetical protein [Vitis vinifera] >gi|157336444|emb|CAO71129.1| unnamed protein product [Vitis vinifera]	97.2	143	8E-75
Consensus16	gi|147822222|emb|CAN63940.1|	hypothetical protein [Vitis vinifera] >gi|157358439|emb|CAO66099.1| unnamed	73.6	197	4E-83

IP : 14.49.138.138, 2017-11-03 13:30:33

		protein product [Vitis vinifera]			
Consensus160	gi|2822483|gb|AAC15418.1|	14-3-3 protein homolog [Maackia amurensis]	90.48	189	9E-86
Consensus161	gi|157338341|emb|CAO39385.1|	unnamed protein product [Vitis vinifera]	66.41	131	1E-33
Consensus162	gi|15234910|ref|NP_192742.1|	CYTC-2 (CYTOCHROME C-2); electron carrier [Arabidopsis thaliana] >gi|27734261|sp|Q9T0G2|CYC3_ARATH RecName: Full=Probable cytochrome c At4g10040 >gi|4539007|emb|CAB39628.1| cytochrome c [Arabidopsis thaliana] >gi|7267700|emb|CAB78127.1| cytochrome c [Arabidopsis thaliana] >gi|15028283|gb|AAK76618.1| putative cytochrome c protein [Arabidopsis thaliana] >gi|19310747|gb|AAL85104.1| putative cytochrome c protein [Arabidopsis thaliana] >gi|21592668|gb|AAM64617.1| cytochrome c [Arabidopsis thaliana]	95.54	112	2E-58
Consensus164	gi|147778109|emb|CAN69730.1|	hypothetical protein [Vitis vinifera]	80.23	258	7E-107
Consensus165	gi|118487777|gb|ABK95712.1|	unknown [Populus trichocarpa]	67.1	155	4E-54
Consensus168	gi|208964722|gb|ACI31551.1|	heat shock protein 90-2 [Glycine max]	93.68	174	6E-70
Consensus169	gi|1061408|gb|AAB52963.1|	citrin	73.35	484	3E-165
Consensus17	gi|42567801|ref|NP_568258.2|	dihydropyrimidinase / DHPase / dihydropyrimidine amidohydrolase / hydantoinase (PYD2) [Arabidopsis thaliana] >gi|28194047|gb|AAO33381.1|AF465755_1 dihydropyrimidine amidohydrolase [Arabidopsis thaliana] >gi|9759387|dbj|BAB10038.1| dihydropyrimidinase [Arabidopsis thaliana]	76.97	152	1E-61
Consensus170	gi|192338746|gb|ACF04278.1|	UTP-glucose 1 phosphate uridylyltransferase [Eucalyptus grandis]	86.36	66	2E-24
Consensus171	gi|157329340|emb|CAO39818.1|	unnamed protein product [Vitis vinifera]	72.81	217	8E-83
Consensus173	gi|157336826|emb|CAO71511.1|	unnamed protein product [Vitis vinifera]	56.72	67	9E-14
Consensus174	gi|7024449|dbj|BAA92155.1|	glycine-rich protein [Citrus unshiu]	100	35	6E-11
Consensus175	gi|147838438|emb|CAN63254.1|	hypothetical protein [Vitis vinifera]	71.79	117	6E-37
Consensus176	gi|157359341|emb|CAO67498.1|	unnamed protein product [Vitis vinifera]	97.37	190	2E-101
Consensus177	gi|288112|emb|CAA45621.1|	polyubiquitin [Petroselinum crispum] >gi|288114|emb|CAA45622.1| polyubiquitin [Petroselinum crispum]	100	306	1E-167
Consensus178	gi|147809367|emb|CAN64491.1|	hypothetical protein [Vitis vinifera]	78.69	183	2E-87
Consensus179	gi|195979199|gb|ACG63707.1|	transcription factor APETALA2 [Poncirus trifoliata]	99.5	199	2E-95
Consensus18	gi|6911553|emb|CAB72130.1|	heat shock protein 70 [Cucumis sativus]	80.12	166	5E-69
Consensus180	gi|157356328|emb|CAO62480.1|	unnamed protein product [Vitis vinifera]	71.79	117	1E-36
Consensus181	gi|147775908|emb|CAN71375.1|	hypothetical protein [Vitis vinifera]	85.48	310	1E-159
Consensus182	gi|15218420|ref|NP_177978.1|	RHM1/ROL1 (RHAMNOSE BIOSYNTHESIS1); UDP-L-rhamnose synthase/ UDP-glucose 4,6-dehydratase/ catalytic [Arabidopsis thaliana] >gi|62901057|sp|Q9SYM5|RHM1_ARATH RecName: Full=Probable rhamnose biosynthetic enzyme 1 >gi|4836876|gb|AAD30579.1|AC007260_10 Similar to dTDP-D-glucose 4,6-dehydratase [Arabidopsis thaliana] >gi|14596091|gb|AAK68773.1| Similar to dTDP-D-glucose 4,6-dehydratase [Arabidopsis thaliana] >gi|20148285|gb|AAM10033.1| similar to dTDP-D-glucose 4,6-dehydratase [Arabidopsis thaliana]	93.15	219	9E-117
Consensus183	gi|151547430|gb|ABS12459.1|	cysteine protease Cp [Citrus sinensis]	99.45	181	2E-93
Consensus185	gi|18404062|ref|NP_565836.1|	ubiquitin extension protein 2 (UBQ2) / 60S ribosomal protein L40 (RPL40A) [Arabidopsis thaliana] >gi|18409639|ref|NP_566969.1| UBQ1 (EARLY-RESPONSIVE TO DEHYDRATION 16, UBIQUITIN EXTENSION PROTEIN 1); protein binding [Arabidopsis thaliana] >gi|13430798|gb|AAK26021.1|AF360311_1 putative ubiquitin extension protein UBQ2 [Arabidopsis thaliana] >gi|166930|gb|AAA32904.1| ubiquitin extension protein (UBQ1) >gi|166932|gb|AAA32905.1| ubiquitin extension protein (UBQ2) >gi|4886268|emb|CAB43405.1| ubiquitin / ribosomal protein CEP52 [Arabidopsis thaliana] >gi|14334950|gb|AAK59652.1| putative ubiquitin extension protein UBQ1 [Arabidopsis thaliana] >gi|15810643|gb|AAL07246.1| putative ubiquitin extension protein UBQ2 [Arabidopsis thaliana] >gi|16323384|gb|AAL15186.1| putative ubiquitin extension protein UBQ1 [Arabidopsis thaliana] >gi|20198116|gb|AAM15407.1| ubiquitin extension protein (UBQ2) [Arabidopsis thaliana] >gi|21553955|gb|AAM63036.1| ubiquitin extension protein UBQ1 [Arabidopsis thaliana]	90.91	110	8E-51
Consensus186	gi|147780003|emb|CAN68893.1|	hypothetical protein [Vitis vinifera]	92.63	95	1E-46
Consensus187	gi|192910700|gb|ACF06458.1|	ADP ribosylation factor 002 [Elaeis guineensis]	100	171	2E-94
Consensus188	gi|7242493|emb|CAB77204.1|	urate oxidase [Cicer arietinum] >gi|7242495|emb|CAB77205.1| urate oxidase [Cicer arietinum]	80.61	165	2E-71

IP : 14.49.138.138, 2017-11-03 13:30:33

Consensus189	gi|122894104|gb|ABM67698.1|	mitogen-activated protein kinase [Citrus sinensis]	100	327	0
Consensus19	gi|187940281|gb|ACD39371.1|	NAC domain protein [Glycine max]	67.35	196	2E-67
Consensus190	gi|170507|gb|AAA34193.1|	ORF >gi|1172167|gb|AAA86424.1| heat shock protein	58.33	96	2E-18
Consensus191	gi|152032030|gb|ABS28874.1|	steroleosin-A [Arachis hypogaea] >gi|160373189|gb|ABX38844.1| steroleosin A [Arachis hypogaea]	59.47	264	4E-90
Consensus192	gi|118486081|gb|ABK94884.1|	unknown [Populus trichocarpa]	67.57	111	1E-32
Consensus193	gi|157350752|emb|CAO40843.1|	unnamed protein product [Vitis vinifera]	97.17	106	3E-56
Consensus194	gi|1061408|gb|AAB52963.1|	citrin	88.54	471	0
Consensus195	gi|157329488|emb|CAO40461.1|	unnamed protein product [Vitis vinifera] >gi|157329861|emb|CAO42765.1| unnamed protein product [Vitis vinifera]	71.43	70	3E-21
Consensus198	gi|108710978|gb|ABF98773.1|	Serine hydroxymethyltransferase, mitochondrial precursor, putative, expressed [Oryza sativa (japonica cultivar-group)]	80	85	1E-30
Consensus2	gi|8778823|gb|AAF79822.1|AC026875_2	T6D22.2 [Arabidopsis thaliana]	78.25	285	1E-114
Consensus20	gi|7406712|emb|CAB85635.1|	putative ripening-related P-450 enzyme [Vitis vinifera]	57.53	219	2E-70
Consensus201	gi|157350818|emb|CAO40933.1|	unnamed protein product [Vitis vinifera]	66.67	240	2E-82
Consensus202	gi|2463569|dbj|BAA22559.1|	squalene synthase [Glycine max]	90.91	132	5E-67
Consensus203	gi|77812440|gb|ABB03801.1|	ADP ribosylation factor 002 [Daucus carota] >gi|118482447|gb|ABK93146.1| unknown [Populus trichocarpa] >gi|118482485|gb|ABK93165.1| unknown [Populus trichocarpa]	100	181	6E-100
Consensus205	gi|12659208|gb|AAK01236.1|AF327623_1	minor allergen hazelnut profilin [Corylus avellana]	93.88	98	4.0E-48
Consensus206	gi|147810156|emb|CAN71454.1|	hypothetical protein [Vitis vinifera]	87.5	152	7.0E-75
Consensus207	gi|158323772|gb|ABW34390.1|	glutathione S-transferase 5 [Vitis vinifera]	75.23	214	2.0E-93
Consensus208	gi|31745704|gb|AAP56259.1|	dehydrin [Citrus sinensis]	98.45	193	1.0E-57
Consensus209	gi|22138108|gb|AAM93434.1|	40S ribosomal S4 protein [Glycine max]	95.95	173	3.0E-94
Consensus21	gi|147771931|emb|CAN77946.1|	hypothetical protein [Vitis vinifera] >gi|157353272|emb|CAO45195.1| unnamed protein product [Vitis vinifera]	97.97	148	3.0E-82
Consensus210	gi|157347768|emb|CAO22224.1|	unnamed protein product [Vitis vinifera]	90.11	91	4.0E-42
Consensus211	gi|147788379|emb|CAN76662.1|	hypothetical protein [Vitis vinifera] >gi|157335113|emb|CAO60943.1| unnamed protein product [Vitis vinifera]	92.41	158	3.0E-71
Consensus213	gi|23506611|gb|AAN37904.1|	histone H1D [Nicotiana tabacum]	79.25	53	1.0E-17
Consensus214	gi|157352236|emb|CAO43264.1|	unnamed protein product [Vitis vinifera]	84.62	182	6.0E-88
Consensus215	gi|125538883|gb|EAY85278.1|	hypothetical protein OsI_006511 [Oryza sativa (indica cultivar-group)]	97.3	148	1.0E-81
Consensus216	gi|19352190|dbj|BAB85987.1|	Acyl-CoA-binding protein [Panax ginseng]	94.19	86	8.0E-40
Consensus217	gi|118489542|gb|ABK96573.1|	unknown [Populus trichocarpa x Populus deltoides]	87.58	153	5.0E-64
Consensus218	gi|4903139|dbj|BAA77836.1|	CiFT [Citrus unshiu]	98.64	147	2.0E-71
Consensus219	gi|157336548|emb|CAO71233.1|	unnamed protein product [Vitis vinifera]	82.91	158	4.0E-74
Consensus22	gi|145334215|ref|NP_001078488.1|	unknown protein [Arabidopsis thaliana] >gi|3549657|emb|CAA20568.1| putative protein [Arabidopsis thaliana] >gi|7270303|emb|CAB80072.1| putative protein [Arabidopsis thaliana]	48.35	91	7.0E-15
Consensus220	gi|157344386|emb|CAO69769.1|	unnamed protein product [Vitis vinifera]	77.63	219	1.0E-84
Consensus221	gi|18401177|ref|NP_566555.1|	RALFL23 (RALF-LIKE 23) [Arabidopsis thaliana] >gi|11994611|dbj|BAB02748.1| unnamed protein product [Arabidopsis thaliana] >gi|15081817|gb|AAK82563.1| AT3g16570/MGL6_2 [Arabidopsis thaliana] >gi|18252281|gb|AAL62021.1| AT3g16570/MGL6_2 [Arabidopsis thaliana] >gi|21536821|gb|AAM61153.1| unknown [Arabidopsis thaliana]	85.48	62	3.0E-24
Consensus222	gi|157346154|emb|CAO15851.1|	unnamed protein product [Vitis vinifera]	65	100	5.0E-18
Consensus223	gi|118482893|gb|ABK93361.1|	unknown [Populus trichocarpa]	48.91	184	1.0E-14
Consensus224	gi|188509981|gb|ACD56663.1|	putative ribosomal protein [Gossypium arboreum]	96.85	127	4.0E-55
Consensus225	gi|159505446|gb|ABW97699.1|	putative bHLH transcription factor [Citrus sinensis]	98.71	155	8.0E-41
Consensus226	gi|15223001|ref|NP_172256.1|	RPS15A (RIBOSOMAL PROTEIN S15A); structural constituent of ribosome [Arabidopsis thaliana] >gi|15238544|ref|NP_200793.1| 40S ribosomal protein S15A (RPS15aF) [Arabidopsis thaliana] >gi|42571385|ref|NP_973783.1| RPS15A (RIBOSOMAL PROTEIN S15A); structural constituent of ribosome [Arabidopsis thaliana] >gi|1173218|sp|P42798|R15A1_ARATH 40S ribosomal protein S15a-1	97.69	130	1.0E-67

IP : 14.49.138.138, 2017-11-03 13:30:33

		>gi|8439890|gb|AAF75076.1|AC007583_12 Strong similarity to 40S ribosomal protein S15A from Arabidopsis thaliana gb|L27461. EST gb|R30315 comes from this gene >gi|12083302|gb|AAG48810.1|AF332447_1 putative ribosomal protein S15 [Arabidopsis thaliana] >gi|13430744|gb|AAK25994.1|AF360284_1 putative ribosomal protein S15 [Arabidopsis thaliana] >gi|14423370|gb|AAK62367.1|AF386922_1 40S ribosomal protein S15A [Arabidopsis thaliana] >gi|440824|gb|AAA61608.1| ribosomal protein S15 >gi|2150130|gb|AAB58750.1| cytoplasmic ribosomal protein S15a [Arabidopsis thaliana] >gi|9757906|dbj|BAB08353.1| 40S ribosomal protein S15A [Arabidopsis thaliana] >gi|14334968|gb|AAK59661.1| putative cytoplasmic ribosomal protein S15a [Arabidopsis thaliana] >gi|14596085|gb|AAK68770.1| Putative 40S ribosomal protein S15A [Arabidopsis thaliana] >gi|15293213|gb|AAK93717.1| putative ribosomal protein S15 [Arabidopsis thaliana] >gi|17104627|gb|AAL34202.1| putative cytoplasmic ribosomal protein S15a [Arabidopsis thaliana] >gi|20148287|gb|AAM10034.1| similar to 40S ribosomal protein S15A [Arabidopsis thaliana] >gi|20148721|gb|AAM10251.1| similar to 40S ribosomal protein S15A [Arabidopsis thaliana] >gi|21593169|gb|AAM65118.1| cytoplasmic ribosomal protein S15a-like [Arabidopsis thaliana] >gi|21593909|gb|AAM65874.1| cytoplasmic ribosomal protein S15a-like [Arabidopsis thaliana] >gi|23397065|gb|AAN31818.1| putative cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]			
Consensus227	gi|18398038|ref|NP_566316.1|	kelch repeat-containing protein [Arabidopsis thaliana] >gi|6466955|gb|AAF13090.1|AC009176_17 unknown protein [Arabidopsis thaliana] >gi|6648184|gb|AAF21182.1|AC013483_6 unknown protein [Arabidopsis thaliana] >gi|11692832|gb|AAG40019.1|AF324668_1 MLP3.17 [Arabidopsis thaliana] >gi|11993873|gb|AAG42920.1|AF329503_1 unknown protein [Arabidopsis thaliana] >gi|14517448|gb|AAK62614.1| AT3g07720/F17A17_6 [Arabidopsis thaliana] >gi|21280883|gb|AAM44920.1| unknown protein [Arabidopsis thaliana] >gi|23507767|gb|AAN38687.1| At3g07720/F17A17_6 [Arabidopsis thaliana]	73.17	41	4.0E-11
Consensus228	gi|6094476|sp|O23787|THI4_CITSI	RecName: Full=Thiazole biosynthetic enzyme, chloroplastic; Flags: Precursor >gi|2582665|emb|CAB05370.1| thi [Citrus sinensis]	100	130	2.0E-65
Consensus23	gi|118485403|gb|ABK94558.1|	unknown [Populus trichocarpa]	83.02	106	4.0E-40
Consensus231	gi|157340053|emb|CAO45730.1|	unnamed protein product [Vitis vinifera]	85.23	149	7.0E-72
Consensus232	gi|116078097|dbj|BAF34912.1|	MADS-box protein [Citrus unshiu]	94.61	241	1.0E-123
Consensus233	gi|111218904|gb|ABH08753.1|	ubiquitin [Arabidopsis thaliana]	99.36	156	1.0E-80
Consensus234	gi|147812549|emb|CAN77331.1|	hypothetical protein [Vitis vinifera]	76.52	132	6.0E-57
Consensus235	gi|118482686|gb|ABK93262.1|	unknown [Populus trichocarpa]	87.5	160	4.0E-57
Consensus236	gi|24473800|gb|AAL91665.1|	2s albumin [Anacardium occidentale]	52.17	138	1.0E-18
Consensus237	gi|6573171|gb|AAF17578.1|AF202184_1	isoflavone reductase homolog 2 [Glycine max]	79.45	73	2.0E-25
Consensus238	gi|118483361|gb|ABK93582.1|	unknown [Populus trichocarpa]	89.54	239	5.0E-99
Consensus239	gi|157344960|emb|CAO71688.1|	unnamed protein product [Vitis vinifera]	59.12	159	1.0E-25
Consensus24	gi|157358842|emb|CAO66722.1|	unnamed protein product [Vitis vinifera]	58.82	170	7.0E-43
Consensus240	gi|157781823|gb|ABV72237.1|	caleosin [Ficus pumila var. awkeotsang]	81.58	190	5.0E-90
Consensus241	gi|15222613|ref|NP_173923.1|	unknown protein [Arabidopsis thaliana] >gi|12321501|gb|AAG50804.1|AC079281_6 transmembrane protein, putative [Arabidopsis thaliana] >gi|27754432|gb|AAO22664.1| putative transmembrane protein [Arabidopsis thaliana] >gi|28394045|gb|AAO42430.1| putative transmembrane protein [Arabidopsis thaliana]	77.78	198	2.0E-81
Consensus242	gi|157353657|emb|CAO46181.1|	unnamed protein product [Vitis vinifera]	66.42	137	4.0E-48
Consensus243	gi|1169534|sp|P42896|ENO_RICCO	RecName: Full=Enolase; AltName: Full=2-phosphoglycerate dehydratase; AltName: Full=2-phospho-D-glycerate hydro-lyase >gi|433609|emb|CAA82232.1| enolase [Ricinus communis]	88.89	162	1.0E-78
Consensus244	gi|147839972|emb|CAN61687.1|	hypothetical protein [Vitis vinifera] >gi|157351323|emb|CAO41510.1| unnamed protein product [Vitis vinifera]	79.82	228	8.0E-110
Consensus245	gi|157351143|emb|CAO41330.1|	unnamed protein product [Vitis vinifera]	86.56	320	1.0E-132
Consensus246	gi|10798652|emb|CAC12826.1|	malate dehydrogenase [Nicotiana tabacum]	94.42	233	1.0E-121
Consensus247	gi|15241359|ref|NP_199917.1|	unknown protein [Arabidopsis thaliana] >gi|9758251|dbj|BAB08750.1| unnamed protein product [Arabidopsis thaliana] >gi|9960953|gb|ABF58960.1| At5g51040 [Arabidopsis thaliana] >gi|110738284|dbj|BAF01071.1| hypothetical protein [Arabidopsis thaliana]	77.08	48	3.0E-16
Consensus248	gi|163929884|dbj|BAF95941.1|	SEPALLATA1 homolog [Citrus unshiu]	100	108	1.0E-57
Consensus249	gi|147858860|emb|CAN78689.1|	hypothetical protein [Vitis vinifera]	71.08	83	2.0E-21
Consensus250	gi|15241727|ref|NP_201026.1|	embryo-specific protein-related [Arabidopsis thaliana] >gi|38603856|gb|AAR24673.1| At5g62200 [Arabidopsis thaliana] >gi|51968404|dbj|BAD42894.1| unknown protein [Arabidopsis thaliana] >gi|51970212|dbj|BAD43798.1| unknown protein [Arabidopsis thaliana]	63.75	80	3.0E-24
Consensus251	gi|119367479|gb|ABL67655.1|	putative cyclophilin [Citrus cv. Shiranuhi]	98.37	123	6.0E-58
Consensus252	gi|145334271|ref|NP_001078516.1|	histone H3.2 [Arabidopsis thaliana]	99.21	127	4.0E-64

IP : 14.49.138.138, 2017-11-03 13:30:33

Consensus253	gi|118484599|gb|ABK94173.1|	unknown [Populus trichocarpa]	79.41	68	8.0E-26
Consensus254	gi|157342373|emb|CAO64486.1|	unnamed protein product [Vitis vinifera]	69.57	138	6.0E-47
Consensus255	gi|157338270|emb|CAO39314.1|	unnamed protein product [Vitis vinifera]	91.56	225	5.0E-119
Consensus257	gi|118481085|gb|ABK92496.1|	unknown [Populus trichocarpa] >gi|118481952|gb|ABK92908.1| unknown [Populus trichocarpa] >gi|118481968|gb|ABK92915.1| unknown [Populus trichocarpa] >gi|118485439|gb|ABK94576.1| unknown [Populus trichocarpa]	81.44	291	7.0E-146
Consensus258	gi|157338993|emb|CAO42344.1|	unnamed protein product [Vitis vinifera]	45.45	132	6.0E-12
Consensus259	gi|147854340|emb|CAN83423.1|	hypothetical protein [Vitis vinifera]	80	125	2.0E-42
Consensus26	gi|118483152|gb|ABK93482.1|	unknown [Populus trichocarpa]	88.71	62	2.0E-22
Consensus260	gi|15234987|ref|NP_192765.1|	wound-responsive family protein [Arabidopsis thaliana] >gi|3695408|gb|AAC62808.1| contains similarity to Solanum lycopersicum (tomato) wound-induced protein (GB:X59882) [Arabidopsis thaliana] >gi|4538956|emb|CAB39780.1| probable wound-induced protein [Arabidopsis thaliana] >gi|7267724|emb|CAB78150.1| probable wound-induced protein [Arabidopsis thaliana] >gi|21553934|gb|AAM63015.1| probable wound-induced protein [Arabidopsis thaliana] >gi|90962948|gb|ABE02398.1| At4g10270 [Arabidopsis thaliana]	51.85	81	6.0E-14
Consensus261	gi|205364122|gb|ACI04518.1|	translationally controlled tumor protein [Hevea brasiliensis]	94.05	168	4.0E-75
Consensus262	gi|124484511|dbj|BAF46352.1|	alpha chain of nascent polypeptide associated complex [Nicotiana benthamiana]	88.82	152	4.0E-59
Consensus263	gi|115449893|ref|NP_001048577.1|	Os02g0824700 [Oryza sativa (japonica cultivar-group)] >gi|48717094|dbj|BAD22867.1| putative Vacuolar ATP synthase subunit F [Oryza sativa Japonica Group] >gi|113538108|dbj|BAF10491.1| Os02g0824700 [Oryza sativa (japonica cultivar-group)] >gi|125547097|gb|EAY92919.1| hypothetical protein OsI_014152 [Oryza sativa (indica cultivar-group)] >gi|125589239|gb|EAZ29589.1| hypothetical protein OsJ_013072 [Oryza sativa (japonica cultivar-group)]	84.62	130	1.0E-54
Consensus264	gi|157338672|emb|CAO42023.1|	unnamed protein product [Vitis vinifera]	50.57	176	2.0E-36
Consensus265	gi|157358430|emb|CAO66090.1|	unnamed protein product [Vitis vinifera]	79.11	158	7.0E-63
Consensus266	gi|74486736|gb|ABA12221.1|	translation elongation factor 1A-5 [Gossypium hirsutum]	97.25	436	0.0E+0
Consensus267	gi|7381207|gb|AAF61436.1|AF137353_1	lipid transfer protein precursor [Pisum sativum]	57.95	88	1.0E-25
Consensus27	gi|147858412|emb|CAN83511.1|	hypothetical protein [Vitis vinifera]	74.59	244	1.0E-91
Consensus270	gi|47716659|gb|AAT37529.1|	purple acid phosphatase 1 [Solanum tuberosum]	65.72	318	3.0E-122
Consensus28	gi|156900676|gb|ABU96744.1|	chloroplast acyl-ACP thioesterase [Jatropha curcas]	64.29	70	2.0E-13
Consensus29	gi|40646966|gb|AAQ19680.1|	chloroplast small heat shock protein class I [Capsicum frutescens]	76.73	159	1.0E-55
Consensus3	gi|157356762|emb|CAO62964.1|	unnamed protein product [Vitis vinifera]	65.79	190	1.0E-63
Consensus30	gi|145333578|ref|NP_001078417.1|	unknown protein [Arabidopsis thaliana] >gi|145333595|ref|NP_001078418.1| unknown protein [Arabidopsis thaliana] >gi|11074950|dbj|BAE99808.1| hypothetical protein [Arabidopsis thaliana]	86.67	60	4.0E-26
Consensus31	gi|212960264|gb|ACJ38662.1|	actin [Betula luminifera]	100	219	4.0E-123
Consensus32	gi|14422444|dbj|BAB60848.1|	BURP domain-containing protein [Bruguiera gymnorrhiza]	64.32	199	6.0E-51
Consensus33	gi|147790682|emb|CAN61026.1|	hypothetical protein [Vitis vinifera]	84.76	328	1.0E-158
Consensus34	gi|119367470|gb|ABL67651.1|	putative auxin-repressed/dormancy-associated protein [Citrus cv. Shiranuhi]	97.54	122	2.0E-50
Consensus35	gi|94958151|gb|ABF47216.1|	cathepsin B [Nicotiana benthamiana]	64.78	159	5.0E-54
Consensus36	gi|157345721|emb|CAO15019.1|	unnamed protein product [Vitis vinifera]	45.66	219	8.0E-32
Consensus37	gi|171451994|dbj|BAG15861.1|	hypothetical protein [Bruguiera gymnorhiza]	82.86	35	6.0E-11
Consensus38	gi|147845872|emb|CAN82178.1|	hypothetical protein [Vitis vinifera]	92.86	168	2.0E-90
Consensus39	gi|85068596|gb|ABC69378.1|	CYP81B2v1 [Nicotiana tabacum] >gi|158635852|dbj|BAF91366.1| cytochrome P450 [Nicotiana tabacum]	55.21	192	3.0E-58
Consensus4	gi|147795381|emb|CAN67602.1|	hypothetical protein [Vitis vinifera]	95.28	127	3.0E-65
Consensus40	gi|147854126|emb|CAN83419.1|	hypothetical protein [Vitis vinifera]	75.47	53	3.0E-14
Consensus41	gi|75171219|sp|Q9FKA5|Y5957_ARATH	Uncharacterized protein At5g39570 >gi|9758332|dbj|BAB08888.1| unnamed protein product [Arabidopsis thaliana] >gi|16604364|gb|AAL24188.1| AT5g39570/MIJ24_40 [Arabidopsis thaliana] >gi|23308191|gb|AAN18065.1| At5g39570/MIJ24_40 [Arabidopsis thaliana]	66.15	65	2.0E-18

IP : 14.49.138.138, 2017-11-03 13:30:33

Consensus44	gi|157336417|emb|CAO71102.1|	unnamed protein product [Vitis vinifera]	65.52	87	2.0E-26
Consensus45	gi|148372097|gb|ABQ62980.1|	TINY-like protein [Populus trichocarpa]	61.86	118	2.0E-17
Consensus46	gi|15239967|ref|NP_196805.1|	EMB3011 (EMBRYO DEFECTIVE 3011); RNA helicase [Arabidopsis thaliana] >gi|7630057|emb|CAB88265.1| pre-mRNA splicing factor ATP-dependent RNA helicase-like protein [Arabidopsis thaliana]	90.53	243	4.0E-123
Consensus47	gi|95925785|gb|ABF57559.1|	OleI [Camellia oleifera]	65.94	138	2.0E-21
Consensus48	gi|157352981|emb|CAO44871.1|	unnamed protein product [Vitis vinifera]	82.75	284	8.0E-129
Consensus49	gi|157352996|emb|CAO44886.1|	unnamed protein product [Vitis vinifera]	82.22	315	2.0E-158
Consensus5	gi|35186896|gb|AAQ84111.1|	Clt1 [Poncirus trifoliata]	90.38	52	3.0E-20
Consensus50	gi|18424977|ref|NP_569016.1|	hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] >gi|75180377|sp|Q9LSK9|Y5566_ARATH RecName: Full=Uncharacterized protein At5g65660 >gi|8978294|dbj|BAA98185.1| unnamed protein product [Arabidopsis thaliana] >gi|21554387|gb|AAM63494.1| unknown [Arabidopsis thaliana] >gi|30102568|gb|AAP21202.1| At5g65660 [Arabidopsis thaliana] >gi|110743764|dbj|BAE99718.1| hypothetical protein [Arabidopsis thaliana]	70.07	137	3.0E-46
Consensus51	gi|157348920|emb|CAO23998.1|	unnamed protein product [Vitis vinifera]	92.59	216	2.0E-120
Consensus52	gi|147811710|emb|CAN72669.1|	hypothetical protein [Vitis vinifera]	80	110	6.0E-44
Consensus53	gi|157335805|emb|CAO61635.1|	unnamed protein product [Vitis vinifera]	45.77	201	8.0E-29
Consensus55	gi|157340035|emb|CAO45712.1|	unnamed protein product [Vitis vinifera]	73.44	305	2.0E-124
Consensus56	gi|147834848|emb|CAN68309.1|	hypothetical protein [Vitis vinifera]	89.83	59	3.0E-23
Consensus57	gi|1346735|sp|P35493|PMGI_RICCO	RecName: Full=2,3-bisphosphoglycerate-independent phosphoglycerate mutase; Short=BPG-independent PGAM; Short=Phosphoglyceromutase; AltName: Full=PGAM-I >gi|474170|emb|CAA49995.1| phosphoglycerate mutase [Ricinus communis]	81.07	169	2.0E-78
Consensus58	gi|2501187|sp|Q38709|THI4_ALNGL	RecName: Full=Thiazole biosynthetic enzyme, chloroplastic; AltName: Full=AG6; Flags: Precursor >gi|1289204|emb|CAA66064.1| thaizole biosynthetic enzmye [Alnus glutinosa]	100	45	5.0E-18
Consensus59	gi|118482787|gb|ABK93311.1|	unknown [Populus trichocarpa] >gi|118485213|gb|ABK94467.1| unknown [Populus trichocarpa] >gi|118487438|gb|ABK95547.1| unknown [Populus trichocarpa]	66.97	109	1.0E-27
Consensus60	gi|683553|emb|CAA88360.1|	oleosin-like protein [Citrus sinensis] >gi|1582679|prf||2119230A oleosin homolog	97.73	132	2.0E-58
Consensus61	gi|157350923|emb|CAO41038.1|	unnamed protein product [Vitis vinifera]	90.79	76	9.0E-33
Consensus62	gi|118486471|gb|ABK95075.1|	unknown [Populus trichocarpa]	73.02	189	6.0E-74
Consensus63	gi|12321311|gb|AAG50732.1|AC079041_25	30S ribosomal protein S11, putative [Arabidopsis thaliana]	70.73	82	3.0E-27
Consensus64	gi|18416995|ref|NP_567775.1|	unknown protein [Arabidopsis thaliana] >gi|14030723|gb|AAK53036.1|AF375452_1 AT4g27450/F27G19_50 [Arabidopsis thaliana] >gi|15028057|gb|AAK76559.1| unknown protein [Arabidopsis thaliana] >gi|20259059|gb|AAM14245.1| unknown protein [Arabidopsis thaliana] >gi|21593019|gb|AAM64968.1| unknown [Arabidopsis thaliana]	84.11	214	1.0E-102
Consensus65	gi|147838864|emb|CAN61394.1|	hypothetical protein [Vitis vinifera]	55.4	213	1.0E-50
Consensus66	gi|1360725|emb|CAA87068.1|	non-photosynthetic ferredoxin [Citrus sinensis]	97.33	150	9.0E-79
Consensus67	gi|147800891|emb|CAN75568.1|	hypothetical protein [Vitis vinifera] >gi|157335268|emb|CAO61098.1| unnamed protein product [Vitis vinifera]	99.66	292	2.0E-162
Consensus68	gi|118482499|gb|ABK93172.1|	unknown [Populus trichocarpa]	85.44	103	7.0E-32
Consensus69	gi|157342912|emb|CAO65624.1|	unnamed protein product [Vitis vinifera]	73.87	111	2.0E-34
Consensus7	gi|4836473|gb|AAD30454.1|AF123257_1	17.6 kD class I small heat shock protein [Lycopersicon esculentum] >gi|24954791|gb|AAN64315.1| type I small heat shock protein 17.6 kDa isoform [Lycopersicon esculentum]	76.62	154	9.0E-33
Consensus70	gi|3308980|dbj|BAA31561.1|	metallothionein-like protein [Citrus unshiu]	100	40	7.0E-14
Consensus71	gi|118481263|gb|ABK92579.1|	unknown [Populus trichocarpa] >gi|118489027|gb|ABK96321.1| unknown [Populus trichocarpa x Populus deltoides]	90.58	138	6.0E-66
Consensus72	gi|157336230|emb|CAO70915.1|	unnamed protein product [Vitis vinifera]	78.01	141	3.0E-47
Consensus73	gi|157338183|emb|CAO39227.1|	unnamed protein product [Vitis vinifera]	80.08	241	1.0E-99
Consensus74	gi|147809687|emb|CAN73348.1|	hypothetical protein [Vitis vinifera] >gi|157345578|emb|CAO14876.1| unnamed protein product [Vitis vinifera]	88.68	159	5.0E-80
Consensus75	gi|157352524|emb|CAO43630.1|	unnamed protein product [Vitis vinifera]	74.76	103	2.0E-36
Consensus76	gi|157335195|emb|CAO61025.1|	unnamed protein product [Vitis vinifera]	63.59	206	1.0E-71
Consensus77	gi|147815376|emb|CAN74416.1|	hypothetical protein [Vitis vinifera]	75.37	203	3.0E-90

IP : 14.49.138.138, 2017-11-03 13:30:33

Consensus78	gi|8099682|gb|AAF72202.1|AF265551_1	cysteine protease inhibitor [Manihot esculenta]	62.63	99	7.0E-25
Consensus79	gi|157358030|emb|CAO65068.1|	unnamed protein product [Vitis vinifera]	86.88	282	1.0E-130
Consensus8	gi|114324485|gb|ABI63585.1|	biotin synthase [Brassica rapa subsp. pekinensis]	88.38	198	7.0E-103
Consensus80	gi|5257560|gb|AAD41409.1|AF159562_1	cytosolic class II low molecular weight heat shock protein [Prunus dulcis]	57.69	156	3.0E-42
Consensus82	gi|147840877|emb|CAN73187.1|	hypothetical protein [Vitis vinifera]	82.22	135	2.0E-44
Consensus83	gi|147778657|emb|CAN62897.1|	hypothetical protein [Vitis vinifera]	93.98	216	1.0E-116
Consensus84	gi|87201358|gb|AAX07458.2|	ethylene-responsive element binding protein ERF2 [Gossypium hirsutum]	47.2	125	2.0E-15
Consensus85	gi|15242248|ref|NP_197636.1|	60S ribosomal protein L10A (RPL10aC) [Arabidopsis thaliana] >gi|145334533|ref|NP_001078612.1| 60S ribosomal protein L10A (RPL10aC) [Arabidopsis thaliana] >gi|27923990|sp|P59231|R10A3_ARATH 60S ribosomal protein L10a-3 >gi|9757825|dbj|BAB08343.1| 60S ribosomal protein L10A [Arabidopsis thaliana] >gi|14335148|gb|AAK59854.1| AT5g22440/MWD9_24 [Arabidopsis thaliana] >gi|18655359|gb|AAL76135.1| AT5g22440/MWD9_24 [Arabidopsis thaliana]	92.49	213	2.0E-97
Consensus86	gi|188509919|gb|ACD56608.1|	putative protein disulfide [Gossypioides kirkii]	82.35	136	4.0E-62
Consensus87	gi|116265932|gb|ABJ91214.1|	CBL-interacting protein kinase 7 [Populus trichocarpa] >gi|116265934|gb|ABJ91215.1| CBL-interacting protein kinase 8 [Populus trichocarpa]	89.55	134	6.0E-53
Consensus88	gi|9988412|dbj|BAB12722.1|	gamma tonoplast intrinsic protein [Pyrus communis]	86.84	114	2.0E-39
Consensus89	gi|119367485|gb|ABL67657.1|	putative copper chaperone [Citrus cv. Shiranuhi]	98.86	88	4.0E-42
Consensus9	gi|157349972|emb|CAO39871.1|	unnamed protein product [Vitis vinifera]	65.84	161	3.0E-50
Consensus90	gi|12830830|gb|AAK08208.1|AF320905_1	metallothionein-like protein [Citrus unshiu] >gi|12830832|gb|AAK08209.1|AF320906_1 metallothionein-like protein [Citrus unshiu] >gi|3308982|dbj|BAA31562.1| metallothionein-like protein [Citrus unshiu] >gi|158936952|dbj|BAF91493.1| metallothionein type 3 [Citrus unshiu]	100	68	7.0E-35
Consensus92	gi|7441288|pir||T10253	membrane protein MP28 - cucurbit >gi|1109614|dbj|BAA08108.1| MP28 [Cucurbita cv. Kurokawa Amakuri]	68.87	151	1.0E-42
Consensus93	gi|78191410|gb|ABB29926.1|	fructose-bisphosphate aldolase-like [Solanum tuberosum]	94.52	219	4.0E-116
Consensus94	gi|147789144|emb|CAN60339.1|	hypothetical protein [Vitis vinifera]	76.39	216	8.0E-92
Consensus95	gi|157337910|emb|CAO38954.1|	unnamed protein product [Vitis vinifera]	74.11	112	5.0E-43
Consensus96	gi|118481986|gb|ABK92924.1|	unknown [Populus trichocarpa]	81.23	293	3.0E-142
Consensus97	gi|118486725|gb|ABK95198.1|	unknown [Populus trichocarpa] >gi|118487202|gb|ABK95429.1| unknown [Populus trichocarpa]	83.23	167	5.0E-79
Consensus98	gi|10334840|gb|AAG15415.1|	seed maturation protein [Glycine tabacina]	55.93	118	1.0E-29
Consensus99	gi|22653808|sp|Q39644|LEA5_CITSI	Late embryogenesis abundant protein Lea5 >gi|599726|emb|CAA86851.1| Lea5 protein [Citrus sinensis]	98.97	97	5.0E-47

8) 지각 미숙과실

Clone No.	Accession No.	Definition of Putative homologue[Organism]	Matching %	Matching Length	E-value
CAI_1A_TripleX5_A03	gi|224090181|ref|XP_002308949.1|	predicted protein [Populus trichocarpa] >gi|222854925|gb|EEE92472.1| predicted protein [Populus trichocarpa]	68.57	210	5e-72
CAI_1A_TripleX5_A04	gi|255578691|ref|XP_002530205.1|	glutathione-s-transferase theta, gst, putative [Ricinus communis] >gi|223530281|gb|EEF32179.1| glutathione-s-transferase theta, gst, putative [Ricinus communis]	73.27	101	6e-38
CAI_1A_TripleX5_A07	gi|225463817|ref|XP_002271306.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|147820518|emb|CAN76575.1| hypothetical protein [Vitis vinifera]	60.33	121	3e-33
CAI_1A_TripleX5_B01	gi|960291|gb|AAA74901.1|	anthranilate synthase alpha subunit [Ruta graveolens]	83.26	233	3e-110
CAI_1A_TripleX5_B02	gi|225458800|ref|XP_002285206.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|147785069|emb|CAN62217.1| hypothetical protein [Vitis vinifera] >gi|270252811|emb|CBI19422.1| unnamed protein product [Vitis vinifera]	89.74	78	6e-36
CAI_1A_TripleX5_B03	gi|255557172|ref|XP_002519617.1|	protein translocase, putative [Ricinus communis] >gi|223541207|gb|EEF42762.1| protein translocase, putative [Ricinus communis]	68.85	260	4e-52
CAI_1A_TripleX5_B08	gi|255559398|ref|XP_002520719.1|	40S ribosomal protein S18, putative [Ricinus communis] >gi|223540104|gb|EEF41681.1| 40S ribosomal protein S18, putative [Ricinus communis]	96.71	152	4e-70
CAI_1A_TripleX5_B09	gi|255587054|ref|XP_002534116.1|	protein farnesyltransferase alpha subunit, putative [Ricinus communis] >gi|223525828|gb|EEF28267.1| protein farnesyltransferase alpha subunit, putative [Ricinus communis]	63.96	111	1e-37

IP : 14.49.138.138, 2017-11-03 13:30:33

CAI_1A_TriplEX5_B10	gi|224125608|ref|XP_002319630.1|	predicted protein [Populus trichocarpa] >gi|222858006|gb|EEE95553.1| predicted protein [Populus trichocarpa]	50.99	202	5e-41
CAI_1A_TriplEX5_B12	gi|211906490|gb|ACJ11738.1|	malate dehydrogenase [Gossypium hirsutum]	96.25	267	2e-137
CAI_1A_TriplEX5_C04	gi|224128015|ref|XP_002329233.1|	predicted protein [Populus trichocarpa] >gi|222871014|gb|EEF08145.1| predicted protein [Populus trichocarpa]	81.4	258	2e-111
CAI_1A_TriplEX5_C05	gi|224089721|ref|XP_002308803.1|	predicted protein [Populus trichocarpa] >gi|118482707|gb|ABK93272.1| unknown [Populus trichocarpa] >gi|118483785|gb|ABK93785.1| unknown [Populus trichocarpa] >gi|222854779|gb|EEE92326.1| predicted protein [Populus trichocarpa]	90.48	105	2e-49
CAI_1A_TriplEX5_C06	gi|255565105|ref|XP_002523545.1|	conserved hypothetical protein [Ricinus communis] >gi|223537252|gb|EEF38884.1| conserved hypothetical protein [Ricinus communis]	60.71	84	1e-19
CAI_1A_TriplEX5_C11	gi|224082550|ref|XP_002306738.1|	predicted protein [Populus trichocarpa] >gi|222856187|gb|EEE93734.1| predicted protein [Populus trichocarpa]	32.06	262	3e-17
CAI_1A_TriplEX5_D03	gi|224088689|ref|XP_002308514.1|	predicted protein [Populus trichocarpa] >gi|222854490|gb|EEE92037.1| predicted protein [Populus trichocarpa]	69.44	108	5e-36
CAI_1A_TriplEX5_E03	gi|224060423|ref|XP_002300192.1|	predicted protein [Populus trichocarpa] >gi|118482123|gb|ABK92992.1| unknown [Populus trichocarpa] >gi|222847450|gb|EEE84997.1| predicted protein [Populus trichocarpa]	95.82	239	4e-104
CAI_1A_TriplEX5_E04	gi|224140647|ref|XP_002323693.1|	predicted protein [Populus trichocarpa] >gi|222868323|gb|EEF05454.1| predicted protein [Populus trichocarpa]	61.11	162	5e-52
CAI_1A_TriplEX5_E07	gi|255568460|ref|XP_002525204.1|	glutathione-s-transferase omega, putative [Ricinus communis] >gi|223535501|gb|EEF37170.1| glutathione-s-transferase omega, putative [Ricinus communis]	77.31	238	7e-107
CAI_1A_TriplEX5_E10	gi|147798444|emb|CAN67908.1|	hypothetical protein [Vitis vinifera]	80.45	179	4e-79
CAI_1A_TriplEX5_F01	gi|224108357|ref|XP_002314819.1|	predicted protein [Populus trichocarpa] >gi|222863859|gb|EEF00990.1| predicted protein [Populus trichocarpa]	68.21	195	2e-68
CAI_1A_TriplEX5_F04	gi|224117120|ref|XP_002317481.1|	aminotransferase family protein [Populus trichocarpa] >gi|222860546|gb|EEE98093.1| aminotransferase family protein [Populus trichocarpa]	81.4	301	3e-133
CAI_1A_TriplEX5_F07	gi|147769055|emb|CAN72018.1|	hypothetical protein [Vitis vinifera]	90	40	4e-12
CAI_1A_TriplEX5_F08	gi|225462908|ref|XP_002264571.1|	PREDICTED: hypothetical protein isoform 1 [Vitis vinifera] >gi|270258053|emb|CBI40092.1| unnamed protein product [Vitis vinifera]	76.44	191	9e-79
CAI_1A_TriplEX5_F09	gi|163929884|dbj|BAF95941.1|	SEPALLATA1 homolog [Citrus unshiu]	98.08	52	6e-24
CAI_1A_TriplEX5_G01	gi|118482052|gb|ABK92957.1|	unknown [Populus trichocarpa]	97	100	2e-38
CAI_1A_TriplEX5_G05	gi|255583933|ref|XP_002532714.1|	conserved hypothetical protein [Ricinus communis] >gi|223527541|gb|EEF29663.1| conserved hypothetical protein [Ricinus communis]	55.65	230	9e-52
CAI_1A_TriplEX5_G08	gi|255579087|ref|XP_002530392.1|	conserved hypothetical protein [Ricinus communis] >gi|223530078|gb|EEF31998.1| conserved hypothetical protein [Ricinus communis]	74.82	278	3e-104
CAI_1A_TriplEX5_G10	gi|224068735|ref|XP_002302812.1|	predicted protein [Populus trichocarpa] >gi|222844538|gb|EEE82085.1| predicted protein [Populus trichocarpa]	78.75	80	4e-31
CAI_1A_TriplEX5_G11	gi|114329665|ref|YP_740484.1|	acetyl-CoA carboxylase carboxyltransferase beta subunit [Citrus sinensis] >gi|122166174|sp|Q09MG9|ACCD_CITSI RecName: Full=Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta, chloroplastic; Short=Acetyl-CoA carboxylase carboxyltransferase subunit beta; Short=ACCase subunit beta >gi|113952631|gb|ABI49029.1| acetyl-CoA carboxylase carboxyltransferase beta subunit [Citrus sinensis]	100	74	2e-38
CAI_1A_TriplEX5_G12	gi|255573101|ref|XP_002527480.1|	conserved hypothetical protein [Ricinus communis] >gi|223533120|gb|EEF34878.1| conserved hypothetical protein [Ricinus communis]	35.79	271	5e-36
CAI_1A_TriplEX5_H07	gi|18423805|ref|NP_568832.1|	emb2731 (embryo defective 2731) [Arabidopsis thaliana] >gi|18202899|sp|Q9FG71|U172_ARATH RecName: Full=UPF0172 protein At5g55940; AltName: Full=Protein EMBRYO DEFECTIVE 2731 >gi|9758214|dbj|BAB08659.1| unnamed protein product [Arabidopsis thaliana] >gi|18086571|gb|AAL57709.1| AT5g55940/MYN21_5 [Arabidopsis thaliana] >gi|21689597|gb|AAM67420.1| AT5g55940/MYN21_5 [Arabidopsis thaliana] >gi|110741034|dbj|BAE98611.1| hypothetical protein [Arabidopsis thaliana]	77.61	201	2e-80
CAI_1A_TriplEX5_H11	gi|255628065|gb|ACU14377.1|	unknown [Glycine max]	88.51	87	2e-43
CAI_1B_5SP_A03	gi|224119132|ref|XP_002317993.1|	predicted protein [Populus trichocarpa] >gi|222858666|gb|EEE96213.1| predicted protein [Populus trichocarpa]	77.34	278	1e-125
CAI_1B_5SP_A07	gi|122894106|gb|ABM67699.1|	NAC domain protein [Citrus sinensis]	91.94	62	1e-27
CAI_1B_5SP_A12	gi|114329641|ref|YP_740460.1|	ATP synthase CF1 alpha subunit [Citrus sinensis] >gi|122166198|sp|Q09MJ3|ATPA_CITSI RecName: Full=ATP synthase subunit alpha, chloroplastic; AltName: Full=F-ATPase subunit alpha; AltName: Full=ATP synthase F1 sector subunit alpha >gi|113952607|gb|ABI49005.1| ATP synthase CF1 alpha subunit [Citrus sinensis]	100	89	4e-31
CAI_1B_5SP_B01	gi|224090173|ref|XP_002308948.1|	predicted protein [Populus trichocarpa] >gi|222854924|gb|EEE92471.1| predicted protein [Populus trichocarpa]	75.94	212	2e-91
CAI_1B_5SP_B02	gi|255563790|ref|XP_002522896.1|	conserved hypothetical protein [Ricinus communis] >gi|223537881|gb|EEF39496.1| conserved hypothetical protein [Ricinus communis]	56.57	99	6e-25
CAI_1B_5SP_B05	gi|225469185|ref|XP_002275624.1|	PREDICTED: hypothetical protein [Vitis vinifera]	80.36	224	7e-79
CAI_1B_5SP_B06	gi|224075453|ref|XP_002304640.1|	AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222842072|gb|EEE79619.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	62.5	184	9e-40

IP : 14.49.138.138, 2017-11-03 13:30:33

CAI_1B_5SP_B10	gi|255578538|ref|XP_002530132.1|	Heme-binding protein, putative [Ricinus communis] >gi|223530357|gb|EEF32248.1| Heme-binding protein, putative [Ricinus communis]	78.31	189	2e-81
CAI_1B_5SP_C08	gi|13603408|dbj|BAB40974.1|	isopentenyl diphosphate isomerase 2 [Nicotiana tabacum]	91.24	194	2e-99
CAI_1B_5SP_C09	gi|151347490|gb|ABS01354.1|	translation initiation factor [Carica papaya]	95.6	159	4e-84
CAI_1B_5SP_C11	gi|110740644|dbj|BAE98425.1|	hypothetical protein [Arabidopsis thaliana]	95.35	43	4e-18
CAI_1B_5SP_D01	gi|270251971|emb|CBI35336.1|	unnamed protein product [Vitis vinifera]	62.79	215	2e-69
CAI_1B_5SP_D02	gi|224134565|ref|XP_002321854.1|	predicted protein [Populus trichocarpa] >gi|222868850|gb|EEF05981.1| predicted protein [Populus trichocarpa]	63.41	123	5e-29
CAI_1B_5SP_D07	gi|147843847|emb|CAN79450.1|	hypothetical protein [Vitis vinifera]	80.46	87	3e-31
CAI_1B_5SP_D12	gi|257196367|gb|ACV49920.1|	ubiquitin-conjugating enzyme variant [Citrus sinensis]	98.63	146	8e-78
CAI_1B_5SP_E01	gi|77999293|gb|ABB16993.1|	unknown [Solanum tuberosum]	100	142	3e-76
CAI_1B_5SP_E05	gi|255556366|ref|XP_002519217.1|	conserved hypothetical protein [Ricinus communis] >gi|223541532|gb|EEF43081.1| conserved hypothetical protein [Ricinus communis]	82.32	164	1e-74
CAI_1B_5SP_E07	gi|225430261|ref|XP_002285072.1|	PREDICTED: hypothetical protein [Vitis vinifera]	91.48	270	1e-134
CAI_1B_5SP_E10	gi|255573806|ref|XP_002527822.1|	Squamous cell carcinoma antigen recognized by T-cells, putative [Ricinus communis] >gi|223532746|gb|EEF34525.1| Squamous cell carcinoma antigen recognized by T-cells, putative [Ricinus communis]	77.27	44	6e-11
CAI_1B_5SP_F07	gi|225425529|ref|XP_002264590.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270241301|emb|CBI28525.1| unnamed protein product [Vitis vinifera]	63.91	230	4e-78
CAI_1B_5SP_F10	gi|225456624|ref|XP_002266530.1|	PREDICTED: hypothetical protein [Vitis vinifera]	77.97	118	2e-46
CAI_1B_5SP_G01	gi|217073804|gb|ACJ85262.1|	unknown [Medicago truncatula]	95.59	68	6e-30
CAI_1B_5SP_G02	gi|149941196|emb|CAO02530.1|	putative 23S ribosomal RNA [Vigna unguiculata]	100	51	9e-23
CAI_1B_5SP_G04	gi|224091134|ref|XP_002309192.1|	thioredoxin h [Populus trichocarpa] >gi|118482588|gb|ABK93214.1| unknown [Populus trichocarpa] >gi|222855168|gb|EEE92715.1| thioredoxin h [Populus trichocarpa]	74.1	139	3e-56
CAI_1B_5SP_G05	gi|224137706|ref|XP_002327192.1|	predicted protein [Populus trichocarpa] >gi|222835507|gb|EEE73942.1| predicted protein [Populus trichocarpa]	84.06	69	5e-32
CAI_1B_5SP_G09	gi|224077760|ref|XP_002305397.1|	predicted protein [Populus trichocarpa] >gi|222848361|gb|EEE85908.1| predicted protein [Populus trichocarpa]	92.31	143	2e-73
CAI_1B_5SP_G10	gi|224128087|ref|XP_002329078.1|	predicted protein [Populus trichocarpa] >gi|118484386|gb|ABK94070.1| unknown [Populus trichocarpa] >gi|222869747|gb|EEF06878.1| predicted protein [Populus trichocarpa]	82.98	282	5e-113
CAI_1B_5SP_G11	gi|224058639|ref|XP_002299579.1|	cytochrome P450 [Populus trichocarpa] >gi|222846837|gb|EEE84384.1| cytochrome P450 [Populus trichocarpa]	57.92	259	4e-83
CAI_1B_5SP_H02	gi|224090803|ref|XP_002309088.1|	predicted protein [Populus trichocarpa] >gi|222855064|gb|EEE92611.1| predicted protein [Populus trichocarpa]	90.87	208	1e-100
CAI_1B_5SP_H03	gi|255571107|ref|XP_002526504.1|	protein with unknown function [Ricinus communis] >gi|223534179|gb|EEF35895.1| protein with unknown function [Ricinus communis]	97.6	208	1e-100
CAI_1B_5SP_H05	gi|255563224|ref|XP_002522615.1|	pentatricopeptide repeat-containing protein, putative [Ricinus communis] >gi|223538091|gb|EEF39702.1| pentatricopeptide repeat-containing protein, putative [Ricinus communis]	65.19	293	8e-89
CAI_1B_5SP_H08	gi|225470769|ref|XP_002268078.1|	PREDICTED: hypothetical protein [Vitis vinifera]	90.6	117	7e-57
CAI_1B_5SP_H09	gi|255548433|ref|XP_002515273.1|	ATP-dependent Clp protease proteolytic subunit, putative [Ricinus communis] >gi|223545753|gb|EEF47257.1| ATP-dependent Clp protease proteolytic subunit, putative [Ricinus communis]	81.07	206	3e-88
CAI_1C_5SP_A01	gi|115487294|ref|NP_001066134.1|	Os12g0143100 [Oryza sativa (japonica cultivar-group)] >gi|77553656|gb|ABA96452.1| GRF zinc finger family protein [Oryza sativa (japonica cultivar-group)]	88.75	80	4e-35
CAI_1C_5SP_A02	gi|225452304|ref|XP_002272292.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270251473|emb|CBI34846.1| unnamed protein product [Vitis vinifera]	83.27	257	2e-123
CAI_1C_5SP_B01	gi|118482830|gb|ABK93331.1|	unknown [Populus trichocarpa]	93.62	47	4e-18
CAI_1C_5SP_B04	gi|225432280|ref|XP_002272645.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270238829|emb|CBI26065.1| unnamed protein product [Vitis vinifera]	61.38	189	2e-47
CAI_1C_5SP_B08	gi|83628260|gb|ABC26010.1|	9-cis-epoxycarotenoid dioxygenase 5 [Citrus clementina]	99.62	265	6e-152
CAI_1C_5SP_C03	gi|224098612|ref|XP_002311223.1|	predicted protein [Populus trichocarpa] >gi|222851043|gb|EEE88590.1| predicted protein [Populus trichocarpa]	86.3	146	1e-71
CAI_1C_5SP_C06	gi|147794982|emb|CAN71764.1|	hypothetical protein [Vitis vinifera]	70.3	101	2e-33
CAI_1C_5SP_C10	gi|255575782|ref|XP_002528790.1|	protein binding protein, putative [Ricinus communis] >gi|223531793|gb|EEF33612.1| protein binding protein, putative [Ricinus communis]	57.25	138	3e-29
CAI_1C_5SP_C12	gi|224112110|ref|XP_002316086.1|	predicted protein [Populus trichocarpa] >gi|222865126|gb|EEF02257.1| predicted protein [Populus trichocarpa]	88.32	274	8e-142
CAI_1C_5SP_D01	gi|224103687|ref|XP_002313154.1|	predicted protein [Populus trichocarpa] >gi|222849562|gb|EEE87109.1| predicted protein [Populus trichocarpa]	68.49	73	1e-23
CAI_1C_5SP_	gi|147820291|emb|CAN7147	hypothetical protein [Vitis vinifera]	82.54	126	2e-51

IP : 14.49.138.138, 2017-11-03 13:30:33

D02	0.1|				
CAI_1C_5SP_D03	gi|114329693|ref|YP_740514.1|	ribosomal protein S3 [Citrus sinensis] >gi|122166145|sp|Q09MD9|RR3_CITSI RecName: Full=30S ribosomal protein S3, chloroplastic >gi|113952659|gb|ABI49057.1| ribosomal protein S3 [Citrus sinensis]	100	165	1e-87
CAI_1C_5SP_D05	gi|119367488|gb|ABL67658.1|	putative multiple stress-responsive zinc-finger protein [Citrus hybrid cultivar]	96.49	171	3e-85
CAI_1C_5SP_D09	gi|255553454|ref|XP_002517768.1|	conserved hypothetical protein [Ricinus communis] >gi|223543040|gb|EEF44575.1| conserved hypothetical protein [Ricinus communis]	77.06	279	3e-95
CAI_1C_5SP_D10	gi|225440638|ref|XP_002278975.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270243477|emb|CBI30417.1| unnamed protein product [Vitis vinifera]	95.24	252	2e-134
CAI_1C_5SP_E02	gi|255547962|ref|XP_002515038.1|	chaperonin containing t-complex protein 1, epsilon subunit, tcpe, putative [Ricinus communis] >gi|223546089|gb|EEF47592.1| chaperonin containing t-complex protein 1, epsilon subunit, tcpe, putative [Ricinus communis]	91.67	216	2e-107
CAI_1C_5SP_E03	gi|225432304|ref|XP_002273548.1|	PREDICTED: hypothetical protein isoform 2 [Vitis vinifera] >gi|225432306|ref|XP_002273516.1| PREDICTED: hypothetical protein isoform 1 [Vitis vinifera] >gi|147862660|emb|CAN83594.1| hypothetical protein [Vitis vinifera] >gi|270238839|emb|CBI26075.1| unnamed protein product [Vitis vinifera]	91.36	81	1e-37
CAI_1C_5SP_E06	gi|225425366|ref|XP_002270179.1|	PREDICTED: hypothetical protein [Vitis vinifera]	58.46	195	4e-43
CAI_1C_5SP_E11	gi|11596186|gb|AAG38521.1|AF283536_1	cystatin-like protein [Citrus x paradisi]	100	118	2e-62
CAI_1C_5SP_F01	gi|255577891|ref|XP_002529818.1|	alcohol dehydrogenase, putative [Ricinus communis] >gi|223530695|gb|EEF32567.1| alcohol dehydrogenase, putative [Ricinus communis]	80.07	291	1e-137
CAI_1C_5SP_F02	gi|224080967|ref|XP_002306247.1|	predicted protein [Populus trichocarpa] >gi|222855696|gb|EEE93243.1| predicted protein [Populus trichocarpa]	83.62	116	5e-52
CAI_1C_5SP_F05	gi|15239401|ref|NP_197918.1|	unknown protein [Arabidopsis thaliana] >gi|28973729|gb|AAO64181.1| unknown protein [Arabidopsis thaliana] >gi|29824197|gb|AAP04059.1| unknown protein [Arabidopsis thaliana] >gi|110736786|dbj|BAF00354.1| hypothetical protein [Arabidopsis thaliana]	63.96	111	2e-33
CAI_1C_5SP_F09	gi|224126083|ref|XP_002319751.1|	predicted protein [Populus trichocarpa] >gi|118484516|gb|ABK94133.1| unknown [Populus trichocarpa] >gi|222858127|gb|EEE95674.1| predicted protein [Populus trichocarpa]	78.57	56	3e-16
CAI_1C_5SP_F10	gi|255560725|ref|XP_002521376.1|	dead box ATP-dependent RNA helicase, putative [Ricinus communis] >gi|223539454|gb|EEF41044.1| dead box ATP-dependent RNA helicase, putative [Ricinus communis]	96.85	254	1e-136
CAI_1C_5SP_G03	gi|225424114|ref|XP_002282753.1|	PREDICTED: hypothetical protein [Vitis vinifera]	87.22	266	8e-129
CAI_1C_5SP_G05	gi|224064398|ref|XP_002301456.1|	predicted protein [Populus trichocarpa] >gi|222843182|gb|EEE80729.1| predicted protein [Populus trichocarpa]	76.56	64	8e-24
CAI_1C_5SP_H09	gi|29423617|gb|AAO73433.1|	vacuolar membrane ATPase subunit c'' [Citrus limon]	100	181	2e-85
CAI_1C_5SP_H10	gi|255536943|ref|XP_002509538.1|	conserved hypothetical protein [Ricinus communis] >gi|223549437|gb|EEF50925.1| conserved hypothetical protein [Ricinus communis]	60.33	242	2e-71
CAI_1C_5SP_H12	gi|224061141|ref|XP_002300356.1|	predicted protein [Populus trichocarpa] >gi|222847614|gb|EEE85161.1| predicted protein [Populus trichocarpa]	77.5	80	9e-16
CAI_1D_5SP_A05	gi|224116330|ref|XP_002317271.1|	predicted protein [Populus trichocarpa] >gi|222860336|gb|EEE97883.1| predicted protein [Populus trichocarpa]	76.52	247	3e-106
CAI_1D_5SP_A06	gi|224100821|ref|XP_002312026.1|	predicted protein [Populus trichocarpa] >gi|222851846|gb|EEE89393.1| predicted protein [Populus trichocarpa]	76.74	258	2e-86
CAI_1D_5SP_A09	gi|90991006|dbj|BAE92957.1|	carotenoid cleavage dioxygenase1 [Citrus unshiu] >gi|90991010|dbj|BAE92959.1| carotenoid cleavage dioxygenase1 [Citrus limon]	98.55	275	5e-160
CAI_1D_5SP_A11	gi|225431285|ref|XP_002275719.1|	PREDICTED: hypothetical protein [Vitis vinifera]	81.5	200	5e-95
CAI_1D_5SP_B01	gi|118485826|gb|ABK94760.1|	unknown [Populus trichocarpa] >gi|118487675|gb|ABK95662.1| unknown [Populus trichocarpa] >gi|118489562|gb|ABK96583.1| unknown [Populus trichocarpa x Populus deltoides]	81.9	105	1e-44
CAI_1D_5SP_B02	gi|224103849|ref|XP_002313218.1|	predicted protein [Populus trichocarpa] >gi|222849626|gb|EEE87173.1| predicted protein [Populus trichocarpa]	74.9	243	2e-91
CAI_1D_5SP_B04	gi|255582148|ref|XP_002531868.1|	glutathione-s-transferase theta, gst, putative [Ricinus communis] >gi|223528476|gb|EEF30505.1| glutathione-s-transferase theta, gst, putative [Ricinus communis]	73.33	210	3e-85
CAI_1D_5SP_B06	gi|147777746|emb|CAN60302.1|	hypothetical protein [Vitis vinifera]	57.53	73	2e-13
CAI_1D_5SP_B10	gi|225435255|ref|XP_002285011.1|	PREDICTED: hypothetical protein isoform 1 [Vitis vinifera] >gi|225435257|ref|XP_002285012.1| PREDICTED: hypothetical protein isoform 2 [Vitis vinifera] >gi|270227551|emb|CBI16284.1| unnamed protein product [Vitis vinifera]	83.15	89	3e-14
CAI_1D_5SP_C03	gi|225440057|ref|XP_002282270.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270247397|emb|CBI32772.1| unnamed protein product [Vitis vinifera]	83.84	99	1e-49
CAI_1D_5SP_C05	gi|255536969|ref|XP_002509551.1|	conserved hypothetical protein [Ricinus communis] >gi|223549450|gb|EEF50938.1| conserved hypothetical protein [Ricinus communis]	81.37	102	3e-40
CAI_1D_5SP_C06	gi|255545146|ref|XP_002513634.1|	NADH dehydrogenase, putative [Ricinus communis] >gi|223547542|gb|EEF49037.1| NADH dehydrogenase, putative [Ricinus communis]	87.5	168	7e-79
CAI_1D_5SP_C08	gi|224122518|ref|XP_002330501.1|	predicted protein [Populus trichocarpa] >gi|222872435|gb|EEF09566.1| predicted protein [Populus trichocarpa]	80.37	326	1e-146
CAI_1D_5SP_C11	gi|255542742|ref|XP_002512434.1|	26S protease regulatory subunit 6a, putative [Ricinus communis] >gi|223548395|gb|EEF49886.1| 26S protease regulatory subunit 6a, putative [Ricinus	95.95	296	3e-159

IP : 14.49.138.138, 2017-11-03 13:30:33

		communis]			
CAI_1D_5SP_D02	gi|125532450|gb|EAY79015.1|	hypothetical protein OsI_34124 [Oryza sativa Indica Group] >gi|125575223|gb|EAZ16507.1| hypothetical protein OsJ_31979 [Oryza sativa Japonica Group]	92	75	3e-18
CAI_1D_5SP_E02	gi|225442553|ref|XP_002279009.1|	PREDICTED: hypothetical protein [Vitis vinifera]	56.28	247	2e-62
CAI_1D_5SP_E07	gi|224057724|ref|XP_002299302.1|	predicted protein [Populus trichocarpa] >gi|118481338|gb|ABK92612.1| unknown [Populus trichocarpa] >gi|222846560|gb|EEE84107.1| predicted protein [Populus trichocarpa]	86.21	87	7e-40
CAI_1D_5SP_E11	gi|225440831|ref|XP_002282071.1|	PREDICTED: similar to ubiquitin fusion protein [Vitis vinifera] >gi|255578906|ref|XP_002530306.1| ubiquitin, putative [Ricinus communis] >gi|255578975|ref|XP_002530340.1| ubiquitin, putative [Ricinus communis] >gi|71040673|gb|AAZ20285.1| ubiquitin fusion protein [Arachis hypogaea] >gi|147769165|emb|CAN60770.1| hypothetical protein [Vitis vinifera] >gi|148908659|gb|ABR17437.1| unknown [Picea sitchensis] >gi|192910738|gb|ACF06477.1| ubiquitin fusion protein [Elaeis guineensis] >gi|223530144|gb|EEF32056.1| ubiquitin, putative [Ricinus communis] >gi|223530162|gb|EEF32073.1| ubiquitin, putative [Ricinus communis] >gi|270243382|emb|CBI30322.1| unnamed protein product [Vitis vinifera]	100	128	1e-67
CAI_1D_5SP_F02	gi|147857446|emb|CAN78649.1|	hypothetical protein [Vitis vinifera]	41.75	103	1e-13
CAI_1D_5SP_F05	gi|255627787|gb|ACU14238.1|	unknown [Glycine max]	87.69	65	5e-11
CAI_1D_5SP_F10	gi|10834829|gb|AAG23841.1|AF302808_1	metallothionein-like protein [Sesamum indicum] >gi|40732882|gb|AAR88997.1| seed-specific metallothionein-like protein [Sesamum indicum]	69.14	81	7e-21
CAI_1D_5SP_G05	gi|255580868|ref|XP_002531253.1|	conserved hypothetical protein [Ricinus communis] >gi|223529138|gb|EEF31117.1| conserved hypothetical protein [Ricinus communis]	73.52	253	6e-92
CAI_1D_5SP_G08	gi|147667132|gb|ABQ45848.1|	beta-1,3-glucanase [Citrus unshiu]	90.41	73	4e-32
CAI_1D_5SP_H02	gi|224108403|ref|XP_002314835.1|	predicted protein [Populus trichocarpa] >gi|222863875|gb|EEF01006.1| predicted protein [Populus trichocarpa]	58.82	187	8e-25
CAI_1D_5SP_H03	gi|224091044|ref|XP_002309157.1|	predicted protein [Populus trichocarpa] >gi|222855133|gb|EEE92680.1| predicted protein [Populus trichocarpa]	77.65	170	2e-75
CAI_2A_5SP_A02	gi|233955417|gb|ACQ91204.1|	truncated hemoglobin [Carica papaya]	85.8	169	4e-81
CAI_2A_5SP_A04	gi|224101747|ref|XP_002312405.1|	predicted protein [Populus trichocarpa] >gi|222852225|gb|EEE89772.1| predicted protein [Populus trichocarpa]	75	76	6e-28
CAI_2A_5SP_A05	gi|147833901|emb|CAN66492.1|	hypothetical protein [Vitis vinifera]	95.65	46	1e-19
CAI_2A_5SP_B01	gi|225464130|ref|XP_002264979.1|	PREDICTED: similar to NFU4 (NFU domain protein 4) [Vitis vinifera]	77.27	242	2e-100
CAI_2A_5SP_B03	gi|224121522|ref|XP_002330721.1|	predicted protein [Populus trichocarpa] >gi|8515890|gb|AAF76227.1|AF272573_1 14-3-3 protein [Populus tremula x Populus alba] >gi|222872497|gb|EEF09628.1| predicted protein [Populus trichocarpa]	87.35	253	1e-120
CAI_2A_5SP_B06	gi|225453078|ref|XP_002270339.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270248446|emb|CBI33578.1| unnamed protein product [Vitis vinifera]	76.52	115	3e-41
CAI_2A_5SP_B07	gi|270235577|emb|CBI24704.1|	unnamed protein product [Vitis vinifera]	86.33	300	3e-139
CAI_2A_5SP_B12	gi|224082818|ref|XP_002306852.1|	predicted protein [Populus trichocarpa] >gi|222856301|gb|EEE93848.1| predicted protein [Populus trichocarpa]	71.71	205	1e-77
CAI_2A_5SP_C01	gi|255571119|ref|XP_002526510.1|	uridylate kinase plant, putative [Ricinus communis] >gi|223534185|gb|EEF35901.1| uridylate kinase plant, putative [Ricinus communis]	88.11	185	2e-87
CAI_2A_5SP_C02	gi|224083811|ref|XP_002307132.1|	predicted protein [Populus trichocarpa] >gi|224096326|ref|XP_002310604.1| predicted protein [Populus trichocarpa] >gi|222853507|gb|EEE91054.1| predicted protein [Populus trichocarpa] >gi|222856581|gb|EEE94128.1| predicted protein [Populus trichocarpa]	96.38	138	8e-70
CAI_2A_5SP_C08	gi|224056258|ref|XP_002298779.1|	predicted protein [Populus trichocarpa] >gi|222846037|gb|EEE83584.1| predicted protein [Populus trichocarpa]	95.43	175	4e-92
CAI_2A_5SP_C11	gi|270258263|emb|CBI40297.1|	unnamed protein product [Vitis vinifera]	66.67	291	3e-103
CAI_2A_5SP_C12	gi|158828372|gb|ABW81204.1|	alcohol acyl transferase [Citrus sinensis]	89.63	164	8e-74
CAI_2A_5SP_D04	gi|224096318|ref|XP_002310603.1|	predicted protein [Populus trichocarpa] >gi|222853506|gb|EEE91053.1| predicted protein [Populus trichocarpa]	76.42	106	2e-34
CAI_2A_5SP_D09	gi|224145996|ref|XP_002325841.1|	predicted protein [Populus trichocarpa] >gi|222862716|gb|EEF00223.1| predicted protein [Populus trichocarpa]	56.52	161	5e-30
CAI_2A_5SP_D12	gi|224091686|ref|XP_002309328.1|	predicted protein [Populus trichocarpa] >gi|222855304|gb|EEE92851.1| predicted protein [Populus trichocarpa]	91.46	199	5e-103
CAI_2A_5SP_E01	gi|225438184|ref|XP_002263670.1|	PREDICTED: hypothetical protein [Vitis vinifera]	94.08	169	5e-85
CAI_2A_5SP_E05	gi|224105305|ref|XP_002313761.1|	predicted protein [Populus trichocarpa] >gi|222850169|gb|EEE87716.1| predicted protein [Populus trichocarpa]	44.93	227	7e-43
CAI_2A_5SP_E11	gi|224069294|ref|XP_002326322.1|	predicted protein [Populus trichocarpa] >gi|222833515|gb|EEE71992.1| predicted protein [Populus trichocarpa]	70.67	225	1e-80
CAI_2A_5SP_E12	gi|224130796|ref|XP_002320928.1|	predicted protein [Populus trichocarpa] >gi|222861701|gb|EEE99243.1| predicted protein [Populus trichocarpa]	55.32	141	3e-25
CAI_2A_5SP_F01	gi|15233044|ref|NP_191670.1|	ARS27A (ARABIDOPSIS RIBOSOMAL PROTEIN S27); structural constituent of ribosome [Arabidopsis thaliana] >gi|73917991|sp|Q9M2F1|RS272_ARATH RecName: Full=40S ribosomal protein S27-2 >gi|15724226|gb|AAL06506.1|AF412053_1 AT3g61110/T27I15_200 [Arabidopsis thaliana] >gi|4193382|gb|AAD10029.1| ribosomal protein S27 [Arabidopsis thaliana] >gi|4193384|gb|AAD10030.1| ribosomal protein S27 [Arabidopsis thaliana] >gi|8388627|emb|CAB94147.1| ribosomal protein S27 [Arabidopsis thaliana] >gi|19699108|gb|AAL90920.1| AT3g61110/T27I15_200 [Arabidopsis thaliana]	95.35	86	8e-37

IP : 14.49.138.138, 2017-11-03 13:30:33

CAI_2A_5SP_F04	gi|77744899|gb|ABB02403.1|	temperature-induced lipocalin [Citrus sinensis]	100	186	6e-96
CAI_2A_5SP_G01	gi|225456252|ref|XP_002279421.1|	PREDICTED: hypothetical protein [Vitis vinifera]	55.56	252	1e-58
CAI_2A_5SP_G08	gi|224142207|ref|XP_002324450.1|	predicted protein [Populus trichocarpa] >gi|222865884|gb|EEF03015.1| predicted protein [Populus trichocarpa]	90.43	209	2e-105
CAI_2A_5SP_G11	gi|255545564|ref|XP_002513842.1|	Beta-1,3-galactosyltransferase sqv-2, putative [Ricinus communis] >gi|223546928|gb|EEF48425.1| Beta-1,3-galactosyltransferase sqv-2, putative [Ricinus communis]	65.26	213	9e-66
CAI_2A_5SP_H02	gi|233955399|gb|ACQ91203.1|	calreticulin [Carica papaya]	93.01	186	2e-102
CAI_2A_5SP_H04	gi|255576254|ref|XP_002529020.1|	DNA topoisomerase type I, putative [Ricinus communis] >gi|223531500|gb|EEF33331.1| DNA topoisomerase type I, putative [Ricinus communis]	43.37	249	3e-24
CAI_2A_5SP_H11	gi|224168295|ref|XP_002339136.1|	predicted protein [Populus trichocarpa] >gi|222874471|gb|EEF11602.1| predicted protein [Populus trichocarpa]	93.62	47	9e-18
CAI_2A_5SP_H12	gi|224128754|ref|XP_002328958.1|	predicted protein [Populus trichocarpa] >gi|222839192|gb|EEE77543.1| predicted protein [Populus trichocarpa]	88.06	201	1e-96
CAI_2B_5SP_A03	gi|255558698|ref|XP_002520373.1|	Cell division protein ftsH, putative [Ricinus communis] >gi|223540420|gb|EEF41989.1| Cell division protein ftsH, putative [Ricinus communis]	89.69	262	1e-117
CAI_2B_5SP_A05	gi|255625693|gb|ACU13191.1|	unknown [Glycine max]	90.98	122	9e-58
CAI_2B_5SP_A09	gi|225431343|ref|XP_002278070.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|225467618|ref|XP_002265867.1| PREDICTED: hypothetical protein [Vitis vinifera] >gi|225468570|ref|XP_002262972.1| PREDICTED: hypothetical protein [Vitis vinifera]	78.57	126	6e-57
CAI_2B_5SP_B01	gi|225452328|ref|XP_002273410.1|	PREDICTED: hypothetical protein [Vitis vinifera]	70.83	264	9e-101
CAI_2B_5SP_B02	gi|255559913|ref|XP_002520975.1|	trytophan synthase alpha subunit, putative [Ricinus communis] >gi|223539812|gb|EEF41392.1| trytophan synthase alpha subunit, putative [Ricinus communis]	76.57	286	4e-109
CAI_2B_5SP_B11	gi|224062948|ref|XP_002300943.1|	predicted protein [Populus trichocarpa] >gi|222842669|gb|EEE80216.1| predicted protein [Populus trichocarpa]	88.73	71	5e-30
CAI_2B_5SP_C01	gi|225448713|ref|XP_002280844.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270236079|emb|CBI25348.1| unnamed protein product [Vitis vinifera]	61.62	198	1e-63
CAI_2B_5SP_C07	gi|147777526|emb|CAN75944.1|	hypothetical protein [Vitis vinifera]	30.14	146	6e-14
CAI_2B_5SP_D02	gi|255543701|ref|XP_002512913.1|	conserved hypothetical protein [Ricinus communis] >gi|223547924|gb|EEF49416.1| conserved hypothetical protein [Ricinus communis]	69.61	181	1e-64
CAI_2B_5SP_D05	gi|255549228|ref|XP_002515668.1|	40S ribosomal protein S4, putative [Ricinus communis] >gi|223545211|gb|EEF46720.1| 40S ribosomal protein S4, putative [Ricinus communis]	82.94	252	1e-114
CAI_2B_5SP_D10	gi|225443932|ref|XP_002271718.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270243997|emb|CBI30936.1| unnamed protein product [Vitis vinifera]	43.66	142	1e-18
CAI_2B_5SP_D11	gi|255545896|ref|XP_002514008.1|	conserved hypothetical protein [Ricinus communis] >gi|223547094|gb|EEF48591.1| conserved hypothetical protein [Ricinus communis]	74.81	262	9e-111
CAI_2B_5SP_E01	gi|224088144|ref|XP_002308342.1|	predicted protein [Populus trichocarpa] >gi|222854318|gb|EEE91865.1| predicted protein [Populus trichocarpa]	88.89	36	7e-12
CAI_2B_5SP_E04	gi|270254970|emb|CBI37358.1|	unnamed protein product [Vitis vinifera]	78.23	147	2e-54
CAI_2B_5SP_E06	gi|224079155|ref|XP_002305772.1|	predicted protein [Populus trichocarpa] >gi|222848736|gb|EEE86283.1| predicted protein [Populus trichocarpa]	80.92	152	3e-65
CAI_2B_5SP_E09	gi|224054124|ref|XP_002298104.1|	predicted protein [Populus trichocarpa] >gi|222845362|gb|EEE82909.1| predicted protein [Populus trichocarpa]	80.56	180	4e-74
CAI_2B_5SP_E10	gi|224136089|ref|XP_002322237.1|	predicted protein [Populus trichocarpa] >gi|118483341|gb|ABK93572.1| unknown [Populus trichocarpa] >gi|222869233|gb|EEF06364.1| predicted protein [Populus trichocarpa]	89.19	111	5e-52
CAI_2B_5SP_E11	gi|164605535|dbj|BAF98601.1|	CM0545.290.nc [Lotus japonicus]	91.11	45	5e-18
CAI_2B_5SP_F01	gi|225434032|ref|XP_002273924.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270235509|emb|CBI24636.1| unnamed protein product [Vitis vinifera]	90.41	73	2e-32
CAI_2B_5SP_F08	gi|255557997|ref|XP_002520027.1|	conserved hypothetical protein [Ricinus communis] >gi|223540791|gb|EEF42351.1| conserved hypothetical protein [Ricinus communis]	80.39	102	8e-44
CAI_2B_5SP_G10	gi|255556496|ref|XP_002519282.1|	tex protein-relatedtranscription accessory protein, putative [Ricinus communis] >gi|223541597|gb|EEF43146.1| tex protein-relatedtranscription accessory protein, putative [Ricinus communis]	68.55	283	9e-90
CAI_2B_5SP_G11	gi|224073736|ref|XP_002304148.1|	predicted protein [Populus trichocarpa] >gi|222841580|gb|EEE79127.1| predicted protein [Populus trichocarpa]	74	50	1e-11
CAI_2B_5SP_H04	gi|225425766|ref|XP_002277517.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270260163|emb|CBI31997.1| unnamed protein product [Vitis vinifera]	93.51	185	1e-97
CAI_2B_5SP_H05	gi|255639553|gb|ACU20071.1|	unknown [Glycine max]	84.89	225	1e-67
CAI_2B_5SP_H07	gi|224085421|ref|XP_002307570.1|	hypothetical protein POPTRDRAFT_818640 [Populus trichocarpa] >gi|118488107|gb|ABK95873.1| unknown [Populus trichocarpa] >gi|222857019|gb|EEE94566.1| hypothetical protein POPTRDRAFT_818640 [Populus trichocarpa]	80.92	262	8e-118

IP : 14.49.138.138, 2017-11-03 13:30:33

CAI_2C_5SP_A01	gi|255546227|ref|XP_002514173.1|	60S ribosomal protein L31, putative [Ricinus communis] >gi|223546629|gb|EEF48127.1| 60S ribosomal protein L31, putative [Ricinus communis]	92.5	120	1e-45
CAI_2C_5SP_A03	gi|6466940|gb|AAF13075.1| AC009176_2	unknown protein [Arabidopsis thaliana]	63.16	57	5e-14
CAI_2C_5SP_B05	gi|118486839|gb|ABK95254.1|	unknown [Populus trichocarpa]	96.81	94	1e-36
CAI_2C_5SP_B08	gi|147858661|emb|CAN80823.1|	hypothetical protein [Vitis vinifera]	89.29	84	8e-38
CAI_2C_5SP_B11	gi|6094476|sp|O23787|THI4_CITSI	RecName: Full=Thiazole biosynthetic enzyme, chloroplastic; Flags: Precursor >gi|2582665|emb|CAB05370.1| thi [Citrus sinensis]	98.44	64	3e-28
CAI_2C_5SP_B12	gi|217072560|gb|ACJ84640.1|	unknown [Medicago truncatula]	73.17	123	1e-48
CAI_2C_5SP_C01	gi|255576103|ref|XP_002528946.1|	eif-1a, putative [Ricinus communis] >gi|223531592|gb|EEF33420.1| eif-1a, putative [Ricinus communis]	97.98	99	4e-50
CAI_2C_5SP_C02	gi|255542062|ref|XP_002512095.1|	Protein KTI12, putative [Ricinus communis] >gi|223549275|gb|EEF50764.1| Protein KTI12, putative [Ricinus communis]	84.25	127	4e-50
CAI_2C_5SP_C08	gi|62526569|gb|AAX84670.1|	ethylene response factor [Manihot esculenta]	75	44	3e-12
CAI_2C_5SP_C09	gi|224117592|ref|XP_002317617.1|	predicted protein [Populus trichocarpa] >gi|222860682|gb|EEE98229.1| predicted protein [Populus trichocarpa]	75.36	138	8e-56
CAI_2C_5SP_D02	gi|255556948|ref|XP_002519507.1|	conserved hypothetical protein [Ricinus communis] >gi|223541370|gb|EEF42921.1| conserved hypothetical protein [Ricinus communis]	80	105	2e-42
CAI_2C_5SP_D08	gi|15224217|ref|NP_179464.1|	small nuclear ribonucleoprotein E, putative / snRNP-E, putative / Sm protein E, putative [Arabidopsis thaliana] >gi|4185140|gb|AAD08943.1| putative small nuclear ribonucleoprotein E [Arabidopsis thaliana] >gi|21592486|gb|AAM64436.1| putative small nuclear ribonucleoprotein E [Arabidopsis thaliana] >gi|26452632|dbj|BAC43399.1| putative small nuclear ribonucleoprotein E [Arabidopsis thaliana] >gi|28973515|gb|AAO64082.1| putative small nuclear ribonucleoprotein E [Arabidopsis thaliana]	92.86	84	1e-36
CAI_2C_5SP_D12	gi|255538108|ref|XP_002510119.1|	Xylem serine proteinase 1 precursor, putative [Ricinus communis] >gi|223550820|gb|EEF52306.1| Xylem serine proteinase 1 precursor, putative [Ricinus communis]	78.95	57	5e-19
CAI_2C_5SP_E04	gi|255550209|ref|XP_002516155.1|	copper transporter, putative [Ricinus communis] >gi|223544641|gb|EEF46157.1| copper transporter, putative [Ricinus communis]	61.76	68	1e-18
CAI_2C_5SP_E12	gi|1351408|sp|P49043|VPE_CITSI	RecName: Full=Vacuolar-processing enzyme; Short=VPE; Flags: Precursor >gi|633185|emb|CAA87720.1| cystein proteinase (by similarity) [Citrus sinensis] >gi|1588548|prf||2208463A vascular processing protease	98.18	55	1e-24
CAI_2C_5SP_F02	gi|225443227|ref|XP_002270610.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270306550|emb|CBI25248.1| unnamed protein product [Vitis vinifera]	83.95	162	6e-58
CAI_2C_5SP_F03	gi|255566540|ref|XP_002524255.1|	conserved hypothetical protein [Ricinus communis] >gi|223536532|gb|EEF38179.1| conserved hypothetical protein [Ricinus communis]	72.09	86	2e-20
CAI_2C_5SP_F09	gi|225453818|ref|XP_002276807.1|	PREDICTED: hypothetical protein [Vitis vinifera]	74.45	137	4e-49
CAI_2C_5SP_F12	gi|225426693|ref|XP_002281735.1|	PREDICTED: hypothetical protein [Vitis vinifera]	54.9	255	9e-75
CAI_2C_5SP_G01	gi|224139328|ref|XP_002323058.1|	predicted protein [Populus trichocarpa] >gi|222867688|gb|EEF04819.1| predicted protein [Populus trichocarpa]	61.7	188	6e-60
CAI_2C_5SP_G04	gi|255582050|ref|XP_002531822.1|	conserved hypothetical protein [Ricinus communis] >gi|223528556|gb|EEF30579.1| conserved hypothetical protein [Ricinus communis]	55.06	89	4e-19
CAI_2C_5SP_G05	gi|225451136|ref|XP_002269746.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|147767146|emb|CAN75647.1| hypothetical protein [Vitis vinifera] >gi|270306789|emb|CBI34293.1| unnamed protein product [Vitis vinifera]	83.77	154	1e-67
CAI_2C_5SP_H04	gi|225438241|ref|XP_002264612.1|	PREDICTED: hypothetical protein [Vitis vinifera]	66.67	57	2e-15
CAI_2C_5SP_H05	gi|13991882|gb|AAK51545.1|	phytoene desaturase [Citrus x paradisi]	100	37	4e-12
CAI_2C_5SP_H07	gi|255548479|ref|XP_002515296.1|	conserved hypothetical protein [Ricinus communis] >gi|223545776|gb|EEF47280.1| conserved hypothetical protein [Ricinus communis]	71.24	153	7e-53
CAI_2C_5SP_H10	gi|188509931|gb|ACD56620.1|	unknown predicted protein [Gossypioides kirkii]	73.89	157	7e-54
CAI_2C_5SP_H11	gi|225467729|ref|XP_002263101.1|	PREDICTED: hypothetical protein [Vitis vinifera]	86.99	246	2e-109
CAI_2C_5SP_H12	gi|225464047|ref|XP_002267841.1|	PREDICTED: similar to cysteine proteinase inhibitor [Vitis vinifera]	73.97	73	1e-25
CAI_2D_5SP_A03	gi|14210375|gb|AAK57011.1| AF378333_1	cinnamate 4-hydroxylase [Citrus x paradisi]	100	268	8e-142
CAI_2D_5SP_A04	gi|255545018|ref|XP_002513570.1|	protein phosphatase 2c, putative [Ricinus communis] >gi|223547478|gb|EEF48973.1| protein phosphatase 2c, putative [Ricinus communis]	75.35	142	9e-47
CAI_2D_5SP_A07	gi|224104361|ref|XP_002313411.1|	copper transporter [Populus trichocarpa] >gi|118485983|gb|ABK94836.1| unknown [Populus trichocarpa] >gi|222849819|gb|EEE87366.1| copper transporter [Populus trichocarpa]	73.98	123	1e-38
CAI_2D_5SP_A10	gi|224063217|ref|XP_002301046.1|	predicted protein [Populus trichocarpa] >gi|118481505|gb|ABK92695.1| unknown [Populus trichocarpa] >gi|222842772|gb|EEE80319.1| predicted protein [Populus trichocarpa]	78.92	223	1e-91
CAI_2D_5SP_A12	gi|225440908|ref|XP_002282804.1|	PREDICTED: hypothetical protein [Vitis vinifera]	75	100	2e-43
CAI_2D_5SP_B02	gi|68138979|gb|AAY86035.1|	pyruvate kinase [Citrus sinensis]	99.57	232	9e-123

IP : 14.49.138.138, 2017-11-03 13:30:33

CAI_2D_5SP_B06	gi|225459233|ref|XP_002284081.1|	PREDICTED: hypothetical protein [Vitis vinifera]	70.15	67	7e-21
CAI_2D_5SP_B11	gi|129770485|gb|ABO31358.1|	starch branching enzyme II-1 [Malus x domestica]	44.33	194	8e-31
CAI_2D_5SP_B12	gi|82621170|gb|ABB86273.1|	cytoplasmic ribosomal protein S13-like [Solanum tuberosum]	98.68	151	5e-79
CAI_2D_5SP_C01	gi|255558218|ref|XP_002520136.1|	Protein PPLZ12, putative [Ricinus communis] >gi|223540628|gb|EEF42191.1| Protein PPLZ12, putative [Ricinus communis]	88.69	274	3e-132
CAI_2D_5SP_C02	gi|255566955|ref|XP_002524460.1|	mutt/nudix hydrolase, putative [Ricinus communis] >gi|223536248|gb|EEF37900.1| mutt/nudix hydrolase, putative [Ricinus communis]	71.73	283	1e-109
CAI_2D_5SP_C05	gi|224066593|ref|XP_002302153.1|	predicted protein [Populus trichocarpa] >gi|224082516|ref|XP_002306725.1| predicted protein [Populus trichocarpa] >gi|118485172|gb|ABK94447.1| unknown [Populus trichocarpa] >gi|222843879|gb|EEE81426.1| predicted protein [Populus trichocarpa] >gi|222856174|gb|EEE93721.1| predicted protein [Populus trichocarpa]	97.4	154	1e-62
CAI_2D_5SP_C10	gi|224116446|ref|XP_002317303.1|	predicted protein [Populus trichocarpa] >gi|222860368|gb|EEE97915.1| predicted protein [Populus trichocarpa]	84.34	83	3e-33
CAI_2D_5SP_D03	gi|224139616|ref|XP_002323194.1|	predicted protein [Populus trichocarpa] >gi|222867824|gb|EEF04955.1| predicted protein [Populus trichocarpa]	90.52	116	3e-57
CAI_2D_5SP_E04	gi|118483069|gb|ABK93444.1|	unknown [Populus trichocarpa]	82.94	211	2e-88
CAI_2D_5SP_E08	gi|224144403|ref|XP_002325278.1|	nucleosome/chromatin assembly factor group [Populus trichocarpa] >gi|222862153|gb|EEE99659.1| nucleosome/chromatin assembly factor group [Populus trichocarpa]	71.88	96	5e-34
CAI_2D_5SP_E09	gi|224085982|ref|XP_002307764.1|	predicted protein [Populus trichocarpa] >gi|222857213|gb|EEE94760.1| predicted protein [Populus trichocarpa]	73.62	235	9e-99
CAI_2D_5SP_E10	gi|224067834|ref|XP_002302556.1|	predicted protein [Populus trichocarpa] >gi|222844282|gb|EEE81829.1| predicted protein [Populus trichocarpa]	91.4	279	1e-134
CAI_2D_5SP_F02	gi|270231826|emb|CBI21151.1|	unnamed protein product [Vitis vinifera]	61.54	247	4e-62
CAI_2D_5SP_F07	gi|225429686|ref|XP_002280034.1|	PREDICTED: hypothetical protein [Vitis vinifera]	61.11	252	4e-72
CAI_2D_5SP_F08	gi|255628253|gb|ACU14471.1|	unknown [Glycine max]	88.03	142	3e-63
CAI_2D_5SP_F09	gi|225435247|ref|XP_002284990.1|	PREDICTED: hypothetical protein isoform 2 [Vitis vinifera]	83.61	244	2e-115
CAI_2D_5SP_F10	gi|225429271|ref|XP_002266390.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270242169|emb|CBI29381.1| unnamed protein product [Vitis vinifera]	84.03	288	1e-139
CAI_2D_5SP_G06	gi|224089575|ref|XP_002308763.1|	predicted protein [Populus trichocarpa] >gi|222854739|gb|EEE92286.1| predicted protein [Populus trichocarpa]	69.67	122	7e-31
CAI_2D_5SP_G09	gi|270238748|emb|CBI25984.1|	unnamed protein product [Vitis vinifera]	99.45	182	2e-99
CAI_2D_5SP_H01	gi|149349541|gb|ABR24115.1|	eugenol synthase 1 [Petunia x hybrida]	78.65	281	9e-128
CAI_2D_5SP_H07	gi|255560111|ref|XP_002521073.1|	ubiquitin-associated uba/ubx domain-containing protein, putative [Ricinus communis] >gi|223539642|gb|EEF41224.1| ubiquitin-associated uba/ubx domain-containing protein, putative [Ricinus communis]	74.58	59	4e-17
CAI_2D_5SP_H08	gi|255551849|ref|XP_002516970.1|	chaperone binding protein, putative [Ricinus communis] >gi|223544058|gb|EEF45584.1| chaperone binding protein, putative [Ricinus communis]	59.77	174	4e-42
CAI_2D_5SP_H09	gi|255537037|ref|XP_002509585.1|	21 kDa protein precursor, putative [Ricinus communis] >gi|223549484|gb|EEF50972.1| 21 kDa protein precursor, putative [Ricinus communis]	76.4	178	1e-63
CAI_3A_5SP_A01	gi|255572672|ref|XP_002527269.1|	conserved hypothetical protein [Ricinus communis] >gi|223533362|gb|EEF35113.1| conserved hypothetical protein [Ricinus communis]	77.65	255	1e-102
CAI_3A_5SP_A04	gi|147812118|emb|CAN65782.1|	hypothetical protein [Vitis vinifera]	70.71	239	1e-92
CAI_3A_5SP_A07	gi|147778443|emb|CAN63032.1|	hypothetical protein [Vitis vinifera]	37.76	98	2e-11
CAI_3A_5SP_B03	gi|255562070|ref|XP_002522043.1|	phosphate abc transporter, putative [Ricinus communis] >gi|223538642|gb|EEF40243.1| phosphate abc transporter, putative [Ricinus communis]	77.74	265	1e-103
CAI_3A_5SP_B05	gi|224123016|ref|XP_002318973.1|	predicted protein [Populus trichocarpa] >gi|222857349|gb|EEE94896.1| predicted protein [Populus trichocarpa]	55.76	278	2e-75
CAI_3A_5SP_B06	gi|225443980|ref|XP_002274093.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|147853333|emb|CAN82327.1| hypothetical protein [Vitis vinifera] >gi|270244031|emb|CBI30970.1| unnamed protein product [Vitis vinifera]	64.26	277	3e-86
CAI_3A_5SP_C01	gi|224100581|ref|XP_002311932.1|	predicted protein [Populus trichocarpa] >gi|118481700|gb|ABK92790.1| unknown [Populus trichocarpa] >gi|222851752|gb|EEE89299.1| predicted protein [Populus trichocarpa]	83.33	48	6e-12
CAI_3A_5SP_C03	gi|225437963|ref|XP_002271401.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270254809|emb|CBI37199.1| unnamed protein product [Vitis vinifera]	79.31	290	5e-123
CAI_3A_5SP_C08	gi|255560207|ref|XP_002521121.1|	conserved hypothetical protein [Ricinus communis] >gi|223539690|gb|EEF41272.1| conserved hypothetical protein [Ricinus communis]	74.62	197	7e-66
CAI_3A_5SP_C11	gi|225456295|ref|XP_002283673.1|	PREDICTED: hypothetical protein [Vitis vinifera]	82.61	230	3e-64
CAI_3A_5SP_D05	gi|225439856|ref|XP_002278124.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270247296|emb|CBI32671.1| unnamed protein product [Vitis vinifera]	92.13	89	4e-42
CAI_3A_5SP_E01	gi|225451804|ref|XP_002281338.1|	PREDICTED: brassinosteroid-6-oxidase [Vitis vinifera] >gi|270306130|emb|CBI16941.1| unnamed protein product [Vitis vinifera]	78.46	311	3e-132
CAI_3A_5SP_	gi|225431233|ref|XP_002273	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270228486|emb|CBI17423.1|	73.5	117	3e-39

IP : 14.49.138.138, 2017-11-03 13:30:33

E05	15.1|	unnamed protein product [Vitis vinifera]			
CAI_3A_5SP_E07	gi|24461867|gb|AAN62354.1|AF506028_23	CTV.22 [Citrus trifoliata]	50	116	2e-21
CAI_3A_5SP_E09	gi|255570396|ref|XP_002526157.1|	glycogenin, putative [Ricinus communis] >gi|223534534|gb|EEF36233.1| glycogenin, putative [Ricinus communis]	95	80	3e-44
CAI_3A_5SP_E12	gi|224111368|ref|XP_002315829.1|	predicted protein [Populus trichocarpa] >gi|222864869|gb|EEF02000.1| predicted protein [Populus trichocarpa]	73.81	84	6e-32
CAI_3A_5SP_F01	gi|225426492|ref|XP_002277375.1|	PREDICTED: hypothetical protein [Vitis vinifera]	82.87	216	5e-91
CAI_3A_5SP_F12	gi|225437402|ref|XP_002268231.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270254483|emb|CBI36873.1| unnamed protein product [Vitis vinifera]	64.42	208	8e-61
CAI_3A_5SP_G06	gi|255550417|ref|XP_002516259.1|	Adipocyte plasma membrane-associated protein, putative [Ricinus communis] >gi|223544745|gb|EEF46261.1| Adipocyte plasma membrane-associated protein, putative [Ricinus communis]	60.33	242	4e-81
CAI_3A_5SP_G08	gi|225449288|ref|XP_002276871.1|	PREDICTED: hypothetical protein [Vitis vinifera]	55.69	246	1e-67
CAI_3A_5SP_G10	gi|6635838|gb|AAF20002.1|AF213936_1	amino acid/peptide transporter [Prunus dulcis]	85.56	277	2e-142
CAI_3A_5SP_H04	gi|35187454|gb|AAQ84318.1|	fiber protein Fb27 [Gossypium barbadense]	88.21	195	6e-74
CAI_3A_5SP_H06	gi|225452905|ref|XP_002284020.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270232943|emb|CBI22260.1| unnamed protein product [Vitis vinifera]	75	116	5e-33
CAI_3A_5SP_H08	gi|270234638|emb|CBI23240.1|	unnamed protein product [Vitis vinifera]	42.45	139	1e-18
CAI_3A_5SP_H10	gi|255627641|gb|ACU14165.1|	unknown [Glycine max]	70.98	224	6e-67
CAI_3A_5SP_H11	gi|115450713|ref|NP_001048957.1|	Os03g0146300 [Oryza sativa (japonica cultivar-group)] >gi|75127295|sp|Q6PS57|CKS1_ORYSJ RecName: Full=Cyclin-dependent kinases regulatory subunit 1 >gi|158512867|sp|A2XCH8|CKS1_ORYSI RecName: Full=Cyclin-dependent kinases regulatory subunit 1 >gi|15451612|gb|AAK98736.1|AC090485_15 Putative cyclin-dependent kinase regulatory subunit [Oryza sativa Japonica Group] >gi|46487749|gb|AAS99236.1| cyclin-dependent kinase subunit [Oryza sativa Japonica Group] >gi|108706167|gb|ABF93962.1| cyclin-dependent kinases regulatory subunit, putative, expressed [Oryza sativa (japonica cultivar-group)] >gi|113547428|dbj|BAF10871.1| Os03g0146300 [Oryza sativa Japonica Group] >gi|125542399|gb|EAY88538.1| hypothetical protein OsI_10011 [Oryza sativa Indica Group] >gi|125584911|gb|EAZ25575.1| hypothetical protein OsJ_09400 [Oryza sativa Japonica Group] >gi|215768237|dbj|BAH00466.1| unnamed protein product [Oryza sativa Japonica Group]	97.18	71	1e-34
CAI_3B_5SP_A10	gi|224133658|ref|XP_002321629.1|	predicted protein [Populus trichocarpa] >gi|222868625|gb|EEF05756.1| predicted protein [Populus trichocarpa]	67.3	159	1e-51
CAI_3B_5SP_A12	gi|225452043|ref|XP_002283875.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270248516|emb|CBI33648.1| unnamed protein product [Vitis vinifera]	65.45	246	2e-79
CAI_3B_5SP_B01	gi|255569476|ref|XP_002525705.1|	BTB/POZ domain-containing protein KCTD9, putative [Ricinus communis] >gi|223535005|gb|EEF36688.1| BTB/POZ domain-containing protein KCTD9, putative [Ricinus communis]	82.05	195	4e-75
CAI_3B_5SP_B03	gi|225443952|ref|XP_002279808.1|	PREDICTED: hypothetical protein [Vitis vinifera]	85.57	201	4e-94
CAI_3B_5SP_B06	gi|224145979|ref|XP_002325835.1|	predicted protein [Populus trichocarpa] >gi|222862710|gb|EEF00217.1| predicted protein [Populus trichocarpa]	88.14	236	4e-113
CAI_3B_5SP_B11	gi|225460369|ref|XP_002264046.1|	PREDICTED: hypothetical protein [Vitis vinifera]	64.14	145	8e-43
CAI_3B_5SP_C01	gi|18395946|ref|NP_564250.1|	peptidyl-prolyl cis-trans isomerase PPIC-type family protein [Arabidopsis thaliana] >gi|9797744|gb|AAF98562.1|AC013427_5 Contains similarity to peptidyl-prolyl cis-trans isomerase EPVH from Homo sapiens gb|AF143096 and contains a Rotamase (PPIC-type PPIASE) PF|00639 domain. ESTs gb|T45176, gb|F14479, gb|AA586142, gb|F14459, gb|AI997648 come from this gene [Arabidopsis thaliana] >gi|12083236|gb|AAG48777.1|AF332414_1 unknown protein [Arabidopsis thaliana] >gi|21553425|gb|AAM62518.1| unknown [Arabidopsis thaliana]	95.28	106	2e-55
CAI_3B_5SP_C05	gi|224117970|ref|XP_002317701.1|	predicted protein [Populus trichocarpa] >gi|222858374|gb|EEE95921.1| predicted protein [Populus trichocarpa]	66.95	239	1e-73
CAI_3B_5SP_C06	gi|217071160|gb|ACJ83940.1|	unknown [Medicago truncatula]	73.79	145	4e-61
CAI_3B_5SP_D02	gi|15230358|ref|NP_191320.1|	ADSS (ADENYLOSUCCINATE SYNTHASE); adenylosuccinate synthase [Arabidopsis thaliana] >gi|2500026|sp|Q96529|PURA_ARATH RecName: Full=Adenylosuccinate synthetase, chloroplastic; Short=AMPSase; Short=AdSS; AltName: Full=IMP--aspartate ligase; Flags: Precursor >gi|1616657|gb|AAB16828.1| adenylosuccinate synthetase [Arabidopsis thaliana] >gi|4678286|emb|CAB41194.1| adenylosuccinate synthetase [Arabidopsis thaliana] >gi|15451052|gb|AAK96797.1| adenylosuccinate synthetase [Arabidopsis thaliana] >gi|20148265|gb|AAM10023.1| adenylosuccinate synthetase [Arabidopsis thaliana]	75.09	281	2e-111
CAI_3B_5SP_D03	gi|225428065|ref|XP_002279626.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270255471|emb|CBI37855.1| unnamed protein product [Vitis vinifera]	97.08	137	4e-72
CAI_3B_5SP_D04	gi|217075044|gb|ACJ85882.1|	unknown [Medicago truncatula]	77.66	94	7e-36
CAI_3B_5SP_D05	gi|225435452|ref|XP_002285455.1|	PREDICTED: hypothetical protein isoform 3 [Vitis vinifera] >gi|225435454|ref|XP_002285453.1| PREDICTED: hypothetical protein isoform 2 [Vitis vinifera] >gi|225435456|ref|XP_002285450.1| PREDICTED: hypothetical protein isoform 1 [Vitis vinifera] >gi|270227646|emb|CBI16379.1| unnamed protein product [Vitis	78.24	216	6e-94

IP : 14.49.138.138, 2017-11-03 13:30:33

		vinifera]			
CAI_3B_5SP_D06	gi|225449018|ref|XP_002272669.1|	PREDICTED: hypothetical protein [Vitis vinifera]	89.37	254	8e-131
CAI_3B_5SP_E03	gi|225434179|ref|XP_002275474.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270235598|emb|CBI24725.1| unnamed protein product [Vitis vinifera]	50.9	167	1e-34
CAI_3B_5SP_F02	gi|255545490|ref|XP_002513805.1|	heat shock protein 70 (HSP70)-interacting protein, putative [Ricinus communis] >gi|223546891|gb|EEF48388.1| heat shock protein 70 (HSP70)-interacting protein, putative [Ricinus communis]	61.19	268	5e-83
CAI_3B_5SP_F06	gi|224085938|ref|XP_002307747.1|	predicted protein [Populus trichocarpa] >gi|222857196|gb|EEE94743.1| predicted protein [Populus trichocarpa]	67	200	6e-76
CAI_3B_5SP_F07	gi|147768776|emb|CAN60456.1|	hypothetical protein [Vitis vinifera]	81.63	49	2e-14
CAI_3B_5SP_F08	gi|255580252|ref|XP_002530956.1|	multidrug resistance pump, putative [Ricinus communis] >gi|223529471|gb|EEF31428.1| multidrug resistance pump, putative [Ricinus communis]	74.28	276	4e-109
CAI_3B_5SP_F09	gi|225440831|ref|XP_002282071.1|	PREDICTED: similar to ubiquitin fusion protein [Vitis vinifera] >gi|255578906|ref|XP_002530306.1| ubiquitin, putative [Ricinus communis] >gi|255578975|ref|XP_002530340.1| ubiquitin, putative [Ricinus communis] >gi|71040673|gb|AAZ20285.1| ubiquitin fusion protein [Arachis hypogaea] >gi|147769165|emb|CAN60770.1| hypothetical protein [Vitis vinifera] >gi|148908659|gb|ABR17437.1| unknown [Picea sitchensis] >gi|192910738|gb|ACF06477.1| ubiquitin fusion protein [Elaeis guineensis] >gi|223530144|gb|EEF32056.1| ubiquitin, putative [Ricinus communis] >gi|223530162|gb|EEF32073.1| ubiquitin, putative [Ricinus communis] >gi|270243382|emb|CBI30322.1| unnamed protein product [Vitis vinifera]	100	128	2e-67
CAI_3B_5SP_F10	gi|15242248|ref|NP_197636.1|	60S ribosomal protein L10A (RPL10aC) [Arabidopsis thaliana] >gi|145334533|ref|NP_001078612.1| 60S ribosomal protein L10A (RPL10aC) [Arabidopsis thaliana] >gi|27923990|sp|P59231|R10A3_ARATH RecName: Full=60S ribosomal protein L10a-3 >gi|9757825|dbj|BAB08343.1| 60S ribosomal protein L10A [Arabidopsis thaliana] >gi|14335148|gb|AAK59854.1| AT5g22440/MWD9_24 [Arabidopsis thaliana] >gi|18655359|gb|AAL76135.1| AT5g22440/MWD9_24 [Arabidopsis thaliana]	95.61	114	5e-56
CAI_3B_5SP_G01	gi|225424719|ref|XP_002265302.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270260285|emb|CBI32119.1| unnamed protein product [Vitis vinifera]	88.72	257	4e-129
CAI_3B_5SP_G06	gi|224100023|ref|XP_002311714.1|	predicted protein [Populus trichocarpa] >gi|222851534|gb|EEE89081.1| predicted protein [Populus trichocarpa]	87.34	79	1e-23
CAI_3B_5SP_G07	gi|224053018|ref|XP_002297666.1|	predicted protein [Populus trichocarpa] >gi|222844924|gb|EEE82471.1| predicted protein [Populus trichocarpa]	77.39	230	6e-95
CAI_3B_5SP_G09	gi|56693965|gb|AAW22771.1|	p33 [Citrus tristeza virus]	91.11	45	9e-17
CAI_3B_5SP_H01	gi|224105367|ref|XP_002333826.1|	predicted protein [Populus trichocarpa] >gi|222838645|gb|EEE77010.1| predicted protein [Populus trichocarpa]	53.88	245	3e-64
CAI_3B_5SP_H07	gi|255565846|ref|XP_002523912.1|	ccaat-binding transcription factor subunit A, putative [Ricinus communis] >gi|223536842|gb|EEF38481.1| ccaat-binding transcription factor subunit A, putative [Ricinus communis]	90.29	175	3e-86
CAI_3C_5SP_A01	gi|225442114|ref|XP_002273796.1|	PREDICTED: hypothetical protein [Vitis vinifera]	78.62	145	7e-62
CAI_3C_5SP_A03	gi|224056895|ref|XP_002299077.1|	predicted protein [Populus trichocarpa] >gi|222846335|gb|EEE83882.1| predicted protein [Populus trichocarpa]	79.31	116	2e-52
CAI_3C_5SP_A05	gi|224099151|ref|XP_002311384.1|	predicted protein [Populus trichocarpa] >gi|222851204|gb|EEE88751.1| predicted protein [Populus trichocarpa]	68.99	158	2e-48
CAI_3C_5SP_A08	gi|255561905|ref|XP_002521961.1|	cyclophilin, putative [Ricinus communis] >gi|223538765|gb|EEF40365.1| cyclophilin, putative [Ricinus communis]	91.91	173	3e-82
CAI_3C_5SP_A12	gi|225464515|ref|XP_002270104.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270234082|emb|CBI22689.1| unnamed protein product [Vitis vinifera]	77.11	284	3e-106
CAI_3C_5SP_B01	gi|224131676|ref|XP_002321150.1|	predicted protein [Populus trichocarpa] >gi|222861923|gb|EEE99465.1| predicted protein [Populus trichocarpa]	93.94	99	1e-47
CAI_3C_5SP_B02	gi|147862409|emb|CAN81911.1|	hypothetical protein [Vitis vinifera]	49.36	233	2e-49
CAI_3C_5SP_B03	gi|225461730|ref|XP_002283370.1|	PREDICTED: hypothetical protein [Vitis vinifera]	72.46	236	4e-89
CAI_3C_5SP_B04	gi|147857906|emb|CAN80393.1|	hypothetical protein [Vitis vinifera]	75.61	41	5e-13
CAI_3C_5SP_B05	gi|255576619|ref|XP_002529200.1|	conserved hypothetical protein [Ricinus communis] >gi|223531378|gb|EEF33214.1| conserved hypothetical protein [Ricinus communis]	43.65	252	1e-32
CAI_3C_5SP_B08	gi|224133592|ref|XP_002327633.1|	predicted protein [Populus trichocarpa] >gi|222836718|gb|EEE75111.1| predicted protein [Populus trichocarpa]	64.12	170	5e-41
CAI_3C_5SP_B09	gi|255560527|ref|XP_002521278.1|	expressed protein, putative [Ricinus communis] >gi|223539546|gb|EEF41134.1| expressed protein, putative [Ricinus communis]	63.41	164	1e-36
CAI_3C_5SP_B10	gi|225444609|ref|XP_002274986.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270240524|emb|CBI27753.1| unnamed protein product [Vitis vinifera]	86.33	139	1e-64
CAI_3C_5SP_B11	gi|225454328|ref|XP_002277525.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270258388|emb|CBI40422.1| unnamed protein product [Vitis vinifera]	83.94	274	1e-124
CAI_3C_5SP_C10	gi|224120428|ref|XP_002318327.1|	predicted protein [Populus trichocarpa] >gi|222859000|gb|EEE96547.1| predicted protein [Populus trichocarpa]	88.59	263	5e-128
CAI_3C_5SP_D04	gi|255574159|ref|XP_002527995.1|	proteasome subunit beta type 6,9, putative [Ricinus communis] >gi|223532621|gb|EEF34407.1| proteasome subunit beta type 6,9, putative [Ricinus communis]	90	230	2e-114
CAI_3C_5SP_D05	gi|255547630|ref|XP_002514872.1|	conserved hypothetical protein [Ricinus communis] >gi|223545923|gb|EEF47426.1| conserved hypothetical protein [Ricinus communis]	55.19	212	1e-34

IP : 14.49.138.138, 2017-11-03 13:30:33

CAI_3C_5SP_E01	gi|255555863|ref|XP_002518967.1|	conserved hypothetical protein [Ricinus communis] >gi|223541954|gb|EEF43500.1| conserved hypothetical protein [Ricinus communis]	80.86	209	6e-78
CAI_3C_5SP_E02	gi|224100509|ref|XP_002311904.1|	predicted protein [Populus trichocarpa] >gi|222851724|gb|EEE89271.1| predicted protein [Populus trichocarpa]	61.11	144	4e-38
CAI_3C_5SP_E05	gi|224061641|ref|XP_002300581.1|	amino acid permease [Populus trichocarpa] >gi|118487470|gb|ABK95562.1| unknown [Populus trichocarpa] >gi|222847839|gb|EEE85386.1| amino acid permease [Populus trichocarpa]	65.25	118	5e-41
CAI_3C_5SP_E06	gi|225449603|ref|XP_002284071.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270244781|emb|CBI31714.1| unnamed protein product [Vitis vinifera]	98.38	185	2e-85
CAI_3C_5SP_F01	gi|18410584|ref|NP_565083.1|	ATHSP101 (ARABIDOPSIS THALIANA HEAT SHOCK PROTEIN 101); ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding / protein binding [Arabidopsis thaliana] >gi|21264430|sp|P42730|HS101_ARATH RecName: Full=Heat shock protein 101 >gi|6715468|gb|AAF26423.1|AF218796_1 heat shock protein 101 [Arabidopsis thaliana] >gi|12324908|gb|AAG52410.1|AC020579_12 heat shock protein 101; 13093-16240 [Arabidopsis thaliana]	86.15	260	3e-121
CAI_3C_5SP_F05	gi|224138380|ref|XP_002326588.1|	predicted protein [Populus trichocarpa] >gi|222833910|gb|EEE72387.1| predicted protein [Populus trichocarpa]	90	90	3e-40
CAI_3C_5SP_F06	gi|224063601|ref|XP_002301222.1|	predicted protein [Populus trichocarpa] >gi|118481753|gb|ABK92816.1| unknown [Populus trichocarpa] >gi|222842948|gb|EEE80495.1| predicted protein [Populus trichocarpa]	79.84	124	2e-47
CAI_3C_5SP_F11	gi|289540890|gb|ADD09567.1|	adeninephosphoribosyl transferase [Trifolium repens] >gi|289540907|gb|ADD09581.1| adeninephosphoribosyl transferase [Trifolium repens]	91.67	108	4e-50
CAI_3C_5SP_G11	gi|225431279|ref|XP_002275676.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270228515|emb|CBI17452.1| unnamed protein product [Vitis vinifera]	76.47	119	1e-46
CAI_3C_5SP_H01	gi|224083394|ref|XP_002307009.1|	predicted protein [Populus trichocarpa] >gi|118489570|gb|ABK96587.1| unknown [Populus trichocarpa x Populus deltoides] >gi|222856458|gb|EEE94005.1| predicted protein [Populus trichocarpa]	81.14	175	4e-75
CAI_3C_5SP_H04	gi|224100423|ref|XP_002311870.1|	predicted protein [Populus trichocarpa] >gi|118487147|gb|ABK95402.1| unknown [Populus trichocarpa] >gi|222851690|gb|EEE89237.1| predicted protein [Populus trichocarpa] >gi|283135858|gb|ADB11320.1| tau class glutathione transferase GSTU22 [Populus trichocarpa]	75.27	182	1e-71
CAI_3C_5SP_H05	gi|255539334|ref|XP_002510732.1|	hmg-CoA reductase, putative [Ricinus communis] >gi|223551433|gb|EEF52919.1| hmg-CoA reductase, putative [Ricinus communis]	94.02	117	1e-54
CAI_3C_5SP_H09	gi|225440484|ref|XP_002273256.1|	PREDICTED: similar to pyrroline-5-carboxylate synthetase [Vitis vinifera] >gi|270243553|emb|CBI30493.1| unnamed protein product [Vitis vinifera]	88	50	2e-19
CAI_3C_5SP_H11	gi|225450215|ref|XP_002265394.1|	PREDICTED: hypothetical protein [Vitis vinifera]	83.72	86	7e-20
CAI_3C_5SP_H12	gi|225439749|ref|XP_002274570.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|147769777|emb|CAN63391.1| hypothetical protein [Vitis vinifera]	100	105	6e-40
CAI_3D_5SP_A07	gi|242129052|gb|ACS83605.1|	ATP synthase epsilon subunit 1 [Gossypium hirsutum]	92.86	70	4e-32
CAI_3D_5SP_B10	gi|225451048|ref|XP_002284948.1|	PREDICTED: hypothetical protein [Vitis vinifera]	77.84	185	5e-83
CAI_3D_5SP_B12	gi|255565362|ref|XP_002523672.1|	Alpha-N-arabinofuranosidase 1 precursor, putative [Ricinus communis] >gi|223537072|gb|EEF38707.1| Alpha-N-arabinofuranosidase 1 precursor, putative [Ricinus communis]	73.7	308	8e-108
CAI_3D_5SP_C04	gi|147819145|emb|CAN78082.1|	hypothetical protein [Vitis vinifera]	81.76	159	2e-72
CAI_3D_5SP_C05	gi|225459126|ref|XP_002285696.1|	PREDICTED: hypothetical protein isoform 1 [Vitis vinifera]	80.95	63	7e-21
CAI_3D_5SP_C06	gi|255635604|gb|ACU18152.1|	unknown [Glycine max]	66.56	302	2e-95
CAI_3D_5SP_C09	gi|255539122|ref|XP_002510626.1|	chaperonin containing t-complex protein 1, beta subunit, tcpb, putative [Ricinus communis] >gi|223551327|gb|EEF52813.1| chaperonin containing t-complex protein 1, beta subunit, tcpb, putative [Ricinus communis]	66.1	118	1e-29
CAI_3D_5SP_D01	gi|270496068|ref|ZP_06213060.1|	hypothetical protein AcavDRAFT_4806 [Acidovorax avenae subsp. avenae ATCC 19860] >gi|270327086|gb|EFA37945.1| hypothetical protein AcavDRAFT_4806 [Acidovorax avenae subsp. avenae ATCC 19860]	47.22	144	1e-24
CAI_3D_5SP_D02	gi|11131528|sp|Q9SEA0|CCS_CITSI	RecName: Full=Capsanthin/capsorubin synthase, chromoplast; Flags: Precursor >gi|6580973|gb|AAF18389.1|AF169241_1 capsanthin/capsorubin synthase [Citrus sinensis] >gi|237664127|gb|ACR09634.1| lycopene beta-cyclase [Citrus sinensis]	100	239	5e-134
CAI_3D_5SP_D06	gi|224064017|ref|XP_002301350.1|	predicted protein [Populus trichocarpa] >gi|222843076|gb|EEE80623.1| predicted protein [Populus trichocarpa]	77.21	272	1e-103
CAI_3D_5SP_D07	gi|145408590|ref|YP_001152214.1|	ORF124 [Pinus koraiensis] >gi|145048839|gb|ABP35456.1| ORF124 [Pinus koraiensis]	91.53	59	6e-25
CAI_3D_5SP_D10	gi|118482586|gb|ABK93213.1|	unknown [Populus trichocarpa] >gi|118485561|gb|ABK94632.1| unknown [Populus trichocarpa]	96.63	178	2e-97
CAI_3D_5SP_E01	gi|225444313|ref|XP_002263767.1|	PREDICTED: hypothetical protein [Vitis vinifera]	82.97	229	7e-106
CAI_3D_5SP_E04	gi|166343818|gb|ABY86652.1|	phytoene synthase [Citrus maxima]	98.36	244	4e-123
CAI_3D_5SP_E08	gi|224106894|ref|XP_002314320.1|	predicted protein [Populus trichocarpa] >gi|118481365|gb|ABK92625.1| unknown [Populus trichocarpa] >gi|222850728|gb|EEE88275.1| predicted protein [Populus trichocarpa]	77.11	83	8e-32
CAI_3D_5SP_E09	gi|255587510|ref|XP_002534297.1|	conserved hypothetical protein [Ricinus communis] >gi|223525556|gb|EEF28089.1| conserved hypothetical protein [Ricinus communis]	84.64	267	3e-115
CAI_3D_5SP_E11	gi|255540017|ref|XP_002511073.1|	conserved hypothetical protein [Ricinus communis] >gi|223550188|gb|EEF51675.1| conserved hypothetical protein [Ricinus communis]	49.52	105	6e-19

IP : 14.49.138.138, 2017-11-03 13:30:33

CAI_3D_5SP_E12	gi|224112078|ref|XP_002332837.1|	predicted protein [Populus trichocarpa] >gi|222833276|gb|EEE71753.1| predicted protein [Populus trichocarpa]	95.58	113	1e-56
CAI_3D_5SP_F01	gi|224064456|ref|XP_002301485.1|	predicted protein [Populus trichocarpa] >gi|222843211|gb|EEE80758.1| predicted protein [Populus trichocarpa]	93.38	136	5e-68
CAI_3D_5SP_F05	gi|118488433|gb|ABK96031.1|	unknown [Populus trichocarpa]	80	100	1e-26
CAI_3D_5SP_G04	gi|255542388|ref|XP_002512257.1|	cysteine synthase, putative [Ricinus communis] >gi|223548218|gb|EEF49709.1| cysteine synthase, putative [Ricinus communis]	82.32	198	2e-79
CAI_3D_5SP_G06	gi|225452574|ref|XP_002280727.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270251610|emb|CBI34983.1| unnamed protein product [Vitis vinifera]	66.67	195	7e-67
CAI_3D_5SP_G07	gi|225453329|ref|XP_002270593.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|147854591|emb|CAN82778.1| hypothetical protein [Vitis vinifera] >gi|270227977|emb|CBI16690.1| unnamed protein product [Vitis vinifera]	72.32	112	5e-32
CAI_3D_5SP_G10	gi|188529683|gb|ACD62528.1|	bet1-like snare 1-1 [Malus x domestica]	86.89	122	1e-55
CAI_3D_5SP_H02	gi|224137502|ref|XP_002327142.1|	predicted protein [Populus trichocarpa] >gi|222835457|gb|EEE73892.1| predicted protein [Populus trichocarpa]	42.8	257	6e-42
CAI_3D_5SP_H05	gi|224122988|ref|XP_002318966.1|	predicted protein [Populus trichocarpa] >gi|222857342|gb|EEE94889.1| predicted protein [Populus trichocarpa]	80.7	57	2e-20
CAI_3D_5SP_H06	gi|270254448|emb|CBI36838.1|	unnamed protein product [Vitis vinifera]	93.39	121	2e-50
CAI_3D_5SP_H08	gi|68138979|gb|AAY86035.1|	pyruvate kinase [Citrus sinensis]	99.5	202	8e-113
CAI_3D_5SP_H10	gi|255567234|ref|XP_002524598.1|	transcription factor, putative [Ricinus communis] >gi|223536151|gb|EEF37806.1| transcription factor, putative [Ricinus communis]	84.57	162	2e-56
CAI_3D_5SP_H12	gi|255543899|ref|XP_002513012.1|	amidophosphoribosyltransferase, putative [Ricinus communis] >gi|223548023|gb|EEF49515.1| amidophosphoribosyltransferase, putative [Ricinus communis]	82.86	35	5e-11
CAI_4A_5SP_A01	gi|224120092|ref|XP_002318240.1|	predicted protein [Populus trichocarpa] >gi|222858913|gb|EEE96460.1| predicted protein [Populus trichocarpa]	90.91	143	7e-45
CAI_4A_5SP_A07	gi|225465631|ref|XP_002268271.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270233752|emb|CBI22361.1| unnamed protein product [Vitis vinifera]	62.34	77	1e-21
CAI_4A_5SP_A10	gi|225436297|ref|XP_002266076.1|	PREDICTED: hypothetical protein isoform 2 [Vitis vinifera]	85.51	69	2e-24
CAI_4A_5SP_A12	gi|224125568|ref|XP_002319618.1|	predicted protein [Populus trichocarpa] >gi|118482627|gb|ABK93233.1| unknown [Populus trichocarpa] >gi|222857994|gb|EEE95541.1| predicted protein [Populus trichocarpa]	93.04	273	2e-132
CAI_4A_5SP_B01	gi|225446742|ref|XP_002282652.1|	PREDICTED: hypothetical protein [Vitis vinifera]	81.25	48	7e-15
CAI_4A_5SP_B02	gi|225454026|ref|XP_002281096.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270259774|emb|CBI38907.1| unnamed protein product [Vitis vinifera]	60.12	163	5e-30
CAI_4A_5SP_B06	gi|122894104|gb|ABM67698.1|	mitogen-activated protein kinase [Citrus sinensis]	99.62	260	5e-148
CAI_4A_5SP_B08	gi|224083147|ref|XP_002306954.1|	predicted protein [Populus trichocarpa] >gi|222856403|gb|EEE93950.1| predicted protein [Populus trichocarpa]	64.29	182	6e-61
CAI_4A_5SP_B12	gi|255626029|gb|ACU13359.1|	unknown [Glycine max]	86.9	145	1e-76
CAI_4A_5SP_C03	gi|225444355|ref|XP_002266186.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|147833195|emb|CAN68644.1| hypothetical protein [Vitis vinifera] >gi|270234583|emb|CBI23185.1| unnamed protein product [Vitis vinifera]	94.05	84	8e-44
CAI_4A_5SP_C04	gi|255588871|ref|XP_002534747.1|	conserved hypothetical protein [Ricinus communis] >gi|255604001|ref|XP_002538152.1| conserved hypothetical protein [Ricinus communis] >gi|223513575|gb|EEF24232.1| conserved hypothetical protein [Ricinus communis] >gi|223524644|gb|EEF27638.1| conserved hypothetical protein [Ricinus communis]	91.3	46	2e-16
CAI_4A_5SP_C08	gi|255575997|ref|XP_002528894.1|	conserved hypothetical protein [Ricinus communis] >gi|223531648|gb|EEF33474.1| conserved hypothetical protein [Ricinus communis]	84.13	126	7e-58
CAI_4A_5SP_C12	gi|255554312|ref|XP_002518196.1|	Beta-amylase, putative [Ricinus communis] >gi|223542792|gb|EEF44329.1| Beta-amylase, putative [Ricinus communis]	65.81	234	1e-78
CAI_4A_5SP_D11	gi|255580317|ref|XP_002530987.1|	conserved hypothetical protein [Ricinus communis] >gi|223529439|gb|EEF31399.1| conserved hypothetical protein [Ricinus communis]	91.16	249	2e-127
CAI_4A_5SP_E01	gi|225456629|ref|XP_002266656.1|	PREDICTED: hypothetical protein [Vitis vinifera]	74.84	306	4e-112
CAI_4A_5SP_E05	gi|255547908|ref|XP_002515011.1|	oligopeptidase, putative [Ricinus communis] >gi|223546062|gb|EEF47565.1| oligopeptidase, putative [Ricinus communis]	80.93	215	3e-85
CAI_4A_5SP_E06	gi|225449456|ref|XP_002283210.1|	PREDICTED: hypothetical protein isoform 2 [Vitis vinifera] >gi|225449458|ref|XP_002283206.1| PREDICTED: hypothetical protein isoform 1 [Vitis vinifera] >gi|270244720|emb|CBI31653.1| unnamed protein product [Vitis vinifera]	84.09	132	1e-60
CAI_4A_5SP_E08	gi|225448142|ref|XP_002263770.1|	PREDICTED: hypothetical protein [Vitis vinifera]	71.26	261	2e-99
CAI_4A_5SP_E09	gi|255536923|ref|XP_002509528.1|	structural constituent of ribosome, putative [Ricinus communis] >gi|223549427|gb|EEF50915.1| structural constituent of ribosome, putative [Ricinus communis]	45.97	124	6e-18
CAI_4A_5SP_E10	gi|146454784|gb|ABQ42058.1|	putative translation factor [Sonneratia caseolaris]	94.87	78	6e-35
CAI_4A_5SP_F09	gi|255539132|ref|XP_002510631.1|	conserved hypothetical protein [Ricinus communis] >gi|223551332|gb|EEF52818.1| conserved hypothetical protein [Ricinus communis]	74.74	95	2e-33
CAI_4A_5SP_G01	gi|15222552|ref|NP_176568.1|	proline-rich family protein [Arabidopsis thaliana] >gi|42571987|ref|NP_974084.1| proline-rich family protein [Arabidopsis thaliana] >gi|12325014|gb|AAG52456.1|AC010852_13 unknown protein; 55304-53614 [Arabidopsis thaliana] >gi|19424093|gb|AAL87329.1| unknown protein [Arabidopsis thaliana] >gi|21436183|gb|AAM51379.1| unknown protein [Arabidopsis thaliana]	82.04	206	2e-101

IP : 14.49.138.138, 2017-11-03 13:30:33

CAI_4A_5SP_G04	gi|118486563|gb|ABK95120.1|	unknown [Populus trichocarpa]	69.14	81	3e-20
CAI_4A_5SP_G05	gi|224054958|ref|XP_002298393.1|	predicted protein [Populus trichocarpa] >gi|222845651|gb|EEE83198.1| predicted protein [Populus trichocarpa]	90.83	109	3e-55
CAI_4A_5SP_G07	gi|255574436|ref|XP_002528131.1|	conserved hypothetical protein [Ricinus communis] >gi|223532470|gb|EEF34261.1| conserved hypothetical protein [Ricinus communis]	68.18	110	9e-37
CAI_4A_5SP_H07	gi|242199340|gb|ACS87991.1|	UDP-glucosyltransferase family 1 protein [Citrus sinensis]	98.55	276	8e-150
CAI_4A_5SP_H09	gi|224122442|ref|XP_002330482.1|	predicted protein [Populus trichocarpa] >gi|222872416|gb|EEF09547.1| predicted protein [Populus trichocarpa]	93.5	123	3e-45
CAI_4A_5SP_H10	gi|224128482|ref|XP_002320343.1|	predicted protein [Populus trichocarpa] >gi|222861116|gb|EEE98658.1| predicted protein [Populus trichocarpa]	85.37	82	2e-32
CAI_4A_5SP_H12	gi|225452304|ref|XP_002272292.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270251473|emb|CBI34846.1| unnamed protein product [Vitis vinifera]	80.46	87	1e-34
CAI_4C_5SP_A04	gi|116830901|gb|ABK28407.1|	unknown [Arabidopsis thaliana]	89.13	46	3e-16
CAI_4C_5SP_A08	gi|224138378|ref|XP_002322799.1|	predicted protein [Populus trichocarpa] >gi|222867429|gb|EEF04560.1| predicted protein [Populus trichocarpa]	53.85	130	9e-22
CAI_4C_5SP_A09	gi|22327930|ref|NP_680453.1|	unknown protein [Arabidopsis thaliana] >gi|79331263|ref|NP_001032092.1| unknown protein [Arabidopsis thaliana] >gi|19423921|gb|AAL87352.1| unknown protein [Arabidopsis thaliana] >gi|21689763|gb|AAM67525.1| unknown protein [Arabidopsis thaliana] >gi|26452952|dbj|BAC43552.1| unknown protein [Arabidopsis thaliana] >gi|222423651|dbj|BAH19793.1| AT5G58005 [Arabidopsis thaliana]	76.64	107	5e-42
CAI_4C_5SP_C02	gi|224069760|ref|XP_002326407.1|	predicted protein [Populus trichocarpa] >gi|118480989|gb|ABK92448.1| unknown [Populus trichocarpa] >gi|222833600|gb|EEE72077.1| predicted protein [Populus trichocarpa]	90.49	263	7e-130
CAI_4C_5SP_C04	gi|2270994|gb|AAB71227.1|	Ca+2-binding EF hand protein [Glycine max] >gi|255625919|gb|ACU13304.1| unknown [Glycine max]	71.3	115	3e-44
CAI_4C_5SP_C07	gi|255556842|ref|XP_002519454.1|	ankyrin repeat-containing protein, putative [Ricinus communis] >gi|223541317|gb|EEF42868.1| ankyrin repeat-containing protein, putative [Ricinus communis]	78.43	204	1e-88
CAI_4C_5SP_C08	gi|225468749|ref|XP_002274350.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|225469368|ref|XP_002262939.1| PREDICTED: hypothetical protein [Vitis vinifera]	81.67	251	1e-116
CAI_4C_5SP_D06	gi|224108151|ref|XP_002314739.1|	predicted protein [Populus trichocarpa] >gi|222863779|gb|EEF00910.1| predicted protein [Populus trichocarpa]	53.93	178	1e-37
CAI_4C_5SP_D09	gi|221327587|gb|ACM17463.1|	ascorbate peroxidase [Citrus maxima]	98.6	143	8e-59
CAI_4C_5SP_D11	gi|9864189|gb|AAG01339.1|	terpene synthase [Citrus junos]	53.45	116	4e-27
CAI_4C_5SP_E01	gi|255578068|ref|XP_002529904.1|	gaba(A) receptor-associated protein, putative [Ricinus communis] >gi|223530581|gb|EEF32458.1| gaba(A) receptor-associated protein, putative [Ricinus communis]	98.33	120	6e-60
CAI_4C_5SP_E03	gi|15229784|ref|NP_189967.1|	CAM7 (CALMODULIN 7); calcium ion binding [Arabidopsis thaliana] >gi|224086697|ref|XP_002307936.1| predicted protein [Populus trichocarpa] >gi|224106642|ref|XP_002314234.1| predicted protein [Populus trichocarpa] >gi|224137536|ref|XP_002322582.1| predicted protein [Populus trichocarpa] >gi|225435971|ref|XP_002270925.1| PREDICTED: hypothetical protein [Vitis vinifera] >gi|225440224|ref|XP_002283763.1| PREDICTED: hypothetical protein [Vitis vinifera] >gi|255549096|ref|XP_002515603.1| calmodulin, putative [Ricinus communis] >gi|255572905|ref|XP_002527384.1| calmodulin, putative [Ricinus communis] >gi|27805429|sp|P59220|CALM7_ARATH RecName: Full=Calmodulin-7; Short=CaM-7 >gi|49037479|sp|P62199|CALM1_PETHY RecName: Full=Calmodulin-1; Short=CaM-1 >gi|49037480|sp|P62200|CALM1_DAUCA RecName: Full=Calmodulin-1/11/16; Short=CaM-1/11/16 >gi|49037481|sp|P62201|CALM_LILLO RecName: Full=Calmodulin; Short=CaM >gi|49037482|sp|P62202|CALM_BRYDI RecName: Full=Calmodulin; Short=CaM; AltName: Full=BC329 >gi|62286560|sp|Q7Y052|CALM_EUPCH RecName: Full=Calmodulin; Short=CaM >gi|5825598|gb|AAD53313.1|AF178073_1 calmodulin 7 [Arabidopsis thaliana] >gi|9992891|gb|AAG11418.1|AF292108_1 calmodulin [Prunus avium] >gi|21913285|gb|AAM81202.1|AF494219_1 calmodulin 1 [Medicago truncatula] >gi|18326|emb|CAA42423.1| calmodulin [Daucus carota] >gi|19447|emb|CAA78301.1| calmodulin [Lilium longiflorum] >gi|169207|gb|AAA33706.1| calmodulin [Petunia x hybrida] >gi|308900|gb|AAA33397.1| calmodulin [Lilium longiflorum] >gi|505154|emb|CAA43143.1| Calmodulin [Malus x domestica] >gi|535444|gb|AAA92681.1| calmodulin [Pisum sativum] >gi|7362781|emb|CAB83153.1| calmodulin 7 [Arabidopsis thaliana] >gi|11036952|gb|AAG27432.1| calmodulin [Elaeis guineensis] >gi|14625405|dbj|BAB61909.1| calmodulin NtCaM3 [Nicotiana tabacum] >gi|14625407|dbj|BAB61910.1| calmodulin NtCaM4 [Nicotiana tabacum] >gi|14625409|dbj|BAB61911.1| calmodulin NtCaM5 [Nicotiana tabacum] >gi|14625411|dbj|BAB61912.1| calmodulin NtCaM6 [Nicotiana tabacum] >gi|14625413|dbj|BAB61913.1| calmodulin NtCaM7 [Nicotiana tabacum] >gi|14625415|dbj|BAB61914.1| calmodulin NtCaM8 [Nicotiana tabacum] >gi|14625421|dbj|BAB61917.1| calmodulin NtCaM11 [Nicotiana tabacum] >gi|14625423|dbj|BAB61918.1| calmodulin NtCaM12 [Nicotiana tabacum] >gi|21594484|gb|AAM66013.1| calmodulin 7 [Arabidopsis thaliana] >gi|40365136|gb|AAP55717.2| calmodulin [Euphorbia characias] >gi|45181612|gb|AAS55460.1| calmodulin cam-11 [Daucus carota] >gi|45181614|gb|AAS55461.1| calmodulin cam-16 [Daucus carota] >gi|50299503|gb|AAT73615.1| calmodulin cam-202 [Daucus carota] >gi|50299507|gb|AAT73617.1| calmodulin cam-204 [Daucus carota] >gi|50299515|gb|AAT73621.1| calmodulin cam-208 [Daucus carota] >gi|50299517|gb|AAT73622.1| calmodulin cam-209 [Daucus carota] >gi|52851162|emb|CAH58629.1| calmodulin [Plantago major] >gi|52851164|emb|CAH58630.1| calmodulin [Plantago major]	100	149	6e-79

IP : 14.49.138.138, 2017-11-03 13:30:33

		>gi|60729719|emb|CAH57707.1| calmodulin [Quercus petraea] >gi|62125396|gb|AAX63770.1| calmodulin [Populus tomentosa] >gi|75756242|gb|ABA27138.1| calmodulin 2 [Catharanthus roseus] >gi|98960891|gb|ABF58929.1| At3g43810 [Arabidopsis thaliana] >gi|110742424|dbj|BAE99131.1| calmodulin 7 [Arabidopsis thaliana] >gi|118136471|gb|ABK62856.1| calmodulin [Scoparia dulcis] >gi|118481324|gb|ABK92605.1| unknown [Populus trichocarpa] >gi|118481354|gb|ABK92620.1| unknown [Populus trichocarpa] >gi|118481535|gb|ABK92710.1| unknown [Populus trichocarpa] >gi|118482590|gb|ABK93215.1| unknown [Populus trichocarpa] >gi|118483779|gb|ABK93782.1| unknown [Populus trichocarpa] >gi|118484140|gb|ABK93953.1| unknown [Populus trichocarpa] >gi|118484730|gb|ABK94234.1| unknown [Populus trichocarpa] >gi|118484977|gb|ABK94353.1| unknown [Populus trichocarpa] >gi|118485441|gb|ABK94577.1| unknown [Populus trichocarpa] >gi|118485636|gb|ABK94668.1| unknown [Populus trichocarpa] >gi|118485771|gb|ABK94734.1| unknown [Populus trichocarpa] >gi|118485950|gb|ABK94820.1| unknown [Populus trichocarpa] >gi|146403792|gb|ABQ32302.1| putative calmodulin [Artemisia annua] >gi|147837821|emb|CAN63123.1| hypothetical protein [Vitis vinifera] >gi|151500327|gb|ABS12105.1| calmodulin 1 [Morus nigra] >gi|189031544|gb|ACD74910.1| calmodulin [Vitis quinquangularis] >gi|192910746|gb|ACF06481.1| calmodulin 8 [Elaeis guineensis] >gi|192910748|gb|ACF06482.1| calmodulin 8 [Elaeis guineensis] >gi|192910750|gb|ACF06483.1| calmodulin 8 [Elaeis guineensis] >gi|192910752|gb|ACF06484.1| calmodulin 8 [Elaeis guineensis] >gi|197312869|gb|ACH63215.1| calmodulin [Rheum australe] >gi|222850642|gb|EEE88189.1| predicted protein [Populus trichocarpa] >gi|222853912|gb|EEE91459.1| predicted protein [Populus trichocarpa] >gi|222867212|gb|EEF04343.1| predicted protein [Populus trichocarpa] >gi|223533255|gb|EEF35009.1| calmodulin, putative [Ricinus communis] >gi|223545241|gb|EEF46748.1| calmodulin, putative [Ricinus communis] >gi|224612147|gb|ACN60147.1| calmodulin [Lonicera japonica] >gi|226377531|gb|ACO52511.1| calmodulin [Panax ginseng] >gi|247421773|gb|ACS96443.1| calmodulin 7 [Jatropha curcas] >gi|255039654|gb|ACT99605.1| calmodulin [Morus alba var. multicaulis] >gi|282935436|gb|ADB03783.1| calmodulin [Ipomoea batatas] >gi|445602|prf||1909349A calmodulin			
CAI_4C_5SP_E06	gi|224053793|ref|XP_002297982.1|	predicted protein [Populus trichocarpa] >gi|222845240|gb|EEE82787.1| predicted protein [Populus trichocarpa]	77.21	136	4e-53
CAI_4C_5SP_E08	gi|255573655|ref|XP_002527750.1|	arf gtpase-activating protein, putative [Ricinus communis] >gi|223532891|gb|EEF34663.1| arf gtpase-activating protein, putative [Ricinus communis]	78.31	249	3e-104
CAI_4C_5SP_F03	gi|122187475|sp|Q1SF86|ATG12_MEDTR	RecName: Full=Putative autophagy-related protein 12	84.21	95	1e-39
CAI_4C_5SP_F09	gi|225457124|ref|XP_002283556.1|	PREDICTED: hypothetical protein [Vitis vinifera]	74.76	103	8e-35
CAI_4C_5SP_G10	gi|225435108|ref|XP_002284515.1|	PREDICTED: hypothetical protein [Vitis vinifera]	75.77	227	7e-98
CAI_4C_5SP_G12	gi|224142863|ref|XP_002324755.1|	predicted protein [Populus trichocarpa] >gi|118483071|gb|ABK93445.1| unknown [Populus trichocarpa] >gi|222866189|gb|EEF03320.1| predicted protein [Populus trichocarpa]	97.5	40	6e-16
CAI_4C_5SP_H02	gi|112253903|ref|YP_717158.1|	hypothetical protein BrnapMp061 [Brassica napus] >gi|37591105|dbj|BAC98907.1| hypothetical protein [Brassica napus]	92.74	248	1e-111
CAI_4C_5SP_H08	gi|255576607|ref|XP_002529194.1|	(S)-2-hydroxy-acid oxidase, putative [Ricinus communis] >gi|223531372|gb|EEF33208.1| (S)-2-hydroxy-acid oxidase, putative [Ricinus communis]	78.91	256	5e-107
CAI_4C_5SP_H09	gi|255536923|ref|XP_002509528.1|	structural constituent of ribosome, putative [Ricinus communis] >gi|223549427|gb|EEF50915.1| structural constituent of ribosome, putative [Ricinus communis]	63.78	185	4e-43
CAI_4C_5SP_H10	gi|224057529|ref|XP_002299252.1|	predicted protein [Populus trichocarpa] >gi|118481982|gb|ABK92922.1| unknown [Populus trichocarpa] >gi|222846510|gb|EEE84057.1| predicted protein [Populus trichocarpa]	82.61	115	8e-36
CAI_4D_5SP_A05	gi|124359550|gb|ABN05967.1|	GroEL-like chaperone, ATPase [Medicago truncatula]	91.4	221	6e-109
CAI_4D_5SP_B01	gi|255583802|ref|XP_002532653.1|	ubiquitin-conjugating enzyme E2, putative [Ricinus communis] >gi|223527613|gb|EEF29726.1| ubiquitin-conjugating enzyme E2, putative [Ricinus communis]	97.97	148	4e-82
CAI_4D_5SP_B08	gi|255557943|ref|XP_002520000.1|	conserved hypothetical protein [Ricinus communis] >gi|223540764|gb|EEF42324.1| conserved hypothetical protein [Ricinus communis]	60.61	132	1e-33
CAI_4D_5SP_C06	gi|224086146|ref|XP_002307832.1|	predicted protein [Populus trichocarpa] >gi|222857281|gb|EEE94828.1| predicted protein [Populus trichocarpa]	50.25	201	4e-37
CAI_4D_5SP_C07	gi|211906450|gb|ACJ11718.1|	phosphoglycerate kinase [Gossypium hirsutum]	90.41	271	2e-128
CAI_4D_5SP_C09	gi|114329713|ref|YP_740533.1|	NADH-plastoquinone oxidoreductase subunit 7 [Citrus sinensis] >gi|122166135|sp|Q09MC0|NDHH_CITSI RecName: Full=NAD(P)H-quinone oxidoreductase subunit H, chloroplastic; AltName: Full=NAD(P)H dehydrogenase subunit H; AltName: Full=NADH-plastoquinone oxidoreductase subunit H; AltName: Full=NADH-plastoquinone oxidoreductase 49 kDa subunit >gi|113952679|gb|ABI49077.1| NADH-plastoquinone oxidoreductase subunit 7 [Citrus sinensis]	100	105	2e-49
CAI_4D_5SP_C10	gi|224060923|ref|XP_002300288.1|	predicted protein [Populus trichocarpa] >gi|222847546|gb|EEE85093.1| predicted protein [Populus trichocarpa]	83.33	48	6e-15
CAI_4D_5SP_C11	gi|255627661|gb|ACU14175.1|	unknown [Glycine max]	94.55	55	1e-21
CAI_4D_5SP_D04	gi|255576842|ref|XP_002529307.1|	conserved hypothetical protein [Ricinus communis] >gi|223531231|gb|EEF33076.1| conserved hypothetical protein [Ricinus communis]	82.05	156	2e-47
CAI_4D_5SP_D08	gi|255568426|ref|XP_002525187.1|	Nodulation receptor kinase precursor, putative [Ricinus communis] >gi|223535484|gb|EEF37153.1| Nodulation receptor kinase precursor, putative [Ricinus communis]	85.86	198	1e-82
CAI_4D_5SP_E01	gi|270253659|emb|CBI36057.1|	unnamed protein product [Vitis vinifera]	60.94	128	1e-29

IP : 14.49.138.138, 2017-11-03 13:30:33

CAI_4D_5SP_E04	gi|225439505|ref|XP_002271217.1|	PREDICTED: hypothetical protein isoform 1 [Vitis vinifera] >gi|270229212|emb|CBI18141.1| unnamed protein product [Vitis vinifera]	78.31	166	3e-74
CAI_4D_5SP_F01	gi|225445503|ref|XP_002285199.1|	PREDICTED: hypothetical protein isoform 1 [Vitis vinifera] >gi|147782859|emb|CAN70098.1| hypothetical protein [Vitis vinifera]	74.52	259	8e-93
CAI_4D_5SP_F06	gi|255570280|ref|XP_002526100.1|	pearli, putative [Ricinus communis] >gi|223534597|gb|EEF36294.1| pearli, putative [Ricinus communis]	80.51	272	3e-120
CAI_4D_5SP_F07	gi|255546267|ref|XP_002514193.1|	Protein-tyrosine phosphatase mitochondrial 1, mitochondrial precursor, putative [Ricinus communis] >gi|223546649|gb|EEF48147.1| Protein-tyrosine phosphatase mitochondrial 1, mitochondrial precursor, putative [Ricinus communis]	78.62	145	3e-56
CAI_4D_5SP_F11	gi|225459136|ref|XP_002285702.1|	PREDICTED: hypothetical protein [Vitis vinifera]	80.45	179	1e-72
CAI_4D_5SP_G01	gi|255558526|ref|XP_002520288.1|	conserved hypothetical protein [Ricinus communis] >gi|223540507|gb|EEF42074.1| conserved hypothetical protein [Ricinus communis]	70.85	199	6e-71
CAI_4D_5SP_G02	gi|225431908|ref|XP_002276743.1|	PREDICTED: hypothetical protein [Vitis vinifera]	97.93	193	8e-92
CAI_4D_5SP_G07	gi|255550842|ref|XP_002516469.1|	conserved hypothetical protein [Ricinus communis] >gi|223544289|gb|EEF45810.1| conserved hypothetical protein [Ricinus communis]	70.82	257	2e-107
CAI_4D_5SP_G08	gi|224075543|ref|XP_002304675.1|	predicted protein [Populus trichocarpa] >gi|222842107|gb|EEE79654.1| predicted protein [Populus trichocarpa]	91.3	69	4e-28
CAI_4D_5SP_G10	gi|255567650|ref|XP_002524804.1|	conserved hypothetical protein [Ricinus communis] >gi|223535988|gb|EEF37647.1| conserved hypothetical protein [Ricinus communis]	58.15	184	5e-39
CAI_4D_5SP_G12	gi|255575938|ref|XP_002528866.1|	conserved hypothetical protein [Ricinus communis] >gi|223531717|gb|EEF33540.1| conserved hypothetical protein [Ricinus communis]	61.36	176	2e-57
CAI_4D_5SP_H02	gi|224106846|ref|XP_002314304.1|	predicted protein [Populus trichocarpa] >gi|222850712|gb|EEE88259.1| predicted protein [Populus trichocarpa]	83.91	174	7e-95
CAI_4D_5SP_H03	gi|225441092|ref|XP_002263561.1|	PREDICTED: hypothetical protein [Vitis vinifera]	75.37	203	9e-84
CAI_4D_5SP_H07	gi|11596184|gb|AAG38520.1|AF283535_1	proteinase inhibitor se60-like protein [Citrus x paradisi]	97.26	73	3e-29
CAI_4D_5SP_H10	gi|224133682|ref|XP_002321635.1|	predicted protein [Populus trichocarpa] >gi|222868631|gb|EEF05762.1| predicted protein [Populus trichocarpa]	63.49	189	2e-49
CAI_5A_5SP_A02	gi|118489548|gb|ABK96576.1|	unknown [Populus trichocarpa x Populus deltoides]	76.22	143	9e-61
CAI_5A_5SP_A03	gi|225445955|ref|XP_002264997.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270228957|emb|CBI17889.1| unnamed protein product [Vitis vinifera]	66.67	66	6e-19
CAI_5A_5SP_A06	gi|147827008|emb|CAN62285.1|	hypothetical protein [Vitis vinifera]	81.25	64	3e-25
CAI_5A_5SP_B03	gi|255637791|gb|ACU19217.1|	unknown [Glycine max]	81.63	49	8e-16
CAI_5A_5SP_B04	gi|225435800|ref|XP_002285750.1|	PREDICTED: hypothetical protein [Vitis vinifera]	74.32	74	9e-13
CAI_5A_5SP_B05	gi|255567977|ref|XP_002524966.1|	sigma factor sigb regulation protein rsbq, putative [Ricinus communis] >gi|223535801|gb|EEF37463.1| sigma factor sigb regulation protein rsbq, putative [Ricinus communis]	90	40	2e-13
CAI_5A_5SP_B09	gi|255538078|ref|XP_002510104.1|	conserved hypothetical protein [Ricinus communis] >gi|223550805|gb|EEF52291.1| conserved hypothetical protein [Ricinus communis]	71.43	77	5e-22
CAI_5A_5SP_B11	gi|147804918|emb|CAN78050.1|	hypothetical protein [Vitis vinifera]	60.92	174	3e-50
CAI_5A_5SP_B12	gi|114329687|ref|YP_740508.1|	RNA polymerase alpha subunit [Citrus sinensis] >gi|122166151|sp|Q09ME5|RPOA_CITSI RecName: Full=DNA-directed RNA polymerase subunit alpha; Short=PEP; AltName: Full=Plastid-encoded RNA polymerase subunit alpha; Short=RNA polymerase subunit alpha >gi|113952653|gb|ABI49051.1| RNA polymerase alpha subunit [Citrus sinensis]	91.21	91	8e-30
CAI_5A_5SP_C05	gi|118488288|gb|ABK95963.1|	unknown [Populus trichocarpa]	91.81	232	4e-115
CAI_5A_5SP_C08	gi|150251526|ref|YP_001312258.1|	hypothetical protein CYtaCp093 [Cycas taitungensis] >gi|150251548|ref|YP_001312280.1| hypothetical protein CYtaCp115 [Cycas taitungensis] >gi|149941576|dbj|BAF65000.1| hypothetical protein [Cycas taitungensis] >gi|149941598|dbj|BAF65022.1| hypothetical protein [Cycas taitungensis]	96.23	53	6e-22
CAI_5A_5SP_C09	gi|115452579|ref|NP_001049890.1|	Os03g0306800 [Oryza sativa (japonica cultivar-group)] >gi|108707737|gb|ABF95532.1| CP12, putative, expressed [Oryza sativa (japonica cultivar-group)] >gi|113548361|dbj|BAF11804.1| Os03g0306800 [Oryza sativa Japonica Group] >gi|125585993|gb|EAZ26657.1| hypothetical protein OsJ_10560 [Oryza sativa Japonica Group] >gi|215737299|dbj|BAG96228.1| unnamed protein product [Oryza sativa Japonica Group]	86.21	58	1e-23
CAI_5A_5SP_D04	gi|283132359|dbj|BAI63585.1|	ACT-domain-containing protein kinase [Lotus japonicus]	71.35	171	3e-58
CAI_5A_5SP_D06	gi|225444171|ref|XP_002271024.1|	PREDICTED: hypothetical protein [Vitis vinifera]	48.35	91	8e-14
CAI_5A_5SP_D07	gi|224127630|ref|XP_002329325.1|	predicted protein [Populus trichocarpa] >gi|222870779|gb|EEF07910.1| predicted protein [Populus trichocarpa]	57.84	268	1e-71
CAI_5A_5SP_D12	gi|225424633|ref|XP_002282325.1|	PREDICTED: hypothetical protein [Vitis vinifera]	63.75	80	2e-17
CAI_5A_5SP_E02	gi|224106141|ref|XP_002314058.1|	silencing group B protein [Populus trichocarpa] >gi|222850466|gb|EEE88013.1| silencing group B protein [Populus trichocarpa]	94.05	84	8e-40
CAI_5A_5SP_E03	gi|12231174|dbj|BAB20970.1|	aspartic proteinase 2 [Nepenthes alata]	78.52	135	5e-59

IP : 14.49.138.138, 2017-11-03 13:30:33

CAI_5A_5SP_E12	gi|55168340|gb|AAV44205.1|	unknow protein [Oryza sativa Japonica Group]	94.74	38	2e-14
CAI_5A_5SP_F03	gi|225428772|ref|XP_002282024.1|	PREDICTED: hypothetical protein [Vitis vinifera]	59.92	257	6e-69
CAI_5A_5SP_F07	gi|255646523|gb|ACU23739.1|	unknown [Glycine max]	77.27	88	2e-40
CAI_5A_5SP_F09	gi|224119574|ref|XP_002331194.1|	cytochrome P450 [Populus trichocarpa] >gi|222873315|gb|EEF10446.1| cytochrome P450 [Populus trichocarpa]	65.89	129	5e-34
CAI_5A_5SP_F12	gi|147791931|emb|CAN67897.1|	hypothetical protein [Vitis vinifera]	70.5	200	6e-64
CAI_5A_5SP_G03	gi|224099815|ref|XP_002311631.1|	predicted protein [Populus trichocarpa] >gi|222851451|gb|EEE88998.1| predicted protein [Populus trichocarpa]	82.14	140	1e-58
CAI_5A_5SP_G05	gi|225428637|ref|XP_002284808.1|	PREDICTED: hypothetical protein [Vitis vinifera]	70.63	126	3e-31
CAI_5A_5SP_G09	gi|118489959|gb|ABK96776.1|	unknown [Populus trichocarpa x Populus deltoides]	86.34	183	3e-88
CAI_5A_5SP_G10	gi|225432374|ref|XP_002276206.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|226713609|sp|A7NW78|U4974_VITVI RecName: Full=UPF0497 membrane protein 4	59.29	113	9e-17
CAI_5A_5SP_G12	gi|15219147|ref|NP_173069.1|	TMS membrane family protein / tumour differentially expressed (TDE) family protein [Arabidopsis thaliana] >gi|6587821|gb|AAF18512.1|AC010924_25 Contains similarity to gb|AF181686 membrane protein TMS1d from Drosophila melanogaster. ESTs gb|R64994, gb|AI994832, gb|Z47674 come from this gene [Arabidopsis thaliana]	85.9	78	9e-28
CAI_5A_5SP_H01	gi|118483216|gb|ABK93511.1|	unknown [Populus trichocarpa]	42.49	193	1e-27
CAI_5A_5SP_H03	gi|255550147|ref|XP_002516124.1|	peroxisome assembly protein, putative [Ricinus communis] >gi|223544610|gb|EEF46126.1| peroxisome assembly protein, putative [Ricinus communis]	62.5	64	3e-14
CAI_5A_5SP_H05	gi|18394539|ref|NP_564038.1|	unknown protein [Arabidopsis thaliana] >gi|9665061|gb|AAF97263.1|AC034106_6 Strong similarity to a hypothetical protein T18K17.12 gi|6598871 from Arabidopsis thaliana BAC T18K17 gb|AC010556. EST gb|AI996552 comes from this gene >gi|182623792|gb|ACB88835.1| At1g17830 [Arabidopsis thaliana]	40.69	231	6e-33
CAI_5A_5SP_H10	gi|255569345|ref|XP_002525640.1|	NudC domain-containing protein, putative [Ricinus communis] >gi|223535076|gb|EEF36758.1| NudC domain-containing protein, putative [Ricinus communis]	53.8	158	9e-37
CAI_5B_5SP_A03	gi|194466229|gb|ACF74345.1|	mago nashi-like protein [Arachis hypogaea]	87.68	138	1e-62
CAI_5B_5SP_A04	gi|217072634|gb|ACJ84677.1|	unknown [Medicago truncatula]	61.7	188	4e-25
CAI_5B_5SP_A05	gi|21554004|gb|AAM63085.1|	putative ubiquinol--cytochrome-c reductase [Arabidopsis thaliana]	75.36	69	6e-28
CAI_5B_5SP_A06	gi|255548421|ref|XP_002515267.1|	hypothetical protein RCOM_1346600 [Ricinus communis] >gi|223545747|gb|EEF47251.1| hypothetical protein RCOM_1346600 [Ricinus communis]	85.82	261	4e-115
CAI_5B_5SP_A07	gi|270255888|emb|CBI38263.1|	unnamed protein product [Vitis vinifera]	69.09	165	3e-54
CAI_5B_5SP_A11	gi|225456230|ref|XP_002283095.1|	PREDICTED: hypothetical protein [Vitis vinifera]	88.83	206	2e-101
CAI_5B_5SP_A12	gi|255574492|ref|XP_002528158.1|	conserved hypothetical protein [Ricinus communis] >gi|223532456|gb|EEF34249.1| conserved hypothetical protein [Ricinus communis]	83.51	194	2e-65
CAI_5B_5SP_B04	gi|147790324|emb|CAN61200.1|	hypothetical protein [Vitis vinifera]	76.26	139	1e-51
CAI_5B_5SP_B08	gi|224124396|ref|XP_002319321.1|	predicted protein [Populus trichocarpa] >gi|222857697|gb|EEE95244.1| predicted protein [Populus trichocarpa]	74.32	183	7e-72
CAI_5B_5SP_B11	gi|255540363|ref|XP_002511246.1|	nucleoside diphosphate kinase, putative [Ricinus communis] >gi|223550361|gb|EEF51848.1| nucleoside diphosphate kinase, putative [Ricinus communis]	75.41	244	3e-85
CAI_5B_5SP_C05	gi|225443859|ref|XP_002276421.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270243950|emb|CBI30889.1| unnamed protein product [Vitis vinifera]	78.34	217	2e-92
CAI_5B_5SP_D03	gi|147770310|emb|CAN75675.1|	hypothetical protein [Vitis vinifera]	47.42	194	2e-29
CAI_5B_5SP_D05	gi|118486383|gb|ABK95032.1|	unknown [Populus trichocarpa]	88.37	43	3e-13
CAI_5B_5SP_D06	gi|224090539|ref|XP_002309020.1|	predicted protein [Populus trichocarpa] >gi|118488449|gb|ABK96039.1| unknown [Populus trichocarpa] >gi|222854996|gb|EEE92543.1| predicted protein [Populus trichocarpa]	84.06	69	1e-29
CAI_5B_5SP_D08	gi|255574019|ref|XP_002527927.1|	abc transporter, putative [Ricinus communis] >gi|223532702|gb|EEF34484.1| abc transporter, putative [Ricinus communis]	91.67	48	7e-15
CAI_5B_5SP_D11	gi|224133686|ref|XP_002321636.1|	predicted protein [Populus trichocarpa] >gi|222868632|gb|EEF05763.1| predicted protein [Populus trichocarpa]	38.76	129	1e-12
CAI_5B_5SP_E06	gi|225424416|ref|XP_002285043.1|	PREDICTED: hypothetical protein [Vitis vinifera]	95.33	107	3e-52
CAI_5B_5SP_E09	gi|118485567|gb|ABK94635.1|	unknown [Populus trichocarpa]	79.41	68	1e-22
CAI_5B_5SP_E11	gi|255628763|gb|ACU14726.1|	unknown [Glycine max]	94.48	145	5e-59
CAI_5B_5SP_F02	gi|224088583|ref|XP_002308484.1|	predicted protein [Populus trichocarpa] >gi|118482513|gb|ABK93179.1| unknown [Populus trichocarpa] >gi|118483135|gb|ABK93474.1| unknown [Populus trichocarpa] >gi|118489825|gb|ABK96712.1| unknown [Populus trichocarpa x Populus deltoides] >gi|222854460|gb|EEE92007.1| predicted protein [Populus trichocarpa]	94.31	123	6e-56
CAI_5B_5SP_F10	gi|7433647|pir||S72532	acetyl-CoA C-acyltransferase (EC 2.3.1.16) precursor - cucurbit >gi|1694621|dbj|BAA11117.1| 3-ketoacyl-CoA thiolase [Cucurbita cv. Kurokawa Amakuri]	77.27	44	2e-11

IP : 14.49.138.138, 2017-11-03 13:30:33

CAI_5B_5SP_F12	gi|225455517|ref|XP_002266824.1|	PREDICTED: hypothetical protein [Vitis vinifera]	68.75	176	2e-62
CAI_5B_5SP_G04	gi|255575719|ref|XP_002528759.1|	conserved hypothetical protein [Ricinus communis] >gi|223531853|gb|EEF33671.1| conserved hypothetical protein [Ricinus communis]	57.14	112	5e-24
CAI_5B_5SP_G05	gi|270232894|emb|CBI22211.1|	unnamed protein product [Vitis vinifera]	85.47	179	3e-82
CAI_5B_5SP_G11	gi|255540867|ref|XP_002511498.1|	Epstein-Barr nuclear antigen, putative [Ricinus communis] >gi|223550613|gb|EEF52100.1| Epstein-Barr nuclear antigen, putative [Ricinus communis]	85.45	110	2e-30
CAI_5B_5SP_G12	gi|255581566|ref|XP_002531588.1|	conserved hypothetical protein [Ricinus communis] >gi|223528784|gb|EEF30791.1| conserved hypothetical protein [Ricinus communis]	83.68	190	4e-87
CAI_5B_5SP_H06	gi|255566183|ref|XP_002524079.1|	Phosphatidylglycerol/phosphatidylinositol transfer protein precursor, putative [Ricinus communis] >gi|223536647|gb|EEF38289.1| Phosphatidylglycerol/phosphatidylinositol transfer protein precursor, putative [Ricinus communis]	64.02	164	6e-48
CAI_5B_5SP_H07	gi|225469778|ref|XP_002274430.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270230330|emb|CBI18704.1| unnamed protein product [Vitis vinifera]	79.12	91	1e-26
CAI_5B_5SP_H09	gi|224146254|ref|XP_002325938.1|	predicted protein [Populus trichocarpa] >gi|222862813|gb|EEF00320.1| predicted protein [Populus trichocarpa]	70.91	55	4e-15
CAI_5C_5SP_A04	gi|224072013|ref|XP_002303609.1|	predicted protein [Populus trichocarpa] >gi|222841041|gb|EEE78588.1| predicted protein [Populus trichocarpa]	60	175	6e-44
CAI_5C_5SP_A08	gi|18413797|ref|NP_568096.1|	zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|20466490|gb|AAM20562.1| unknown protein [Arabidopsis thaliana] >gi|23198148|gb|AAN15601.1| unknown protein [Arabidopsis thaliana]	94.59	37	9e-13
CAI_5C_5SP_A09	gi|225432169|ref|XP_002267688.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270238772|emb|CBI26008.1| unnamed protein product [Vitis vinifera]	70	80	2e-21
CAI_5C_5SP_A10	gi|255548932|ref|XP_002515522.1|	xenotropic and polytropic murine leukemia virus receptor ids-4, putative [Ricinus communis] >gi|223545466|gb|EEF46971.1| xenotropic and polytropic murine leukemia virus receptor ids-4, putative [Ricinus communis]	76.56	64	3e-19
CAI_5C_5SP_B04	gi|224100741|ref|XP_002311995.1|	predicted protein [Populus trichocarpa] >gi|222851815|gb|EEE89362.1| predicted protein [Populus trichocarpa]	80.52	77	8e-22
CAI_5C_5SP_B06	gi|224106672|ref|XP_002314245.1|	predicted protein [Populus trichocarpa] >gi|118483965|gb|ABK93870.1| unknown [Populus trichocarpa] >gi|222850653|gb|EEE88200.1| predicted protein [Populus trichocarpa]	94.74	133	1e-55
CAI_5C_5SP_B10	gi|114329698|ref|YP_740519.1|	hypothetical chloroplast RF2 [Citrus sinensis] >gi|114329720|ref|YP_740539.1| hypothetical chloroplast RF2 [Citrus sinensis] >gi|122166130|sp|Q09MB4|YCF2_CITSI RecName: Full=Protein ycf2 >gi|113952664|gb|ABI49062.1| hypothetical chloroplast RF2 [Citrus sinensis] >gi|113952686|gb|ABI49084.1| hypothetical chloroplast RF2 [Citrus sinensis]	82.48	137	2e-56
CAI_5C_5SP_C01	gi|255632386|gb|ACU16543.1|	unknown [Glycine max]	83.81	105	1e-47
CAI_5C_5SP_C04	gi|224060307|ref|XP_002300134.1|	predicted protein [Populus trichocarpa] >gi|222847392|gb|EEE84939.1| predicted protein [Populus trichocarpa]	60	105	8e-30
CAI_5C_5SP_C05	gi|255542370|ref|XP_002512248.1|	Guanine deaminase, putative [Ricinus communis] >gi|223548209|gb|EEF49700.1| Guanine deaminase, putative [Ricinus communis]	78.08	146	5e-32
CAI_5C_5SP_C08	gi|47271332|emb|CAG27839.1|	calcium-dependent protein kinase 8 [Nicotiana plumbaginifolia]	87.72	57	1e-21
CAI_5C_5SP_D01	gi|255553793|ref|XP_002517937.1|	ribosomal-protein-alanine acetyltransferase, putative [Ricinus communis] >gi|223542919|gb|EEF44455.1| ribosomal-protein-alanine acetyltransferase, putative [Ricinus communis]	72.84	81	6e-26
CAI_5C_5SP_D03	gi|255557443|ref|XP_002519752.1|	60S ribosomal protein L32, putative [Ricinus communis] >gi|223541169|gb|EEF42725.1| 60S ribosomal protein L32, putative [Ricinus communis]	93.86	114	1e-55
CAI_5C_5SP_D04	gi|15219188|ref|NP_173624.1|	MUB6 (MEMBRANE-ANCHORED UBIQUITIN-FOLD PROTEIN 6 PRECURSOR) [Arabidopsis thaliana] >gi|75150987|sp|Q8GWJ6|MUB6_ARATH RecName: Full=Membrane-anchored ubiquitin-fold protein 6; Short=Membrane-anchored ub-fold protein 6; Short=AtMUB6; Flags: Precursor >gi|26452618|dbj|BAC43392.1| unknown protein [Arabidopsis thaliana] >gi|28973097|gb|AAO63873.1| unknown protein [Arabidopsis thaliana]	60	65	2e-11
CAI_5C_5SP_D06	gi|225434897|ref|XP_002283328.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270227374|emb|CBI16107.1| unnamed protein product [Vitis vinifera]	43.38	136	6e-17
CAI_5C_5SP_D07	gi|30686484|ref|NP_849433.1|	unknown protein [Arabidopsis thaliana] >gi|5051771|emb|CAB45064.1| putative protein [Arabidopsis thaliana] >gi|7269279|emb|CAB79339.1| putative protein [Arabidopsis thaliana]	63.51	74	6e-17
CAI_5C_5SP_D09	gi|224133102|ref|XP_002327961.1|	predicted protein [Populus trichocarpa] >gi|222837370|gb|EEE75749.1| predicted protein [Populus trichocarpa]	87.42	151	6e-57
CAI_5C_5SP_E10	gi|26454627|sp|Q07511|FDH_SOLTU	RecName: Full=Formate dehydrogenase, mitochondrial; AltName: Full=NAD-dependent formate dehydrogenase; Short=FDH; Flags: Precursor >gi|11991527|emb|CAA79702.2| mitochondrial formate dehydrogenase precursor [Solanum tuberosum]	82.2	118	2e-50
CAI_5C_5SP_E11	gi|255625819|gb|ACU13254.1|	unknown [Glycine max]	79.79	94	9e-33
CAI_5C_5SP_F03	gi|224077306|ref|XP_002305204.1|	predicted protein [Populus trichocarpa] >gi|222848168|gb|EEE85715.1| predicted protein [Populus trichocarpa]	90.85	164	3e-69
CAI_5C_5SP_F12	gi|224144381|ref|XP_002336141.1|	multidrug resistance protein ABC transporter family [Populus trichocarpa] >gi|222873976|gb|EEF11107.1| multidrug resistance protein ABC transporter family [Populus trichocarpa]	60.62	160	2e-42
CAI_5C_5SP_G06	gi|11414871|dbj|BAB18529.1|	25-kDa coat protein [Citrus tristeza virus] >gi|61742859|gb|AAX55222.1| coat protein [Citrus tristeza virus] >gi|190401235|gb|ACE77164.1| coat protein [Citrus tristeza virus]	92.45	53	4e-20

IP : 14.49.138.138, 2017-11-03 13:30:33

CAI_5C_5SP_H01	gi|255553181|ref|XP_002517633.1|	Nucleosome-binding protein, putative [Ricinus communis] >gi|223543265|gb|EEF44797.1| Nucleosome-binding protein, putative [Ricinus communis]	64.57	127	3e-19
CAI_5C_5SP_H02	gi|4539543|emb|CAB39974.1|	glyceraldehyde-3-phosphate dehydrogenase [Nicotiana tabacum]	65.14	218	9e-64
CAI_5C_5SP_H05	gi|147801241|emb|CAN72326.1|	hypothetical protein [Vitis vinifera]	54.32	81	3e-20
CAI_5C_5SP_H08	gi|224071369|ref|XP_002303426.1|	predicted protein [Populus trichocarpa] >gi|222840858|gb|EEE78405.1| predicted protein [Populus trichocarpa]	49.77	213	3e-33
CAI_5C_5SP_H09	gi|225424114|ref|XP_002282753.1|	PREDICTED: hypothetical protein [Vitis vinifera]	84.62	52	2e-17
CAI_5C_5SP_H10	gi|116788849|gb|ABK25024.1|	unknown [Picea sitchensis]	78.26	46	2e-12
CAI_5D_5SP_A01	gi|255553837|ref|XP_002517959.1|	conserved hypothetical protein [Ricinus communis] >gi|223542941|gb|EEF44477.1| conserved hypothetical protein [Ricinus communis]	84.74	249	4e-125
CAI_5D_5SP_A04	gi|270240115|emb|CBI27347.1|	unnamed protein product [Vitis vinifera]	75	108	5e-41
CAI_5D_5SP_A06	gi|224061525|ref|XP_002300523.1|	predicted protein [Populus trichocarpa] >gi|222847781|gb|EEE85328.1| predicted protein [Populus trichocarpa]	86.67	45	8e-14
CAI_5D_5SP_A08	gi|224156922|ref|XP_002337775.1|	predicted protein [Populus trichocarpa] >gi|222869695|gb|EEF06826.1| predicted protein [Populus trichocarpa]	80.49	41	8e-11
CAI_5D_5SP_B06	gi|224136005|ref|XP_002322215.1|	predicted protein [Populus trichocarpa] >gi|222869211|gb|EEF06342.1| predicted protein [Populus trichocarpa]	88.58	289	8e-156
CAI_5D_5SP_B09	gi|224133432|ref|XP_002321566.1|	predicted protein [Populus trichocarpa] >gi|222868562|gb|EEF05693.1| predicted protein [Populus trichocarpa]	78.57	98	4e-40
CAI_5D_5SP_C01	gi|255578951|ref|XP_002530328.1|	signal recognition particle protein, putative [Ricinus communis] >gi|223530132|gb|EEF32044.1| signal recognition particle protein, putative [Ricinus communis]	92.96	142	4e-62
CAI_5D_5SP_C02	gi|225462013|ref|XP_002273244.1|	PREDICTED: similar to heat shock protein 90 [Vitis vinifera]	95.8	143	3e-73
CAI_5D_5SP_C03	gi|255626947|gb|ACU13818.1|	unknown [Glycine max]	75.42	118	7e-46
CAI_5D_5SP_C04	gi|119367465|gb|ABL67649.1|	putative thioredoxin-dependent peroxidase [Citrus hybrid cultivar]	98.77	162	3e-85
CAI_5D_5SP_C05	gi|255631930|gb|ACU16332.1|	unknown [Glycine max]	62.67	75	7e-15
CAI_5D_5SP_C06	gi|147772934|emb|CAN73821.1|	hypothetical protein [Vitis vinifera]	79.35	92	8e-40
CAI_5D_5SP_C08	gi|255557929|ref|XP_002519993.1|	conserved hypothetical protein [Ricinus communis] >gi|223540757|gb|EEF42317.1| conserved hypothetical protein [Ricinus communis]	75.9	166	2e-44
CAI_5D_5SP_D01	gi|145208313|gb|ABP38063.1|	acyl carrier protein [Jatropha curcas] >gi|257187683|gb|ACV49879.1| acyl carrier protein [Jatropha curcas]	91.23	57	6e-22
CAI_5D_5SP_D04	gi|224131164|ref|XP_002328470.1|	predicted protein [Populus trichocarpa] >gi|222838185|gb|EEE76550.1| predicted protein [Populus trichocarpa]	52.04	98	6e-16
CAI_5D_5SP_D08	gi|17402597|dbj|BAB78733.1|	zeaxanthin epoxidase [Citrus unshiu]	98.95	286	7e-147
CAI_5D_5SP_D09	gi|224138226|ref|XP_002322761.1|	cinnamyl alcohol dehydrogenase-like protein [Populus trichocarpa] >gi|222867391|gb|EEF04522.1| cinnamyl alcohol dehydrogenase-like protein [Populus trichocarpa]	83.4	259	4e-117
CAI_5D_5SP_D10	gi|13430174|gb|AAK25754.1|AF334834_1	putative chaperon P13.9 [Castanea sativa]	73.28	131	4e-52
CAI_5D_5SP_E01	gi|255572513|ref|XP_002527191.1|	Cucumber peeling cupredoxin, putative [Ricinus communis] >gi|223533456|gb|EEF35204.1| Cucumber peeling cupredoxin, putative [Ricinus communis]	45.67	127	4e-23
CAI_5D_5SP_E04	gi|118484619|gb|ABK94182.1|	unknown [Populus trichocarpa]	94.03	134	1e-41
CAI_5D_5SP_E05	gi|255626921|gb|ACU13805.1|	unknown [Glycine max]	70.54	129	1e-47
CAI_5D_5SP_E08	gi|255584507|ref|XP_002532982.1|	DNA binding protein, putative [Ricinus communis] >gi|223527246|gb|EEF29406.1| DNA binding protein, putative [Ricinus communis]	84.15	82	3e-21
CAI_5D_5SP_E11	gi|18400602|ref|NP_566496.1|	unknown protein [Arabidopsis thaliana] >gi|25091502|sp|Q9LKA5|UMP1_ARATH RecName: Full=Uncharacterized protein At3g15000, mitochondrial >gi|16226543|gb|AAL16196.1|AF428427_1 AT3g15000/K15M2_14 [Arabidopsis thaliana] >gi|8777483|dbj|BAA97063.1| unnamed protein product [Arabidopsis thaliana] >gi|53828643|gb|AAU94431.1| At3g15000 [Arabidopsis thaliana] >gi|110740938|dbj|BAE98564.1| hypothetical protein [Arabidopsis thaliana]	47.87	94	5e-13
CAI_5D_5SP_F07	gi|224115142|ref|XP_002316953.1|	predicted protein [Populus trichocarpa] >gi|222860018|gb|EEE97565.1| predicted protein [Populus trichocarpa]	95.57	203	4e-100
CAI_5D_5SP_F08	gi|255563108|ref|XP_002522558.1|	50S ribosomal protein L34, chloroplast precursor, putative [Ricinus communis] >gi|223538249|gb|EEF39858.1| 50S ribosomal protein L34, chloroplast precursor, putative [Ricinus communis]	63.75	160	4e-36
CAI_5D_5SP_F09	gi|157093363|gb|ABV22336.1|	calmodulin [Noctiluca scintillans]	96.36	55	2e-22
CAI_5D_5SP_G03	gi|255583729|ref|XP_002532618.1|	serine-threonine protein kinase, plant-type, putative [Ricinus communis] >gi|223527674|gb|EEF29784.1| serine-threonine protein kinase, plant-type, putative [Ricinus communis]	56.48	108	3e-26
CAI_5D_5SP_G06	gi|151347490|gb|ABS01354.1|	translation initiation factor [Carica papaya]	93.08	159	3e-80
CAI_5D_5SP_G07	gi|225440831|ref|XP_002282071.1|	PREDICTED: similar to ubiquitin fusion protein [Vitis vinifera] >gi|255578906|ref|XP_002530306.1| ubiquitin, putative [Ricinus communis] >gi|255578975|ref|XP_002530340.1| ubiquitin, putative [Ricinus communis] >gi|71040673|gb|AAZ20285.1| ubiquitin fusion protein [Arachis hypogaea] >gi|147769165|emb|CAN60770.1| hypothetical protein [Vitis vinifera]	100	128	2e-67

IP : 14.49.138.138, 2017-11-03 13:30:33

		>gi|148908659|gb|ABR17437.1| unknown [Picea sitchensis] >gi|192910738|gb|ACF06477.1| ubiquitin fusion protein [Elaeis guineensis] >gi|223530144|gb|EEF32056.1| ubiquitin, putative [Ricinus communis] >gi|223530162|gb|EEF32073.1| ubiquitin, putative [Ricinus communis] >gi|270243382|emb|CBI30322.1| unnamed protein product [Vitis vinifera]			
CAI_5D_5SP_G10	gi|147794019|emb|CAN60112.1|	hypothetical protein [Vitis vinifera]	83.17	101	1e-35
CAI_5D_5SP_G12	gi|255539226|ref|XP_002510678.1|	conserved hypothetical protein [Ricinus communis] >gi|223551379|gb|EEF52865.1| conserved hypothetical protein [Ricinus communis]	63.7	270	2e-72
CAI_5D_5SP_H03	gi|225464373|ref|XP_002265455.1|	PREDICTED: hypothetical protein isoform 1 [Vitis vinifera]	54.7	287	8e-92
CAI_5D_5SP_H11	gi|224096790|ref|XP_002310737.1|	predicted protein [Populus trichocarpa] >gi|222853640|gb|EEE91187.1| predicted protein [Populus trichocarpa]	72.46	69	6e-24
CAI_5D_5SP_H12	gi|224052982|ref|XP_002297648.1|	predicted protein [Populus trichocarpa] >gi|118484908|gb|ABK94320.1| unknown [Populus trichocarpa] >gi|222844906|gb|EEE82453.1| predicted protein [Populus trichocarpa]	65.24	187	5e-63
CAI_6A_5SP_A03	gi|259156773|gb|ACV96635.1|	cytochrome c oxidase subunit 1 [Citrullus lanatus]	100	143	3e-82
CAI_6A_5SP_A04	gi|224128201|ref|XP_002329106.1|	predicted protein [Populus trichocarpa] >gi|222869775|gb|EEF06906.1| predicted protein [Populus trichocarpa]	74.26	272	2e-109
CAI_6A_5SP_A07	gi|217071202|gb|ACJ83961.1|	unknown [Medicago truncatula]	72.16	176	2e-67
CAI_6A_5SP_A10	gi|225450919|ref|XP_002284549.1|	PREDICTED: hypothetical protein [Vitis vinifera]	62.16	111	1e-30
CAI_6A_5SP_B04	gi|224126343|ref|XP_002319815.1|	predicted protein [Populus trichocarpa] >gi|222858191|gb|EEE95738.1| predicted protein [Populus trichocarpa]	44.06	202	7e-27
CAI_6A_5SP_B10	gi|224104343|ref|XP_002313405.1|	predicted protein [Populus trichocarpa] >gi|222849813|gb|EEE87360.1| predicted protein [Populus trichocarpa]	76.24	101	6e-41
CAI_6A_5SP_C03	gi|255576671|ref|XP_002529225.1|	Cysteine protease ATG4B, putative [Ricinus communis] >gi|223531343|gb|EEF33181.1| Cysteine protease ATG4B, putative [Ricinus communis]	68.66	201	3e-53
CAI_6A_5SP_C04	gi|255538698|ref|XP_002510414.1|	proteasome subunit alpha type, putative [Ricinus communis] >gi|223551115|gb|EEF52601.1| proteasome subunit alpha type, putative [Ricinus communis]	81.65	218	7e-92
CAI_6A_5SP_C06	gi|170522964|gb|ACB20694.1|	putative cold-inducible protein [Camellia sinensis] >gi|259018359|gb|ACV89762.1| putative light-inducible protein [Camellia sinensis]	60.62	193	1e-50
CAI_6A_5SP_C08	gi|114329687|ref|YP_740508.1|	RNA polymerase alpha subunit [Citrus sinensis] >gi|122166151|sp|Q09ME5|RPOA_CITSI RecName: Full=DNA-directed RNA polymerase subunit alpha; Short=PEP; AltName: Full=Plastid-encoded RNA polymerase subunit alpha; Short=RNA polymerase subunit alpha >gi|113952653|gb|ABI49051.1| RNA polymerase alpha subunit [Citrus sinensis]	96.99	133	1e-66
CAI_6A_5SP_C09	gi|115444425|ref|NP_001045992.1|	Os02g0164800 [Oryza sativa (japonica cultivar-group)] >gi|49388054|dbj|BAD25168.1| unknown protein [Oryza sativa Japonica Group] >gi|49388411|dbj|BAD25544.1| unknown protein [Oryza sativa Japonica Group] >gi|113535523|dbj|BAF07906.1| Os02g0164800 [Oryza sativa Japonica Group]	90.91	44	2e-16
CAI_6A_5SP_D03	gi|225462930|ref|XP_002267401.1|	PREDICTED: hypothetical protein [Vitis vinifera]	79.56	181	2e-83
CAI_6A_5SP_D10	gi|224102619|ref|XP_002312750.1|	predicted protein [Populus trichocarpa] >gi|222852570|gb|EEE90117.1| predicted protein [Populus trichocarpa]	76.17	277	6e-125
CAI_6A_5SP_E08	gi|224029765|gb|ACN33958.1|	unknown [Zea mays]	77	100	3e-37
CAI_6A_5SP_E11	gi|225448213|ref|XP_002265950.1|	PREDICTED: hypothetical protein [Vitis vinifera]	76.14	285	2e-116
CAI_6A_5SP_E12	gi|224123390|ref|XP_002319067.1|	predicted protein [Populus trichocarpa] >gi|222857443|gb|EEE94990.1| predicted protein [Populus trichocarpa]	51.59	126	1e-31
CAI_6A_5SP_F02	gi|225427923|ref|XP_002275216.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|147821778|emb|CAN77171.1| hypothetical protein [Vitis vinifera] >gi|270255536|emb|CBI37920.1| unnamed protein product [Vitis vinifera]	81.36	220	7e-101
CAI_6A_5SP_F03	gi|255539843|ref|XP_002510986.1|	conserved hypothetical protein [Ricinus communis] >gi|223550101|gb|EEF51588.1| conserved hypothetical protein [Ricinus communis]	37.9	124	1e-15
CAI_6A_5SP_F04	gi|255548295|ref|XP_002515204.1|	s-adenosylmethionine synthetase, putative [Ricinus communis] >gi|223545684|gb|EEF47188.1| s-adenosylmethionine synthetase, putative [Ricinus communis]	96.6	265	3e-149
CAI_6A_5SP_F06	gi|225423648|ref|XP_002276237.1|	PREDICTED: hypothetical protein [Vitis vinifera]	78.85	52	4e-18
CAI_6A_5SP_F09	gi|255573874|ref|XP_002527856.1|	conserved hypothetical protein [Ricinus communis] >gi|223532780|gb|EEF34559.1| conserved hypothetical protein [Ricinus communis]	73.82	275	1e-119
CAI_6A_5SP_F10	gi|114329681|ref|YP_740502.1|	photosystem II CP47 chlorophyll apoprotein [Citrus sinensis] >gi|122166157|sp|Q09MF1|PSBB_CITSI RecName: Full=Photosystem II CP47 chlorophyll apoprotein; AltName: Full=PSII 47 kDa protein; AltName: Full=Protein CP-47 >gi|113952647|gb|ABI49045.1| photosystem II CP47 chlorophyll apoprotein [Citrus sinensis]	99.39	164	1e-89
CAI_6A_5SP_F11	gi|225462543|ref|XP_002266917.1|	PREDICTED: hypothetical protein isoform 2 [Vitis vinifera] >gi|225462545|ref|XP_002266877.1| PREDICTED: hypothetical protein isoform 1 [Vitis vinifera] >gi|147799989|emb|CAN77245.1| hypothetical protein [Vitis vinifera]	95.6	250	4e-123
CAI_6A_5SP_F12	gi|255557022|ref|XP_002519544.1|	conserved hypothetical protein [Ricinus communis] >gi|223541407|gb|EEF42958.1| conserved hypothetical protein [Ricinus communis]	61.35	207	6e-53
CAI_6A_5SP_G06	gi|255582541|ref|XP_002532054.1|	heat shock protein, putative [Ricinus communis] >gi|223528276|gb|EEF30326.1| heat shock protein, putative [Ricinus communis]	69.03	226	3e-69
CAI_6A_5SP_G07	gi|226491834|ref|NP_001147590.1|	chloroplast oxygen-evolving complex/thylakoid lumenal 25.6kDa protein [Zea mays] >gi|195612378|gb|ACG28019.1| chloroplast oxygen-evolving complex/thylakoid lumenal	76.74	43	1e-12

IP : 14.49.138.138, 2017-11-03 13:30:33

		25.6kDa protein [Zea mays] >gi|238006362|gb|ACR34216.1| unknown [Zea mays]			
CAI_6A_5SP_G10	gi|255587494|ref|XP_002534292.1|	protein with unknown function [Ricinus communis] >gi|223525564|gb|EEF28091.1| protein with unknown function [Ricinus communis]	99.46	185	1e-85
CAI_6A_5SP_G12	gi|225440849|ref|XP_002282193.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270243373|emb|CBI30313.1| unnamed protein product [Vitis vinifera]	93.75	80	1e-35
CAI_6A_5SP_H03	gi|530207|gb|AAA66338.1|	heat shock protein [Glycine max]	94.55	55	1e-21
CAI_6A_5SP_H04	gi|224053517|ref|XP_002297852.1|	predicted protein [Populus trichocarpa] >gi|222845110|gb|EEE82657.1| predicted protein [Populus trichocarpa]	71.84	245	8e-91
CAI_6A_5SP_H05	gi|255647070|gb|ACU24003.1|	unknown [Glycine max]	97.62	42	2e-14
CAI_6A_5SP_H07	gi|255576844|ref|XP_002529308.1|	conserved hypothetical protein [Ricinus communis] >gi|223531232|gb|EEF33077.1| conserved hypothetical protein [Ricinus communis]	73.97	146	3e-47
CAI_6A_5SP_H08	gi|225454694|ref|XP_002270877.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270239235|emb|CBI26470.1| unnamed protein product [Vitis vinifera]	77.5	160	7e-63
CAI_6A_5SP_H10	gi|255641136|gb|ACU20846.1|	unknown [Glycine max]	83.09	207	2e-86
CAI_6A_5SP_H11	gi|15234910|ref|NP_192742.1|	CYTC-2 (cytochrome c-2); electron carrier/ heme binding / iron ion binding [Arabidopsis thaliana] >gi|27734261|sp|Q9T0G2|CYC3_ARATH RecName: Full=Probable cytochrome c At4g10040 >gi|4539007|emb|CAB39628.1| cytochrome c [Arabidopsis thaliana] >gi|7267700|emb|CAB78127.1| cytochrome c [Arabidopsis thaliana] >gi|15028283|gb|AAK76618.1| putative cytochrome c protein [Arabidopsis thaliana] >gi|19310747|gb|AAL85104.1| putative cytochrome c protein [Arabidopsis thaliana] >gi|21592668|gb|AAM64617.1| cytochrome c [Arabidopsis thaliana]	94.64	112	3e-57
CAI_6A_5SP_H12	gi|225442341|ref|XP_002281000.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270253580|emb|CBI35978.1| unnamed protein product [Vitis vinifera]	84.42	276	2e-129
CAI_6B_5SP_A03	gi|225441589|ref|XP_002281591.1|	PREDICTED: hypothetical protein [Vitis vinifera]	85.83	254	7e-115
CAI_6B_5SP_A08	gi|4519260|dbj|BAA75515.1|	vacuolar H+-ATPase c subunit [Citrus unshiu] >gi|6721527|dbj|BAA89594.1| vacuolar H+-ATPase c subunit [Citrus unshiu]	99.39	165	8e-56
CAI_6B_5SP_A10	gi|270236352|emb|CBI25619.1|	unnamed protein product [Vitis vinifera]	87.1	62	1e-24
CAI_6B_5SP_B04	gi|255628315|gb|ACU14502.1|	unknown [Glycine max]	78.95	95	1e-36
CAI_6B_5SP_B06	gi|225454381|ref|XP_002279076.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270258412|emb|CBI40446.1| unnamed protein product [Vitis vinifera]	63.11	122	2e-36
CAI_6B_5SP_B07	gi|147839732|emb|CAN61780.1|	hypothetical protein [Vitis vinifera]	80.9	89	1e-32
CAI_6B_5SP_B08	gi|154091338|gb|ABS57463.1|	brother of FT and TFL1 protein [Glycine max] >gi|255630264|gb|ACU15487.1| unknown [Glycine max]	89.23	130	4e-65
CAI_6B_5SP_B12	gi|147782757|emb|CAN63437.1|	hypothetical protein [Vitis vinifera] >gi|270306402|emb|CBI23878.1| unnamed protein product [Vitis vinifera]	62.56	227	1e-38
CAI_6B_5SP_C03	gi|224112100|ref|XP_002316082.1|	predicted protein [Populus trichocarpa] >gi|222865122|gb|EEF02253.1| predicted protein [Populus trichocarpa]	87.72	57	2e-21
CAI_6B_5SP_C05	gi|116109058|gb|ABJ74162.1|	H+-ATPase proteolipid [Acanthus ebracteatus]	98.59	142	6e-52
CAI_6B_5SP_C06	gi|224085111|ref|XP_002307496.1|	predicted protein [Populus trichocarpa] >gi|222856945|gb|EEE94492.1| predicted protein [Populus trichocarpa]	89.69	97	5e-42
CAI_6B_5SP_C07	gi|224055715|ref|XP_002298617.1|	predicted protein [Populus trichocarpa] >gi|222845875|gb|EEE83422.1| predicted protein [Populus trichocarpa]	95.29	85	1e-40
CAI_6B_5SP_C11	gi|12585474|sp|Q9MB46|VATE_CITUN	RecName: Full=V-type proton ATPase subunit E; Short=V-ATPase subunit E; AltName: Full=Vacuolar proton pump subunit E >gi|6729085|dbj|BAA89661.1| vacuolar H+-ATPase E subunit-1 [Citrus unshiu]	99.57	230	5e-113
CAI_6B_5SP_D10	gi|224074217|ref|XP_002304305.1|	predicted protein [Populus trichocarpa] >gi|118485751|gb|ABK94725.1| unknown [Populus trichocarpa] >gi|222841737|gb|EEE79284.1| predicted protein [Populus trichocarpa]	96.55	203	2e-107
CAI_6B_5SP_D11	gi|270232559|emb|CBI21880.1|	unnamed protein product [Vitis vinifera]	83.15	184	4e-71
CAI_6B_5SP_E02	gi|224105037|ref|XP_002313663.1|	predicted protein [Populus trichocarpa] >gi|118484510|gb|ABK94130.1| unknown [Populus trichocarpa] >gi|118485202|gb|ABK94462.1| unknown [Populus trichocarpa] >gi|118487376|gb|ABK95516.1| unknown [Populus trichocarpa] >gi|118488119|gb|ABK95879.1| unknown [Populus trichocarpa] >gi|222850071|gb|EEE87618.1| predicted protein [Populus trichocarpa]	82.3	113	3e-22
CAI_6B_5SP_E04	gi|225441927|ref|XP_002284555.1|	PREDICTED: hypothetical protein isoform 2 [Vitis vinifera] >gi|225441929|ref|XP_002284557.1| PREDICTED: hypothetical protein isoform 3 [Vitis vinifera] >gi|225441931|ref|XP_002284553.1| PREDICTED: hypothetical protein isoform 1 [Vitis vinifera] >gi|270248245|emb|CBI33380.1| unnamed protein product [Vitis vinifera]	55.88	136	4e-35
CAI_6B_5SP_E06	gi|224060307|ref|XP_002300134.1|	predicted protein [Populus trichocarpa] >gi|222847392|gb|EEE84939.1| predicted protein [Populus trichocarpa]	55.34	253	3e-61
CAI_6B_5SP_E07	gi|224107767|ref|XP_002333468.1|	predicted protein [Populus trichocarpa] >gi|222836988|gb|EEE75381.1| predicted protein [Populus trichocarpa]	64.29	56	4e-16
CAI_6B_5SP_E11	gi|225469270|ref|XP_002267760.1|	PREDICTED: hypothetical protein [Vitis vinifera]	84.76	269	5e-125

IP : 14.49.138.138, 2017-11-03 13:30:33

CAI_6B_5SP_F02	gi|255547213|ref|XP_002514664.1|	activating signal cointegrator 1 complex subunit 3, helc1, putative [Ricinus communis] >gi|223546268|gb|EEF47770.1| activating signal cointegrator 1 complex subunit 3, helc1, putative [Ricinus communis]	70.15	134	5e-45
CAI_6B_5SP_F04	gi|224132980|ref|XP_002321457.1|	predicted protein [Populus trichocarpa] >gi|222868453|gb|EEF05584.1| predicted protein [Populus trichocarpa]	60.61	66	2e-13
CAI_6B_5SP_F06	gi|224067088|ref|XP_002302349.1|	predicted protein [Populus trichocarpa] >gi|222844075|gb|EEE81622.1| predicted protein [Populus trichocarpa]	80.51	313	6e-127
CAI_6B_5SP_F07	gi|224101081|ref|XP_002312134.1|	predicted protein [Populus trichocarpa] >gi|222851954|gb|EEE89501.1| predicted protein [Populus trichocarpa]	74.51	153	4e-62
CAI_6B_5SP_F08	gi|255560810|ref|XP_002521418.1|	nucleic acid binding protein, putative [Ricinus communis] >gi|223539317|gb|EEF40908.1| nucleic acid binding protein, putative [Ricinus communis]	56.25	128	4e-17
CAI_6B_5SP_F11	gi|224146482|ref|XP_002326022.1|	predicted protein [Populus trichocarpa] >gi|222862897|gb|EEF00404.1| predicted protein [Populus trichocarpa]	87.01	77	3e-15
CAI_6B_5SP_G01	gi|255556858|ref|XP_002519462.1|	conserved hypothetical protein [Ricinus communis] >gi|223541325|gb|EEF42876.1| conserved hypothetical protein [Ricinus communis]	63.11	122	2e-36
CAI_6B_5SP_G06	gi|15230232|ref|NP_191274.1|	NAP57 (Arabidopsis thaliana homologue of NAP57); pseudouridine synthase >gi|67460428|sp|Q9LD90|DKC1_ARATH RecName: Full=H/ACA ribonucleoprotein complex subunit 4; AltName: Full=Nucleolar protein NAP57 homolog; AltName: Full=Nopp-140-associated protein of 57 kDa homolog; Short=AtNAP57 >gi|8901186|gb|AAF43210.2|AF234984_1 putative pseudouridine synthase [Arabidopsis thaliana] >gi|6911885|emb|CAB72185.1| putative protein [Arabidopsis thaliana] >gi|28392852|gb|AAO41863.1| unknown protein [Arabidopsis thaliana] >gi|225898727|dbj|BAH30494.1| hypothetical protein [Arabidopsis thaliana]	63.74	91	3e-22
CAI_6B_5SP_G10	gi|30385248|gb|AAP23943.1|	CCR protein [x Citrofortunella mitis]	98.23	113	1e-46
CAI_6B_5SP_G12	gi|225466653|ref|XP_002273608.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270259577|emb|CBI38710.1| unnamed protein product [Vitis vinifera]	65.89	258	5e-82
CAI_6B_5SP_H01	gi|110747150|gb|ABG89394.1|	gibberellic acid receptor [Gossypium hirsutum]	85.92	142	4e-71
CAI_6B_5SP_H02	gi|225452968|ref|XP_002284346.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|147778657|emb|CAN62897.1| hypothetical protein [Vitis vinifera]	94.87	273	1e-144
CAI_6B_5SP_H05	gi|224069236|ref|XP_002326308.1|	SAUR family protein [Populus trichocarpa] >gi|222833501|gb|EEE71978.1| SAUR family protein [Populus trichocarpa]	87.01	77	2e-31
CAI_6B_5SP_H07	gi|110349911|emb|CAJ19269.1|	putative stress-induced protein [Solanum commersonii]	95.12	41	1e-13
CAI_6B_5SP_H09	gi|224106191|ref|XP_002314079.1|	cinnamoyl CoA reductase-like protein [Populus trichocarpa] >gi|222850487|gb|EEE88034.1| cinnamoyl CoA reductase-like protein [Populus trichocarpa]	81.69	284	2e-124
CAI_6B_5SP_H10	gi|225441809|ref|XP_002283878.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270242913|emb|CBI29853.1| unnamed protein product [Vitis vinifera]	76.25	80	3e-30
CAI_6C_5SP_A02	gi|224058639|ref|XP_002299579.1|	cytochrome P450 [Populus trichocarpa] >gi|222846837|gb|EEE84384.1| cytochrome P450 [Populus trichocarpa]	74.62	130	2e-50
CAI_6C_5SP_A06	gi|255555073|ref|XP_002518574.1|	transcription regulator, putative [Ricinus communis] >gi|223542419|gb|EEF43961.1| transcription regulator, putative [Ricinus communis]	42.51	287	2e-30
CAI_6C_5SP_A08	gi|225444850|ref|XP_002281014.1|	PREDICTED: hypothetical protein [Vitis vinifera]	67.16	201	4e-69
CAI_6C_5SP_A10	gi|18403942|ref|NP_565821.1|	unknown protein [Arabidopsis thaliana] >gi|20197521|gb|AAM15109.1| hypothetical protein [Arabidopsis thaliana]	74.47	47	9e-15
CAI_6C_5SP_A11	gi|255555853|ref|XP_002518962.1|	conserved hypothetical protein [Ricinus communis] >gi|223541949|gb|EEF43495.1| conserved hypothetical protein [Ricinus communis]	63.57	140	8e-42
CAI_6C_5SP_C05	gi|255575865|ref|XP_002528830.1|	60S ribosomal protein L14, putative [Ricinus communis] >gi|223531742|gb|EEF33564.1| 60S ribosomal protein L14, putative [Ricinus communis]	90.38	52	2e-19
CAI_6C_5SP_C06	gi|225459577|ref|XP_002285862.1|	PREDICTED: hypothetical protein [Vitis vinifera]	75	100	2e-42
CAI_6C_5SP_C10	gi|224143686|ref|XP_002325040.1|	predicted protein [Populus trichocarpa] >gi|222866474|gb|EEF03605.1| predicted protein [Populus trichocarpa]	86.38	213	7e-91
CAI_6C_5SP_D10	gi|255566472|ref|XP_002524221.1|	Serine/threonine-protein kinase Nek8, putative [Ricinus communis] >gi|223536498|gb|EEF38145.1| Serine/threonine-protein kinase Nek8, putative [Ricinus communis]	71.64	67	7e-18
CAI_6C_5SP_D12	gi|225440288|ref|XP_002284203.1|	PREDICTED: similar to UBC9 (UBIQUITIN CONJUGATING ENZYME 9); ubiquitin-protein ligase isoform 2 [Vitis vinifera] >gi|225440290|ref|XP_002284197.1|	97.97	148	3e-82

IP : 14.49.138.138, 2017-11-03 13:30:33

		PREDICTED: similar to UBC9 (UBIQUITIN CONJUGATING ENZYME 9); ubiquitin-protein ligase isoform 1 [Vitis vinifera] >gi|225454440|ref|XP_002280356.1| PREDICTED: similar to UBC9 (UBIQUITIN CONJUGATING ENZYME 9); ubiquitin-protein ligase isoform 1 [Vitis vinifera] >gi|225454442|ref|XP_002280366.1| PREDICTED: similar to UBC9 (UBIQUITIN CONJUGATING ENZYME 9); ubiquitin-protein ligase isoform 2 [Vitis vinifera] >gi|147803053|emb|CAN77754.1| hypothetical protein [Vitis vinifera] >gi|147852846|emb|CAN81281.1| hypothetical protein [Vitis vinifera] >gi|270247513|emb|CBI32888.1| unnamed protein product [Vitis vinifera] >gi|270258437|emb|CBI40471.1| unnamed protein product [Vitis vinifera]			
CAI_6C_5SP_E01	gi|270236191|emb|CBI25460.1|	unnamed protein product [Vitis vinifera]	77.32	97	2e-25
CAI_6C_5SP_E02	gi|238014838|gb|ACR38454.1|	unknown [Zea mays]	90.77	65	2e-26
CAI_6C_5SP_E03	gi|224133624|ref|XP_002327641.1|	predicted protein [Populus trichocarpa] >gi|222836726|gb|EEE75119.1| predicted protein [Populus trichocarpa]	83.43	175	9e-72
CAI_6C_5SP_E05	gi|255541746|ref|XP_002511937.1|	conserved hypothetical protein [Ricinus communis] >gi|223549117|gb|EEF50606.1| conserved hypothetical protein [Ricinus communis]	65.87	252	4e-85
CAI_6C_5SP_E07	gi|147792162|emb|CAN68575.1|	hypothetical protein [Vitis vinifera]	97.37	38	2e-12
CAI_6C_5SP_E10	gi|170507|gb|AAA34193.1|	ORF [Solanum lycopersicum] >gi|1172167|gb|AAA86424.1| heat shock protein [Solanum lycopersicum]	58.33	96	1e-18
CAI_6C_5SP_F01	gi|224072532|ref|XP_002303772.1|	predicted protein [Populus trichocarpa] >gi|222841204|gb|EEE78751.1| predicted protein [Populus trichocarpa]	71.11	225	7e-62
CAI_6C_5SP_F02	gi|225459372|ref|XP_002284238.1|	PREDICTED: hypothetical protein [Vitis vinifera]	75.32	77	2e-11
CAI_6C_5SP_F09	gi|270258328|emb|CBI40362.1|	unnamed protein product [Vitis vinifera]	90.18	112	1e-51
CAI_6C_5SP_F11	gi|224145992|ref|XP_002325840.1|	predicted protein [Populus trichocarpa] >gi|222862715|gb|EEF00222.1| predicted protein [Populus trichocarpa]	73.39	233	2e-80
CAI_6C_5SP_F12	gi|225463173|ref|XP_002269418.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270240484|emb|CBI27714.1| unnamed protein product [Vitis vinifera]	90	100	2e-47
CAI_6C_5SP_G02	gi|225448367|ref|XP_002268645.1|	PREDICTED: hypothetical protein [Vitis vinifera]	91.96	199	9e-91
CAI_6C_5SP_G05	gi|15240969|ref|NP_198681.1|	proteasome maturation factor UMP1 family protein [Arabidopsis thaliana] >gi|10176833|dbj|BAB10155.1| unnamed protein product [Arabidopsis thaliana] >gi|19347883|gb|AAL85998.1| unknown protein [Arabidopsis thaliana] >gi|21281209|gb|AAM45059.1| unknown protein [Arabidopsis thaliana] >gi|21593744|gb|AAM65711.1| unknown [Arabidopsis thaliana]	66.67	141	3e-51
CAI_6C_5SP_G06	gi|114329661|ref|YP_740480.1|	NADH-plastoquinone oxidoreductase subunit 3 [Citrus sinensis] >gi|122166178|sp|Q09MH3|NU3C_CITSI RecName: Full=NAD(P)H-quinone oxidoreductase subunit 3, chloroplastic; AltName: Full=NAD(P)H dehydrogenase subunit 3; AltName: Full=NADH-plastoquinone oxidoreductase subunit 3 >gi|113952627|gb|ABI49025.1| NADH-plastoquinone oxidoreductase subunit 3 [Citrus sinensis]	98.02	101	5e-50
CAI_6C_5SP_G08	gi|2501850|gb|AAB80717.1|	GDP dissociation inhibitor [Nicotiana tabacum]	92.01	288	3e-153
CAI_6C_5SP_G09	gi|147766193|emb|CAN72381.1|	hypothetical protein [Vitis vinifera]	83.09	136	1e-50
CAI_6C_5SP_H05	gi|255553201|ref|XP_002517643.1|	conserved hypothetical protein [Ricinus communis] >gi|223543275|gb|EEF44807.1| conserved hypothetical protein [Ricinus communis]	78.51	121	2e-45
CAI_6D_5SP_A02	gi|224068845|ref|XP_002326214.1|	predicted protein [Populus trichocarpa] >gi|222833407|gb|EEE71884.1| predicted protein [Populus trichocarpa]	85.09	114	6e-49
CAI_6D_5SP_A03	gi|146747227|gb|ABQ44212.1|	galactinol synthase [Capsicum annuum]	85.45	213	1e-109
CAI_6D_5SP_A07	gi|224138698|ref|XP_002322879.1|	predicted protein [Populus trichocarpa] >gi|222867509|gb|EEF04640.1| predicted protein [Populus trichocarpa]	53.14	175	5e-34
CAI_6D_5SP_B12	gi|255550572|ref|XP_002516336.1|	RNA polymerase II transcriptional coactivator KIWI, putative [Ricinus communis] >gi|223544566|gb|EEF46083.1| RNA polymerase II transcriptional coactivator KIWI, putative [Ricinus communis]	74.68	79	2e-23
CAI_6D_5SP_C02	gi|255578581|ref|XP_002530152.1|	peroxiredoxins, prx-1, prx-2, prx-3, putative [Ricinus communis] >gi|223530313|gb|EEF32207.1| peroxiredoxins, prx-1, prx-2, prx-3, putative [Ricinus communis]	88.26	230	1e-111
CAI_6D_5SP_C07	gi|255587476|ref|XP_002534285.1|	conserved hypothetical protein [Ricinus communis] >gi|223525573|gb|EEF28096.1| conserved hypothetical protein [Ricinus communis]	66.37	226	5e-77
CAI_6D_5SP_C12	gi|114329642|ref|YP_740461.1|	ATP synthase CF0 subunit I [Citrus sinensis] >gi|122166197|sp|Q09MJ2|ATPF_CITSI RecName: Full=ATP synthase subunit b, chloroplastic; AltName: Full=ATPase subunit I; AltName: Full=ATP synthase F(0) sector subunit b >gi|113952608|gb|ABI49006.1| ATP synthase CF0 subunit I [Citrus sinensis]	96.47	85	2e-37
CAI_6D_5SP_D02	gi|114329678|ref|YP_740497.1|	ribosomal protein S18 [Citrus sinensis] >gi|122166161|sp|Q09MF6|RR18_CITSI RecName: Full=30S ribosomal protein S18, chloroplastic >gi|113952644|gb|ABI49042.1| ribosomal protein S18 [Citrus sinensis]	99.01	101	4e-48
CAI_6D_5SP_	gi|118482762|gb|ABK93299.	unknown [Populus trichocarpa] >gi|118483053|gb|ABK93436.1| unknown [Populus	95.38	173	6e-83

IP : 14.49.138.138, 2017-11-03 13:30:33

D04	1|	trichocarpa] >gi|118483119|gb|ABK93468.1| unknown [Populus trichocarpa] >gi|118483283|gb|ABK93544.1| unknown [Populus trichocarpa] >gi|118489714|gb|ABK96658.1| unknown [Populus trichocarpa x Populus deltoides]			
CAI_6D_5SP_D08	gi|224142377|ref|XP_002324535.1|	predicted protein [Populus trichocarpa] >gi|222865969|gb|EEF03100.1| predicted protein [Populus trichocarpa]	77.55	196	4e-73
CAI_6D_5SP_E08	gi|255586225|ref|XP_002533767.1|	short-chain dehydrogenase, putative [Ricinus communis] >gi|223526304|gb|EEF28612.1| short-chain dehydrogenase, putative [Ricinus communis]	90.62	96	7e-40
CAI_6D_5SP_F03	gi|224138062|ref|XP_002322720.1|	predicted protein [Populus trichocarpa] >gi|222867350|gb|EEF04481.1| predicted protein [Populus trichocarpa]	82.27	282	3e-124
CAI_6D_5SP_F04	gi|247421835|gb|ACS96445.1|	S18.A ribosomal protein [Jatropha curcas]	98.59	71	2e-35
CAI_6D_5SP_F07	gi|255550415|ref|XP_002516258.1|	proteasome subunit alpha type, putative [Ricinus communis] >gi|223544744|gb|EEF46260.1| proteasome subunit alpha type, putative [Ricinus communis]	92.68	246	1e-127
CAI_6D_5SP_F08	gi|224056335|ref|XP_002298808.1|	global transcription factor group [Populus trichocarpa] >gi|222846066|gb|EEE83613.1| global transcription factor group [Populus trichocarpa]	62.41	274	3e-77
CAI_6D_5SP_G01	gi|255563242|ref|XP_002522624.1|	immunophilin, putative [Ricinus communis] >gi|223538100|gb|EEF39711.1| immunophilin, putative [Ricinus communis]	84.82	112	9e-55
CAI_6D_5SP_G07	gi|255538564|ref|XP_002510347.1|	BRASSINAZOLE-RESISTANT 1 protein, putative [Ricinus communis] >gi|223551048|gb|EEF52534.1| BRASSINAZOLE-RESISTANT 1 protein, putative [Ricinus communis]	67.15	277	4e-74
CAI_6D_5SP_H03	gi|224092675|ref|XP_002309697.1|	predicted protein [Populus trichocarpa] >gi|222855673|gb|EEE93220.1| predicted protein [Populus trichocarpa]	55.97	159	2e-19
CAI_6D_5SP_H05	gi|151347486|gb|ABS01352.1|	methionine synthase [Carica papaya]	90.23	266	5e-128
CAI_6D_5SP_H06	gi|255563689|ref|XP_002522846.1|	Trafficking protein particle complex subunit, putative [Ricinus communis] >gi|223537930|gb|EEF39544.1| Trafficking protein particle complex subunit, putative [Ricinus communis]	94.62	186	3e-97
CAI_6D_5SP_H07	gi|255574131|ref|XP_002527981.1|	conserved hypothetical protein [Ricinus communis] >gi|223532607|gb|EEF34393.1| conserved hypothetical protein [Ricinus communis]	67.07	246	3e-77
CAI_6D_5SP_H09	gi|225432031|ref|XP_002280085.1|	PREDICTED: hypothetical protein [Vitis vinifera]	87.04	108	6e-49
CAI_6D_5SP_H11	gi|74486736|gb|ABA12221.1|	translation elongation factor 1A-5 [Gossypium hirsutum]	97.32	299	2e-169
CAI_7A_5SP_A01	gi|270231282|emb|CBI20607.1|	unnamed protein product [Vitis vinifera]	73.38	263	4e-103
CAI_7A_5SP_A02	gi|255570065|ref|XP_002525995.1|	ankyrin repeat-containing protein, putative [Ricinus communis] >gi|223534727|gb|EEF36419.1| ankyrin repeat-containing protein, putative [Ricinus communis]	75.69	218	4e-87
CAI_7A_5SP_A03	gi|225449698|ref|XP_002267817.1|	PREDICTED: hypothetical protein [Vitis vinifera]	88.97	263	1e-126
CAI_7A_5SP_A06	gi|255554134|ref|XP_002518107.1|	60S ribosomal protein L13a, putative [Ricinus communis] >gi|223542703|gb|EEF44240.1| 60S ribosomal protein L13a, putative [Ricinus communis]	91.26	206	1e-98
CAI_7A_5SP_A12	gi|270230992|emb|CBI20319.1|	unnamed protein product [Vitis vinifera]	68.78	189	3e-60
CAI_7A_5SP_B04	gi|225423741|ref|XP_002277028.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|147836213|emb|CAN75429.1| hypothetical protein [Vitis vinifera]	83.33	228	3e-104
CAI_7A_5SP_B08	gi|255539735|ref|XP_002510932.1|	21 kDa protein precursor, putative [Ricinus communis] >gi|223550047|gb|EEF51534.1| 21 kDa protein precursor, putative [Ricinus communis]	69.19	172	2e-62
CAI_7A_5SP_B09	gi|255546147|ref|XP_002514133.1|	dead box ATP-dependent RNA helicase, putative [Ricinus communis] >gi|223546589|gb|EEF48087.1| dead box ATP-dependent RNA helicase, putative [Ricinus communis]	65.59	279	7e-99
CAI_7A_5SP_B12	gi|224128117|ref|XP_002320248.1|	predicted protein [Populus trichocarpa] >gi|222861021|gb|EEE98563.1| predicted protein [Populus trichocarpa]	61.95	113	7e-29
CAI_7A_5SP_C01	gi|18499|emb|CAA38374.1|	late embryogenesis abundant protein [Gossypium hirsutum] >gi|167330|gb|AAA33057.1| embryogensis abundant protein [Gossypium hirsutum] >gi|167353|gb|AAB00728.1| water-stress protectant protein [Gossypium hirsutum] >gi|167355|gb|AAA33064.1| late embryogenesis-abundant protein 2-D [Gossypium hirsutum]	88.64	44	3e-14
CAI_7A_5SP_C02	gi|255574605|ref|XP_002528213.1|	cytochrome C oxidase polypeptide vib, putative [Ricinus communis] >gi|223532374|gb|EEF34170.1| cytochrome C oxidase polypeptide vib, putative [Ricinus communis]	89.47	76	8e-38
CAI_7A_5SP_C03	gi|255583557|ref|XP_002532535.1|	lupus la ribonucleoprotein, putative [Ricinus communis] >gi|223527747|gb|EEF29851.1| lupus la ribonucleoprotein, putative [Ricinus communis]	56.76	222	7e-58
CAI_7A_5SP_C07	gi|60498651|dbj|BAD90709.1|	plastid DNA-binding protein [Prunus x yedoensis]	52.17	69	1e-12
CAI_7A_5SP_C12	gi|225445170|ref|XP_002284107.1|	PREDICTED: hypothetical protein isoform 1 [Vitis vinifera] >gi|225445172|ref|XP_002284110.1| PREDICTED: hypothetical protein isoform 2 [Vitis vinifera]	90.36	197	1e-96
CAI_7A_5SP_D08	gi|147815437|emb|CAN63831.1|	hypothetical protein [Vitis vinifera]	90.32	93	2e-41
CAI_7A_5SP_D09	gi|255563727|ref|XP_002522865.1|	electron transport oxidoreductase, putative [Ricinus communis] >gi|223537949|gb|EEF39563.1| electron transport oxidoreductase, putative [Ricinus communis]	74.28	276	3e-105
CAI_7A_5SP_E03	gi|225435925|ref|XP_002267920.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270235178|emb|CBI24308.1| unnamed protein product [Vitis vinifera]	86.31	241	6e-116
CAI_7A_5SP_E05	gi|255630399|gb|ACU15556.1|	unknown [Glycine max]	85.19	108	3e-49
CAI_7A_5SP_E07	gi|225443700|ref|XP_002264921.1|	PREDICTED: hypothetical protein [Vitis vinifera]	37.5	240	4e-36

IP : 14.49.138.138, 2017-11-03 13:30:33

CAI_7A_5SP_E09	gi|255546115|ref|XP_002514117.1|	Density-regulated protein, putative [Ricinus communis] >gi|223546573|gb|EEF48071.1| Density-regulated protein, putative [Ricinus communis]	81.63	196	1e-72
CAI_7A_5SP_E11	gi|225440566|ref|XP_002276610.1|	PREDICTED: hypothetical protein [Vitis vinifera]	88.72	133	6e-64
CAI_7A_5SP_E12	gi|68164987|gb|AAY87459.1|	omega-6 fatty acid desaturase [Hevea brasiliensis]	81.43	210	9e-106
CAI_7A_5SP_F02	gi|224083783|ref|XP_002307122.1|	predicted protein [Populus trichocarpa] >gi|222856571|gb|EEE94118.1| predicted protein [Populus trichocarpa]	88.27	307	2e-153
CAI_7A_5SP_F06	gi|224099925|ref|XP_002311676.1|	predicted protein [Populus trichocarpa] >gi|118483982|gb|ABK93878.1| unknown [Populus trichocarpa] >gi|222851496|gb|EEE89043.1| predicted protein [Populus trichocarpa]	97.65	85	6e-43
CAI_7A_5SP_F10	gi|225457225|ref|XP_002284112.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270226393|emb|CBI15127.1| unnamed protein product [Vitis vinifera]	81.61	87	4e-40
CAI_7A_5SP_F11	gi|21304463|emb|CAD29834.2|	putative ribosomal protein L2 [Vitis vinifera]	96.43	140	9e-74
CAI_7A_5SP_G06	gi|15228314|ref|NP_188300.1|	60S ribosomal protein L19 (RPL19B) [Arabidopsis thaliana] >gi|17865565|sp|Q9LUQ6|RL192_ARATH RecName: Full=60S ribosomal protein L19-2 >gi|11994633|dbj|BAB02770.1| 60S ribosome protein L19-like [Arabidopsis thaliana] >gi|15010618|gb|AAK73968.1| AT3g16780/MGL6_23 [Arabidopsis thaliana] >gi|19699260|gb|AAL90996.1| AT3g16780/MGL6_23 [Arabidopsis thaliana]	54.74	95	2e-13
CAI_7A_5SP_G08	gi|224064456|ref|XP_002301485.1|	predicted protein [Populus trichocarpa] >gi|222843211|gb|EEE80758.1| predicted protein [Populus trichocarpa]	94.25	174	6e-88
CAI_7A_5SP_G11	gi|26224736|gb|AAN76362.1|	serpin-like protein [Citrus x paradisi]	98.17	273	2e-148
Consensus100	gi|270260171|emb|CBI32005.1|	unnamed protein product [Vitis vinifera]	93.29	164	2e-85
Consensus101	gi|114329639|ref|YP_740458.1|	photosystem II protein K [Citrus sinensis] >gi|122166200|sp|Q09MJ5|PSBK_CITSI RecName: Full=Photosystem II reaction center protein K; Short=PSII-K; Flags: Precursor >gi|113952605|gb|ABI49003.1| photosystem II protein K [Citrus sinensis]	100	61	7e-26
Consensus102	gi|57013900|ref|YP_173374.1|	hypothetical protein NitaMp027 [Nicotiana tabacum] >gi|57014030|ref|YP_173501.1| hypothetical protein NitaMp164 [Nicotiana tabacum] >gi|56806536|dbj|BAD83437.1| hypothetical protein [Nicotiana tabacum] >gi|56806666|dbj|BAD83567.1| hypothetical protein [Nicotiana tabacum]	98.78	82	9e-42
Consensus103	gi|1360725|emb|CAA87068.1|	non-photosynthetic ferredoxin [Citrus sinensis]	98	150	6e-79
Consensus104	gi|217071440|gb|ACJ84080.1|	unknown [Medicago truncatula]	87.93	116	2e-49
Consensus105	gi|209168551|gb|ACI42271.1|	glutathione S-transferase Tau2 [Citrus sinensis] >gi|225676730|gb|ACO05907.1| glutathione transferase Tau2 [Citrus sinensis]	89.95	219	8e-102
Consensus106	gi|255558872|ref|XP_002520459.1|	heat-shock protein, putative [Ricinus communis] >gi|223540301|gb|EEF41872.1| heat-shock protein, putative [Ricinus communis]	33.33	189	1e-12
Consensus107	gi|119367470|gb|ABL67651.1|	putative auxin-repressed/dormancy-associated protein [Citrus hybrid cultivar]	98.36	122	1e-50
Consensus108	gi|255585824|ref|XP_002533590.1|	heat-shock protein, putative [Ricinus communis] >gi|223526534|gb|EEF28795.1| heat-shock protein, putative [Ricinus communis]	84.42	154	2e-55
Consensus109	gi|224074873|ref|XP_002304470.1|	f-box family protein [Populus trichocarpa] >gi|222841902|gb|EEE79449.1| f-box family protein [Populus trichocarpa]	79.29	140	4e-64
Consensus110	gi|153012222|ref|YP_001381737.1|	photosystem I assembly protein ycf3 [Medicago truncatula]	97.44	78	4e-38
Consensus111	gi|76446335|gb|ABA42952.1|	RING-H2 finger protein [Citrus trifoliata]	98.1	158	5e-82
Consensus112	gi|255571441|ref|XP_002526668.1|	ferritin, plant, putative [Ricinus communis] >gi|223533968|gb|EEF35690.1| ferritin, plant, putative [Ricinus communis]	82.64	144	1e-44
Consensus113	gi|225457979|ref|XP_002275717.1|	PREDICTED: hypothetical protein isoform 2 [Vitis vinifera]	71.79	78	5e-30
Consensus114	gi|26418686|gb|AAN78125.1|	dehydrin [Citrus x paradisi]	97.46	118	6e-30
Consensus115	gi|255540985|ref|XP_002511557.1|	40S ribosomal protein S9, putative [Ricinus communis] >gi|223550672|gb|EEF52159.1| 40S ribosomal protein S9, putative [Ricinus communis]	95.51	178	9e-93
Consensus116	gi|224087579|ref|XP_002308192.1|	predicted protein [Populus trichocarpa] >gi|222854168|gb|EEE91715.1| predicted protein [Populus trichocarpa]	80.69	145	9e-46
Consensus118	gi|18404892|ref|NP_565897.1|	hydrophobic protein, putative / low temperature and salt responsive protein, putative [Arabidopsis thaliana] >gi|15529214|gb|AAK97701.1| unknown protein [Arabidopsis thaliana] >gi|16974383|gb|AAL31117.1| At2g38901/At2g38901 [Arabidopsis thaliana] >gi|20197443|gb|AAM15078.1| Expressed protein [Arabidopsis thaliana]	96.3	54	2e-23
Consensus119	gi|225433734|ref|XP_002269806.1|	PREDICTED: similar to Histone-lysine N-methyltransferase ATX2 [Vitis vinifera] >gi|270256645|emb|CBI39462.1| unnamed protein product [Vitis vinifera]	69.67	122	2e-44
Consensus11	gi|34541994|gb|AAQ74889.1|	A1-induced protein [Gossypium hirsutum]	86.86	236	1e-113
Consensus120	gi|116078097|dbj|BAF34912.1|	MADS-box protein [Citrus unshiu]	99.58	237	3e-131
Consensus122	gi|255571087|ref|XP_002526494.1|	40S ribosomal protein S11, putative [Ricinus communis] >gi|223534169|gb|EEF35885.1| 40S ribosomal protein S11, putative [Ricinus communis]	98.74	159	5e-78
Consensus123	gi|255539248|ref|XP_002510689.1|	DNA-binding protein MNB1B, putative [Ricinus communis] >gi|223551390|gb|EEF52876.1| DNA-binding protein MNB1B, putative [Ricinus communis]	81.74	115	8e-42
Consensus124	gi|89276295|gb|ABD66504.1|	actin depolymerizing factor 8 [Gossypium hirsutum] >gi|119388970|gb|AAY88048.2| actin depolymerizing factor [Gossypium hirsutum]	92.81	139	1e-67

IP : 14.49.138.138, 2017-11-03 13:30:33

Consensus125	gi|224081999|ref|XP_002306550.1|	predicted protein [Populus trichocarpa] >gi|222855999|gb|EEE93546.1| predicted protein [Populus trichocarpa]	73.03	89	1e-23
Consensus126	gi|255543727|ref|XP_002512926.1|	40S ribosomal protein S25-1, putative [Ricinus communis] >gi|223547937|gb|EEF49429.1| 40S ribosomal protein S25-1, putative [Ricinus communis]	97.22	72	6e-31
Consensus127	gi|225459477|ref|XP_002285835.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270252453|emb|CBI19064.1| unnamed protein product [Vitis vinifera]	94.57	92	1e-41
Consensus128	gi|224105881|ref|XP_002313965.1|	predicted protein [Populus trichocarpa] >gi|222850373|gb|EEE87920.1| predicted protein [Populus trichocarpa]	78.57	70	3e-27
Consensus12	gi|18416995|ref|NP_567775.1|	unknown protein [Arabidopsis thaliana] >gi|14030723|gb|AAK53036.1|AF375452_1 AT4g27450/F27G19_50 [Arabidopsis thaliana] >gi|15028057|gb|AAK76559.1| unknown protein [Arabidopsis thaliana] >gi|20259059|gb|AAM14245.1| unknown protein [Arabidopsis thaliana] >gi|21593019|gb|AAM64968.1| unknown [Arabidopsis thaliana]	82.73	249	9e-119
Consensus131	gi|1061408|gb|AAB52963.1|	citrin [Citrus sinensis]	77.92	240	4e-69
Consensus132	gi|224076226|ref|XP_002304909.1|	predicted protein [Populus trichocarpa] >gi|118487860|gb|ABK95753.1| unknown [Populus trichocarpa] >gi|222847873|gb|EEE85420.1| predicted protein [Populus trichocarpa] >gi|225626261|gb|ACN97180.1| peroxidase [Populus trichocarpa]	88.26	247	2e-130
Consensus133	gi|1061408|gb|AAB52963.1|	citrin [Citrus sinensis]	94.38	89	7e-41
Consensus134	gi|225458049|ref|XP_002280438.1|	PREDICTED: hypothetical protein [Vitis vinifera]	72.5	160	4e-67
Consensus135	gi|225850691|ref|YP_002730925.1|	hypothetical protein PERMA_1142 [Persephonella marina EX-H1] >gi|225851462|ref|YP_002731696.1| hypothetical protein PERMA_1936 [Persephonella marina EX-H1] >gi|225645989|gb|ACO04175.1| conserved hypothetical protein [Persephonella marina EX-H1] >gi|225646335|gb|ACO04521.1| conserved hypothetical protein [Persephonella marina EX-H1]	53.12	160	3e-26
Consensus136	gi|37524017|gb|AAQ92310.1|	COR15 [Citrus clementina x Citrus reticulata]	100	101	5e-27
Consensus138	gi|255561012|ref|XP_002521518.1|	WD-repeat protein, putative [Ricinus communis] >gi|223539196|gb|EEF40789.1| WD-repeat protein, putative [Ricinus communis]	68.44	244	6e-61
Consensus139	gi|225440308|ref|XP_002262887.1|	PREDICTED: hypothetical protein [Vitis vinifera]	100	52	8e-25
Consensus13	gi|255571742|ref|XP_002526814.1|	peptidase, putative [Ricinus communis] >gi|223533818|gb|EEF35549.1| peptidase, putative [Ricinus communis]	66.67	120	3e-36
Consensus140	gi|147774374|emb|CAN72399.1|	hypothetical protein [Vitis vinifera]	58.8	233	2e-62
Consensus141	gi|13486942|dbj|BAB40143.1|	plasma membrane intrinsic protein 2-2 [Pyrus communis]	90.95	243	2e-114
Consensus142	gi|75214626|gb|ABA18098.1|	putative ring-box Roc1/Rbx1/Hrt1 protein [Olimarabidopsis pumila]	89.47	95	5e-48
Consensus143	gi|225462474|ref|XP_002267488.1|	PREDICTED: hypothetical protein [Vitis vinifera]	81	221	6e-97
Consensus146	gi|270243649|emb|CBI30588.1|	unnamed protein product [Vitis vinifera]	43.8	258	7e-29
Consensus147	gi|224131896|ref|XP_002321205.1|	predicted protein [Populus trichocarpa] >gi|222861978|gb|EEE99520.1| predicted protein [Populus trichocarpa]	80.98	205	2e-95
Consensus149	gi|34851176|gb|AAP15200.1|	profilin-like protein [Humulus scandens]	93.89	131	1e-67
Consensus14	gi|270247896|emb|CBI33233.1|	unnamed protein product [Vitis vinifera]	73.26	187	2e-76
Consensus150	gi|255546295|ref|XP_002514207.1|	conserved hypothetical protein [Ricinus communis] >gi|223546663|gb|EEF48161.1| conserved hypothetical protein [Ricinus communis]	59.49	79	6e-19
Consensus151	gi|225458701|ref|XP_002284973.1|	PREDICTED: hypothetical protein [Vitis vinifera]	82.28	237	5e-106
Consensus152	gi|89258491|gb|ABD65459.1|	putative ribosomal protein L28 [Gossypium hirsutum]	83.33	150	3e-66
Consensus153	gi|255629069|gb|ACU14879.1|	unknown [Glycine max]	90.95	221	6e-102
Consensus154	gi|224095003|ref|XP_002310323.1|	predicted protein [Populus trichocarpa] >gi|118487937|gb|ABK95790.1| unknown [Populus trichocarpa] >gi|222853226|gb|EEE90773.1| predicted protein [Populus trichocarpa]	72.55	102	2e-38
Consensus155	gi|255631250|gb|ACU15992.1|	unknown [Glycine max]	71.82	110	1e-30
Consensus157	gi|255540809|ref|XP_002511469.1|	conserved hypothetical protein [Ricinus communis] >gi|223550584|gb|EEF52071.1| conserved hypothetical protein [Ricinus communis]	85.06	87	3e-37
Consensus15	gi|224073041|ref|XP_002303955.1|	predicted protein [Populus trichocarpa] >gi|222841387|gb|EEE78934.1| predicted protein [Populus trichocarpa]	71.63	208	9e-75
Consensus160	gi|224130632|ref|XP_002320889.1|	predicted protein [Populus trichocarpa] >gi|222861662|gb|EEE99204.1| predicted protein [Populus trichocarpa]	67.33	251	2e-82
Consensus161	gi|209967449|gb|ACJ02353.1|	60S ribosomal protein L27A [Vernicia fordii]	95.21	146	2e-78
Consensus162	gi|224064886|ref|XP_002301600.1|	predicted protein [Populus trichocarpa] >gi|222843326|gb|EEE80873.1| predicted protein [Populus trichocarpa]	95.6	91	4e-43
Consensus163	gi|19570344|dbj|BAB86292.1|	nucleoside diphosphate kinase 1 [Brassica rapa] >gi|19744165|dbj|BAB86841.1| NDPK I [Brassica rapa]	84.46	148	4e-68
Consensus164	gi|110349085|gb|ABG73110.1|	Pis v 2.0201 allergen 11S globulin precusor [Pistacia vera]	56.54	260	5e-64

IP : 14.49.138.138, 2017-11-03 13:30:33

Consensus165	gi|119367472|gb|ABL67652.1|	putative thioredoxin H protein [Citrus hybrid cultivar]	100	57	1e-25
Consensus166	gi|170522964|gb|ACB20694.1|	putative cold-inducible protein [Camellia sinensis] >gi|259018359|gb|ACV89762.1| putative light-inducible protein [Camellia sinensis]	61.14	193	5e-52
Consensus167	gi|255626425|gb|ACU13557.1|	unknown [Glycine max]	81.42	113	3e-50
Consensus168	gi|255646355|gb|ACU23657.1|	unknown [Glycine max]	83.61	122	1e-49
Consensus169	gi|224120428|ref|XP_002318327.1|	predicted protein [Populus trichocarpa] >gi|222859000|gb|EEE96547.1| predicted protein [Populus trichocarpa]	49.33	150	5e-28
Consensus16	gi|78191410|gb|ABB29926.1|	fructose-bisphosphate aldolase-like [Solanum tuberosum]	93.84	276	2e-146
Consensus171	gi|147856966|emb|CAN81809.1|	hypothetical protein [Vitis vinifera]	77.12	437	8e-177
Consensus172	gi|544437|sp|Q06652|GPX4_CITSI	RecName: Full=Probable phospholipid hydroperoxide glutathione peroxidase; Short=PHGPx; AltName: Full=Salt-associated protein >gi|296358|emb|CAA47018.1| CIT-SAP [Citrus sinensis] >gi|119367482|gb|ABL67656.1| putative phospholipid hydroperoxide glutathione peroxidase [Citrus hybrid cultivar]	100	166	1e-90
Consensus173	gi|109156608|ref|YP_654227.1|	cytochrome b6/f complex subunit V [Oryza sativa Indica Group] >gi|42795500|gb|AAS46067.1| cytochrome b6/f complex subunit V [Oryza sativa Indica Group] >gi|42795567|gb|AAS46133.1| cytochrome b6/f complex subunit V [Oryza sativa Japonica Group] >gi|42795631|gb|AAS46196.1| cytochrome b6/f complex subunit V [Oryza sativa Japonica Group]	94.74	38	6e-12
Consensus174	gi|116078097|dbj|BAF34912.1|	MADS-box protein [Citrus unshiu]	94.05	252	4e-129
Consensus175	gi|225437704|ref|XP_002280035.1|	PREDICTED: hypothetical protein [Vitis vinifera]	86.11	108	6e-46
Consensus177	gi|111218904|gb|ABH08753.1|	ubiquitin [Arabidopsis thaliana]	90.85	142	2e-63
Consensus178	gi|293338698|gb|ADE43669.1|	heat shock protein 17.5 cytosolic class II [Jatropha curcas]	61.98	121	5e-27
Consensus179	gi|224124980|ref|XP_002329861.1|	predicted protein [Populus trichocarpa] >gi|222871098|gb|EEF08229.1| predicted protein [Populus trichocarpa]	52.71	203	2e-49
Consensus17	gi|224058427|ref|XP_002299504.1|	predicted protein [Populus trichocarpa] >gi|118482989|gb|ABK93406.1| unknown [Populus trichocarpa] >gi|222846762|gb|EEE84309.1| predicted protein [Populus trichocarpa]	76.16	151	8e-44
Consensus180	gi|224123696|ref|XP_002319143.1|	NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222857519|gb|EEE95066.1| NAC domain protein, IPR003441 [Populus trichocarpa]	55.96	277	6e-66
Consensus181	gi|224104357|ref|XP_002313410.1|	predicted protein [Populus trichocarpa] >gi|222849818|gb|EEE87365.1| predicted protein [Populus trichocarpa]	77.91	163	1e-53
Consensus182	gi|255575865|ref|XP_002528830.1|	60S ribosomal protein L14, putative [Ricinus communis] >gi|223531742|gb|EEF33564.1| 60S ribosomal protein L14, putative [Ricinus communis]	94.03	134	2e-65
Consensus183	gi|24473800|gb|AAL91665.1|	2s albumin [Anacardium occidentale]	51.45	138	3e-18
Consensus184	gi|119367477|gb|ABL67654.1|	putative H-type thioredoxin [Citrus hybrid cultivar]	99.16	119	7e-61
Consensus185	gi|25992541|gb|AAN77150.1|	fiber protein Fb11 [Gossypium barbadense]	84.38	64	1e-22
Consensus186	gi|14423860|sp|Q9M7N0|PROF3_HEVBR	RecName: Full=Profilin-3; AltName: Full=Pollen allergen Hev b 8.0201; AltName: Allergen=Hev b 8.0201 >gi|6979167|gb|AAF34341.1|AF119365_1 latex profilin Hev b 8 [Hevea brasiliensis]	91.6	131	2e-58
Consensus187	gi|217384814|gb|ACK43223.1|	alpha-expansin [Ziziphus jujuba]	88.05	226	6e-104
Consensus189	gi|1169534|sp|P42896|ENO_RICCO	RecName: Full=Enolase; AltName: Full=2-phosphoglycerate dehydratase; AltName: Full=2-phospho-D-glycerate hydro-lyase >gi|433609|emb|CAA82232.1| enolase [Ricinus communis]	92.81	445	0
Consensus18	gi|225452222|ref|XP_002268255.1|	PREDICTED: hypothetical protein [Vitis vinifera]	76.73	275	7e-112
Consensus190	gi|255641581|gb|ACU21063.1|	unknown [Glycine max]	74.12	255	1e-91
Consensus191	gi|255584110|ref|XP_002532797.1|	conserved hypothetical protein [Ricinus communis] >gi|223527457|gb|EEF29590.1| conserved hypothetical protein [Ricinus communis]	66.29	89	1e-20
Consensus193	gi|225450883|ref|XP_002284334.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270254425|emb|CBI36816.1| unnamed protein product [Vitis vinifera]	73.06	219	2e-79
Consensus194	gi|255538870|ref|XP_002510500.1|	cytochrome P450, putative [Ricinus communis] >gi|223551201|gb|EEF52687.1| cytochrome P450, putative [Ricinus communis]	62.86	280	7e-96
Consensus196	gi|114329641|ref|YP_740460.1|	ATP synthase CF1 alpha subunit [Citrus sinensis] >gi|122166198|sp|Q09MJ3|ATPA_CITSI RecName: Full=ATP synthase subunit alpha, chloroplastic; AltName: Full=F-ATPase subunit alpha; AltName: Full=ATP synthase F1 sector subunit alpha >gi|113952607|gb|ABI49005.1| ATP synthase CF1 alpha subunit [Citrus sinensis]	96.77	341	8e-179
Consensus197	gi|224163581|ref|XP_002338573.1|	early light-inducible protein [Populus trichocarpa] >gi|118488109|gb|ABK95874.1| unknown [Populus trichocarpa] >gi|222872878|gb|EEF10009.1| early light-inducible protein [Populus trichocarpa]	63.02	192	2e-57
Consensus198	gi|225436662|ref|XP_002276538.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270235125|emb|CBI24255.1| unnamed protein product [Vitis vinifera]	82.07	184	3e-84
Consensus19	gi|225441339|ref|XP_002276510.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|147782754|emb|CAN70573.1| hypothetical protein [Vitis vinifera]	61.63	172	1e-48

IP : 14.49.138.138, 2017-11-03 13:30:33

Consensus1	gi|255579735|ref|XP_002530706.1|	conserved hypothetical protein [Ricinus communis] >gi|223529720|gb|EEF31660.1| conserved hypothetical protein [Ricinus communis]	72.63	274	3e-104
Consensus200	gi|225426900|ref|XP_002263737.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|225470331|ref|XP_002267121.1| PREDICTED: hypothetical protein [Vitis vinifera]	44.42	475	3e-97
Consensus201	gi|255539487|ref|XP_002510808.1|	steroid binding protein, putative [Ricinus communis] >gi|223549923|gb|EEF51410.1| steroid binding protein, putative [Ricinus communis]	76.19	231	7e-89
Consensus202	gi|106073473|gb|ABF82026.1|	PSI P700 apoprotein A2 [Solanum lycopersicum]	100	145	3e-84
Consensus203	gi|255541508|ref|XP_002511818.1|	conserved hypothetical protein [Ricinus communis] >gi|223548998|gb|EEF50487.1| conserved hypothetical protein [Ricinus communis]	92.75	69	2e-34
Consensus204	gi|14279437|gb|AAK58599.1| AF269158_1	ethylene-induced esterase [Citrus sinensis]	98.12	266	3e-150
Consensus206	gi|224079149|ref|XP_002305769.1|	predicted protein [Populus trichocarpa] >gi|222848733|gb|EEE86280.1| predicted protein [Populus trichocarpa]	88.61	79	4e-25
Consensus208	gi|255537227|ref|XP_002509680.1|	conserved hypothetical protein [Ricinus communis] >gi|223549579|gb|EEF51067.1| conserved hypothetical protein [Ricinus communis]	76.21	269	5e-117
Consensus209	gi|261280336|gb|ACM67308.2|	triosphosphate isomerase-like protein type I [Dimocarpus longan]	93.6	250	4e-116
Consensus20	gi|255569887|ref|XP_002525907.1|	gaba(A) receptor-associated protein, putative [Ricinus communis] >gi|223534821|gb|EEF36511.1| gaba(A) receptor-associated protein, putative [Ricinus communis]	98.36	122	5e-53
Consensus211	gi|270235765|emb|CBI24890.1|	unnamed protein product [Vitis vinifera]	90.6	117	3e-57
Consensus214	gi|55375985|gb|AAV50005.1|	14-3-3 family protein [Malus x domestica]	96.09	230	1e-117
Consensus215	gi|20138097|sp|Q9ZWQ7|DAD1_CITUN	RecName: Full=Defender against cell death 1; Short=DAD-1; AltName: Full=CitDAD-1-1 >gi|4126405|dbj|BAA36555.1| homolog to defender against apoptotic death 1 [Citrus unshiu]	96.52	115	5e-56
Consensus216	gi|2274917|emb|CAA03881.1|	Cu/Zn superoxide dismutase [Citrus sinensis]	44.34	106	7e-13
Consensus217	gi|255566991|ref|XP_002524478.1|	ribosomal protein l7ae, putative [Ricinus communis] >gi|223536266|gb|EEF37918.1| ribosomal protein l7ae, putative [Ricinus communis]	96.09	128	8e-54
Consensus218	gi|224072410|ref|XP_002303722.1|	predicted protein [Populus trichocarpa] >gi|222841154|gb|EEE78701.1| predicted protein [Populus trichocarpa]	80	130	8e-44
Consensus21	gi|225438389|ref|XP_002275222.1|	PREDICTED: hypothetical protein [Vitis vinifera]	76.26	198	1e-84
Consensus220	gi|255578850|ref|XP_002530279.1|	60S ribosomal protein L12, putative [Ricinus communis] >gi|223530177|gb|EEF32086.1| 60S ribosomal protein L12, putative [Ricinus communis]	96.39	166	2e-85
Consensus221	gi|6094476|sp|O23787|THI4_CITSI	RecName: Full=Thiazole biosynthetic enzyme, chloroplastic; Flags: Precursor >gi|2582665|emb|CAB05370.1| thi [Citrus sinensis]	98.49	265	7e-137
Consensus222	gi|255537325|ref|XP_002509729.1|	60S ribosomal protein L24, putative [Ricinus communis] >gi|223549628|gb|EEF51116.1| 60S ribosomal protein L24, putative [Ricinus communis]	95.04	141	9e-62
Consensus223	gi|270243310|emb|CBI30250.1|	unnamed protein product [Vitis vinifera]	64.86	74	2e-18
Consensus225	gi|12830830|gb|AAK08208.1| AF320905_1	metallothionein-like protein [Citrus unshiu] >gi|12830832|gb|AAK08209.1|AF320906_1 metallothionein-like protein [Citrus unshiu] >gi|3308982|dbj|BAA31562.1| metallothionein-like protein [Citrus unshiu] >gi|158936952|dbj|BAF91493.1| metallothionein type 3 [Citrus unshiu]	98.53	68	4e-34
Consensus226	gi|224124306|ref|XP_002329990.1|	stress-induced hydrophobic peptide [Populus trichocarpa] >gi|222871415|gb|EEF08546.1| stress-induced hydrophobic peptide [Populus trichocarpa]	91.23	57	2e-16
Consensus227	gi|257219544|gb|ACV50425.1|	cold induced plasma membrane protein [Jatropha curcas]	91.23	57	2e-22
Consensus228	gi|225448725|ref|XP_002280954.1|	PREDICTED: hypothetical protein [Vitis vinifera]	69.09	55	2e-14
Consensus22	gi|7024451|dbj|BAA92156.1|	glycine-rich RNA-binding protein [Citrus unshiu]	97.75	89	3e-43
Consensus230	gi|147804852|emb|CAN64691.1|	hypothetical protein [Vitis vinifera]	60.69	145	3e-45
Consensus232	gi|255582024|ref|XP_002531809.1|	conserved hypothetical protein [Ricinus communis] >gi|223528543|gb|EEF30566.1| conserved hypothetical protein [Ricinus communis]	75.76	66	1e-21
Consensus234	gi|205364122|gb|ACI04518.1|	translationally controlled tumor protein [Hevea brasiliensis]	93.45	168	8e-75
Consensus235	gi|224091437|ref|XP_002309251.1|	predicted protein [Populus trichocarpa] >gi|222855227|gb|EEE92774.1| predicted protein [Populus trichocarpa]	80.7	114	3e-46
Consensus236	gi|224130140|ref|XP_002320762.1|	predicted protein [Populus trichocarpa] >gi|118489542|gb|ABK96573.1| unknown [Populus trichocarpa x Populus deltoides] >gi|222861535|gb|EEE99077.1| predicted protein [Populus trichocarpa]	90.56	233	3e-108
Consensus237	gi|225452110|ref|XP_002284213.1|	PREDICTED: hypothetical protein [Vitis vinifera]	70	70	4e-25
Consensus23	gi|224056234|ref|XP_002298768.1|	predicted protein [Populus trichocarpa] >gi|222846026|gb|EEE83573.1| predicted protein [Populus trichocarpa]	92.86	56	4e-27
Consensus24	gi|224120008|ref|XP_002318220.1|	predicted protein [Populus trichocarpa] >gi|222858893|gb|EEE96440.1| predicted protein [Populus trichocarpa]	92.11	76	1e-22

IP : 14.49.138.138, 2017-11-03 13:30:33

Consensus25	gi|225455521|ref|XP_002267233.1|	PREDICTED: hypothetical protein [Vitis vinifera]	57.77	251	1e-78
Consensus26	gi|225426803|ref|XP_002283042.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|147854517|emb|CAN80707.1| hypothetical protein [Vitis vinifera]	61.29	62	3e-15
Consensus27	gi|255578511|ref|XP_002530119.1|	conserved hypothetical protein [Ricinus communis] >gi|223530373|gb|EEF32263.1| conserved hypothetical protein [Ricinus communis]	91.25	80	4e-36
Consensus28	gi|224020985|ref|YP_002608218.1|	ATPase subunit 9 [Carica papaya] >gi|170522397|gb|ACB20507.1| ATPase subunit 9 [Carica papaya]	97.53	81	2e-23
Consensus29	gi|255629416|gb|ACU15054.1|	unknown [Glycine max]	92.06	126	3e-44
Consensus2	gi|225350102|gb|ACN87961.1|	expansin 2 [Citrus sinensis]	100	243	8e-129
Consensus30	gi|224059690|ref|XP_002299972.1|	predicted protein [Populus trichocarpa] >gi|222847230|gb|EEE84777.1| predicted protein [Populus trichocarpa]	80.41	97	8e-40
Consensus31	gi|224132064|ref|XP_002328176.1|	predicted protein [Populus trichocarpa] >gi|118481731|gb|ABK92805.1| unknown [Populus trichocarpa] >gi|222837691|gb|EEE76056.1| predicted protein [Populus trichocarpa]	83.1	71	9e-29
Consensus32	gi|151547430|gb|ABS12459.1|	cysteine protease Cp [Citrus sinensis]	98.89	361	0
Consensus33	gi|225448398|ref|XP_002269398.1|	PREDICTED: hypothetical protein isoform 1 [Vitis vinifera] >gi|147854340|emb|CAN83423.1| hypothetical protein [Vitis vinifera]	80.8	125	1e-42
Consensus34	gi|217075040|gb|ACJ85880.1|	unknown [Medicago truncatula]	62.69	134	1e-31
Consensus35	gi|255625999|gb|ACU13344.1|	unknown [Glycine max]	48.54	103	2e-16
Consensus36	gi|225427377|ref|XP_002282974.1|	PREDICTED: similar to protein synthesis initiation factor-like [Vitis vinifera]	100	92	9e-47
Consensus37	gi|224120364|ref|XP_002318311.1|	predicted protein [Populus trichocarpa] >gi|222858984|gb|EEE96531.1| predicted protein [Populus trichocarpa]	71.67	293	2e-114
Consensus38	gi|225433728|ref|XP_002269474.1|	PREDICTED: hypothetical protein [Vitis vinifera]	82.67	150	4e-74
Consensus39	gi|179744409|gb|ACB86853.1|	mannitol transporter [Citrus sinensis]	98	150	6e-77
Consensus3	gi|225436349|ref|XP_002269322.1|	PREDICTED: hypothetical protein [Vitis vinifera]	61.34	194	4e-48
Consensus40	gi|255582815|ref|XP_002532181.1|	Iron-sulfur assembly protein IscA, chloroplast precursor, putative [Ricinus communis] >gi|223528129|gb|EEF30199.1| Iron-sulfur assembly protein IscA, chloroplast precursor, putative [Ricinus communis]	73.74	179	6e-59
Consensus42	gi|156567559|gb|ABU82739.1|	cold acclimation WCOR413-like protein [Citrus trifoliata]	95.63	206	9e-99
Consensus43	gi|224286458|gb|ACN40936.1|	unknown [Picea sitchensis]	100	230	1e-123
Consensus44	gi|255582174|ref|XP_002531881.1|	peripheral-type benzodiazepine receptor, putative [Ricinus communis] >gi|223528489|gb|EEF30518.1| peripheral-type benzodiazepine receptor, putative [Ricinus communis]	62.96	162	1e-50
Consensus45	gi|147800088|emb|CAN70933.1|	hypothetical protein [Vitis vinifera]	84.14	145	9e-60
Consensus46	gi|1170745|sp|P46518|LEA14_GOSHI	RecName: Full=Late embryogenesis abundant protein Lea14-A >gi|167326|gb|AAA18542.1| Group 4 late embryogenesis-abundant protein [Gossypium hirsutum] >gi|167328|gb|AAA18543.1| Group 4 late embryogenesis-abundant protein [Gossypium hirsutum]	76.82	151	4e-62
Consensus47	gi|255539022|ref|XP_002510576.1|	skp1, putative [Ricinus communis] >gi|223551277|gb|EEF52763.1| skp1, putative [Ricinus communis]	93.04	158	1e-71
Consensus48	gi|26418686|gb|AAN78125.1|	dehydrin [Citrus x paradisi]	95.51	89	3e-33
Consensus49	gi|111218906|gb|ABH08754.1|	ubiquitin [Arabidopsis thaliana]	99.48	193	3e-102
Consensus4	gi|255547686|ref|XP_002514900.1|	nuclear transport factor, putative [Ricinus communis] >gi|223545951|gb|EEF47454.1| nuclear transport factor, putative [Ricinus communis]	94.31	123	1e-62
Consensus50	gi|192910730|gb|ACF06473.1|	light-inducible protein ATLS1 [Elaeis guineensis]	89.57	115	4e-53
Consensus51	gi|225460636|ref|XP_002265125.1|	PREDICTED: hypothetical protein [Vitis vinifera]	90.34	207	3e-94
Consensus52	gi|224075782|ref|XP_002304765.1|	predicted protein [Populus trichocarpa] >gi|118482084|gb|ABK92973.1| unknown [Populus trichocarpa] >gi|118483879|gb|ABK93830.1| unknown [Populus trichocarpa] >gi|118486451|gb|ABK95065.1| unknown [Populus trichocarpa] >gi|222842197|gb|EEE79744.1| predicted protein [Populus trichocarpa]	80.23	172	2e-77
Consensus53	gi|224060514|ref|XP_002300227.1|	predicted protein [Populus trichocarpa] >gi|222847485|gb|EEE85032.1| predicted protein [Populus trichocarpa]	89.33	150	1e-71
Consensus54	gi|147804843|emb|CAN66875.1|	hypothetical protein [Vitis vinifera]	95.24	84	7e-39
Consensus55	gi|224062149|ref|XP_002300779.1|	predicted protein [Populus trichocarpa] >gi|118482922|gb|ABK93374.1| unknown [Populus trichocarpa] >gi|118484750|gb|ABK94244.1| unknown [Populus trichocarpa] >gi|222842505|gb|EEE80052.1| predicted protein [Populus trichocarpa]	92.47	146	1e-65
Consensus57	gi|134286711|dbj|BAF50334.1|	hypothetical protein [Crucihimalaya wallichii] >gi|134286725|dbj|BAF50348.1| hypothetical protein [Crucihimalaya wallichii] >gi|134286888|dbj|BAF50509.1| hypothetical protein [Lepidium virginicum] >gi|134286902|dbj|BAF50523.1| hypothetical protein [Lepidium virginicum] >gi|134286977|dbj|BAF50597.1| hypothetical protein [Lobularia maritima] >gi|134286991|dbj|BAF50611.1| hypothetical protein [Lobularia	86.81	91	5e-34

IP : 14.49.138.138, 2017-11-03 13:30:33

		maritima]			
Consensus58	gi|209484089|gb|ACI47519.1|	iron-sulfer cluster scaffold protein ISU1 [Eucalyptus grandis]	83.33	156	1e-64
Consensus59	gi|225440308|ref|XP_002262887.1|	PREDICTED: hypothetical protein [Vitis vinifera]	94.55	55	2e-25
Consensus5	gi|270234205|emb|CBI22810.1|	unnamed protein product [Vitis vinifera]	86.57	67	3e-25
Consensus60	gi|225461330|ref|XP_002284579.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270231039|emb|CBI20366.1| unnamed protein product [Vitis vinifera]	77.45	102	4e-32
Consensus62	gi|270243017|emb|CBI29957.1|	unnamed protein product [Vitis vinifera]	87.93	58	4e-21
Consensus63	gi|224131142|ref|XP_002321011.1|	multidrug resistance protein ABC transporter family [Populus trichocarpa] >gi|222861784|gb|EEE99326.1| multidrug resistance protein ABC transporter family [Populus trichocarpa]	82.35	51	2e-16
Consensus64	gi|260401128|gb|ACX37092.1|	cyclophilin [Citrus sinensis]	99.42	172	1e-87
Consensus65	gi|255548684|ref|XP_002515398.1|	conserved hypothetical protein [Ricinus communis] >gi|223545342|gb|EEF46847.1| conserved hypothetical protein [Ricinus communis]	68.85	61	6e-14
Consensus66	gi|255556846|ref|XP_002519456.1|	tonoplast intrinsic protein, putative [Ricinus communis] >gi|223541319|gb|EEF42870.1| tonoplast intrinsic protein, putative [Ricinus communis]	90.44	251	2e-116
Consensus67	gi|224060236|ref|XP_002300099.1|	predicted protein [Populus trichocarpa] >gi|118488638|gb|ABK96131.1| unknown [Populus trichocarpa] >gi|222847357|gb|EEE84904.1| predicted protein [Populus trichocarpa]	89.22	167	8e-83
Consensus68	gi|225438619|ref|XP_002281037.1|	PREDICTED: hypothetical protein [Vitis vinifera] >gi|270232151|emb|CBI21474.1| unnamed protein product [Vitis vinifera]	95.1	102	3e-51
Consensus69	gi|270240437|emb|CBI27668.1|	unnamed protein product [Vitis vinifera]	87.84	74	6e-19
Consensus6	gi|224056230|ref|XP_002298766.1|	predicted protein [Populus trichocarpa] >gi|222846024|gb|EEE83571.1| predicted protein [Populus trichocarpa]	89.18	194	5e-99
Consensus70	gi|22653808|sp|Q39644|LEA5_CITSI	RecName: Full=Late embryogenesis abundant protein Lea5 >gi|599726|emb|CAA86851.1| Lea5 protein [Citrus sinensis]	97.94	97	5e-46
Consensus71	gi|224146587|ref|XP_002326061.1|	predicted protein [Populus trichocarpa] >gi|222862936|gb|EEF00443.1| predicted protein [Populus trichocarpa]	67.72	158	5e-54
Consensus72	gi|255557985|ref|XP_002520021.1|	NADH-ubiquinone oxidoreductase subunit B17.2, putative [Ricinus communis] >gi|223540785|gb|EEF42345.1| NADH-ubiquinone oxidoreductase subunit B17.2, putative [Ricinus communis]	82.47	154	3e-73
Consensus74	gi|147862659|emb|CAN83593.1|	hypothetical protein [Vitis vinifera]	68	100	1e-28
Consensus75	gi|270228659|emb|CBI17596.1|	unnamed protein product [Vitis vinifera]	97.14	70	1e-31
Consensus76	gi|50844679|gb|AAT84461.1|	cytochrome b5 isoform Cb5-D [Vernicia fordii]	74.63	134	3e-53
Consensus77	gi|270256806|emb|CBI23573.1|	unnamed protein product [Vitis vinifera]	99.28	138	8e-70
Consensus78	gi|224059690|ref|XP_002299972.1|	predicted protein [Populus trichocarpa] >gi|222847230|gb|EEE84777.1| predicted protein [Populus trichocarpa]	82.47	97	6e-39
Consensus79	gi|15229784|ref|NP_189967.1|	CAM7 (CALMODULIN 7); calcium ion binding [Arabidopsis thaliana] >gi|224086697|ref|XP_002307936.1| predicted protein [Populus trichocarpa] >gi|224106642|ref|XP_002314234.1| predicted protein [Populus trichocarpa] >gi|224137536|ref|XP_002322582.1| predicted protein [Populus trichocarpa] >gi|225435971|ref|XP_002270925.1| PREDICTED: hypothetical protein [Vitis vinifera] >gi|225440224|ref|XP_002283763.1| PREDICTED: hypothetical protein [Vitis vinifera] >gi|255549096|ref|XP_002515603.1| calmodulin, putative [Ricinus communis] >gi|255572905|ref|XP_002527384.1| calmodulin, putative [Ricinus communis] >gi|27805429|sp|P59220|CALM7_ARATH RecName: Full=Calmodulin-7; Short=CaM-7 >gi|49037479|sp|P62199|CALM1_PETHY RecName: Full=Calmodulin-1; Short=CaM-1 >gi|49037480|sp|P62200|CALM1_DAUCA RecName: Full=Calmodulin-1/11/16; Short=CaM-1/11/16 >gi|49037481|sp|P62201|CALM_LILLO RecName: Full=Calmodulin; Short=CaM >gi|49037482|sp|P62202|CALM_BRYDI RecName: Full=Calmodulin; Short=CaM; AltName: Full=BC329 >gi|62286560|sp|Q7Y052|CALM_EUPCH RecName: Full=Calmodulin; Short=CaM >gi|5825598|gb|AAD53313.1|AF178073_1 calmodulin 7 [Arabidopsis thaliana] >gi|9992891|gb|AAG11418.1|AF292108_1 calmodulin [Prunus avium] >gi|21913285|gb|AAM81202.1|AF494219_1 calmodulin 1 [Medicago truncatula] >gi|18326|emb|CAA42423.1| calmodulin [Daucus carota] >gi|19447|emb|CAA78301.1| calmodulin [Lilium longiflorum] >gi|169207|gb|AAA33706.1| calmodulin [Petunia x hybrida] >gi|308900|gb|AAA33397.1| calmodulin [Lilium longiflorum] >gi|505154|emb|CAA43143.1| Calmodulin [Malus x domestica] >gi|535444|gb|AAA92681.1| calmodulin [Pisum sativum] >gi|7362781|emb|CAB83153.1| calmodulin 7 [Arabidopsis thaliana] >gi|11036952|gb|AAG27432.1| calmodulin [Elaeis guineensis] >gi|14625405|dbj|BAB61909.1| calmodulin NtCaM3 [Nicotiana tabacum] >gi|14625407|dbj|BAB61910.1| calmodulin NtCaM4 [Nicotiana tabacum] >gi|14625409|dbj|BAB61911.1| calmodulin NtCaM5 [Nicotiana tabacum] >gi|14625411|dbj|BAB61912.1| calmodulin NtCaM6 [Nicotiana tabacum] >gi|14625413|dbj|BAB61913.1| calmodulin NtCaM7 [Nicotiana tabacum] >gi|14625415|dbj|BAB61914.1| calmodulin NtCaM8 [Nicotiana tabacum] >gi|14625421|dbj|BAB61917.1| calmodulin NtCaM11 [Nicotiana tabacum] >gi|14625423|dbj|BAB61918.1| calmodulin NtCaM12 [Nicotiana tabacum] >gi|21594484|gb|AAM66013.1| calmodulin 7 [Arabidopsis thaliana] >gi|40365136|gb|AAP55717.2| calmodulin [Euphorbia characias] >gi|45181612|gb|AAS55460.1| calmodulin cam-11 [Daucus carota] >gi|45181614|gb|AAS55461.1| calmodulin cam-16 [Daucus carota] >gi|50299503|gb|AAT73615.1| calmodulin cam-202 [Daucus carota] >gi|50299507|gb|AAT73617.1| calmodulin cam-204 [Daucus carota] >gi|50299515|gb|AAT73621.1| calmodulin cam-208 [Daucus carota] >gi|50299517|gb|AAT73622.1| calmodulin cam-209 [Daucus carota] >gi|52851162|emb|CAH58629.1| calmodulin [Plantago major] >gi|52851164|emb|CAH58630.1| calmodulin [Plantago major] >gi|60729719|emb|CAH57707.1| calmodulin [Quercus petraea] >gi|62125396|gb|AAX63770.1| calmodulin [Populus tomentosa] >gi|75756242|gb|ABA27138.1| calmodulin 2 [Catharanthus roseus] >gi|98960891|gb|ABF58929.1| At3g43810 [Arabidopsis thaliana] >gi|110742424|dbj|BAE99131.1| calmodulin 7 [Arabidopsis thaliana] >gi|118136471|gb|ABK62856.1| calmodulin [Scoparia dulcis] >gi|118481324|gb|ABK92605.1| unknown [Populus trichocarpa]	100	149	6e-79

IP : 14.49.138.138, 2017-11-03 13:30:33

		>gi|118481354|gb|ABK92620.1| unknown [Populus trichocarpa] >gi|118481535|gb|ABK92710.1| unknown [Populus trichocarpa] >gi|118482590|gb|ABK93215.1| unknown [Populus trichocarpa] >gi|118483779|gb|ABK93782.1| unknown [Populus trichocarpa] >gi|118484140|gb|ABK93953.1| unknown [Populus trichocarpa] >gi|118484730|gb|ABK94234.1| unknown [Populus trichocarpa] >gi|118484977|gb|ABK94353.1| unknown [Populus trichocarpa] >gi|118485441|gb|ABK94577.1| unknown [Populus trichocarpa] >gi|118485636|gb|ABK94668.1| unknown [Populus trichocarpa] >gi|118485771|gb|ABK94734.1| unknown [Populus trichocarpa] >gi|118485950|gb|ABK94820.1| unknown [Populus trichocarpa] >gi|146403792|gb|ABQ32302.1| putative calmodulin [Artemisia annua] >gi|147837821|emb|CAN63123.1| hypothetical protein [Vitis vinifera] >gi|151500327|gb|ABS12105.1| calmodulin 1 [Morus nigra] >gi|189031544|gb|ACD74910.1| calmodulin [Vitis quinquangularis] >gi|192910746|gb|ACF06481.1| calmodulin 8 [Elaeis guineensis] >gi|192910748|gb|ACF06482.1| calmodulin 8 [Elaeis guineensis] >gi|192910750|gb|ACF06483.1| calmodulin 8 [Elaeis guineensis] >gi|192910752|gb|ACF06484.1| calmodulin 8 [Elaeis guineensis] >gi|197312869|gb|ACH63215.1| calmodulin [Rheum australe] >gi|222850642|gb|EEE88189.1| predicted protein [Populus trichocarpa] >gi|222853912|gb|EEE91459.1| predicted protein [Populus trichocarpa] >gi|222867212|gb|EEF04343.1| predicted protein [Populus trichocarpa] >gi|223533255|gb|EEF35009.1| calmodulin, putative [Ricinus communis] >gi|223545241|gb|EEF46748.1| calmodulin, putative [Ricinus communis] >gi|224612147|gb|ACN60147.1| calmodulin [Lonicera japonica] >gi|226377531|gb|ACO52511.1| calmodulin [Panax ginseng] >gi|247421773|gb|ACS96443.1| calmodulin 7 [Jatropha curcas] >gi|255039654|gb|ACT99605.1| calmodulin [Morus alba var. multicaulis] >gi|282935436|gb|ADB03783.1| calmodulin [Ipomoea batatas] >gi|445602|prf||1909349A calmodulin			
Consensus7	gi|225437346|ref|XP_002265489.1|	PREDICTED: hypothetical protein [Vitis vinifera]	86.36	88	1e-37
Consensus80	gi|255565162|ref|XP_002523573.1|	Caltractin, putative [Ricinus communis] >gi|223537135|gb|EEF38768.1| Caltractin, putative [Ricinus communis]	87.06	170	1e-77
Consensus82	gi|3308980|dbj|BAA31561.1|	metallothionein-like protein [Citrus unshiu] >gi|281181704|dbj|BAI58031.1| metallothionein [Citrus jambhiri]	100	40	5e-14
Consensus83	gi|255628751|gb|ACU14720.1|	unknown [Glycine max]	78.35	97	4e-34
Consensus84	gi|37524017|gb|AAQ92310.1|	COR15 [Citrus clementina x Citrus reticulata]	100	62	2e-19
Consensus85	gi|255626469|gb|ACU13579.1|	unknown [Glycine max]	66.42	134	5e-47
Consensus86	gi|224074171|ref|XP_002304285.1|	predicted protein [Populus trichocarpa] >gi|224138624|ref|XP_002326649.1| predicted protein [Populus trichocarpa] >gi|118484142|gb|ABK93954.1| unknown [Populus trichocarpa] >gi|222833971|gb|EEE72448.1| predicted protein [Populus trichocarpa] >gi|222841717|gb|EEE79264.1| predicted protein [Populus trichocarpa]	96.75	154	3e-68
Consensus87	gi|255543030|ref|XP_002512578.1|	cysteine desulfurylase, putative [Ricinus communis] >gi|223548539|gb|EEF50030.1| cysteine desulfurylase, putative [Ricinus communis]	67.04	267	8e-98
Consensus88	gi|225442221|ref|XP_002277703.1|	PREDICTED: hypothetical protein [Vitis vinifera]	99.06	106	1e-52
Consensus89	gi|225430906|ref|XP_002276581.1|	PREDICTED: hypothetical protein [Vitis vinifera]	73.48	279	2e-100
Consensus8	gi|224116926|ref|XP_002331848.1|	predicted protein [Populus trichocarpa] >gi|224118148|ref|XP_002317742.1| predicted protein [Populus trichocarpa] >gi|118484605|gb|ABK94176.1| unknown [Populus trichocarpa] >gi|118486683|gb|ABK95178.1| unknown [Populus trichocarpa] >gi|192910722|gb|ACF06469.1| ubiquitin conjugating enzyme [Elaeis guineensis] >gi|222858415|gb|EEE95962.1| predicted protein [Populus trichocarpa] >gi|222875086|gb|EEF12217.1| predicted protein [Populus trichocarpa] >gi|257219556|gb|ACV50431.1| ubiquitin conjugating enzyme 2 [Jatropha curcas]	99.32	148	5e-83
Consensus90	gi|119367485|gb|ABL67657.1|	putative copper chaperone [Citrus hybrid cultivar]	97.73	88	3e-41
Consensus91	gi|255567721|ref|XP_002524839.1|	carboxymethylenebutenolidase, putative [Ricinus communis] >gi|223535899|gb|EEF37559.1| carboxymethylenebutenolidase, putative [Ricinus communis]	74.89	223	5e-90
Consensus92	gi|2463569|dbj|BAA22559.1|	squalene synthase [Glycine max]	90.67	268	3e-142
Consensus93	gi|270243212|emb|CBI30152.1|	unnamed protein product [Vitis vinifera]	66.29	89	2e-27
Consensus94	gi|2213425|emb|CAB09799.1|	hypothetical protein [Citrus x paradisi]	99.12	227	1e-128
Consensus95	gi|118487795|gb|ABK95721.1|	unknown [Populus trichocarpa]	83.33	258	1e-119
Consensus96	gi|224140583|ref|XP_002323661.1|	predicted protein [Populus trichocarpa] >gi|116265958|gb|ABJ91227.1| CBL-interacting protein kinase 21 [Populus trichocarpa] >gi|222868291|gb|EEF05422.1| predicted protein [Populus trichocarpa]	64.94	348	4e-108
Consensus97	gi|221327589|gb|ACM17464.1|	ascorbate peroxidase 2 [Citrus maxima]	96.49	57	3e-12
Consensus98	gi|255581937|ref|XP_002531767.1|	Photosystem I reaction center subunit V, chloroplast precursor, putative [Ricinus communis] >gi|223528603|gb|EEF30623.1| Photosystem I reaction center subunit V, chloroplast precursor, putative [Ricinus communis]	78.48	158	4e-61
Consensus99	gi|50199132|emb|CAH03799.1|	lipid transfer protein [Citrus sinensis]	76.09	92	5e-33

IP : 14.49.138.138, 2017-11-03 13:30:33

9) 병귤 미숙과실

Accession No.	Definition of putative homologues [organism]	Matching (%)	Matching (length)	E-value
NM_118317	peroxidase 42 (PRXR1) mRNA [Arabidopsis thaliana]	77	813	2.00E-163
NM_120882	glucan endo-1,3-beta-glucosidase-like protein 3 (E13L3) mRNA [Arabidopsis thaliana]	72	266	4.00E-32
NM_105269	peroxiredoxin-2C (TPX2) mRNA [Arabidopsis thaliana]	78	497	5.00E-106
NM_114735	putative S-acyltransferase (AT3G48760) mRNA [Arabidopsis thaliana]	73	767	2.00E-117
NM_118980	ADP/ATP carrier 3 protein (AAC3) mRNA [Arabidopsis thaliana]	76	837	2.00E-163
NM_001036720	BEL1-like homeodomain protein 2 (BLH2) mRNA [Arabidopsis thaliana]	87	30	0.5
NM_113623	DCD (Development and Cell Death) domain protein (AT3G27090) mRNA [Arabidopsis thaliana]	81	383	4.00E-94
NM_113623	DCD (Development and Cell Death) domain protein (AT3G27090) mRNA [Arabidopsis thaliana]	81	383	4.00E-94
AK318644	AT3G52120 mRNA [Arabidopsis thaliana]	76	221	3.00E-35
NM_106531	curculin-like (mannose-binding) lectin-like protein (AT1G78830) mRNA [Arabidopsis thaliana]	84	43	0.61
NM_001203599	ubiquitin-conjugating enzyme E2 10 (UBC10) mRNA [Arabidopsis thaliana]	86	449	1.00E-146
AK317712	AT3G10720 mRNA [Arabidopsis thaliana]	81	47	0.013
AK226902	mRNA for ubiquitin extension protein [Arabidopsis thaliana]	85	455	5.00E-143
NM_106555	photosystem II subunit R (PSBR) mRNA [Arabidopsis thaliana]	76	426	8.00E-77
NM_120019	farnesylated protein 6 (FP6) mRNA [Arabidopsis thaliana]	74	442	1.00E-69
NM_100596	uncharacterized protein (AT1G07220) mRNA [Arabidopsis thaliana]	93	26	1.9
NM_124714	CLP protease regulatory subunit X (CLPX) mRNA [Arabidopsis thaliana]	73	814	3.00E-116
NM_001160906	dormancy-associated protein-like 1 (DYL1) mRNA [Arabidopsis thaliana]	72	363	1.00E-43
NM_105399	calmodulin-binding transcription activator 4 (AT1G67310) mRNA [Arabidopsis thaliana]	75	343	3.00E-54
NM_125361	histone H4 (AT5G59690) mRNA [Arabidopsis thaliana]	81	316	1.00E-75
AY039912	At1g55460 mRNA sequence [Arabidopsis thaliana]	86	35	0.27
NM_112618	S-adenosylmethionine synthase 4 (MTO3) mRNA [Arabidopsis thaliana]	80	582	2.00E-144
AK319078	AT4G25910 mRNA [Arabidopsis thaliana]	83	41	0.011
NM_124489	Fe superoxide dismutase 2 (FSD2) mRNA [Arabidopsis thaliana]	76	649	5.00E-120
NM_129093	RNA-binding (RRM/RBD/RNP motifs) family protein (AT2G35410) mRNA [Arabidopsis thaliana]	68	377	2.00E-23
AY144108	hypothetical protein (At2g39490/F12L6.15) mRNA [Arabidopsis thaliana]	92	57	2.00E-13
NM_129316	60S ribosomal protein L36-1 (AT2G37600) mRNA [Arabidopsis thaliana]	74	299	1.00E-42
NM_100144	beta-glucosidase (BXL2) mRNA [Arabidopsis thaliana]	84	42	0.037
NM_001035615	Ribosomal protein L34 (AT3G13882) mRNA [Arabidopsis thaliana]	79	223	1.00E-43
NM_001198478	gibberellin-regulated protein 1 (GASA1) mRNA [Arabidopsis thaliana]	67	303	3.00E-19
NM_105269	peroxiredoxin-2C (TPX2) mRNA [Arabidopsis thaliana]	78	497	5.00E-106
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	81	51	3.00E-04
NM_119019	photosystem I reaction center subunit IV A (PSAE-1) mRNA [Arabidopsis thaliana]	80	167	1.00E-34
NM_001036720	BEL1-like homeodomain protein 2 (BLH2) mRNA [Arabidopsis thaliana]	87	30	0.56
NM_001036983	uncharacterized protein (HCF208) mRNA [Arabidopsis thaliana]	91	31	1.8
AK228689	mRNA for hypothetical protein [Arabidopsis thaliana]	72	446	6.00E-55
NM_102497	Ribosome associated membrane protein RAMP4 (AT1G27350) mRNA [Arabidopsis thaliana]	82	214	5.00E-53
NM_111754	60S acidic ribosomal protein P0-2 (AT3G09200) mRNA [Arabidopsis thaliana]	82	636	1.00E-170

IP : 14.49.138.138, 2017-11-03 13:30:33

NM_111161	AIG2-like (avirulence induced gene) family protein (AT3G02910) mRNA [Arabidopsis thaliana]	79	57	0.003
NM_103611	VIER F-box protein 1 (VFB1) mRNA [Arabidopsis thaliana]	74	650	6.00E-100
NM_120653	pleckstrin homology domain-containing protein (AT5G05710) mRNA [Arabidopsis thaliana]	79	362	2.00E-80
NM_001036342	BRCA1-associated protein (BRIZ2) mRNA [Arabidopsis thaliana]	72	556	1.00E-52
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	80	49	0.002
NM_127284	Calcium-dependent protein kinase family protein (CPK6) mRNA [Arabidopsis thaliana]	84	153	8.00E-38
NM_126087	serine/threonine-protein kinase SRK2I (SNRK2.3) mRNA [Arabidopsis thaliana]	87	30	0.56
NM_120882	glucan endo-1,3-beta-glucosidase-like protein 3 (E13L3) mRNA [Arabidopsis thaliana]	72	266	4.00E-32
NM_129462	hydroxyproline-rich glycoprotein-like protein (AT2G39050) mRNA [Arabidopsis thaliana]	72	423	8.00E-55
NM_102725	double-stranded DNA-binding-like protein (AT1G29850) mRNA [Arabidopsis thaliana]	80	374	5.00E-86
NM_106396	replication factor C subunit 3 (RFC3) mRNA [Arabidopsis thaliana]	97	26	0.033
NM_103323	serine hydroxymethyltransferase 7 (SHM7) mRNA [Arabidopsis thaliana]	75	365	2.00E-56
NM_126278	tobamovirus multiplication protein 3 (TOM3) mRNA [Arabidopsis thaliana]	81	503	2.00E-124
AK317161	AT1G78460 mRNA [Arabidopsis thaliana]	85	38	0.47
NM_001160906	dormancy-associated protein-like 1 (DYL1) mRNA [Arabidopsis thaliana]	72	363	7.00E-41
NM_101433	uncharacterized protein (AT1G15640) mRNA [Arabidopsis thaliana]	93	26	0.35
NM_118980	ADP/ATP carrier 3 protein (AAC3) mRNA [Arabidopsis thaliana]	75	810	2.00E-144
NM_113224	ethylene-responsive transcription factor ERF098 (AT3G23230) mRNA [Arabidopsis thaliana]	79	56	4.00E-04
NM_121956	Elongation factor 1-beta 2 (AT5G19510) mRNA [Arabidopsis thaliana]	73	678	2.00E-105
NM_129093	RNA-binding (RRM/RBD/RNP motifs) family protein (AT2G35410) mRNA [Arabidopsis thaliana]	69	496	7.00E-42
NM_001203188	DNA helicase INO80 complex-like 1 (INO80) mRNA [Arabidopsis thaliana]	84	36	1.6
AY059815	AIM1 protein (At4g29010; F19B15.40) mRNA [Arabidopsis thaliana]	74	783	6.00E-119
NM_106090	esterase/lipase/thioesterase family protein (AT1G74300) mRNA [Arabidopsis thaliana]	92	25	1
NM_120882	glucan endo-1,3-beta-glucosidase-like protein 3 (E13L3) mRNA [Arabidopsis thaliana]	72	266	4.00E-32
NM_180537	Uridylate kinase (PYR6) mRNA [Arabidopsis thaliana]	78	563	2.00E-122
NM_122667	60S ribosomal protein L18-3 (AT5G27850) mRNA [Arabidopsis thaliana]	80	570	6.00E-137
AY059815	AIM1 protein (At4g29010; F19B15.40) mRNA [Arabidopsis thaliana]	74	782	4.00E-121
NM_126747	F-type H+-transporting ATPase subunit alpha (AT2G07698) mRNA [Arabidopsis thaliana]	94	987	0
NM_180537	Uridylate kinase (PYR6) mRNA [Arabidopsis thaliana]	78	563	2.00E-123
NM_124967	RPM1-interacting protein 4 (RIN4) family protein (NOI) mRNA [Arabidopsis thaliana]	89	126	1.00E-37
NM_130025	Ras-related protein RABH1B (RAB6A) mRNA [Arabidopsis thaliana]	82	640	1.00E-170
AK316936	AT1G65270 mRNA [Arabidopsis thaliana]	75	587	2.00E-105
NM_123982	uncharacterized protein (AT5G46130) mRNA [Arabidopsis thaliana]	80	53	0.41
NM_122912	DNA binding and zinc-finger domain-containing protein (AT5G35210) mRNA [Arabidopsis thaliana]	93	26	0.16
NM_001036737	cytochrome P450 [Arabidopsis thaliana]	69	529	2.00E-42
NM_112661	uncharacterized protein (AT3G17800) mRNA [Arabidopsis thaliana]	96	21	1.5
NM_123058	Exostosin family protein (AT5G37000) mRNA [Arabidopsis thaliana]	88	33	0.12
NM_113448	60S ribosomal protein L5-1 (ATL5) mRNA [Arabidopsis thaliana]	77	758	3.00E-147
NM_130025	Ras-related protein RABH1B (RAB6A) mRNA [Arabidopsis thaliana]	81	623	3.00E-166
NM_105029	Protein kinase protein with tetratricopeptide repeat domain (AT1G63500) mRNA [Arabidopsis thaliana]	89	27	1.1

IP : 14.49.138.138, 2017-11-03 13:30:33

NM_128872	vesicle-associated membrane protein 722 (SAR1) mRNA [Arabidopsis thaliana]	77	542	2.00E-105
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	80	49	0.002
AK220588	mRNA for hypothetical protein [Arabidopsis thaliana]	78	162	8.00E-22
NM_129462	hydroxyproline-rich glycoprotein-like protein (AT2G39050) mRNA [Arabidopsis thaliana]	71	371	7.00E-42
NM_115882	dynamin-related protein 1E (DL1E) mRNA [Arabidopsis thaliana]	77	651	4.00E-133
NM_105651	alpha-amylase-like 3 (AMY3) mRNA [Arabidopsis thaliana]	93	26	0.087
NM_104336	acyl carrier protein 2 (ACP2) mRNA [Arabidopsis thaliana]	71	257	2.00E-23
AK227568	mRNA for metallothionein 2b [Arabidopsis thaliana]	71	260	3.00E-26
NM_128994	light-harvesting complex II chlorophyll a/b binding protein 1 (LHB1B2) mRNA [Arabidopsis thaliana]	76	808	9.00E-155
NM_127534	profilin 1 (PRF1) mRNA [Arabidopsis thaliana]	77	387	3.00E-76
NM_001160781	Mob1/phocein family protein (AT4G19045) mRNA [Arabidopsis thaliana]	80	222	3.00E-48
NM_180420	LURP-one-related 15 protein (AT5G01750) mRNA [Arabidopsis thaliana]	69	212	3.00E-15
NM_123107	uncharacterized protein (AT5G37480) mRNA [Arabidopsis thaliana]	70	222	1.00E-12
NM_117028	gibberellin-regulated protein 3 (GASA3) mRNA [Arabidopsis thaliana]	73	149	5.00E-15
NM_127534	profilin 1 (PRF1) mRNA [Arabidopsis thaliana]	77	387	3.00E-76
NM_125384	histone H2B (HTB4) mRNA [Arabidopsis thaliana]	80	466	5.00E-112
BT026113	At1g61620 mRNA [Arabidopsis thaliana]	73	911	4.00E-134
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	79	75	6.00E-10
NM_103729	thioesterase-like protein (AT1G48320) mRNA [Arabidopsis thaliana]	77	209	2.00E-36
NM_111682	uncharacterized protein (AT3G08030) mRNA [Arabidopsis thaliana]	73	731	5.00E-108
EU031443	ecotype Cvi-0 TAO1 gene [Arabidopsis thaliana]	83	34	1.3
NM_123256	germin-like protein subfamily 1 member 11 (AT5G38940) mRNA [Arabidopsis thaliana]	69	633	1.00E-51
NM_111146	Isopentenyl-diphosphate Delta-isomerase II (IPP2) mRNA [Arabidopsis thaliana]	81	687	4.00E-178
NM_104768	maternal effect embryo arrest 9 protein (MEE9) mRNA [Arabidopsis thaliana]	70	170	5.00E-11
NM_122658	Hypoxia-responsive family protein (AT5G27760) mRNA [Arabidopsis thaliana]	74	237	3.00E-34
NM_123272	germin-like protein 6 (GLP6) mRNA [Arabidopsis thaliana]	71	425	2.00E-49
NM_001160925	uncharacterized protein (AT1G42480) mRNA [Arabidopsis thaliana]	77	171	9.00E-26
NM_001036720	BEL1-like homeodomain protein 2 (BLH2) mRNA [Arabidopsis thaliana]	87	30	0.56
NM_124796	Quercetin 3-O-methyltransferase 1 (OMT1) mRNA [Arabidopsis thaliana]	70	374	1.00E-37
NM_126597	proteasome subunit alpha type-6-B (PAA2) mRNA [Arabidopsis thaliana]	80	551	8.00E-136
AK318964	AT2G37660 mRNA [Arabidopsis thaliana]	89	27	3.7
NM_112545	RING-H2 finger protein ATL2 (ATL2) mRNA [Arabidopsis thaliana]	78	144	7.00E-23
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.067
NM_121645	thioredoxin F2 (TRXF2) mRNA [Arabidopsis thaliana]	77	323	7.00E-66
NM_001198478	gibberellin-regulated protein 1 (GASA1) mRNA [Arabidopsis thaliana]	67	303	1.00E-17
AK227661	mRNA for putative AP2 domain transcription factor [Arabidopsis thaliana]	93	26	0.1
AY800586	clone H0000001110 hypothetical protein (AT1G18510) mRNA [Arabidopsis thaliana]	100	36	1.00E-09
NM_121396	chalcone synthase (TT4) mRNA [Arabidopsis thaliana]	75	434	2.00E-77
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	80	49	0.002
NM_124371	zinc knuckle (CCHC-type) family protein (emb1441) mRNA [Arabidopsis thaliana]	77	242	3.00E-41

IP : 14.49.138.138, 2017-11-03 13:30:33

NM_104534	pentatricopeptide repeat-containing protein (AT1G56570) mRNA [Arabidopsis thaliana]	87	30	0.89
NM_125630	plant invertase/pectin methylesterase inhibitor domain-containing protein (AT5G62360) mRNA [Arabidopsis thaliana]	67	502	9.00E-33
NM_102942	putative membrane protein (AT1G32080) mRNA [Arabidopsis thaliana]	77	776	7.00E-168
NM_121843	40S ribosomal protein S16-3 (AT5G18380) mRNA [Arabidopsis thaliana]	80	418	4.00E-100
AK229276	mRNA for ABA-responsive protein - like [Arabidopsis thaliana]	73	669	5.00E-101
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	80	49	0.002
NM_123272	germin-like protein 6 (GLP6) mRNA [Arabidopsis thaliana]	71	425	2.00E-48
NM_127899	poly(A) binding protein 4 (PAB4) mRNA [Arabidopsis thaliana]	80	58	0.036
AK317341	AT3G52880 mRNA [Arabidopsis thaliana]	81	337	8.00E-77
NM_100830	emp24/gp25L/p24 family/GOLD domain-containing protein (AT1G09580) mRNA [Arabidopsis thaliana]	75	404	1.00E-64
NM_202521	zinc finger protein CONSTANS-LIKE 9 (COL9) mRNA [Arabidopsis thaliana]	81	42	0.59
AY800586	clone H0000001110 hypothetical protein (AT1G18510) mRNA [Arabidopsis thaliana]	100	36	1.00E-09
AK227650	mRNA for hypothetical protein [Arabidopsis thaliana]	75	134	1.00E-15
-	-	-	-	-
NM_104534	pentatricopeptide repeat-containing protein (AT1G56570) mRNA [Arabidopsis thaliana]	87	30	0.37
AB425271	At1g58520 orthologue [Arabidopsis thaliana]	96	21	3.1
NM_121645	thioredoxin F2 (TRXF2) mRNA [Arabidopsis thaliana]	79	334	1.00E-74
NM_102646	protein trichome birefringence-like 38 (TBL38) mRNA [Arabidopsis thaliana]	74	677	2.00E-112
DQ446773	clone pENTR221-At3g57270 glycosyl hydrolase family 17 protein (At3g57270) mRNA [Arabidopsis thaliana]	67	353	3.00E-16
NM_180233	40S ribosomal protein S5-2 (RPS5A) mRNA [Arabidopsis thaliana]	80	587	3.00E-141
NM_111300	GDSL esterase/lipase LTL1 (LTL1) mRNA [Arabidopsis thaliana]	76	435	1.00E-75
NM_113062	major facilitator protein (AT3G21670) mRNA [Arabidopsis thaliana]	73	892	3.00E-135
NM_120426	uncharacterized protein (AT5G03460) mRNA [Arabidopsis thaliana]	69	129	0.002
AY800612	clone H0000001186 hypothetical protein (AT1G67540) mRNA [Arabidopsis thaliana]	83	52	4.00E-06
AK226427	mRNA for hypothetical protein [Arabidopsis thaliana]	75	183	4.00E-25
AY501358	hypothetical protein (At2g47340) mRNA [Arabidopsis thaliana]	100	28	4.00E-05
AK317128	AT1G07840 mRNA [Arabidopsis thaliana]	69	643	1.00E-57
AY630778	hypothetical protein (At3G52550) mRNA [Arabidopsis thaliana]	92	35	1.00E-04
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	75	55	0.064
AK117225	At2g26070 mRNA for unknown protein [Arabidopsis thaliana]	80	48	0.031
NM_103274	annexin D1 (ANNAT1) mRNA [Arabidopsis thaliana]	73	517	2.00E-79
NM_119960	cinnamyl alcohol dehydrogenase 8 (ELI3-2) mRNA [Arabidopsis thaliana]	71	829	2.00E-95
AF386970	Unknown protein (At2g44650; F16B22.14) mRNA [Arabidopsis thaliana]	73	432	2.00E-58
NM_121432	DNA-binding storekeeper protein-like protein (AT5G14280) mRNA [Arabidopsis thaliana]	71	689	2.00E-86
NM_001202912	ubiquitin-conjugating enzyme E2 11 (UBC11) mRNA [Arabidopsis thaliana]	82	444	1.00E-120
NM_118706	40S ribosomal protein S10-1 (AT4G25740) mRNA [Arabidopsis thaliana]	79	547	5.00E-131
NM_121517	putative WRKY transcription factor 72 (WRKY72) mRNA [Arabidopsis thaliana]	92	24	0.3
NM_111493	ribosomal protein L34e-like protein (AT3G06180) mRNA [Arabidopsis thaliana]	88	33	0.017
AK227371	mRNA for hypothetical protein [Arabidopsis thaliana]	78	45	1.3
NM_001203991	aquaporin PIP2-7 (PIP3) mRNA [Arabidopsis thaliana]	82	613	6.00E-162

IP : 14.49.138.138, 2017-11-03 13:30:33

NM_117028	gibberellin-regulated protein 3 (GASA3) mRNA [Arabidopsis thaliana]	72	149	2.00E-13
NM_129238	aquaporin TIP1-1 (GAMMA-TIP) mRNA [Arabidopsis thaliana]	78	749	6.00E-163
NM_001203991	aquaporin PIP2-7 (PIP3) mRNA [Arabidopsis thaliana]	82	798	0
AK227380	mRNA for hypothetical protein [Arabidopsis thaliana]	80	268	1.00E-62
NM_123258	putative germin-like protein subfamily 1 member 12 (AT5G38960) mRNA [Arabidopsis thaliana]	69	519	2.00E-47
AY144114	hypothetical protein (At2g42720/F7D19.28) mRNA [Arabidopsis thaliana]	85	39	2.00E-04
AK228192	mRNA for hypothetical protein [Arabidopsis thaliana]	77	499	8.00E-104
NM_178945	myb domain protein 3r2 (MYB3R2) mRNA [Arabidopsis thaliana]	84	31	1.2
NM_115584	beta-1,3-glucanase 3 (BG3) mRNA [Arabidopsis thaliana]	72	307	5.00E-37
-	-	-	-	-
NM_119682	O-methyltransferase family 2 protein (AT4G35160) mRNA [Arabidopsis thaliana]	100	19	4.2
NM_119682	O-methyltransferase family 2 protein (AT4G35160) mRNA [Arabidopsis thaliana]	100	19	4.8
NM_001203108	U-box domain-containing protein 32 (AT3G49060) mRNA [Arabidopsis thaliana]	72	195	1.00E-20
NM_126233	Ribophorin I (AT2G01720) mRNA [Arabidopsis thaliana]	76	830	6.00E-158
AK316891	AT3G02470 mRNA [Arabidopsis thaliana]	92	37	2.00E-04
NM_116468	exocyst complex component sec15B (SEC15B) mRNA [Arabidopsis thaliana]	80	44	0.36
BT030622	unknown protein (At1g70640) mRNA [Arabidopsis thaliana]	76	270	2.00E-42
AK318870	AT5G14920 mRNA [Arabidopsis thaliana]	72	98	1.00E-05
AK229596	mRNA for ribosomal protein GL41 - like [Arabidopsis thaliana]	93	78	2.00E-24
NM_130081	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein (AT2G45180) mRNA [Arabidopsis thaliana]	72	274	3.00E-32
NM_100133	P-glycoprotein 11 (PGP11) mRNA [Arabidopsis thaliana]	96	22	2.1
NM_102305	zinc finger protein 7 (ZFP7) mRNA [Arabidopsis thaliana]	80	120	2.00E-22
NM_120082	protein RER1A (ATRER1A) mRNA [Arabidopsis thaliana]	76	430	6.00E-74
NM_122982	exosome complex exonuclease RRP6 (AT5G35910) mRNA [Arabidopsis thaliana]	75	372	3.00E-54
AK117372	At5g48970 mRNA for putative mitochondrial carrier protein [Arabidopsis thaliana]	87	38	0.02
NM_129425	5'-nucleotidase / magnesium ion binding protein (AT2G38680) mRNA [Arabidopsis thaliana]	75	801	5.00E-145
NM_117843	60S ribosomal protein L15-2 (AT4G17390) mRNA [Arabidopsis thaliana]	82	613	4.00E-165
NM_127729	40S ribosomal protein S25-2 (AT2G21580) mRNA [Arabidopsis thaliana]	84	153	8.00E-38
NM_117683	drought-induced 21 protein (DI21) mRNA [Arabidopsis thaliana]	83	46	3.00E-04
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.12
GQ177366	ecotype Nd-1 GA1 gene [Arabidopsis thaliana]	86	28	8
NM_111283	glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]	82	660	0
AK228164	mRNA for bis(5'-adenosyl)-triphosphatase-like [Arabidopsis thaliana]	72	418	2.00E-54
NM_104590	ATP phosphoribosyl transferase 1 (ATP-PRT1) mRNA [Arabidopsis thaliana]	85	33	0.57
AK228770	mRNA for hypothetical protein [Arabidopsis thaliana]	75	187	4.00E-28
-	-	-	-	-
AB117776	AT3G27920.1 gene [Arabidopsis thaliana]	93	26	0.24
NM_001197990	putative E3 ubiquitin-protein ligase ARI12 (ARI12) mRNA [Arabidopsis thaliana]	90	30	0.077
NM_102646	protein trichome birefringence-like 38 (TBL38) mRNA [Arabidopsis thaliana]	71	634	3.00E-79
NM_001085085	40S ribosomal protein S15-4 (AT5G09510) mRNA [Arabidopsis thaliana]	82	435	8.00E-116

IP : 14.49.138.138, 2017-11-03 13:30:33

NM_112682	WUSCHEL-related homeobox 1 (WOX1) mRNA [Arabidopsis thaliana]	91	33	5.00E-04
AK316937	AT2G46340 mRNA [Arabidopsis thaliana]	100	19	3.3
NM_124714	CLP protease regulatory subunit X (CLPX) mRNA [Arabidopsis thaliana]	71	351	2.00E-34
AB493591	At2g45120 mRNA for hypothetical protein [Arabidopsis thaliana]	81	77	1.00E-11
NM_113623	DCD (Development and Cell Death) domain protein (AT3G27090) mRNA [Arabidopsis thaliana]	81	383	4.00E-94
NM_126150	voltage dependent anion channel 2 (VDAC2) mRNA [Arabidopsis thaliana]	78	510	2.00E-109
NM_100308	40S ribosomal protein S15-1 (RPS15) mRNA [Arabidopsis thaliana]	79	409	3.00E-88
NM_001203966	uncharacterized protein (AT4G32930) mRNA [Arabidopsis thaliana]	100	18	6.1
GU293333	ecotype Bl-1 rpoB-trnC intergenic spacer [Arabidopsis thaliana]	72	180	5.00E-13
NM_121374	cycloartenol-c-24-methyltransferase (SMT1) mRNA [Arabidopsis thaliana]	83	603	4.00E-170
AK317336	AT5G48000 mRNA [Arabidopsis thaliana]	85	45	0.001
NM_122081	plant invertase/pectin methylesterase inhibitor domain-containing protein (AT5G20740) mRNA [Arabidopsis thaliana]	71	184	3.00E-14
NM_114242	leucine-rich repeat-containing protein (AT3G43740) mRNA [Arabidopsis thaliana]	72	257	1.00E-31
NM_119043	RNA-binding-related protein (AT4G28990) mRNA [Arabidopsis thaliana]	67	519	7.00E-23
NM_100484	Salt tolerance protein (STO) mRNA [Arabidopsis thaliana]	95	20	5.7
NM_129411	non-specific lipid-transfer protein 1 (LP1) mRNA [Arabidopsis thaliana]	80	67	2.00E-07
NM_100484	Salt tolerance protein (STO) mRNA [Arabidopsis thaliana]	96	21	1.6
NM_129907	60S ribosomal protein L38 (AT2G43460) mRNA [Arabidopsis thaliana]	85	215	9.00E-62
NM_112303	uncharacterized protein (AT3G14430) mRNA [Arabidopsis thaliana]	72	130	3.00E-10
NM_120882	glucan endo-1,3-beta-glucosidase-like protein 3 (E13L3) mRNA [Arabidopsis thaliana]	72	266	4.00E-32
AK228346	mRNA for putative two-component response regulator 3 protein [Arabidopsis thaliana]	92	25	0.56
NM_119850	LIM domain-containing protein (AT4G36860) mRNA [Arabidopsis thaliana]	72	216	3.00E-21
NM_124238	putative disease resistance RPP8-like protein 4 (AT5G48620) mRNA [Arabidopsis thaliana]	86	28	4.2
NM_102090	class-II DAHP synthetase-like protein (AT1G22410) mRNA [Arabidopsis thaliana]	82	512	8.00E-141
NM_105125	glutaredoxin-like protein (AT1G64500) mRNA [Arabidopsis thaliana]	92	24	2.2
NM_001202613	putative protein kinase (AT2G17530) mRNA [Arabidopsis thaliana]	86	28	4.2
AK318920	AT3G07300 mRNA [Arabidopsis thaliana]	77	971	0
NM_112530	rapid alkalinization factor 23 (RALF23) mRNA [Arabidopsis thaliana]	84	186	1.00E-48
NM_124967	RPM1-interacting protein 4 (RIN4) family protein (NOI) mRNA [Arabidopsis thaliana]	89	126	1.00E-37
NM_001203288	protein iron regulated 2 (IREG2) mRNA [Arabidopsis thaliana]	79	41	3.2
AK230014	mRNA for hypothetical protein [Arabidopsis thaliana]	79	267	2.00E-53
NM_124796	Quercetin 3-O-methyltransferase 1 (OMT1) mRNA [Arabidopsis thaliana]	70	340	4.00E-24
NM_125736	Leucine-rich repeat protein kinase family protein (AT5G63410) mRNA [Arabidopsis thaliana]	85	44	0.55
AK227380	mRNA for hypothetical protein [Arabidopsis thaliana]	83	288	1.00E-74
NM_105849	uncharacterized protein (AT1G71910) mRNA [Arabidopsis thaliana]	87	29	1.5
NM_125736	Leucine-rich repeat protein kinase family protein (AT5G63410) mRNA [Arabidopsis thaliana]	85	44	0.54
NM_001203991	aquaporin PIP2-7 (PIP3) mRNA [Arabidopsis thaliana]	82	558	1.00E-152
NM_180629	phosphatidylinositol 4-kinase alpha (ATPI4K ALPHA) mRNA [Arabidopsis thaliana]	83	34	1.7
NM_118980	ADP/ATP carrier 3 protein (AAC3) mRNA [Arabidopsis thaliana]	76	947	0
NM_121956	Elongation factor 1-beta 2 (AT5G19510) mRNA [Arabidopsis thaliana]	75	383	2.00E-66

IP : 14.49.138.138, 2017-11-03 13:30:33

NM_202091	photosystem II oxygen-evolving enhancer protein (PQL2) mRNA [Arabidopsis thaliana]	87	30	1
NM_001203991	aquaporin PIP2-7 (PIP3) mRNA [Arabidopsis thaliana]	81	591	3.00E-160
NM_103889	tubulin alpha-2/alpha-4 chain (TUA2) mRNA [Arabidopsis thaliana]	86	856	0
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.06
NM_001036737	cytochrome P450 [Arabidopsis thaliana]	69	523	4.00E-39
NM_001123746	E3 ubiquitin-protein ligase BAH1 (NLA) mRNA [Arabidopsis thaliana]	96	22	1.3
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	81	51	2.00E-04
NM_001202668	formin-like protein 18 (AT2G25050) mRNA [Arabidopsis thaliana]	96	24	1.1
NM_123058	Exostosin family protein (AT5G37000) mRNA [Arabidopsis thaliana]	88	33	0.23
NM_130113	cytochrome P450 [Arabidopsis thaliana]	100	21	0.16
AY800632	clone H00000001192 hypothetical protein (AT4G12760) mRNA [Arabidopsis thaliana]	100	23	0.068
AY800632	clone H00000001192 hypothetical protein (AT4G12760) mRNA [Arabidopsis thaliana]	100	23	0.066
NM_001203991	aquaporin PIP2-7 (PIP3) mRNA [Arabidopsis thaliana]	82	560	6.00E-156
NM_148478	VQ motif-containing protein (AT1G21326) mRNA [Arabidopsis thaliana]	83	35	0.5
NM_129083	B3 domain-containing protein (AT2G35310) mRNA [Arabidopsis thaliana]	88	32	0.58
AY079112	AT3g15140/F4B12_5 mRNA [Arabidopsis thaliana]	83	75	6.00E-13
NM_105651	alpha-amylase-like 3 (AMY3) mRNA [Arabidopsis thaliana]	93	26	0.15
BX814564	Full-length cDNA Complete sequence from clone GSLTFB80ZF12 of Flowers and buds of strain col-0 of Arabidopsis thaliana (thale cress) [Arabidopsis thaliana]	86	41	0.005
NM_001203991	aquaporin PIP2-7 (PIP3) mRNA [Arabidopsis thaliana]	83	462	1.00E-132
NM_001124033	phosphoglycerate kinase (AT1G56190) mRNA [Arabidopsis thaliana]	92	23	3.4
NM_123058	Exostosin family protein (AT5G37000) mRNA [Arabidopsis thaliana]	88	33	0.23
NM_123256	germin-like protein subfamily 1 member 11 (AT5G38940) mRNA [Arabidopsis thaliana]	69	633	5.00E-56
NM_121520	protein banquo 2 (BNQ2) mRNA [Arabidopsis thaliana]	71	271	2.00E-26
NM_124457	nodulin MtN3-like protein (AT5G50790) mRNA [Arabidopsis thaliana]	92	24	1.1
AK229545	mRNA for hypothetical protein [Arabidopsis thaliana]	80	96	7.00E-14
NM_100012	aspartyl protease-like protein (AT1G01300) mRNA [Arabidopsis thaliana]	74	641	4.00E-101
AK228480	mRNA for S-adenosyl-L-methionine:jasmonic acid carboxyl methyltransferase [Arabidopsis thaliana]	92	36	3.00E-05
AK227018	mRNA for hypothetical protein [Arabidopsis thaliana]	96	44	4.00E-11
NM_115990	remorin-like protein (AT3G61260) mRNA [Arabidopsis thaliana]	77	364	2.00E-72
NM_203166	AP-2 complex subunit mu-1 (AT5G46630) mRNA [Arabidopsis thaliana]	84	759	0
NM_129978	histone-lysine N-methyltransferase ASHH3 (ASHH3) mRNA [Arabidopsis thaliana]	96	21	9.2
NM_103264	protease-associated and C3HC4-type RING finger domain-containing protein (AT1G35630) mRNA [Arabidopsis thaliana]	89	26	4.9
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.12
NM_100588	Ran-binding protein 1-a (SIRANBP) mRNA [Arabidopsis thaliana]	79	555	4.00E-121
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	80	75	2.00E-10
NM_115694	Ubiquitin-specific protease family C19-related protein (AT3G58320) mRNA [Arabidopsis thaliana]	88	33	0.2
NM_180220	reticulon-like protein B8 (AT3G10260) mRNA [Arabidopsis thaliana]	93	27	0.7
NM_001124033	phosphoglycerate kinase (AT1G56190) mRNA [Arabidopsis thaliana]	92	23	3.4
AK229402	mRNA for hypothetical protein [Arabidopsis thaliana]	80	49	0.052
-	-	-	-	-

IP : 14.49.138.138, 2017-11-03 13:30:33

NM_112957	organic cation/carnitine transporter4 (4-Oct) mRNA [Arabidopsis thaliana]	72	317	6.00E-36
-	-	-	-	-
NM_001198509	protein kinase domain-containing protein (AT1G79640) mRNA [Arabidopsis thaliana]	92	24	1.6
HM053469	ecotype KZ-10 accelerated cell death 6 (ACD6) gene [Arabidopsis thaliana]	88	41	3.00E-05
NM_121702	2-alkenal reductase (AT5G16960) mRNA [Arabidopsis thaliana]	90	30	0.22
NM_123256	germin-like protein subfamily 1 member 11 (AT5G38940) mRNA [Arabidopsis thaliana]	69	633	3.00E-53
AB493609	At3g11260 mRNA for hypothetical protein [Arabidopsis thaliana]	87	36	0.21
NM_105728	60S ribosomal protein L27a-3 (AT1G70600) mRNA [Arabidopsis thaliana]	83	452	1.00E-130
NM_100285	HAD superfamily [Arabidopsis thaliana]	67	508	3.00E-34
AK319078	AT4G25910 mRNA [Arabidopsis thaliana]	83	41	0.011
NM_123272	germin-like protein 6 (GLP6) mRNA [Arabidopsis thaliana]	72	424	1.00E-51
NM_123923	maintenance of ploidy protein MOB1 (MPS1 binder 1) (AT5G45550) mRNA [Arabidopsis thaliana]	82	638	3.00E-172
NM_120466	40S ribosomal protein S28-1 (AT5G03850) mRNA [Arabidopsis thaliana]	83	202	9.00E-50
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.062
NM_102311	microtubule-associated proteins 70-2 (MAP70-2) mRNA [Arabidopsis thaliana]	92	23	6.7
NM_122861	GDSL esterase/lipase (AT5G33370) mRNA [Arabidopsis thaliana]	81	51	2.00E-04
NM_202787	polyubiquitin 10 (UBQ10) mRNA [Arabidopsis thaliana]	82	770	0
AK229405	mRNA for putative cytosolic factor protein [Arabidopsis thaliana]	90	29	0.27
NM_104043	ATP synthase subunit epsilon (AT1G51650) mRNA [Arabidopsis thaliana]	81	225	2.00E-52
NM_125991	3-hydroxyisobutyryl-CoA hydrolase 1 (CHY1) mRNA [Arabidopsis thaliana]	83	136	3.00E-31
NM_115539	calmodulin 3 (CAM3) mRNA [Arabidopsis thaliana]	86	460	5.00E-150
AK317612	AT1G55490 mRNA [Arabidopsis thaliana]	100	21	0.39
NM_117551	early light-inducible protein 2 (ELIP2) mRNA [Arabidopsis thaliana]	73	336	5.00E-48
AK317104	AT5G58005 mRNA [Arabidopsis thaliana]	71	290	4.00E-31
NM_123272	germin-like protein 6 (GLP6) mRNA [Arabidopsis thaliana]	72	425	2.00E-52
NM_147270	NADH dehydrogenase I subunit 3 (AT2G07751) mRNA [Arabidopsis thaliana]	90	68	4.00E-17
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.06
NM_112085	chitinase (HCHIB) mRNA [Arabidopsis thaliana]	65	589	2.00E-23
NM_201749	protein kinase domain-containing protein (AT2G17220) mRNA [Arabidopsis thaliana]	71	707	8.00E-73
NM_121400	uncharacterized protein (AT5G13970) mRNA [Arabidopsis thaliana]	90	29	0.34
NM_127223	Iron-sulfur assembly protein IscA-like 1 (AT2G16710) mRNA [Arabidopsis thaliana]	78	280	9.00E-58
NM_106064	60S ribosomal protein L6-3 (AT1G74050) mRNA [Arabidopsis thaliana]	80	622	3.00E-147
NM_119840	aminopeptidase P1 (APP1) mRNA [Arabidopsis thaliana]	72	539	2.00E-73
NM_117386	60S ribosomal protein L13a-3 (AT4G13170) mRNA [Arabidopsis thaliana]	77	73	1.00E-06
AK230360	mRNA for hypothetical protein [Arabidopsis thaliana]	73	707	1.00E-102
BT046121	unknown protein (At3g26600) mRNA [Arabidopsis thaliana]	66	732	6.00E-30
NM_203243	transducin/WD40 domain-containing protein (AT5G60940) mRNA [Arabidopsis thaliana]	76	206	8.00E-34
NM_001123884	protein SPIRAL1-like1 (SP1L1) mRNA [Arabidopsis thaliana]	79	191	5.00E-37
NM_128994	light-harvesting complex II chlorophyll a/b binding protein 1 (LHB1B2) mRNA [Arabidopsis thaliana]	82	673	3.00E-179
NM_001203599	ubiquitin-conjugating enzyme E2 10 (UBC10) mRNA [Arabidopsis thaliana]	86	449	1.00E-146

IP : 14.49.138.138, 2017-11-03 13:30:33

NM_117761	GT8-glycogenin domain-containing protein (AT4G16600) mRNA [Arabidopsis thaliana]	90	29	0.69
NM_117386	60S ribosomal protein L13a-3 (AT4G13170) mRNA [Arabidopsis thaliana]	77	73	1.00E-06
NM_115162	60S ribosomal protein L24-2 (STV1) mRNA [Arabidopsis thaliana]	77	504	2.00E-103
NM_101028	xyloglucan:xyloglucosyl transferase (XTH8) mRNA [Arabidopsis thaliana]	75	812	1.00E-139
NM_121919	aluminum induced protein with YGL and LRDR motifs (AILP1) mRNA [Arabidopsis thaliana]	76	681	1.00E-127
AY572784	CDC48-interacting UBX-domain protein (PUX4) mRNA [Arabidopsis thaliana]	69	250	7.00E-20
AY572784	CDC48-interacting UBX-domain protein (PUX4) mRNA [Arabidopsis thaliana]	69	250	7.00E-20
NM_129411	non-specific lipid-transfer protein 1 (LP1) mRNA [Arabidopsis thaliana]	75	80	3.00E-06
NM_001160906	dormancy-associated protein-like 1 (DYL1) mRNA [Arabidopsis thaliana]	72	363	1.00E-43
NM_123764	mitochondrial import receptor subunit TOM22-2 (TOM22-V) mRNA [Arabidopsis thaliana]	77	134	2.00E-19
NM_119432	Exostosin family protein (AT4G32790) mRNA [Arabidopsis thaliana]	92	24	1.8
NM_122824	RNA recognition motif (RRM)-containing protein (AT5G32450) mRNA [Arabidopsis thaliana]	76	408	5.00E-74
NM_123764	mitochondrial import receptor subunit TOM22-2 (TOM22-V) mRNA [Arabidopsis thaliana]	77	134	2.00E-19
NM_001160906	dormancy-associated protein-like 1 (DYL1) mRNA [Arabidopsis thaliana]	72	363	7.00E-41
NM_202361	26 proteasome complex subunit DSS1 (DSS1(I)) mRNA [Arabidopsis thaliana]	79	206	1.00E-41
NM_101788	RING/U-box domain-containing protein (AT1G19310) mRNA [Arabidopsis thaliana]	76	97	8.00E-10
AY093388	ribulose bisphosphate carboxylase [Arabidopsis thaliana]	78	494	1.00E-101
NM_111300	GDSL esterase/lipase LTL1 (LTL1) mRNA [Arabidopsis thaliana]	72	831	1.00E-108
NM_130285	ADP-ribosylation factor 1 (ARF1A1C) mRNA [Arabidopsis thaliana]	87	550	0
NM_125630	plant invertase/pectin methylesterase inhibitor domain-containing protein (AT5G62360) mRNA [Arabidopsis thaliana]	67	485	6.00E-30
NM_119613	glucan endo-1,3-beta-glucosidase 7 (AT4G34480) mRNA [Arabidopsis thaliana]	76	414	4.00E-76
BT028904	unknown protein (At1g66230) mRNA [Arabidopsis thaliana]	100	21	0.13
AK317327	AT2G43640 mRNA [Arabidopsis thaliana]	77	309	3.00E-57
NM_180643	NHL domain-containing protein (AT1G70280) mRNA [Arabidopsis thaliana]	83	46	0.052
NM_125991	3-hydroxyisobutyryl-CoA hydrolase 1 (CHY1) mRNA [Arabidopsis thaliana]	83	136	3.00E-31
AB493667	At4g01260 gene for hypothetical protein [Arabidopsis thaliana]	87	30	0.79
AY144108	hypothetical protein (At2g39490/F12L6.15) mRNA [Arabidopsis thaliana]	95	56	4.00E-16
NM_001202645	RING/FYVE/PHD zinc finger-containing protein (AT2G22120) mRNA [Arabidopsis thaliana]	82	158	5.00E-36
DQ132706	clone 01268 hypothetical protein (At4g18660) mRNA [Arabidopsis thaliana]	90	46	2.00E-07
NM_104590	ATP phosphoribosyl transferase 1 (ATP-PRT1) mRNA [Arabidopsis thaliana]	85	33	0.57
NM_121328	RING finger protein (AT5G13250) mRNA [Arabidopsis thaliana]	96	23	0.91
NM_118847	protein translation factor SUI1-1 (AT4G27130) mRNA [Arabidopsis thaliana]	82	404	6.00E-105
NM_123256	germin-like protein subfamily 1 member 11 (AT5G38940) mRNA [Arabidopsis thaliana]	69	633	1.00E-51
BT050412	unknown protein (At5g14550) mRNA [Arabidopsis thaliana]	76	541	2.00E-104
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	85	114	5.00E-24
NM_128997	high mobility group (HMG1/2) domain-containing protein (AT2G34450) mRNA [Arabidopsis thaliana]	80	255	1.00E-57
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	28	0.21
NM_111327	uncharacterized protein (AT3G04560) mRNA [Arabidopsis thaliana]	73	714	4.00E-101
NM_116250	Mechanosensitive ion channel protein (AT4G00290) mRNA [Arabidopsis thaliana]	73	318	1.00E-39
NM_117683	drought-induced 21 protein (DI21) mRNA [Arabidopsis thaliana]	79	103	5.00E-16

IP : 14.49.138.138, 2017-11-03 13:30:33

NM_117683	drought-induced 21 protein (DI21) mRNA [Arabidopsis thaliana]	79	103	5.00E-16
NM_001123884	protein SPIRAL1-like1 (SP1L1) mRNA [Arabidopsis thaliana]	72	344	2.00E-39
NM_116120	putative adenine nucleotide alpha hydrolase domain-containing universal stress protein (AT3G62550) mRNA [Arabidopsis thaliana]	68	443	3.00E-33
NM_104206	4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis (AT1G53280) mRNA [Arabidopsis thaliana]	77	378	4.00E-73
NM_101038	heat shock protein 70 (Hsp 70) family protein (AT1G11660) mRNA [Arabidopsis thaliana]	72	153	2.00E-14
NM_105541	protein kinase-like protein (AT1G68690) mRNA [Arabidopsis thaliana]	80	921	0
NM_001160906	dormancy-associated protein-like 1 (DYL1) mRNA [Arabidopsis thaliana]	71	363	2.00E-36
NM_119764	uncharacterized protein (AT4G35980) mRNA [Arabidopsis thaliana]	75	252	1.00E-37
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.06
NM_100043	glycerol-3-phosphate acyltransferase (GPAT4) mRNA [Arabidopsis thaliana]	76	622	3.00E-120
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	30	0.034
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	30	0.034
NM_116497	protein kinase family protein (AT4G02630) mRNA [Arabidopsis thaliana]	81	47	0.046
NM_202381	protein SPIRAL1-like2 (SP1L2) mRNA [Arabidopsis thaliana]	78	127	1.00E-21
NM_122606	DNAJ heat shock N-terminal domain-containing protein (AT5G27240) mRNA [Arabidopsis thaliana]	92	25	3.5
NM_122606	DNAJ heat shock N-terminal domain-containing protein (AT5G27240) mRNA [Arabidopsis thaliana]	92	25	0.32
NM_113490	uncharacterized protein (AT3G25870) mRNA [Arabidopsis thaliana]	79	55	0.002
NM_122606	DNAJ heat shock N-terminal domain-containing protein (AT5G27240) mRNA [Arabidopsis thaliana]	92	25	0.31
NM_001198478	gibberellin-regulated protein 1 (GASA1) mRNA [Arabidopsis thaliana]	67	303	3.00E-19
NM_114963	thioredoxin H1 (TRX1) mRNA [Arabidopsis thaliana]	79	332	3.00E-75
NM_128207	putative cytochrome b6f complex subunit (AT2G26500) mRNA [Arabidopsis thaliana]	68	292	3.00E-19
NM_128476	pumilio 1 (PUM1) mRNA [Arabidopsis thaliana]	96	23	1.2
NM_148478	VQ motif-containing protein (AT1G21326) mRNA [Arabidopsis thaliana]	83	35	0.49
NM_001198055	uncharacterized protein (AT1G13360) mRNA [Arabidopsis thaliana]	68	112	0.077
NM_112622	Nucleotide-sugar transporter family protein (AT3G17430) mRNA [Arabidopsis thaliana]	81	803	0
NM_122069	polyubiquitin 4 (UBQ4) mRNA [Arabidopsis thaliana]	86	148	7.00E-39
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.12
NM_103558	uncharacterized protein (AT1G44770) mRNA [Arabidopsis thaliana]	69	658	2.00E-56
NM_102391	putative phosphatidylinositol 4-kinase type 2-beta (AT1G26270) mRNA [Arabidopsis thaliana]	70	202	2.00E-16
NM_001198104	uncharacterized protein (AT1G19330) mRNA [Arabidopsis thaliana]	90	60	2.00E-14
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	80	75	2.00E-10
AK318752	AT1G20440 mRNA [Arabidopsis thaliana]	76	83	1.00E-08
NM_101446	uncharacterized protein (AT1G15780) mRNA [Arabidopsis thaliana]	92	25	0.61
NM_119711	thioredoxin reductase 1 (NTRB) mRNA [Arabidopsis thaliana]	80	585	2.00E-144
NM_121822	glutamate dehydrogenase 1 (GDH1) mRNA [Arabidopsis thaliana]	89	27	0.64
NM_121822	glutamate dehydrogenase 1 (GDH1) mRNA [Arabidopsis thaliana]	89	27	0.63
NM_119894	protein maternal effect embryo arrest 59 (MEE59) mRNA [Arabidopsis thaliana]	76	122	2.00E-15
NM_114288	serine/threonine-protein kinase Nek5 (NEK6) mRNA [Arabidopsis thaliana]	93	28	0.26
NM_127885	UDP-glycosyltransferase-like protein (AT2G23210) mRNA [Arabidopsis thaliana]	70	170	2.00E-10
NM_113074	UTP-glucose glucosyltransferase-like protein (AT3G21790) mRNA [Arabidopsis thaliana]	73	551	1.00E-76

IP : 14.49.138.138, 2017-11-03 13:30:33

AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.06
AK118654	At2g26600 mRNA for putative beta-1,3-glucanase [Arabidopsis thaliana]	74	726	2.00E-105
NM_119263	uncharacterized protein (AT4G31130) mRNA [Arabidopsis thaliana]	72	457	5.00E-61
NM_001160806	putative low temperature and salt responsive protein (AT4G30660) mRNA [Arabidopsis thaliana]	74	199	5.00E-26
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	78	57	0.003
NM_125093	calcium-transporting ATPase 8 (ACA8) mRNA [Arabidopsis thaliana]	74	276	3.00E-38
NM_118727	putative clathrin assembly protein (AT4G25940) mRNA [Arabidopsis thaliana]	75	67	0.17
NM_121822	glutamate dehydrogenase 1 (GDH1) mRNA [Arabidopsis thaliana]	89	27	1.2
NM_102732	chlorophyll a-b binding protein 2/3 (CAB2) mRNA [Arabidopsis thaliana]	79	812	0
NM_116938	protein SAH7 (SAH7) mRNA [Arabidopsis thaliana]	68	391	3.00E-26
NM_123256	germin-like protein subfamily 1 member 11 (AT5G38940) mRNA [Arabidopsis thaliana]	79	52	0.002
AK317040	AT4G12400 mRNA [Arabidopsis thaliana]	80	417	9.00E-101
NM_118398	glycoprotease M22 family protein (AT4G22720) mRNA [Arabidopsis thaliana]	77	465	5.00E-93
NM_119071	HAD superfamily [Arabidopsis thaliana]	75	116	1.00E-11
NM_001160906	dormancy-associated protein-like 1 (DYL1) mRNA [Arabidopsis thaliana]	72	363	1.00E-43
NM_127532	60S ribosomal protein L31-1 (AT2G19740) mRNA [Arabidopsis thaliana]	78	363	3.00E-76
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	91	31	0.005
NM_001203061	cysteine/histidine-rich C1 domain-containing protein (AT3G27480) mRNA [Arabidopsis thaliana]	84	36	0.21
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	79	75	2.00E-09
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	80	75	2.00E-10
NM_118669	Double Clp-N motif protein (AT4G25370) mRNA [Arabidopsis thaliana]	75	483	1.00E-82
NM_104046	4-coumarate--CoA ligase 1 (4CL1) mRNA [Arabidopsis thaliana]	74	618	2.00E-99
BT030019	At1g23000 mRNA [Arabidopsis thaliana]	78	264	2.00E-54
NM_001084797	uncharacterized protein (AT3G50170) mRNA [Arabidopsis thaliana]	81	46	0.033
BX814287	Full-length cDNA Complete sequence from clone GSLTFB66ZC08 of Flowers and buds of strain col-0 of Arabidopsis thaliana (thale cress) [Arabidopsis thaliana]	84	36	1.2
NM_001036455	14-3-3-like protein GF14 mu (GRF9) mRNA [Arabidopsis thaliana]	80	796	0
NM_103681	AP-2 complex subunit sigma (AT1G47830) mRNA [Arabidopsis thaliana]	84	261	1.00E-74
NM_113122	uncharacterized protein (AT3G22240) mRNA [Arabidopsis thaliana]	75	148	2.00E-17
AK229367	mRNA for hypothetical protein [Arabidopsis thaliana]	68	411	4.00E-30
NM_130358	chlororespiratory reduction 6 (CRR6) mRNA [Arabidopsis thaliana]	74	395	2.00E-64
NM_128872	vesicle-associated membrane protein 722 (SAR1) mRNA [Arabidopsis thaliana]	77	542	9.00E-102
NM_128872	vesicle-associated membrane protein 722 (SAR1) mRNA [Arabidopsis thaliana]	76	677	1.00E-132
NM_104336	acyl carrier protein 2 (ACP2) mRNA [Arabidopsis thaliana]	71	257	2.00E-23
NM_203039	cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG8 (AT5G11950) mRNA [Arabidopsis thaliana]	80	397	1.00E-92
NM_113371	Late embryogenesis abundant protein [Arabidopsis thaliana]	74	123	2.00E-09
NM_111871	protein pumilio 4 (PUM4) mRNA [Arabidopsis thaliana]	78	177	7.00E-33
AY800632	clone H0000001192 hypothetical protein (AT4G12760) mRNA [Arabidopsis thaliana]	92	24	2.8
NM_001203505	alpha-1,3-glucosyltransferase (AT5G38460) mRNA [Arabidopsis thaliana]	96	24	0.052
NM_123516	40S ribosomal protein S10-2 (AT5G41520) mRNA [Arabidopsis thaliana]	76	411	2.00E-76
NM_180810	RNA-binding protein (AT5G46250) mRNA [Arabidopsis thaliana]	76	153	6.00E-22

IP : 14.49.138.138, 2017-11-03 13:30:33

NM_100458	vacuolar ATPase assembly integral membrane protein VMA21-like domain-containing protein (AT1G05780) mRNA [Arabidopsis thaliana]	75	260	2.00E-41
AY065137	60S ribosomal protein L13 [Arabidopsis thaliana]	77	623	6.00E-131
AK227568	mRNA for metallothionein 2b [Arabidopsis thaliana]	69	260	5.00E-23
NM_125477	uncharacterized protein (AT5G60840) mRNA [Arabidopsis thaliana]	80	43	1.2
NM_121982	tubulin alpha-3/alpha-5 chain (TUA3) mRNA [Arabidopsis thaliana]	80	524	1.00E-131
NM_001203331	H/ACA ribonucleoprotein complex subunit 2-like protein (AT5G08180) mRNA [Arabidopsis thaliana]	72	320	1.00E-42
NM_121982	tubulin alpha-3/alpha-5 chain (TUA3) mRNA [Arabidopsis thaliana]	80	813	0
NM_124858	thiazole biosynthetic enzyme (THI1) mRNA [Arabidopsis thaliana]	80	625	2.00E-156
AB493557	At2g22540 mRNA for hypothetical protein [Arabidopsis thaliana]	76	120	2.00E-15
NM_119633	40S ribosomal protein S3a-2 (AT4G34670) mRNA [Arabidopsis thaliana]	79	792	0
NM_105097	ubiquitin-conjugating enzyme E2 28 (UBC28) mRNA [Arabidopsis thaliana]	85	444	9.00E-134
AK226392	mRNA for cyclophilin [Arabidopsis thaliana]	77	533	4.00E-107
NM_129411	non-specific lipid-transfer protein 1 (LP1) mRNA [Arabidopsis thaliana]	75	80	3.00E-06
NM_001125215	KRR1 family protein (AT3G24080) mRNA [Arabidopsis thaliana]	90	40	2.00E-05
NM_112047	omega-6 fatty acid desaturase [Arabidopsis thaliana]	72	697	5.00E-93
NM_001198176	dormancy-associated protein-like 1 (DYL1) mRNA [Arabidopsis thaliana]	71	241	1.00E-19
AK316712	AT3G08720 mRNA [Arabidopsis thaliana]	74	532	1.00E-82
NM_123920	Leucine-rich repeat (LRR) family protein (AT5G45520) mRNA [Arabidopsis thaliana]	96	22	3.9
NM_123590	alcohol dehydrogenase-like 7 (AT5G42250) mRNA [Arabidopsis thaliana]	77	77	3.00E-07
NM_116892	glycine-rich protein (AT4G08230) mRNA [Arabidopsis thaliana]	70	338	8.00E-32
NM_148640	uncharacterized protein (AT1G67785) mRNA [Arabidopsis thaliana]	82	158	3.00E-36
NM_001198176	dormancy-associated protein-like 1 (DYL1) mRNA [Arabidopsis thaliana]	72	393	1.00E-44
NM_100045	protein sec fourteen-like protein-20 (AT1G01630) mRNA [Arabidopsis thaliana]	72	638	2.00E-86
NM_119566	putative caffeoyl-CoA O-methyltransferase (CCoAOMT1) mRNA [Arabidopsis thaliana]	76	688	3.00E-128
NM_001202912	ubiquitin-conjugating enzyme E2 11 (UBC11) mRNA [Arabidopsis thaliana]	82	444	3.00E-122
NM_001036869	uncharacterized protein (AT5G26770) mRNA [Arabidopsis thaliana]	72	601	4.00E-75
NM_100757	Superoxide dismutase [Cu-Zn] (CSD1) mRNA [Arabidopsis thaliana]	77	507	6.00E-104
NM_106225	gibberellin-regulated protein 1 (GASA1) mRNA [Arabidopsis thaliana]	66	300	3.00E-12
NM_111146	Isopentenyl-diphosphate Delta-isomerase II (IPP2) mRNA [Arabidopsis thaliana]	79	566	2.00E-136
NM_111871	protein pumilio 4 (PUM4) mRNA [Arabidopsis thaliana]	80	174	5.00E-35
NM_103274	annexin D1 (ANNAT1) mRNA [Arabidopsis thaliana]	73	788	1.00E-120
NM_001202967	transcription factor TCP4 (TCP4) mRNA [Arabidopsis thaliana]	70	145	8.00E-09
NM_118847	protein translation factor SUI1-1 (AT4G27130) mRNA [Arabidopsis thaliana]	81	404	3.00E-102
NM_106245	S-phase kinase-associated protein 1 (SKP1) mRNA [Arabidopsis thaliana]	75	481	7.00E-85
NM_101983	extensin 3 (EXT3) mRNA [Arabidopsis thaliana]	69	306	1.00E-30
DQ062416	ecotype Tsu-0 chalcone synthase family protein (At5g13930) mRNA [Arabidopsis thaliana]	76	848	1.00E-165
NM_104009	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase (AT1G51310) mRNA [Arabidopsis thaliana]	92	23	5.2
NM_001198469	myb family transcription factor (AT1G74840) mRNA [Arabidopsis thaliana]	72	464	2.00E-54
FJ441355	clone L At1g58100 gene [Arabidopsis thaliana]	100	18	1.9
NM_106477	transferase (AT1G78280) mRNA [Arabidopsis thaliana]	100	22	0.075

IP : 14.49.138.138, 2017-11-03 13:30:33

NM_180529	calmodulin 6 (CAM6) mRNA [Arabidopsis thaliana]	81	450	1.00E-119
NM_121381	peptide alpha-N-acetyltransferase (AT5G13780) mRNA [Arabidopsis thaliana]	78	554	2.00E-123
NM_102497	Ribosome associated membrane protein RAMP4 (AT1G27350) mRNA [Arabidopsis thaliana]	82	214	5.00E-53
NM_115282	protein scarecrow (SCR) mRNA [Arabidopsis thaliana]	78	145	1.00E-23
NM_001124981	fructose-bisphosphate aldolase [Arabidopsis thaliana]	77	236	9.00E-44
NM_129275	60S ribosomal protein L12-1 (AT2G37190) mRNA [Arabidopsis thaliana]	79	492	7.00E-116
NM_121263	tubulin beta-6 chain (TUB6) mRNA [Arabidopsis thaliana]	82	530	2.00E-148
NM_106534	putative glycoprotein (EP1) (AT1G78860) mRNA [Arabidopsis thaliana]	70	287	3.00E-27
NM_106534	putative glycoprotein (EP1) (AT1G78860) mRNA [Arabidopsis thaliana]	70	287	3.00E-27
NM_202361	26 proteasome complex subunit DSS1 (DSS1(I)) mRNA [Arabidopsis thaliana]	81	206	2.00E-45
NM_202361	26 proteasome complex subunit DSS1 (DSS1(I)) mRNA [Arabidopsis thaliana]	81	206	2.00E-45
NM_129209	bifunctional enolase 2/transcriptional activator (LOS2) mRNA [Arabidopsis thaliana]	80	764	0
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.06
NM_125664	tubulin beta-2/beta-3 chain (TUB2) mRNA [Arabidopsis thaliana]	84	710	0
NM_100901	glutamine-rich protein 23 (GRP23) mRNA [Arabidopsis thaliana]	89	27	1.5
NM_117683	drought-induced 21 protein (DI21) mRNA [Arabidopsis thaliana]	78	103	2.00E-14
NM_202361	26 proteasome complex subunit DSS1 (DSS1(I)) mRNA [Arabidopsis thaliana]	81	206	2.00E-45
AY261783	clone At2g15130/F15A23.13 hypothetical protein mRNA [Arabidopsis thaliana]	92	46	2.00E-09
NM_121527	gibberellin-regulated protein 4 (GASA4) mRNA [Arabidopsis thaliana]	70	328	1.00E-30
NM_104319	dehydrin family protein (AT1G54410) mRNA [Arabidopsis thaliana]	70	177	2.00E-10
NM_117035	uncharacterized oxidoreductase (AT4G09670) mRNA [Arabidopsis thaliana]	69	812	3.00E-83
NM_116415	S-adenosylmethionine synthase 2 (SAM-2) mRNA [Arabidopsis thaliana]	80	560	7.00E-142
NM_121124	CBS domain-containing protein (AT5G10860) mRNA [Arabidopsis thaliana]	79	627	4.00E-145
NM_103731	50S ribosomal protein L18 (AT1G48350) mRNA [Arabidopsis thaliana]	80	367	3.00E-83
NM_102417	peptidyl-prolyl cis-trans isomerase NIMA-interacting 4 (AT1G26550) mRNA [Arabidopsis thaliana]	80	416	3.00E-101
NM_119209	uncharacterized protein (AT4G30630) mRNA [Arabidopsis thaliana]	77	93	2.00E-10
NM_124128	cysteine proteinase inhibitor 5 (AT5G47550) mRNA [Arabidopsis thaliana]	69	219	1.00E-10
AK229545	mRNA for hypothetical protein [Arabidopsis thaliana]	78	103	6.00E-14
NM_124128	cysteine proteinase inhibitor 5 (AT5G47550) mRNA [Arabidopsis thaliana]	69	219	1.00E-10
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.06
AK317389	AT5G65220 mRNA [Arabidopsis thaliana]	76	331	9.00E-58
NM_202361	26 proteasome complex subunit DSS1 (DSS1(I)) mRNA [Arabidopsis thaliana]	81	206	2.00E-45
NM_106245	S-phase kinase-associated protein 1 (SKP1) mRNA [Arabidopsis thaliana]	78	475	2.00E-97
NM_127548	malate dehydrogenase (oxaloacetate-decarboxylating)(NADP+) (NADP-ME1) mRNA [Arabidopsis thaliana]	76	558	3.00E-108
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	78	68	1.00E-06
NM_202361	26 proteasome complex subunit DSS1 (DSS1(I)) mRNA [Arabidopsis thaliana]	81	206	2.00E-45
NM_103508	stearoyl-acyl-carrier protein desaturase-like protein (AT1G43800) mRNA [Arabidopsis thaliana]	72	645	2.00E-91
NM_111311	60S ribosomal protein L23 (emb2171) mRNA [Arabidopsis thaliana]	86	424	5.00E-136
NM_001123884	protein SPIRAL1-like1 (SP1L1) mRNA [Arabidopsis thaliana]	80	191	7.00E-39
NM_120653	pleckstrin homology domain-containing protein (AT5G05710) mRNA [Arabidopsis thaliana]	79	362	1.00E-80

IP : 14.49.138.138, 2017-11-03 13:30:33

NM_105684	uncharacterized protein (AT1G70160) mRNA [Arabidopsis thaliana]	77	685	3.00E-141
NM_116685	peroxisomal membrane protein PMP22 (PMP22) mRNA [Arabidopsis thaliana]	72	551	2.00E-72
NM_148143	U-box domain-containing protein kinase family protein (AT5G57035) mRNA [Arabidopsis thaliana]	93	27	0.05
NM_001125215	KRR1 family protein (AT3G24080) mRNA [Arabidopsis thaliana]	90	40	2.00E-05
AK317712	AT3G10720 mRNA [Arabidopsis thaliana]	82	48	0.045
NM_124945	calcium-activated outward-rectifying potassium channel 1 (ATKCO1) mRNA [Arabidopsis thaliana]	69	466	1.00E-38
NM_117035	uncharacterized oxidoreductase (AT4G09670) mRNA [Arabidopsis thaliana]	69	884	7.00E-86
NM_125664	tubulin beta-2/beta-3 chain (TUB2) mRNA [Arabidopsis thaliana]	84	710	0
NM_106477	transferase (AT1G78280) mRNA [Arabidopsis thaliana]	100	22	0.095
NM_106634	30S ribosomal protein S17 (RPS17) mRNA [Arabidopsis thaliana]	75	187	3.00E-24
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.06
NM_105728	60S ribosomal protein L27a-3 (AT1G70600) mRNA [Arabidopsis thaliana]	83	452	1.00E-130
NM_117499	E3 ubiquitin-protein ligase RHF1A (RHF1A) mRNA [Arabidopsis thaliana]	82	38	0.69
NM_124128	cysteine proteinase inhibitor 5 (AT5G47550) mRNA [Arabidopsis thaliana]	69	219	1.00E-10
BX816829	Full-length cDNA Complete sequence from clone GSLTPGH70ZC01 of Hormone Treated Callus of strain col-0 of Arabidopsis thaliana (thale cress) [Arabidopsis thaliana]	95	20	8.9
AK317460	AT5G23090 mRNA [Arabidopsis thaliana]	78	432	7.00E-98
NM_001160906	dormancy-associated protein-like 1 (DYL1) mRNA [Arabidopsis thaliana]	72	363	7.00E-41
NM_106455	putative beta-D-xylosidase 7 (AT1G78060) mRNA [Arabidopsis thaliana]	71	1000	1.00E-122
AY800632	clone H00000001192 hypothetical protein (AT4G12760) mRNA [Arabidopsis thaliana]	94	31	6.00E-04
NM_128773	transmembrane receptor protein (AT2G32140) mRNA [Arabidopsis thaliana]	85	40	0.03
NM_125664	tubulin beta-2/beta-3 chain (TUB2) mRNA [Arabidopsis thaliana]	81	926	0
AK317460	AT5G23090 mRNA [Arabidopsis thaliana]	81	432	2.00E-110
NM_116744	ubiquitin 11 (UBQ11) mRNA [Arabidopsis thaliana]	84	698	0
NM_122149	60S ribosomal protein L10a-3 (AT5G22440) mRNA [Arabidopsis thaliana]	85	208	1.00E-59
NM_100939	ADP-ribosylation factor A1F (ARFA1F) mRNA [Arabidopsis thaliana]	88	548	0
NM_128773	transmembrane receptor protein (AT2G32140) mRNA [Arabidopsis thaliana]	85	40	0.03
NM_100133	P-glycoprotein 11 (PGP11) mRNA [Arabidopsis thaliana]	96	22	1.7
NM_129114	SWIB/MDM2 domain-containing protein (AT2G35605) mRNA [Arabidopsis thaliana]	73	193	2.00E-23
NM_115117	esterase/lipase domain-containing protein (AT3G52570) mRNA [Arabidopsis thaliana]	76	743	1.00E-140
NM_101921	high mobility group B3 protein (HMGB3) mRNA [Arabidopsis thaliana]	77	533	5.00E-100
AK317257	AT4G40040 mRNA [Arabidopsis thaliana]	81	426	5.00E-112
NM_105608	translation initiation factor eIF-5A (ELF5A-3) mRNA [Arabidopsis thaliana]	80	478	8.00E-116
NM_001203123	uncharacterized protein (AT3G51290) mRNA [Arabidopsis thaliana]	73	174	1.00E-20
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	81	51	4.00E-04
NM_111634	peroxin 13 (PEX13) mRNA [Arabidopsis thaliana]	75	146	7.00E-17
NM_117499	E3 ubiquitin-protein ligase RHF1A (RHF1A) mRNA [Arabidopsis thaliana]	82	38	0.68
NM_001123732	protein IQ-domain 18 (IQD18) mRNA [Arabidopsis thaliana]	78	80	1.00E-08
NM_106545	lupeol synthase 2 (LUP2) mRNA [Arabidopsis thaliana]	96	24	3.6
NM_202644	mini zinc finger 2 (MIF2) mRNA [Arabidopsis thaliana]	71	323	6.00E-35
NM_116228	UDP-D-glucuronate 4-epimerase 3 (GAE3) mRNA [Arabidopsis thaliana]	93	27	0.089

IP : 14.49.138.138, 2017-11-03 13:30:33

NM_106477	transferase (AT1G78280) mRNA [Arabidopsis thaliana]	100	22	0.092
NM_001160906	dormancy-associated protein-like 1 (DYL1) mRNA [Arabidopsis thaliana]	72	363	7.00E-41
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.06
NM_121018	actin 7 (ACT7) mRNA [Arabidopsis thaliana]	87	832	0
NM_001125215	KRR1 family protein (AT3G24080) mRNA [Arabidopsis thaliana]	90	40	2.00E-05
NM_128676	actin depolymerizing factor 6 (ADF6) mRNA [Arabidopsis thaliana]	78	419	4.00E-88
NM_001123822	uncharacterized protein (AT1G15320) mRNA [Arabidopsis thaliana]	71	241	6.00E-24
NM_120082	protein RER1A (ATRER1A) mRNA [Arabidopsis thaliana]	76	369	9.00E-60
-	-	-	-	-
NM_202644	mini zinc finger 2 (MIF2) mRNA [Arabidopsis thaliana]	72	323	1.00E-37
NM_202310	60S ribosomal protein L41 (AT1G56045) mRNA [Arabidopsis thaliana]	89	71	2.00E-18
NM_118013	MADS-box transcription factor (AG) mRNA [Arabidopsis thaliana]	73	715	8.00E-105
NM_111201	calcineurin-like metallo-phosphoesterase-like protein (AT3G03305) mRNA [Arabidopsis thaliana]	67	216	2.00E-09
AK316712	AT3G08720 mRNA [Arabidopsis thaliana]	72	359	2.00E-35
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.042
NM_103950	RAV-like factor (AT1G50680) mRNA [Arabidopsis thaliana]	96	21	1.2
NM_116744	ubiquitin 11 (UBQ11) mRNA [Arabidopsis thaliana]	84	698	0
NM_111489	RING/U-box domain-containing protein (AT3G06140) mRNA [Arabidopsis thaliana]	89	34	0.044
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	80	75	2.00E-10
NM_115539	calmodulin 3 (CAM3) mRNA [Arabidopsis thaliana]	84	460	3.00E-141
NM_127686	translocon-associated protein subunit alpha (AT2G21160) mRNA [Arabidopsis thaliana]	71	782	2.00E-86
-	-	-	-	-
AK230360	mRNA for hypothetical protein [Arabidopsis thaliana]	71	167	4.00E-14
NM_114140	Putative membrane lipoprotein (AT3G42725) mRNA [Arabidopsis thaliana]	65	377	6.00E-10
NM_122281	putative copper transport protein (AT5G23760) mRNA [Arabidopsis thaliana]	79	46	8.6
NM_101398	tetratricopeptide repeat-containing protein (AT1G15290) mRNA [Arabidopsis thaliana]	93	26	0.28
BT026490	At1g09850 mRNA [Arabidopsis thaliana]	74	256	3.00E-34
NM_121843	40S ribosomal protein S16-3 (AT5G18380) mRNA [Arabidopsis thaliana]	79	418	2.00E-97
NM_105627	transcription factor (AT1G69580) mRNA [Arabidopsis thaliana]	70	94	0.21
AK226392	mRNA for cyclophilin [Arabidopsis thaliana]	77	533	4.00E-107
NM_001203599	ubiquitin-conjugating enzyme E2 10 (UBC10) mRNA [Arabidopsis thaliana]	80	447	1.00E-107
NM_127548	malate dehydrogenase (oxaloacetate-decarboxylating)(NADP+) (NADP-ME1) mRNA [Arabidopsis thaliana]	77	558	5.00E-112
NM_126071	C2H2-like zinc finger protein (AT5G66730) mRNA [Arabidopsis thaliana]	88	33	0.028
AK316842	AT4G02890 mRNA [Arabidopsis thaliana]	88	109	4.00E-30
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.12
X52322	rRNA repeat unit [A. thaliana]	85	313	3.00E-69
NM_125822	protein EXORDIUM like 2 (EXL2) mRNA [Arabidopsis thaliana]	73	403	5.00E-56
NM_126483	OB-fold nucleic acid binding domain-containing protein (AT2G04520) mRNA [Arabidopsis thaliana]	84	449	8.00E-135
NM_112618	S-adenosylmethionine synthase 4 (MTO3) mRNA [Arabidopsis thaliana]	81	791	0
NM_121073	RNA recognition motif-containing protein (AT5G10350) mRNA [Arabidopsis thaliana]	83	245	9.00E-63

IP : 14.49.138.138, 2017-11-03 13:30:33

AY800632	clone H00000001192 hypothetical protein (AT4G12760) mRNA [Arabidopsis thaliana]	100	25	0.006
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	91	31	0.005
NM_001161300	exocyst complex component 84B (EXO84B) mRNA [Arabidopsis thaliana]	93	26	0.85
AK227568	mRNA for metallothionein 2b [Arabidopsis thaliana]	72	262	1.00E-29
NM_114278	MD-2-related lipid recognition domain-containing protein (AT3G44100) mRNA [Arabidopsis thaliana]	67	325	8.00E-15
AY800632	clone H00000001192 hypothetical protein (AT4G12760) mRNA [Arabidopsis thaliana]	100	25	0.005
AK221900	mRNA for hypothetical protein [Arabidopsis thaliana]	84	712	0
NM_001203698	branched-chain-amino-acid aminotransferase 5 (ATBCAT-5) mRNA [Arabidopsis thaliana]	97	26	0.26
NM_148143	U-box domain-containing protein kinase family protein (AT5G57035) mRNA [Arabidopsis thaliana]	93	27	0.05
NM_112755	protein MKS1 (MKS1) mRNA [Arabidopsis thaliana]	66	284	3.00E-08
NM_001202762	galactose oxidase/kelch repeat-containing protein (AT2G36360) mRNA [Arabidopsis thaliana]	81	904	0
NM_118467	uncharacterized protein (AT4G23380) mRNA [Arabidopsis thaliana]	75	52	1.8
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	30	0.034
NM_121982	tubulin alpha-3/alpha-5 chain (TUA3) mRNA [Arabidopsis thaliana]	81	826	0
NM_104319	dehydrin family protein (AT1G54410) mRNA [Arabidopsis thaliana]	70	177	2.00E-10
NM_001160906	dormancy-associated protein-like 1 (DYL1) mRNA [Arabidopsis thaliana]	72	363	1.00E-43
NM_129411	non-specific lipid-transfer protein 1 (LP1) mRNA [Arabidopsis thaliana]	75	80	3.00E-06
NM_001203988	Rac-like GTP-binding protein ARAC3 (RAC3) mRNA [Arabidopsis thaliana]	82	603	3.00E-160
NM_111898	nudix hydrolase 26 (NUDX26) mRNA [Arabidopsis thaliana]	76	458	4.00E-89
NM_120466	40S ribosomal protein S28-1 (AT5G03850) mRNA [Arabidopsis thaliana]	85	202	4.00E-54
NM_100614	class I heat shock protein (AT1G07400) mRNA [Arabidopsis thaliana]	77	328	1.00E-62
NM_111889	transducin/WD40 domain-containing protein (AT3G10530) mRNA [Arabidopsis thaliana]	76	574	7.00E-99
NM_104730	actin-related protein C3 (ARPC3) mRNA [Arabidopsis thaliana]	82	232	2.00E-57
AK317320	AT3G54800 mRNA [Arabidopsis thaliana]	75	302	9.00E-51
NM_102056	uncharacterized protein (AT1G22060) mRNA [Arabidopsis thaliana]	96	22	9
NM_113062	major facilitator protein (AT3G21670) mRNA [Arabidopsis thaliana]	73	862	1.00E-132
AY800632	clone H00000001192 hypothetical protein (AT4G12760) mRNA [Arabidopsis thaliana]	94	29	0.002
DQ446998	clone pENTR221-At5g33340 aspartyl protease family protein (At5g33340) mRNA [Arabidopsis thaliana]	68	206	3.00E-08
NM_001198509	protein kinase domain-containing protein (AT1G79640) mRNA [Arabidopsis thaliana]	92	24	1.7
NM_114963	thioredoxin H1 (TRX1) mRNA [Arabidopsis thaliana]	79	332	3.00E-75
NM_103926	7-dehydrocholesterol reductase (DWF5) mRNA [Arabidopsis thaliana]	77	643	5.00E-133
NM_179061	heat shock factor binding protein (HSBP) mRNA [Arabidopsis thaliana]	85	213	2.00E-59
NM_001203988	Rac-like GTP-binding protein ARAC3 (RAC3) mRNA [Arabidopsis thaliana]	78	531	3.00E-109
NM_121018	actin 7 (ACT7) mRNA [Arabidopsis thaliana]	86	918	0
NM_121024	cellulose synthase A catalytic subunit 5 [UDP-forming] (CESA5) mRNA [Arabidopsis thaliana]	74	492	3.00E-78
AK318870	AT5G14920 mRNA [Arabidopsis thaliana]	69	135	4.00E-06
NM_179618	bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein (AT2G10940) mRNA [Arabidopsis thaliana]	72	165	9.00E-11
NM_116783	temperature sensing protein-like protein (EDA35) mRNA [Arabidopsis thaliana]	100	19	1.7
NM_120913	Succinyl-CoA ligase [GDP-forming] subunit alpha-1 (AT5G08300) mRNA [Arabidopsis thaliana]	83	770	0
NM_180843	arginine/serine-rich-splicing factor RSP41 (ATRSP41) mRNA [Arabidopsis thaliana]	75	741	2.00E-137

IP : 14.49.138.138, 2017-11-03 13:30:33

AK229545	mRNA for hypothetical protein [Arabidopsis thaliana]	76	79	2.00E-08
NM_001084942	putative CTP synthase (AT4G20320) mRNA [Arabidopsis thaliana]	88	32	0.052
NM_117741	uncharacterized protein (AT4G16444) mRNA [Arabidopsis thaliana]	69	490	1.00E-44
NM_123127	ADP-ribosylation factor-like A1A (ARLA1A) mRNA [Arabidopsis thaliana]	84	272	6.00E-75
NM_105623	protein agamous-like 94 (AGL94) mRNA [Arabidopsis thaliana]	79	42	6.1
NM_001202839	ubiquitin-40S ribosomal protein S27a-2 (UBQ6) mRNA [Arabidopsis thaliana]	84	466	3.00E-139
BT026484	At3g19990 mRNA [Arabidopsis thaliana]	73	761	2.00E-113
NM_117251	Hydroxymethylglutaryl-CoA synthase (MVA1) mRNA [Arabidopsis thaliana]	78	788	3.00E-174
NM_001084864	tetratricopeptide repeat-containing protein-like protein (AT3G63095) mRNA [Arabidopsis thaliana]	90	28	1.5
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	99	542	0
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.06
NM_113597	histone-lysine N-methyltransferase (AT3G26850) mRNA [Arabidopsis thaliana]	72	252	4.00E-30
NM_128088	uncharacterized protein (AT2G25310) mRNA [Arabidopsis thaliana]	80	443	2.00E-105
NM_115282	protein scarecrow (SCR) mRNA [Arabidopsis thaliana]	78	145	1.00E-23
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	99	542	0
NM_128945	uncharacterized protein (AT2G33850) mRNA [Arabidopsis thaliana]	80	86	5.00E-12
NM_115772	callose synthase (GSL11) mRNA [Arabidopsis thaliana]	85	33	1.3
NM_100254	switch 2 (SWI2) mRNA [Arabidopsis thaliana]	93	26	0.22
NM_129995	calcium-binding EF-hand-containing protein (AT2G44310) mRNA [Arabidopsis thaliana]	72	418	2.00E-52
NM_001197952	endoribonuclease Dicer (DCL1) mRNA [Arabidopsis thaliana]	93	26	3.6
NM_123256	germin-like protein subfamily 1 member 11 (AT5G38940) mRNA [Arabidopsis thaliana]	79	52	0.002
NM_001203061	cysteine/histidine-rich C1 domain-containing protein (AT3G27480) mRNA [Arabidopsis thaliana]	84	36	0.21
AK229008	mRNA for ARG1 protein [Arabidopsis thaliana]	81	729	0
NM_125095	Clp amino terminal domain-containing protein (AT5G57130) mRNA [Arabidopsis thaliana]	87	29	3.2
NM_105410	60S ribosomal protein L17-2 (AT1G67430) mRNA [Arabidopsis thaliana]	81	510	4.00E-132
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.06
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.12
NM_101398	tetratricopeptide repeat-containing protein (AT1G15290) mRNA [Arabidopsis thaliana]	93	26	0.29
AC004708	4870 from: 1 to: 167234 [CIC5B11.1 check:]	97	171	6.00E-75
NM_123383	RNA ligase/cyclic nucleotide phosphodiesterase family protein (AT5G40190) mRNA [Arabidopsis thaliana]	72	542	4.00E-76
FJ154118	At3g13062 mRNA [Arabidopsis thaliana]	75	568	5.00E-95
NM_106225	gibberellin-regulated protein 1 (GASA1) mRNA [Arabidopsis thaliana]	68	300	9.00E-19
AK318910	AT5G12080 mRNA [Arabidopsis thaliana]	69	178	4.00E-05
NM_123267	HXXXD-type acyl-transferase-like protein (AT5G39050) mRNA [Arabidopsis thaliana]	80	67	2.00E-07
NM_001085133	Cytokine-induced anti-apoptosis inhibitor 1 [Arabidopsis thaliana]	73	428	3.00E-58
NM_120082	protein RER1A (ATRER1A) mRNA [Arabidopsis thaliana]	76	369	9.00E-60
NM_112551	60S ribosomal protein L19-2 (AT3G16780) mRNA [Arabidopsis thaliana]	84	470	1.00E-140
NM_125361	histone H4 (AT5G59690) mRNA [Arabidopsis thaliana]	84	78	5.00E-13
NM_125192	outer membrane lipoprotein Blc (TIL) mRNA [Arabidopsis thaliana]	72	556	5.00E-74
NM_124103	small subunit ribosomal protein S19 (RPS19) mRNA [Arabidopsis thaliana]	75	150	2.00E-20

IP : 14.49.138.138, 2017-11-03 13:30:33

AK319016	AT3G46000 mRNA [Arabidopsis thaliana]	81	51	3.00E-04
AK226459	mRNA for Lhcb4- protein [Arabidopsis thaliana]	76	501	7.00E-98
NM_104319	dehydrin family protein (AT1G54410) mRNA [Arabidopsis thaliana]	79	85	2.00E-10
NM_111461	anaphase-promoting complex subunit 11 (APC11) mRNA [Arabidopsis thaliana]	93	27	0.18
GU005953	ecotype Ws-0 CDKF-1 gene [Arabidopsis thaliana]	83	35	0.33
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	30	0.034
AK317069	AT1G52300 mRNA [Arabidopsis thaliana]	83	302	7.00E-83
DQ062415	ecotype Mv-0 chalcone synthase family protein (At5g13930) mRNA [Arabidopsis thaliana]	77	965	0
NM_124123	putative pectinesterase 68 (AT5G47500) mRNA [Arabidopsis thaliana]	87	37	0.004
NM_127165	non-symbiotic hemoglobin 1 (HB1) mRNA [Arabidopsis thaliana]	77	447	2.00E-92
AB493630	At3g24010 mRNA for hypothetical protein [Arabidopsis thaliana]	74	340	1.00E-50
NM_104504	F-box protein PP2-B14 (PP2-B14) mRNA [Arabidopsis thaliana]	91	32	0.007
NM_001203732	cullin 1 (CUL1) mRNA [Arabidopsis thaliana]	76	931	0
AK227324	mRNA for hypothetical protein [Arabidopsis thaliana]	75	98	4.00E-09
NM_123258	putative germin-like protein subfamily 1 member 12 (AT5G38960) mRNA [Arabidopsis thaliana]	70	512	1.00E-50
AK227147	mRNA for putative UDP-glucose glucosyltransferase [Arabidopsis thaliana]	67	374	1.00E-12
NM_119135	choline monooxygenase (AT4G29890) mRNA [Arabidopsis thaliana]	71	818	6.00E-94
NM_001161128	protein Fes1A (Fes1A) mRNA [Arabidopsis thaliana]	71	776	2.00E-86
NM_126333	leucine-rich repeat protein kinase-like protein (AT2G02780) mRNA [Arabidopsis thaliana]	68	716	3.00E-53
NM_001160906	dormancy-associated protein-like 1 (DYL1) mRNA [Arabidopsis thaliana]	72	363	9.00E-41
NM_117683	drought-induced 21 protein (DI21) mRNA [Arabidopsis thaliana]	79	103	5.00E-16
NM_102769	metallo-beta-lactamase domain-containing protein (AT1G30300) mRNA [Arabidopsis thaliana]	78	862	0
NM_112046	actin-11 (ACT11) mRNA [Arabidopsis thaliana]	80	420	2.00E-105
NM_102056	uncharacterized protein (AT1G22060) mRNA [Arabidopsis thaliana]	96	22	8.9
NM_102363	putative transmembrane protein (AT1G25520) mRNA [Arabidopsis thaliana]	77	694	4.00E-147
NM_202722	putative galactinol--sucrose galactosyltransferase 2 (SIP2) mRNA [Arabidopsis thaliana]	73	634	1.00E-96
NM_202722	putative galactinol--sucrose galactosyltransferase 2 (SIP2) mRNA [Arabidopsis thaliana]	69	406	4.00E-43
AK230285	mRNA for predicted GPI-anchored protein [Arabidopsis thaliana]	76	228	9.00E-35
NM_111366	cysteine synthase D1 (CYSD1) mRNA [Arabidopsis thaliana]	73	362	1.00E-56
NM_113046	histidine-containing phosphotransmitter 1 (AHP1) mRNA [Arabidopsis thaliana]	75	443	3.00E-71
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	80	75	2.00E-10
NM_120080	40S ribosomal protein S25-4 (AT4G39200) mRNA [Arabidopsis thaliana]	85	328	1.00E-97
NM_130109	FASCICLIN-like arabinogalactan protein 8 (FLA8) mRNA [Arabidopsis thaliana]	89	26	5.5
NM_001198111	BEL1-like homeodomain 10 (BEL10) mRNA [Arabidopsis thaliana]	85	32	2.5
NM_001203010	lipid-binding serum glycoprotein-like protein (AT3G20270) mRNA [Arabidopsis thaliana]	93	27	0.019
AY800632	clone H0000001192 hypothetical protein (AT4G12760) mRNA [Arabidopsis thaliana]	100	23	0.026
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	71	85	0.27
AK318734	AT1G56340 mRNA [Arabidopsis thaliana]	81	958	0
NM_104929	bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein (AT1G62500) mRNA [Arabidopsis thaliana]	79	263	1.00E-56
NM_102158	GroES-like protein (AT1G23100) mRNA [Arabidopsis thaliana]	70	293	8.00E-28

IP : 14.49.138.138, 2017-11-03 13:30:33

NM_104390	uncharacterized protein (AT1G55170) mRNA [Arabidopsis thaliana]	90	29	3.4
AK318955	AT5G06440 mRNA [Arabidopsis thaliana]	100	23	0.01
NM_116013	Quinoprotein amine dehydrogenase [Arabidopsis thaliana]	85	39	0.53
NM_112093	heat shock protein 70-4 (HSP70) mRNA [Arabidopsis thaliana]	80	86	5.00E-12
NM_117646	indole-3-acetate beta-D-glucosyltransferase (IAGLU) mRNA [Arabidopsis thaliana]	65	507	1.00E-12
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.061
AB425270	At1g58470 orthologue [Arabidopsis thaliana]	83	34	2.7
NM_130159	aquaporin PIP1-2 (PIP1B) mRNA [Arabidopsis thaliana]	82	690	0
NM_001198429	Hypersensitive-induced response protein 2 (AT1G69840) mRNA [Arabidopsis thaliana]	80	830	0
NM_129083	B3 domain-containing protein (AT2G35310) mRNA [Arabidopsis thaliana]	88	32	0.72
NM_128939	30S ribosomal protein S5 (AT2G33800) mRNA [Arabidopsis thaliana]	75	701	8.00E-123
NM_112618	S-adenosylmethionine synthase 4 (MTO3) mRNA [Arabidopsis thaliana]	82	639	5.00E-170
NM_100553	histone H1.1 (AT1G06760) mRNA [Arabidopsis thaliana]	76	246	3.00E-39
NM_126136	subtilisin-like protease (ARA12) mRNA [Arabidopsis thaliana]	69	310	2.00E-23
NM_104929	bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein (AT1G62500) mRNA [Arabidopsis thaliana]	69	177	3.00E-08
NM_121610	14-3-3-like protein GF14 upsilon (GRF5) mRNA [Arabidopsis thaliana]	83	763	0
NM_124485	Respiratory burst oxidase-C (RHD2) mRNA [Arabidopsis thaliana]	70	789	7.00E-86
AK317612	AT1G55490 mRNA [Arabidopsis thaliana]	100	21	0.33
NM_105982	nascent polypeptide-associated complex subunit beta (AT1G73230) mRNA [Arabidopsis thaliana]	78	459	4.00E-100
NM_103788	C3HC zinc finger-like protein (AT1G48950) mRNA [Arabidopsis thaliana]	70	820	1.00E-89
NM_115023	uncharacterized protein (AT3G51640) mRNA [Arabidopsis thaliana]	100	17	6.1
AK317722	AT1G35720 mRNA [Arabidopsis thaliana]	69	131	2.00E-04
AK227544	mRNA for putative cytochrome P450 [Arabidopsis thaliana]	85	33	0.5
NM_116182	Chalcone-flavanone isomerase family protein (AT3G63170) mRNA [Arabidopsis thaliana]	70	183	5.00E-11
NM_001203183	magnesium-protoporphyrin IX monomethyl ester [oxidative] cyclase (CRD1) mRNA [Arabidopsis thaliana]	83	766	0
NM_101570	SOUL heme-binding protein (AT1G17100) mRNA [Arabidopsis thaliana]	69	556	1.00E-50
NM_104373	protein auxin RESPONSE 4 (AXR4) mRNA [Arabidopsis thaliana]	66	600	1.00E-32
NM_106362	alcohol dehydrogenase class-P (ADH1) mRNA [Arabidopsis thaliana]	78	867	0
NM_121996	peroxidase 59 (AT5G19890) mRNA [Arabidopsis thaliana]	70	266	5.00E-24
NM_203088	translation initiation factor eIF-2 beta subunit (EIF2 BETA) mRNA [Arabidopsis thaliana]	76	765	2.00E-143
NM_001084507	mitochondrial import inner membrane translocase subunit Tim10 (TIM10) mRNA [Arabidopsis thaliana]	81	226	2.00E-52
NM_125035	uncharacterized protein (AT5G56520) mRNA [Arabidopsis thaliana]	86	34	0.99
NM_127268	pentatricopeptide repeat-containing protein (AT2G17140) mRNA [Arabidopsis thaliana]	81	42	0.36
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	28	0.41
AK316826	AT5G20830 mRNA [Arabidopsis thaliana]	71	455	1.00E-56
NM_113528	cytochrome P450 71B23 (CYP71B23) mRNA [Arabidopsis thaliana]	73	255	4.00E-31
NM_001203818	pleckstrin homology (PH) domain-containing protein (AT4G17140) mRNA [Arabidopsis thaliana]	90	29	0.069
NM_001198061	uncharacterized protein (AT1G13930) mRNA [Arabidopsis thaliana]	67	225	7.00E-09
AK316989	AT1G72370 mRNA [Arabidopsis thaliana]	80	635	3.00E-161
NM_001084288	SLAC1 homologue 4 (SLAH4) mRNA [Arabidopsis thaliana]	87	29	3.3

IP : 14.49.138.138, 2017-11-03 13:30:33

NM_129410	non-specific lipid-transfer protein 2 (LTP2) mRNA [Arabidopsis thaliana]	77	52	0.041
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.12
NM_125822	protein EXORDIUM like 2 (EXL2) mRNA [Arabidopsis thaliana]	70	666	4.00E-76
NM_001125979	60S acidic ribosomal protein P3-2 (AT5G57290) mRNA [Arabidopsis thaliana]	79	51	0.008
NM_106064	60S ribosomal protein L6-3 (AT1G74050) mRNA [Arabidopsis thaliana]	78	702	8.00E-155
NM_112270	oxidoreductase [Arabidopsis thaliana]	87	36	3.5
NM_130285	ADP-ribosylation factor 1 (ARF1A1C) mRNA [Arabidopsis thaliana]	87	550	0
NM_100945	uncharacterized protein (AT1G10690) mRNA [Arabidopsis thaliana]	71	103	2.00E-04
NM_103831	mitochondrial import receptor subunit TOM6-like protein (TOM6) mRNA [Arabidopsis thaliana]	73	175	5.00E-19
NM_103831	mitochondrial import receptor subunit TOM6-like protein (TOM6) mRNA [Arabidopsis thaliana]	73	175	7.00E-19
NM_112530	rapid alkalinization factor 23 (RALF23) mRNA [Arabidopsis thaliana]	83	186	2.00E-47
NM_179782	exostosin-like protein (FRA8) mRNA [Arabidopsis thaliana]	86	28	3
AY045968	putative ethylene responsive element binding factor (At5g61590) mRNA [Arabidopsis thaliana]	85	33	0.94
NM_179213	oxidoreductase [Arabidopsis thaliana]	68	835	4.00E-76
NM_119566	putative caffeoyl-CoA O-methyltransferase (CCoAOMT1) mRNA [Arabidopsis thaliana]	76	688	3.00E-129
NM_180444	alfin-like 1 protein (AL1) mRNA [Arabidopsis thaliana]	73	708	9.00E-111
NM_119682	O-methyltransferase family 2 protein (AT4G35160) mRNA [Arabidopsis thaliana]	73	110	1.00E-07
NM_105168	cytochrome P450 [Arabidopsis thaliana]	68	437	2.00E-29
NM_001085128	uncharacterized protein (AT5G17165) mRNA [Arabidopsis thaliana]	68	261	2.00E-14
GU011206	ecotype Ws-0 CYCD4-2 5' flanking region genomic sequence [Arabidopsis thaliana]	83	41	0.1
NM_115790	Protein Transporter [Arabidopsis thaliana]	78	340	2.00E-67
NM_115816	60S ribosomal protein L38 (AT3G59540) mRNA [Arabidopsis thaliana]	85	192	1.00E-52
NM_106717	PPPDE putative thiol peptidase family protein (AT1G80690) mRNA [Arabidopsis thaliana]	83	40	0.27
NM_123039	uncharacterized protein (AT5G36810) mRNA [Arabidopsis thaliana]	92	23	4.6
AK227687	mRNA for hypothetical protein [Arabidopsis thaliana]	78	298	3.00E-55
NM_100711	photosystem I subunit O (PSAO) mRNA [Arabidopsis thaliana]	94	31	5.00E-04
-	-	-	-	-
NM_106111	F-box/kelch-repeat protein (AT1G74510) mRNA [Arabidopsis thaliana]	90	29	0.16
NM_115202	aquaporin PIP2-1 (PIP2A) mRNA [Arabidopsis thaliana]	77	763	9.00E-161
AK316754	AT4G14960 mRNA [Arabidopsis thaliana]	83	911	0
AK318680	AT2G46920 mRNA [Arabidopsis thaliana]	91	31	0.021
-	-	-	-	-
NM_119711	thioredoxin reductase 1 (NTRB) mRNA [Arabidopsis thaliana]	74	875	2.00E-145
AY072530	unknown protein (At2g44650; F16B22.14) mRNA [Arabidopsis thaliana]	73	398	1.00E-54
NM_119625	G-box binding factor 6 (GBF6) mRNA [Arabidopsis thaliana]	73	249	4.00E-31
NM_129877	Proline-rich extensin-like family protein (AT2G43150) mRNA [Arabidopsis thaliana]	77	101	2.00E-11
AK229060	mRNA for hypothetical protein [Arabidopsis thaliana]	96	25	0.05
NM_102220	Proline-rich extensin-like family protein (AT1G23720) mRNA [Arabidopsis thaliana]	82	58	2.00E-04
AK316878	AT2G45960 mRNA [Arabidopsis thaliana]	79	637	1.00E-139
AK318680	AT2G46920 mRNA [Arabidopsis thaliana]	91	31	0.011

IP : 14.49.138.138, 2017-11-03 13:30:33

AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.12
NM_001161322	DEK domain-containing chromatin associated protein (AT5G63550) mRNA [Arabidopsis thaliana]	92	25	7.4
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.12
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.12
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	30	0.034
AY800632	clone H00000001192 hypothetical protein (AT4G12760) mRNA [Arabidopsis thaliana]	79	47	0.1
AY800632	clone H00000001192 hypothetical protein (AT4G12760) mRNA [Arabidopsis thaliana]	85	45	9.00E-05
NM_101543	V-ATPase-related protein (AT1G16820) mRNA [Arabidopsis thaliana]	99	76	1.00E-29
NM_001161300	exocyst complex component 84B (EXO84B) mRNA [Arabidopsis thaliana]	93	26	1.3
NM_001203050	peroxiredoxin Q (ATPRX Q) mRNA [Arabidopsis thaliana]	96	23	0.62
-	-	-	-	-
NM_120715	NDR1/HIN1-Like protein 3 (NHL3) mRNA [Arabidopsis thaliana]	94	30	9.00E-04
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	89	26	4.9
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	89	26	4.9
AK227610	mRNA for hypothetical protein [Arabidopsis thaliana]	77	110	3.00E-14
NM_101070	NEDD8-like protein RUB3 (RUB3) mRNA [Arabidopsis thaliana]	88	32	0.044
NM_112200	transcription repressor MYB5 (MYB5) mRNA [Arabidopsis thaliana]	78	63	4.00E-05
BX841865	Full-length cDNA Complete sequence from clone GSLTPGH20ZE10 of Hormone Treated Callus of strain col-0 of Arabidopsis thaliana (thale cress) [Arabidopsis thaliana]	87	30	6.9
AY800632	clone H00000001192 hypothetical protein (AT4G12760) mRNA [Arabidopsis thaliana]	100	23	0.059
NM_148612	uncharacterized protein (AT1G59885) mRNA [Arabidopsis thaliana]	92	25	2.6
NM_129584	myb family transcription factor (AT2G40260) mRNA [Arabidopsis thaliana]	90	29	0.089
NM_122329	lipase class 3-related protein (AT5G24230) mRNA [Arabidopsis thaliana]	93	26	0.16
NM_001198384	protein ILITYHIA (ILA) mRNA [Arabidopsis thaliana]	90	30	0.11
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	98	159	2.00E-71
NM_180420	LURP-one-related 15 protein (AT5G01750) mRNA [Arabidopsis thaliana]	70	171	2.00E-09
NM_117509	60S ribosomal protein L36a (AT4G14320) mRNA [Arabidopsis thaliana]	86	319	3.00E-100
NM_120080	40S ribosomal protein S25-4 (AT4G39200) mRNA [Arabidopsis thaliana]	83	328	6.00E-90
AB493587	At2g43000 mRNA for hypothetical protein [Arabidopsis thaliana]	85	45	1.00E-04
NM_102220	Proline-rich extensin-like family protein (AT1G23720) mRNA [Arabidopsis thaliana]	83	52	3.00E-04
AK226902	mRNA for ubiquitin extension protein [Arabidopsis thaliana]	85	455	6.00E-142
NM_112537	translationally-controlled tumor protein-like protein (TCTP) mRNA [Arabidopsis thaliana]	80	509	5.00E-125
NM_001036042	patellin-4 (AT1G30690) mRNA [Arabidopsis thaliana]	85	33	1.7
NM_114688	uncharacterized protein (AT3G48185) mRNA [Arabidopsis thaliana]	100	25	0.001
NM_001203652	protein disulfide-isomerase A1 (PDIL1-4) mRNA [Arabidopsis thaliana]	72	543	5.00E-68
NM_001125215	KRR1 family protein (AT3G24080) mRNA [Arabidopsis thaliana]	90	40	2.00E-05
NM_112867	vacuolar sorting protein 9 domain-containing protein (VPS9A) mRNA [Arabidopsis thaliana]	96	22	3.7
NM_120167	histone H3 (AT4G40030) mRNA [Arabidopsis thaliana]	90	77	4.00E-21
NM_111118	regulator of chromosome condensation domain-containing protein (AT3G02510) mRNA [Arabidopsis thaliana]	96	24	0.11
NM_001036557	Polyadenylate-binding protein-interacting protein 2 (AT4G14270) mRNA [Arabidopsis thaliana]	68	121	0.022
NM_112085	chitinase (HCHIB) mRNA [Arabidopsis thaliana]	66	486	1.00E-20

IP : 14.49.138.138, 2017-11-03 13:30:33

NM_116485	translocase of chloroplast 159 (TOC159) mRNA [Arabidopsis thaliana]	76	706	4.00E-133
NM_001160995	Histidinol-phosphate aminotransferase (HISN6B) mRNA [Arabidopsis thaliana]	77	626	2.00E-124
NM_120167	histone H3 (AT4G40030) mRNA [Arabidopsis thaliana]	90	77	4.00E-21
AK228577	mRNA for peroxidase [Arabidopsis thaliana]	83	39	0.075
AK228010	mRNA for hypothetical protein [Arabidopsis thaliana]	79	423	8.00E-99
NM_001202738	uncharacterized protein (AT2G33510) mRNA [Arabidopsis thaliana]	86	42	1.00E-04
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	30	0.017
NM_129411	non-specific lipid-transfer protein 1 (LP1) mRNA [Arabidopsis thaliana]	87	46	8.00E-07
AK228864	mRNA for xyloglucan endo-1,4-beta-D-glucanase precursor [Arabidopsis thaliana]	92	23	6.8
NM_113528	cytochrome P450 71B23 (CYP71B23) mRNA [Arabidopsis thaliana]	67	278	8.00E-14
NM_115368	ABC transporter G family member 17 (AT3G55100) mRNA [Arabidopsis thaliana]	83	35	1.1
NM_128773	transmembrane receptor protein (AT2G32140) mRNA [Arabidopsis thaliana]	85	40	0.032
NM_001202735	vesicle-associated membrane protein 722 (SAR1) mRNA [Arabidopsis thaliana]	77	124	7.00E-18
NM_104206	4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis (AT1G53280) mRNA [Arabidopsis thaliana]	70	738	4.00E-83
NM_117000	nucleoside diphosphate kinase 1 (NDPK1) mRNA [Arabidopsis thaliana]	76	358	9.00E-64
NM_122329	lipase class 3-related protein (AT5G24230) mRNA [Arabidopsis thaliana]	93	26	0.15
AY800632	clone H00000001192 hypothetical protein (AT4G12760) mRNA [Arabidopsis thaliana]	100	24	0.021
NM_112200	transcription repressor MYB5 (MYB5) mRNA [Arabidopsis thaliana]	78	70	4.00E-06
NM_102125	40S ribosomal protein S18 (PFL) mRNA [Arabidopsis thaliana]	92	69	2.00E-19
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.12
NM_202645	SNF1-related protein kinase catalytic subunit alpha KIN11 (KIN11) mRNA [Arabidopsis thaliana]	92	24	1.4
GU009019	ecotype Ws-0 CYCA3-2 gene [Arabidopsis thaliana]	92	24	2.2
AK226226	mRNA for 60S ribosomal protein L39 [Arabidopsis thaliana]	84	167	1.00E-42
NM_112200	transcription repressor MYB5 (MYB5) mRNA [Arabidopsis thaliana]	78	63	4.00E-05
NM_119254	CemA-like proton extrusion protein-like protein (AT4G31040) mRNA [Arabidopsis thaliana]	89	27	1.7
NM_120225	S-adenosyl-L-methionine-dependent methyltransferase family protein (AT5G01470) mRNA [Arabidopsis thaliana]	88	31	0.1
NM_001124033	phosphoglycerate kinase (AT1G56190) mRNA [Arabidopsis thaliana]	92	23	3.4
NM_106609	sodium/hydrogen exchanger 6 (NHX6) mRNA [Arabidopsis thaliana]	89	54	5.00E-11
NM_111344	hevein-like protein (PR4) mRNA [Arabidopsis thaliana]	70	365	6.00E-34
NM_001203599	ubiquitin-conjugating enzyme E2 10 (UBC10) mRNA [Arabidopsis thaliana]	86	449	5.00E-144
-	-	-	-	-
NM_112200	transcription repressor MYB5 (MYB5) mRNA [Arabidopsis thaliana]	78	70	2.00E-06
NM_125207	uric acid degradation bifunctional protein TTL (TTL) mRNA [Arabidopsis thaliana]	67	427	3.00E-29
NM_001036042	patellin-4 (AT1G30690) mRNA [Arabidopsis thaliana]	85	33	1.7
NM_115119	60S ribosomal protein L40-2 (UBQ1) mRNA [Arabidopsis thaliana]	89	393	2.00E-140
NM_125699	embryo defective 2759 protein (EMB2759) mRNA [Arabidopsis thaliana]	68	734	1.00E-51
NM_125699	embryo defective 2759 protein (EMB2759) mRNA [Arabidopsis thaliana]	67	823	2.00E-56
NM_113489	2-oxoacid dehydrogenases acyltransferase family protein (LTA2) mRNA [Arabidopsis thaliana]	70	552	2.00E-55
AF190297	ecotype Columbia transparent testa 1 (TT1) gene [Arabidopsis thaliana]	91	32	0.13
AF190297	ecotype Columbia transparent testa 1 (TT1) gene [Arabidopsis thaliana]	91	32	0.099

IP : 14.49.138.138, 2017-11-03 13:30:33

NM_111311	60S ribosomal protein L23 (emb2171) mRNA [Arabidopsis thaliana]	86	432	1.00E-137
NM_129967	6,7-dimethyl-8-ribityllumazine synthase (COS1) mRNA [Arabidopsis thaliana]	80	488	2.00E-117
-	-	-	-	-
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.12
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	30	0.034
NM_105835	Polyadenylate-binding protein 5 (PAB5) mRNA [Arabidopsis thaliana]	81	71	2.00E-08
AK318939	AT1G49975 mRNA [Arabidopsis thaliana]	100	26	0.002
NM_114467	histone H2B (HTB9) mRNA [Arabidopsis thaliana]	96	23	0.39
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.12
BX826934	Full-length cDNA Complete sequence from clone GSLTFB78ZA04 of Flowers and buds of strain col-0 of Arabidopsis thaliana (thale cress) [Arabidopsis thaliana]	82	38	0.97
NM_001203082	phytosulfokine-beta (PSK3) mRNA [Arabidopsis thaliana]	83	63	4.00E-09
AK317640	AT5G19330 mRNA [Arabidopsis thaliana]	86	34	0.24
NM_001203385	mitochondrial outer membrane protein porin 2 (VDAC3) mRNA [Arabidopsis thaliana]	74	830	3.00E-141
NM_102942	putative membrane protein (AT1G32080) mRNA [Arabidopsis thaliana]	74	621	5.00E-95
NM_123256	germin-like protein subfamily 1 member 11 (AT5G38940) mRNA [Arabidopsis thaliana]	69	633	3.00E-52
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	91	31	0.005
NM_113185	aluminum induced protein with YGL and LRDR motif (AT3G22850) mRNA [Arabidopsis thaliana]	77	713	1.00E-145
NM_122006	regulatory particle triple-A ATPase 6A (RPT6A) mRNA [Arabidopsis thaliana]	81	945	0
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	91	31	0.01
AK229545	mRNA for hypothetical protein [Arabidopsis thaliana]	80	96	7.00E-14
NM_104336	acyl carrier protein 2 (ACP2) mRNA [Arabidopsis thaliana]	81	72	5.00E-11
NM_102056	uncharacterized protein (AT1G22060) mRNA [Arabidopsis thaliana]	96	22	8.8
NM_112085	chitinase (HCHIB) mRNA [Arabidopsis thaliana]	84	42	0.006
NM_101651	basic transcription factor 3 (BTF3) mRNA [Arabidopsis thaliana]	74	498	1.00E-88
NM_001203943	small nuclear ribonucleoprotein F (RUXF) mRNA [Arabidopsis thaliana]	75	204	8.00E-38
NM_112484	photosystem I reaction center subunit VI-1 (PSAH-1) mRNA [Arabidopsis thaliana]	79	437	2.00E-96
NM_118357	uncharacterized protein (AT4G22310) mRNA [Arabidopsis thaliana]	80	125	2.00E-22
NM_106593	ALA-interacting subunit 5 (ALIS5) mRNA [Arabidopsis thaliana]	92	25	4.8
GU293556	ecotype ZJjds ycf3-trnS intergenic spacer [Arabidopsis thaliana]	85	252	2.00E-72
NM_115611	Polygalacturonase ADPG1 (ADPG1) mRNA [Arabidopsis thaliana]	88	31	2.7
NM_001035681	ubiquinone biosynthesis monooxygenase Coq6 (AT3G24200) mRNA [Arabidopsis thaliana]	92	23	4.6
NM_106595	inosine-5'-monophosphate dehydrogenase (AT1G79470) mRNA [Arabidopsis thaliana]	90	29	0.25
NM_121429	COP9 signalosome complex subunit 3 (COP13) mRNA [Arabidopsis thaliana]	96	24	1.5
NM_100425	putative RNA helicase SDE3 (SDE3) mRNA [Arabidopsis thaliana]	81	42	0.62
NM_147273	uncharacterized protein (AT2G07774) mRNA [Arabidopsis thaliana]	85	39	0.006
NM_001203962	transcriptional corepressor LEUNIG (LUG) mRNA [Arabidopsis thaliana]	81	36	4
NM_111086	60S ribosomal protein L39-2 (AT3G02190) mRNA [Arabidopsis thaliana]	85	159	5.00E-42
NM_001202887	embryo defective 2016 protein (EMB2016) mRNA [Arabidopsis thaliana]	100	19	1.6
AY800632	clone H0000001192 hypothetical protein (AT4G12760) mRNA [Arabidopsis thaliana]	100	23	0.062
BX827908	Full-length cDNA Complete sequence from clone GSLTPGH33ZF09 of Hormone Treated Callus of strain col-0 of Arabidopsis thaliana (thale cress) [Arabidopsis	88	32	0.93

IP : 14.49.138.138, 2017-11-03 13:30:33

	thaliana]			
BX827908	Full-length cDNA Complete sequence from clone GSLTPGH33ZF09 of Hormone Treated Callus of strain col-0 of Arabidopsis thaliana (thale cress) [Arabidopsis thaliana]	88	32	0.93
NM_122329	lipase class 3-related protein (AT5G24230) mRNA [Arabidopsis thaliana]	93	26	0.14
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	80	75	3.00E-10
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	28	0.41
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	80	75	3.00E-10
NM_001198509	protein kinase domain-containing protein (AT1G79640) mRNA [Arabidopsis thaliana]	92	24	3.3
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.12
NM_001198509	protein kinase domain-containing protein (AT1G79640) mRNA [Arabidopsis thaliana]	92	24	3.3
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	87	30	0.41
NM_100326	uncharacterized protein (AT1G04470) mRNA [Arabidopsis thaliana]	88	31	0.083
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.12
NM_104739	naphthoate synthase (ECHID) mRNA [Arabidopsis thaliana]	90	28	0.28
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.12
NM_120134	Lipase/lipooxygenase [Arabidopsis thaliana]	71	114	4.00E-05
AK227055	mRNA for protein kinase [Arabidopsis thaliana]	81	52	1.00E-04
AK229461	mRNA for hypothetical protein [Arabidopsis thaliana]	92	24	1.2
NM_001203822	DWNN domain-containing protein (AT4G17410) mRNA [Arabidopsis thaliana]	96	22	2.3
NM_126283	F-box protein PP2-B1 (PP2-B1) mRNA [Arabidopsis thaliana]	96	22	1.5
-	-	-	-	-
NM_101103	putative calcium-binding protein CML13 (AT1G12310) mRNA [Arabidopsis thaliana]	92	23	5
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.12
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	28	0.41
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.12
NM_001125945	Glucose-methanol-choline (GMC) oxidoreductase family protein (AT5G51950) mRNA [Arabidopsis thaliana]	84	36	0.27
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	80	75	3.00E-10
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.12
FJ441344	clone E At1g51990 gene [Arabidopsis thaliana]	88	41	0.031
NM_121649	Isopentenyl-diphosphate Delta-isomerase I (IPP1) mRNA [Arabidopsis thaliana]	100	18	3.4
NM_104531	TIR-NBS-LRR class disease resistance protein (AT1G56540) mRNA [Arabidopsis thaliana]	87	36	0.12
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.12
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	30	0.034
AY600577	hypothetical protein (At3g18300) mRNA [Arabidopsis thaliana]	86	41	0.002
NM_119934	phytosulfokine-beta (PSK6) mRNA [Arabidopsis thaliana]	76	50	0.86
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.12
NM_129414	uncharacterized protein (AT2G38570) mRNA [Arabidopsis thaliana]	90	28	0.72
NM_111844	40S ribosomal protein S28-1 (AT3G10090) mRNA [Arabidopsis thaliana]	93	26	1
DQ473520	ARR2 (ARR2) gene [Arabidopsis thaliana]	86	35	0.3
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	80	75	3.00E-10
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	81	51	1.00E-04

IP : 14.49.138.138, 2017-11-03 13:30:33

NM_117467	serine hydroxymethyltransferase 4 (SHM4) mRNA [Arabidopsis thaliana]	80	178	4.00E-37
NM_203095	Remorin family protein (AT5G23750) mRNA [Arabidopsis thaliana]	77	185	4.00E-30
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.12
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	81	51	2.00E-04
NM_103975	protein Disulfide Isomerase (PDIa) family [Arabidopsis thaliana]	86	42	5.00E-05
NM_122010	Plant Tudor-like RNA-binding protein (AT5G20030) mRNA [Arabidopsis thaliana]	100	20	0.43
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.12
NM_001203130	uncharacterized protein (AT3G51760) mRNA [Arabidopsis thaliana]	77	81	2.00E-07
BX819802	Full-length cDNA Complete sequence from clone GSLTLS2ZE12 of Adult vegetative tissue of strain col-0 of Arabidopsis thaliana (thale cress) [Arabidopsis thaliana]	85	39	2.1
NM_001202902	component of IIS longevity pathway SMK-1 domain-containing protein (AT3G06670) mRNA [Arabidopsis thaliana]	81	51	0.007
NM_112325	cytochrome P450 [Arabidopsis thaliana]	100	20	0.59
GQ176917	ecotype Nd-1 ATC gene [Arabidopsis thaliana]	87	29	3.2
BX813433	Full-length cDNA Complete sequence from clone GSLTFB17ZD10 of Flowers and buds of strain col-0 of Arabidopsis thaliana (thale cress) [Arabidopsis thaliana]	100	18	3.7
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.12
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.12
NM_111851	DHFS-FPGS homolog C (DFC) mRNA [Arabidopsis thaliana]	89	26	4.9
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	99	199	7.00E-94
NM_001203471	pentatricopeptide repeat-containing protein (AT5G25630) mRNA [Arabidopsis thaliana]	85	32	1.6
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	87	37	0.003
NM_128693	delta-9 acyl-lipid desaturase 2 (DS2) mRNA [Arabidopsis thaliana]	89	26	2.5
-	-	-	-	-
NM_127151	CSL zinc finger domain-containing protein (AT2G15910) mRNA [Arabidopsis thaliana]	96	21	6.8
AK317544	AT1G11910 mRNA [Arabidopsis thaliana]	79	172	1.00E-30
AK229596	mRNA for ribosomal protein GL41 - like [Arabidopsis thaliana]	94	78	3.00E-25
BX827147	Full-length cDNA Complete sequence from clone GSLTLS16ZC07 of Adult vegetative tissue of strain col-0 of Arabidopsis thaliana (thale cress) [Arabidopsis thaliana]	88	33	0.18
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.12
NM_001084435	Ribosomal protein L27 family protein (AT2G16930) mRNA [Arabidopsis thaliana]	88	31	1.5
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.12
EU550191	isolate CS6626 At1g27340 (At1g27340) gene [Arabidopsis thaliana]	75	137	2.00E-16
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.12
AK316912	AT1G50630 mRNA [Arabidopsis thaliana]	88	33	0.25
AY735627	chromosome 3 hypothetical protein AT3G61410 mRNA [Arabidopsis thaliana]	82	49	0.001
NM_101431	uncharacterized protein (AT1G15620) mRNA [Arabidopsis thaliana]	88	31	0.2
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.12
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.12
AY064995	At1g66920/T4O24_7 mRNA sequence [Arabidopsis thaliana]	92	24	9.7
BX831142	Full-length cDNA Complete sequence from clone GSLTLS60ZG11 of Adult vegetative tissue of strain col-0 of Arabidopsis thaliana (thale cress) [Arabidopsis thaliana]	96	24	2.9
BT004310	clone RAFL15-32-E21 (R50090) unknown protein (At5g55530) mRNA [Arabidopsis thaliana]	96	24	0.13
AY735627	chromosome 3 hypothetical protein AT3G61410 mRNA [Arabidopsis thaliana]	86	50	1.00E-04

IP : 14.49.138.138, 2017-11-03 13:30:33

NM_124404	chloroplast RNA-binding protein 31B (CP31B) mRNA [Arabidopsis thaliana]	96	21	4.7
NM_119332	Phototropic-responsive NPH3 family protein (ENP) mRNA [Arabidopsis thaliana]	100	21	0.2
NM_001160770	uncharacterized protein (AT4G16180) mRNA [Arabidopsis thaliana]	100	17	9.8
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.12
BX827147	Full-length cDNA Complete sequence from clone GSLTLS16ZC07 of Adult vegetative tissue of strain col-0 of Arabidopsis thaliana (thale cress) [Arabidopsis thaliana]	88	33	0.21
EU550191	isolate CS6626 At1g27340 (At1g27340) gene [Arabidopsis thaliana]	75	137	2.00E-16
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	97	188	2.00E-82
-	-	-	-	-
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	80	49	0.002
NM_124415	ATP binding / damaged DNA binding / nucleoside-triphosphatase/ nucleotide binding protein (AT5G50340) mRNA [Arabidopsis thaliana]	89	26	4.2
NM_001203589	phosphoprotein phosphatase inhibitor (AT5G52200) mRNA [Arabidopsis thaliana]	100	19	1.1
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.12
BT028908	unknown protein (At3g06070) mRNA [Arabidopsis thaliana]	78	58	0.001
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.12
NM_001036567	uncharacterized protein (AT4G14819) mRNA [Arabidopsis thaliana]	96	21	4.2
BT046195	unknown protein (At2g38410) mRNA [Arabidopsis thaliana]	87	29	1.1
-	-	-	-	-
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	30	0.034
NM_127877	Lysine-rich arabinogalactan protein 17 (AGP17) mRNA [Arabidopsis thaliana]	83	47	1.00E-04
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	80	75	3.00E-10
NM_001202689	Pollen Ole e 1 allergen and extensin family protein (AT2G27385) mRNA [Arabidopsis thaliana]	92	23	8.4
NM_116924	electron carrier/ protein disulfide oxidoreductase (AT4G08550) mRNA [Arabidopsis thaliana]	77	52	0.25
NM_116388	serine protease inhibitor [Arabidopsis thaliana]	92	23	2.6
NM_114510	uncharacterized protein (AT3G46430) mRNA [Arabidopsis thaliana]	73	158	2.00E-15
AK319148	AT4G25880 mRNA [Arabidopsis thaliana]	92	24	8.2
AY090986	At3g41950 mRNA sequence [Arabidopsis thaliana]	91	97	1.00E-30
AK318644	AT3G52120 mRNA [Arabidopsis thaliana]	79	142	8.00E-25
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	28	0.41
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	78	57	0.006
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.12
NM_102193	Peptidase C15 [Arabidopsis thaliana]	90	29	0.21
AK317315	AT2G47240 mRNA [Arabidopsis thaliana]	92	23	5.4
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.12
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	81	51	5.00E-04
NM_129209	bifunctional enolase 2/transcriptional activator (LOS2) mRNA [Arabidopsis thaliana]	75	168	2.00E-22
AY800632	clone H00000001192 hypothetical protein (AT4G12760) mRNA [Arabidopsis thaliana]	100	24	0.017
NM_121819	chaperone DnaJ-domain containing protein (AT5G18140) mRNA [Arabidopsis thaliana]	92	25	8.7
AK228213	mRNA for putative protein import receptor [Arabidopsis thaliana]	82	48	0.001
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	28	0.41
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.12

IP : 14.49.138.138, 2017-11-03 13:30:33

AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	81	51	3.00E-04
NM_128638	glutathione S-transferase (GSTF9) mRNA [Arabidopsis thaliana]	81	66	3.00E-08
DQ446396	clone pENTR221-At1g65445 transferase-like (At1g65445) mRNA [Arabidopsis thaliana]	87	29	0.83
BX819890	Full-length cDNA Complete sequence from clone GSLTLS44ZB10 of Adult vegetative tissue of strain col-0 of Arabidopsis thaliana (thale cress) [Arabidopsis thaliana]	74	151	7.00E-15
AY045968	putative ethylene responsive element binding factor (At5g61590) mRNA [Arabidopsis thaliana]	85	33	0.63
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	80	64	1.00E-06
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.12
NM_114187	sucrose synthase 4 (SUS4) mRNA [Arabidopsis thaliana]	83	118	3.00E-25
NM_117665	calcium-dependent lipid-binding domain-containing protein (AT4G15740) mRNA [Arabidopsis thaliana]	78	50	0.17
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	30	0.034
NM_001198367	uncharacterized protein (AT1G62981) mRNA [Arabidopsis thaliana]	92	25	0.35
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	30	0.034
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	80	75	3.00E-10
NM_120134	Lipase/lipooxygenase [Arabidopsis thaliana]	83	39	1.6
AY144111	hypothetical protein (At2g47360/T8I13.20) mRNA [Arabidopsis thaliana]	82	38	2.6
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	90	29	0.12
NM_001036039	ABC transporter C family member 1 (MRP1) mRNA [Arabidopsis thaliana]	82	33	3.2
AK229323	mRNA for putative jasmonate inducible protein [Arabidopsis thaliana]	88	49	7.00E-07
NM_001203414	uncharacterized protein (AT5G19930) mRNA [Arabidopsis thaliana]	95	37	1.00E-04
NM_129316	60S ribosomal protein L36-1 (AT2G37600) mRNA [Arabidopsis thaliana]	79	76	1.00E-09
-	-	-	-	-
AK226566	mRNA for putative transketolase precursor [Arabidopsis thaliana]	76	69	4.00E-04
NM_129611	Uroporphyrinogen decarboxylase 2 (HEME2) mRNA [Arabidopsis thaliana]	76	197	7.00E-32
AY096798	At2g07707 mRNA sequence [Arabidopsis thaliana]	80	75	3.00E-10
AK229008	mRNA for ARG1 protein [Arabidopsis thaliana]	89	27	0.84

Accession No.	Definition of putative homologues [organism]	Matching (%)	Matching (length)	E-value
XM_002304873	predicted protein [Populus trichocarpa]	85	950	0
EF147768	unknown mRNA [Populus trichocarpa]	70	835	6.00E-88
EF122396	putative thioredoxin-dependent peroxidase mRNA [Citrus cv.]	99	489	0
XM_002284216	hypothetical protein [Vitis vinifera]	81	752	0
XM_002275489	hypothetical protein [Vitis vinifera]	80	895	0
EF175925	putative DNA binding protein (V03-3) mRNA [Citrus sinensis]	73	405	5.00E-40
AJ001304	mRNA for hypothetical protein [Citrus paradisi]	97	713	0
AJ001304	mRNA for hypothetical protein [Citrus paradisi]	97	713	0
XM_002513143	arginine/serine rich splicing factor sf4/14 [Ricinus communis]	87	220	1.00E-66
XM_002515254	Beta-glucosidase [Ricinus communis]	81	123	7.00E-20
EF147148	unknown mRNA [Populus trichocarpa]	90	449	6.00E-169
EF175924	putative DNA binding protein (V03-1) mRNA [Citrus sinensis]	73	443	3.00E-49

IP : 14.49.138.138, 2017-11-03 13:30:33

GU991549	cultivar Zhi ubiquitin/ribosomal fusion protein mRNA [Citrus trifoliata]	93	683	0
GU937873	chloroplast photosystem II-like (psbR) [Morus alba]	80	427	5.00E-99
XM_002306149	predicted protein [Populus trichocarpa]	81	436	1.00E-107
XM_002532058	AMP deaminase [Ricinus communis]	72	274	4.00E-29
XM_002516624	ATP-dependent clp protease ATP-binding subunit clpx [Ricinus communis]	79	798	1.00E-173
EF122398	putative auxin-repressed/dormancy-associated protein mRNA [Citrus cv.]	99	369	0
XM_002270829	hypothetical protein [Vitis vinifera]	75	701	2.00E-125
FQ393484	clone SS0AFA25YM13 [Vitis vinifera]	84	351	5.00E-99
XM_002267239	hypothetical protein [Vitis vinifera]	75	539	2.00E-92
HM067359	s-adenosylmethionine synthetase-like mRNA [Dimocarpus longan]	85	713	0
AK378472	mRNA [Bombyx mori]	96	49	9.00E-11
EU883637	iron superoxide dismutase mRNA [Citrus maxima]	99	489	0
XM_002279649	hypothetical protein [Vitis vinifera]	73	424	7.00E-62
AK251553	cDNA clone: FLbaf118i17 [Hordeum vulgare sp.]	88	95	1.00E-21
XM_002317387	predicted protein [Populus trichocarpa]	85	338	5.00E-99
CU233142	EST from severe drought-stressed opposite wood [Populus]	78	103	9.00E-11
XM_002521340	structural constituent of ribosome [Ricinus communis]	81	278	5.00E-62
EU717678	GAST-like protein mRNA [Litchi chinensis]	76	323	7.00E-53
EF122396	putative thioredoxin-dependent peroxidase mRNA [Citrus cv.]	99	489	0
X05910	cistron for 26S ribosomal RNA [Citrus limon]	99	367	6.00E-178
AB002095	PSI reaction center subunit III [Citrus sinensis]	99	322	1.00E-156
EF175925	putative DNA binding protein (V03-3) mRNA [Citrus sinensis]	73	444	1.00E-47
BC033654	cDNA clone IMAGE:3901849 [Homo sapiens]	86	97	2.00E-20
AK336838	cDNA [Lotus japonicus]	78	395	7.00E-74
XM_002277120	hypothetical protein [Vitis vinifera]	79	305	2.00E-59
FQ393610	clone SS0AFA25YC04 [Vitis vinifera]	84	685	0
AC022379	chromosome 3 clone 996C6 map 3p [Homo sapiens]	89	51	2.00E-07
XM_002301129	f-box family protein [Populus trichocarpa]	76	1008	0
AM448318	whole genome shotgun sequence [Vitis vinifera,]	84	396	2.00E-111
XM_002530405	brca1-associated protein [Ricinus communis]	75	566	3.00E-81
CU229117	EST from severe drought-stressed leaves [Populus]	98	208	4.00E-94
AM437734	contig VV78X024535.5 [Vitis vinifera]	80	408	1.00E-86
EF175925	putative DNA binding protein (V03-3) mRNA [Citrus sinensis]	73	444	3.00E-42
EF147768	unknown mRNA [Populus trichocarpa]	70	835	6.00E-88
XM_002525420	conserved hypothetical protein [Ricinus communis]	82	423	1.00E-109
XM_002331828	predicted protein [Populus trichocarpa]	85	418	3.00E-121
XM_002305491	predicted protein [Populus trichocarpa]	77	329	7.00E-62
XM_002513800	serine hydroxymethyltransferase [Ricinus communis]	75	374	8.00E-55
XM_002275143	hypothetical protein [Vitis vinifera]	86	501	6.00E-151
EU957706	clone 1612279 mRNA sequence [Zea mays]	86	61	1.00E-08

IP : 14.49.138.138, 2017-11-03 13:30:33

EF122398	Shiranuhi putative auxin-repressed/dormancy-associated protein mRNA [Citrus cv.]	99	369	0
XM_002269599	hypothetical protein [Vitis vinifera]	69	358	6.00E-18
XM_002275489	hypothetical protein [Vitis vinifera]	77	921	0
XM_002336783	AP2/ERF domain-containing transcription factor (DREB55) [Populus trichocarpa]	77	278	4.00E-49
FJ356252	elongation factor-like mRNA [Citrus maxima]	97	720	0
XM_002279649	hypothetical protein [Vitis vinifera]	76	646	4.00E-121
EF175926	putative DNA binding protein (V03-2) mRNA [Citrus sinensis]	75	225	2.00E-26
EF148118	unknown mRNA [Populus trichocarpa]	80	835	0
AF506028	citrus tristeza virus resistance gene locus [Poncirus trifoliata]	67	356	7.00E-10
EF147768	unknown mRNA [Populus trichocarpa]	70	835	6.00E-88
XM_002302444	predicted protein [Populus trichocarpa]	86	560	0
FQ392128	clone SS0AFA7YF24 [Vitis vinifera]	81	650	1.00E-171
EF148118	unknown mRNA [Populus trichocarpa]	80	834	0
AK154432	NOD-derived CD11c +ve dendritic cells cDNA [Mus musculus]	95	1054	0
XM_002302444	predicted protein [Populus trichocarpa]	86	560	0
XM_002316746	predicted protein [Populus trichocarpa]	74	462	3.00E-70
XM_002526458	unknown protein [Ricinus communis]	86	638	0
FQ393371	clone SS0AFA26YF16 [Vitis vinifera]	79	694	2.00E-162
EF175927	putative DNA binding protein (V03-4) mRNA [Citrus sinensis]	72	241	2.00E-19
AC123927	BAC clone RP24-329L20 from chromosome 18 [Mus musculus]	87	51	8.00E-06
XM_002321821	cytochrome P450 (CYP96A16v1) [Populus trichocarpa]	71	690	1.00E-77
AC244194	strain Heinz 1706 chromosome 4 clone hba-4l19 map 4 [Solanum lycopersicum]	84	53	0.003
AC102550	chromosome 18 [Mus musculus]	83	47	0.13
XM_002321190	predicted protein [Populus trichocarpa]	82	764	0
XM_002526458	unknown protein [Ricinus communis]	86	637	0
XM_002283369	hypothetical protein [Vitis vinifera]	83	112	1.00E-19
XM_002530099	Vesicle-associated membrane protein [Ricinus communis]	85	563	2.00E-169
CU229117	severe drought-stressed leaves [Populus]	98	207	1.00E-93
CU233272	severe drought-stressed opposite wood [Populus]	84	174	2.00E-36
XM_002525420	hypothetical protein [Ricinus communis]	79	423	5.00E-95
XM_002326846	predicted protein [Populus trichocarpa]	82	660	6.00E-176
CU223893	EST from leave [Populus]	80	70	4.00E-07
EU717697	plastid acyl carrier protein (ACP) mRNA [Camellia oleifera]	79	443	1.00E-95
AB008100	metallothionein-like protein [Citrus unshiu]	92	654	0
AY198376	chlorophyll a/b-binding protein precursor [Citrus limon]	96	650	0
AJ243325	profilin (pro1 gene) [Hevea brasiliensis]	89	400	9.00E-141
XM_002326725	predicted protein [Populus trichocarpa]	87	223	2.00E-69
AK245634	cDNA [Glycine max]	73	332	1.00E-45
XM_002263498	hypothetical protein [Vitis vinifera]	74	485	4.00E-69
EU717678	GAST-like protein mRNA [Litchi chinensis]	75	339	3.00E-51

IP : 14.49.138.138, 2017-11-03 13:30:33

AJ243325	profilin (pro1 gene) [Hevea brasiliensis]	89	400	9.00E-141
FQ383541	clone SS0ABG1YJ04 [Vitis vinifera]	84	448	4.00E-133
XM_002263065	hypothetical protein [Vitis vinifera]	82	893	0
CU227213	severe drought-stressed leaves [Populus]	95	256	7.00E-111
NM_001248656	uncharacterized [Glycine max]	75	292	1.00E-45
XM_002517751	hypothetical protein [Ricinus communis]	78	866	0
AK386657	mRNA [Bombyx mori]	76	73	0.034
XM_002284264	hypothetical protein [Vitis vinifera]	75	601	3.00E-103
EF553533	isopentenyl pyrophosphate isomerase mRNA [Corylus avellana]	86	690	0
XM_002308716	predicted protein [Populus trichocarpa]	77	441	3.00E-84
DQ001729	hypoxia-responsive family protein mRNA [Citrus sinensis]	99	587	0
XM_002284264	hypothetical protein [Vitis vinifera]	76	555	4.00E-96
XM_002273316	hypothetical protein [Vitis vinifera]	80	266	1.00E-55
EF175924	putative DNA binding protein (V03-1) mRNA [Citrus sinensis]	73	442	5.00E-47
XM_003626569	Caffeic acid 3-O-methyltransferase (MTR_7g118320) mRNA [Medicago truncatula]	69	599	3.00E-58
XM_003541061	proteasome subunit alpha type-6-like [Glycine max]	86	567	0
JN572691	aquaporin PIP1 (PIP1) [Dimocarpus longan]	83	51	0.028
AM488634	whole genome shotgun sequence [Vitis vinifera]	80	144	5.00E-26
CU229117	severe drought-stressed leaves [Populus]	97	205	2.00E-90
XM_003624144	Thioredoxin (MTR_7g080250) mRNA [Medicago truncatula]	78	354	1.00E-76
EU717678	GAST-like protein mRNA [Litchi chinensis]	76	323	6.00E-53
AL009126	168 complete genome [Bacillus subtilis sp.]	92	36	0.033
AM910996	chromosome 14 [Plasmodium knowlesi]	100	40	1.00E-09
AB009351	mRNA for chalcone synthase [Citrus sinensis]	99	619	0
CU229117	severe drought-stressed leaves [Populus]	98	208	4.00E-94
XM_002273886	hypothetical protein [Vitis vinifera]	88	231	1.00E-73
AE014187	3D7 chromosome 14 [Plasmodium falciparum]	82	61	1.00E-06
XM_002322369	predicted protein [Populus trichocarpa]	72	622	2.00E-79
XM_002518958	hypothetical protein [Ricinus communis]	84	791	0
NM_001248604	uncharacterized [Glycine max]	84	414	3.00E-121
XM_002263329	hypothetical protein [Vitis vinifera]	79	697	2.00E-158
CU229117	severe drought-stressed leaves [Populus]	96	209	1.00E-87
XM_002284264	hypothetical protein [Vitis vinifera]	75	601	2.00E-99
XM_639636	AX4 hypothetical protein (DDB_G0273339) mRNA [Dictyostelium discoideum]	80	79	2.00E-07
XM_002326216	predicted protein [Populus trichocarpa]	85	338	9.00E-96
XM_002298137	predicted protein [Populus trichocarpa]	83	428	8.00E-118
HQ603732	microsatellite sequence [Eurycoma longifolia]	77	130	1.00E-16
AM910996	chromosome 14 [Plasmodium knowlesi]	100	40	1.00E-09
AM458863	contig VV78X003272.4 [Vitis vinifera]	74	347	4.00E-54
CU233582	severe drought-stressed opposite wood [Populus]	95	210	1.00E-87

IP : 14.49.138.138, 2017-11-03 13:30:33

XM_002171673	yFS275 DNA repair protein rad26 [Schizosaccharomyces japonicus]	92	34	0.42
EF175925	putative DNA binding protein (V03-3) mRNA [Citrus sinensis]	72	175	3.00E-07
XM_003624144	Thioredoxin (MTR_7g080250) mRNA [Medicago truncatula]	81	364	4.00E-89
XM_003542938	uncharacterized protein [Glycine max]	77	704	4.00E-147
AJ000081	mRNA for beta-1,3-glucanase [Citrus sinensis]	96	1042	0
XM_002534266	40S ribosomal protein S5 [Ricinus communis]	83	587	2.00E-170
XM_003521734	GDSL esterase/lipase LTL1-like [Glycine max]	78	504	2.00E-105
XM_002525277	oligopeptide transporter [Ricinus communis]	81	847	0
XM_003542472	uncharacterized protein [Glycine max]	78	158	1.00E-24
AF283533	miraculin-like protein 2 [Citrus x paradisi]	99	837	0
XM_002532899	Pectinesterase-3 precursor [Ricinus communis]	66	787	2.00E-43
AF283533	miraculin-like protein 2 [Citrus x paradisi]	94	557	0
XM_002283696	hypothetical protein [Vitis vinifera]	76	761	3.00E-150
AM906072	putative metallotionein [Citrus medica]	93	245	3.00E-95
EU544401	26S ribosomal RNA gene [Spragueanella rhamnifolia]	93	69	7.00E-21
AK382749	mRNA [Bombyx mori]	95	35	2.00E-04
XM_002302255	predicted protein [Populus trichocarpa]	80	570	8.00E-136
XM_002322725	cinnamyl alcohol dehydrogenase-like protein (CADL4) [Populus trichocarpa]	78	903	0
FQ389175	clone SS0AEB20YK02 [Vitis vinifera]	82	304	4.00E-75
XM_002871566	lyrata predicted protein [Arabidopsis lyrata sp.]	73	683	3.00E-98
FQ381610	clone SS0ABP1YC07 [Vitis vinifera]	89	458	6.00E-163
XM_002513602	40S ribosomal protein S10 [Ricinus communis]	86	537	3.00E-172
XM_002521755	Patellin-3 [Ricinus communis]	93	56	1.00E-11
XM_002314249	predicted protein [Populus trichocarpa]	75	176	3.00E-18
XM_002509537	21 kDa protein precursor [Ricinus communis]	71	380	3.00E-41
XM_002306151	aquaporin [Populus trichocarpa]	85	623	0
EU717678	GAST-like protein mRNA [Litchi chinensis]	75	309	2.00E-45
FJ851080	tonoplast intrinsic protein (TIP1;1) mRNA [Hevea brasiliensis]	82	743	0
XM_002521246	Aquaporin PIP2.7 [Ricinus communis]	85	808	0
AK227380	hypothetical protein [Arabidopsis thaliana]	80	268	2.00E-60
XM_002284264	hypothetical protein [Vitis vinifera]	74	615	4.00E-95
FQ381884	clone SS0ABG80YG19 [Vitis vinifera]	78	72	0.003
XM_002512083	hypothetical protein [Ricinus communis]	81	538	7.00E-137
FR797721	plastid rps16-trnK intergenic spacer [Jacobaea carniolica]	84	53	0.009
AJ000081	mRNA for beta-1,3-glucanase [Citrus sinensis]	96	872	0
AC189319	pekinensis [Brassica rapa sp.]	85	40	0.038
XM_002331924	flavonoid o-methyltransferase related (FOMT8) [Populus trichocarpa]	68	869	1.00E-76
XM_002331924	flavonoid o-methyltransferase related (FOMT8) [Populus trichocarpa]	68	869	7.00E-75
XM_002318773	predicted protein [Populus trichocarpa]	69	642	3.00E-67
XM_002316337	predicted protein [Populus trichocarpa]	81	852	0

IP : 14.49.138.138, 2017-11-03 13:30:33

AB573149	genomic DNA [Citrus unshiu]	77	311	9.00E-54
AM456108	contig VV78X264310.14 [Vitis vinifera]	89	36	0.033
XM_002271603	hypothetical protein [Vitis vinifera]	82	318	2.00E-80
XM_002280183	hypothetical protein [Vitis vinifera]	79	216	7.00E-42
FQ393524	clone SS0AFA25YJ14 [Vitis vinifera]	98	83	2.00E-30
FQ387947	clone SS0AEB24YL24 [Vitis vinifera]	81	392	2.00E-93
DQ864733	chloroplast [Citrus sinensis]	99	495	0
XM_002311507	predicted protein [Populus trichocarpa]	77	539	2.00E-106
XM_002300726	predicted protein [Populus trichocarpa]	82	585	2.00E-157
XM_002525656	3'-5' exonuclease [Ricinus communis]	75	462	3.00E-67
AM473379	contig VV78X073156.7 [Vitis vinifera]	93	38	5.00E-04
XM_002264452	hypothetical protein [Vitis vinifera]	82	843	0
XM_002510931	ribosomal protein L15 [Ricinus communis]	89	650	0
EF148047	unknown mRNA [Populus trichocarpa]	82	231	5.00E-50
DQ424891	group 5 late embryogenesis abundant protein (LEA5) gene [Citrus unshiu]	99	259	4.00E-127
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	179	2.00E-85
XM_002270930	hypothetical protein [Vitis vinifera]	84	61	1.00E-07
FJ694012	isolate GAPDH-L2 glyceraldehyde-3-phosphate dehydrogenase mRNA [Dimocarpus longan]	87	684	0
XM_002326025	predicted protein [Populus trichocarpa]	75	447	9.00E-78
XM_002273611	hypothetical protein [Vitis vinifera]	77	123	7.00E-13
XM_003544439	uncharacterized protein [Glycine max]	84	185	4.00E-48
XM_002996004	hypothetical protein [Nosema ceranae]	71	117	0.49
AC216543	clone POP015-B14 [Populus trichocarpa]	74	106	2.00E-06
AC093864	BAC clone RP11-557J10 from 4 [Homo sapiens]	83	56	0.002
XM_002274628	hypothetical protein [Vitis vinifera]	75	615	2.00E-112
XM_002314616	predicted protein [Populus trichocarpa]	85	511	4.00E-158
AY866481	pheromone-degrading enzyme 2 mRNA [Antheraea polyphemus]	89	44	0.003
JF934877	pAA56 [Cloning vector]	91	381	9.00E-154
XM_002516624	ATP-dependent clp protease ATP-binding subunit clpx [Ricinus communis]	71	553	2.00E-61
XM_002301228	predicted protein [Populus trichocarpa]	71	289	4.00E-30
AJ001304	mRNA for hypothetical protein [Citrus paradisi]	97	713	0
XM_002306471	porin/voltage-dependent anion-selective channel protein [Populus trichocarpa]	80	545	6.00E-136
XM_002314616	predicted protein [Populus trichocarpa]	85	452	6.00E-130
XM_002519842	hypothetical protein [Ricinus communis]	86	223	1.00E-65
DQ864733	chloroplast [Citrus sinensis]	99	363	2.00E-176
XM_002313279	predicted protein [Populus trichocarpa]	88	661	0
EF175924	putative DNA binding protein (V03-1) mRNA [Citrus sinensis]	75	209	9.00E-24
XM_002326267	predicted protein [Populus trichocarpa]	76	513	2.00E-93
XM_002263652	hypothetical protein [Vitis vinifera]	81	560	1.00E-140
XM_002514231	hypothetical protein [Ricinus communis]	75	831	1.00E-152

IP : 14.49.138.138, 2017-11-03 13:30:33

AE014185	3D7 chromosome 10 [Plasmodium falciparum]	81	56	0.51
AF369931	lipid-transfer protein mRNA [Citrus sinensis]	80	413	8.00E-90
AC003101	chromosome 17 [Homo sapiens]	88	40	0.042
XM_002309747	predicted protein [Populus trichocarpa]	91	211	3.00E-75
FQ394196	clone SS0AFA22YB24 [Vitis vinifera]	80	145	5.00E-27
XM_002284076	hypothetical protein [Vitis vinifera]	72	605	9.00E-79
CU468326	DNA sequence from clone CH242-208H7 on chromosome X [Pig]	100	24	0.29
XM_002310160	predicted protein [Populus trichocarpa]	74	355	3.00E-47
BC155773	vacuolar protein sorting 26 homolog A (yeast) [Danio rerio]	94	47	1.00E-09
DQ166521	putative 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase 3 mRNA [Fagus sylvatica]	86	580	0
AM910990	strain H chromosome 8 [Plasmodium knowlesi]	84	56	3.00E-06
AB007819	glycine-rich RNA-binding protein [Citrus unshiu]	96	158	2.00E-64
FQ386279	clone SS0AEB2YH24 [Vitis vinifera]	83	991	0
EU024484	rapid alkalinization factor precursor [Litchi chinensis]	79	408	9.00E-83
XM_002316746	predicted protein [Populus trichocarpa]	75	462	6.00E-73
AE014186	3D7 chromosome 11 [Plasmodium falciparum]	80	67	0.002
DQ864733	chloroplast [Citrus sinensis]	96	609	0
EF520737	O-methyltransferase mRNA [Citrus sinensis x Citrus reticulata]	95	711	0
AC239143	BAC clone 22E07 [Carica papaya]	74	149	6.00E-14
AK227380	hypothetical protein [Arabidopsis thaliana]	83	288	2.00E-72
DQ864733	chloroplast [Citrus sinensis]	99	365	1.00E-179
AC239143	BAC clone 22E07 [Carica papaya]	76	122	7.00E-13
FJ971058	plasma intrinsic protein 2;5 [Juglans regia]	85	573	5.00E-176
AC164123	BAC clone RP24-390M17 from chromosome 9 [Mus musculus]	80	60	0.001
XM_002275489	hypothetical protein [Vitis vinifera]	80	1031	0
FJ356252	elongation factor-like mRNA [Citrus maxima]	94	588	0
XM_002313665	predicted protein [Populus trichocarpa]	73	468	3.00E-65
EU599222	aquaporin (AQP) gene [Manihot esculenta]	84	629	0
EF144256	unknown [Populus trichocarpa]	87	955	0
FQ378026	mitochondrion [Beta macrocarpa]	99	184	1.00E-86
XM_002321821	cytochrome P450 [Populus trichocarpa]	70	653	5.00E-70
AB007818	gene for glycine-rich protein [Citrus unshiu]	99	319	2.00E-157
X05910	cistron for 26S ribosomal RNA [Citrus limon]	98	368	1.00E-172
XM_001138482	uncharacterized protein C9orf68-like [Pan troglodytes]	94	29	0.16
AC140221	BAC clone RP23-281K10 [Mus musculus]	89	34	0.43
AC165951	BAC clone RP24-137B13 [Mus musculus]	85	57	1.00E-06
FN568061	microsatellite DNA [Schizothorax richardsonii]	85	485	8.00E-137
FN568061	microsatellite DNA [Schizothorax richardsonii]	74	424	2.00E-43
FJ971058	plasma intrinsic protein 2;5 Juglans regia]	85	575	8.00E-180
EF175924	putative DNA binding protein (V03-1) mRNA [Citrus sinensis]	75	209	9.00E-24

IP : 14.49.138.138, 2017-11-03 13:30:33

CP002913	XI [Methanococcus maripaludis]	90	38	0.3
AP010403	genomic DNA [Lotus japonicus]	80	170	3.00E-32
CT033766	mth4-42c9 [Medicago truncatula]	81	56	0.002
JF430587	pDC-KHT [Cloning vector]	91	474	1.00E-166
FJ971058	plasma intrinsic protein 2;5 [Juglans regia]	85	483	2.00E-150
CP002582	DSM 5427 [Clostridium lentocellum]	97	27	0.14
AC140221	BAC clone RP23-281K10 [Mus musculus]	89	34	0.43
XM_002284264	hypothetical protein [Vitis vinifera]	76	602	2.00E-106
FR692356	microsatellite DNA [Citrus reshni]	97	309	8.00E-141
BC099789	cDNA clone [Rattus norvegicus]	96	44	2.00E-09
AF320905	metallothionein-like protein (MT45) mRNA [Citrus unshiu]	99	551	0
XM_002320832	predicted protein [Populus trichocarpa]	78	651	4.00E-134
AY008435	S-adenosyl-L-methionine:jasmonic acid carboxyl methyltransferase (JMT) gene [Arabidopsis thaliana]	92	37	9.00E-06
XM_003517188	uncharacterized protein [Glycine max]	95	55	3.00E-13
XM_002511787	Remorin [Ricinus communis]	77	542	1.00E-108
XM_002326679	predicted protein [Populus trichocarpa]	89	763	0
CP002686	chromosome 3 [Arabidopsis thaliana]	100	20	0.76
EF126560	atpB-rbcL intergenic spacer [Oxanthera sp.]	100	334	2.00E-169
JF729202	ecotype Landsberg erecta mitochondrion [Arabidopsis thaliana]	99	181	4.00E-84
FQ378967	clone SS0AEB11YN22 [Vitis vinifera]	79	680	1.00E-146
FQ378026	mitochondrion [Beta macrocarpa]	99	252	3.00E-122
XM_003417055	zinc finger homeobox 3 (ZFHX3) [Loxodonta africana]	73	102	0.018
AC106873	BAC clone RP11-374M7 from 7 [Homo sapiens]	89	43	0.005
CP002686	chromosome 3 [Arabidopsis thaliana]	93	26	0.079
AM906072	putative metallotionein [Citrus medica]	96	245	5.00E-104
CP002688	chromosome 5 [Arabidopsis thaliana]	96	24	0.99
XM_003543233	organic cation transporter protein-like [Glycine max]	76	336	2.00E-55
CP002685	chromosome 2 [Arabidopsis thaliana]	96	22	3
EF175924	putative DNA binding protein (V03-1) mRNA [Citrus sinensis]	72	333	1.00E-33
AM474008	contig VV78X064218.12 [Vitis vinifera]	75	184	2.00E-20
FQ397517	clone SS0AEB6YI22 [Vitis vinifera]	75	132	8.00E-14
XM_002284264	hypothetical protein [Vitis vinifera]	76	601	3.00E-104
AF283532	paradisi miraculin-like protein mRNA [Citrus x]	99	592	0
XM_002322742	predicted protein [Populus trichocarpa]	87	452	7.00E-148
XM_002301818	predicted protein [Populus trichocarpa]	75	746	3.00E-135
AK378472	mRNA [Bombyx mori]	96	49	9.00E-11
XM_002284264	hypothetical protein [Vitis vinifera]	75	614	6.00E-100
FQ394010	clone SS0AFA23YB07 [Vitis vinifera]	88	642	0
XM_002531546	ribosomal protein S28 [Ricinus communis]	85	210	6.00E-59
FQ378026	mitochondrion [Beta macrocarpa]	93	188	2.00E-71

IP : 14.49.138.138, 2017-11-03 13:30:33

EF126532	voucher RJB GH06-122 atpB-rbcL intergenic spacer [Citrus myrtifolia]	99	449	0
FQ380516	clone SS0ACG53YH11 [Vitis vinifera]	93	54	6.00E-12
AP009383	genomic DNA [Lotus japonicus]	83	768	0
CP002688	chromosome 5 [Arabidopsis thaliana]	88	31	0.27
XM_002517182	ATP synthase epsilon chain [Ricinus communis]	83	233	2.00E-59
XM_002264149	hypothetical protein [Vitis vinifera]	83	233	9.00E-58
FJ825754	calmodulin (Cam) mRNA [Panax ginseng]	90	448	5.00E-164
AF194001	small subunit ribosomal RNA (mtSSU) gene [Crossosoma bigelovii]	96	1091	0
FQ389288	clone SS0AEB20YE23 [Vitis vinifera]	80	323	2.00E-73
FQ383946	clone SS0AAG6YP01 [Vitis vinifera]	76	258	8.00E-41
XM_002284176	hypothetical protein [Vitis vinifera]	76	520	4.00E-93
AF506028	citrus tristeza virus resistance gene locus [Poncirus trifoliata]	92	256	1.00E-94
FQ378026	mitochondrion [Beta macrocarpa]	100	183	1.00E-87
AB081944	RlemAchiI mRNA for acidic class I chitinase [Citrus jambhiri]	94	938	0
XM_002332325	predicted protein [Populus trichocarpa]	82	726	0
XM_002512787	hypothetical protein [Ricinus communis]	67	779	8.00E-48
XM_002310976	predicted protein [Populus trichocarpa]	85	324	1.00E-95
FQ387152	clone SS0AEB27YI08 [Vitis vinifera]	79	788	3.00E-173
XM_002525056	xaa-pro aminopeptidase [Ricinus communis]	80	515	9.00E-122
CU231309	EST from mild drought-stressed leaves [Populus]	89	95	2.00E-24
AK338074	cDNA [Lotus japonicus]	78	838	2.00E-176
XM_003519782	uncharacterized protein [Glycine max]	71	827	5.00E-101
XM_002514584	Cleavage stimulation factor 50 kDa subunit [Ricinus communis]	84	206	1.00E-51
EF146374	unknown mRNA [Populus trichocarpa]	75	511	3.00E-84
AY198376	chlorophyll a/b-binding protein precursor [Citrus limon]	98	520	0
EF147148	clone WS01228_E06 unknown mRNA [Populus trichocarpa]	90	449	7.00E-169
AY221088	cellulose synthase (StCesA4) mRNA [Solanum tuberosum]	81	67	1.00E-04
CU231309	EST from mild drought-stressed leaves [Populus]	89	95	2.00E-24
XM_002509683	60S ribosomal protein L24 [Ricinus communis]	88	493	1.00E-169
XM_002518482	Xyloglucan endotransglucosylase/hydrolase protein A precursor [Ricinus communis]	84	881	0
FQ393279	clone SS0AFA26YM15 [Vitis vinifera]	83	679	0
XM_002518373	NSFL1 cofactor p47 [Ricinus communis]	79	408	2.00E-90
XM_002518373	NSFL1 cofactor p47 [Ricinus communis]	79	409	2.00E-90
AF369931	lipid-transfer protein mRNA [Citrus sinensis]	81	413	3.00E-95
EF122398	Shiranuhi putative auxin-repressed/dormancy-associated protein mRNA [Citrus cv.]	99	369	0
NM_001053427	Japonica Group Os02g0496900 (Os02g0496900) mRNA [Oryza sativa]	86	154	3.00E-38
EF175926	putative DNA binding protein (V03-2) mRNA [Citrus sinensis]	72	439	1.00E-40
XM_002325814	predicted protein [Populus trichocarpa]	78	595	4.00E-126
NM_001053427	Japonica Group Os02g0496900 (Os02g0496900) mRNA [Oryza sativa]	86	154	3.00E-38
EF122398	Shiranuhi putative auxin-repressed/dormancy-associated protein mRNA	99	369	0

IP : 14.49.138.138, 2017-11-03 13:30:33

	[Citrus cv.]			
EF146402	clone WS0117_O21 unknown mRNA [Populus trichocarpa]	75	371	2.00E-58
XM_002519010	rnf5 [Ricinus communis]	75	737	4.00E-128
AF312228	ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit precursor [Citrus reticulata]	98	354	7.00E-168
XM_002319088	predicted protein [Populus trichocarpa]	80	834	0
XM_002515184	ADP-ribosylation factor [Ricinus communis]	84	762	0
XM_002322367	predicted protein [Populus trichocarpa]	73	601	5.00E-82
XM_002306063	predicted protein [Populus trichocarpa]	72	776	1.00E-101
AC216543	clone POP015-B14 [Populus trichocarpa]	75	102	6.00E-07
NM_001248909	uncharacterized [Glycine max]	82	327	5.00E-80
AM906072	putative metallotionein (mt gene) [Citrus medica]	96	245	2.00E-102
XM_002264149	hypothetical protein [Vitis vinifera]	83	233	9.00E-58
DQ864733	chloroplast [Citrus sinensis]	99	324	2.00E-158
NM_001156243	protein Mo25 (LOC100283342) [Zea mays]	98	80	7.00E-29
XM_002533881	protein binding protein [Ricinus communis]	92	157	3.00E-55
X65320	pCAT-Promoter [Cloning vector]	96	556	0
XM_002273611	hypothetical protein [Vitis vinifera]	77	123	7.00E-13
AC216543	clone POP015-B14 [Populus trichocarpa]	75	106	1.00E-07
HQ268025	eukaryotic translation initiation factor 3 mRNA [Hevea brasiliensis]	85	408	2.00E-119
XM_002284264	hypothetical protein [Vitis vinifera]	76	601	3.00E-104
XM_002524613	hypothetical protein [Ricinus communis]	83	564	4.00E-159
GU363534	americana isolate mt67326 mitochondrial sequence [Fragaria vesca sp.]	94	918	0
XM_002305960	high mobility group family (HMGB914) [Populus trichocarpa]	83	314	7.00E-80
FQ378026	mitochondrion [Beta macrocarpa]	100	179	2.00E-85
XM_002319060	predicted protein [Populus trichocarpa]	78	722	2.00E-157
XM_002301333	predicted protein [Populus trichocarpa]	74	555	3.00E-91
Z46824	mRNA for Lea5 protein [C. sinensis]	99	588	0
Z46824	mRNA for Lea5 protein [C. sinensis]	99	588	0
EF145997	clone WS0114_M21 unknown mRNA [Populus trichocarpa]	74	572	1.00E-88
XM_002302724	predicted protein [Populus trichocarpa]	76	446	2.00E-80
XM_002316832	predicted protein [Populus trichocarpa]	87	392	3.00E-127
AC215419	chromosome 2 clone C02HBa0204D01 [Solanum lycopersicum]	82	122	2.00E-20
XM_002514476	ATP binding protein [Ricinus communis]	86	952	0
EF122398	Shiranuhi putative auxin-repressed/dormancy-associated protein mRNA [Citrus cv.]	99	369	9.00E-180
XM_002327618	predicted protein [Populus trichocarpa]	81	262	1.00E-59
FQ378026	mitochondrion [Beta macrocarpa]	100	183	1.00E-87
XM_002511827	ER glycerol-phosphate acyltransferase [Ricinus communis]	81	614	2.00E-156
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	179	2.00E-85
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	99	179	6.00E-84
AC090712	strain C57BL6/J chromosome 6 clone RP23-230F22 [Mus musculus]	92	36	0.002

IP : 14.49.138.138, 2017-11-03 13:30:33

EF146374	unknown mRNA [Populus trichocarpa]	77	296	2.00E-50
AB168838	testis cDNA [Macaca fascicularis]	88	123	1.00E-34
XM_002509736	AMP dependent CoA ligase [Ricinus communis]	77	109	6.00E-11
FQ394333	clone SS0AFA21YF07 [Vitis vinifera]	72	287	8.00E-29
XM_002509736	AMP dependent CoA ligase [Ricinus communis]	77	108	4.00E-13
EU717678	GAST-like protein mRNA [Litchi chinensis]	76	323	6.00E-53
EF122401	putative H-type thioredoxin mRNA [Citrus cv. Shiranuhi]	100	360	0
CU224107	EST from leave [Populus]	77	384	1.00E-69
XM_002279033	hypothetical protein [Vitis vinifera]	74	737	1.00E-120
EF175925	putative DNA binding protein (V03-3) mRNA [Citrus sinensis]	72	326	2.00E-26
FQ394333	clone SS0AFA21YF07 [Vitis vinifera]	70	231	6.00E-17
XM_002328538	predicted protein [Populus trichocarpa]	86	791	0
X73156	polyubiquitin repeats [L. esculentum]	86	148	4.00E-38
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	181	1.00E-86
XM_002306592	predicted protein [Populus trichocarpa]	72	846	2.00E-119
XM_002281882	hypothetical protein [Vitis vinifera]	77	265	3.00E-45
XM_002326859	predicted protein [Populus trichocarpa]	70	397	3.00E-30
FQ378026	mitochondrion [Beta macrocarpa]	99	252	7.00E-124
AY160772	paradisi dehydrin mRNA [Citrus x]	93	363	5.00E-153
XM_002527741	clathrin assembly protein [Ricinus communis]	76	262	5.00E-41
XM_002528476	disulfide oxidoreductase [Ricinus communis]	81	593	3.00E-155
AC244191	Y Chr BAC RNAEX-139A07 (Amplicon Express Rat SHR-Akr BAC library) complete sequence [Rattus norvegicus]	92	35	0.016
AC244191	Y Chr BAC RNAEX-139A07 (Amplicon Express Rat SHR-Akr BAC library) complete sequence [Rattus norvegicus]	92	35	0.016
XM_002283389	hypothetical protein [Vitis vinifera]	74	352	7.00E-48
XM_002307225	predicted protein [Populus trichocarpa]	82	95	1.00E-13
GQ221686	UDP-glucosyltransferase family 1 protein (UGT1) gene [Citrus sinensis]	97	996	0
XM_002520530	UDP-glucosyltransferase [Ricinus communis]	75	660	1.00E-108
FQ378026	mitochondrion [Beta macrocarpa]	99	183	5.00E-86
XM_002325178	predicted protein [Populus trichocarpa]	82	776	0
XM_002521075	hypothetical protein [Ricinus communis]	79	502	1.00E-113
EF145633	unknown mRNA [Populus trichocarpa]	82	225	4.00E-54
X05910	cistron for 26S ribosomal RNA [Citrus limon]	99	358	3.00E-174
XM_003595057	Plasma membrane calcium-transporting ATPase (MTR_2g038310) [Medicago truncatula]	78	325	1.00E-62
XM_002527741	clathrin assembly protein [Ricinus communis]	76	261	1.00E-41
AC244191	Y Chr BAC RNAEX-139A07 (Amplicon Express Rat SHR-Akr BAC library) complete sequence [Rattus norvegicus]	92	35	0.015
AY198376	chlorophyll a/b-binding protein precursor [Citrus limon]	98	647	0
FQ387945	clone SS0AEB24YM02 [Vitis vinifera]	77	467	4.00E-88
XM_003245863	HEAT repeat-containing protein 7A-like [Acyrthosiphon pisum]	89	35	0.089
XM_002329866	predicted protein [Populus trichocarpa]	82	443	1.00E-118
XM_002327941	predicted protein [Populus trichocarpa]	83	466	4.00E-132

IP : 14.49.138.138, 2017-11-03 13:30:33

XM_002309195	predicted protein [Populus trichocarpa]	74	601	1.00E-88
EF122398	Shiranuhi putative auxin-repressed/dormancy-associated protein mRNA [Citrus cv.]	99	369	0
CU224964	EST from leave [Populus]	86	357	5.00E-111
FQ378026	mitochondrion [Beta macrocarpa]	99	183	5.00E-86
CP002582	DSM 5427 [Clostridium lentocellum]	90	38	0.069
FQ378026	mitochondrion [Beta macrocarpa]	99	257	4.00E-121
FQ378026	mitochondrion [Beta macrocarpa]	100	246	1.00E-121
FQ392409	clone SS0AFA5YM07 [Vitis vinifera]	80	523	5.00E-127
AF239686	4-coumarate:coA ligase 2 [Rubus idaeus]	82	637	6.00E-170
XM_002284096	hypothetical protein [Vitis vinifera]	82	530	4.00E-146
XM_002303811	predicted protein [Populus trichocarpa]	69	450	1.00E-34
BN001303	nidulans FGSC A4 chromosome III [TPA_reasm: Aspergillus]	100	24	0.17
XM_003540351	14-3-3-like protein D-like [Glycine max]	85	795	0
XM_002306889	predicted protein [Populus trichocarpa]	93	254	1.00E-98
EF144565	clone WS01110_O01 unknown mRNA [Populus trichocarpa]	75	220	9.00E-28
DQ244772	clone 10582 mRNA sequence [Zea mays]	71	416	2.00E-46
XM_002268024	hypothetical protein [Vitis vinifera]	84	443	9.00E-127
NM_001249705	uncharacterized LOC100500089 (LOC100500089) [Glycine max]	85	532	1.00E-157
XM_002530099	Vesicle-associated membrane protein [Ricinus communis]	84	699	0
EU717697	plastid acyl carrier protein (ACP) mRNA [Camellia oleifera]	79	443	1.00E-95
XM_002278269	hypothetical protein [Vitis vinifera]	85	422	3.00E-127
XM_002304168	predicted protein [Populus trichocarpa]	79	578	8.00E-130
XM_002273467	hypothetical protein [Vitis vinifera]	81	211	6.00E-47
XM_002266850	hypothetical protein [Vitis vinifera]	70	235	3.00E-20
AC187853	clone Pop1-117C24 [Populus trichocarpa]	84	53	4.00E-04
XM_002509807	40S ribosomal protein S10 [Ricinus communis]	80	433	2.00E-104
XM_002316690	predicted protein [Populus trichocarpa]	74	532	1.00E-89
FQ388729	clone SS0AEB22YC15 [Vitis vinifera]	78	324	1.00E-63
XM_002519950	60S ribosomal protein L13 [Ricinus communis]	83	620	1.00E-178
AB008100	metallothionein-like protein [Citrus unshiu]	95	618	0
XM_002317197	predicted protein [Populus trichocarpa]	83	63	1.00E-06
XM_002285685	hypothetical protein [Vitis vinifera]	85	521	2.00E-161
XM_002269667	hypothetical protein [Vitis vinifera]	76	468	3.00E-90
XM_002285685	hypothetical protein [Vitis vinifera]	85	810	0
Z82983	thi mRNA [C. sinensis]	97	861	0
XM_002318854	predicted protein [Populus trichocarpa]	70	682	8.00E-73
XM_002517039	40S ribosomal protein S3a [Ricinus communis]	83	777	0
XM_002299458	predicted protein [Populus trichocarpa]	85	598	9.00E-179
GQ853548	cyclophilin (CYP) mRNA [Citrus sinensis]	99	578	0
AF369931	lipid-transfer protein mRNA [Citrus sinensis]	81	413	1.00E-94

IP : 14.49.138.138, 2017-11-03 13:30:33

XM_002323122	predicted protein [Populus trichocarpa]	79	113	4.00E-13
DQ023609	omega-6 fatty acid desaturase (FAD) mRNA [Hevea brasiliensis]	80	692	4.00E-171
EF122398	Shiranuhi putative auxin-repressed/dormancy-associated protein mRNA [Citrus cv.]	97	240	5.00E-107
XM_002528656	ribosomal protein S6 kinase [Ricinus communis]	82	626	1.00E-172
BA000042	mitochondrial DNA [Nicotiana tabacum]	99	893	0
XM_002324658	predicted protein [Populus trichocarpa]	72	628	2.00E-85
EF144478	unknown mRNA [Populus trichocarpa]	80	320	1.00E-74
XM_003531273	uncharacterized protein [Glycine max]	84	155	7.00E-38
EF122398	Shiranuhi putative auxin-repressed/dormancy-associated protein mRNA [Citrus cv.]	99	329	4.00E-159
XM_002284660	hypothetical protein [Vitis vinifera]	81	642	3.00E-168
FQ392971	clone SS0AFA3YF01 [Vitis vinifera]	78	686	3.00E-148
FQ381610	clone SS0ABP1YC07 [Vitis vinifera]	89	458	1.00E-165
XM_002276603	hypothetical protein [Vitis vinifera]	81	632	1.00E-164
AF318938	copper/zinc superoxide dismutase mRNA [Citrus limon]	96	693	0
EU717678	GAST-like protein mRNA [Litchi chinensis]	75	320	1.00E-48
EF553533	isopentenyl pyrophosphate isomerase mRNA [Corylus avellana]	84	574	2.00E-169
XM_002273467	hypothetical protein [Vitis vinifera]	82	212	1.00E-49
XM_002302255	predicted protein [Populus trichocarpa]	82	843	0
XM_002323867	predicted protein [Populus trichocarpa]	82	344	1.00E-88
HQ268025	eukaryotic translation initiation factor 3 mRNA [Hevea brasiliensis]	85	408	1.00E-119
FJ851401	SKP1-like protein mRNA [Citrus maxima]	99	556	0
XM_002300894	predicted protein [Populus trichocarpa]	76	233	7.00E-34
AB009351	mRNA for chalcone synthase [Citrus sinensis]	99	905	0
EF122397	Shiranuhi putative miraculin-like protein 2 mRNA [Citrus cv.]	99	219	3.00E-105
XM_002511432	DNA binding protein [Ricinus communis]	73	663	6.00E-94
FN543123	mating type locus [Dictyostelium discoideum]	97	28	0.047
AF283533	miraculin-like protein 2 mRNA [Citrus x paradisi]	99	649	0
AY830128	calmodulin (CaM) mRNA [Hevea brasiliensis]	86	447	6.00E-143
XM_002314022	silencing group B protein (SGB901) [Populus trichocarpa]	84	536	6.00E-156
XM_002277120	hypothetical protein [Vitis vinifera]	79	305	2.00E-59
XM_002323076	GRAS family transcription factor (GRAS1) [Populus trichocarpa]	85	146	1.00E-35
XM_002528547	fructose-bisphosphate aldolase [Ricinus communis]	83	240	1.00E-62
XM_002331407	predicted protein [Populus trichocarpa]	83	503	3.00E-140
XM_002307924	tubulin [Populus trichocarpa]	86	540	1.00E-176
XM_002317426	predicted protein [Populus trichocarpa]	74	518	7.00E-80
XM_002317426	predicted protein [Populus trichocarpa]	74	518	7.00E-80
EF146402	unknown mRNA [Populus trichocarpa]	84	229	1.00E-61
EF146402	unknown mRNA [Populus trichocarpa]	84	229	1.00E-61
GQ144341	2-phospho-D-glycerate hydrolase (LOS2) mRNA [Citrus trifoliata]	98	880	0
FQ378026	mitochondrion [Beta macrocarpa]	99	183	5.00E-86

IP : 14.49.138.138, 2017-11-03 13:30:33

XM_002283020	hypothetical protein [Vitis vinifera]	87	715	0
EF175926	putative DNA binding protein (V03-2) mRNA [Citrus sinensis]	72	229	3.00E-22
DQ424890	group 5 late embryogenesis abundant protein (LEA5) mRNA [Citrus unshiu]	99	584	0
EF146402	clone WS0117_O21 unknown mRNA [Populus trichocarpa]	84	229	1.00E-61
AF320905	metallothionein-like protein (MT45) mRNA [Citrus unshiu]	97	550	0
DQ889532	clone 1Y22 gibberellin-regulated protein mRNA [Arachis hypogaea]	79	329	5.00E-68
AY327515	COR15 mRNA [Citrus clementina x Citrus reticulata]	97	732	0
XM_002527076	oxidoreductase [Ricinus communis]	76	789	4.00E-153
EU703623	S-adenosylmethionine synthetase mRNA [Panax ginseng]	81	602	4.00E-158
XM_002319955	predicted protein [Populus trichocarpa]	84	653	0
XM_002509866	50S ribosomal protein L18 [Ricinus communis]	86	367	6.00E-111
FQ387365	clone SS0AEB26YL13 [Vitis vinifera]	84	462	1.00E-132
XM_002325090	predicted protein [Populus trichocarpa]	71	583	9.00E-65
AF283536	paradisi cystatin-like protein mRNA [Citrus x]	99	509	0
AF320905	metallothionein-like protein (MT45) mRNA [Citrus unshiu]	99	531	0
AF283536	paradisi cystatin-like protein mRNA [Citrus x]	99	506	0
FQ378026	mitochondrion [Beta macrocarpa]	99	185	4.00E-87
XM_002310525	predicted protein [Populus trichocarpa]	85	349	7.00E-104
EF146402	unknown mRNA [Populus trichocarpa]	84	229	1.00E-61
XM_002510531	skp1 [Ricinus communis]	83	481	2.00E-131
XM_003525237	NADP-dependent malic enzyme-like [Glycine max]	86	556	0
FQ378026	mitochondrion [Beta macrocarpa]	97	248	2.00E-110
EF146402	unknown mRNA [Populus trichocarpa]	84	229	1.00E-61
XM_002307442	predicted protein [Populus trichocarpa]	80	674	2.00E-163
XM_003570330	60S ribosomal protein L23-like [Brachypodium distachyon]	89	431	3.00E-152
EF146374	unknown mRNA [Populus trichocarpa]	75	512	1.00E-86
AM448318	whole genome shotgun sequence [Vitis vinifera,]	84	396	2.00E-111
XM_002311825	predicted protein [Populus trichocarpa]	84	661	0
XM_002316511	predicted protein [Populus trichocarpa]	81	560	6.00E-144
XM_002528972	Glycine-rich protein DC7.1 precursor [Ricinus communis]	86	95	7.00E-20
XM_002323122	predicted protein [Populus trichocarpa]	79	113	4.00E-13
EF175926	putative DNA binding protein (V03-2) mRNA [Citrus sinensis]	72	446	4.00E-41
XM_002310888	outward rectifying potassium channel [Populus trichocarpa]	72	753	2.00E-100
XM_002527076	oxidoreductase [Ricinus communis]	76	860	4.00E-159
XM_002283020	hypothetical protein [Vitis vinifera]	87	715	0
AF283533	paradisi miraculin-like protein 2 mRNA [Citrus x]	99	838	0
XM_002515978	30S ribosomal protein S17 [Ricinus communis]	84	202	2.00E-51
FQ378026	mitochondrion [Beta macrocarpa]	99	183	5.00E-86
XM_002322742	predicted protein [Populus trichocarpa]	87	452	7.00E-148
XM_002336774	cytochrome P450 (CYP82C8v1) [Populus trichocarpa]	71	309	1.00E-29

IP : 14.49.138.138, 2017-11-03 13:30:33

AF283536	cystatin-like protein mRNA [Citrus x paradisi]	99	506	0
AP007150	RIB40 DNA [Aspergillus oryzae]	97	27	0.1
XM_002328654	predicted protein [Populus trichocarpa]	81	519	6.00E-137
EF122398	Shiranuhi putative auxin-repressed/dormancy-associated protein mRNA [Citrus cv.]	99	369	0
XM_002302249	predicted protein [Populus trichocarpa]	81	998	0
X65320	pCAT-Promoter [Cloning vector]	98	714	0
FQ397517	clone SS0AEB6YI22 [Vitis vinifera]	75	132	1.00E-13
XM_002307924	tubulin [Populus trichocarpa]	86	930	0
XM_002272151	hypothetical protein [Vitis vinifera]	79	697	1.00E-152
GQ890686	ubiquitin mRNA [Guzmania wittmackii]	90	678	0
FQ388800	clone SS0AEB21YN14 [Vitis vinifera]	83	242	2.00E-58
XM_002318899	predicted protein [Populus trichocarpa]	91	549	0
FQ397517	clone SS0AEB6YI22 [Vitis vinifera]	75	132	1.00E-13
DQ864733	chloroplast [Citrus sinensis]	99	406	0
XM_002270671	hypothetical protein [Vitis vinifera]	75	244	7.00E-35
FQ382413	clone SS0ABG58YI09 [Vitis vinifera]	79	884	0
AM851105	microsatellite DNA [Theobroma cacao]	79	785	2.00E-168
AF024716	histone 3 mRNA [Gossypium hirsutum]	83	413	7.00E-118
FQ388467	clone SS0AEB23YB08 [Vitis vinifera]	88	478	4.00E-164
XM_002327620	predicted protein [Populus trichocarpa]	71	464	5.00E-44
AY177420	26S ribosomal RNA gene [Citrus aurantium]	99	329	3.00E-161
XM_003543528	uncharacterized protein [Glycine max]	78	504	7.00E-100
XM_002336774	cytochrome P450 (CYP82C8v1) [Populus trichocarpa]	71	309	1.00E-29
XM_002317745	predicted protein [Populus trichocarpa]	67	945	8.00E-62
AF506028	citrus tristeza virus resistance gene locus [Poncirus trifoliata]	70	316	8.00E-22
XM_002323819	predicted protein [Populus trichocarpa]	80	331	5.00E-74
XM_002308916	predicted protein [Populus trichocarpa]	75	669	7.00E-118
AF283533	miraculin-like protein 2 mRNA [Citrus x paradisi]	99	837	0
EF122398	Shiranuhi putative auxin-repressed/dormancy-associated protein mRNA [Citrus cv.]	99	369	0
FQ378026	mitochondrion [Beta macrocarpa]	99	183	5.00E-86
HQ615689	actin (ACT) mRNA [Litchi chinensis]	92	839	0
XM_002323122	predicted protein [Populus trichocarpa]	79	113	5.00E-13
XM_002300743	predicted protein [Populus trichocarpa]	87	454	1.00E-151
XM_002517611	hypothetical protein [Ricinus communis]	73	666	3.00E-98
XM_002521514	rer1 protein [Ricinus communis]	79	520	5.00E-120
NG_009102	phosphodiesterase 6A [Homo sapiens]	94	33	0.018
XM_002323819	predicted protein [Populus trichocarpa]	81	331	1.00E-75
AC142498	clone mth2-24a18 [Medicago truncatula]	98	70	9.00E-24
AB218610	CitMADS1 mRNA for MADS-box protein [Citrus unshiu]	99	738	0
XM_002266850	hypothetical protein [Vitis vinifera]	72	237	9.00E-26

IP : 14.49.138.138, 2017-11-03 13:30:33

XM_002272976	hypothetical protein [Vitis vinifera]	71	983	4.00E-109
FQ378026	mitochondrion [Beta macrocarpa]	99	134	2.00E-57
AL928758	chromosome 12 [Oryza sativa]	100	25	0.031
GQ890686	ubiquitin mRNA [Guzmania wittmackii]	90	678	0
GQ398765	microsatellite CL50 sequence [Calopogonium mucunoides]	81	139	3.00E-24
FQ378026	mitochondrion [Beta macrocarpa]	100	250	7.00E-124
FJ825754	calmodulin (Cam) mRNA [Panax ginseng]	88	448	2.00E-155
GQ451654	putative translocon-associated protein alpha subunit mRNA [Jatropha curcas]	84	778	0
L39006	(clone CORc410) cold stress protein mRNA [Poncirus trifoliata]	96	249	5.00E-107
AY160772	dehydrin mRNA [Citrus x paradisi]	97	996	0
AM458981	contig VV78X211450.17 [Vitis vinifera]	81	630	3.00E-166
AC131386	chromosome 5 clone CTD-3179P9 [Homo sapiens]	97	27	0.37
EF122397	Shiranuhi putative miraculin-like protein 2 mRNA [Citrus cv.]	99	642	0
XM_002305707	predicted protein [Populus trichocarpa]	77	936	0
NM_001248604	uncharacterized [Glycine max]	85	414	6.00E-124
XM_002322948	predicted protein [Populus trichocarpa]	76	360	1.00E-62
GQ853548	cultivar Pera cyclophilin (CYP) mRNA [Citrus sinensis]	99	578	0
XM_002330540	predicted protein [Populus trichocarpa]	88	447	5.00E-157
XM_003525237	NADP-dependent malic enzyme-like [Glycine max]	87	556	0
XM_002520770	hypothetical protein [Ricinus communis]	67	524	5.00E-31
X64344	mRNA Pcubi4-1 for polyubiquitin [P. crispum]	90	109	5.00E-32
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	179	2.00E-85
X05910	cistron for 26S ribosomal RNA [Citrus limon]	89	312	3.00E-86
XM_002513902	hypothetical protein [Ricinus communis]	75	817	4.00E-147
HQ268023	eukaryotic translation initiation factor 1Ab mRNA [Hevea brasiliensis]	88	444	2.00E-155
AY259227	S-adenosylmethionine synthetase (SAMS) mRNA [Litchi chinensis]	84	795	0
XM_002306264	predicted protein [Populus trichocarpa]	88	255	2.00E-79
JF430587	pDC-KHT [Cloning vector]	98	613	0
FQ378026	mitochondrion [Beta macrocarpa]	99	183	5.00E-86
DQ424891	group 5 late embryogenesis abundant protein (LEA5) gene [Citrus unshiu]	97	212	6.00E-92
AB008100	metallothionein-like protein [Citrus unshiu]	93	596	0
FQ395642	clone SS0AFA14YN09 [Vitis vinifera]	71	434	5.00E-50
JF430587	pDC-KHT [Cloning vector]	97	591	0
XM_002306380	predicted protein [Populus trichocarpa]	88	717	0
XM_002334484	predicted protein [Populus trichocarpa]	78	142	2.00E-21
XM_002528972	Glycine-rich protein DC7.1 precursor [Ricinus communis]	86	95	7.00E-20
AK245941	cDNA [Glycine max]	73	229	2.00E-23
XM_002267781	hypothetical protein [Vitis vinifera]	84	924	0
FP245400	DNA sequence from clone CH242-512I21 on chromosome X [Pig]	90	37	0.56
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	180	4.00E-86

IP : 14.49.138.138, 2017-11-03 13:30:33

XM_002285685	hypothetical protein [Vitis vinifera]	85	895	0
AY327515	x Citrus reticulata COR15 mRNA [Citrus clementina]	97	731	0
EF122398	Shiranuhi putative auxin-repressed/dormancy-associated protein mRNA [Citrus cv.]	99	369	8.00E-180
AF369931	lipid-transfer protein mRNA [Citrus sinensis]	81	413	3.00E-95
FQ393928	clone SS0AFA23YH16 [Vitis vinifera]	89	606	0
XM_002310960	predicted protein [Populus trichocarpa]	82	501	1.00E-134
XM_002531546	ribosomal protein S28 [Ricinus communis]	86	210	4.00E-61
EU223835	low molecular weight heat shock protein (LMWHSP4) mRNA [Gossypium hirsutum]	79	436	1.00E-95
XM_002269942	hypothetical protein [Vitis vinifera]	84	620	3.00E-167
FQ381769	clone SS0ABG84YH08 [Vitis vinifera]	88	232	3.00E-73
XM_002311051	predicted protein [Populus trichocarpa]	82	304	4.00E-75
FQ378026	mitochondrion [Beta macrocarpa]	95	170	4.00E-68
XM_002525277	oligopeptide transporter [Ricinus communis]	81	817	0
FQ378026	mitochondrion [Beta macrocarpa]	99	176	2.00E-82
XM_002523947	Aspartic proteinase nepenthesin-1 precursor [Ricinus communis]	66	790	7.00E-37
EF175927	putative DNA binding protein (V03-4) mRNA [Citrus sinensis]	73	331	2.00E-38
EF122401	Shiranuhi putative H-type thioredoxin mRNA [Citrus cv.]	100	360	0
AY465906	sterol delta-7 reductase [Tropaeolum majus]	84	686	0
HM003258	clone U10BCDNA 2736 hypothetical protein mRNA [Camellia sinensis]	83	279	8.00E-71
FQ393928	clone SS0AFA23YH16 [Vitis vinifera]	85	536	2.00E-162
HQ615689	actin (ACT) mRNA [Litchi chinensis]	90	972	0
XM_002306671	predicted protein [Populus trichocarpa]	81	558	4.00E-140
XM_002280183	hypothetical protein [Vitis vinifera]	82	216	2.00E-48
AB601114	hypothetical protein [Vitis hybrid]	81	225	3.00E-49
AL928966	DNA sequence from clone RP24-388A9 on chromosome 2 Contains the Olfr1113 gene for olfactory receptor 1113 [Mouse]	89	42	0.002
XM_002318311	predicted protein [Populus trichocarpa]	85	764	0
XM_002322400	predicted protein [Populus trichocarpa]	79	888	0
AF320905	metallothionein-like protein (MT45) mRNA [Citrus unshiu]	93	532	0
XM_002309248	predicted protein [Populus trichocarpa]	73	174	6.00E-15
XM_002307178	predicted protein [Populus trichocarpa]	76	554	2.00E-106
XM_002530972	ADP-ribosylation factor [Ricinus communis]	88	272	5.00E-90
CU179672	DNA sequence from clone CH242-371G3 on chromosome 4 [Pig]	80	65	9.00E-05
AM442845	contig VV78X064871.6 [Vitis vinifera]	88	473	4.00E-164
XM_002310324	predicted protein [Populus trichocarpa]	78	787	7.00E-164
AY534617	HMG-CoA synthase 2 (HMGS2) mRNA [Hevea brasiliensis]	83	805	0
XM_002514966	cytochrome P450 [Ricinus communis]	73	310	3.00E-42
DQ864733	chloroplast [Citrus sinensis]	99	542	0
FQ378026	mitochondrion [Beta macrocarpa]	99	184	1.00E-86
XM_002265476	hypothetical protein [Vitis vinifera]	82	402	6.00E-105
XM_002515435	hypothetical protein [Ricinus communis]	81	560	3.00E-142

IP : 14.49.138.138, 2017-11-03 13:30:33

XM_002323076	GRAS family transcription factor (GRAS1) [Populus trichocarpa]	85	146	1.00E-35
DQ864733	chloroplast [Citrus sinensis]	99	542	0
EF144899	unknown mRNA [Populus trichocarpa]	83	113	3.00E-21
GQ995665	voucher Salinas & Tenorio 5843 (MICH) clone 6 psbA-trnH intergenic spacer [Ruellia speciosa]	79	57	0.036
XM_003518958	uncharacterized protein [Glycine max]	86	113	2.00E-27
XM_002330863	predicted protein [Populus trichocarpa]	77	438	3.00E-83
XM_002280952	hypothetical protein [Vitis vinifera]	71	518	1.00E-57
AC078868	3 BAC RP11-758B20 (Roswell Park Cancer Institute Human BAC Library) complete sequence [Homo sapiens]	94	30	0.087
CP002582	DSM 5427 [Clostridium lentocellum]	90	38	0.068
XM_002314814	predicted protein [Populus trichocarpa]	86	693	0
AY217785	subtilase (cg12) gene [Casuarina glauca]	75	101	9.00E-08
HM003240	clone U10BCDNA 1298 ribosomal petrp-like protein mRNA [Camellia sinensis]	86	528	4.00E-171
FQ378026	mitochondrion [Beta macrocarpa]	100	183	1.00E-87
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	179	2.00E-85
EF122397	Shiranuhi putative miraculin-like protein 2 mRNA [Citrus cv.]	99	643	0
AY177421	26S ribosomal RNA gene [Bursera inaguensis]	100	171	3.00E-81
XM_002517332	calmodulin binding protein [Ricinus communis]	78	552	3.00E-117
XM_002269681	hypothetical protein [Vitis vinifera]	79	635	4.00E-141
EU717678	GAST-like protein mRNA [Litchi chinensis]	76	320	1.00E-54
XM_002514018	hypothetical protein [Ricinus communis]	76	346	3.00E-57
AC213153	clone POP047-O16 [Populus trichocarpa]	83	74	3.00E-08
FQ381288	clone SS0ACG13YK06 [Vitis vinifera]	79	653	1.00E-153
XM_002521514	rer1 protein [Ricinus communis]	79	520	6.00E-120
FJ362591	60s ribosome protein L19 (RPL19B) mRNA [Vernicia fordii]	82	646	8.00E-168
AM474507	contig VV78X220546.3 [Vitis vinifera]	73	291	4.00E-33
DQ223001	temperature-induced lipocalin (TIL) mRNA [Citrus sinensis]	99	561	0
X61030	mitochondrion rps19 and rps3 (exon 1) genes for ribosomal protein S19 and ribosomal protein S3 [O. berteriana]	86	174	1.00E-48
AK342129	mRNA [Acyrthosiphon pisum]	84	65	3.00E-07
EF148536	unknown mRNA [Populus trichocarpa]	81	705	0
AY327515	COR15 mRNA [Citrus clementina]	94	728	0
JF754917	isolate CLM134-NW cytochrome oxidase subunit 1 (COI) gene [Bemisia tabaci]	89	35	0.68
XM_002300894	predicted protein [Populus trichocarpa]	74	119	8.00E-06
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	180	4.00E-86
XM_002894326	lyrata 60S ribosomal protein L37 [Arabidopsis lyrata sp.]	84	302	5.00E-86
AB009351	mRNA for chalcone synthase [Citrus sinensis]	99	1117	0
BC072690	cardiotrophin 1 [Rattus norvegicus]	97	32	4.00E-04
AY026338	non-symbiotic hemoglobin class 1 (Glb1) mRNA [Citrus unshiu]	98	813	0
XM_002518124	Inhibitor of growth protein [Ricinus communis]	84	453	6.00E-131
XM_002297778	predicted protein [Populus trichocarpa]	80	77	1.00E-07
XM_002330328	predicted protein [Populus trichocarpa]	86	972	0

IP : 14.49.138.138, 2017-11-03 13:30:33

HM003293	hypothetical protein [Camellia sinensis]	72	348	8.00E-38
XM_002284264	hypothetical protein [Vitis vinifera]	75	506	2.00E-82
XM_002334122	predicted protein [Populus trichocarpa]	69	727	2.00E-63
XM_002308064	predicted protein [Populus trichocarpa]	79	839	0
XM_002531510	Hsp70-binding protein [Ricinus communis]	79	850	0
XM_002326459	predicted protein [Populus trichocarpa]	74	704	7.00E-113
EF122398	Shiranuhi putative auxin-repressed/dormancy-associated protein mRNA [Citrus cv.]	99	369	0
Z46824	mRNA for Lea5 protein [C. sinensis]	99	591	0
XM_002317254	predicted protein [Populus trichocarpa]	81	818	0
HQ588866	actin (ACT7) mRNA [Litchi chinensis]	77	809	2.00E-162
FQ378026	mitochondrion [Beta macrocarpa]	97	163	2.00E-71
XM_002529102	Transmembrane protein TPARL [Ricinus communis]	83	738	0
XM_002308921	predicted protein [Populus trichocarpa]	78	693	3.00E-155
XM_002308921	predicted protein [Populus trichocarpa]	75	453	3.00E-82
XM_002518443	hypothetical protein [Ricinus communis]	77	426	2.00E-87
XM_002512211	cysteine synthase [Ricinus communis]	76	432	6.00E-86
XM_002516788	Histidine-containing phosphotransfer protein [Ricinus communis]	82	468	1.00E-125
FQ378026	mitochondrion [Beta macrocarpa]	97	251	4.00E-114
NM_001249412	uncharacterized LOC100499810 (LOC100499810) [Glycine max]	89	329	9.00E-114
AC160143	BAC clone CH251-565M18 from chromosome unknown [Pan troglodytes]	83	45	0.23
XM_002298592	predicted protein [Populus trichocarpa]	79	215	2.00E-41
GU559961	NADH dehydrogenase subunit I (ND1) gene [Anevrina curvinervis]	87	37	0.26
NM_001103321	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 4 (GalNAc-T4) (GALNT4) [Bos taurus]	94	101	7.00E-32
GU928159	28S ribosomal RNA gene [Uncultured eukaryote]	76	365	3.00E-61
EF146676	unknown mRNA [Populus trichocarpa]	86	943	0
FQ391059	clone SS0AEB15YM24 [Vitis vinifera]	81	347	4.00E-84
XM_002299936	predicted protein [Populus trichocarpa]	82	295	1.00E-69
BX324212	DNA sequence from clone CH211-209N20 in linkage group 4 Contains three novel genes and eight CpG islands [Zebrafish]	77	99	2.00E-05
BC040229	adenosine deaminase domain containing 1 (testis-specific) [Homo sapiens]	91	109	2.00E-33
XM_003174240	CBS 118893 HCO3-transporter (MGYG_04466) mRNA [Arthroderma gypseum]	94	29	0.27
BT132380	clone RRlibB00690 mRNA sequence [Oryza sativa]	88	78	3.00E-16
AM426630	contig VV78X173797.4 [Vitis vinifera]	67	890	6.00E-49
FQ378026	mitochondrion [Beta macrocarpa]	99	184	1.00E-86
AM468657	whole genome shotgun sequence [Vitis vinifera,]	87	46	8.00E-04
JN572691	aquaporin PIP1 (PIP1) mRNA [Dimocarpus longan]	81	944	0
XM_002520090	Protein PPLZ12 [Ricinus communis]	86	835	0
AK285402	cDNA [Glycine max]	78	75	2.00E-05
XM_002509411	30S ribosomal protein S5 [Ricinus communis]	79	716	3.00E-167
AY259227	S-adenosylmethionine synthetase (SAMS) mRNA [Litchi chinensis]	85	647	0
XM_002520951	histone h1/h5 [Ricinus communis]	73	677	1.00E-90

IP : 14.49.138.138, 2017-11-03 13:30:33

XM_002510073	Xylem serine proteinase 1 precursor [Ricinus communis]	81	796	0
XM_003601427	Proline rich protein (MTR_3g082100) mRNA [Medicago truncatula]	71	302	5.00E-31
FJ479618	14-3-3 protein mRNA [Dimocarpus longan]	88	839	0
XM_002318757	predicted protein [Populus trichocarpa]	76	970	0
AF194001	small subunit ribosomal RNA (mtSSU) gene [Crossosoma bigelovii]	98	931	0
FQ390134	clone SS0AEB18YK02 [Vitis vinifera]	84	477	5.00E-138
XM_002511948	conserved hypothetical protein [Ricinus communis]	78	583	1.00E-127
AL590105	DNA sequence from clone RP11-273H7 on chromosome 10 Contains the 5' end of the gene for protein kinase (PKE) [Human]	85	46	0.15
XM_002299179	predicted protein [Populus trichocarpa]	75	905	4.00E-159
EF175927	putative DNA binding protein (V03-4) mRNA [Citrus sinensis]	74	331	2.00E-39
XM_002300806	predicted protein [Populus trichocarpa]	83	235	8.00E-60
XM_002523631	Magnesium-protoporphyrin IX monomethyl ester [oxidative] cyclase [Ricinus communis]	89	798	0
CU227612	EST from severe drought-stressed leaves [Populus]	79	559	7.00E-124
XM_002318974	predicted protein [Populus trichocarpa]	71	663	3.00E-78
DQ083539	paradisi alcohol dehydrogenase mRNA [Citrus x]	96	938	0
FJ157351	peroxidase 1 mRNA [Litchi chinensis]	81	882	0
FQ378861	clone SS0AEB12YD19 [Vitis vinifera]	83	816	0
FQ390699	clone SS0AEB16YP05 [Vitis vinifera]	84	232	1.00E-61
CP000552	str. MIT 9515 [Prochlorococcus marinus]	86	49	5.00E-05
XM_002300751	predicted protein [Populus trichocarpa]	74	101	1.00E-04
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	178	5.00E-85
AB022092	CitSUS1 mRNA for sucrose synthase [Citrus unshiu]	99	493	0
JN792547	cultivar Valencia putative cytochrome P450 (SUR) mRNA [Citrus sinensis]	85	460	1.00E-140
AJ002213	repeated element highly similar to the BamHI repeated sequence families of Vicia faba [Pisum sativum]	100	27	0.006
FQ390878	clone SS0AEB16YG08 [Vitis vinifera]	70	393	3.00E-32
XM_003602525	40S ribosomal protein SA (MTR_3g095810) mRNA [Medicago truncatula]	81	653	5.00E-172
DQ864733	chloroplast [Citrus sinensis]	99	382	0
AF369931	lipid-transfer protein mRNA [Citrus sinensis]	94	409	6.00E-172
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	180	4.00E-86
XM_002864846	hypothetical protein [Arabidopsis lyrata sp.]	71	662	5.00E-82
AK328666	cDNA [Solanum lycopersicum]	85	52	2.00E-05
FQ387152	clone SS0AEB27YI08 [Vitis vinifera]	80	804	0
HQ860792	Calypso chromosome 1 [Cucumis sativus]	78	160	2.00E-24
XM_002515184	ADP-ribosylation factor [Ricinus communis]	84	762	0
XM_002527873	hypothetical protein [Ricinus communis]	74	324	2.00E-43
AK325570	cDNA [Solanum lycopersicum]	80	173	4.00E-34
AK325570	cDNA [Solanum lycopersicum]	80	173	5.00E-34
EU024484	rapid alkalinization factor precursor [Litchi chinensis]	77	482	1.00E-87
AC190187	BAC clone CH251-582J15 from chromosome 7 [Pan troglodytes]	84	49	0.036
AC154654	BAC clone RP24-262O15 from chromosome 16 [Mus musculus]	95	39	2.00E-06

IP : 14.49.138.138, 2017-11-03 13:30:33

EF147098	clone WS01227_I14 unknown mRNA [Populus trichocarpa]	76	836	5.00E-165
FQ392971	clone SS0AFA3YF01 [Vitis vinifera]	78	686	3.00E-149
HM122433	domestica ALF domain class transcription factor (ALF7) mRNA [Malus x]	83	723	0
XM_002331924	flavonoid o-methyltransferase related (FOMT8) [Populus trichocarpa]	68	801	3.00E-66
XM_002523990	cytochrome P450 [Ricinus communis]	69	658	5.00E-51
XM_002519954	hypothetical protein [Ricinus communis]	76	265	3.00E-37
DQ864733	chloroplast [Citrus sinensis]	96	997	0
FQ387337	clone SS0AEB26YN10 [Vitis vinifera]	82	359	4.00E-89
XM_002309747	predicted protein [Populus trichocarpa]	91	192	1.00E-66
FN561630	ITGAX gene for integrin [Equus caballus]	90	37	0.039
DQ864733	chloroplast [Citrus sinensis]	99	314	6.00E-151
XM_002263890	hypothetical protein [Vitis vinifera]	82	346	4.00E-86
AF322910	23S ribosomal RNA [Vigna radiata]	78	111	9.00E-08
AC144709	clone CH211-204P11 [Danio rerio]	87	37	0.18
EF175925	putative DNA binding protein (V03-3) mRNA [Citrus sinensis]	72	448	5.00E-40
XM_002530234	Aquaporin PIP2.1 [Ricinus communis]	83	872	0
EF144256	clone PX0011_P23 unknown mRNA [Populus trichocarpa]	84	1009	0
EF010853	stress-related protein (PR) [Citrus sinensis]	99	679	0
EF010853	stress-related protein (PR)[Citrus sinensis]	91	498	0
AK337757	cDNA [Lotus japonicus]	77	895	0
FQ389175	clone SS0AEB20YK02 [Vitis vinifera]	80	304	2.00E-71
XM_002301980	predicted protein [Populus trichocarpa]	73	530	9.00E-72
XM_002320417	predicted protein [Populus trichocarpa]	70	240	1.00E-16
DQ122179	sterol delta-7 reductase DWF5 mRNA [Gossypium hirsutum]	81	98	2.00E-15
X65718	mRNA for extensin [P. amygdalus]	81	73	4.00E-08
DQ402075	aquaporin 1 (AQP1) [Gossypium hirsutum]	86	649	0
EF010853	stress-related protein (PR) [Citrus sinensis]	99	358	5.00E-178
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	179	2.00E-85
AB239721	metallothionein type 3 [Citrus unshiu]	98	256	6.00E-118
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	180	4.00E-86
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	180	4.00E-86
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	179	2.00E-85
AB290349	DFR mRNA for dihydroflavonol 4-reductase [Humulus lupulus]	88	39	0.015
HQ712167	cytochrome P45017 mRNA [Sebastes schlegelii]	97	33	2.00E-04
AP009634	genomic DNA [Lotus japonicus]	92	198	4.00E-70
Z46824	mRNA for Lea5 protein [C. sinensis]	100	164	2.00E-77
DQ864733	chloroplast [Citrus sinensis]	99	261	3.00E-128
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	116	1.00E-51
CP002688	chromosome 5 [Arabidopsis thaliana]	94	30	0.067
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	99	177	8.00E-83

IP : 14.49.138.138, 2017-11-03 13:30:33

FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	99	177	8.00E-83
XM_002264475	hypothetical protein [Vitis vinifera]	74	223	2.00E-24
XM_002302117	predicted protein [Populus trichocarpa]	89	54	2.00E-09
XM_002280020	hypothetical protein [Vitis vinifera]	81	196	3.00E-41
BX548062	DNA sequence from clone CH211-223K23 in linkage group 20 Contains two genes for a novel protein similar to vertebrate immune-related [Zebrafish]	86	49	0.002
BT018951	clone Contig123.F mRNA sequence [Zea mays]	75	340	3.00E-53
AC104770	chromosome 17 [Homo sapiens]	100	25	0.03
AC216417	clone POP051-F19 [Populus trichocarpa]	77	116	2.00E-11
EF175925	putative DNA binding protein (V03-3) mRNA [Citrus sinensis]	72	436	2.00E-39
AP011961	DNA [Jatropha curcas]	81	274	1.00E-64
HQ664548	ribosomal protein L2 (rpl2) and ribosomal protein L23 (rpl23) genes [Schinus terebinthifolius]	99	162	1.00E-73
AK245634	cDNA [Glycine max]	72	330	1.00E-38
U64678	ribosomal protein L44 isoform b (RL44) [Gossypium hirsutum]	90	323	8.00E-115
EF148047	clone WS0127_B15 unknown mRNA [Populus trichocarpa]	82	413	3.00E-107
XM_003617334	NAC domain protein IPR003441 (MTR_5g090970) mRNA [Medicago truncatula]	81	165	9.00E-33
XM_003592090	hypothetical protein (MTR_1g099150) mRNA [Medicago truncatula]	78	88	1.00E-08
GU991549	cultivar Zhi ubiquitin/ribosomal fusion protein mRNA [Citrus trifoliata]	94	653	0
HQ640232	translationally controlled tumor protein (TCTP) mRNA [Hevea brasiliensis]	87	546	0
EF175927	putative DNA binding protein (V03-4) mRNA [Citrus sinensis]	72	236	8.00E-18
XM_002511412	hypothetical protein [Ricinus communis]	94	61	2.00E-14
XM_002313476	predicted protein [Populus trichocarpa]	74	846	1.00E-120
XM_002323122	predicted protein [Populus trichocarpa]	79	113	5.00E-13
AF283532	paradisi miraculin-like protein mRNA [Citrus x]	98	809	0
AP009728	genomic DNA [Lotus japonicus]	92	84	8.00E-24
XR_078025	hypothetical protein [Vitis vinifera]	82	82	6.00E-12
FQ387238	clone SS0AEB27YD20 [Vitis vinifera]	73	454	5.00E-62
Z70032	mRNA for class II acidic chitinase [C. sinensis]	93	989	0
XM_002531839	protein translocase [Ricinus communis]	84	762	0
XM_002523182	histidinol-phosphate aminotransferase [Ricinus communis]	79	816	2.00E-177
AP009728	genomic DNA [Lotus japonicus]	92	84	8.00E-24
AC131965	CH230-6E20 (Children's Hospital Oakland Research Institute Rat (BN/SsNHsd/MCW) BAC library) complete sequence [Rattus norvegicus]	90	39	6.00E-04
XM_002279475	hypothetical protein [Vitis vinifera]	83	429	3.00E-117
XM_002278252	hypothetical protein [Vitis vinifera]	70	159	8.00E-07
FQ378026	mitochondrion [Beta macrocarpa]	90	182	4.00E-61
AF369931	lipid-transfer protein mRNA [Citrus sinensis]	79	413	1.00E-87
FQ397991	clone SS0AEB5YB01 [Vitis vinifera]	80	126	1.00E-22
XM_002264012	hypothetical protein [Vitis vinifera]	71	423	4.00E-43
AF283536	paradisi cystatin-like protein mRNA [Citrus x]	99	253	7.00E-124
FQ397517	clone SS0AEB6YI22 [Vitis vinifera]	75	132	1.00E-13

IP : 14.49.138.138, 2017-11-03 13:30:33

XM_002530099	Vesicle-associated membrane protein [Ricinus communis]	90	158	1.00E-47
XM_002316832	predicted protein [Populus trichocarpa]	75	889	9.00E-156
XM_002526422	nucleoside diphosphate kinase [Ricinus communis]	83	367	8.00E-97
EF175925	putative DNA binding protein (V03-3) mRNA [Citrus sinensis]	73	452	2.00E-44
AB022092	CitSUS1 mRNA for sucrose synthase [Citrus unshiu]	94	222	5.00E-83
XM_002280020	hypothetical protein [Vitis vinifera]	83	196	4.00E-47
XM_002174013	yFS275 40S ribosomal protein S18 [Schizosaccharomyces japonicus]	96	65	4.00E-19
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	180	4.00E-86
AF283533	miraculin-like protein 2 [Citrus x paradisi]	100	158	4.00E-74
AC012490	BAC clone RP11-164G2 from 7 [Homo sapiens]	80	63	0.002
FJ362595	60S ribosomal protein L39 (RPL39C) mRNA [Vernicia fordii]	92	166	4.00E-59
XM_002280020	hypothetical protein [Vitis vinifera]	81	196	3.00E-41
AE013599	chromosome 2R [Drosophila melanogaster]	82	50	0.021
AC162276	chromosome 7 BAC clone mth2-145k10 [Medicago truncatula]	84	50	0.001
CP002582	DSM 5427 [Clostridium lentocellum]	97	27	0.14
AM474450	whole genome shotgun sequence [Vitis vinifera,]	75	224	2.00E-30
DQ007450	putative PR4-type protein mRNA [Ruta graveolens]	77	473	9.00E-96
EF147148	unknown mRNA [Populus trichocarpa]	90	449	3.00E-166
XM_002519842	hypothetical protein [Ricinus communis]	87	223	9.00E-67
XM_002280020	hypothetical protein [Vitis vinifera]	84	196	9.00E-49
XM_002268757	hypothetical protein [Vitis vinifera]	76	651	3.00E-111
EF175927	putative DNA binding protein (V03-4) mRNA [Citrus sinensis]	72	236	8.00E-18
XM_002530294	ubiquitin [Ricinus communis]	90	387	1.00E-143
XM_002263428	hypothetical protein [Vitis vinifera]	74	831	4.00E-134
XM_002263428	hypothetical protein [Vitis vinifera]	74	852	2.00E-139
XM_002315910	predicted protein [Populus trichocarpa]	75	538	7.00E-88
AC130186	clone LB4-244I20 [Atelerix albiventris]	83	57	3.00E-04
AC130186	clone LB4-244I20 [Atelerix albiventris]	83	57	2.00E-04
XM_002335754	predicted protein [Populus trichocarpa]	88	441	1.00E-151
XM_002280391	hypothetical protein [Vitis vinifera]	81	596	9.00E-149
FQ310508	chromosome sequence corresponding to linkage group 18 [Dicentrarchus labrax]	78	62	0.056
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	180	4.00E-86
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	179	2.00E-85
NM_001075952	asialoglycoprotein receptor 2 (ASGR2) [Bos taurus]	95	94	2.00E-31
NM_001075952	asialoglycoprotein receptor 2 (ASGR2) [Bos taurus]	94	95	7.00E-31
CR936950	DNA sequence from clone CH211-58J23 in linkage group 14 [Zebrafish]	84	50	0.2
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	180	4.00E-86
NM_152418	DDB1 and CUL4 associated factor 4-like 2 (DCAF4L2) [Homo sapiens]	84	43	0.14
AM423532	contig VV78X272044.7 [Vitis vinifera]	84	75	1.00E-12
BT099892	MIP14221 full insert cDNA [Drosophila melanogaster]	94	33	8.00E-04

IP : 14.49.138.138, 2017-11-03 13:30:33

EF146047	unknown mRNA [Populus trichocarpa]	82	832	0
XM_002518958	hypothetical protein [Ricinus communis]	81	656	5.00E-159
XM_002284264	hypothetical protein [Vitis vinifera]	76	614	1.00E-108
FQ378026	mitochondrion [Beta macrocarpa]	99	182	2.00E-85
XM_002315712	predicted protein [Populus trichocarpa]	83	746	0
AJ251819	mRNA for 26S proteasome subunit 8 (Tat binding protein) (a1 gene) [Fagus sylvatica]	86	908	0
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	99	182	2.00E-85
AF320905	metallothionein-like protein (MT45) mRNA [Citrus unshiu]	99	551	0
EU717697	plastid acyl carrier protein (ACP) mRNA [Camellia oleifera]	76	424	2.00E-79
FQ378026	mitochondrion [Beta macrocarpa]	90	183	2.00E-66
Z70032	mRNA for class II acidic chitinase [C. sinensis]	96	350	2.00E-158
FQ390134	clone SS0AEB18YK02 [Vitis vinifera]	81	467	1.00E-120
XM_002272210	hypothetical protein [Vitis vinifera]	75	255	4.00E-49
CU223377	EST from leave [Populus]	86	462	5.00E-150
FP100153	cDNA clone: bphyem123g18 [Phyllostachys edulis]	83	134	3.00E-29
AB007819	gene for glycine-rich RNA-binding protein [Citrus unshiu]	98	173	4.00E-74
DQ864733	chloroplast [Citrus sinensis]	99	290	6.00E-144
AC136520	Japonica Group chromosome 5 clone OSJNBa0017O06 [Oryza sativa]	88	39	1.4
X70378	fht gene for narigenin 3-dioxygenase [D. caryophyllus]	90	160	8.00E-51
AL353585	DNA sequence from clone RP11-43I13 on chromosome 1 [Human]	89	42	9.00E-04
XM_002307256	predicted protein [Populus trichocarpa]	90	66	2.00E-14
FM992691	CD36 chromosome 4 [Candida dubliniensis]	84	53	0.008
DQ864733	chloroplast [Citrus sinensis]	99	386	0
CP000725	str. Challis substr. CH1 [Streptococcus gordonii]	84	50	0.001
XM_002336877	predicted protein [Populus trichocarpa]	86	207	1.00E-59
AC147448	BAC clone CH261-2D18 from chromosome unknown [Gallus gallus]	91	32	0.24
AB364106	pombe expression vector pDUAL-YFH81c DNA [S.]	80	392	1.00E-83
EF175926	putative DNA binding protein (V03-2) mRNA [Citrus sinensis]	75	225	1.00E-26
EF175926	putative DNA binding protein (V03-2) mRNA [Citrus sinensis]	75	225	1.00E-26
EF175925	putative DNA binding protein (V03-3) mRNA [Citrus sinensis]	73	192	2.00E-10
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	196	1.00E-94
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	179	2.00E-85
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	196	1.00E-94
EF175924	putative DNA binding protein (V03-1) mRNA [Citrus sinensis]	72	333	1.00E-33
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	181	1.00E-86
EF175924	putative DNA binding protein (V03-1) mRNA [Citrus sinensis]	72	333	1.00E-33
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	99	179	6.00E-84
AC197394	BAC clone CH250-409H15 from chromosome 20 [MACACA MULATTA]	87	44	3.00E-04
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	181	1.00E-86
AE014298	chromosome X [Drosophila melanogaster]	93	28	0.49

IP : 14.49.138.138, 2017-11-03 13:30:33

FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	180	4.00E-86
XM_002307058	predicted protein [Populus trichocarpa]	78	144	1.00E-20
CT573420	DNA sequence from clone MTH2-17L3 on chromosome 3 [M. truncatula]	73	139	2.00E-11
AY664413	cultivar B73 locus 9002 [Zea mays]	85	40	0.048
FN357472	genome sequence supercontig Smp_scaff000181 [Schistosoma mansoni]	91	32	0.34
XM_001329041	G3 hypothetical protein (TVAG_150040) partial mRNA [Trichomonas vaginalis]	92	35	0.063
AC188569	BAC clone CH251-684O22 from chromosome 7 [Pan troglodytes]	85	44	0.18
DQ864733	chloroplast [Citrus sinensis]	100	179	1.00E-85
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	180	4.00E-86
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	178	5.00E-85
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	179	2.00E-85
XM_002284334	hypothetical protein [Vitis vinifera]	78	81	3.00E-04
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	246	9.00E-122
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	99	180	2.00E-84
CU179759	DNA sequence from clone CH73-97A24 in linkage group 7 [Zebrafish]	81	78	2.00E-06
FN543123	mating type locus [Dictyostelium discoideum]	97	28	0.041
CR759910	DNA sequence from clone DKEYP-79C4 in linkage group 19 Contains the 5' end of the gene for a novel protein similar to vertebrate runt-related transcription factor 1 translocated to and 1 (cyclin D-related) (RUNX1T1) and two CpG islands [Zebrafish]	86	48	0.018
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	99	180	2.00E-83
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	179	2.00E-85
NM_001113817	tropicalis sterile alpha motif domain containing 13 (samd13) [Xenopus (Silurana)]	93	116	6.00E-38
XM_002301106	predicted protein [Populus trichocarpa]	82	102	3.00E-16
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	180	4.00E-86
CR352283	DNA sequence from clone CH211-105M14 in linkage group 12 [Zebrafish]	78	75	0.11
FJ802556	isolate MN146 NADH dehydrogenase subunit 4 (ND4) gene [Metilia brunnerii]	78	63	0.003
CR388147	DNA sequence from clone DKEYP-72E1 in linkage group 3 [Zebrafish]	85	46	0.004
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	243	4.00E-120
DQ123012	26S ribosomal RNA gene [Turnera subulata]	100	100	6.00E-43
XM_002298642	serine hydroxymethyltransferase 1 (SHMT1) [Populus trichocarpa]	87	191	6.00E-57
M77811	vector [BlueScribe cloning]	94	444	0
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	99	179	6.00E-84
AY177421	26S ribosomal RNA gene [Bursera inaguensis]	99	181	5.00E-85
XM_002319778	predicted protein [Populus trichocarpa]	91	42	8.00E-06
XM_001434908	hypothetical protein [Paramecium tetraurelia]	89	35	0.22
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	179	2.00E-85
EU251692	pAW34 [Cloning vector]	80	449	2.00E-94
FP104544	DNA sequence from clone MEKBa-163H18 [Wallaby]	100	23	1.1
AC154302	BAC clone RP23-378K2 from chromosome 9 [Mus musculus]	86	49	0.012
XM_002307357	predicted protein [Populus trichocarpa]	80	75	3.00E-08
AC162887	chromosome 19 [Mus musculus]	84	54	0.001

IP : 14.49.138.138, 2017-11-03 13:30:33

FN357486	genome sequence supercontig Smp_scaff000195 [Schistosoma mansoni]	78	63	0.54
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	99	180	2.00E-84
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	179	2.00E-85
CR628343	DNA sequence from clone CH211-38E16 in linkage group 20 [Zebrafish]	90	37	0.005
HQ664548	ribosomal protein L2 (rpl2) and ribosomal protein L23 (rpl23) genes [Schinus terebinthifolius]	99	202	2.00E-96
XM_001524949	NRRL YB-4239 methionyl-tRNA synthetase [Lodderomyces elongisporus]	86	41	0.02
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	191	5.00E-92
XM_002284256	hypothetical protein [Vitis vinifera]	83	93	1.00E-13
FJ525432	virus isolate NZRB-G90 [Citrus tristeza]	99	362	9.00E-175
XM_002314541	predicted protein [Populus trichocarpa]	82	59	5.00E-05
AJ313385	aspartic proteinase (ap2 gene) [Theobroma cacao]	87	172	7.00E-49
EF146222	clone WS0116_F12 [Populus trichocarpa]	95	90	6.00E-30
DQ650639	peroxidase (POD1) mRNA [Citrus maxima]	79	74	6.00E-04
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	180	4.00E-86
AL663078	DNA sequence from clone RP23-440P13 on chromosome 11 Contains the gene for a novel protein (6230425C22Rik) similar to Homo sapiens CGI-48 protein [Mouse]	83	52	0.064
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	181	1.00E-86
FJ502241	F-box family protein mRNA [Poncirus trifoliata]	96	363	9.00E-162
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	179	2.00E-85
XM_002284623	hypothetical protein [Vitis vinifera]	82	196	6.00E-44
M77811	vector [BlueScribe cloning]	92	438	5.00E-158
AC215624	clone POP006-B08 [Populus trichocarpa]	95	35	0.002
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	180	4.00E-86
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	181	1.00E-86
XM_001491891	uncharacterized protein C18orf8-like [Equus caballus]	100	24	0.11
AL590395	DNA sequence from clone RP11-390H11 on chromosome 6 [Human]	92	35	0.01
NM_001096941	small nuclear ribonucleoprotein 35kDa (U11/U12) (snrnp35) [Xenopus laevis]	92	36	0.002
HQ207194	cloning vector pVCC [Transformation and]	79	283	9.00E-47
FN554965	gambiense DAL972 chromosome 2 [Trypanosoma brucei]	84	37	2.4
CP000807	ATCC 51142 linear chromosome [Cyanothece sp.]	91	33	0.1
CP002684	chromosome 1 [Arabidopsis thaliana]	96	25	1.4
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	181	1.00E-86
DQ650639	peroxidase (POD1) mRNA [Citrus maxima]	78	108	2.00E-11
FJ502241	F-box family protein mRNA [Poncirus trifoliata]	96	363	9.00E-162
DQ864733	chloroplast [Citrus sinensis]	99	188	9.00E-89
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	99	180	2.00E-84
EU002156	26S ribosomal RNA gene [Phyllanthus calycinus]	100	112	2.00E-49
AC240777	clone OB__Ba0079B10 [Oryza brachyantha]	91	32	0.17
XM_002284299	hypothetical protein [Vitis vinifera]	79	70	3.00E-05
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	99	179	6.00E-84
AM473047	whole genome shotgun sequence [Vitis vinifera,]	77	199	2.00E-29

IP : 14.49.138.138, 2017-11-03 13:30:33

FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	179	2.00E-85
XM_646909	HM-1:IMSS protein tyrosine kinase domain-containing protein [Entamoeba histolytica]	85	40	0.62
NG_009904	Janus kinase 2 (JAK2) [Homo sapiens]	89	34	0.16
FR833047	Alem1 [Albugo laibachii]	100	21	4.4
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	179	2.00E-85
XM_740051	chabaudi hypothetical protein (PC000648.02.0) partial mRNA [Plasmodium chabaudi]	88	49	2.00E-05
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	225	2.00E-110
CP002198	PCC 7822 [Cyanothece sp.]	89	34	0.36
X65320	pCAT-Promoter [Cloning vector]	91	531	0
AC210441	clone OG_BBa0001E03 [Oryza glaberrima]	100	23	0.38
XM_002262851	hypothetical protein [Vitis vinifera]	85	182	4.00E-47
HQ664664	rpl23 pseudogene and tRNA-Ile (trnI-CAU) gene [Tamarix pentandra]	100	95	3.00E-40
EF135616	26S ribosomal RNA gene [Rhizanthes zippelii]	100	97	2.00E-41
XM_002513143	arginine/serine rich splicing factor sf4/14 [Ricinus communis]	91	141	9.00E-46
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	178	5.00E-85
X05910	cistron for 26S ribosomal RNA [Citrus limon]	99	361	1.00E-178
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	180	4.00E-86
AM449295	contig VV78X154793.4 [Vitis vinifera]	87	163	1.00E-44
EU401918	sapporoensis mitochondrion [Bombus hypocrita]	85	44	0.065
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	99	179	6.00E-84
X05910	26S ribosomal RNA [Citrus limon]	99	368	0
GQ144341	2-phospho-D-glycerate hydrolase (LOS2) mRNA [Citrus trifoliata]	99	388	0
AB022092	sucrose synthase [Citrus unshiu]	94	221	1.00E-83
CU914536	DNA sequence from clone CH73-57G1 [Zebrafish]	100	25	0.11
HQ527558	clone NBRI_Gh_E_EYT27PB03G850Q simple sequence repeat marker [Gossypium herbaceum]	84	49	7.00E-04
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	179	2.00E-85
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	179	2.00E-85
AF479138	26S ribosomal RNA gene [Aesculus pavia]	99	201	8.00E-96
XM_002530159	glutathione-s-transferase theta [Ricinus communis]	87	84	7.00E-19
BC031875	family with sequence similarity 71 [Homo sapiens]	94	43	1.00E-07
XM_002319969	predicted protein [Populus trichocarpa]	81	166	4.00E-33
AC164123	BAC clone RP24-390M17 from chromosome 9 [Mus musculus]	82	61	1.00E-05
X05910	26S ribosomal RNA [Citrus limon]	99	380	0
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	181	1.00E-86
AB022092	sucrose synthase [Citrus unshiu]	99	334	9.00E-162
BX255887	DNA sequence from clone CH211-272F3 in linkage group 18 Contains the 5' end of the veph gene for ventricular zone expressed PH domain protein [Zebrafish]	83	58	5.00E-05
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	180	4.00E-86
CP002688	chromosome 5 [Arabidopsis thaliana]	97	27	0.18
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	99	179	6.00E-84
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	246	9.00E-122

IP : 14.49.138.138, 2017-11-03 13:30:33

XM_001021876	hypothetical protein [Tetrahymena thermophila]	91	33	0.07
AP000037	genomic DNA [Homo sapiens]	84	59	5.00E-06
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	181	1.00E-86
CU467636	DNA sequence from clone CH73-325A8 in linkage group 6 [Zebrafish]	90	37	0.003
FJ389180	pHC95 [Cloning vector]	86	244	9.00E-66
AB015619	pCHR8 DNA [Cloning vector]	79	323	3.00E-59
XM_002317387	predicted protein [Populus trichocarpa]	85	98	9.00E-21
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	100	173	3.00E-82
XM_002511644	transketolase [Ricinus communis]	77	181	2.00E-29
HQ526422	clone NBRI_Gh_C_7664 simple sequence repeat marker [Gossypium herbaceum]	85	194	9.00E-53
FP885871	maritima genotype male-fertile G mitochondrion [Beta vulgaris sp.]	99	246	4.00E-120
AE014298	chromosome X [Drosophila melanogaster]	90	37	0.035

IP : 14.49.138.138, 2017-11-03 13:30:33

첨부자료 2. 《Microarray Data》

O Posttranslational modification, protein turnover, chaperones관련 유전자 중 당유자에서 발현이 많은 것

CITRUS0003664|Cclementina_Contig4283	Predicted E3 ubiquitin ligase
CITRUS0009361|Cclementina_DY257832	Predicted E3 ubiquitin ligase
CITRUS0031029|Csinensis_CB610826	Molecular chaperones HSP70/HSC70, HSP70 superfamily
CITRUS0040297|Csinensis_Contig3651	Molecular chaperones HSP70/HSC70, HSP70 superfamily
CITRUS0014022|Cclementina_DY271345	Molecular chaperone (small heat-shock protein Hsp26/Hsp42)
CITRUS0044303|GGB_illhan--06-R-D03.ab1	Molecular chaperone (DnaJ superfamily)
CITRUS0024598|Csinensis_Contig250	Molecular chaperone (small heat-shock protein Hsp26/Hsp42)
CITRUS0011925|Cclementina_DY264432	Molecular chaperone (DnaJ superfamily)
CITRUS0012462|Cclementina_DY266551	Molecular chaperone (small heat-shock protein Hsp26/Hsp42)
CITRUS0043557|GGB_Contig270	Molecular chaperone (small heat-shock protein Hsp26/Hsp42)
CITRUS0014011|Cclementina_DY271313	Molecular chaperone (small heat-shock protein Hsp26/Hsp42)
CITRUS0007177|Cclementina_CX292523	Glutaredoxin and related proteins
CITRUS0027204|Csinensis_Contig3793	Molecular chaperone (small heat-shock protein Hsp26/Hsp42)
CITRUS0026757|Csinensis_Contig3108	Protein disulfide isomerase (prolyl 4-hydroxylase beta subunit)
CITRUS0024498|Csinensis_Contig84	Molecular chaperone (small heat-shock protein Hsp26/Hsp42)
CITRUS0025720|Csinensis_Contig1812	Mitochondrial chaperonin
CITRUS0043664|GGB_Contig1081	Glutaredoxin and related proteins
CITRUS0021769|Cclementina_DY301046	Ubiquitin-like protein
CITRUS0034659|Csinensis_DN618782	Chaperone HSP104 and related ATP-dependent Clp proteases
CITRUS0042134|Csinensis_CF836629	Predicted E3 ubiquitin ligase
CITRUS0040915|Csinensis_Contig6133	Molecular chaperones HSP70/HSC70, HSP70 superfamily
CITRUS0036122|GGB_Contig38	SCF ubiquitin ligase, Skp1 component
CITRUS0026461|Csinensis_Contig2719	FOG: Predicted E3 ubiquitin ligase
CITRUS0000520|Cclementina_Contig694	Molecular chaperone (small heat-shock protein Hsp26/Hsp42)
CITRUS0043866|GGB_mct--01-j23.g1	Molecular chaperone (small heat-shock protein Hsp26/Hsp42)

O Posttranslational modification, protein turnover, chaperones관련 유전자 중 청견에서 발현이 많은 것

CITRUS0014796|Cclementina_DY274501	Transport protein Sec61, alpha subunit

IP : 14.49.138.138, 2017-11-03 13:30:33

O Cell cycle control, cell division, chromosome partitioning관련 유전자 중 궁천조생 에서 발현이 많은 것

CITRUS0041035|Csinensis_Contig6631	Cyclin B and related kinase-activating proteins
CITRUS0040494|Csinensis_Contig4437	G2/Mitotic-specific cyclin A
CITRUS0027869|Csinensis_Contig5197	Cyclin B and related kinase-activating proteins
CITRUS0028276|Csinensis_Contig5897	Serine/threonine protein kinase
CITRUS0008553|Cclementina_CX299803	G1/S-specific cyclin D
CITRUS0025364|Csinensis_Contig1251	G1/S-specific cyclin D
CITRUS0008966|Cclementina_CX308141	Anaphase promoting complex, Cdc20, Cdh1, and Ama1 subunits
CITRUS0003198|Cclementina_Contig3761	Cyclin B and related kinase-activating proteins
CITRUS0040544|Csinensis_Contig4636	Cyclin B and related kinase-activating proteins
CITRUS0028670|Csinensis_Contig6711	Cyclin B and related kinase-activating proteins
CITRUS0043816|GGB_CT--03-F-H21.ab1	Cyclin B and related kinase-activating proteins

O Lipid transport and metabolism관련 유전자 중 하귤에서 발현이 많은 것

CITRUS0040434|Csinensis_Contig4167	Cytochrome P450 CYP4/CYP19/CYP26 subfamilies
CITRUS0000810|Cclementina_Contig1072	Diacylglycerol kinase
CITRUS0024557|Csinensis_Contig165	Cytochrome P450 CYP4/CYP19/CYP26 subfamilies
CITRUS0012146|Cclementina_DY265017	Predicted lipase
CITRUS0021367|Cclementina_DY299846	Lysophospholipase
CITRUS0014824|Cclementina_DY274592	Soluble epoxide hydrolase
CITRUS0039798|Creticulata_CF831678	Cytochrome P450 CYP4/CYP19/CYP26 subfamilies
CITRUS0012709|Cclementina_DY267402	Soluble epoxide hydrolase
CITRUS0043347|Csinensis_DN620225	Diacylglycerol kinase
CITRUS0020649|Cclementina_DY296582	Lysophospholipase

O Signal transduction mechanisms관련 유전자 중 당유자에서 발현이 적은 것

CITRUS0012732|Cclementina_DY267461	Serine/threonine protein phosphatase
CITRUS0001656|Cclementina_Contig2014	Mitogen-activated protein kinase kinase (MAP2K)
CITRUS0024784|Csinensis_Contig563	Mitogen-activated protein kinase kinase (MAP2K)
CITRUS0001259|Cclementina_Contig1582	Serine/threonine protein phosphatase
CITRUS0044135|GGB_HAN--03-F-O22.ab1	Mitogen-activated protein kinase
CITRUS0019862|Cclementina_DY294756	Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily
CITRUS0021180|Cclementina_DY299280	Phosphatidylinositol 4-kinase
CITRUS0002248|Cclementina_Contig2673	Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily
CITRUS0034053|Csinensis_CX078540	Retinoblastoma pathway protein LIN-9/chromatin-associated protein Aly
CITRUS0018740|Cclementina_DY290716	Serine/threonine protein phosphatase 2A, regulatory subunit
CITRUS0022879|Cclementina_DY302824	ARK protein kinase family
CITRUS0019232|Cclementina_DY292355	Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs
CITRUS0008885|Cclementina_CX307883	Predicted seven transmembrane receptor - rhodopsin family
CITRUS0044236|GGB_illhan--04-R-J17.ab1	Calmodulin and related proteins (EF-Hand superfamily)

IP : 14.49.138.138, 2017-11-03 13:30:33

O Signal transduction mechanisms관련 유전자 중 하귤에서 발현이 많은 것

CITRUS0031152|Csinensis_CF417899	Serine/threonine protein kinase
CITRUS0000810|Cclementina_Contig1072	Diacylglycerol kinase
CITRUS0043074|Csinensis_CX671645	Serine/threonine protein kinase
CITRUS0019063|Cclementina_DY291407	Serine/threonine protein phosphatase
CITRUS0010909|Cclementina_DY262031	Serine/threonine protein kinase
CITRUS0025579|Csinensis_Contig1597	Serine/threonine protein kinase
CITRUS0024840|Csinensis_Contig638	MEKK and related serine/threonine protein kinases
CITRUS0038061|GGB_illhan--01-R-D03.ab1	Serine/threonine protein phosphatase
CITRUS0031976|Csinensis_CF510001	Serine/threonine protein kinase
CITRUS0017963|Cclementina_DY287998	Serine/threonine protein phosphatase
CITRUS0019304|Cclementina_DY292890	Calmodulin and related proteins (EF-Hand superfamily)
CITRUS0043347|Csinensis_DN620225	Diacylglycerol kinase
CITRUS0014766|Cclementina_DY274418	Serine/threonine protein phosphatase
CITRUS0016249|Cclementina_DY279105	Serine/threonine protein kinase

IP : 14.49.138.138, 2017-11-03 13:30:33

첨부자료 3. 《보유 연구소재 목록 : 전체 염기서열 정보》

(감귤류 glycosyltransferase 유전자 클론의 삽입유전자 전체 염기서열 정보)

>HAN-06-M14 : Full-length cDNA
GAGAGAGCAAAAATAAATGGCGAAAAATGAAAAGAAAGCTTCCTCCAGCAAATTGGCTCACTGTTTGGTCTTAACCTATCCAGGACAAGG
CCATATAAATCCCATGCTCCAATTCTCCAAGCGCTTACAACACAAAGGAATCAAAGTCACTTTCGTTACTACTCATTTTTTCAACAAATCC
TTGCATAGAAATTCATCACCCATCCCCATTGCTCTCGAGGCAATCTCCGACGGCTACGATGAAGGAGGTGCTGCACAAGCAGAGAGTATTG
ACGCTTACTTGGAGAGATTTTGGCAAATTGGCCCGCAAACTCTTACTGAGCTAGTCGAGAAGATGAATGCCTCAAGTGTTCCTGTTGATTG
CATTGTATATGATTCAATTTTGCCTTGGGCTCTTGATGTTGCTAAGAAGTTTGGCTTGCTTGGAGCTACTTTTCTTACTCAATCTTGTGCT
GTTTATTGCATATATTACCATGCGAA
TAGGGGCTTTCTCAAACTTCCACTTACGGGCAATGAAATTTTGCTGCCCGGAATGCCCCCACTTGAGCCTCAAGACATGCCTTCATTCGTTT
ACGATTTGGGCTTATATCCTGCTATCTCTGATTTGGTGCTGAAAAATCAATTTGATAATATTGACAAAGCTGATTGGGTTCTTTCCAACA
CATTTTACGATTTGGAGGAAGGGGTAGTTGAATGGCTGGGGAGGCACTGGTCATTGAGGACAATTGGACCAACCGTACCGTCCACGTACTT
GGATAAGCAACTTGAAGATGACAAAGACTATGGTTTCAGCATGTTTAAGCAAAATAATGAATCTTGCATTAAATGGTTGAACGATCAGGC
AAAAGGGTCAGTTGTTTATGTATCATTTGGGAGTATGGCAACACTAAAAATAGAGGAAATGGAAGAATTGGCTTGGGGTCTGAAAGCAAG
TGACAAGTATTTCTTGTGGGTTGTAAG
GGAATCCGAACAATCTAAGCTTCCGGAAAACTTTTCAGAAGAAACATCCCAGAAAGGCTTGGTGGTGAATTGGTGTCCGCAATTAGAAGT
TTTGGCACATGAAGCAACAGGATGTTTTTTGACACACTGTGGCTGGAACTCTACGTTGGAGGCTCTGAGCTTGGGAGTTCCAATGGTGGCA
ATGCCACAATGGACTGATCAGAGCACTAATTCCAAGTACATTATGGATGTTTGGAAAATGGGACTTAAAGCTCCCGCGGATGAGAAAGGA
ATTGTCAGAAGAGAAGCAATTGCACATTGCATTAGTGAGATATTGGAGGGTGAGAGAGGCAAAGAGATAAGACGGAATGCTGGTAAATGG
AGAAATTTTGCCAAAGAAGCCGTGGCTAAAGGCGGAAGTTCAGACAAAAATATTGATGAATTTGTTGCCAATTTGGTTTGCTCCAAATGC
TTGTAATTCTTTGTGTGGTTGTTGACATA
AAATAGAGAATGGCTACGGAACTTTTAGCTTCATTGCAACAGCACCTTCAGATTTGGGATAATGAATCCCAGTTTGTTAAGATTTTGTAA
TAAATTGCCTCGTGC

>HAN-04-H11 : Full-length cDNA
TTTTTTTTCACCCAATCTTTTGTCGCAGAGTAAAATAACATAAATTCATTCGTATAAAAATTTGACTCTATAACCCAAAAACCGTTTAAC
CCCAAAATTTTAAGCCAACAGATTAGTACTTTTTTTTTTTTTTTTTGTTAAAGGAAATAAATAACTACATTAAGATAAAAACATCACG
TAATTATAAAGTAGCGCAAAATATGATTATTATGAAGCTTTTCATTTACGACAAGTGCTTTGAGTCAGAACTTCCAATCAATACTCTACA
CGTGTCCATCAAGACTCCACCAATTCTACCTTCTCATTTGCCGTTGCCGTCTTCTCCACTAATTCCTTAACTCTGTGGACTGACTTCCACTT
GCTGCTGGTTATAATCTCGACACTTCTCCTTCTTACTTCATCAACGAAAGCCTGAATGTTCGTATCCCACGAGCCACCATCGGCCACAGCTT
CCTCCGCCTCCTTCTTCCACTTCAGCGCGTTCTCCTTCAACTCCGCCTCCTTAAGTCCGGCCGTGGCCTCGAGCAAGCACTTCTCCACTTCAT
CCCTTGAAATATATCCTGTTCTCTGCCTCTCCACGGCACAATCTTAAACCGGTCATGAACACATCACACAAATACATGGCATCAGTTACTT
GATCACCCCATTGCGGGAAGGTGATCACCGGCACCCCCGATGCCAACGACTCCATGGCTGAGATCCAACCGCAGTGAGTCACAAAGCAAGCA
ACACTAGGGTGAGCCAACACCTTTTCTTGTGGACTCCATTGCACAACTTTGCCCTTATCTCCAACTTTCTCCAAGAACCCATCTGGCAGCTC
AACAATTTTAACGCCAGAGTCTTCAGGCGGCGGCTTCATCACCCACAAGAACGAAATCCCCGAGTTCAACAATGCATAGCCAATTTCTTCA
ACTTGTTCTTGCTTCAAGTAGACAACCGTGCCGAAAGAGATGTACACAACGGATGATGGTGGCTTTTTGTCGAGCCAGTCTATGCATTCAT
CGGGTTTCATGCAGTCATCGCGGACGGTTAAGGTTGGAGCTTTAGGGTTTTTGAACAGAGGGCCGGACGGGTTTAATAGGGCAGATTTTTG
CCATGTAATCGATAATCTCTTTCTCAAGCTCATAGAAAGTGTCCAACAATATGCAAAANACGGCCNTTGCCCAAGATTTTCGTACTGCCCC
CAAAATAGNCTCTTCTCCAAGNAAAGNGATAAGGAGTTGACGGATGCAAGAAGCTAGGCACTTCATCCATGCTTCAGTAGTGGCATGCACG
GCAACTGAACATCAATTTCGGGTTCCTTTTCACTAGGAAATGGAACCAAACCGTGGAAGTAATGGTAATAAGCAGCAAAACAAGCACAAG
ATTGAACCCAAAGCATAGCAGACGGAAGCCCTAGGGATTCAGCAACATCAGAAACCCAAGGGATAAATGGGTTATTGATCAGGCAAGAAA
CGGGGCGATATTCTTCAGCGCTTTTCCTGATTATTTTTGGAATCACTTGTTTGCCAATAAGCTCAAGTTGAGCCATGTATTGGTCAAGATC
TCCGCGTCTTGGATCGTCTTCGTCCCATCCATCCTCGAAGAATTCGAAGCGAATGAAGCCGTCGCCAACTGGAGTAGGCTCGTAGGTGAAGT
TACCCGCTTTTCTCATTTGTTTGCCAAAGCTTTCAGGTGTGGTCAAGGTGAGAAAGAAACCCTTTGAAGCAAGGAGTCTGCCGAGCCTCAG
AAGCGGGTTTACGTGGCCATGGCCGGGGAATGAAACTAGTAAGACGTGAACAAGGGATTCAGTTCCCATTATTCTCGAATAATTTGTTCTA
AAATTGGCTAGCTAGCAATTTAAATGACAGCCTCGTGC

>HAN-06-P04 : Full-length cDNA
TTTTTTTGATTTGGAATTTAAATTTATTGACTAATCAAATAAAACTGTTTACGGGTCCCAAAGATAATAGCATTTAGCAACTTGCAAAA
AGCGTGTACATTTGATAAAATCAAAAAGAACACTCAAGGAAATAAAGCATGACTTGAAGTGGCTGACCCACATTTCTTAGGAGTCAAAAA
CTGCACATCATTGATGAATTGATTAAAGTTCTTTTGTGACGATCCATCGGCGGATAATGCATTCTCTAGTTTCTTTCTTACCTCCTTGATA
TTCTTCCTTAATTCATCACTTGATTTTCCACTCATCAAACTGTTGATTTTCTCAGAGACTTCCTCCTTTGTGATTGATGATTTCTTTTGAT
CACAAAGATTGAGCCCAATCTTCCAATCATCAACCACTAATTTTCTATTAGTGAATTGATCAGTCAACAGAGGGAAACACAACAATGGGA
CACTACACCACATACTTTCCTGTATTGAATTCCACCCACAATGAGTTAAGAACCCTCCGATAGCCGAATGTGAGATCACATCAATCTGGCT
GCACCACGGAACAATCAATCCTCTACCGCTGATCTTTATCTTTTCTTCAAATCCAACGGGTAAAAAGTCGGTTTCATCAGAACTAACAATA
TCAGGGCGAAGCACCCAAACAAAGCTCACTTCACTAAGCAAAAGCCCTAGTGCAATCTCCACAATATCATTCTTACTTGCGTGAGCATAGC

IP : 14.49.138.138, 2017-11-03 13:30:33

TACCGAATGACACATACAAAACTGACCCACGAGGCTTTGTGTTGAGCCATTGGGTGCACTCAGACTCGGACCACAGGCTCGTAGGAACTAA
ACTTTTGGTGAACCCTGCTGGGAAAATGGGACCAATGGCATATGTTGGCTGCTTTTGGTGTAGGGCTGAGATTGTTTCTGATTCAAGCTCA
TGCACTGTGTTGCAGAGGATAAAATCAACTCTCTTTACGTCCTCAAAGGCCTTTTGTATTATACGGTGAACCACAGTTGATGTGTCTGTAG
CTTGAAGATATGACATCAAGTCCTTTCGTTCTATTGCCCGAACTCCCGGTATATAGTCAATGGTGTTCTCACGATTATCAGTAGAAGCAAA
GTGGCCATGACTTCTTAGGAGATCCATGTGATAATAAAGAGTTAAAACCAGAGCTGGTTCAGTCCAAAACGAGATATTAACAAGGTTATA
TTTCTTGGCAATCATTGAGGACCAAACAAAAAAAGTGTCGGTAACTAAGCAATTCATTTCGGGGTTCAATTGGATTAAATTTCCAACAAG
TTCATCAACATGTGCAGAGAACACATGTAAAAGACATTCCATGAACTGGTCATGGTTGAGTGATCGGTCAAAATTTAAAGGAAGCCCATC
ACTGACCGTTGCGTAACGTATATCTAGACCGGCTTTACGTGCGCCGGCAAAGATGTCGTCCTCGTCACCGTTGGATTGAGCCTTGGTTATTT
GGTGATGGATTGAATGAGTGTTGACAAAGGTGATGGTAAAGCCACTGGAGGCGAGCTTCAGGGCTAGATTCACAAAAGGAATAACGTGAC
CTTGGAGAGGGTAGCAGATCGCAATTGCATGAGGCTTAGGTTTTTTGTGATTGTTCTCCATCTCTAGCTTTTTATGATGGGAATGACAAA
TTTT

>illhan-06-J10 : Full-length cDNA
AGATAAGATGGAATACAAAAGGTCCAGTCTTTTCGAACTTACCATGTAGGAAATTGCATGGAAATGATTAAATTGTTCAATAATACTTCA
TAGACCTCTTAACTTTCCTCCAGAAAAATTTAAGAATCATACCCCACTCCCCTTCTCTACCACTTAATCCTCCACTTTTTCTCCTTCTGATC
CTCATCAACAACAATGGCACAGAGGAAAGAAACCATAGTTTTGTTTCCATTCATGGCACAAGGCCATATAATCCCTTTCCTGGCATTAGCC
CTTCACTTAGAGAAAACAAATAAATACACCATAACTTTTGTTAACACCCCTTTGAACCTCAGGAAACTCAAATCTTCTGTCCCTCAAAACT
CCTCCATTAACCTTCTTGAAATTCCCTTCGATAGCATAGATCATAATCTCCCTCCTTGTACTGAGAACACAGATTCTGTTCCTTATCATCT
AGTTTCCAAACTCATTGAGGCTACTTTATCGTTTAAGCCCCATTTCAAGAAACTCGTCAATGATCTTATTGATGAACAAAATGGCTATAA
ACCACTTTGTATCATCACAGATATGTTCTTTGGTTGGTGCAAAGAGATAGCACAAGAATATGGTATTTTTCATGCGATATTTATAGGAGG
TGGTGGATTTGGCTTTGCTTGTTACTACTCTCTGTGGGTAAACTTGCCTCATCGGAACATGGATTCTGATGAATGTGTATTGCCGGATTTT
CCTGAAGCTTCTACAATTCATGCAACTCAGCTGGCAGATTATCTAANAGTTGCGGATGGAAGTGATTCTTTTTCAGCGATTCTACAGAAAG
TGCTTCCTCAGTGGATGAATGCCGATGGAATTTTGGTTAACACAGTTGAGGAACTTGACAAGATTGGACTGATGTATTTCAAGAGAAAAT
TGGGCCGGTCGGTTTGGCCAATAGGACCTGTTCTTTTGTCCACAGAAAACAGAGGTGGGGCTGGAAAAGAGTACGGAATCTCCACAGAGTT
GTGTAAAAAATGGCTCGATACCAAGCCGTACACTTCAGTTCTGTATGTATCATTTGGTTCACAAAACAAAATAGCCACATCACAAATGAT
GCAATTGGCAATGGCTTTAGAGGCTAGTGGCAAGAATTTCATTTGGGTTGTTAGGCCTCCGATTGGCTTTGACATAAATTCTGAGTTTTA
AAGCCAACGAGTGGCTGCCTTGAGGATTCGAAGAAAGAATCAAATGTTCAGGACAAGGGCTAGTGGTACACAAATGGGCACCTCAGGTGGA
GATTTTATCTCATAGGTCTGTATCTGTATTTTTGAGTCACTGCGGATGGAACTCTGTACTTGAAGCTTTAAGTCATGGGGTGCCGATAAT
AGGGTGGCCATTGGCAGCAGAGCAGTTTTACAATTCTAAGCTGTTGGAAGAAGAGATTGGGGTTTGTGTGGAGGTAGCTAGAGGGAAGAG
CAGTGAGGTTCTGAAAAAAGACATAGCGGCAAAAATTGAGTTGGTGATGAATGAGACTGAGAAAGGAATAGAGTTGAGAAAGAATGCTT
ATGAGGTTAGGGAGATTATTAAGAATGCCTTTAAAAATGAAGAAAATTTTCAGGGTTCTTCAGTGAAAGCCATGAATCAATTCCTGAATG
CTGCATCGATGGTGAAGGAGACAATTAATTGATCAAAGAATGAAGTTTTTGATGCATGAACCTAGCCATTTTAATGGTGTTACTTGAAAA
TGACGCATCTTTTTTTTCGTTTTTGGGTTTGGCCAATCTTATAATAATTGGTGGCCGGCACGGC

>YHANP-03-D10 : Full-length cDNA
GCACGAGGCAAGCAGTCAAAGTCTGAGTCAGAGATGGAGAAGCAGGATCATGTTCATGTTGCGATACTCCCGCTTCCAGCCGTAGGCCATG
TCAACTCCATGCTGAACCTTGCAGAGCTGCTCGGCCACGCCGGCATCAAGATTACGTTTCTCAACACCGAACATTATTACGATCGCGTCATC
CGTCACAGCAGTGATGCCTTTTCGCGTTACATGCAAATTCCGGGATTTCAATTCAAGACCTTAACAGATGGACTTCCCAGGGATCATCCTC
GAACTCCAGATAAATTCCCTGAGCTTGTTGATTCATTGAACTGCGCCACTCCACCCCTTTTGAAAGAGATGGTCAGTGATTCTAAGTCGCC
GGTGAACTGTATTATCACAGATGGGTATATGAGCCGTGCAATTGACGCTGCCAGAGAAGTTGGAGTTTCCATTATTTATTTTCGCACTAT
TAGTGCTTGTGCATTTTGGTCATTCCATTGCATCCCTGATATCATTGATGCAGGCGAGCTTCCGATCAAAGGAACTGAAGACATGGATCGC
CTGATAACCACTGTACCTGGAATGGAAGGTTTTCTCAGGTGCCGTGATCTTCCGAGCTTCTGTCGAGTTAACGACCCAATGGATCCGCACCT
CCTACTCTTTGCACGCGAGACCCGATTATCTGCTCATGCAGACGGTCTCATATTGAACACATTTGAAGATCTGGAAGGACCCATCTTGTCCC
AAATCCGCAACCACTCATGCCCGAATATCTACAGCATTGGACCTCTTAATGCTCATCTCAAAGTAAGAATCCCAGAAAAAACATATTCCTC
AAGCAGTTTGTGGAAAATTGACAGAAGCTGCATGGCATGGCTTGACAAGCAACCCAAGCAATCTGTTATCTATGTCAGCTTTGGTAGCATT
GCAGTAATGTCAAGAGATCAACTAATAGAGTTTTATTACGGCCTTGTTCATAGCAAGAAAAATTTCTTATGGGTCATCAGGCCTGACTTG
ATTTCAGGAAAAGATGGTGAGAATCAAATTCCTGAGGAGCTTCTGGAGGCAACCAAGGAAAGAGGATGCATTGCGGGATGGGTTCCACAG
GAAGAAGTTTTAGCCCACAGCGCGGTTGGTGGATTTTTGACCCACTGTGGCTGGAACTCGACCCTGGAGAGTATCGTGGCTGGAATGCCTA
TGATTTGTTGGCCATCTTTTGCTGATCAGCAGATCAATAGTAGGTTTGTTGGTGAAGTGTGGAAGCTGGGGTTAGATATAAAGGATTTGT
GTGATAGAAATATTGTTGAGAAGACGGTGAATGATCTAATGGTGGAGAGGAAGGAAGAGTTCATGGAATCAGCTGATCGGATGGCTAATT
TGGCTAAAAAAAAGTGTTAATAAAGGCGGATCCTCATATTGCAATTTGGACCGTCTGGTAAATGATATAAAAATGATGAGCTCACAACCAC
AAAATTGCTGAAAGCTTGGTGCAAGATGCCACTATATGCTTGACTTCCAAGTAATTTCAAGTTTGGAAGTGTTTGCCAATGAAATAAATT
AAATCACGCCAAAGGACTAGTACTTATTTTTATTTTACTTTCTTCTGTTGTCTTTGAATTATCCTCTGTTAGTCTGTTTTATGTTGTTTA
AAAAAAAAA

>YHANP-01-H03 : Full-length cDNA
GCACGAGGAAACTAACAAGATTTTACCTGACCAAGCACCGGCACCAATTCCAATACCATGGAACAAACACTCCAAGCGCAAGCAGCACCCC
ATATAGTCCTATTACCGAGTCCGGGTATGGGTCACCTCATCCCACTCATCGAGTTTGCAAAGCGACTCGTTCATCGTCATCATTTTCTCGTC
ACTTTTTTTATCCCCTCGGACGGCCCTCCCTCTGAAGCTCAAAAATCTACCCTTGAGTCTCTCCCTAGTTCCATAAACTCCGTCTTTCTTCC
CGTTTCATTAAACGACGTCGCAGAAGACGCAAGAGCCGAGACTGTTATTTCTCTCACCGTCTTACGCTCTCTACCCTGTCTTCGCCAAGAGT

IP : 14.49.138.138, 2017-11-03 13:30:33

TGACGTCGCTTGTAGCCAAGGCTACAGTTGCGGCCTTGGTCGTCGATCTTTTTGGCACCGACGCTTTTGATGTTGCTCAAGAATTTAACAT
TTCGCCCTACATTTTTTACCCTTCCACGGCTATGTGCTTGTCTTTGTTTCTTCATCTTGAAAAGCTTGATCAAATGGTTCCACGCGATTGC
GAGTACAGAGACATGTCAGAACCCGTTCAGATTCCCGGGTGCATACCCGTCCACGGCGGATACTTGCTCGACCCGGTTCAAGACCGGAAGAA
TGAGGCCTATCGATGGGTCCTCCATCACGCAAAAAGGTATAAGCTGGCTGAGGGTATTATCGTAAACAGCTTCACGGACCTGGAAAGAGGA
GCTCTAAAGGCCTTACAACATCAGGATGAGCCCGGCAAACCTCCGGTTTACCCGGTCGGACCGCTCGTGAAAACGGGTTCGACTGCCGAGTC
CAAGAACGAGGGATGTTTAAAGTGGTTAGATGATCAGCCACTCGGTTCGGTTCTATTTGTTTCTTTTGGCAGTGGTGGGACCCTCTCCTGT
GAACAGTTGAATGAATTGGCCTTGGGGTTGGAGATGAGCGAACAAAGATTCTTGTGGGTCGTGAGAAGCCCCAACAATGCTGCTAATTCGA
CGTTTTTTAGTGTGAACAGTCATAAGGACCCTTATGATTTTTTGCCAAAAGGGTTCTTGGACAGGACCAAGGGGCGGGGGATGTTGGTTCC
GTCATGGGCACCACAGGCACAAGTGCTGAGCCATGGCTCCACCGGAGGGTTCCTATGTCACTGTGGGTGGAACTCTGTACTCGAAAGTGTAG
TCAATGGGGTGCCGCTGATAGCCTGGCCACTTTATGCTGAGCAAAAGATGAATGCCGTGATACTCACCGAGGACGTGAAATTGGCTTTGAG
ACCAAAAGCTAATGAAAATGGGATCGTGGGAAGAGATGAAATTGCTAAAGTTGTCAAAGCTCTAATGGAAGGTGAACAGGGTAAAGAAGT
TCGTAATAAAATGAAAGACTTAAAAGATGCGGCCGCCGCGGTGCTGAGTGAAAATGGATCTTCTACCAAAGCCCTCTCTCAGTTGGCTTCC
AAGTGGAACAACAACGAAGGGAAACCATGCAGTTTGCAGATTTAAATTCAATATTATAATTTTCTACATAGAATTTAAAATTTTTAATC
TCAGAGTTTTTTTTTTTTAATTTGTTTAATCTAATTTCCCTTCCGGTTGTACGCTCTAGCCTCTAGCAGTAGGTCGTGTGTGTTTCCTTTC
TCTGATACATTGCCGTTTCAATGTATATATAAATTCAATAAATAATAATGCAGCATTCACTTGAAACGTCCCCACCACATCACCCTTACGT
CTATGCATCTCCCCCTCCTCCTTACCACTACTAGAAAGTGGCCACGAATAGCTCATGCTTTTTTATGGAGAGGCGATTCGCATGCAAATAA
AGAAAGCGAAAGCTGATTAAGAGACTTTACCGTGAGAAAAAGAAAAGCGAGTTGCCGCGTTTTAATTATCTTTATCTTTTTTCCTTTTTG
CCCCCCGAAGAGGAATAAACAGTTACATGTAGAAAAGCAAAGTGCTTATCATTTTCATGTATGGATCGTTGCTGTGTGTAATTCGCATCTC
ACGTCTTTTGTAATTGTCAACCTTTTTGCATGCAGATGCAAGAGGTTGGTCGTATAATA

>YHANP-03-O14 : Full-length cDNA
GCACGAGGAATGGAGAGGCAGAAAGAATCCAATGTGCAACAAAAGAAGGGGCGCCGGGTGATACTCTTTCCTCTGCCTTTGCAAGGCCACA
TAAACCCCATGCTTCAGCTTGCAAGCATTCTATATAGTAAAGGCTTTTCCATCACCATAATTCACACCAACTTCAACTCTCCAAACCCTTC
TAACTATCCTCACTTCAGCTTCAATTCCATCTCTGAGAGCCTGTGGGAAAGCGAAGTCTCCACCGAGAATGCCATATCTCTTCTTACAGTCC
TTAATGACAAGTGTGTTGTGCCATTTCAGGATTGCCTGGCTAAGTTGATTTCAAATGGTGATCAGGAGGAGCCCGTCACCTGCTTAATCAC
AGACGCTATCTGGCACTTCGCACAAACTGTTGCTGATACCCTAAGGCTTCCGAGGATCGTGCTAAGAACTAGTAGTATCTCTTCTTTTCTC
GCTTTTTCTGCCTTCCAAATTCTACTGGAAAAGGGTTACCTTGCCGAACAAGATTCCCAGTTAGAAAAACCAGTGACAGAGTTACCACCGC
TGAGAGTGAAAGACATTCCGATTATTGTAACACATGATACAAGGAATTTTCATCAACTGATATCAGCGGTGGTTAGTAAGACAAAGGCTT
GTTCAGGATTGATATGGAACTCTTTTGAGGACCTTGAACAAACCGAACTCACAAGATTACACAAGGACTTTCCCATCCCAATGTTCCCAAT
AGGCCCATTTCACAAGTACTGTCTAGCTTCTTCAAGTAGCTTACTATCTCAAGACCAAAGTTGCATTTCCTGGTTAGACAAACAAGCAGCA
AAATCTGTAATGTATGTGAGTTTTGGAAGTATTGTTGTTGTAAATGTGACCGAATTTTTGGAGATAGCTTGGGGGCTAGCGAATAGCAGG
GTACCCTTTCTCTGGGTGGTTCGACCAGGATTAGTCCCTGGAGTAGAATGGCTTGAACCTTTGCCAAAAGGGTTCCTGGAAATGCTGGATG
GAAGAGGGCATATAGTAAAATGGGCTCCCCAACAAGAGGTTTTAGCTCATCCTGCTGTTGGAGGGTTTTGGACACACAATGGTTGGAACTC
AACATTGGAGAGCATATGTGAAGGCGTCCCCATGATTTGCCAACCCTGTTTTGGTGATCAATTGGTGAATGCAAGATATGTTAGTCATGT
TTGGAGGGTTGGATTGCATTTAGAAAGGAAGTTTGAGAGAAGGGAGATCGAAACAGCAATCAGAAGAGTAACTGTTGAAGCTGAAGGCCA
GGAAATGAGAGAGAGGATTATGCACTTGAAGGAGAAACTGGAACTTTCCTTATTAGAAGCTGGTTCTTCATATCAATCTCTAGAGAGATT
GGTTGATCACATACTTTCATTCTAGTTTTTTCAATCCTATGGTGTAACAAGTATTGATCGTCCAAACTTACTTAAAGATGATCGCACAAG
AAATAAAGCTCAATTTTCTGGCTTCAAGTCGATCCCATTGTTTTGTTGGAAGCTTTGAATAATTGTCCAATTTTCTGTTATCAATTCAAC
TGAAGCACTGATGCTAATTGTTTACGTAACCAATTTGACGAGACTTGTCTCAACGTACTCCGTCTCTAAATTCCAGACGAATCATGTCATA
AACTTTGTGATTTTCTTTTATATTCATTTATTGAATTATATGATTTTGATATAAAAAAAAAAAA

>YHANP-04-K12 : Full-length cDNA
GGCACGCATCTAGCAACTAGTGGGATCCCCCGGGCTTTTAGTGAATTCGGCACGAGGCTGAAAACTCGCTCTTTATTGATTGCAGTACTAT
GGCTTACTCAAAAAATTTTACTCTGCTCATCTCTATAGCAATCAGCTCTTTGATGGTTGCTTCTGCTAGTAATTTCTACCAAGACTTTGAT
ATCACTTGGGGAGATGGCCGTGGTAAGATACTCAACAACGGCCAGCTTCTCTCCCTCTCCCTTGACAAAGCCTCAGGCTCAGGCTTCCAGTC
CAAGAGCGAGTACCTTTTTGGCAAAATCGACATGCAACTCAAGCTTGTCCCTGGCAATTCTGCCGGCACAGTCACCGCCTACTACTTAAAA
TCACCAGGATCAACATGGGATGAGATAGACTTTGAATTCTTGGGGAATTTAAGTGGTGATCCTTATACTCTTCATACTAATGTGTTCACA
AATGGCAAAGGTGACAGAGAACAACAATTCCACCTCTGGTTTGACCCCACTGCTGACTTTCACACCTATTCCGTTCTCTGGAATCCCCAACG
TATTGTCTTCTATGTTGATGGCTCGCCAATTAGAGAGTTCAAGAACTTGGAATCAAACGGCGTACTCTTTCCCAAAAACCAGCCGATGAGG
ATTTACTCGAGTCTCTGGAACGCCGATGACTGGGCCACGAGAGGTGGCCTTATCAAAACTGACTGGACCCAAGCTCCCTTCACTGCTTCTTA
CAGAAACTTCAATGCCAATGCTTGCGTCTGGTCTAATGGAAAATCCTCTTGCAACTCAAAAAATAATAATCCATGGTTCTCGCAAGAACTT
GATGCCACTGGCCAAGAGAGACTCAAATGGGTGCAGAAGAATTACATGATATATAATTATTGCAAGGACTCAAAACGATTTCCCCAAGGG
CTCCCAAAAGAATGTGCATTCAATATATAACTGATCCATTTGCCATATGTCTTTGTTTATAGCTTTTTTAATCTTCAGTTTTGATGTTTT
GGTTCTTTTATTCTGTGCACTAATGTTTAGTGACAAATAAAATGTATGGTTCATTCTTTTTTGTACTATAAGTGCTACGTGTAATAAAAT
ATTGTTACTTTTGTTAAAAAAAAAAAAAAAAAAACTC

>YjinA-01-E02 : Full-length cDNA
GCTCGCAAAACCTGACTTATATCTATTTTTATATTTGAATGAAAATGGGATGACAAACTCAGAGAGGGTTGGGGCGGGGTTATATCTATG
TAACTTAGGGATGCTAGCATTAAACAATGGGGCCAATGGAGCCAAATCCTGCGATCAAAAAGGGAATTGTTTGGAGGAAAAGGTATATGA
AGTAATTGTTCTTCCCATGGACAAAATCATAGCATCCGCAAAAAAAAAAAGAACACTCCAAATCCCCGCTCCCAAGTATGCATTCTCTCAGC

IP : 14.49.138.138, 2017-11-03 13:30:33

AAATTTGATTTTAGGTTTTTTGGGAGCTTTGGTATTTGTTTTGTTCTTCCCATCAGCTGCCTTATTCTTGAAAGCATCTCCAAGTTTTTC
GGGGACAACCCATTCATTGGCCCTTCCAGCTTCGAACAAACCAATAAATGGGGCCTTGGTTCGATGCAAAAACATCACATTCTCAAAAAGA
ATCCAGTAAAACAATAGGGGAATAGACCTTGGAGTCCAAACTGAATTTAAAATGGGGATTATGGAAGGAATATAAACAGCTCCCCAGAAT
GGAACTTGAACTTCAGGAACCAAAATGGTTAGCGGAAGCACGACGCAATAGAAGGAAAATGTGACCATATGGGCAATTATCTTCCGGACA
AAGAAGAAACTGTAGATAACATAAACTTTCTTCCAGAATTTAACTTTCTTATTTCTAATAATCTCCATCACCATTTTCCTGAATAAATTG
GCAGGACCACAAGACCATCGGTGCTGCTGGAATCGGAAAGCTTTGAAAGTACTAGGAAGTTCACTTTTCACCTGGAGATCACCGAGGTACA
CAAATTTCCATCCCTTGAGACTAGCTCGAACAGCAAGGTCCATGTCCTCCACTGTAGTTCGATCCTTCCAGCCACCTGCCTCATTGATAGCA
GCAATTCTCCATACACCAGCAGTTCCATTGAAGCCAAAGAAAGCATGAGTTGCTGATCCCACTTCTTGCTCCACTTTAAAATGGTAATCCA
ATGACATCTCTTGCATTCTTGTCAACAAGCATTCATTTGCATTTACGAATCTCCAGCGAGCTTGAACAAGGGCAATGTCAGAGTTTTGGAC
TAAGTAAGGAATGGCACGTCGGAGATNAATCGGGCTCCGGCCGGAAATCGGCGTCGAAGATGGCCACGTATTCACAATGTTTAACATAGCT
TCTTTTGAGCCCTTCTTTGAGAGCACCAGCTTTGTATCCCGTGCGATTCTCTCTGATTTGGTACCTTATGTTAATGCCTTTGGCCGCCCATC
TTTGGCACTCTTGCTCCACCATTTGCTTGATGGCAGGGTCAGTTGAATCGTCAAGGACTTGGATCACGAGACGATCGGACGGCCAAGAGAG
TCCGCAAGCTGCTCCAATGGAGATTTTGTAAACCTCTTTTTCATTGAACATTGGGATTTGAATAAGAACAACGGGGAAATTAGAGCTGCCC
AATTCGACATCGTCTTCAATAGGTTGCCAATTGTAACGCTTCTCAGGTTTTGGCCAAAACAGCTTAACAAGGATTATAACAATGCCCATGT
AAACCCTTTCCATGAAGAGCATGAGTGACATGGCCAAGCAAATGTAGACGCCGAGTTTAAGCAAAGGGACTATCAATGGGGCTTTGAGTAG
TTCCCAAATCAAACCAATTTGGCCTGCAATGTCCTCTCTTGACACTTGGAATGACTCTGGTATGAAAAATTTTGGTGAAATTTGAGCCATT
TTCTCTAGCAGAGCAAAACAGGGGAGGCGATAAAGAGATTTTTTTGGCTAATGCTGGTTTAAAAACAAGAAACAAGAAGGAAAATTTTTC
ACAATGTGATTGAATTGGAACAAATCTTGGCTTTTACATGGAAACTTGAACACAATGGGCAAAAATTAAAACGCAAATTAAAAGACTTTC
TCTCTTTCTCTATTTTTTTTCCCCCTAGTTAAGGGAAGAACAGAAAGATCTTTACTTACTGGTCTTTTAGCCAATACTTGCTCTGTTTTTT
TTTTTTTTCTCTCTACCAAAATGAAGCAGAGACAGAGCCTCGTGC

>YjinA-01-H01 : Full-length cDNA
TAGAATTCGGCACGAGGCTGAGTCAGAGATGGAGAAGCAGGATCATGTTCATGTTGCGATACTCCCGCTTCCAGCCGTAGGCCATGTCAAC
TCCATGCTGAACCTTGCAGAGCTGCTCGGCCACGCCGGCATCAAGATTACGTTTCTCAACACCGAACATTATTACGATCGCGTCATCCGTCA
CAGCAGTGATGCCTTTTCGCGTTACATGCAAATTCCGGGATTTCAATTCAAGACCTTAACAGATGGACTTCCCAGGGATCATCCTCGAACT
CCAGATAAATTCCCTGAGCTTGTTGATTCATTGAACTGCGCCACTCCACCCCTTTTGAAAGAGATGGTCAGTGATTCTAAGTCGCCGGTGA
ACTGTATTATCACAGATGGGTATATGAGCCGTGCAATTGACGCTGCCAGAGAAGTTGGAATTTCCATTATTAATTTTCGCACTATTAGTG
CTTGTGCATTTTGGTCATTCCATTGCATCCCTGATATCATCGATGCAGGCGAGCTTCCGATCAAAGGAACTGAAGACATGGATCGCCTGAT
AACCACTGTACCTGGAATGGAAGGTTTTCTCAGGTGCCGTGATCTTCCGAGCTTCTGTCGAGTTAACGACCCAATGGATCCGCAACTCCTAC
TCTTTGCACGCGAGACCCGATTATCTGCTCATGCAGACGGTCTCATATTGAATACATTTGAAGATCTGGAAGGACCCATCTTGTCCCAAAT
CCGCAACCACTCATGCCCGAATATCTACAGCAATGGGACCTCTTAATGCTCATCTCAAAGTAAGAATCCCAGAAAAAACATATTCCTCAAG
CAGTTTGTGGAAAATTGACAGAAGCTGCATGGCATGGCTTGACAAGCAACCCAAGCAATCTGTTATCTATGTCAGCTTTGGTAGCATTGCA
GTAATGTCAAGAGATCAACTAACAGAGTTTTATTACGGCCTTGTTCATAGCAAGAAAAGTTTCTTATGGGTCATCAGGCCTGACTTGATT
ACAGGAAAAGATGGTGAGAATCAAATTCCGGAGGAGCTTCTGGAGGCAACCAAGGAAAGAGGATACATTGCGGGATGGGTTCCACAGGAA
GAAGTTTTAGCCCACAGCGCAGTTGGTGGATTTTTGACTCACTGTGGCTGGAACTCGACTCTGGAGAGTATCGTGGCTGGAATGCCTATGA
TTTGTTGGCCATCTTTTGCTGATCAGCAGATCAATAGTAGGTTTGTTGGTGAAGTGTGGAAGCTGGGGTTAGATATAAAGGATTTGTGTG
ATAGAAATATTGTTGAGAAGACGGTGAATGATCTAATGGTGGAGAGGAAGGAAGAGTTCATGGAATCAGCTGATCGGATGGCTAATTTGG
CAAAAAAAAAGTGTTAATAAAGGCGGATCCTCATATTGCAATTTGGACCGTCTGGTAAATGATATAAAAATGATGAGCTCACAACCACAAA
ATTGCTGAAAGCTTGGTGCAAGATGCCACTACATGCTTGACTTCAAGTAATTTCAAGTTTGGAAGTGTTTGCCAATGAAATAAATTAAAT
CATGCCAAAGGACTAGTACTTATTTTTATTTTACTT

>YjinA-03-E04 : Full-length cDNA
CTTAAATAAAATTGTATGATCACAAAAAAATCAATAGCATCCAATACAACTCTAATTTCATTTGTTTGAAATAGCTCATAAATAGGACCC
AAAAAAAAAGGGATAAAACAACTACGGGAGCTTGATGCTGGACATCTTAATAAAATTTTGATTATAAAAACCTTAATGTGGGTACATAG
GCTTCTCTAAGGTTTCTTTATTGAAATGGCTACCCAAGTGAAATGTCCCTGAAAAAAGCATCAAGGTTAGTAATAAATGATCCATTTTCT
GCAACTGCTTCTCGACAAATCTCTTGAACTTCTCTAGCCCTTAAACTCATCTGTTTCCTCTCATCACTATTCAAATCCATAAACCTTTTCA
CTAGCTCTGTAATTTCATCTCTTGTCACCAAACTTTCACTTGCTATGTCAGGTTTCTTTACTCTCCATCCAGTCTTCCAATCTTGTACAAT
TTGCTTACTATTTGGAACTTGATCCCAAAATATCGGAAAAGTAAGCATTGGGACACCAGCATAAAGACTTTCGATAGTTGAATTTAAACC
ACAATGAGTCCAAAATCCCCCAGTAGAAGCATGGCACAGCACCCTCAGTTGGTCACACCAAGGCACCACAATGCCCCGATCATCAGCATGGC
CATCTTTAAACCGAGAAGTATCACCTCTTGTCACCCACAAATATCTGACGCCACTGTTGCGGNATACCAGCTATAATTTCATCCATTTGTG
CACTTGAAACCGACAAAAAGCTTCCCAAGGAGACGTACAAAACTGAGCCAACAGGCTGAGTTTCCAACCACTCAAAGTATTTGGGACCATT
GTGACCAGTAATTGATGATACGTTGAAGTAGGGAATGGTTGGTCCAATTGGGTACACTGGAAATGAAAATTCTTCTTTTAAAGCGTCAAT
AGTTTTGGCTTCCAGCTTGTAGACCGAAGAAAGCAAAAGATATTGAGCTTTTGAGACCTTTGATGCACTTTGCAGGGCCGCCATGCAAAAT
TTTTCTGCCAGCTCCGTGAAAAATTGTAGGAAAATCAGCCAACTTCGTCGGTTCAAGTCCTGGGATGTAGTCCACAAGCTCGTCTCCCTTT
TCTGAGAGATCAAACGGAAAATGGCCGTTTCTTTCAAGAAGCTCAAAGTGATGAAAAACAGAGAACACAAGTGCAGACATCGTCCACAAG
GAAGCTACGGGAATGTTCCTGCGGTTGCCAACGTCAACAACCCAAGGCAAGTAAGTATCTGCTATAATAGCAGTCAGTGCCGCCGGAGGTT
GCTCATCATCATCAAGAAGCAGACGATCAAGGAGCTCTTCAAAAGGAGCTTCCATCTTTGTAAACACAGCCTCCAGGAAGCCGGCAAAGTC
ATTGGCGCGCCCATGCTCTGAGGGTATGGTATTAGGCAATGTACGGAATCGAATGTTATGGGGCTTGCTCTGTGAGCCAATGAATCCGAGC
CACTCTTCTGTCACAACAAAGGTGATGAGGATATCAGGCTGCCTTGAAACTAAGAGCTTGCAAATGTTCATCATGGGGTTGACGTGTCCTC
TCCCGGGATAAGGCAGGGCCAGCACGTGGCAGAGGCTGGTTGGTTTTACTTGGGCAGGATGAGGATCCATGAGTACCACTTGATATATGGG

IP : 14.49.138.138, 2017-11-03 13:30:33

AGCTAATTCAGCTGGCTGGCTGGCTGGCTGGCTGGCTGGTGGCTTGCAAGAGTAAAACGCAGAGACAGAATGAGCCTCGTGC

>YjinA-03-F24 : Full-length cDNA
AGCCAGACAGACACAGCCAGACATTCAATCGCAGAGAAGACAAAGTTACACAAGAAACGCTAAATCAAGAAGGCTGAATGTTATTTATTT
TAGTTTAAATTAAGCTAAGGCTTTGAGATCCTTGACGAAATCTGCAATAATCTTATCCTGAATCTGGCCGTTCAACAAAAACTCCCTCCAC
CGTTTCTGATTAGCCCTGATTGAAGCTCCAGGCTCCTTGTTCACATCCACCATAACTGTTTTAATAGCCTTAAAAATATCCTCCTTCCCAA
AATGCCCATCATGATCCCTCCTATTTACCTCCACTCCAGCTTTCAAGTCTCCAGCAACGAGCTTGGAGTTCAAGAATTGGTCACCTTTTAA
AGGCAGAAGCACCAATTGACAGTCGCTAATCACAGCTTCAGTTACCGAACTAAATCCTGAGTGACACACGTAACATCCAACGCTCTCATGT
CTTAAAATGAGCTGCTGTTGCACCCATACTGTGTGCACCACTCCCCTGTCTTTCACCCTGTCCATGAACCCTGGAGGCAGAGTCCGGACCAG
CTCACTCTGACCATCGACGTTAGGCGGGAAATTTAAGACCAGGAAGAAGGGCAATCCCGTAATTTCCAACCCAATGGCTAACTCTTTGATC
TGATCAACGGTGAGGAATGTTTCACTTCCGAAGGAGCAATAAATAACAGACTTGGGAGGATACTTACAGAGCCATTTAGCCCATCTCTCTT
CAAGCTCCCCTGATGGCGGCTCAGGATTAACAAGTGGACCGGTTAGAAGAACCGGTTTCTTGAACTGGGTTCTCACGAAATCCAGGTAAGG
ACCCTCCATTTCATTACATGTCTTGATGGCAAGAACATCGCAGCCATCAACGCCCTGAATCCCTCTCTCATAAACACTCGGGCCGCCCATTG
AACTTTGTATAAACATACAAGTAATCTCGAGCCACAAATTCATCGAGCGAGGTAATGGAAGTTGCAGGGAACCCATCGGGAGATTTCATT
AGATCTGCTAAACTGTTGTTGAGTTTCCTGGCGGGGACCACGAGATAGGCTTGTGAAATGGCAGAGAAAACAGAGAAGTTAACTGTTTTG
ATGCCAAGTTGAGAACCAGCAAGACCCGGCAACCAGTAATGGGTAAAATCAAAGAACACAAAATGGGGTTCGAGCTGTGACAACAAAGTT
TTGATTTGTGGTTGCATGAGGTCCAAGGCTTGCTTTAGGAGCTCAGCCATGTGAGGTGTCATCTCTGAGGTGCTATCAAGACCAGGAGGGA
GGCCATCGACGTGTGGGATTTGAAGAGGGATAATGTCGGCCATGGGAGTTAAATTGAGCGATGATTTGATGCGGGGAATGTTACCAGGAGC
CGAAAAGAAAGAGACCTTGACTCCATGAAGTGAGAGCTTGTTGGAAAGTTGTACAAAGGGGCTTATGTGACCAAAAGCAAACCATGGGAA
CATCACCACGTGAAGTTGATCAGCTTCAGCTGATTCAGTTCCCATTTTGTGGTGTTGGTTCGAAGGGGCGTGCATGTTCGAAGAGGCGTGT
ATGGTCTCTGTCTCCCTCGTGC

>YjinA-03-I06 : Full-length cDNA
GCACGAGGCCAGTTTGAAAATAGAAAAAAGAAAAAGGAAAATGAAAAATGACAAATCAGGACTCAACTGGATTCACACGGCACAGCCAGA
TCCACGTTTATTACTTATATGCGAAGGAGAGGGAGACAGAGCTTTGACCTCCATCGCTTGAAGGCTTGAACACGCATCGAGGCTTTGAGTG
TAACGTACTTGTTGTGCCAGATCAAGATTCAAGCATGTCAGATTCCGGCGGCTTTGATTCCCATCCACATGTAGCTCTCATCCCAAGTGCT
GGCATGGGCCATCTAACGCCCTTTCTTCGACTTGCTGCATCGCTTGTTCAGCATCACTGTCGCGTCACCTTAATAACCACTTACCCCACTGT
CTCACTTGCTGAGACTCAACATGTTTCTCACTTTCTATCTGCTTATCCTCAGGTCACCGAAAAGCGGTTTCATCTCCTCCCTTTTGATCCCA
ATTCAGCCAACGCTACTGACCCTTTCTTGCTCCGGTGGGAAGCCATTCGCCGCTCAGCTCACCTTCTTGCTCCTCTGCTTTCTCCCCCGCTCT
CTGCTCTCATCACAGATGTGACTCTGATCTCCGCCGTTCTTCCTGTTACCATAAATTTACATCTCCCAAACTACGTCCTTTTCACAGCATCT
GCCAAAATGTTTTCTCTTACCGCGTCTTTTCCTGCCATTGTTGCATCCAAATCAACCAGCTCTGGTTCTGTTGAATTTGATGATGATTTTA
TTGAAATTCCAGGCCTTCCTCCAATACCCTTATCATCAGTCCCTCCGGCGGTTATGGATTCTAAGAGTCTATTTGCAACTTCATTCCTTGA
AAATGGTAATAGTTTCGTAAAATCGAATGGTGTGTTGATCAACAGCTTTGATGCATTAGAAGCAGACACTCTGGTTGCACTTAATGGAAG
AAGAGTTGTTGCTGGACTTCCCCCGGTGTACGCCGTTGGACCTCTTTTGCCTTGTGAGTTTGAAAAAAGAGACGACCCTAGTACATCTCTG
ATTCTGAAGTGGCTCGATGATCAACCAGAAGGGTCGGTAGTGTATGTCAGTTTTGGCAGTCGATTGGCCTTGTCAATGGAGCAAACGAAGG
AGCTGGGAGATGGGTTACTAAGCAGTGGCTGCAGATTTTTGTGGGTGGTGAAAGGTAAGATCGTTGACAAGGAAGATGAGGAAAGCTTAA
AAAATGTGCTTGGTCATGAACTCACGGAGAAGATCAAAGATCAGGGGTTGGTGGTAAAGAATTGGGTGGATCAAGATAAGGTACTGAGTC
ACAGGGCTGTCGGTGGATTCGTTTCTCATGGCGGTTGGAACTCACTGGTTGAGGCTGCACGGCACGGGGTGCCTCTGTTAGTTTGGCCGCAT
TTTGGGGATCAGAAGATCAATGCAGAGGCAGTGGAGAGAGCTGGGTTGGGGATGTGGGTCAGGAGCTGGGGTTGGGGTACAGAGCTGAGGG
CGAAAGGAGATGAAATTGGTTTGAAAATTAAAGATTTGATGGCAAACGACTTTTTGAGAGAGCAAGCTAAACGTATTGAAGAAGAGGCA
AGGAAAGCCATTGGAGTTGGTGGAAGCTCCGAGAGAACATTCAAGGAGCTCATTGACAAGTGGAAGTGCAACAACAACACCCATTAAAAT
GAAAAATTGAATGTTTTTGGCTTCAGTTTTATTCAAAACTGAATTCTAGCTTTCCTATCCTGCTTGCTTTGATTTTTGATATGTAGAATG
TGTATCATTATGTGTCAATGCAAGATTGAAAATAAAATAATTATCTATGTATGAATTATGATCCCAATTTAGAATGGTTTGATTTGTGA
TAAGCTTATTTTACTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAACTCGAGGGGGGGCCCGGTACCC

>YjinA-04-J04 : Full-length cDNA
GCACGAGGGCCAAGCCCATCTGTCATTTAAATTGCTAGCTAGCCAATTTTAGAACAAATTATTCGAGAATAATGGGAACTGAATCCCTTGT
TCACGTCTTACTAGTTTCATTCCCCGGCCATGGCCACGTAAACCCGCTTCTGAGGCTCGGCAGACTCCTTGCTTCGAAGGGCTTCTTTCTCA
CCTTGACCACACCTGAAAGCTTTGGCAAACAAATGAGAAAAGCGGGTAACTTCACCTACGAGCCTACTCCAGTTGGCGACGGCTTCATTCGC
TTCGAATTCTTCGAGGATGGATGGGACGAAGACGATCCAAGACGCGGAGATCTTGACCAATACATGTCTCAACTTGAGCTTATTGGCAAAC
AAGTGATTCCAAAAATAATCAGGAAAAGCGCTGAAGAATATCGCCCCGTTTCTTGCCTGATCAATAACCCATTTATCCCTTGGGTTTCTGA
TTTTGCTGAATCCCTAGGGCTTCCGTCTGCTATGCTTTGGGTTCAATCTTGTGCTTGTTTTGCTGCTTATTACCATTACTTCCACGGTTTG
GTTCCATTTCCTAGTGAAAAGGAACCCGAAATTGATGTTCAGTTGCCGTGCATGCCACTACTGAAGCATGATGAAGTGCCTAGCTTCTTGC
ATCCGTCAACTCCTTATCCTTTCTTGAGAAGAGCTATTTTGGGGCAGTACGAAAATCTTGGCAAGCCGTTTTGCATATTGTTGGACACTTT
CTATGAGCTTGAGAAAGAGATTATCGATTACATGGCAAAAATCTGCCCTATTAAACCCCGTCGGCCCTCTGTTCAAAAACCCTAAAGCTCC
AACCTTAACCGTCCGCGATGACTGCATGAAACCCGATGAATGCATAGACTGGCTCGACAAAAAGCCACCATCATCCGTTGTGTACATCTCT
TTCGGCACGGTTGTCTACTTGGAGCAAGAACAAGTTGAAGAAATTGGCTATGCATTGTTGAACTCGGGGATTTCGTTCTTGTGGGTGATGA
AGCCGCCGCCTGAAGACTCTGGCGTTAAAATTGTTGAGCTGCCAGATGGGTTCTTGGAGAAAGTTGCAGATAAGGGCAAAGTTGTGCAATG
GAGTCCACAAGAAAAGGTGTTGGCTCACCCTAGTGTTGCTTGCTTTGTGACTCACTGCGGCTGGAACTCAACCATGGAGTCGTTGGCATCG
GGGGTGCCGGTGATCACCTTCCCGCAATGGGGTGATCAAGTAACTGATGCCATGTATTTGTGTGATGTGTTCAAGACCGGTTTAAGATTGT

IP : 14.49.138.138, 2017-11-03 13:30:33

GCCGTGGAGAGGCAGAGAACAGGATAATTTCAAGGGATGAAGTGGAGAAGTGCTTGCTCGAGGCCACGGCCGGACCTAAGGAGGCGGAGCT
GAAGGAGAACGCGCTGAAGTGGAAGAAGGAGGCGGAGGAAGCTGTGGCCGATGGTGGCTCGTCGGATAGGAACATTCAGGCTTTCGTTGAT
GAAGTAAGAAGGAGAAGTGTCGAGATTATAACCAGCAGCAAGTCGAAGTCAGTCCACAGAGTTAAGGAATTAGTGGAGAAGACGGCAACG
GCAAATG

>YjinA-04-J10 : Full-length cDNA
GCAGGAATTCGGCACGAGGCTCATCTCATCTGCACAAATAAAAAAAAAATGTCCAAAACCAAACCTCCACATCACCAGCAGTTCCTCCTCCT
CCTCCTCCTCCTCTTCCTCCTCATCGTCACCGCCACCAATGCCGCCACCAAATACAAATTCAAAGAAGCCCCGCAATTCTACAACTCACAAA
ACTGCCCAAACATCATCATCAACCAGCAAGGTGATGAGGATCATCTCATAAATACGTGCTCTGCAGAAGCGATCCACGTAGCCATGACTTT
AGACGCCCCATACCTCCGTGGGTCAATGGCCGCCATTCACTCCGTCCTACAACACTCCTCTTGCCCACAAAACGTCCTCTTTCACTTTGTCTC
CTCCGACAAAGACGCAAACAACCTTCTTCATGAAACAATCTCCCACTCCTTTCCTTCCCTCAGTTTCCAAATCTATCCCTTCGACGACACTG
CCGTTTCAGGCCTCATCTCAACATCCATCCGCTCAGCTCTCGACTGTCCACTCAACTACGCCCGCAACTACCTGGCCAATCTCCTTCCGCCAT
GTGCCCACAAAGTCGTCTACCTAGACTCCGACTTAGTCCTCGTCGATGATATCTCAAAACTCGCCGCTACCCCACTTGGGGACCATGCAGTT
TTGGCTGCACCCGAGTACTGCAATGCTAACTTCACTTCATATTTCACCCCAACGTTTTGGTCTAACCCTACGTTATCTCTAACATTTTCTG
GACGCAATGCGTGTTACTTTAACACAGGAGTAATGGTGATTGATTTGGAGAGATGGCGAAAAGGAGACTACACGAGGAAGATCGTTGAAT
GGATGGAGCTGCAAAAGAGAATGAGGATCTACGAGTTGGGTTCCTTGCCTCCGTTTCTGTTAGTGTTTGCAGGAAACATAGCGCCAGTCGA
TCACAGATGGAACCAACATGGCCTTGGAGGTGACAACTATAGAGGTTTGTGCAGGGATTTGCATCCGGGTCCGGTGAGTTTGTTGCATTGG
AGTGGCAAAGGCAAGCCCTGGGTCAGACTTGACGCCAACAGGCCCTGCCCTTTGGACGCTTTGTGGGCACCTTATGATCTTTTGCAAACACC
CTTTCTTCTCGAGTCTTAGATATATTAATTTTGTAGTACAATTGTATCATATATATCATATATTAGTCTTAGATACACTAATAAATGTT
CACCCCCTCCCCCACCACCACCCTTTTTTCCCTTCTTGAATATACATATATATGTTTGAGGTGTTTGTTCATGTACAATCTCAGCAGGAGAG
GAAAGGAGAGGAGAGGAGAGATCTAAATCCAAGAGTACGTAGCGGAATTCAATTAGAAGATCTCTGGGTCTGTAAATTTGAATCTGATCG
ATGGTGATGAGGGAAGACGGTATTCATATATATAAAAAATGTACGCAGGTACAGCAGCCATAAAAACGTTTACAATATTTTTGTTTTGTT
TTTGTTTTTTTTCCATACACCTGAGAACTATTAATCATAGTCACAACTAGCCATTGAACAAGCTTTTCCATTTCTGGCCGTGACGTCTGAT
CTGTATTTCTGATTATTTTCATTTCATCAACGTTACATTCTAAAAAAAAAAAAAAAAAAAAAAAAAC

>YjinA-05-G03 : Full-length cDNA
NGAGTTTTTTTTTTTTTTTTTTTTTTTGAAGCAGAAACTATTCTATTTATATGAANGAANNTTGAGGACAAATATATGTGGTCGTTCACA
GACCTTTTTGACAGCAGTACACCTATCCAATTACATTCAATTCGTATGTTGACAAAATAAAAAAAAATAAAAAAACATATAAATTTAAAT
CTTTGTATAAATACCCCCCTTGTATCCTCAAAGAAGTATAGGAACATATGTTGAACACCGTCAATTTTCATAGATTCACATACAAGCAGG
TTGAAGAATCAGCTCCTATGCATCGAATGCACGAAGATTTTTTGCTTTCAAAAGCTTTAAGTGGAATCACCAAAATGATGGAATTTTTAT
TAGACTTGTATTTCCCCTCTCTATATACTTCTTTCCCTACATCAACTCTCTCATTGAATGCATGTTTGTCTGTGAAACATGCATCCACTGT
TACTGATTCAAACACGGACGCCCCAAATAGCAGAATCCTCTTCACCACATTTTTCATGAACACTTCTTATTTTTTCCACTGACTTGCAGAT
TCCACTGCAGCTCCAATCAAATGATGCAACGCAAACATTACCAGCCTGAGCTTTCCACTCACAATCTGGAGGAGTCTGGCAACACATATTG
CGGTCATCGATGTGCTCGACTTCCAGACCAATAAACCATGAACCAAGTGACACATCTTCATTGGCAAACTTATGCAATATGGGCTGGTTGA
TAGAAATATATGTGGCAAGATCCTTCGAAATGGCATAAATCTGCCCAGTTGCATGCCGGAAGTATTTGTTCCCCTCCTCGCCAAATTTCCA
GTACTCTGGCTCATGGTACTTGACATTCTTTTGAGAAAGAACAGGTCCGGATTTCATACACCCAATATATACTCGAGGCTTTGAACGGTGA
CGAGAAAGAGTAGTTGCTAGCATACCAAGATTTACATGGACATCGTCATCCACCTTAACATAGAAATCAGCATCCCATTTTGCAACAGCAG
TGGAAAAGAAAATCTTTGTTTTTGCAGACAATTCATGATATCCTTCAATGTGCTCCAGCCGTAGGAAGTCCTTGTGCTGTGCATCTTCTGA
ATCAATAGCTTTATCTAAAATGCTGTTGGATGTCGCACTGTGGCCAATCATGAATCGGATGATTATTCCCTTCTCACGTTCTAATTGAAT
AAGTTTTCCCCCTTGAGGCATCCAAGTGTCCCTAACAGAATCACGTCGCTTCCTACTACTAAAAGCAGTATTAATTCCAATAACCACGAAA
ACTTTTGGCCTTCTGGAGTTCGTACTTGCATTGGCAGCAGAACTTTCCAAGCCAGGCATTTCCCGACTACTCCGGGAAGCAGCCAGCTCCAT
CTGAAGCTGCCCAATCGGCTTGTCCAAAGTCCTATCCGATTCAACAGAACCATCATGAATTGCTCCACGGGTTTTCAAAACTTCCTTCGCCA
CATCTTGATCTTGAAAAGCTTTTTTAGCGCAATCAGTTGAAGCAACTGCCACTTGCTGCTCACGTCTGCGCACGTTTAACGATGGACGTCC
ATCCGATTCCGGTGGGTTCCACGTCAAGTTGCTGAAGAGAATCCCGAGAGCAAAGCAAAATAAGCATAAAAAAGGAATCCATTTTGTGGA
GATAATAGTAGTAGTACTCGTTCGATACTTCATTTTCTTTCTTTTTCTTTTCCTTTTTCTCTCGGAGCAAACAAGAAAAGAGAGAAGAAA
AAGAAAGCGCGTGCAGGAGGGAAGATGGGGGTTGAAAAGTCGCCTCGTGC

>YjinA-01-C06 : Full-length cDNA
AGGCACGAGGAGAAAACGAGCAAGAGAGACACAGAGACCATGCACGCCTCTTCGAACATGCACGCCCCTTCGAACCAACACCACAAAATGG
GAACTGAATCAGCTGAAGCTGATCAGCTTCACGTGGTGATGTTCCCATGGTTTGCTTTTGGTCACATAAGCCCCTTTGTACAACTTTCCAA
CAAGCTCTCACTTCATGGAGTCAAGGTCTCTTTCTTTTCGGCTCCTGGTAACATTCCCCGCATCAAATCATCGCTCAATTTAACTCCCATGG
CCGACATTATCCCTCTTCAAATCCCACACGTCGATGGCCTCCCTCCTGGTCTTGATAGCACCTCAGAAATGACACCTCACATGGCTGAGCTC
CTAAAGCAAGCCTTGGACCTCATGCAACCACAAATCAAAACTTTGTTGTCACAGCTCAAACCCCATTTTGTGTTCTTTGATTTTACCCATT
ACTGGTTGCCGGGTCTTGTTGGTTCTCAACTTGGCATCAAAACAGTTAACTTCTCTGTTTTCTCTGCCATTTCACAAGCCTATCTCGTGGT
CCCCGCCAGGAAACTCAACAACAGTTTAGCAGATCTAATGAAATCTCCCGATGGGTTCCCTGCAACTTCCATTACCTCGCTCGATGAATTT
GTGGCTCGAGATTACTTGTATGTTTATACAAAGTTCAATGGCGGCCCGAGTGTTTATGAGAGAGGGATTCAGGGCGTTGATGGCTGCGATG
TTCTTGCCATCAAGACATGTAATGAAATGGAGGGTCCTTACCTGGATTTCGTGAGAACCCAGTTCAAGAAACCGGTTCTTCTAACCGGTCC
ACTTGTTAATCCTGAGCCGCCATCCGGGGAGCTTGAAGAGAGATGGGCTAAATGGCTCTGTAAGTATCCTCCCAAGTCTGTTATTTATTGC
TCCTTCGGAAGTGAAACATTCCTCACCGTTGATCAGATCAAAGAGTTAGCCATTGGGTTGGAAATTACGGGATTGCCCTTCTTCCTGGTCT
TAAATTTCCCGCCTAACGTCGATGCTCAGAGTGAGCTGGTCCGGACTCTGCCTCCAGGGTTCATGGACAGGGTGAAAGACAGGGGAGTGGT

IP : 14.49.138.138, 2017-11-03 13:30:33

GCACACAGGATGGGTGCAACAGCAGCTCATTTTAAGACATGAGAGCGTTGGATGTTACGTGTGTCACTCAGGATTTAGTTCGGTAACTGAA
GCTGTGATTAGCGATTGTCAATTGGTGCTTCTGCCTTTAAAAGGTGACCAATTCTTGAACTCCAAGCTCGTTGCTGGAGACTTGAAAGCTG
GAGTGGAGGTAAATAGGAGGGATCATGATGGGCATTTTGGGAAGGAGGATATTTTTAAGGCTGTTAAAACAGTTATG
>HAN-02-I17
AAAAAAATAATTGAATATATTTTAATGAAAACAAATATAAAGCATAATGCTTTAGGTAATTTTTCAAACTATAGAAGCTAACTAGCTCG
AACCCGGGGACTAAATTAACATTTATCCAATTTATTACAAAATCTTAACAAACTGGGATTCATTATCCCAAATCTGAAGGTGCTGTTGCA
ATGAAGCTAAAAGTTCCGTAGCCATTCTCTATTTTATGTCAACAACCACACAAAGAATTACAAGCATTTGGAGCAAACCAAATTGGCAAC
AAATTCATCAATATTTTTGTCTGAACTTCCGCCTTTAGCCACGGCTTCTTTGGCAAAATTTCTCCATTTACCAGCATTCCGTCTTATCTCT
TTGCCTCTCTCACCCTCCAATATCTCACTAATGCAATGTGCAATTGCTTCTCTTCTGACAATTCCTTTCTCATCCGCGGGAGCTTTAAGTCC
CATTTTCCAAACATCCATAATGTACTTG
GAATTAGTGCTCTGATCAGTCCATTGTGGCATTGCCACCATTGGAACTCCCAAGCTCAGAGCCTCCAACGTAGAGTTCCAGCCACAGTGTGT
CAAAAAACATCCTGTTGCTTCATGTGCCAAAACTTCTAATTGCGGACACCAATTCACCACCAAGCCTTTCTGGGATGTTTCTTCTGAAAAG
TTTTCCGGAAGCTTAGATTGTTCGGATTCCCTTACAACCCACAAGAAATACTTGTCACTTGCTTTCAGACCCCAAGCCAATTCTTCCATTT
CCTCTATTTTTAGTGTTGCCATACTCCCAAATGATACATAAACAACTGACCCTTTTGCCTGATCGTTCAACCATTTAATGCAAGATTCATT
ATTTTGCTTAAACATGCTGAAACCATAGTCTTTGTCATCTTCAAGTTGCTTATCCAAGTACGTGGACGGTACGGTTGGTCCAATTGTCCTC
AATGACCAGTGCCTCCCCAGCCAT
TCACTACCCTTCTC

>HAN-03-L10
TAATGTGGTATGAATAGCTAGGCATTTAACAAAGATGACCGCACTATAGGCTAAGGAGAAGGCACCAACTTGCTAAAAAATTTCTTTAAA
CTGAAATCACATGAGATCAGCCAGGCTATGCAATTCCTGAACAAAACCATCAACATAAGAATTCTCAAGCCCTGGGCTGATTAAGAACTCT
CTCAGTTCAGCATGATTTTGCCTTGCATCCTTGCCCACTTCACTATCATCATCCATCACAGCCTTCACAGCCTTGCATACACCATCTCTTGT
AAATAATCCATCTTCATCGCCTCTCTCAACTTCCACTCCAACTTTCAGATCTTCACCCATCAGTCTTGAATTTATAATTTGGTCACCAACA
TTTGGGAGCAGCACTAATTGGCACTCATTGACCATAGCCTCTGACAGTGATCCTGATCCACAGTGGGTCACAAAACACCCAACAGAGGGAT
GTTTCAAGATCAACTGTTGCTGAAC
CCAACCTCCATGAACAAATCCTCTTCCTTTGACTCTGTCTTCGAATCCTTCAGGGAGTGCTGACTCTATTGTATCATGTCCCGTCGGTGGTT
TCAGGGCAGCGAAAAAGGGGAGACCTGTAAGCTCAAAACCTAAGATCAGTTCTTGGAACTGGTCCTTCTTGAGAACACATTCACTCCCAAG
TGCACAGAATATTAAGCTTTTCGCTTTAAAGCTGCTGAACAACATTTCGAACTCCTCTTCTAAAACAGAAGCAGGAGGCTCCGGCAACACT
GGCCCTGCCAAAATCACTCGCTTTTCGAACTGGCTCTCAACGTAATCACAATAAGCACCTTCAATCTCCCTGCACGTTTTGAAACCAATCGC
ATCACACTCGGTTAAACAGAGTAATAATCGCTCCATGAACGAAAGGCCACCAAAGTCTTTAACAGTTGCAGCAGCTAGTCCTCTAGCTTCA
TGGGCACGTAACTTGA

>HAN-05-A11
GCACGAGGATCACAATCAGTTCCGCGTATCGCGACCAAATCGAGTCCCCTCAGTTTCATGAAGTCCAAGCTCGTTCTCTTGGTCTCACACGA
ACTCTCTCTTTCTGGTGGTCCATTGCTGCTGATGGAGCTAGCATTTCTATTAAGGGGTGTGGGTACTAAGGTTAATTGGATCACTATCCAG
AAGCCATCTGAAGAAGATGAAGTGATATACAGTTTGGAGCATAAGATGTGGGACAGAGGAGTACAGGTCATTTCTGCTAAAGGTCAAGAA
ACTATAAACACAGCTCTTAAAGCAGATTTGATTGTCTTGAACACTGCAGTTGCTGGCAAATGGCTGGATGCTGTTCTCAAGGAAGATGTTC
CTCGTGTTCTACCAAATGTATTGTGGTGGATCCACGAAATGCGAGGGAATTACTTTAAATTGGACTATGTTAAGCACCTTCCTTTGGTTGC
TGGTGCTATGATTGATTCACATGTT
ACAGCAGAATACTGGAAGAATAGGA

>HAN-06-L11
CCCGGAAAACTTTGCAGAAGAAACATCCCAGAAAGGCTTGGTTGTGAATTGGTGCCCGCAATTAGAAGTTTTGGCACATGAAGCAACAGGA
TGCTTTTTGACACATTGTGGCTGGAACTCTACAATGGAGGCCCTGAGCTTGGGAGTGCCAATGGTGGCAATGCCACAATGGACTGATCAGA
GCACTAATTCCAAGTGCATGATGGATGTCTGGAAAACGGGACTTAAAGTTCCAGCGGATGACAAAGGAATTGTCAGAAGAGAAGCAATTG
CACATTGCATTCGTGAAATATTAGAGGGTGAGAGAGGCAAAGAGATAAGACAGAATGCTGGTAAATGGAGCAATTTTGCCAAAGAAGCCG
TGGCTAAAGGTGGAAGTTCGGACAAAAATATTGATGACTTTGTTGCCAACTTGATTTCCTCCAAAAGCTTTTAATATCTTTAATTTTGTT
GGATTTTTGTAATATCTTTAATTTGTAA
TACTTTTTACCAAAGCAAGGACAAAAATAAAAATTATAATGCTAGCGGGTGCTTGTTTCTACCCTCGTGC

>HAN-03-M15
GTTGAAGTTGTGCGTCTCTTCTGGCCTCTGCCATTGAAGACTAAAATGGCCATCACCTTTTCAGATCTCCACACAGAGTCAGGCCTTAAGT
CTCTCGATCAGTATCTTTCTGGGAAATCTTATATCTCCGGTGATCAACTGACAAAAGATGACATCAAGGTCTACGCTGCCGTTTTGAAGAA
ACCTGCCGATTCTTTCCCCAACGCCAGCAGCTGGTACGACAGCGTTTCTTCACATATCGCCCCAAGCTTCCCTGGCAAAGCCCTTGGTGTGA
GAGTTGATGGCAAAGGTGCTCCAGTTGACGCCGCCGCAGCCAAGCCTGCTGCTGTTGGAGGTGGTGATGATGATGATTTGGATCTCTTCGG
AGATGAGACTGAGGAGGATAAGAAAGCAGCAGAGGAGAGGGAGGCTGCTAAAAAGCAATCATCCAAGAAGAAAGAGAGTGGAAAATCATC
GGTACTTTTGGATGTAAAGCCTTGG
GATGACGAGACAGACATGAAAAAGCTAGAAGAGGCAGTTAGGAGTGTTGAGATGCCGGGTCTCTTTTGGGGAGCATCAAAATTGGTCCCA
GTCGGTTATGGGATTAAGAAGATGCAGATCATGATGACAATCATTGATGATCTTGTTTCTGTGGATTCACTCATAGAGGAACACCTCACA
GTTGAGCCCTGCAATGAGTATGTTCAGAGCTGCGACATCGTTGCCTTCAATAAAATTTAAGAATCCTCTCACTGTTTTGCCTTATAGTGCA

IP : 14.49.138.138, 2017-11-03 13:30:33

GCCATTTTTGGCTGCAATTTAGTTTTTGTCGTTTTAATTGTGTTCTGGGTTTTAATGGTTTTGCTTGGCCTGCATTTTCCGTTGCTAAAT
TGAGAAGAAATGACAAAATTTCATCTATATATATATATTTTCTAATCACAAAACAAAGCTATACGTTAAAACAAAAAAAACAAAAAAAA
AAAAATCATGAGCATAAAACCAACACCACA
ATAAATTAATTTACATGTCCGGATCCTCGGAATTTGAAGCTCCCGGCTGCCGCCTCGACCTATGTCTATGACTCTTATGGCTGCCGCCGAAT
TTCAACCTACCGGTGTCTTTAAAACGTTGTCGTTCTGATGGAACAAGAACACATTCGGGTAATGGCACGGGGTATCGCATTGTATCATAAC
AATATGAATAGTACATGTAACGCTCCCGGAATCTACGCATGGCCCGTCTCCCGGCCGGAGTGATGACGGAGAGGCCTTTCTCGGCAAGCCGG
GAATCGGTGTCTTGGCAGTTGGAGGAGGGGACTTGTTCAATGGGATCAACAGGGCAGCCCTCTAACACAAAGTCTTTAAATTCAGAAGTGA
ATGGTGCGTACTTGTAATTAACTTTGGCTTTGCCACCTGATGTGGCCCAATTTGAGGCATCCCAAATTGTTGTGTACAATGACATTGGCTT
TGATGGGAAATCACCACCCATTG
CCTTTGAGCGCACGACTTCCCTTATCGGTACTTCATCCACATAGAATATAATGTTGTTGCTTGTCCAAAGAATGCTATATCTATGAAATTG
CTTCGTGGGATCAAACCAAAGCTGGTATCTCTCTTCTCTGCCACGTGCCGTGCTCCCATTTCCATAGAAATTTGTTTGGAACCTCCACGGTT
TTCCAGCCACGTTTCCTAGAAACTCAAAGTCTAATTCGTCGTGTGTTTTTGGGAACACGTCTCCGTTTGACGTATAGAATGCAACACATAA
GCCAGCCGTGTGATCCGATGGCAACTTGATCATGGCGCTAAAGAACCCGTGATTGTACAACTTTGACGAAACAAAACCGGACCCGGAGAAG
CGGTTGAGGAGGAGACGAACGTTCTTGCCGTCGGGGGAGCGAATGAGATTGCCGTCGCCGAAAAGATGAGAGTAGCCTTCATCGAAAGAGA
TGGTGGCGAGGTTGAAAGCAGATG
ATGACGACAACGACGACGCTGCGTTTGTGAATGTGAACACAAGTGATGGTGATGAGCAGCAACACAACAGAATTAGAATTAGAGTGAAAG
GGTGCTGATGATTTTTTTGATTGAGAGCAAAGAAACCAATCCATTATTATTTTTGGTTTCTATAAATCCTCGTGC

>HAN-05-N24
GAAAGAGGAAAAAGAGTATGGTGATCATGTGCTAATGGTATCACTCGCAACCCAAAGTCATATTAATCCCTTGCTTAGACTAGGCAAACG
CCTAGTCTCTAAAGGTCTCAGTGTAACGGTTGCCACACCTGAAATTGCCCAACACCAATTGCTCAAATCATTCACCAGCAGCAAAATCAAT
GATTGTGTTTCTGATGATATCCCATGTCTATATTTCTCCGATGGGTTCGATTTAGATTACAACCGCAAATCCGATTTAGATCACTACATGG
AAACTATAGAGAAAGCTGGACCTGGTAACCTCTCAAAACTTATCAAAAACCATTACCATGATAAGCACAAGAAACTCTCTTGCATCATTA
ACAATCCATTTGTTCCATGGGTTGTTGATGTTGCTGCTGAGCTTGGAATCCCGTGTGCCATGCTTTGGATTCAACCATGTTCACTTTTTTC
TATTTACTATCGTTTCTATAACAAATTAAACCCATTTCCCACCTCGGAGAATCCAAATTCAAGTGTTGAGTTACCAGGGTTACAAACTTT
GCACACACATGATTTGCCTTCATTTGTTCTCCATTCAAATCCATTTGGTAGCTTCACAAGAATTCTCAATGACTTGTTCCAAAACCTGAAT
AAGCAATACAAGTGGGTATTAGCAAATTCTTTCTTTGAGTTAGAGAAAGAAGCCACTGAGTCTATGTCTCAGCTTTGTCCAATACGACCT
GTCGGTCCTTTAGTCCCTCATTCATTGCTAGGCCAAGATGAAAAGCTTGATGTTGGAGTTGAAAGGTGGAAGCCTGAAGATTGTTGCTTAG
AATGGCTTAACAAACAATCAAATTCTTCAGTTGTTTACATATCATTTGGTAGCCTTACCCAGTTATCAGCTAATCAAATGGAGGTCATAG
CCACAGCTTTGAAGAACATTAAGCTTCCATTTTTGTGGATTGTTAAGCAATCAGAATCTGCTTCTTCTGATGGTGAGGGTACTTTGCCGTT
ATGGTTTCTTGAAGAAACTAAAAACCGAGGCCTTGTGGTATCAT

>HAN-06-D23
GCACGAGGCAATGAAATGTAAAATCAACTTTTAAGGAATGTCCCATTTTCTGAAATTCAATCAATTGGGGAAAGAAAAAAAAAAACGCGCC
CTAAAAGTATAGTTATAAATAAGATATATACGGCACAGTTTTAGCAGTACAACACAATTCTGTAAGGATCTATTGACCAATTCACAATTC
AATTTTCAAACTACCAAAGTTTCCGTGATTTAAAATCAAAGATCAACCTCTCCCAAATTGATTTGAAAGCTAAATCGGACTACATGGAGA
TGGAACGAGCCTTGTACATGCAAATGTATGCCATATGCCAATCACCTCCTCCAGACAGTTTAGTGATGTCTTCCTCTCGCTGAGGAAGGGG
ATTATCATCATCATATTCAATCCATTTTCCACTTTCTTGCTTCACCCAAGCAACATAATGCCCTGAATCAGCACTCCTACCCTTGTGGGTC
AGCACAGCAACCAGATCGTAGATTCCAGTTAGATGTGTTTCCTTGTCAGTGTCAGTAGTAACCCCATCTTGAGATGAAGCTACTGATGATT
CTCCACTTCCATTTGATGCTGATCCCTCGGCTTCTGTCATTTTGACGTCATTATCCTTCGAATTAGAGCTCTTCTCACCACCTTTTTTTAA
ACCAAGCTTTTTACCCTCCTCATCCCTTAGTTTCTGACGAGGGGCATCCAATTTTTTGCGAAGATCATCAGAACAGAAATCGTAAACATCC
AACTCCAGCGGGTAATCCACTTTCCTCAAAATCTTGGCTTTCTGGTTTGACTCCCTCTTCCAGAAAAAGCGAACAAACTGAATGGTCAAGT
ACCTAGGCAAGCCATTAATACAAGACTCTTTCAAGTAAACTGCACTACGACCCAAGGCAGGAGAAGCCTTCTCCAGTTCTGATTTCAAACC
ATGCTTTAGTCCTTCATGCAAATGGTTCACCTCATGTGATATGTGACATTAAAGAGCATAAATTGATTCCGTTTCCGAGCTTTCCTCACCA
CTTTCTTGGCAATGCACTCTGCTCACAATATCAATACCGAAAAGGGCTTTCACTGTATCGGGAATTTCACTAGCATTTACTGATCTTAGAG
ACTGTGAAAGCGTATACAAAAGCTGTGTCCAACACTCTTCAGCATCCTGCTGCATGAAGGTACCATTGTGCAACTGGCCAAACTGAGGATA
CTTTTTACGCAACAGCATCCAAAACTGCATAGGAGCCACAGGCTTCACACTTTTATCAAGATCATTAAATAATTCAGAAGTAGCAACTGTC
AACATATGAGAGCTTTGATCCACATCATTGCTTCTTCCAGACTGTGAATACTTAATTAAAGCAGACTTCAACTCTGGAACAGAATGCAGGC
ACTGGATGGTGGAGTTCATGTAGCAGGTGTTTCCCAAATTGAACAGGCCAGCACTATGACCCAGTGATAACACTTGTTCTTCTTCAGGAAG
ATCTTCCACAAAAACAGGTCCCTTCTCAGGAGCCTTCACAATCTCATCTGCTGTTCCCATCATCATCAATCTTTGACCCTGTTTCACTCCTA
ACATTGACCAATCTGAATCATCCTTCAGTAAACCGCCCTTTACCATAATCTTCTGCCTTTCTGGTGGCACACCAGTCAGATCATACAATTG
ACACTTGAAAACATAAGGGGTCTGGCTAGTGTCAATTTCCACATTCGAAAAGACCTCCTTTTGCCATTTCACACTCACTGTTAGCATGATT
GAAGAGGCTTAGAGAAATCGAGAAAAATGTGTAAATGGGTTTTTGAACAGTTCGGTTTTTC

>HAN-03-E09
NTCGAGTTTTTTTTTTTTTTTTTTAACTAATCTCTTTTATAATATAATTGATAATGGAAATTCACATTGACAAAAGGCAAATTACACAC
TGACTGGGCAAAATAAAAAAAAAAAAAACAGAGTCTCTCAAAAGCAATAATAATTTAAACACAACACCACCTTGAGTAGACACCCCAAAAA
TAAAGCAGCAAGCTCTTACTGTGACCACACACACACACACACACACCAAATTTTTATTATAAAATAAATCTAAAATGATGGATGATGATG
CTGATGTTGATGCGTCACATAAAAGTTCATTAATTTAATCGCTGTCACTGCTGCTGCTGCTCTCGTGTCCGTCCTCGTGCTTCTTCTTCTCC
TTCTTCTTTTTCTTCTTCTCTTCACCGTGGGCGGCGCCCTCGCCGCCGCCGACACCGGGGATCTTCTGCTTGATCTTGTCCACCAAGCCCTCC

IP : 14.49.138.138, 2017-11-03 13:30:33

TTGTGTTCGCCCTCCCTGTGTTCCCCGCCGTGATACTGCTGCTGCTGCTGATGGTGAACATCAGTAGTACCGACACCGGGGATCTGCTGCTT
GATCTTGTCCACCAAGCCTTCCTTGTGTTCGCCGCCGTGATACTGCTGCTGATGGTGAACATCAGTAGTGTGGTGGTCCCCACTATGGTGCT
CACCCTTGTGCTTGTCCTCCTCTTTTTGCCCTCCTCCCATGTGAAGGGCTTCTCCGATCTTGTGAATAACTCCTGACATTTTCCCTTAAAAC
GACTATTCCTCTTCTTTTCTTTTCAACGAAAAGAGTTGTTTGCTATCTTCTTTAACACAAACCAACTCACGTCTTTATTCAGCTCACAAAT
ACAAATCCGACTTTTGATTTCCTGTAAGGATCAGAAATATCCAACAAATGCACAAACTTCGGACACTGTTAATGCAAGAAGACTAAAAGA
GAGTGCAGGTCACTATCTTATCAGCTTTTTCTTCAACACCCCACAATTATTGCAAAAAAAAAAAAATCCCCTTAAACAATATAAACTTGGC
CTTGCTACGGATTTTGGATAAGTCGTTCAAGTTTCACTCCTTGGGTTGGGGAACGCTGATCACATAAATATTCAGAAAGATCTCATTGAA
TACGGCCGGGACATGCCATGTTTTAATTTTCATACTGCCCTTATTAGAAAGATAGATGTAAGTATTGGAAAATCTAGTATGACAAAATGT
AACTAATCAAGTTTTCTAGAGATTGATATGAAGAACTGCCTTGCTTTGTACAAAGATCCAGTTTTTCCTTCAGAATCGCAGCTCTGTTCCT
CATTTCCCGCCCCTCGGCATCCACCATTACTCGTCTAATTGCCCTTTCAACCTCCCCTCTCTCCAGCTTCCTTTCCAAATGCAAACCAACTTT
CCAAACATCACTAACATATCTTGCAATCACCATTTGCTCACCATGACAAGGCTGGCATATCATGGGGACACCTTCACACATACTTTCCAAC
GTCGAATTCCAGCCACAATGTGTCCAAAATGCTCCGGTGGCAGGATGAGCTAGCACTTCTTGCTGNNAGCCCATTTCACTATATGCCCTCTT
CCGTCTAACATTTCCAAGAACCCTCGTGGTAATAGCTCAATCCATTCTGCTCCGCGGACTAGTCCTGGCCGTACCACCCACAAGAATGGCAC
CTTGCTGTTGGCTAGGCCCCAAGCTACTTCCAAAAATTTGGTCTCATCAATGGCAGCAATGCTTCCAAAACTTACATAAATTACAGATTTT
GGTGCCTGTTTGTCTAACCTAGAAATGCAGATTCGGTCTTGTGACAATAAGCTACTTGCAGAAGCTGGATAGTACTTGTGAAACGGGCCTA
TAGGGAACGATGGAATGGGGAACTCCCGGTGAAATTTAGCAAGAGAATCTTGTTCAAGTTCCTGAACTGAATTCCATATGCATCCTGAGG
AAGCCTTCATCTGATTGATTGCTTCTGCTGCAAATTGATGCAGTGTCTCTTGATAAAGCGTTTCAATGACAGGAATGTCTTTCATTCTTAG
AGGCGGAAGCTCTGGCACTGGGGCTTCCAAATCATGAGAATCTTGTATGGGAAAGTAACCCTTTTGGCTTAGAACTGGTAAGGCAGCATAA
ACAAGAGAGGAAGAGACACTGAGACTCCTTAACACAATCCTGGGGAGCTTTAGGCTTTCAGCAACATCATGAGTGAAGAACCAACTAGCAT
CTGTGATTAAGCAAGCAATAGGCTCTTCTTCCCCTCGTGC

>illhan-04-I08
TTAGTTCTATATCCACTGGCTAATAAAATTGCTGCAGGCTGAAGAATTTCAAAGCCATATAGAAGCTACATACTTAGCACATCATATACT
GACCTACTCGTCCCACTTGCATAAAGTTTGTCAGATATTGTAACGAAATCCAAAAGGAAGACAACACAAGTTTACAACCGATACATAGTC
AACTAAAATCACACTTGCTTTACAATTCATGACATTCAAAAGCCCACCTCCCCAGAGGAGCAAACGATCCATACCCTTATGCCTCATCTAT
CTGCATATCTGAGGTNCCACAGAGTGAGGTTGTCTCTTAGCAATTGCATGATAAGAGTGCTATCCTTGTAGGATTTCTTCACCCAAAGTGT
CCAGCTCAGCAATGGCCTCCTCAAAGGCCTGTTTGGCCATGGTACAAGCTTTCTCTGATGAATTGAGAATCTCATAGTAAAACACTGAGAA
GTTGAGTGCCAGCCCCAACCTTATAGGGTGTGTTGGCGCCAGATCAGTCAGTGCAATATCCTGAGCCGCCTTATAAGACAACATAGTGTTT
TCAGCGGCGGCCTTCCTCTCATCACCAACTTTAAACTCCGCCAAGTAACGGTAGTAATCTCCCTTCATCTTCAAATAGAAGACTTTGGACTC
ACCAGCAGTAGCCGAAGGCACAAGGTGCGAGTCCAGCAACTTCAATATGCTCCCGCACACGTCAGATAACTCAGACTCTACCTTTGACCGAT
AGTCTTTGACCAGCGAGACGTGTTCCTCGTTCTTGCGGCCTTCCTCTTTCTGCTCGATAGAGGAGATAATACGCCACGCGGCGCGAAGAGAG
CCGATGACGTTCTTGTAAGCAACGGAGAGGAGGTTGCGCTCCTCGACGGTGAGTTCAGTCGCCGGAGTGGAGGAAGTGACGAGGCTGTCCAT
GAACTTAACCATCTCTTCATAGCGCTCGGCTTTGCTCGGCGAGTTTCG
CCAGGTAAAC

>illhan-06-G16
TATCTCCAACTTTCTCCAAGAACCCATTTGGCAGGCCAACAATTTTAACGCCAGAGTCTTCAGACGGCGGCTTCATCACCCACAAGAACGA
AATCCCCGAGTTCAACAATGCATAGCCAATTTCTTCAACTTGTTCTTGCTTCAAGTAGACAACCGTGCCGAAAGAGATGTACACAACGGAT
GATGGTGGCTTTTTGTCGAGCCAGTCTATGCATTCATCGGGTTTCATGCAGTCATCGCGGATGGTTAAGGTTGGAGCTTTAGGGTTTTTGA
ACAGAGGGCCGACGGGTTTAATAGGGCAAATTTTTGCCATGTGATCGATAATCTCTTTCTCAAGCTCATAGAAAGTGTCCAGCAATATGCA
AAACGGCTTGCCAAGATTCTCGTAGTGCCCCAAAATAGCTCTTTTTCAAGAAAGAATAAGGAGTTGACGGATGCAAGAAGCTAGGCACTTC
ATCATGCTTCAGTAGTGGCATGCACGGCAACTGAACATCAATTTCGGGTTCTTTTTCACTAGGAAATGGAACCAAACCGTGAAAGTAATGG
TAATAAGCAGCAAAACAAGCACAAGATTGAACCCAAAGCATAGCAGACGGAAGCCCTAGGGATTCAGCAACATCAGAGACCCAAGGGATA
AATGGGTTATTGATCAGGCAAGAAACGGGGCGATATTCATCAGCGCTTTTCTTGATTATTTTTGGAATCACTTGTTTGCCTATAAGCTCA
AGTTGAGCCATGTATTGGTCAAGATCTCCGCGTCTTGGATCGTTTTCGTCCCATCCATCCTCGAAGAATTCGAAGCGAATGAAGCCGTCGCC
AACTGGAGTAGGCTCGTAGGTGAAGTTACCCGCTTTTCTCATTTGTTTGCCAAAGCTTTCAGGTGTGGTCAAGGTGAGAAAGAAACCCTTT
GAAGCAAGGAGTCGGCCGAGCCTCAGGAGCGGGTTTACGTGGCCATGGCCG
GGGAATGAAACTAGTAAGACATGAACAAGAGATTCAGTTCC

>illhan-06-I09
TTTTTTTTTGTTCATAAAGATTAGTTATTTTACATCACAGAGATCTGTTGCCAAAAAAGTGTCCTCAATAAGGCAAATTACTGCCCAAAA
AATTTCTACAATTAGTCCCTGCCTTGTTAGTTTGTTGCTTTTTGTTGTTGAGTCATCTTTGCATGGAGAAACTTGACAAGCCCGTTAAGGG
AAACTTCAGCATTTGTGCTCTTCATCAACTCACCAGCCACTTCTGCAGGTGTAACATTCACTTCCTTTATCAGCTCTTCAATTTGTTCAAA
AAGGTGGTGATGGCTGATACCCAGATAGTTGAATGCAAGTTGTTTAAACACAGAAGTGTTGCAATATGACATATGAAGATGCATGTCCAT
GCGGCCAGGTCTCAGCAATGCCGGGTCGAGTTTCTCTTTGTGGTTTGTTGTAAAAACAATGATGCGACCCTCACCACAACAAGACCACAAA
CCATCAATGAAATTCAATAGTCCTGAGAGTGTCACCTTGTTCTCCTCTTGATTCGTTGCTTGTACTTCTGATGATTCTCGATTCTGTAGCT
TGACAGAGCAATCAATATCTTCTATTACAAGCATTGATCGGCTTGGCATTGTGAGCAGCAGAAACCTGAGTTCTGAATTGGATTTAACTG
CGCTTAAATCCAGGTCATAGATGTCAAATTTGAGTTGATTAGCCATGGCTGCAATCAAGCTTGACTTGCCAGTCCCCGGAGGGCCATATAG
CAAATACCCACGTTTCCAAGCCTTCCCAATTCTTGTGTAATATTCTTTCCCATTCATAAAATTTTCTAAATCCTCCGTGATTTCCTTCTTG
AGCTCTGAATCAAGAGCAAGAGTCTTGAATGTCATTGGATGCTTAAGCACAATGTTATTTGCATCCCAACGCATATGCATAACTGTATGA

IP : 14.49.138.138, 2017-11-03 13:30:33

AGCTTTACCACTTTGCTTTCTTCTTTGATTGCTTTCGCCTTCTCCAGAACATGGGGCAAGTACAAGTTGAGTACTACGTCTTTATGTTTCT
TGTGAAAACTTAACTCATAATGTCTAACTTCTGATCGAAGAGACGCGTTGTAATCTCCCAAGTTTGGATTTCTGTATTCCATTGATGAGG
GAACTTGTGTGTAGACTAATTTCCATTTCAGCGTTACATCTTTAAAAACATCAAACGTTTCTTCATTTCTATCAAGGGCTATTTCGAAAG
TCTTTTCTTTTTCGCTTTTTCCCACCCGGAATCTTTGAGCGGAGGTGGTAGTTGCCTTGTTACCCAAGTAATAATTTGCTGCTTCAAATAC
CTGGTTTATGGAGAATCCTTGGAATTCTTCGACAACAATGGTGAGTTGAGAAGAGAAGTATTGAGAAACCAAATGTATCTTGGAATCCAA
GTAGCCGTAAAGCTCAGCTGGTAGAAAATCATTGGCAACGCTCCGAATGAGCATGGCGGATGCAGAGAGTGAAGCTGCTGTTGACAAAACT
GTTTTTGGGCTAATAAAATTGCTGCAGGCTGAAGAATTTCAAAGCCATATAGAAGCTACATACTTAGCACATCATATACTGACCTACTCG
TCCCACTTGCATAAAGTTTGTCAGATATTGTAACGAAATCCAAAAGGAAGACAACACAAGTTTACAACCGATACATAGTCAACTAAAATC
ACACTTGCTTTACAATTCATGACATTCAAAAGCCCACCTCCCCAGAGGAGCAAACGATCCATACCCTTATGCCTCATCTATCTGCTCCTGCA
TATCTGAGGTCCACAGAGTGAGGTTGTCTCTTAGCAATTGCATGATAAGAGTGCTATCCTTGTAGGATTCTTCACCCAAAGTGTCCAGCTC
AGCAATGGCCTCCTCAAAGGCCTGTTTGGCCATGGTACAAGCTTTCTCTGATGAATTGAGAATCTCATAGTAAAACACTGAGAAGTTGAGT
GCCAGCCCCAACCTTATAGGGTGTGTTGGCGCCAGATCAGTCAGTGCAATATCCTGAGCCGCCTTATAAGACAACATAGTGTTTTCAGCGGC
GGCCTTCCTCTCATCACCAACTTTAAACTCCGCCAAGTAACGGTAGTAATCTCCCTTCATCTTCAAATAGAAGACTTTGGACTCACCAGCA
GTAGCCGAAGGCACAAGGTGCGAGTCCAGCAACTTCAATATGCTCCCGCACACGTCAGATAACTCAGACTCTACCTTTGACCGATAGTCTTT
GACCAGCGAGACGTGTTCCTCGTTCTTGCGGCCTTCCTCTTTCTGCTCGATAGAGGAGATAATACGCCACGCGGCGCGAAGAGAGCCGATGA
CGTTCTTGTAAGCAACGGAGAGGAGGTTGCGCTCCTCGACGGTGAGTTCAGTCGCCGGAGTGGAGGAAGTGACGAGGCTGTCCATGAACTT
AACCATCTCTTCATAGCGCTCGGCTTGCTCGGCGAGTTTCGCCAGGTAAACGTATTGCTCTCTCGTCGGGGTTCCCATAGCAGAATTGCAGA
AACTGTAAAGTTAACTGGAGGGGAATTGGATCTTC

>YHANP02-O22
GAATTTTTGGCAATGGCACTGAATCAAGCCACACATTGCCTCACTCGGCAACAAGGGCAGCAATGCTGGTGAGAGTCAACACCTTGTTACA
AGGATACTCAGGCATCAGGTTTGAGATCCTGGAAACCATTACCAAGTTCCTTAACCATAACATCACCCCATGCTTGCCGCTACGTGGCACG
ATCACCGCGTCGGGTGACCTGGTCCCACTCTCGTACATTGCTGGGCTTTTGACAGGCAGGCCCAACTCGAAGGCTGTTGGGCCCAACGGCCA
AGTTCTCAACCCCACCGAGGCCTTCAACCTAGCTGGGGTCACTAGTGGATTTTTTGAATTGCAGCCTAAGGAAGGTCTTGCCCTGGTGAAT
GGCACAGCGGTTGGTTCTGGTTTAGCTGCCACGGTACTCTTTGAGGCTAACATATTAGCCATTATGTCTGAAGTTTTATCTGCAATTTTTG
CGGAAGTGATGAATGGAAAACCTGAATTTACGGACCACTTGACGCACAACTTGAACCACCATCCGGGACAAATTGAAGCTGCAGCTATTAT
GGAACACATTTTGGATGGCAGCTCTTATGTTAAAGCAGCACAAAAGTTGCATGAAATCGATCCTCTTCAAAAGCCAAAGCAAGACAGATA
TGCTCTTCGAACATCGCCTCAATGGCTAGGCCCCCAGATTGAAGTGATCAGGGCAGCTACCAAAATGATTGAAAGAGAGATTAACTCCGTG
AATGACAATCCATTGATAGATGTATCAAGGAACAAGGCGCTTCATGGAGGCAATTTCCAGGGGACCCCAATTGGTGTTTCCATGGACAACA
CCCGTCTAGCCATTGCTTCAATTGGCAAGCTCTTGTTTGCACAATTCTCTGAGCTTGTCAATGATTTCTACAACAACGGGTTGCCTTCAAA
TCTTACTGGGGGACGTAATCCAAGCTTGGATTACGGATTCAAGGGTGCCGAAATTGCAATGGCATCATACTGTTCTGAACTCCAATTCCTC
GCCAATCCTGTCACCAATCATGTCCAAAGTGCTGAGCAACACAACCAAGATGTGAACTCTTTAGGCCTCATTTCTTCTAGGAAAACTGCTG
AAGCAGTAGACATATTGAAGCTTATGTCGTCAACTTTCTTAGTTGCTCTATGCCAAGCGATTGACTTGAGGCATCTGGAAGAGAACCTCAA
GAACACAGTGAAGAACACCGTGAGTCAAGTTGCCAAAAGAGTCTTGACCATGGGAGTGAATGGAGAGCTTCACCCTTCAAGATTCTGCGAA
AAAGACTTGATCAAAGTTGTGGACAGAGAATATGTCTTTGCATACATTGATGATCCTTGCAGTGCAAGTTACCCATTGATGCAGAAGCTG
AGGCAGGTGCTTGTTGATCATGCGTTGGACAATGGAGACAGAGAGAAGAATTCAACCACTTCAATCTTCCAAAAGATTGGAGCCTTTGAG
GATGAACTAAAGACCCTTTTGCCTAAAGAGGTCGAAATCGCCAGAACTGAACTTGAGAGTGGAAATGCAGCCATTGCAAACAGGATCAAG
GAATGCAGGTCCTATCCGTTATACAAAATTGTGAGAGAAGAGATTGGAACAAGTTTGTTGACGGGCGAAAAGGTTCGATCCCCAGGTGAA
GAATTCGACAAAGTTTTCGCAGCAATGTGTGAAGGGAAGTTGATTGATCCTATGCTTGAATGCTTGAAGGAGTGGAATGGTGCTCCTCTT
CCTATTTGCCAGAATTAATGGTTTGATTAAGTACAGTTTTATGACAGTGTCTTTTTTTATGCTTCTTGTTCTTATGCTTTTACTTGCCAT
GTTGTGTAGTCAACTTGAAACAGTCAATTCAATTGCTTTTTTGGTTTTTCTGTATTTGGAAAAGTTGGGACAACAACAAATGTAATGTTG
ATAACAAGATCTTTTGTTATTTCAGTTCAAGTTGAATTAATGAAATATGAAGAAATATTTCTGTCGAAAAAAAAAAAAAATGCAAGCGCC
GGATCAATATTACATATGGGCCAATCAACATAAAATTAAGCCTAATAAGATCTTGATATCATGTCTACCAATGCATCAAGATTTTGCATG
GAACTTCCACCGGGA

>YHANP-04-I05
CAGCAATGGCGCAAAGAAAAGAGAATATAGTGATGTTCCCATTCATGGCACAAGGCCATATAATCCCCTTCCTAGCATTAGCCCGTCGCTT
GGAAGAAACAAACAAATACACCATAACTCTTGTTAACACCCCTTTAAACCTTAAGAAGCTCAAATCATCTCTCCCTCAAAATTCCTCTATT
CACCTTCTTGAAATTCCTTTCAATAGCGTAGAGCATGACCTCCCTCCATGTACTGAAAACACAGACTCTATTCCGTATCATCTCTTTCCAA
AATTCCTTCAAGCATCAGCATCGCTCGAACCCCACTTCAAGAAACTAATCTCTGAACTTGTCAATGAACAAAATGGCCAAAAACCACTTTG
TATCATCACTGATACGTTCTTAGGCTGGTGTAAAGAGACAGCACAAGAGTATGGTATTTTTCATGCTATATTCATAGGAGGTGGTGGCTT
TGGCTTTGCTTGTTTGTACTCGATGTTGCTAAACCTACCTCACCGCAGCACGGATTCTGATGAATTTCTGTTGCCGGATTTTCCAGAAGCT
TCAACACTTCATGTAACACAGATATCTCCTTACTTACGTGCTACCGATGGAAGTGATTCTTTTTCAGTGTTTTATAAGAAGTTGCTTCTTC
TATGGAAGGATGCAGATGGAATTTTGGTTAACACGGTTGAGGAACTTGACAAGATTGGACTGATGTATTTCAAGAGAAAATTTGGCCGGC
CGGTTTGGCCAATAGGGCCTGTTCTTTTGTCCACGGAAAGCAGAGCTGGGGCCAGAAAAGAGTACGGAATCTCCACAGAGTTGTGTAAAAA
ATGGCTTGATACAAAGCCGTACACTTCAGTTCTGTATGTATCATTCGGTTCACAAAA

>YjinA-01-E02
GCTCGCAAAACCTGACTTATATCTATTTTTATATTTGAATGAAAATGGGATGACAAACTCAGAGAGGGTTGGGGCGGGGTTATATCTATG
TAACTTAGGGATGCTAGCATTAAACAATGGGGCCAATGGAGCCAAATCCTGCGATCAAAAAGGGAATTGTTTGGAGGAAAAGGTATATGA

IP : 14.49.138.138, 2017-11-03 13:30:33

AGTAATTGTTCTTCCCATGGACAAAATCATAGCATCCGCAAAAAAAAAAGAACACTCCAAATCCCCGCTCCCAAGTATGCATTCTCTCAGC
AAATTTGATTTTAGGTTTTTTGGGAGCTTTGGTATTTGTTTTGTTCTTCCCATCAGCTGCCTTATTCTTGAAAGCATCTCCAAGTTTTTC
GGGGACAACCCATTCATTGGCCCTTCCAGCTTCGAACAAACCAATAAATGGGGCCTTGGTTCGATGCAAAAACATCACATTCTCAAAAAGA
ATCCAGTAAAACAATAGGGGAATAGACCTTGGAGTCCAAACTGAATTTAAAATGGGGATTATGGAAGGAATATAAACAGCTCCCCAGAAT
GGAACTTGAACTTCAGGAACCAAAATGGTTAGCGGAAGCACGACGCAATAGAAGGAAAATGTGACCATATGGGCAATTATCTTCCGGACA
AAGAAGAAACTGTAGATAACATAAACTTTCTTCCAGAATTTAACTTTCTTATTTCTAATAATCTCCATCACCATTTTCCTGAATAAATTG
GCAGGACCACAAGACCATCGGTGCTGCTGGAATCGGAAAGCTTTGAAAGTACTAGGAAGTTCACTTTTCACCTGGAGATCACCGAGGTACA
CAAATTTCCATCCCTTGAGACTAGCTCGAACAGCAAGGTCCATGTCCTCCACTGTAGTTCGATCCTTCCAGCCACCTGCCTCATTGATAGCA
GCAATTCTCCATACACCAGCAGTTCCATTGAAGCCAAAGAAAGCATGAGTTGCTGATCCCACTTCTTGCTCCACTTTAAAATGGTAATCCA
ATGACATCTCTTGCATTCTTGTCAACAAGCATTCATTTGCATTTACGAATCTCCAGCGAGCTTGAACAAGGGCAATGTCAGAGTTTTGGAC
TAAGTAAGGAATGGCACGTCGGAGATNAATCGGGCTCCGGCCGGAAATCGGCGTCGAAGATGGCCACGTATTCACAATGTTTAACATAGCT
TCTTTTGAGCCCTTCTTTGAGAGCACCAGCTTTGTATCCCGTGCGATTCTCTCTGATTTGGTACCTTATGTTAATGCCTTTGGCCGCCCATC
TTTGGCACTCTTGCTCCACCATTTGCTTGATGGCAGGGTCAGTTGAATCGTCAAGGACTTGGATCACGAGACGATCGGACGGCCAAGAGAG
TCCGCAAGCTGCTCCAATGGAGATTTTGTAAACCTCTTTTTCATTGAACATTGGGATTTGAATAAGAACAACGGGGAAATTAGAGCTGCCC
AATTCGACATCGTCTTCAATAGGTTGCCAATTGTAACGCTTCTCAGGTTTTGGCCAAAACAGCTTAACAAGGATTATAACAATGCCCATGT
AAACCCTTTCCATGAAGAGCATGAGTGACATGGCCAAGCAAATGTAGACGCCGAGTTTAAGCAAAGGGACTATCAATGGGGCTTTGAGTAG
TTCCCAAATCAAACCAATTTGGCCTGCAATGTCCTCTCTTGACACTTGGAATGACTCTGGTATGAAAAATTTTGGTGAAATTTGAGCCATT
TTCTCTAGCAGAGCAAAACAGGGGAGGCGATAAAGAGATTTTTTTGGCTAATGCTGGTTTAAAAACAAGAAACAAGAAGGAAAATTTTTC
ACAATGTGATTGAATTGGAACAAATCTTGGCTTTTACATGGAAACTTGAACACAATGGGCAAAAATTAAAACGCAAATTAAAAGACTTTC
TCTCTTTCTCTATTTTTTTTCCCCCTAGTTAAGGGAAGAACAGAAAGATCTTTACTTACTGGTCTTTTAGCCAATACTTGCTCTGTTTTTT
TTTTTTTTCTCTCTACCAAAATGAAGCAGAGACAGAGCCTCGTGC

>YjinA-01-G05
AATGAAAGTATGTGATCAACCAATCTCTTTAGAGATTGATATGAAGAACCAGCTTTTAATAAGGAAAGTTCCAGTTTCTCCTTCAAGTGC
ATAATCCTCTCTCTCATTTCCTGGCCTTCAGCTTCAACAGTTACTCTTCTGATTGCTGTTTCGATCTCCCTTCTCTCAAACTTCCTTTCTAA
ATGCAATCCAACCCTCCAAACATGACTAACATATCTTGCATTCACCAATTGATCACCAAAACAGGGTTGGCAAATCATGGGGACGCCTTCA
CATATGCTCTCCAATGTTGAGTTCCAACCATTGTGTGTCCAAAACCCTCCAACAGCAGGATGAGCTAAAACCTCTTGTTGGGGAGCCCATT
TTACTATATGCCCTCTTCCATCCAGCATTTCCAGGAACCCTTTTGGCAAAGGTTCAAGCCATTCTACTCCAGGGACTGCTCCTGGTCGAACC
ACCCAGAGAAAGGGTACCCTGCTATTCGCTAGCCCCCAAGCTATCTCCAAAAATTCGGTCACATTTACAATAACTATACTTCCAAAACTCA
CATACATTACAGATTTTGCTGCTTGTTTGTCTAACCAGGAAATGCAACTTGGGTCTTGAGATAGTAAGCTACTTGAAGAAGCTAGACAGT
ACTTGTGAAATGGGCCTATTGGGAACATTGGGATGGGAAAGTCCTTGTGTAATCTTGTGAGTTCGGTTTGTTCAAGGTCCTCAAAAGAGT
TCCATATCAATCCTGAACAGGCCTTTGTCTTACTAACCGCCGCTGATATCAGTTGATGAAAATTCCTTGTATCATGTGTTACAATAATCGG
AATGTCTTTCACTCTCAGCGGTGGTAACTCTGACACTGGTTTTTCTAACTGGGAATCTGAGGAAAAAGAAACTGAAAACCATAAATGAAA
TAAAATAATAAAAGAAAGAAAATCAGTGTGCACTTGTTATATTAGTCGAAACAAAAAGCTTATTAATGCTTGTTTGAATCTAAATAATG
TAGGGAGGGACGTGCAAACCTTGTTCGGCAAGGTAACCCTTTTCCAGTAGAATTTGGAAGGCAGAAAAAGCGAGAAAAGAAGAGATACTA
CCAGTTCTTAACACGATCCTCGGAAGCCTTAGGGTATCAGCAACAGTTTGTGCGAAGTGCCAGATAGCGTCTGTGATTAAGCAGGCGACGG
GCTCCTCCTGATCACCATTTGAAATCAACTTAGCCAAGCAATCCTGAAATGGCACAACACACTTGTCATTAAGGACTGTAAGAAGAGATAC
GGTATCCTCGGTGGAGACTTCGCTTTCCCACAGGCTCTCAGAGATGGAATTGAAGCTGAAGTGAGGATAGTTAGAAGGGTTTGGAGAGTTG
AAGTAAGAGTGAATTATGGTGATGGAAAAGCCTTTACTATATAGAATGCTTGCAAGCTGAAGCATGGGGTTTATGTGGCCTTGCAAAGGC
AGAGGAAAGAGTATCACCCGGCGCCCCTTCTTTTGTTGCACATTGGATTCTTCCTCGTGCCGAATTCAAACAGCCCGGGGGATCCACTG

>YjinA-01-H01
TAGAATTCGGCACGAGGCTGAGTCAGAGATGGAGAAGCAGGATCATGTTCATGTTGCGATACTCCCGCTTCCAGCCGTAGGCCATGTCAAC
TCCATGCTGAACCTTGCAGAGCTGCTCGGCCACGCCGGCATCAAGATTACGTTTCTCAACACCGAACATTATTACGATCGCGTCATCCGTCA
CAGCAGTGATGCCTTTTCGCGTTACATGCAAATTCCGGGATTTCAATTCAAGACCTTAACAGATGGACTTCCCAGGGATCATCCTCGAACT
CCAGATAAATTCCCTGAGCTTGTTGATTCATTGAACTGCGCCACTCCACCCCTTTTGAAAGAGATGGTCAGTGATTCTAAGTCGCCGGTGA
ACTGTATTATCACAGATGGGTATATGAGCCGTGCAATTGACGCTGCCAGAGAAGTTGGAATTTCCATTATTAATTTTCGCACTATTAGTG
CTTGTGCATTTTGGTCATTCCATTGCATCCCTGATATCATCGATGCAGGCGAGCTTCCGATCAAAGGAACTGAAGACATGGATCGCCTGAT
AACCACTGTACCTGGAATGGAAGGTTTTCTCAGGTGCCGTGATCTTCCGAGCTTCTGTCGAGTTAACGACCCAATGGATCCGCAACTCCTAC
TCTTTGCACGCGAGACCCGATTATCTGCTCATGCAGACGGTCTCATATTGAATACATTTGAAGATCTGGAAGGACCCATCTTGTCCCAAAT
CCGCAACCACTCATGCCCGAATATCTACAGCAATGGGACCTCTTAATGCTCATCTCAAAGTAAGAATCCCAGAAAAAACATATTCCTCAAG
CAGTTTGTGGAAAATTGACAGAAGCTGCATGGCATGGCTTGACAAGCAACCCAAGCAATCTGTTATCTATGTCAGCTTTGGTAGCATTGCA
GTAATGTCAAGAGATCAACTAACAGAGTTTTATTACGGCCTTGTTCATAGCAAGAAAAGTTTCTTATGGGTCATCAGGCCTGACTTGATT
ACAGGAAAAGATGGTGAGAATCAAATTCCGGAGGAGCTTCTGGAGGCAACCAAGGAAAGAGGATACATTGCGGGATGGGTTCCACAGGAA
GAAGTTTTAGCCCACAGCGCAGTTGGTGGATTTTTGACTCACTGTGGCTGGAACTCGACTCTGGAGAGTATCGTGGCTGGAATGCCTATGA
TTTGTTGGCCATCTTTTGCTGATCAGCAGATCAATAGTAGGTTTGTTGGTGAAGTGTGGAAGCTGGGGTTAGATATAAAGGATTTGTGTG
ATAGAAATATTGTTGAGAAGACGGTGAATGATCTAATGGTGGAGAGGAAGGAAGAGTTCATGGAATCAGCTGATCGGATGGCTAATTTGG
CAAAAAAAAGTGTTAATAAAGGCGGATCCTCATATTGCAATTTGGACCGTCTGGTAAATGATATAAAAATGATGAGCTCACAACCACAAA
ATTGCTGAAAGCTTGGTGCAAGATGCCACTACATGCTTGACTTCAAGTAATTTCAAGTTTGGAAGTGTTTGCCAATGAAATAAATTAAAT
CATGCCAAAGGACTAGTACTTATTTTTATTTTACTT

IP : 14.49.138.138, 2017-11-03 13:30:33

>YjinA02-N10
CTCTTCCCTCTGGCTGTCAGTCGTCTTGTTCGCCTTTGAACTCTGTGCCTATTTTAAAGGCTGGCATTTTGCCACTCCCAATCTGCAACTCC
AGTACATATTTCAGAGCCCATTAGCTATCAAGGGTGCCTTTGATTTGCTTTATTCCAGCTGGGTTTTGGTTCGCGTTCACTATTTGGCTCC
TCCGCTTCAGTTCCTAGCCAATGCTTGTATTGTGCTCTTCCTAATTCAGAGCCTCGACCGGCTTATTCTCTGCTTGGGTTGTTTCTGGATCC
GTTTCAAGAGAATTAAGCCCGTCCCCAAACACGATGACACTTCAGATCTTGAATCCGGCCAAAAAGGATTTTTCCCGATGGTGCTTGTTCA
GATCCCTATGTGTAATGAGAAAGAGGTGTATCAGCAGTCTATTGCCGCGGTGTGTAATTTGGACTGGCCTAAATCAAAGATTTTGATTCA
AGTGCTTGACGATTCCGATGATCCAACGGCGCAGACCTTGATTAAAGAGGAGGTGCTCAAGTGGCAGGAAGCGGGTGCCAACATTGTCTAT
AGGCATCGCATTCTCAGAGATGGTTACAAGGCCGGTAATCTCAAGTCCGCTATGAATTGCAGCTACGTCAAAGACTATGAATTTGTGGCCA
TCTTCGATGCGGATTTTCAACCCAATCCTGATTTTCTCAGAAGAACTGTCCCTCATTTTAAGGATAATGAGGAGCTGGGGTTGGTTCAGGC
AAGATGGTCTTTTGTGAATAAGGATGAGAATTTGTTAACAAGGCTGCAGGACATAAACCTGTCGTTTCATTTTGAAGTAGAGCAGCAAGT
AAATGGTGTGTTTATAAATTTCTTTTGGGTCAATGGCACTGCTGGTGTGTGG

>YjinA-03-E04
CTTAAATAAAATTGTATGATCACAAAAAAATCAATAGCATCCAATACAACTCTAATTTCATTTGTTTGAAATAGCTCATAAATAGGACCC
AAAAAAAAAGGGATAAAACAACTACGGGAGCTTGATGCTGGACATCTTAATAAAATTTTGATTATAAAAACCTTAATGTGGGTACATAG
GCTTCTCTAAGGTTTCTTTATTGAAATGGCTACCCAAGTGAAATGTCCCTGAAAAAAGCATCAAGGTTAGTAATAAATGATCCATTTTCT
GCAACTGCTTCTCGACAAATCTCTTGAACTTCTCTAGCCCTTAAACTCATCTGTTTCCTCTCATCACTATTCAAATCCATAAACCTTTTCA
CTAGCTCTGTAATTTCATCTCTTGTCACCAAACTTTCACTTGCTATGTCAGGTTTCTTTACTCTCCATCCAGTCTTCCAATCTTGTACAAT
TTGCTTACTATTTGGAACTTGATCCCAAAATATCGGAAAAGTAAGCATTGGGACACCAGCATAAAGACTTTCGATAGTTGAATTTAAACC
ACAATGAGTCCAAAATCCCCCAGTAGAAGCATGGCACAGCACCCTCAGTTGGTCACACCAAGGCACCACAATGCCCCGATCATCAGCATGGC
CATCTTTAAACCGAGAAGTATCACCTCTTGTCACCCACAAATATCTGACGCCACTGTTGCGGNATACCAGCTATAATTTCATCCATTTGTG
CACTTGAAACCGACAAAAAGCTTCCCAAGGAGACGTACAAAACTGAGCCAACAGGCTGAGTTTCCAACCACTCAAAGTATTTGGGACCATT
GTGACCAGTAATTGATGATACGTTGAAGTAGGGAATGGTTGGTCCAATTGGGTACACTGGAAATGAAAATTCTTCTTTTAAAGCGTCAAT
AGTTTTGGCTTCCAGCTTGTAGACCGAAGAAAGCAAAAGATATTGAGCTTTTGAGACCTTTGATGCACTTTGCAGGGCCGCCATGCAAAAT
TTTTCTGCCAGCTCCGTGAAAAATTGTAGGAAAATCAGCCAACTTCGTCGGTTCAAGTCCTGGGATGTAGTCCACAAGCTCGTCTCCCTTT
TCTGAGAGATCAAACGGAAAATGGCCGTTTCTTTCAAGAAGCTCAAAGTGATGAAAAACAGAGAACACAAGTGCAGACATCGTCCACAAG
GAAGCTACGGGAATGTTCCTGCGGTTGCCAACGTCAACAACCCAAGGCAAGTAAGTATCTGCTATAATAGCAGTCAGTGCCGCCGGAGGTT
GCTCATCATCATCAAGAAGCAGACGATCAAGGAGCTCTTCAAAAGGAGCTTCCATCTTTGTAAACACAGCCTCCAGGAAGCCGGCAAAGTC
ATTGGCGCGCCCATGCTCTGAGGGTATGGTATTAGGCAATGTACGGAATCGAATGTTATGGGGCTTGCTCTGTGAGCCAATGAATCCGAGC
CACTCTTCTGTCACAACAAAGGTGATGAGGATATCAGGCTGCCTTGAAACTAAGAGCTTGCAAATGTTCATCATGGGGTTGACGTGTCCTC
TCCCGGGATAAGGCAGGGCCAGCACGTGGCAGAGGCTGGTTGGTTTTACTTGGGCAGGATGAGGATCCATGAGTACCACTTGATATATGGG
AGCTAATTCAGCTGGCTGGCTGGCTGGCTGGCTGGCTGGTGGCTTGCAAGAGTAAAACGCAGAGACAGAATGAGCCTCGTGC

>YjinA-03-F24
AGCCAGACAGACACAGCCAGACATTCAATCGCAGAGAAGACAAAGTTACACAAGAAACGCTAAATCAAGAAGGCTGAATGTTATTTATTT
TAGTTTAAATTAAGCTAAGGCTTTGAGATCCTTGACGAAATCTGCAATAATCTTATCCTGAATCTGGCCGTTCAACAAAAACTCCCTCCAC
CGTTTCTGATTAGCCCTGATTGAAGCTCCAGGCTCCTTGTTCACATCCACCATAACTGTTTTAATAGCCTTAAAAATATCCTCCTTCCCAA
AATGCCCATCATGATCCCTCCTATTTACCTCCACTCCAGCTTTCAAGTCTCCAGCAACGAGCTTGGAGTTCAAGAATTGGTCACCTTTTAA
AGGCAGAAGCACCAATTGACAGTCGCTAATCACAGCTTCAGTTACCGAACTAAATCCTGAGTGACACACGTAACATCCAACGCTCTCATGT
CTTAAAATGAGCTGCTGTTGCACCCATACTGTGTGCACCACTCCCCTGTCTTTCACCCTGTCCATGAACCCTGGAGGCAGAGTCCGGACCAG
CTCACTCTGACCATCGACGTTAGGCGGGAAATTTAAGACCAGGAAGAAGGGCAATCCCGTAATTTCCAACCCAATGGCTAACTCTTTGATC
TGATCAACGGTGAGGAATGTTTCACTTCCGAAGGAGCAATAAATAACAGACTTGGGAGGATACTTACAGAGCCATTTAGCCCATCTCTCTT
CAAGCTCCCCTGATGGCGGCTCAGGATTAACAAGTGGACCGGTTAGAAGAACCGGTTTCTTGAACTGGGTTCTCACGAAATCCAGGTAAGG
ACCCTCCATTTCATTACATGTCTTGATGGCAAGAACATCGCAGCCATCAACGCCCTGAATCCCTCTCTCATAAACACTCGGGCCGCCCATTG
AACTTTGTATAAACATACAAGTAATCTCGAGCCACAAATTCATCGAGCGAGGTAATGGAAGTTGCAGGGAACCCATCGGGAGATTTCATT
AGATCTGCTAAACTGTTGTTGAGTTTCCTGGCGGGGACCACGAGATAGGCTTGTGAAATGGCAGAGAAAACAGAGAAGTTAACTGTTTTG
ATGCCAAGTTGAGAACCAGCAAGACCCGGCAACCAGTAATGGGTAAAATCAAAGAACACAAAATGGGGTTCGAGCTGTGACAACAAAGTT
TTGATTTGTGGTTGCATGAGGTCCAAGGCTTGCTTTAGGAGCTCAGCCATGTGAGGTGTCATCTCTGAGGTGCTATCAAGACCAGGAGGGA
GGCCATCGACGTGTGGGATTTGAAGAGGGATAATGTCGGCCATGGGAGTTAAATTGAGCGATGATTTGATGCGGGGAATGTTACCAGGAGC
CGAAAAGAAAGAGACCTTGACTCCATGAAGTGAGAGCTTGTTGGAAAGTTGTACAAAGGGGCTTATGTGACCAAAAGCAAACCATGGGAA
CATCACCACGTGAAGTTGATCAGCTTCAGCTGATTCAGTTCCCATTTTGTGGTGTTGGTTCGAAGGGGCGTGCATGTTCGAAGAGGCGTGT
ATGGTCTCTGTCTCCCTCGTGC

>YjinA-04-K01
GCACGAGGGCTTGGTTTCTTGCTTTTCTATGCGAATCTTGTTTCACCTTCGTCTGGGTTCTCACCACTGGCACCAAATGGACTCCTATATCT
TACAACACTTATCCACAACGGCTCCAAGAACGGATAAAGGAGCTTCCTCCACTAGACATTTTTGTGACAACTGCAGATCCTTATCTAGAGC
CTCCAATCCTCACAGTGAACACAGTACTCTCTTTGTTGGCAGTTGATTATCCAGCTCATAGGCTTGCTTGCTACGTGTCTGATGATGGCTG
CTCACCTCTCAACTTTTACTCTCTCGTTGAAGCATCAAAGTTTGCCAAGCTTTGGGTTCCATTTTGTAAGAAGTATAATATTCGAGTTAGA
GCTCCATTTAGATACTTCTTACGTGAGTCTGATGAACCGCCTTGTGCGAGTTCATGGGAATTCCAGCAAGACTGGGAAAAGATGAAGGAAG

IP : 14.49.138.138, 2017-11-03 13:30:33

AGTACGAGAGACTTTGCGGAAACATTGAAGCTGCAGCCAACAATTCTACTTCATTTGATCTAACAGGGGAATTGGAAGTTTTCTTCAACA
CAGAATGCCAGAATCATCCAACAATAATCAAGGTTATATGGGAGAATATGCAGGGTCTCTCTGATGGGATACCACATTTAATCTACATAT
CCAGAGAGAAAAGGCCAAAGAATCCACATCATTATAAAGCGGGGGCCATGAATGTATTAACTAGAGTCTCCGGCTTGATGACCAATGCACC
ATTCATGCTCAATGTGGATTGCGACATGTATGCCAACAACCCAGAGCTTGTTCTTCATGCAATGTGTTTGTTT

>YjinA-06-I18
GAGCTGGNGCTTTGGTGCACANTGAGNTCAGACAATGTTGCTCATCCCACCAGACCTTTNTCAGCANTGNTGNTGCATTTTTGGCATTATC
GGCANTGCAANNACGCTGGGCACTCACATGCATCAATTTCAAAGCCCTTGTATGATGCAACAAAAGGTGCATGGCTCCAGTCCGTCTTGAC
CCTTCCCCCCCTGTGTGGCCCAGTCATCAGCATTCCATATTGAACTGTACACACCCATGGCTTGGTCCTTTGGGAAGGGAATTCCTTTGTGC
TCCAAGTTAGTGTGCACTCTAATTGGGGTCTCATCCACCAAAAATACAACTTGGCGCTGGTTCCAAAGGAGGGAATAGGTATGAAATTCCT
TTGTTGGGTCGAACCAGAGGTCAAGTCTCTGCTCTCTGTTGCCCACACCATTCACATAAACATTGGTTTGGACTAAGTATGGCTCTCCTGT
AGTGTTCCCCAGGAACTCAAAATCGAACTCGTTGTGATTTGGACCGTCTGATGACATATAGAAGGCAGTGACAGTTCCAGCAGAGTCACCC
CCTACAAGTTTAATTTGGATGGAGACTTTCCCAAACAAATACTTGCTCTTTGACGCAAACCCAGCTCCGGAATAATTATCGAGGTTAAGCT
TGAGAGTGTCCCCATCATACTGAACATGATTAAATGCCCAGCTTGTTTGATAAAGGTCATCAAACTTAGCTGAGCTGACCAAACCTACCAT
TAAAAGACCCACAAACAGACTGAAAATCAAAGACATTTTAACCATTGAAGAATGAAGACAGAAGAACGGGGAGAGGAAGTAAGCGAATGA
GCAGAGCAGGCCCAGTGAAGTGGAGGGAAGTTGAAGCTTCTACTTTGCCTCGTGC
>YjinA-07-H14
AGTTCGAACACTGGGACAAGACTTTATTAAACAGCAAACATAACTGTACATTGGACAAGACTGGATAAAAGGTTAATTTGAAAGCAAACA
CCTAAAAAACTTGAAAGGAGCTATAGCTACAAAGAAAGCTGGGTGCTACATTTCTCACAAGCATACACTATTTCCATTCCAGTTGATGAT
TTTTTGCTACACTCATTTTGTTATTCACATGGACCCTCTTGCAGCTTGCATCCCCACAAACTTTTTTTCCCCCGAACCGCCGATTTTTAACT
GTTGGCTAATATCTCAAGTGGAAAAAAAAAGATCTTCTAACCTTCTACTCTGTGGCTGCAAAAACTGCTGGCCCTTCCACCTTAAATGTAGC
ACCCCAAATCTCTTCTTCCGCAGCAGGAACCGCAGTGATCTTGTTCTTTGGATTCTCAAAGCTTCTCAGTCCTCCAACTGCTGTTGAAAAG
AAACAACCTTGAGGGAAAGAAGCAAGTGACTTGCCGCAAGCACCTTTGAGCAAGTCAGCATCATCAGCAAAGGCAACATGTCCATCAGCAG
TGATTCCCCAATAAAGAGGAACCTTACCAAATTGGTCAGAAGCCACAAACAAGGTGGAGGTGGACTTGTCGTAAACAATGAAGGCAAAGT
ACCCACTAAGGTGGCCAACGACATGGTTCGGTGGGTAAGGGGCCCGATCACGCANANCCTTGTATGCCTCAATCACCNAGATCACTTCATTT
GCCGACTTAGCTAGTCCATATTGGCTGCCTCAGGCTTCCCAAGTTATCAAGTGCTCCCTCAAACAAGCAGAAANATCTCATCTTTCACAGC
AAATGATCTTTGCCGTAAAGGAGACTCGTTCTGATGAGTGTACGCGAGGGTGACGTTGTCCCCGACCTGTACGGACACAGCAGACGAGTTG
GTCTGGAGGAAACGGTCGACCAGTGCCGTCGATGTGGTCTTCGGCGACGGAGTCCGGCTTCCGGCCGCCACCAGCTCCTCTGGAGGTGAAAC
GATCGCGCTGCTGAACACTCCCAACATTTTAAGCTACCAAATTTCCTTTTCTCTCGCTTTCTCGCCCTAGAAATTTCTCTCTCCTACAAGAA
AACTTTGATCCGTTCGGAACTCTTTGGCTTTAACTGGAAAGCCTCGTGCCGAATTCGGCACGAGGCGAGTTTTTTTTTTTTTTTTTTTTTT
TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGAAGCGACAACATTAAATTTTTTTTTGAATTTGGGACGGGCACAACCCAGCCAAATAGAA
ACAGCCCAACATTCCATCCCAAAAAAAACAAAGTTACCCAAAAAACGCTAAATCAAAAAGGGTGAATGTTATCTATTTTAGGAGTGCTAA
ACGTCAAAAATGGCCAAAGAACGCCGAAAGTATGTGAAAAAAGCAAAAGTAGCAAAAAAAAACAAAAGGGGCAAAAGTTCCCATGG

>YjinA-08-J10
GACCGGTTAGAAGAACCGGTTTCTTGAACTGGGTTCTCACGAAATCCAGGTAAGGACCCTCCATTTCATTACATGTCTTGATGGCAAGAAC
ATCGCAGCCATCAACGCCCTGAATCCCTCTCTCATAAACACTCGGGCCGCCATTGAACTTTGTATAAACATACAAGTAATCTCGAGCCACA
AATTCATCGAGCGAGGTAATGGAAGTTGCAGGGAACCCATCGGGAGATTTCATTAGATCTGCTAAACTGTTGTTGAGTTTCCTGGCGGGGA
CCACGAGATAGGCTTGTGAAATGGCAGAGAAAACAGAGAAGTTAACTGTTTTGATGCCAAGTTGAGAACCAGCAAGACCCGGCAACCAGTA
ATGGGTAAAATCAAAGAACACAAAATGGGGTTCGAGCTGTGACAACAAAGTTTTGATTTGTGGTTGCATGAGGTCCAAGGCTTGCTTTAG
GAGCTCAGCCATGTGAGGTGTCATCTCTGAGGTGCTATCAAGACCAGGAGGGAGGCCATCGACGTGTGGGATTTGAAGAGGGATAATGTCG
GCCATGGGAGTTAAATTGAGCGATGATTTGATGCGGGGAATGTTACCAGGAGCCGAAAAGAAAGAGACCTTGACTCCATGAAGTGAGAGC
TTGTTGGAAAGTTGTACAAAGGGGCTTATGTGACCAAAAGCAAACCATGGGAACATCACCACGTGAAGTTGATCAGCTTCAGCTGATTCA
GTTCCCATTTTGTGGTGTTGGTTCGAAGGGGCGTGCATGTTCGAAGAGGCGTGTATGGTCTCCTCGTGC

>YjinA-08-O13
GCACGAGGGAAAGCTGAGCTTGTGTTCATTCCATCGCCAGGCGCCGGCCACCTTGTATCGACGGTGGAGATTGCAAAGATCCTTGTTGATCG
CGACGAACGTATCTCCATCACAGTCCTGATAATCAAGCTTCCATTTGACAACAAAGTCGCCGCCTACACAGAATCACTCGCCGCCTCTAATT
TACCATCTCGTATCAAATTCATTTTCCTTCCAGATGACAACCAATCCCCTACCCCAGGAAAAGTCCCCTATTCTTCCCTCGAAACCAAAAA
AACCCACGTCAAAGAAGCTGTCGCTAAGCTCACTGGGTCACCTGACTCGCCAACACTTGCCGGATTTGTTCTCGACATGTTCTGCATGTGCA
TGGTTGACGTTGCAGATGAACTTAGGGTTCCTAGTTATGTCTTCTTCACGTCGAGTGCAGCTTCATTGGGTTCCTTTCTTAACGGCCAAGC
TCTTTACGACCAAAACAAGCTCACCACTGAGTTGATAGACTCAGGTGCTGATTTGCAAGTTCCGACGCTTGTGAACTCAATTCCTGCTAGG
CTTTTGCCTAGTTCTTTTTTTGATAAAGAGTGGGGCGAATTTTTATTTGGGCAAGCAAGAAGGTACAGACTTGTTAAGGGCATAATGGTA
AACACATTTGAAGAGCTAGAACCCTACGCAGTCAAGTCTTTCTACGATGGTAAGATTAAGATTCCGCCGGTTTATGCCGTGGGGCCCGTTG
TGAATATCACAGGGGACAATTATGCTTTGGGACCCGGAGGAATTGAGAAGAAAGCTGAAGTTATGACGTGGCTGGATGATCAACCGGTAT
CATCAGTCGTGTTCCTGTGCTTCGGGAGCAGGGGATGCTTCGATGTGGATCAAGCAAGAGAGATCGCGCATGCGCTAGAACAATGCGGACA
CCGGTTCTTGTGGTCCCTACGTCAGGCCCCAACCGAGGATAAGACCGAACTGCGGAGTGATTACGCAGATCTCAAGGGCGTACTGCCGGGAG
GGTTTTTGGATCGAACGGCTGAGATAGGGAAGGTGATTGGGTGGGCCCCGCAGGTTGCTGTGCTGAGCCATCCCGCGGTTGGAGGGTTCGT
ATCGCACTGCGGGTGGAATTCAACGCTAGAGAGTATTCGGTTTGGCGTTCCGATCGCCACGTGGCCGATGTACGCCGAGCAACAGGCTAATG
CGTTTCAGTTGGTGATAGAGTTGGGACTGGCGGTGGAGATTAAAATGGATTATAGGAAGGATATTTTCAATAAAATTCCAACGATGGTTA

IP : 14.49.138.138, 2017-11-03 13:30:33

CTGCTGAGGAGATTGAGAGAGGAATCAAGTGCTTGATGAATCCTGAGAGCGAGATTCGGAAAAGAGTGAAGGAAATGAGTGAGAAAGCTG
GAAGAGCGGTGATGGACGGTGGATCTTCATTCTCATCACTGGGCCGCTTTATTGATGATGTATTAGACAACATGTGAACCTAAAGCAGCGT
CAGTGCTTTTAGCTCAATAATTTCAAAGCAGCTCATGTGCCCGGACTGAGGTGCATTTGTCGTCTTGTTATGTTTTATTTTTTATTATCT
TTTTAAGAAGTGTTCTTTTAGTTTAATTTCAAAAAAAAAAAAAAAAAAAAACTCGAGGGGGGGCC

(감귤류 putative ethylene responsive element binding protein유전자 클론의 삽입유전자 전체 염기서열 정보)

EREBP1: Full-length cDNA(507bp)

Atggcgtcctcacgcgagggacactacaggggtgttagaaagaggccatgggggagatacgcagctgaaatacgcgacccgtggaagaagacgagggtttggttgggtacatttgacaccccggaggaagctgca
ctcgcgtacgacggcgctgccaggtctctccgtggagccaaagccaagaccaacttcccagctccggttacaaactctcttcctcttgatctcaacgcaccgtctgatactaataccagtaatcagcaccgttggatcactcc
tggtcaccaccgtcatcagcgctttggattttgtgaatttttgcaaactggggttcttaaagaaatcaactttgctgataggcaagcaacttcagcttctgcacaaactgacgctgcggttattgatggcgctccggtggctga
taatgggtctactccgtccttctttgggattgtgaggcgtgggttgccgattgatttgaatgagccgccaccgtctggctttga

EREBP2: Full-length cDNA)(717bp)

atgtgtggcggttctatcttaggagacttctttcctcgccacggcggcagccgcgtcaccgcttccgacctctcgcccaactcaccctttcgctgctactaaacaactccctcacaactttgaatctactccgttctccgatgaac
accagtcactggccaaaatcaaacgccctcaaccccctcatatctaaactcctgttcagcttcaggtgatgagaaaaagcccaagaggcagaggaagaatctctacaggggaataaggcaacgcccctggggcaaatg
ggcagctgagattcgtgacccaaggaaaggagttcgagtctggctcggcacattcaacactgccgaagaagcagctcgagcctatgacaaagaagcccgcaagattcgcggcaagaaagccaaagtcaacttcccca
acgaagaggacgtcttcaccgtcacccctgctgctgccgcccatgcttaccatcatcatcagcataatcataatcccactcccagtccccttccttctctttcccaagaagatctttttagtcgtaataactcatctataagtagtg
ttggttttggcttgtatggttatgatctgaacccccagattgttacttctggtggtgacgagaattccgggactggttctggttctgtttcagaaggtgggtacgattccacagaacttatgctgaattgcaacccagaatgtca
atga

EREBP3: Full-length cDNA(819bp)

atgtgtggcggttctatcttaggagacttctttcctcgccacggcggcagccgcgtcaccgcttccgacctctggcccaactcaccctttcgctgctactaaacaactccctcacaactttgaatctactccgttctccgatgaac
accagtcactggccaaaatcaaacgccctcaaccccctcatatctaaactcctgttcagcttcaggtgatgagaaaaagcccaagaggcagaggaagaatctctacaggggaataaggcaacgcccctggggcaaatg
ggcagctgagattcgtgacccaaggaaaggagttcgagtctggctcggcacattcaacactgccgaagaagcagctcgagcctatgacaaagaagcccgcaagattcgcggcaagaaagccaaagtcaacttcccca
acgaagaggacgtcttcaccgtcacccctgctgctgccgcccatgcttaccatcatcatcagcataatcataatcccactcccagtccccttccttctctttcccaagaagatctttttagtcgtaataactcatctataagtagtg
ttggttttgacttgtatggttatgatctgaacccccagattgttacttctggtggtgacgagaattccgggactggttctggttctgtttcagaaggtgggtacgattccacagaacttatgctgaattgcaaccagaatgtcaa
tgatggttcgtttgctcaaatgaaggtgaaaagcccaagaacaagaagaagaagaaaaggcgaaaagctgaagaggaaagagaacgaagtgccgaaagctgtctga

(감귤류 putative miraculin-like protein 유전자 클론의 삽입유전자 전체 염기서열 정보)

miraculin-like protein 1mRNA: Full-length cDNA(699bp)

atgaagacttcattagtaacaacactctccttccttatacttgctttggccacaaaacctcagttgggcgcctcagaatctgaacctatcttagatgtctatggcaaccaggtggactccagccacaggtattatcttgtctcagc
actctggggagttaaaaccggcggtggaattagcgcggacaaaggcaaaaatggacagtgtccaacggatgttatccaattaagtcctaaggacaaaaggggaaagaatttaggtttacttccgtatgacaattccacaa
ttgtccgggaatccactaatattaaattgaaattctcaagagtttcttctcttcagcagtgtaacaaagattcgttgtggaaagttgacaacgataacgcttcattaggaaagcagtttataacaatcggtgaaggtaaaacgtg
tcaaaatttttttaaacttgagaaagttagtgcatcaatatttgatatgaaaatagcactagacattccctgtctatacaaaattgttcattgttcaacacttgttaatggttcttgcgatacactctgcaaagacgttggcgtttcta
atgtggatggcgtccaacgtctagttgtggttgatgataatgatcagccaaatctgcctttgcctgttgtgttatttccagctgatagtggaagatctatgttatttccgtctctgtaa

miraculin-like protein 2 mRNA: Full-length cDNA(711bp)

atgaagacttcattgataacaacactctccttccttatccttaccttggccacgcagcctctattgggcatctcatcaaactctgaacctgtcttagatatcattggcaacaaggtcaaatccaccctcgagtataaacttatcccg
gtcctagatggcgccggtggattcagcacacacctaggcacaaatggacagtgtccctggacgttatccaattaagttctcctagcgaaaggggagataatttaagattacttccgtacgacaattacaaaattgtcaagg
tatccactgatgtcaacctgagattccccgtaaaagtttctgttaagccctgtaatgaagaaccattgtggaaagttgatagctatgacgatccattaattgtaaccggcggaagtgagggccacccaggagctgaaacgtt
gctaaattggtttaagattgagaaagctggaaatttttcatatggtggtgtatacaatattgtccattgtccgagtgtctgtctatcttgtcctagacgctgcaacaaaattggcgtttcaactaaggatggcgttcgacgtctgc
ttctagttggtgatcatgaaccggctttgaatgttctgtttttttccatcagaggaaagctcaaggctacttcaagctgctaacgcaatatcaaggttttttgaagctgctgaagcaatatcaatgaccgcgtaa

(감귤류 ZDS 와 GGPS 그리고 CiFT2 전체 염기서열 정보)

[zeta-carotene desaturase (Zds) mRNA(1713)]

ggatccatgggttctt cagttctgtt tcctgcaact tcagtcactg gtgttagttg gtctcgggtt caagagaagt gtcgaagatt ctgtgtacgg gcttctttgg acgctaatgt ttctgatatg agtgttaatg
caccccaggg tttgtttcca ccagaaccag aacattatag aggaccaaag ctgaaagtgg ctattattgg agctgggctt gcgggcatgt caacggcagt ggaattgttg gatcaaggcc acgaggtgga
tatatatgag tcaaggtctt ttattggtgg taaagtgggt tcatttgtcg ataaacgtgg aaaccatatt gaaatgggcc tgcacgtttt ctttggatgc tacaataatc tgttccgatt gatgaaaaag gtcggtgcgg
acaaaaattt acttgtgaag gatcatactc atacatttgt aaatcagggt ggtgaaattg gtgaacttga tttccggttc ccaattggag ctccgttaca tgggattcgc gcatttttgt cgacaaatca gcttaagact
tatgataaag caagaaatgc tcttgctctt gctctgagtc ctgttgtaaa ggcacttgtt atcctgatg gagccttgaa ggacatacga gatttggata gtataagctt ctctgattgg tttttgtcca agggtggtac
acagacgagt attcaaagaa tgtgggatcc tgttgcctat gcccttgggt ttattgattg tgataacatc agtgctcgtt gtatgcttac tatatttgca ctgtttgcga ctaagactga ggcttcccta ttgcggatgc
tcaagggttc tccagatgtt tatttgagtg ggcccataag aaaatatatc acagataaag ggggcaggtt ccatcttagg tggggatgca gagagatact ttatgataaa gctgctaatg cggaaacata
tgtcaaagga cttgccatgt ctaaggccac tgacaagaag gttgtgcaag ctgatgcata tgttgcagca tgtgatgtcc ctggaattaa aagattgctt ccctcatcat ggagggaaat gaaatttttc
aacaatattt atgcgctagt tggagttcct gttgtcacag tgcagcttag atacaatggt tgggttactg agttgcaaga cctagaacgg tcaaggcaat tgaggcgagc tctggggtta gataacctt
tgtatactcc agatgcagat ttctcttgct ttgcagatct agcactcact tcaccagaag actactacag agaagggcaa ggttcattac tccaatgtgt tttgacgcct ggcgatcctt acatgccctt accaaatgat
gaaatcataa ggagagtggc aaagcaggtt ttagctctat ttccatcatc ccaaggttta gaagttattt ggtcgtctgt tgtcaaaatc gggcaatctt tgtaccgtga gggacctggt aaagacccct tcagacctga
tcaaaagaca cctgtgaaga acttcttcct tgctggctca tatacaaaac aggattacat agatagtatg gaaggagcaa ctttgtctgg tagacaagcc tcagcctaca tatgcaatgc cggggaagaa
ttagtagcac tgaggaagca gcttgctgcc tttgaatctc aagaacaaat ggaagctcca actactacta acgatgaact aagtcttgtg tgaagtcgac

[Citrus unshiu geranylgeranyl diphosphate synthase (Ggps) mRNA(1281)]

ggatccatgttaattt atcgtggact ttctcggatt tctagaatct cgaaaaagac tccgtttggc cgccgttggc ttccctctca cccgcttctc tccggtgctt cacactctgc tgctgctgct gcggcggact
cttctgtgaa ggttttgggt tgcagagaag cttattcatg gagtttgcct gccttgcatg gaattagaca tcaaattcat caccagagca gctccgtaat tgaggatact gattcccagg agcagctcga cccattttct
cttgttgctg atgaactgtc aatacttgct aaaaggttgc gctccatggt agttgctgag gtgcctaagc ttgcctcagc tgctgagtat ttctttaaaa tgggggtgga aggaaagagg ttccgtccca cggttttatt
gctgatggcg acagctctga atgttcgagt acctgaacct ctacatgatg gagtagaaga tgctttggcg actgaactac gtacaaggca acaatgtata gctgagatta cagagatgat ccatgtagca

IP : 14.49.138.138, 2017-11-03 13:30:33

agccttcttc atgatgatgt cttggatgat gcagatacca ggcgtggtat tggttcattg aattttgtga tgggcaataa gttagctgta ttagcgggcg attttcttct ttcccgtgct tgtgttgccc ttgcctcttt gaaaaacaca gaggttgtga cgttactggc aaccgttgta gagcatcttg ttactggtga aaccatgcaa atgacaacat catctgacca acgttgtagc atggattatt atatgcaaaa aacatactac aagaccgcat cattaatctc aaacagctgc aaggcaattg cccttcttgc tggacaaaca gccgaagtgg caatattagc ttttgattat ggaaagaatc tgggtctggc atatcaatta atcgacgatg ttctcgattt cactggcaca tcagcctctc ttggaaaggg ttctttatct gacatccagc atggaatcat aacagctcca atattgtttg ccatggaaga gttccctcag ttacgcacag tagttgagca aggcttcgag gattcctcaa atgttgatat agcccttgag taccttggga agagtcgagg gatacaaaag acaagagaac tggccgtgaa gcatgctaat cttgctgcag ctgcgattga ttctctacct gaaaacaatg atgaggatgt tagaaagtca aggcgtgcac ttttagatct cactcataga gtcatcacaa gaaataaata a**gtcgac**

[Citrus unshiu CiFT2 mRNA for flowering]

tctagaatgt ctagcaggga gagagaccct cttattgttg gccgcgttgt tggtgatgtt cttgacaatt ttacaagaac aattccaatg aggattacct attcaaacaa ggatgttaat aatggccgtg agctcaaacc ttctgaagtt ctgaaccagc ctagggttga aattggtggt gatgatctta ggacatttta tactttggta atggttgatc ctgatgcacc aagcccaagt gaccccagcc ttagggagta tttgcattgg ttggtgactg atattccagc aaccacaggg gccagctttg gccaagagat tgtgaactat gaaagcccta gtccaacgat ggggattcac aggtttgtct ttgtgttgtt ccggcaactt gggaggcaga ctgtttatgc accagggtgg cgtcagaact tcagcacgag ggattttgct gagctttaca atctgggacc tccggtggcc gctgtctact tcaactgcca gagggagagc ggatccggcg gaaggcctgt cagacgatga**gtcgac**

(병글 CAD 게놈 유전자)

대문자-엑손, 소문자-인트론

ATGGGGCAAGCACCGGAGCAAGAGCACCCTAAGAACGCCTTTGGATGGGCTGCCAGGGACACTTCTGGCGTTCTCTCCCCCTTTCACTTCTC
CAGAAG

gtatcgttttctctctttttctttccctttctcttcatgccatttccaatcaatctttttaagtcatgtttgcaattaaaattgatcaattataacttaagaattataatataaaatattttataaaaactagttacttttagtttaaaaggtatatt
gatatgatttttttaattattgttaaaaatattatttaaaaattatatttatttcatattattaacgcttatttcatagttatcttttcaatgataaataaaaccttaaattagatatatgcgtgcatttatttttaatatgcatgtctgatgtcta
gtgattagcggttccgctttttttttttttttaattttaattttcgtttgttgttaaatcgtctgtttttgcagagCAACGGGAGAGAAGGATGTGACATTCAAAGTAACTCACTGTGGGATAT
GCCATTCAGATCTTCACTTGATCAAAAATGAATGGGGCAATGCCATTTACCCAATCGTCCCCGGgtatgttttccgctttctcaaatcatatcttgttttcaatttgttcttt
tctttcgaaagaagatgtataaatatatatctgatttaatagttttcagttttgtcatcgtatacagtacgatggctgatttcttattgtgtcttctgttttttttcaataaatttattagtaacgaattaaaataatattaacaataataaaa
aaaatgaaagcgtgtcgatggagtctgcaccacgaaagcacgtgttaaataagccacataaacctcaaaaataaaaatgtttctgtactgtctgatcgctgcgctggaccaacgttatttttttattcatcaattcccttgctatac
taattgaaatatccgcctaagcaaattaggaaagtattaatgaagaaattaaatataatcctctcattagaaagcaaattaggaaagtaataatgaagaaatacatttaacttaccaaatgtatcgaattgtatgcgaatgaata
tgagttttgttggtcctctggtttttattatttgcgtattttgttatgttcaatttttattccatctgaaattcaagtcactaaattaaaaaattgaaccggcaaacggaaatgcagACATGAGATTGTGGGCGTAG
TGACAGAGGTCGGAAGCAAAGTGAGTAAATTCAAAGTCGGAGACAAAGTGGGAGTAGGATGCATGGTGGGATCATGCCGCTCTTGTGATA
GCTGCGCCATTGATCTTGAGAACTACTGCCCCAAAGTTATAATGACCTATGCCAGCAAGTACCATGATGGAACCATCACATACGGAGGCTA
CTCTGACACTATGGTTGCCGATGAGCACTTTGTGGTCCGTATTCCTGAAGGCGCACCACTTGACGCCACTGCCCCTCTCCTCTGTGCTGGTA
TCACAGTCTACAGTCCGTTGAGATCCTATGGACTCGACAAGCCTTGGTATGCATGTGGGTGTCGTCGGCCTGGGCGGTCTAGGCCTGTCGCT
GTCAAATTCGCAAAGGCTATGGGGGTTAAGGTGACCGTGATCAGTACCTCCCCTAGCAAGAAGAGTGAAGCCGTTGAACGTCTTGGCGCTG
ATTCCTTTTTGGTCAGTCGTGTTCAAGATGAGATGCAGgtactgctttttcgccccttttttgtttctgggtgcgcttattttgaacatgtttctttgattgagagttgaggtgaattggtccatc
attcttgcttgctaaattgatttgtttgctaacgttggctgtgaagGCTGCCATGGGCACAATGGATGGTATCATCGATACAGTATCTGCAGTTCACCCGCTAATGCCGT
TGATTGGACTGTTGAAATCTCAAGGAAAGCTTGTACTTCTTGGTGCACCAGAGAAGCCACTAGAGCTACCAGCTTTCCCCCTGCTCACGGgt
gagtgatctgcgcttatgttacttcatttttctttgttataaacacatattactttggaactcttgcggctaacaaaagtgttgtgcaatttcagGGAGGAAGATAGTTGGTGGCAGTCTCATTGGGG
GGTTGAAGGAGACTCAAGAGATGATTGATTTTGCAGCAAAACACAACATCAGAGCTGATATTGAGGTCATACCGGCCGACTATGTGAACA
CAGCCATGGAGCGCCTTGCTAAAGCCGATGTTAGATATCGCTTTGTCATCGACGTTGCAAACACAATGAAGTCCACCCCTTAA

IP : 14.49.138.138, 2017-11-03 13:30:33

첨부 자료 4. 《현재 보유하고 있는 감귤 유전자원 식물체》

1) 감귤 유전자원 식물

No.	은행등록번호	소재명	학명	종명	확보일자
1	CGRB1	유주	citrus	*grandis*	20080520
2	CGRB2	머틀립	citrus	*aurantium*	20080520
3	CGRB3	한라봉	citrus		20080520
4	CGRB4	영파금감	Fortunella	*crassifolia*	20080520
5	CGRB5	사세보	citrus	*C. unshiu*	20080520
6	CGRB6	만백유	citrus	*grandis*	20080520
7	CGRB7	금감	Fortunella	*crassifolia*	20080520
8	CGRB8	불수감	citrus	*medica*	20080520
9	CGRB9	당유자	citrus	*grandis*	20080520
10	CGRB10	청귤	citrus	*nippokoreana*	20090105
11	CGRB11	빈귤	citrus	*leiocarpa*	20090105
12	CGRB12	소유자	citrus	*junos*	20090105
13	CGRB13	인창귤	citrus	*ichangensis*	20090105
14	CGRB14	병귤	citrus	*platymamma*	20090105
15	CGRB15	당유자	citrus	*grandis*	20090105
16	CGRB16	동정귤	citrus	*erythrosa*	20090105
17	CGRB17	진귤	citrus	*sunki*	20090105
18	CGRB18	감자	citrus	*benikoji*	20090105
19	CGRB19	사두감	citrus	*pseudogulgul*	20090105
20	CGRB20	홍귤	citrus	*tachibana*	20090105
21	CGRB21	지각	citrus	*aurantium*	20090105
22	CGRB22	칵테일	citrus	*paradisi*	20090107
23	CGRB23	탐라,	citrus	*unshiu*	20090416
24	CGRB24	하례	citrus	*unshiu*	20090416
25	CGRB25	일남일호	citrus	*unshiu*	20090416
26	CGRB26	상도	citrus	*unshiu*	20090416
27	CGRB27	궁천	citrus	*unshiu*	20090416
28	CGRB28	흥진	citrus	*unshiu*	20090416
29	CGRB29	청견	citrus		20090416
30	CGRB30	클래멘타인	citrus	*sinensis*	20090416
31	CGRB31	sweet	citrus	*limon*	20090416
32	CGRB32	레몬	citrus	*unshiu*	20090416
33	CGRB33	탱자	poncirus	*sulcata*	20090416
34	CGRB34	남감20호	citrus	*tangerina*	20090416
35	CGRB35	편귤	citrus	tangerina	20100415
36	CGRB36	삼보감	*citrus*	*sulcata*	20100408
37	CGRB37	암기조생	*citrus*	*unshiu*	20100415
38	CGRB38	강본조생	*citrus*	*unshiu*	20100415
39	CGRB39	Hamlin	*citrus*	*sinensis*	20100415
40	CGRB40	Succari	*citrus*	*sinensis*	20100415
41	CGRB41	Cara cara	*citrus*	*sinensis*	20100415
42	CGRB42	청도온주	*citrus*	*unshiu*	20100415
43	CGRB43	세또까	*citrus*		20100415
44	CGRB44	다원조생	*citrus*	*unshiu*	20100415
45	CGRB45	대포조생	*citrus*	*unshiu*	20100415

IP : 14.49.138.138, 2017-11-03 13:30:33

No.	은행등록번호	소재명	학명	종명	확보일자
46	CGRB46	궁본조생	*citrus*	*unshiu*	20100415
47	CGRB47	한라조생	*citrus*	*unshiu*	20100415
48	CGRB48	장실금감	*Fortunella*	*crassifolia*	20100415
49	CGRB49	성전온주	*citrus*	*unshiu*	20100415
50	CGRB50	팔정궁천	*citrus*	*unshiu*	20100415
51	CGRB51	북구조생	*citrus*	*unshiu*	20100415
52	CGRB52	삼보조생	*citrus*	*unshiu*	20100415
53	CGRB53	좌좌목	*citrus*	*unshiu*	20100415
54	CGRB54	산화홍	*citrus*	*unshiu*	20100415
55	CGRB55	구능온주	*citrus*	*unshiu*	20100415
56	CGRB56	미택온주	*citrus*	*unshiu*	20100415
57	CGRB57	히로시마 7호	*citrus*	*unshiu*	20100415
58	CGRB58	유라조생	*citrus*	*unshiu*	20100415
59	CGRB59	Sanguinelli	*citrus*	*sinensis*	20100415
60	CGRB60	Pixie	*citrus*	*reticulata*	20100415
61	CGRB61	Orlando	*citrus*	*aurantium*	20100415
62	CGRB62	Tarocco#7	*citrus*	*sinensis*	20100415
63	CGRB63	Nova	*citrus*	*reticulata*	20100415
64	CGRB64	Dancy	*citrus*	*tangerina*	20100415
65	CGRB65	Cleopatra	*citrus*	*reshni*	20100415
66	CGRB66	Sourorange	*citrus*	*aurantium*	20100415
67	CGRB67	Sunburst	*citrus*	*reticulata*	20100415
68	CGRB68	C.macrophylla	*citrus*	*macrophylla*	20100415
69	CGRB69	Minneola	*citrus*	*Tangelo*	20100415
70	CGRB70	남향	*citrus*		20100415
71	CGRB71	삼다조생	*citrus*	*unshiu*	20100415
72	CGRB72	Tarares lemon	*citrus*	*limonia*	20100415
73	CGRB73	Fairchild	*citrus*	*reticulata*	20100415
74	CGRB74	Roubidoux	*poncirus*	*sulcata*	20100415
75	CGRB75	Osceola	*citrus*	*reticulata*	20100415
76	CGRB76	Dweet	*citrus*	*Tangor*	20100415
77	CGRB77	Robinson	*citrus*	*reticulata*	20100415
78	CGRB78	Marrs	*citrus*	*sinensis*	20100415
79	CGRB79	Riogrande	*citrus*	*sinensis*	20100415
80	CGRB80	Dream	*citrus*	*sinensis*	20100415
81	CGRB81	Murcott	*citrus*	*Tangor*	20100415
82	CGRB82	Willow leaf	*citrus*	*deliciosa*	20100415
83	CGRB83	Bergamot	*citrus*	*Tangelo*	20100415
84	CGRB84	진지향	*citrus*		20100415
85	CGRB85	입간조생	*citrus*	*unshiu*	20100415
86	CGRB86	필리핀자몽	*citrus*	*paradisi*	20100805
87	CGRB87	병감	*citrus*	*reticulata*	20120217
88	CGRB88	Minneola Tangelo	*citrus*	*reticulata*	20120217

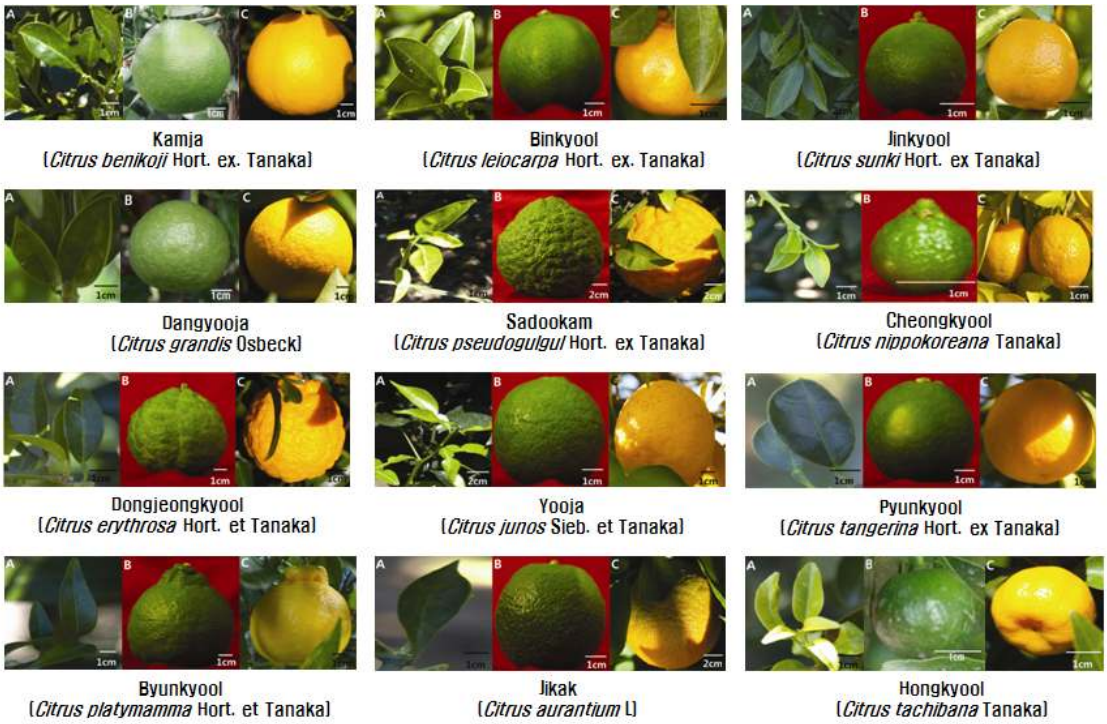
IP : 14.49.138.138, 2017-11-03 13:30:33

2) 감귤 유전자원 캘러스 cell line

No.	은행등록번호	소재명	학명	종명	확보일자
1	CGRB27	궁천조생	*Citrus*	*unshiu*	*2009.06.19*
2	CGRB88	하례조생	*Citrus*	*unshiu*	*2009.06.19*
3	CGRB89	상야조생	*Citrus*	*unshiu*	*2009.06.19*
4	CGRB43	청도온주	*Citrus*	*unshiu*	*2009.06.19*
5	CGRB90	네블오렌지	*Citrus*	*sinensis*	*2009.06.19*
6	CGRB14	병귤	*Citrus*	*platymamma*	*2011.08.01*
7	CGRB15	당유자	*Citrus*	*grandis*	*2011.08.01*
8	CGRB16	동정귤	*Citrus*	*erythrosa* Hort.et Tanaka	*2011.08.01*
9	CGRB10	청귤	*Citrus*	*nippokoreana* Tanaka	*2011.08.01*
10	CGRB35	편귤	*Citrus*	*angerina* Hort.ex Tanaka	*2011.08.01*

IP : 14.49.138.138, 2017-11-03 13:30:33

3) 감귤 유전자원 과실



은행등록번호	일 반 명	학 명	확 보 수 량	
			미숙(확보일)	성숙(확보일)
CGRB15	당유자	*Citrus grandis* Osbeck	9(2010.9.26)	14(2011.2.8)
CGRB10	청귤	*Citrus nippokoreana* Tanaka	16(2010.8.18)	14(2010.12.3)
CGRB11	빈귤	*Citrus. leiocarpa* Hort. ex. Tan.	20(2010.9.26)	10(2011.1.18)
CGRB12	소유자	*Citrus junos* Sieb. et Tanaka	24(2010.9.26)	5(2011.2.8)
CGRB14	병귤	*Citrus platymamma* Hort. et Tanaka	15(2010.9.20)	20(2010.12.1)
CGRB16	동정귤	*Citrus erythrosa* Hort.et Tanaka	14(2010.9.20)	14(2010.11.18)
CGRB17	진귤	*Citrus sunki* Hort. ex Tanaka	39(2010.8.18)	12(2011.1.18)
CGRB18	감자	*Citrus. benikoji* Hort. ex. Tan.	30(2010.8.18)	14(2011.2.8)
CGRB19	사두감	*Citrus.pseudogulgul* Hort.ex Tanaka	18(2010.8.18)	8(2011.2.8)
CGRB20	홍귤	*Cirtus tachibana* Tanaka	49(2010.8.18)	30(2010.11.18)
CGRB22	지각	*Citrus aurantium* L	20(2010.8.18)	12(2011.2.8)
CGRB35	편귤	*Citrus tangerina* Hort.ex Tanaka	20(2010.9.26)	5(2010.11.18)
합 계			274	158

IP : 14.49.138.138, 2017-11-03 13:30:33

첨부자료 5. 《발표자료》

IP : 14.49.138.138, 2017-11-03 13:30:33

첨부자료 6. 《분양신청양식》

감귤유전자원소재은행

제주특별자치도 제주시 제주대학로 66번지 제주대학교 아열대원예산업연구소 104호
http://citrus.cheju.ac.kr TEL. 82-64-724-0706 FAX. 82-64-725-0989

연구소재 분양 신청서

연구소재 분양과 사용에 관한 동의서

1. 분양받은 연구소재는 시험연구, 교육 등을 포함하는 연구목적으로만 사용하여야 한다.
2. 분양받은 연구소재를 이용하여 특허를 신청하거나 상업적 목적으로 사용하고자 할 때는 본 소재은행과 별도의 협의를 하여야 한다.
3. 분양받은 소재를 사용하여 발표하는 논문에는 연구소재를 본 소재은행으로부터 분양받았음을 재료 및 방법 또는 사사에 명기하고, 발표된 논문의 별쇄본, 복사본 또는 file 1부를 본 은행으로 발송하여야 한다. 본 소재은행에 대한 영문표기는 Citrus Genetic Resources Bank(CGRB)(약어 확인하여 기입)이며, 약어로만 표시하여도 된다.
4. 분양받은 소재는 제 3자에게 임의로 제공, 이전, 판매할 수 없다.
5. 본 은행과 연구소재 기탁자는 분양된 소재의 인수, 관리, 보존 또는 사용에 따른 어떠한 책임도 지지 않는다.
6. 명시되지 않은 기타사항에 대해서는 본 소재은행과 협의하여 결정하여야 한다.

연구소재 분양과 사용에 관한 위의 사항을 동의합니다.

신청자명 : **(서명)**

IP : 14.49.138.138, 2017-11-03 13:30:33

* 표시되어 있는 항목은 필수 기입항목입니다.

* 필수: 연구소재의 해외의존율에 관한 설문조사지

1. 분양신청자의 정보를 기입하여 주시기 바랍니다.

신청자 성명*		(서명)	직위*	
소 속 기 관*				
연 락 처*	TEL		HP	
	FAX		e-mail	
주 소*	(〒)			
신 청 일*	200 년 월 일			

2. 연구책임자(또는 기관장)와 연구자의 정보를 기입하여 주시기 바랍니다.

연구책임자 성명			(서명)	직위	
연구자	성 명		(서명)	직위	
	소속기관				
	연 락 처	TEL		HP	
		FAX		e-mail	

※ 연구책임자와 연구자가 분양신청자와 동일한 경우에는 기입하지 않으셔도 됩니다.

3. 연구정보를 기입하여 주시기 바랍니다.

연구과제 번호	
연구과제 제목*	
연 구 목 적	
연구 수행기간	

IP : 14.49.138.138, 2017-11-03 13:30:33

4. 분양신청 연구소재 목록을 작성하여 주시기 바랍니다.

구분	연구소재명*	카달로그 번호*	수량/용량*
1			
2			
3			
4			
5			
6			
7			
8			
9			
10			

※ 분양 신청 목록란이 부족하실 경우 추가하여 작성하여 주시기 바랍니다.

5. 연구소재 배송처를 기입하여 주시기 바랍니다.

배송처	인수자명			소속기관/부서	
	연 락 처	TEL		HP	
		FAX		e-mail	
	주 소	(〒)			
	희망 배송일*	200 년 월 일			
배송방법*		☐ 직접 수령 ☐ 우편배송 ☐ 항공배송			

※ 배송처가 분양신청자와 동일한 경우에는 * 표시되어 있는 사항만 기입하여 주시기 바랍니다.

IP : 14.49.138.138, 2017-11-03 13:30:33

6. 입금처를 기입하여 주시기 바랍니다. (작성하지 않으셔도 됩니다.)

입금처	입금자명			소속기관/부서	
	연 락 처	TEL		HP	
		FAX		e-mail	
	주 소	(〒)			
입금방법*		☐ 직접 현금 납부 ☐ 온라인 계좌 이체 ☐ 신용카드 결제			
신용카드 결제*		카드 종류		카드 번호	
		카드 소유자명		만기일	
결제관련 문서요청*		☐ 견적서 ☐ 납품서			

※ 입금자가 분양신청자와 동일한 경우에는 * 표시되어 있는 사항만 기입하여 주시기 바랍니다.
※ 1개월 이내에 입금되지 않으면 분양신청은 취소됩니다.

<연구소재은행 기입부분>

접수번호		접수일	
접수자		비고	

분양자	(서명)	분양일	
분양 책임자	(서명)	비고	

IP : 14.49.138.138, 2017-11-03 13:30:33

Korea National Research Resource Center (KNRRC)
Seoul Women's Univ. 623 Hwarang-ro, Nowon-gu, Seoul 139-774, Korea
(재)연구소재중앙센터
서울시 노원구 공릉2동 126번지 서울여자대학교 별관
TEL :

연구소재 해외 의존율에 대한 설문조사

교육과학기술부 기초연구인프라구축사업으로 진행되고 있는 연구소재은행에서는 기초과학 및 융합연구 등 다양한 분야로 연구소재와 정보를 제공하고 있습니다. 현재 33개의 국가지정연구소재은행, 소재 분야별 5개의 거점센터와 1개의 중앙센터로 운영되고 있습니다.

연구소재중앙센터에서는 연구자들이 필요로 하는 연구소재에 대한 해외의존도를 분석하여 은행 서비스의 질적 향상과 신규 연구소재의 발굴을 위한 전략적 방안을 마련하고 나아가 연구의 효율성을 꾀하고 국부의 유출을 방지하기 위해 설문조사를 실시하고자 합니다.

분양신청서와 같이 제출해주셔야 분양 신청이 완료됩니다.

대단히 감사합니다.

설문조사지 정보	
설문 목적	연구소재의 수입 의존도 분석 및 신규 소재 발굴
설문 대상	모든 연구소재 분양 신청자
작성 방법	해당 번호에 체크(√)하거나 직접 기입
정보 활용	본 조사는 연구소재은행에서 분양되고 있는 소재 중 수입 대체효과를 나타내는 소재의 규모와 향 후 연구자원에 대한 해외 의존율을 감소시키기 위한 전략적 방안을 마련하는데 기초자료로 활용하고자 함.
조사 시행기관	연구소재중앙센터

IP : 14.49.138.138, 2017-11-03 13:30:33

[분양신청 소재에 관한 사항]

1. 귀하께서 본 소재은행에 분양신청하신 소재의 종류는 무엇입니까? ( ) * 복수응답 가능

① 인체 유래 검체 ② 동물소재 ③ 식물소재

④ 미생물 소재 ⑤ 융합물질 소재 (광물, 결정, 핵산, 단백질 등)

2. 이번에 귀하께서 분양 신청하신 소재의 총수는 몇 개입니까? _____개

[분양 신청 소재 중 해외 의존도]

3. 귀하께서는 이번에 분양 신청하신 소재 중 이전에 해외에서 분양받으신 소재가 있으십니까? ( )

① 있다 ② 없다

4. 귀하께서는 이번에 분양 신청하신 소재 중 이전에 해외에서 분양받으신 소재가 있으시다면 어떻게 확보하셨습니까? ( ) * 복수응답 가능

① 해외의 지인을 통해서 분양받았다.

② 해외의 대학 또는 연구기관을 통해서 분양 받았다.

③ 해외 소재은행을 통해서 분양 받았다.

5. 이번에 분양 신청하신 소재 중 이전에 해외 소재은행에서 구입하셨던 소재는 몇 개입니까? * 복수응답 가능

① 인체 유래 검체 _____개 ② 동물소재 _____개 ③ 식물소재 _____개

④ 미생물 소재 _____개 ⑤ 융합물질 소재 (광물, 결정, 핵산, 단백질 등)_____개

6. 귀하께서는 해외 소재은행에서 구입하셨던 소재를 본 소재은행에서 구입하시게 된 이유는 무엇입니까? ( )

* 복수응답 가능

① 품질이 만족스럽기 때문이다.

② 소재를 빠른 시일 내에 받을 수 있기 때문이다.

③ 소재 가격이 저렴하기 때문이다.

④ 우리나라 소재가 갖는 고유의 특성 때문이다.

⑤ 분양조건이 까다롭지 않아서

7. 귀하께서는 연구소재를 해외 소재은행에서 구입하시게 된 이유는 무엇입니까? ( ) * 복수응답 가능

① 품질이 만족스럽기 때문이다.

② 학술지에 게재되어 있는 소재이기 때문이다.

③ 국내에 없는 소재이기 때문이다

④ 표준자원 (Reference Resource)이기 때문이다.

⑤ 소재에 대한 정보가 정확하고 풍부해서

8. 상기의 설문에서 국내에 없는 소재로 응답하신 경우, 해외 소재은행에서만 구입하셨던 소재는 무엇입니까?

***** 설문에 응해주셔서 대단히 감사합니다. *****

IP : 14.49.138.138, 2017-11-03 13:30:33

첨부자료 7. 《학술지 발표논문》

IP : 14.49.138.138, 2017-11-03 13:30:33

2007-2012.02

소재은행 분양실적

IP : 14.49.138.138, 2017-11-03 13:30:33

[표 7] 보유 연구소재 목록 및 분양 실적

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
진귤 성숙과실 유전자정보	2010	2012-02-28	제주대학교	9	×
진귤 성숙과실 DNA Clone	2010	2012-02-28	제주대학교	4	×
식물체 cell line	2011	2012-02-27	전남 한방산업진흥 약용작물 종자 보급센터	7	×
진귤 성숙과실 유전자정보	2010	2012-02-27	제주대학교	10	×
진귤 성숙과실 DNA Clone	2010	2012-02-27	제주대학교	3	×
온주밀감 미숙과실 유전자정보	2002	2012-02-27	난지농업연구소 감귤시험장	9	×
온주밀감 미숙과실 DNA Clone	2002	2012-02-27	난지농업연구소 감귤시험장	4	×
한라봉 미숙과실 과피 유전자정보	2005	2012-02-24	제주대학교	10	×
한라봉 미숙과실 과피 DNA Clone	2005	2012-02-24	제주대학교	1	×
지각 미숙과실 유전자정보	2011	2012-02-17	분자생명공학부	6	×
지각 미숙과실 DNA Clone	2011	2012-02-17	분자생명공학부	4	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2012-02-17	제주대학교	2	×
한라봉 성숙과실 병반과피 유전자정보	2006	2012-02-17	제주대학교	1	×
지각 미숙과실 DNA Clone	2011	2012-02-17	제주대학교	4	×
지각 미숙과실 유전자정보	2011	2012-02-17	제주대학교	1	×
한라봉 성숙과실 과피 유전자정보	2004	2012-02-13	(주)바이오애그젠엔텍	2	×
한라봉 성숙과실 과피 DNA Clone	2004	2012-02-13	(주)바이오애그젠엔텍	7	×
진귤 미숙과실 DNA Clone	2006	2012-02-13	아열대원예산업연구소	2	×
진귤 성숙과실 유전자정보	2010	2012-02-13	아열대원예산업연구소	5	×
진귤 성숙과실 DNA Clone	2010	2012-02-13	아열대원예산업연구소	1	×
진귤 미숙과실 유전자정보	2006	2012-02-13	제주대학교	1	×
진귤 미숙과실 DNA Clone	2006	2012-02-13	제주대학교	1	×
한라봉 성숙과실 과피 DNA Clone	2004	2012-02-13	제주대학교	1	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
한라봉 성숙과실 과피 유전자정보	2004	2012-02-13	제주대학교	1	×
온주밀감 성숙과실 DNA Clone	2003	2012-02-13	제주대학교	1	×
온주밀감 성숙과실 유전자정보	2003	2012-02-13	제주대학교	2	×
한라봉 미숙과실 과피 유전자정보	2005	2012-02-13	제주대학교	1	×
한라봉 미숙과실 과피 DNA Clone	2005	2012-02-13	제주대학교	2	×
지각 미숙과실 DNA Clone	2011	2012-02-13	제주대학교	2	×
지각 미숙과실 DNA Clone	2011	2012-02-09	제주생물종다양성연구소	7	×
지각 미숙과실 유전자정보	2011	2012-02-09	제주생물종다양성연구소	2	×
진귤 성숙과실 유전자정보	2010	2012-02-09	제주생물종다양성연구소	1	×
진귤 성숙과실 DNA Clone	2010	2012-02-09	제주생물종다양성연구소	3	×
한라봉 성숙과실 병반과피 유전자정보	2006	2012-02-06	제주대학교	3	×
진귤 성숙과실 유전자정보	2010	2012-02-06	제주대학교	2	×
진귤 성숙과실 DNA Clone	2010	2012-02-06	제주대학교	6	×
지각 미숙과실 DNA Clone	2011	2012-02-06	제주대학교	7	×
지각 미숙과실 유전자정보	2011	2012-02-06	제주대학교	1	×
한라봉 성숙과실 병반과피 유전자정보	2006	2012-02-06	제주대학교	3	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2012-02-06	제주대학교	1	×
온주밀감 성숙과실 유전자정보	2003	2012-02-02	아열대원예산업연구소	2	×
온주밀감 성숙과실 DNA Clone	2003	2012-02-02	아열대원예산업연구소	1	×
진귤 성숙과실 DNA Clone	2010	2012-02-02	아열대원예산업연구소	4	×
진귤 성숙과실 유전자정보	2010	2012-02-02	아열대원예산업연구소	1	×
지각 미숙과실 유전자정보	2011	2012-02-02	아열대원예산업연구소	1	×
지각 미숙과실 DNA Clone	2011	2012-02-02	아열대원예산업연구소	3	×
지각 미숙과실 DNA Clone	2011	2012-02-02	난지농업연구소 감귤시험장	3	×
한라봉 성숙과실 병반과피 유전자정보	2006	2012-02-02	난지농업연구소 감귤시험장	3	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2012-02-02	난지농업연구소 감귤시험장	2	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
진귤 성숙과실 DNA Clone	2010	2012-02-02	난지농업연구소 감귤시험장	2	×
진귤 성숙과실 유전자정보	2010	2012-02-02	난지농업연구소 감귤시험장	2	×
진귤 미숙과실 유전자정보	2006	2012-02-02	난지농업연구소 감귤시험장	1	×
진귤 미숙과실 DNA Clone	2006	2012-02-02	난지농업연구소 감귤시험장	3	×
진귤 성숙과실 DNA Clone	2010	2012-01-31	제주대학교	3	×
진귤 성숙과실 유전자정보	2010	2012-01-31	제주대학교	4	×
지각 미숙과실 DNA Clone	2011	2012-01-31	제주대학교	8	×
지각 미숙과실 유전자정보	2011	2012-01-31	제주대학교	3	×
진귤 성숙과실 DNA Clone	2010	2012-01-27	아열대원예산업연구소	3	×
지각 미숙과실 DNA Clone	2011	2012-01-27	아열대원예산업연구소	4	×
진귤 성숙과실 유전자정보	2010	2012-01-27	아열대원예산업연구소	1	×
지각 미숙과실 유전자정보	2011	2012-01-27	난지농업연구소 감귤시험장	3	×
지각 미숙과실 DNA Clone	2011	2012-01-27	난지농업연구소 감귤시험장	9	×
한라봉 미숙과실 과피 유전자정보	2005	2012-01-25	난지농업연구소	11	×
한라봉 미숙과실 과피 DNA Clone	2005	2012-01-25	난지농업연구소	6	×
진귤 성숙과실 DNA Clone	2010	2012-01-25	아열대원예산업연구센터	3	×
진귤 성숙과실 유전자정보	2010	2012-01-25	아열대원예산업연구센터	3	×
온주밀감 성숙과실 유전자정보	2003	2012-01-17	제주대학교	8	×
온주밀감 성숙과실 DNA Clone	2003	2012-01-17	제주대학교	4	×
온주밀감 미숙과실 DNA Clone	2002	2012-01-10	아열대원예산업연구소	7	×
온주밀감 미숙과실 유전자정보	2002	2012-01-10	아열대원예산업연구소	9	×
온주밀감 성숙과실 DNA Clone	2003	2012-01-10	분자생명공학부	5	×
온주밀감 성숙과실 유전자정보	2003	2012-01-10	분자생명공학부	7	×
진귤 성숙과실 유전자정보	2010	2012-01-10	제주대학교	10	×
진귤 성숙과실 DNA Clone	2010	2012-01-10	제주대학교	5	×
한라봉 성숙과실 과피 유전자정보	2004	2012-01-10	제주대학교	7	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
한라봉 성숙과실 과피 DNA Clone	2004	2012-01-10	제주대학교	7	×
식물체 과실	2011	2012-01-03	기초과학지원연구원부산센터하이테크소재연구부	100	×
한라봉 성숙과실 과피 유전자정보	2004	2012-01-01	제주대학교	1	×
한라봉 성숙과실 병반과피 유전자정보	2006	2012-01-01	제주대학교	1	×
진귤 성숙과실 유전자정보	2010	2012-01-01	제주대학교	1	×
지각 미숙과실 유전자정보	2011	2012-01-01	제주대학교	2	×
온주밀감 성숙과실 유전자정보	2003	2011-12-29	제주대학교	3	×
온주밀감 성숙과실 DNA Clone	2003	2011-12-29	제주대학교	2	×
한라봉 성숙과실 과피 유전자정보	2004	2011-12-29	제주대학교	4	×
한라봉 성숙과실 과피 DNA Clone	2004	2011-12-29	제주대학교	2	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2011-12-29	제주대학교	4	×
지각 미숙과실 DNA Clone	2011	2011-12-29	제주대학교	6	×
식물체 cell line	2011	2011-12-27	난지농업연구소 감귤시험장	3	×
한라봉 성숙과실 과피 DNA Clone	2004	2011-12-26	제주생물종다양성연구소	1	×
한라봉 성숙과실 과피 유전자정보	2004	2011-12-26	제주생물종다양성연구소	2	×
한라봉 성숙과실 병반과피 유전자정보	2006	2011-12-26	제주생물종다양성연구소	5	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2011-12-26	제주생물종다양성연구소	4	×
지각 미숙과실 DNA Clone	2011	2011-12-26	제주생물종다양성연구소	6	×
한라봉 성숙과실 병반과피 유전자정보	2006	2011-12-19	난지농업연구소 감귤시험장	1	×
지각 미숙과실 DNA Clone	2011	2011-12-19	난지농업연구소 감귤시험장	3	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2011-12-19	난지농업연구소 감귤시험장	3	×
진귤 미숙과실 DNA Clone	2006	2011-12-19	난지농업연구소 감귤시험장	4	×
진귤 미숙과실 유전자정보	2006	2011-12-19	난지농업연구소 감귤시험장	1	×
진귤 성숙과실 유전자정보	2010	2011-12-19	난지농업연구소 감귤시험장	4	×
한라봉 성숙과실 과피 DNA Clone	2004	2011-12-19	(주)바이오애그젠엔텍	4	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
한라봉 성숙과실 과피 유전자정보	2004	2011-12-19	(주)바이오애그젠엔텍	5	×
지각 미숙과실 DNA Clone	2011	2011-12-19	(주)바이오애그젠엔텍	9	×
지각 미숙과실 유전자정보	2011	2011-12-16	제주특별자치도농업기술원	2	×
지각 미숙과실 DNA Clone	2011	2011-12-16	제주특별자치도농업기술원	2	×
진귤 미숙과실 유전자정보	2006	2011-12-16	제주특별자치도농업기술원	2	×
진귤 미숙과실 DNA Clone	2006	2011-12-16	제주특별자치도농업기술원	1	×
한라봉 성숙과실 과피 유전자정보	2004	2011-12-16	제주특별자치도농업기술원	4	×
한라봉 성숙과실 과피 DNA Clone	2004	2011-12-16	제주특별자치도농업기술원	3	×
한라봉 미숙과실 과피 DNA Clone	2005	2011-12-16	제주특별자치도농업기술원	3	×
한라봉 성숙과실 과피 DNA Clone	2004	2011-12-16	난지농업연구소 감귤시험장	1	×
한라봉 성숙과실 과피 유전자정보	2004	2011-12-16	난지농업연구소 감귤시험장	2	×
한라봉 성숙과실 병반과피 유전자정보	2006	2011-12-16	난지농업연구소 감귤시험장	5	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2011-12-16	난지농업연구소 감귤시험장	7	×
한라봉 미숙과실 과피 DNA Clone	2005	2011-12-16	난지농업연구소 감귤시험장	8	×
지각 미숙과실 유전자정보	2011	2011-12-12	제주대학교	5	×
지각 미숙과실 DNA Clone	2011	2011-12-12	제주대학교	10	×
한라봉 성숙과실 과피 유전자정보	2004	2011-12-12	제주대학교	2	×
한라봉 성숙과실 병반과피 유전자정보	2006	2011-12-12	제주대학교	1	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2011-12-09	제주대학교	16	×
한라봉 성숙과실 병반과피 유전자정보	2006	2011-12-09	제주대학교	4	×
진귤 성숙과실 DNA Clone	2010	2011-12-09	생명공학부	1	×
진귤 성숙과실 유전자정보	2010	2011-12-09	생명공학부	1	×
진귤 미숙과실 DNA Clone	2006	2011-12-09	생명공학부	10	×
진귤 미숙과실 유전자정보	2006	2011-12-09	생명공학부	3	×
온주밀감 성숙과실 DNA Clone	2003	2011-12-06	제주대학교	13	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
온주밀감 성숙과실 유전자정보	2003	2011-12-06	제주대학교	5	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2011-12-05	분자생명공학부	15	×
한라봉 성숙과실 병반과피 유전자정보	2006	2011-12-05	분자생명공학부	1	×
온주밀감 미숙과실 DNA Clone	2002	2011-12-02	제주대학교	6	×
온주밀감 미숙과실 유전자정보	2002	2011-12-02	제주대학교	4	×
온주밀감 미숙과실 DNA Clone	2002	2011-11-30	생명공학부	3	×
온주밀감 미숙과실 유전자정보	2002	2011-11-30	생명공학부	5	×
진귤 성숙과실 유전자정보	2010	2011-11-30	생명공학부	3	×
지각 미숙과실 유전자정보	2011	2011-11-30	바이오애그진엔텍	2	×
지각 미숙과실 DNA Clone	2011	2011-11-30	바이오애그진엔텍	2	×
진귤 미숙과실 유전자정보	2006	2011-11-30	바이오애그진엔텍	5	×
진귤 성숙과실 DNA Clone	2010	2011-11-29	제주대학교	1	×
한라봉 미숙과실 과피 DNA Clone	2005	2011-11-29	제주대학교	1	×
지각 미숙과실 DNA Clone	2011	2011-11-29	제주대학교	2	×
한라봉 미숙과실 과피 유전자정보	2005	2011-11-23	아열대원예산업연구소	5	×
한라봉 미숙과실 과피 DNA Clone	2005	2011-11-23	아열대원예산업연구소	4	×
온주밀감 성숙과실 유전자정보	2003	2011-11-23	아열대원예산업연구센터	5	×
온주밀감 성숙과실 DNA Clone	2003	2011-11-23	아열대원예산업연구센터	4	×
식물체 과실	2011	2011-11-18	기초과학지원연구원부산센터하이테크소재연구부	171	×
진귤 성숙과실 DNA Clone	2010	2011-11-18	제주대학교	2	×
진귤 성숙과실 유전자정보	2010	2011-11-18	제주대학교	5	×
지각 미숙과실 DNA Clone	2011	2011-11-18	분자생명공학부	3	×
지각 미숙과실 유전자정보	2011	2011-11-18	분자생명공학부	7	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2011-11-10	난지농업연구소	5	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
한라봉 성숙과실 병반과피 유전자정보	2006	2011-11-10	난지농업연구소	9	×
진귤 성숙과실 유전자정보	2010	2011-11-10	제주생물종다양성연구소	5	×
진귤 성숙과실 DNA Clone	2010	2011-11-10	제주생물종다양성연구소	4	×
진귤 성숙과실 유전자정보	2010	2011-11-07	제주대학교	8	×
진귤 성숙과실 DNA Clone	2010	2011-11-07	제주대학교	1	×
한라봉 성숙과실 과피 DNA Clone	2004	2011-11-07	생명공학부	2	×
한라봉 성숙과실 과피 유전자정보	2004	2011-11-07	생명공학부	5	×
진귤 미숙과실 DNA Clone	2006	2011-11-01	난지농업연구소 감귤시험장	6	×
진귤 미숙과실 유전자정보	2006	2011-11-01	난지농업연구소 감귤시험장	2	×
한라봉 미숙과실 과피 유전자정보	2005	2011-11-01	제주대학교	4	×
한라봉 미숙과실 과피 DNA Clone	2005	2011-11-01	제주대학교	1	×
한라봉 성숙과실 과피 DNA Clone	2004	2011-10-26	아열대원예산업연구센터	2	×
한라봉 성숙과실 과피 유전자정보	2004	2011-10-26	아열대원예산업연구센터	5	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2011-10-26	제주대학교	3	×
한라봉 성숙과실 병반과피 유전자정보	2006	2011-10-26	제주대학교	5	×
지각 미숙과실 유전자정보	2011	2011-10-26	제주대학교	2	×
한라봉 성숙과실 과피 유전자정보	2004	2011-10-26	(주)바이오애그젠엔텍	5	×
한라봉 성숙과실 과피 DNA Clone	2004	2011-10-26	(주)바이오애그젠엔텍	3	×
진귤 미숙과실 유전자정보	2006	2011-10-26	바이오애그진엔텍	9	×
진귤 미숙과실 DNA Clone	2006	2011-10-26	바이오애그진엔텍	2	×
온주밀감 성숙과실 DNA Clone	2003	2011-10-19	제주대학교	2	×
온주밀감 성숙과실 유전자정보	2003	2011-10-19	제주대학교	8	×
진귤 미숙과실 유전자정보	2006	2011-10-19	아열대원예산업연구소	6	×
진귤 미숙과실 DNA Clone	2006	2011-10-19	아열대원예산업연구소	2	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
지각 미숙과실 DNA Clone	2011	2011-10-19	생명공학부	1	×
지각 미숙과실 유전자정보	2011	2011-10-19	생명공학부	2	×
온주밀감 미숙과실 유전자정보	2002	2011-10-19	생명공학부	4	×
온주밀감 미숙과실 DNA Clone	2002	2011-10-19	생명공학부	2	×
한라봉 미숙과실 과피 DNA Clone	2005	2011-10-14	분자생명공학부	6	×
한라봉 미숙과실 과피 유전자정보	2005	2011-10-14	분자생명공학부	7	×
지각 미숙과실 유전자정보	2011	2011-10-14	난지농업연구소	1	×
온주밀감 미숙과실 유전자정보	2002	2011-10-14	난지농업연구소	3	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2011-10-10	제주특별자치도농업기술원	2	×
한라봉 미숙과실 과피 유전자정보	2005	2011-10-10	제주특별자치도농업기술원	3	×
한라봉 미숙과실 과피 DNA Clone	2005	2011-10-10	제주특별자치도농업기술원	4	×
진귤 성숙과실 유전자정보	2010	2011-10-10	제주특별자치도농업기술원	5	×
진귤 성숙과실 DNA Clone	2010	2011-10-10	제주특별자치도농업기술원	3	×
진귤 성숙과실 DNA Clone	2010	2011-10-10	제주대학교	5	×
진귤 성숙과실 유전자정보	2010	2011-10-10	제주대학교	3	×
한라봉 성숙과실 병반과피 유전자정보	2006	2011-10-10	제주대학교	3	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2011-10-10	제주대학교	4	×
지각 미숙과실 유전자정보	2011	2011-10-10	제주대학교	3	×
지각 미숙과실 DNA Clone	2011	2011-10-10	제주대학교	5	×
두릅 유전자정보	2005	2011-10-05	제주대학교	1	×
지각 미숙과실 DNA Clone	2011	2011-10-05	제주대학교	2	×
지각 미숙과실 유전자정보	2011	2011-10-05	제주대학교	3	×
한라봉 성숙과실 과피 유전자정보	2004	2011-10-05	제주대학교	1	×
한라봉 미숙과실 과피 DNA Clone	2005	2011-10-05	제주대학교	1	×
한라봉 미숙과실 과피 유전자정보	2005	2011-10-05	제주대학교	2	×
지각 미숙과실 DNA Clone	2011	2011-10-04	제주대학교	8	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
진귤 미숙과실 유전자정보	2006	2011-10-04	제주대학교	3	×
진귤 성숙과실 유전자정보	2010	2011-10-04	제주대학교	2	×
진귤 성숙과실 DNA Clone	2010	2011-10-04	제주대학교	6	×
진귤 성숙과실 DNA Clone	2010	2011-09-29	제주대학교	2	×
진귤 성숙과실 유전자정보	2010	2011-09-29	제주대학교	3	×
한라봉 성숙과실 과피 유전자정보	2004	2011-09-29	난지농업연구소 감귤시험장	1	×
한라봉 성숙과실 과피 DNA Clone	2004	2011-09-29	난지농업연구소 감귤시험장	2	×
온주밀감 미숙과실 유전자정보	2002	2011-09-29	난지농업연구소 감귤시험장	3	×
지각 미숙과실 유전자정보	2011	2011-09-23	제주대학교	2	×
지각 미숙과실 DNA Clone	2011	2011-09-23	제주대학교	1	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2011-09-23	제주대학교	1	×
한라봉 성숙과실 병반과피 유전자정보	2006	2011-09-23	제주대학교	2	×
한라봉 성숙과실 과피 유전자정보	2004	2011-09-23	바이오스펙트럼(주)	2	×
한라봉 성숙과실 과피 DNA Clone	2004	2011-09-23	바이오스펙트럼(주)	1	×
진귤 미숙과실 유전자정보	2006	2011-09-23	바이오스펙트럼(주)	2	×
진귤 미숙과실 DNA Clone	2006	2011-09-23	바이오스펙트럼(주)	1	×
진귤 성숙과실 유전자정보	2010	2011-09-19	제주생물종다양성연구소	3	×
지각 미숙과실 유전자정보	2011	2011-09-19	제주생물종다양성연구소	4	×
지각 미숙과실 DNA Clone	2011	2011-09-19	제주생물종다양성연구소	3	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2011-09-19	제주대학교	1	×
한라봉 성숙과실 병반과피 유전자정보	2006	2011-09-19	제주대학교	2	×
진귤 미숙과실 유전자정보	2006	2011-09-19	제주대학교	4	×
진귤 미숙과실 DNA Clone	2006	2011-09-19	제주대학교	3	×
지각 미숙과실 DNA Clone	2011	2011-09-08	제주생물종다양성연구소	5	×
지각 미숙과실 유전자정보	2011	2011-09-08	제주생물종다양성연구소	1	×
진귤 성숙과실 유전자정보	2010	2011-09-08	제주생물종다양성연구소	5	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
진귤 성숙과실 DNA Clone	2010	2011-09-08	제주생물종다양성연구소	3	×
진귤 성숙과실 유전자정보	2010	2011-09-06	바이오애그진엔텍	4	×
두릅 유전자정보	2005	2011-09-06	(주)바이오애그젠엔텍	1	×
지각 미숙과실 유전자정보	2011	2011-09-06	(주)바이오애그젠엔텍	1	×
한라봉 성숙과실 과피 DNA Clone	2004	2011-09-06	(주)바이오애그젠엔텍	1	×
진귤 미숙과실 유전자정보	2006	2011-09-06	(주)바이오애그젠엔텍	3	×
진귤 성숙과실 DNA Clone	2010	2011-09-05	제주대학교	6	×
진귤 성숙과실 유전자정보	2010	2011-09-05	제주대학교	9	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2011-09-05	제주대학교	2	×
지각 미숙과실 DNA Clone	2011	2011-09-05	제주대학교	9	×
한라봉 성숙과실 과피 유전자정보	2004	2011-08-30	제주특별자치도농업기술원	1	×
한라봉 성숙과실 병반과피 유전자정보	2006	2011-08-30	제주특별자치도농업기술원	4	×
진귤 성숙과실 유전자정보	2010	2011-08-30	제주대학교	4	×
온주밀감 미숙과실 유전자정보	2002	2011-08-30	제주대학교	4	×
온주밀감 성숙과실 유전자정보	2003	2011-08-25	난지농업연구소 감귤시험장	4	×
온주밀감 미숙과실 유전자정보	2002	2011-08-25	난지농업연구소 감귤시험장	7	×
지각 미숙과실 유전자정보	2011	2011-08-25	제주생물종다양성연구소	2	×
지각 미숙과실 DNA Clone	2011	2011-08-25	제주생물종다양성연구소	1	×
한라봉 성숙과실 과피 유전자정보	2004	2011-08-25	제주생물종다양성연구소	6	×
지각 미숙과실 유전자정보	2011	2011-08-22	제주대학교	8	×
지각 미숙과실 DNA Clone	2011	2011-08-22	제주대학교	1	×
진귤 성숙과실 DNA Clone	2010	2011-08-22	아열대원예산업연구소	2	×
진귤 성숙과실 유전자정보	2010	2011-08-22	아열대원예산업연구소	8	×
지각 미숙과실 유전자정보	2011	2011-08-16	제주대학교	2	×
한라봉 미숙과실 과피 유전자정보	2005	2011-08-16	제주대학교	7	×
온주밀감 미숙과실 유전자정보	2002	2011-08-16	제주대학교	8	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
진귤 성숙과실 유전자정보	2010	2011-08-16	제주대학교	3	×
한라봉 성숙과실 병반과피 유전자정보	2006	2011-08-09	생명공학부	10	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2011-08-09	생명공학부	1	×
한라봉 성숙과실 과피 유전자정보	2004	2011-08-09	제주대학교	5	×
한라봉 성숙과실 과피 DNA Clone	2004	2011-08-09	제주대학교	2	×
한라봉 미숙과실 과피 유전자정보	2005	2011-08-09	제주대학교	5	×
한라봉 성숙과실 병반과피 유전자정보	2006	2011-08-09	제주대학교	9	×
지각 미숙과실 DNA Clone	2011	2011-08-09	제주대학교	13	×
진귤 미숙과실 유전자정보	2006	2011-08-05	분자생명공학부	9	×
진귤 미숙과실 DNA Clone	2006	2011-08-05	분자생명공학부	1	×
온주밀감 미숙과실 유전자정보	2002	2011-08-05	제주대학교	6	×
진귤 성숙과실 DNA Clone	2010	2011-08-05	제주대학교	1	×
진귤 성숙과실 유전자정보	2010	2011-08-05	제주대학교	4	×
진귤 미숙과실 유전자정보	2006	2011-07-29	바이오스퀙트럼(주)	10	×
한라봉 성숙과실 병반과피 유전자정보	2006	2011-07-29	제주생물종다양성연구소	5	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2011-07-29	제주생물종다양성연구소	2	×
지각 미숙과실 유전자정보	2011	2011-07-29	제주생물종다양성연구소	7	×
한라봉 성숙과실 병반과피 유전자정보	2006	2011-07-28	제주대학교	12	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2011-07-28	제주대학교	3	×
진귤 성숙과실 DNA Clone	2010	2011-07-28	제주대학교	3	×
온주밀감 미숙과실 유전자정보	2002	2011-07-28	제주대학교	9	×
진귤 성숙과실 DNA Clone	2010	2011-07-22	난지농업연구소	1	×
진귤 성숙과실 유전자정보	2010	2011-07-22	난지농업연구소	4	×
지각 미숙과실 유전자정보	2011	2011-07-22	난지농업연구소	10	×
한라봉 미숙과실 과피 유전자정보	2005	2011-07-22	제주대학교	14	×
한라봉 성숙과실 병반과피 유전자정보	2006	2011-07-22	아열대원예산업연구소	9	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
한라봉 성숙과실 과피 유전자정보	2004	2011-07-22	아열대원예산업연구소	6	×
한라봉 성숙과실 과피 DNA Clone	2004	2011-07-22	아열대원예산업연구소	1	×
진귤 미숙과실 유전자정보	2006	2011-07-22	제주대학교	8	×
진귤 미숙과실 DNA Clone	2006	2011-07-22	제주대학교	1	×
온주밀감 성숙과실 DNA Clone	2003	2011-07-22	제주대학교	2	×
온주밀감 성숙과실 유전자정보	2003	2011-07-22	제주대학교	4	×
한라봉 성숙과실 과피 DNA Clone	2004	2011-07-18	생명공학부	2	×
한라봉 성숙과실 과피 유전자정보	2004	2011-07-18	생명공학부	3	×
진귤 성숙과실 유전자정보	2010	2011-07-18	생명공학부	3	×
진귤 성숙과실 DNA Clone	2010	2011-07-18	생명공학부	1	×
온주밀감 미숙과실 DNA Clone	2002	2011-07-18	생명공학부	3	×
온주밀감 미숙과실 유전자정보	2002	2011-07-18	생명공학부	4	×
한라봉 성숙과실 병반과피 유전자정보	2006	2011-07-18	제주대학교	6	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2011-07-18	제주대학교	4	×
지각 미숙과실 DNA Clone	2011	2011-07-18	제주대학교	3	×
지각 미숙과실 유전자정보	2011	2011-07-18	제주대학교	5	×
한라봉 성숙과실 과피 유전자정보	2004	2011-07-18	제주대학교	8	×
한라봉 성숙과실 과피 DNA Clone	2004	2011-07-18	제주대학교	6	×
진귤 성숙과실 유전자정보	2010	2011-07-08	제주특별자치도농업기술원	8	×
진귤 성숙과실 DNA Clone	2010	2011-07-08	제주특별자치도농업기술원	1	×
온주밀감 성숙과실 유전자정보	2003	2011-07-08	제주특별자치도농업기술원	9	×
온주밀감 성숙과실 DNA Clone	2003	2011-07-08	제주대학교	10	×
진귤 미숙과실 유전자정보	2006	2011-07-08	제주대학교	4	×
진귤 성숙과실 유전자정보	2010	2011-07-08	제주대학교	6	×
한라봉 성숙과실 병반과피 유전자정보	2006	2011-07-06	아열대원예산업연구소	3	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2011-07-06	아열대원예산업연구소	3	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
지각 미숙과실 DNA Clone	2011	2011-07-06	아열대원예산업연구소	5	×
한라봉 성숙과실 과피 DNA Clone	2004	2011-07-01	제주대학교	6	×
한라봉 성숙과실 과피 유전자정보	2004	2011-07-01	제주대학교	4	×
온주밀감 성숙과실 DNA Clone	2003	2011-07-01	제주대학교	5	×
온주밀감 성숙과실 유전자정보	2003	2011-07-01	제주대학교	5	×
지각 미숙과실 유전자정보	2011	2011-07-01	난지농업연구소	6	×
지각 미숙과실 DNA Clone	2011	2011-07-01	난지농업연구소	4	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2011-07-01	난지농업연구소	5	×
한라봉 성숙과실 병반과피 유전자정보	2006	2011-07-01	난지농업연구소	5	×
한라봉 성숙과실 과피 DNA Clone	2004	2011-07-01	제주특별자치도농업기술원	5	×
한라봉 성숙과실 과피 유전자정보	2004	2011-07-01	제주특별자치도농업기술원	5	×
한라봉 미숙과실 과피 DNA Clone	2005	2011-07-01	제주특별자치도농업기술원	5	×
한라봉 미숙과실 과피 유전자정보	2005	2011-07-01	제주특별자치도농업기술원	5	×
진귤 성숙과실 DNA Clone	2010	2011-07-01	난지농업연구소 감귤시험장	5	×
진귤 성숙과실 유전자정보	2010	2011-07-01	난지농업연구소 감귤시험장	5	×
진귤 미숙과실 DNA Clone	2006	2011-07-01	난지농업연구소 감귤시험장	5	×
진귤 미숙과실 유전자정보	2006	2011-07-01	난지농업연구소 감귤시험장	5	×
한라봉 성숙과실 과피 DNA Clone	2004	2011-06-29	(주)바이오애그젠엔텍	10	×
한라봉 성숙과실 과피 유전자정보	2004	2011-06-29	(주)바이오애그젠엔텍	10	×
한라봉 미숙과실 과피 DNA Clone	2005	2011-06-29	아열대원예산업연구소	10	×
한라봉 미숙과실 과피 유전자정보	2005	2011-06-29	아열대원예산업연구소	10	×
진귤 미숙과실 DNA Clone	2006	2011-06-27	바이오스펙트럼(주)	10	×
진귤 미숙과실 유전자정보	2006	2011-06-27	바이오스펙트럼(주)	10	×
온주밀감 성숙과실 DNA Clone	2003	2011-06-27	생명공학부	10	×
온주밀감 성숙과실 유전자정보	2003	2011-06-27	생명공학부	10	×
온주밀감 미숙과실 DNA Clone	2002	2011-06-27	제주대학교	10	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
온주밀감 미숙과실 유전자정보	2002	2011-06-27	제주대학교	10	×
지각 미숙과실 DNA Clone	2011	2011-06-22	제주대학교	3	×
진귤 성숙과실 DNA Clone	2010	2011-06-22	제주대학교	3	×
진귤 성숙과실 유전자정보	2010	2011-06-22	제주대학교	9	×
지각 미숙과실 DNA Clone	2011	2011-06-22	제주대학교	5	×
한라봉 성숙과실 병반과피 유전자정보	2006	2011-06-22	제주대학교	4	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2011-06-22	제주대학교	2	×
지각 미숙과실 DNA Clone	2011	2011-06-22	제주생물종다양성연구소	9	×
지각 미숙과실 유전자정보	2011	2011-06-22	제주생물종다양성연구소	10	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2011-06-21	바이오스퀘트럼(주)	9	×
지각 미숙과실 DNA Clone	2011	2011-06-20	제주대학교	7	×
지각 미숙과실 DNA Clone	2011	2011-06-20	바이오애그진엔텍	11	×
지각 미숙과실 유전자정보	2011	2011-06-15	아열대원예산업연구소	3	×
지각 미숙과실 DNA Clone	2011	2011-06-15	아열대원예산업연구소	9	×
지각 미숙과실 유전자정보	2011	2011-06-15	난지농업연구소	4	×
지각 미숙과실 DNA Clone	2011	2011-06-15	난지농업연구소	10	×
지각 미숙과실 유전자정보	2011	2011-06-15	제주대학교	2	×
지각 미숙과실 DNA Clone	2011	2011-06-15	제주대학교	4	×
한라봉 성숙과실 병반과피 유전자정보	2006	2011-06-15	제주대학교	3	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2011-06-15	제주대학교	3	×
한라봉 미숙과실 과피 DNA Clone	2005	2011-06-15	제주대학교	6	×
한라봉 미숙과실 과피 유전자정보	2005	2011-06-15	제주대학교	3	×
지각 미숙과실 DNA Clone	2011	2011-06-13	제주생물종다양성연구소	10	×
진귤 성숙과실 유전자정보	2010	2011-06-13	난지농업연구소 감귤시험장	5	×
진귤 성숙과실 DNA Clone	2010	2011-06-13	난지농업연구소 감귤시험장	2	×
지각 미숙과실 DNA Clone	2011	2011-06-13	난지농업연구소 감귤시험장	10	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
지각 미숙과실 DNA Clone	2011	2011-06-10	제주대학교	13	×
지각 미숙과실 유전자정보	2011	2011-06-10	제주대학교	9	×
한라봉 성숙과실 병반과피 유전자정보	2006	2011-06-07	제주특별자치도농업기술원	5	×
지각 미숙과실 DNA Clone	2011	2011-06-07	제주특별자치도농업기술원	6	×
지각 미숙과실 DNA Clone	2011	2011-06-07	제주대학교	13	×
지각 미숙과실 DNA Clone	2011	2011-06-07	제주대학교	13	×
지각 미숙과실 유전자정보	2011	2011-06-07	(주)바이오애그젠엔텍	5	×
지각 미숙과실 DNA Clone	2011	2011-06-07	(주)바이오애그젠엔텍	12	×
한라봉 성숙과실 과피 DNA Clone	2004	2011-05-25	제주대학교	5	×
한라봉 성숙과실 과피 유전자정보	2004	2011-05-25	제주대학교	10	×
한라봉 미숙과실 과피 DNA Clone	2005	2011-05-25	제주대학교	10	×
한라봉 미숙과실 과피 유전자정보	2005	2011-05-25	제주대학교	10	×
지각 미숙과실 DNA Clone	2011	2011-05-23	제주대학교	6	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2011-05-16	제주대학교	3	×
한라봉 성숙과실 병반과피 유전자정보	2006	2011-05-16	제주대학교	2	×
지각 미숙과실 DNA Clone	2011	2011-05-16	제주대학교	8	×
진귤 성숙과실 DNA Clone	2010	2011-05-16	바이오애그진엔텍	3	×
진귤 성숙과실 유전자정보	2010	2011-05-16	바이오애그진엔텍	3	×
지각 미숙과실 DNA Clone	2011	2011-05-16	바이오애그진엔텍	5	×
지각 미숙과실 DNA Clone	2011	2011-05-13	제주대학교	6	×
한라봉 미숙과실 과피 DNA Clone	2005	2011-05-13	자연과학대학	2	×
한라봉 미숙과실 과피 유전자정보	2005	2011-05-13	자연과학대학	1	×
지각 미숙과실 DNA Clone	2011	2011-05-13	자연과학대학	4	×
지각 미숙과실 DNA Clone	2011	2011-05-13	바이오스펙트럼(주)	2	×
지각 미숙과실 유전자정보	2011	2011-05-13	바이오스펙트럼(주)	1	×
한라봉 성숙과실 과피 유전자정보	2004	2011-05-13	바이오스펙트럼(주)	2	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
진귤 성숙과실 유전자정보	2010	2011-05-13	바이오스펙트럼(주)	1	×
진귤 성숙과실 DNA Clone	2010	2011-05-13	바이오스펙트럼(주)	6	×
진귤 성숙과실 DNA Clone	2010	2011-05-09	제주생물종다양성연구소	6	×
진귤 성숙과실 유전자정보	2010	2011-05-09	제주생물종다양성연구소	2	×
지각 미숙과실 DNA Clone	2011	2011-05-09	제주생물종다양성연구소	5	×
지각 미숙과실 유전자정보	2011	2011-05-09	제주생물종다양성연구소	7	×
진귤 성숙과실 DNA Clone	2010	2011-05-09	난지농업연구소 감귤시험장	3	×
진귤 성숙과실 유전자정보	2010	2011-05-09	난지농업연구소 감귤시험장	4	×
한라봉 성숙과실 병반과피 유전자정보	2006	2011-05-09	난지농업연구소 감귤시험장	5	×
지각 미숙과실 DNA Clone	2011	2011-05-09	난지농업연구소 감귤시험장	9	×
지각 미숙과실 유전자정보	2011	2011-05-09	제주대학교	3	×
진귤 성숙과실 DNA Clone	2010	2011-05-09	제주대학교	3	×
진귤 성숙과실 유전자정보	2010	2011-05-09	제주대학교	1	×
지각 미숙과실 DNA Clone	2011	2011-05-09	제주대학교	6	×
지각 미숙과실 유전자정보	2011	2011-05-06	제주대학교	2	×
지각 미숙과실 DNA Clone	2011	2011-05-06	제주대학교	8	×
진귤 미숙과실 DNA Clone	2006	2011-05-06	제주대학교	3	×
온주밀감 성숙과실 DNA Clone	2003	2011-05-06	제주대학교	5	×
온주밀감 성숙과실 유전자정보	2003	2011-05-06	제주대학교	1	×
온주밀감 미숙과실 유전자정보	2002	2011-05-06	제주대학교	5	×
한라봉 미숙과실 과피 DNA Clone	2005	2011-05-06	제주특별자치도농업기술원	4	×
한라봉 미숙과실 과피 유전자정보	2005	2011-05-06	제주특별자치도농업기술원	2	×
진귤 성숙과실 유전자정보	2010	2011-05-06	제주특별자치도농업기술원	2	×
진귤 성숙과실 DNA Clone	2010	2011-05-06	제주특별자치도농업기술원	2	×
한라봉 미숙과실 과피 DNA Clone	2005	2011-05-06	바이오애그진엔텍	4	×
지각 미숙과실 DNA Clone	2011	2011-05-06	바이오애그진엔텍	4	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
지각 미숙과실 유전자정보	2011	2011-05-06	바이오애그진엔텍	7	×
진귤 성숙과실 유전자정보	2010	2011-05-06	제주대학교	6	×
지각 미숙과실 DNA Clone	2011	2011-05-06	제주대학교	15	×
지각 미숙과실 DNA Clone	2011	2011-04-27	아열대원예산업연구소	9	×
진귤 성숙과실 DNA Clone	2010	2011-04-27	제주대학교	6	×
진귤 성숙과실 유전자정보	2010	2011-04-27	제주대학교	1	×
지각 미숙과실 유전자정보	2011	2011-04-22	생명공학부	12	×
지각 미숙과실 DNA Clone	2011	2011-04-22	생명공학부	9	×
지각 미숙과실 DNA Clone	2011	2011-04-22	제주대학교	13	×
지각 미숙과실 유전자정보	2011	2011-04-22	제주대학교	12	×
지각 미숙과실 DNA Clone	2011	2011-04-22	제주대학교	10	×
지각 미숙과실 유전자정보	2011	2011-04-22	제주대학교	15	×
지각 미숙과실 DNA Clone	2011	2011-04-18	난지농업연구소	8	×
지각 미숙과실 유전자정보	2011	2011-04-18	난지농업연구소	9	×
지각 미숙과실 유전자정보	2011	2011-04-18	바이오스펙트럼(주)	5	×
지각 미숙과실 DNA Clone	2011	2011-04-18	바이오스펙트럼(주)	9	×
한라봉 성숙과실 과피 DNA Clone	2004	2011-04-14	제주대학교	6	×
한라봉 성숙과실 과피 유전자정보	2004	2011-04-14	제주대학교	5	×
한라봉 미숙과실 과피 DNA Clone	2005	2011-04-14	(주)바이오애그젠엔텍	9	×
한라봉 미숙과실 과피 유전자정보	2005	2011-04-14	(주)바이오애그젠엔텍	6	×
지각 미숙과실 DNA Clone	2011	2011-04-14	제주생물종다양성연구소	12	×
지각 미숙과실 유전자정보	2011	2011-04-14	제주생물종다양성연구소	9	×
지각 미숙과실 유전자정보	2011	2011-04-12	제주대학교	5	×
지각 미숙과실 DNA Clone	2011	2011-04-12	제주대학교	12	×
식물체 cell line	2010	2011-04-08	난지농업연구소 감귤시험장	1	×
지각 미숙과실 DNA Clone	2011	2011-04-07	제주대학교	12	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
지각 미숙과실 유전자정보	2011	2011-04-07	제주대학교	10	×
지각 미숙과실 DNA Clone	2011	2011-04-07	난지농업연구소 감귤시험장	8	×
지각 미숙과실 유전자정보	2011	2011-04-07	난지농업연구소 감귤시험장	2	×
지각 미숙과실 DNA Clone	2011	2011-04-07	제주대학교	8	×
지각 미숙과실 유전자정보	2011	2011-04-07	제주대학교	8	×
두릅 DNA Clone	2005	2011-04-07	제주대학교	2	×
두릅 유전자정보	2005	2011-04-06	제주대학교	1	×
식물체 cell line	2010	2011-04-05	난지농업연구소 감귤시험장	2	×
한라봉 성숙과실 병반과피 유전자정보	2006	2011-04-05	바이오애그진엔텍	1	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2011-04-05	바이오애그진엔텍	1	×
지각 미숙과실 DNA Clone	2011	2011-04-05	바이오애그진엔텍	4	×
지각 미숙과실 유전자정보	2011	2011-04-05	바이오애그진엔텍	6	×
지각 미숙과실 DNA Clone	2011	2011-04-05	자연과학대학	2	×
지각 미숙과실 유전자정보	2011	2011-04-05	자연과학대학	1	×
진귤 성숙과실 유전자정보	2010	2011-04-05	자연과학대학	3	×
진귤 성숙과실 DNA Clone	2010	2011-04-05	자연과학대학	2	×
진귤 미숙과실 DNA Clone	2006	2011-04-05	자연과학대학	3	×
진귤 미숙과실 DNA Clone	2006	2011-04-05	제주생물종다양성연구소	3	×
진귤 성숙과실 DNA Clone	2010	2011-04-05	제주생물종다양성연구소	3	×
진귤 성숙과실 유전자정보	2010	2011-04-05	제주생물종다양성연구소	1	×
지각 미숙과실 DNA Clone	2011	2011-04-05	제주생물종다양성연구소	3	×
지각 미숙과실 유전자정보	2011	2011-04-05	제주생물종다양성연구소	7	×
지각 미숙과실 유전자정보	2011	2011-03-30	난지농업연구소 감귤시험장	4	×
지각 미숙과실 DNA Clone	2011	2011-03-30	난지농업연구소 감귤시험장	5	×
지각 미숙과실 DNA Clone	2011	2011-03-30	아열대원예산업연구소	6	×
지각 미숙과실 유전자정보	2011	2011-03-30	아열대원예산업연구소	9	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
식물체 과실	2010	2011-03-25	경상대학교	4	×
지각 미숙과실 DNA Clone	2011	2011-03-25	제주대학교	7	×
지각 미숙과실 DNA Clone	2011	2011-03-23	난지농업연구소 감귤시험장	6	×
지각 미숙과실 유전자정보	2011	2011-03-23	난지농업연구소 감귤시험장	5	×
지각 미숙과실 유전자정보	2011	2011-03-18	생명공학부	6	×
지각 미숙과실 DNA Clone	2011	2011-03-18	생명공학부	11	×
지각 미숙과실 DNA Clone	2011	2011-03-16	난지농업연구소	6	×
지각 미숙과실 유전자정보	2011	2011-03-16	난지농업연구소	9	×
지각 미숙과실 유전자정보	2011	2011-03-16	제주특별자치도농업기술원	6	×
지각 미숙과실 DNA Clone	2011	2011-03-16	제주특별자치도농업기술원	10	×
한라봉 성숙과실 과피 유전자정보	2004	2011-03-14	제주대학교	1	×
지각 미숙과실 유전자정보	2011	2011-03-14	바이오스펙트럼(주)	5	×
지각 미숙과실 DNA Clone	2011	2011-03-14	바이오스펙트럼(주)	8	×
지각 미숙과실 유전자정보	2011	2011-03-14	(주)바이오애그젠엔텍	5	×
지각 미숙과실 DNA Clone	2011	2011-03-14	(주)바이오애그젠엔텍	11	×
지각 미숙과실 DNA Clone	2011	2011-03-10	제주대학교	8	×
지각 미숙과실 유전자정보	2011	2011-03-10	제주대학교	4	×
한라봉 미숙과실 과피 DNA Clone	2005	2011-03-04	제주대학교	1	×
한라봉 미숙과실 과피 유전자정보	2005	2011-03-04	제주대학교	1	×
진귤 미숙과실 DNA Clone	2006	2011-03-04	제주대학교	3	×
진귤 미숙과실 유전자정보	2006	2011-03-04	제주대학교	3	×
온주밀감 성숙과실 DNA Clone	2003	2011-03-04	제주대학교	2	×
온주밀감 성숙과실 유전자정보	2003	2011-03-04	제주대학교	2	×
온주밀감 미숙과실 DNA Clone	2002	2011-03-04	제주대학교	2	×
온주밀감 미숙과실 유전자정보	2002	2011-03-04	제주대학교	2	×
진귤 미숙과실 유전자정보	2006	2011-02-21	바이오스펙트럼(주)	4	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
진귤 미숙과실 DNA Clone	2006	2011-02-21	바이오스펙트럼(주)	6	×
한라봉 미숙과실 과피 DNA Clone	2005	2011-02-21	(주)바이오애그젠엔텍	8	×
한라봉 미숙과실 과피 유전자정보	2005	2011-02-21	(주)바이오애그젠엔텍	3	×
진귤 성숙과실 DNA Clone	2010	2011-02-21	제주대학교	9	×
진귤 성숙과실 유전자정보	2010	2011-02-21	제주대학교	3	×
식물체 잎	2009	2011-02-21	제주대학교	5	×
식물체 잎	2009	2011-02-17	제주대학교	30	×
한라봉 미숙과실 과피 유전자정보	2005	2011-02-10	제주특별자치도농업기술원	5	×
한라봉 미숙과실 과피 DNA Clone	2005	2011-02-10	제주특별자치도농업기술원	5	×
진귤 성숙과실 유전자정보	2010	2011-02-10	(주)바이오애그젠엔텍	3	×
진귤 성숙과실 DNA Clone	2010	2011-02-10	(주)바이오애그젠엔텍	8	×
식물체 과실	2010	2011-02-08	경상대학교	102	○
한라봉 미숙과실 과피 유전자정보	2005	2011-01-31	난지농업연구소	4	×
한라봉 미숙과실 과피 DNA Clone	2005	2011-01-31	난지농업연구소	9	×
진귤 성숙과실 유전자정보	2010	2011-01-28	제주대학교	4	×
진귤 성숙과실 DNA Clone	2010	2011-01-28	제주대학교	10	×
진귤 성숙과실 DNA Clone	2010	2011-01-19	제주대학교	11	×
식물체 과실	2010	2011-01-18	경상대학교	165	○
식물체 과실	2010	2011-01-17	한국식품연구원	64	×
진귤 성숙과실 유전자정보	2010	2011-01-13	제주대학교	10	×
진귤 성숙과실 DNA Clone	2010	2011-01-13	제주대학교	19	×
한라봉 미숙과실 과피 DNA Clone	2005	2011-01-10	제주대학교	3	×
온주밀감 성숙과실 DNA Clone	2003	2011-01-10	제주대학교	1	×
한라봉 미숙과실 과피 DNA Clone	2005	2010-12-27	제주대학교	4	×
진귤 성숙과실 DNA Clone	2010	2010-12-27	제주대학교	12	×
진귤 미숙과실 유전자정보	2006	2010-12-27	난지농업연구소	6	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
진귤 성숙과실 유전자정보	2010	2010-12-27	난지농업연구소	12	×
진귤 성숙과실 유전자정보	2010	2010-12-24	제주대학교	3	×
진귤 성숙과실 DNA Clone	2010	2010-12-24	제주대학교	2	×
진귤 미숙과실 DNA Clone	2006	2010-12-24	제주대학교	4	×
진귤 미숙과실 유전자정보	2006	2010-12-24	제주대학교	2	×
진귤 성숙과실 유전자정보	2010	2010-12-24	생명공학부	11	×
진귤 성숙과실 유전자정보	2010	2010-12-21	난지농업연구소 감귤시험장	10	×
한라봉 미숙과실 과피 유전자정보	2005	2010-12-21	난지농업연구소 감귤시험장	3	×
한라봉 성숙과실 과피 DNA Clone	2004	2010-12-20	(주)바이오애그젠엔텍	3	×
한라봉 성숙과실 과피 유전자정보	2004	2010-12-20	(주)바이오애그젠엔텍	1	×
한라봉 미숙과실 과피 유전자정보	2005	2010-12-20	(주)바이오애그젠엔텍	6	×
온주밀감 성숙과실 DNA Clone	2003	2010-12-20	(주)바이오애그젠엔텍	9	×
한라봉 성숙과실 과피 유전자정보	2004	2010-12-16	아열대원예산업연구소	5	×
한라봉 미숙과실 과피 DNA Clone	2005	2010-12-16	아열대원예산업연구소	3	×
한라봉 미숙과실 과피 유전자정보	2005	2010-12-16	아열대원예산업연구소	11	×
진귤 미숙과실 DNA Clone	2006	2010-12-16	제주대학교	7	×
진귤 성숙과실 DNA Clone	2010	2010-12-16	제주대학교	9	×
한라봉 성숙과실 병반과피 유전자정보	2006	2010-12-14	제주대학교	3	×
한라봉 성숙과실 과피 유전자정보	2004	2010-12-14	제주대학교	3	×
한라봉 미숙과실 과피 유전자정보	2005	2010-12-14	제주대학교	4	×
진귤 성숙과실 유전자정보	2010	2010-12-14	제주대학교	2	×
진귤 미숙과실 유전자정보	2006	2010-12-14	제주대학교	3	×
온주밀감 성숙과실 유전자정보	2003	2010-12-14	제주대학교	5	×
온주밀감 미숙과실 유전자정보	2002	2010-12-14	제주대학교	7	×
진귤 미숙과실 DNA Clone	2006	2010-12-13	바이오스펙트럼(주)	16	×
진귤 성숙과실 DNA Clone	2010	2010-12-10	제주특별자치도농업기술원	1	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
진귤 성숙과실 유전자정보	2010	2010-12-10	제주특별자치도농업기술원	13	×
한라봉 성숙과실 과피 DNA Clone	2004	2010-12-10	(주)바이오애그젠엔텍	4	×
한라봉 미숙과실 과피 유전자정보	2005	2010-12-10	(주)바이오애그젠엔텍	9	×
한라봉 미숙과실 과피 DNA Clone	2005	2010-12-10	(주)바이오애그젠엔텍	2	×
진귤 성숙과실 유전자정보	2010	2010-12-10	제주생물종다양성연구소	9	×
진귤 성숙과실 DNA Clone	2010	2010-12-10	제주생물종다양성연구소	3	×
진귤 미숙과실 유전자정보	2006	2010-12-10	제주생물종다양성연구소	7	×
진귤 미숙과실 DNA Clone	2006	2010-12-10	제주생물종다양성연구소	8	×
진귤 성숙과실 유전자정보	2010	2010-12-09	제주대학교	8	×
진귤 성숙과실 DNA Clone	2010	2010-12-09	제주대학교	6	×
진귤 미숙과실 유전자정보	2006	2010-12-09	제주대학교	9	×
진귤 성숙과실 DNA Clone	2010	2010-12-09	제주대학교	8	×
진귤 미숙과실 DNA Clone	2006	2010-12-09	제주대학교	8	×
한라봉 미숙과실 과피 유전자정보	2005	2010-12-01	제주특별자치도농업기술원	6	×
진귤 성숙과실 유전자정보	2010	2010-12-01	제주특별자치도농업기술원	5	×
진귤 성숙과실 DNA Clone	2010	2010-12-01	제주특별자치도농업기술원	5	×
한라봉 미숙과실 과피 유전자정보	2005	2010-12-01	제주대학교	4	×
진귤 성숙과실 유전자정보	2010	2010-12-01	제주대학교	3	×
진귤 미숙과실 유전자정보	2006	2010-12-01	제주대학교	9	×
온주밀감 성숙과실 유전자정보	2003	2010-12-01	생명공학부	6	×
온주밀감 미숙과실 유전자정보	2002	2010-12-01	생명공학부	6	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2010-11-30	제주대학교	3	×
한라봉 미숙과실 과피 DNA Clone	2005	2010-11-30	제주대학교	4	×
진귤 미숙과실 DNA Clone	2006	2010-11-30	제주대학교	3	×
한라봉 미숙과실 과피 유전자정보	2005	2010-11-30	제주대학교	1	×
한라봉 미숙과실 과피 유전자정보	2005	2010-11-29	난지농업연구소 감귤시험장	4	×
진귤 성숙과실 유전자정보	2010	2010-11-29	난지농업연구소 감귤시험장	3	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
진귤 미숙과실 유전자정보	2006	2010-11-29	난지농업연구소 감귤시험장	5	×
한라봉 성숙과실 과피 유전자정보	2004	2010-11-26	생명자원과학대학	5	×
한라봉 미숙과실 과피 유전자정보	2005	2010-11-26	생명자원과학대학	8	×
진귤 성숙과실 유전자정보	2010	2010-11-25	제주대학교	11	×
진귤 미숙과실 유전자정보	2006	2010-11-25	제주대학교	6	×
진귤 성숙과실 유전자정보	2010	2010-11-25	제주대학교	6	×
진귤 미숙과실 유전자정보	2006	2010-11-25	제주대학교	4	×
진귤 미숙과실 DNA Clone	2006	2010-11-25	제주대학교	3	×
진귤 미숙과실 DNA Clone	2006	2010-11-23	제주대학교	10	×
진귤 성숙과실 DNA Clone	2010	2010-11-23	제주대학교	8	×
진귤 성숙과실 유전자정보	2010	2010-11-23	아열대원예산업연구센터	3	×
진귤 성숙과실 DNA Clone	2010	2010-11-23	아열대원예산업연구센터	4	×
진귤 미숙과실 DNA Clone	2006	2010-11-23	아열대원예산업연구센터	8	×
온주밀감 성숙과실 유전자정보	2003	2010-11-23	아열대원예산업연구센터	6	×
온주밀감 미숙과실 유전자정보	2002	2010-11-23	아열대원예산업연구센터	5	×
진귤 성숙과실 유전자정보	2010	2010-11-22	아열대원예산업연구소	8	×
진귤 미숙과실 DNA Clone	2006	2010-11-22	아열대원예산업연구소	9	×
진귤 미숙과실 유전자정보	2006	2010-11-22	아열대원예산업연구소	1	×
한라봉 성숙과실 과피 DNA Clone	2004	2010-11-22	제주대학교	6	×
한라봉 미숙과실 과피 DNA Clone	2005	2010-11-22	제주대학교	6	×
온주밀감 성숙과실 DNA Clone	2003	2010-11-22	제주대학교	6	×
진귤 성숙과실 DNA Clone	2010	2010-11-22	난지농업연구소	4	×
진귤 미숙과실 DNA Clone	2006	2010-11-22	난지농업연구소	4	×
온주밀감 성숙과실 DNA Clone	2003	2010-11-22	난지농업연구소	6	×
한라봉 미숙과실 과피 DNA Clone	2005	2010-11-16	바이오스펙트럼(주)	6	×
한라봉 미숙과실 과피 유전자정보	2005	2010-11-16	바이오스펙트럼(주)	1	×
진귤 성숙과실 유전자정보	2010	2010-11-16	바이오스펙트럼(주)	8	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
온주밀감 미숙과실 유전자정보	2002	2010-11-16	바이오스펙트럼(주)	5	×
진귤 성숙과실 유전자정보	2010	2010-11-16	(주)바이오애그젠엔텍	6	×
온주밀감 성숙과실 유전자정보	2003	2010-11-16	(주)바이오애그젠엔텍	9	×
온주밀감 미숙과실 유전자정보	2002	2010-11-16	(주)바이오애그젠엔텍	11	×
진귤 미숙과실 유전자정보	2006	2010-11-12	제주대학교	12	×
온주밀감 성숙과실 DNA Clone	2003	2010-11-12	제주대학교	8	×
온주밀감 미숙과실 DNA Clone	2002	2010-11-12	제주대학교	7	×
진귤 성숙과실 유전자정보	2010	2010-11-09	제주대학교	6	×
온주밀감 성숙과실 유전자정보	2003	2010-11-09	제주대학교	11	×
온주밀감 미숙과실 유전자정보	2002	2010-11-09	제주대학교	4	×
한라봉 성숙과실 병반과피 유전자정보	2006	2010-11-05	제주생물종다양성연구소	9	×
한라봉 성숙과실 과피 유전자정보	2004	2010-11-05	제주생물종다양성연구소	7	×
한라봉 미숙과실 과피 유전자정보	2005	2010-11-05	제주생물종다양성연구소	11	×
온주밀감 성숙과실 DNA Clone	2003	2010-11-03	제주대학교	15	×
진귤 성숙과실 유전자정보	2010	2010-11-03	제주대학교	1	×
진귤 성숙과실 유전자정보	2010	2010-10-28	난지농업연구소 감귤시험장	3	×
진귤 미숙과실 유전자정보	2006	2010-10-28	난지농업연구소 감귤시험장	3	×
온주밀감 성숙과실 DNA Clone	2003	2010-10-28	난지농업연구소 감귤시험장	4	×
온주밀감 미숙과실 DNA Clone	2002	2010-10-28	난지농업연구소 감귤시험장	4	×
한라봉 미숙과실 과피 DNA Clone	2005	2010-10-25	제주대학교	1	×
진귤 성숙과실 DNA Clone	2010	2010-10-25	제주대학교	6	×
한라봉 성숙과실 병반과피 유전자정보	2006	2010-10-25	바이오스펙트럼(주)	2	×
한라봉 미숙과실 과피 유전자정보	2005	2010-10-25	바이오스펙트럼(주)	8	×
진귤 성숙과실 유전자정보	2010	2010-10-25	바이오스펙트럼(주)	8	×
한라봉 성숙과실 병반과피 유전자정보	2006	2010-10-21	아열대원예산업연구센터	3	×
한라봉 미숙과실 과피 DNA Clone	2005	2010-10-21	아열대원예산업연구센터	5	×
한라봉 미숙과실 과피 유전자정보	2005	2010-10-21	아열대원예산업연구센터	5	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
진귤 성숙과실 유전자정보	2010	2010-10-21	아열대원예산업연구센터	5	×
한라봉 미숙과실 과피 유전자정보	2005	2010-10-21	제주대학교	5	×
진귤 성숙과실 DNA Clone	2010	2010-10-21	제주대학교	4	×
온주밀감 미숙과실 DNA Clone	2002	2010-10-21	제주대학교	4	×
한라봉 미숙과실 과피 유전자정보	2005	2010-10-19	제주대학교	3	×
진귤 성숙과실 유전자정보	2010	2010-10-19	제주대학교	6	×
진귤 미숙과실 유전자정보	2006	2010-10-19	제주대학교	2	×
온주밀감 성숙과실 DNA Clone	2003	2010-10-19	제주대학교	2	×
온주밀감 미숙과실 DNA Clone	2002	2010-10-19	제주대학교	6	×
진귤 미숙과실 DNA Clone	2006	2010-10-18	자연과학대학	7	×
온주밀감 미숙과실 DNA Clone	2002	2010-10-18	자연과학대학	2	×
온주밀감 미숙과실 유전자정보	2002	2010-10-18	자연과학대학	3	×
두릅 유전자정보	2005	2010-10-18	자연과학대학	3	×
온주밀감 성숙과실 유전자정보	2003	2010-10-18	자연과학대학	2	×
한라봉 성숙과실 병반과피 유전자정보	2006	2010-10-15	난지농업연구소	8	×
한라봉 미숙과실 과피 유전자정보	2005	2010-10-15	난지농업연구소	6	×
한라봉 미숙과실 과피 DNA Clone	2005	2010-10-15	생명공학부	3	×
한라봉 미숙과실 과피 유전자정보	2005	2010-10-15	생명공학부	6	×
진귤 미숙과실 DNA Clone	2006	2010-10-13	(주)바이오애그젠엔텍	9	×
진귤 성숙과실 DNA Clone	2010	2010-10-13	(주)바이오애그젠엔텍	8	×
진귤 미숙과실 DNA Clone	2006	2010-10-11	바이오스펙트럼(주)	3	×
진귤 성숙과실 DNA Clone	2010	2010-10-11	바이오스펙트럼(주)	5	×
한라봉 성숙과실 병반과피 유전자정보	2006	2010-10-07	제주특별자치도농업기술원	5	×
한라봉 성숙과실 과피 유전자정보	2004	2010-10-07	제주특별자치도농업기술원	4	×
한라봉 미숙과실 과피 유전자정보	2005	2010-10-07	제주특별자치도농업기술원	7	×
진귤 성숙과실 DNA Clone	2010	2010-10-07	제주생물종다양성연구소	3	×
진귤 성숙과실 유전자정보	2010	2010-10-07	제주생물종다양성연구소	8	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
한라봉 성숙과실 과피 유전자정보	2004	2010-10-07	제주생물종다양성연구소	1	×
온주밀감 미숙과실 유전자정보	2002	2010-10-05	제주대학교	4	×
진귤 성숙과실 유전자정보	2010	2010-10-05	제주대학교	11	×
한라봉 성숙과실 과피 유전자정보	2004	2010-09-29	바이오스펙트럼(주)	2	×
한라봉 성숙과실 과피 DNA Clone	2004	2010-09-29	바이오스펙트럼(주)	2	×
진귤 성숙과실 DNA Clone	2010	2010-09-29	바이오스펙트럼(주)	8	×
한라봉 성숙과실 과피 유전자정보	2004	2010-09-24	제주대학교	12	×
한라봉 미숙과실 과피 유전자정보	2005	2010-09-24	제주대학교	10	×
진귤 성숙과실 유전자정보	2010	2010-09-16	아열대원예산업연구센터	12	×
진귤 성숙과실 유전자정보	2010	2010-09-16	(주)바이오애그젠엔텍	9	×
진귤 성숙과실 유전자정보	2010	2010-09-14	제주특별자치도농업기술원	7	×
한라봉 미숙과실 과피 유전자정보	2005	2010-09-14	바이오스펙트럼(주)	3	×
한라봉 미숙과실 과피 DNA Clone	2005	2010-09-14	바이오스펙트럼(주)	1	×
진귤 미숙과실 DNA Clone	2006	2010-09-14	바이오스펙트럼(주)	1	×
진귤 미숙과실 유전자정보	2006	2010-09-14	바이오스펙트럼(주)	6	×
한라봉 성숙과실 과피 유전자정보	2004	2010-09-10	제주대학교	1	×
한라봉 성숙과실 과피 DNA Clone	2004	2010-09-10	제주대학교	3	×
진귤 성숙과실 DNA Clone	2010	2010-09-10	제주대학교	1	×
진귤 성숙과실 유전자정보	2010	2010-09-10	제주대학교	4	×
진귤 미숙과실 DNA Clone	2006	2010-09-10	제주대학교	4	×
진귤 미숙과실 유전자정보	2006	2010-09-10	제주대학교	2	×
온주밀감 성숙과실 DNA Clone	2003	2010-09-08	제주대학교	2	×
한라봉 미숙과실 과피 DNA Clone	2005	2010-09-08	제주대학교	3	×
온주밀감 미숙과실 DNA Clone	2002	2010-09-08	제주대학교	5	×
한라봉 성숙과실 과피 DNA Clone	2004	2010-09-08	제주대학교	2	×
한라봉 성숙과실 과피 유전자정보	2004	2010-09-08	제주대학교	1	×
한라봉 미숙과실 과피 DNA Clone	2005	2010-09-08	제주대학교	4	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
한라봉 미숙과실 과피 유전자정보	2005	2010-09-08	제주대학교	4	×
한라봉 성숙과실 병반과피 유전자정보	2006	2010-09-06	아열대원예산업연구소	1	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2010-09-06	아열대원예산업연구소	7	×
한라봉 성숙과실 과피 DNA Clone	2004	2010-08-24	제주특별자치도농업기술원	13	×
식물체 과실	2010	2010-08-20	한국식품연구원	45	×
진귤 성숙과실 DNA Clone	2010	2010-08-19	제주대학교	4	×
진귤 미숙과실 DNA Clone	2006	2010-08-19	제주대학교	7	×
한라봉 성숙과실 과피 유전자정보	2004	2010-08-13	제주대학교	5	×
온주밀감 성숙과실 DNA Clone	2003	2010-08-13	제주대학교	8	×
진귤 성숙과실 DNA Clone	2010	2010-08-13	제주대학교	4	×
진귤 성숙과실 유전자정보	2010	2010-08-13	제주대학교	10	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2010-08-13	제주대학교	9	×
한라봉 성숙과실 병반과피 유전자정보	2006	2010-08-13	제주대학교	10	×
진귤 성숙과실 유전자정보	2010	2010-08-13	제주대학교	1	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2010-08-09	제주특별자치도농업기술원	6	×
진귤 성숙과실 DNA Clone	2010	2010-08-09	생명공학부	7	×
진귤 성숙과실 유전자정보	2010	2010-08-09	생명공학부	10	×
한라봉 미숙과실 과피 유전자정보	2005	2010-08-04	생명공학부	12	×
진귤 성숙과실 유전자정보	2010	2010-08-04	생명공학부	7	×
식물체 과실	2010	2010-07-29	한국식품연구원	15	×
한라봉 성숙과실 과피 DNA Clone	2004	2010-07-20	(주)바이오애그젠엔텍	5	×
한라봉 성숙과실 과피 유전자정보	2004	2010-07-20	(주)바이오애그젠엔텍	3	×
한라봉 미숙과실 과피 유전자정보	2005	2010-07-20	(주)바이오애그젠엔텍	7	×
진귤 성숙과실 DNA Clone	2010	2010-07-20	생명공학부	8	×
진귤 성숙과실 유전자정보	2010	2010-07-20	생명공학부	4	×
한라봉 미숙과실 과피 유전자정보	2005	2010-07-20	아열대원예산업연구센터	17	×
진귤 성숙과실 유전자정보	2010	2010-07-20	제주생물종다양성연구소	18	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
한라봉 미숙과실 과피 DNA Clone	2005	2010-07-14	바이오스펙트럼(주)	7	×
한라봉 미숙과실 과피 유전자정보	2005	2010-07-14	바이오스펙트럼(주)	7	×
진귤 성숙과실 유전자정보	2010	2010-07-14	생명공학부	10	×
진귤 성숙과실 DNA Clone	2010	2010-07-14	생명공학부	7	×
진귤 미숙과실 DNA Clone	2006	2010-07-08	제주대학교	3	×
진귤 미숙과실 유전자정보	2006	2010-07-08	제주대학교	10	×
한라봉 미숙과실 과피 유전자정보	2005	2010-07-05	자연과학대학	13	×
진귤 성숙과실 유전자정보	2010	2010-07-05	제주대학교	14	○
식물체 잎	2009	2010-07-02	경희대학교	8	×
한라봉 성숙과실 병반과피 유전자정보	2006	2010-07-01	제주대학교	1	×
한라봉 성숙과실 과피 유전자정보	2004	2010-07-01	제주대학교	1	×
한라봉 미숙과실 과피 유전자정보	2005	2010-07-01	제주대학교	1	×
진귤 성숙과실 유전자정보	2010	2010-07-01	제주대학교	1	×
진귤 미숙과실 유전자정보	2006	2010-07-01	제주대학교	1	×
온주밀감 미숙과실 유전자정보	2002	2010-07-01	제주대학교	1	×
한라봉 미숙과실 과피 DNA Clone	2005	2010-06-29	바이오애그진엔텍	8	×
온주밀감 미숙과실 DNA Clone	2002	2010-06-29	제주대학교	1	×
온주밀감 미숙과실 유전자정보	2002	2010-06-29	제주대학교	9	×
진귤 성숙과실 DNA Clone	2010	2010-06-25	제주생물종다양성연구소	16	×
온주밀감 미숙과실 유전자정보	2002	2010-06-25	제주대학교	16	×
진귤 성숙과실 유전자정보	2010	2010-06-21	제주대학교	16	×
진귤 성숙과실 DNA Clone	2010	2010-06-21	제주대학교	14	×
진귤 미숙과실 유전자정보	2006	2010-06-21	바이오스펙트럼(주)	13	×
진귤 성숙과실 유전자정보	2010	2010-06-18	아열대원예산업연구소	10	×
온주밀감 성숙과실 유전자정보	2003	2010-06-18	제주대학교	16	×
진귤 성숙과실 유전자정보	2010	2010-06-16	제주대학교	20	×
한라봉 성숙과실 병반과피 유전자정보	2006	2010-06-03	바이오애그진엔텍	3	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
한라봉 성숙과실 병반과피 DNA Clone	2006	2010-06-03	바이오애그진엔텍	9	×
진귤 성숙과실 DNA Clone	2010	2010-06-03	아열대원예산업연구소	5	×
진귤 미숙과실 DNA Clone	2006	2010-05-31	제주대학교	15	×
진귤 미숙과실 유전자정보	2006	2010-05-28	제주특별자치도농업기술원	7	×
한라봉 미숙과실 과피 유전자정보	2005	2010-05-28	제주대학교	9	×
진귤 미숙과실 DNA Clone	2006	2010-05-27	자연과학대학	11	×
진귤 성숙과실 유전자정보	2010	2010-05-27	제주대학교	14	×
진귤 성숙과실 DNA Clone	2010	2010-05-27	제주대학교	7	×
진귤 성숙과실 DNA Clone	2010	2010-05-25	제주대학교	5	×
진귤 성숙과실 유전자정보	2010	2010-05-25	제주대학교	16	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2010-05-20	바이오스펙트럼(주)	15	×
진귤 성숙과실 DNA Clone	2010	2010-05-20	생명공학부	5	×
진귤 성숙과실 유전자정보	2010	2010-05-20	생명공학부	14	×
진귤 성숙과실 DNA Clone	2010	2010-05-17	제주특별자치도농업기술원	8	×
진귤 성숙과실 유전자정보	2010	2010-05-17	제주특별자치도농업기술원	1	×
진귤 미숙과실 DNA Clone	2006	2010-05-17	제주생물종다양성연구소	22	×
진귤 성숙과실 DNA Clone	2010	2010-05-13	바이오애그진엔텍	5	×
진귤 성숙과실 유전자정보	2010	2010-05-13	바이오애그진엔텍	12	×
진귤 성숙과실 DNA Clone	2010	2010-05-10	생명자원과학대학	7	×
진귤 성숙과실 유전자정보	2010	2010-05-10	생명자원과학대학	7	×
진귤 성숙과실 DNA Clone	2010	2010-05-01	난지농업연구소 감귤시험장	15	×
진귤 성숙과실 DNA Clone	2010	2010-05-01	아열대원예산업연구센터	12	×
진귤 성숙과실 DNA Clone	2010	2010-05-01	제주대학교	7	×
진귤 성숙과실 유전자정보	2010	2010-04-30	난지농업연구소	20	×
진귤 성숙과실 유전자정보	2010	2010-04-30	바이오스펙트럼(주)	20	×
진귤 성숙과실 유전자정보	2010	2010-04-30	제주생물종다양성연구소	20	×
진귤 성숙과실 DNA Clone	2010	2010-04-28	난지농업연구소	8	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
진귤 성숙과실 유전자정보	2010	2010-04-28	난지농업연구소	1	×
진귤 미숙과실 유전자정보	2006	2010-04-21	제주대학교	2	×
진귤 성숙과실 유전자정보	2010	2010-04-21	제주대학교	3	×
한라봉 성숙과실 병반과피 유전자정보	2006	2010-04-21	제주대학교	1	×
한라봉 미숙과실 과피 유전자정보	2005	2010-04-21	제주대학교	1	×
진귤 미숙과실 유전자정보	2006	2010-04-21	제주대학교	2	×
진귤 성숙과실 유전자정보	2010	2010-04-21	제주대학교	4	×
진귤 성숙과실 유전자정보	2010	2010-04-20	제주대학교	20	×
진귤 성숙과실 유전자정보	2010	2010-04-20	제주대학교	15	×
진귤 성숙과실 유전자정보	2010	2010-04-20	아열대원예산업연구소	15	×
진귤 성숙과실 DNA Clone	2010	2010-04-20	아열대원예산업연구소	1	×
진귤 성숙과실 DNA Clone	2010	2010-04-19	난지농업연구소 감귤시험장	12	×
감귤 Callus Cell line	2010	2010-04-08	감귤시험장	1	×
진귤 성숙과실 DNA Clone	2010	2010-04-07	제주대학교	20	×
진귤 성숙과실 DNA Clone	2010	2010-04-07	제주대학교	15	×
진귤 성숙과실 DNA Clone	2010	2010-04-07	제주생물종다양성연구소	20	×
온주밀감 성숙과실 유전자정보	2003	2010-04-07	아열대원예산업연구소	20	×
진귤 성숙과실 DNA Clone	2010	2010-03-30	아열대원예산업연구센터	18	×
온주밀감 성숙과실 DNA Clone	2003	2010-03-30	제주대학교	15	×
진귤 성숙과실 DNA Clone	2010	2010-03-30	제주대학교	14	×
온주밀감 성숙과실 DNA Clone	2003	2010-03-30	제주대학교	13	×
진귤 성숙과실 DNA Clone	2010	2010-03-30	아열대원예산업연구소	15	×
진귤 성숙과실 DNA Clone	2010	2010-03-30	난지농업연구소 감귤시험장	1	×
진귤 성숙과실 유전자정보	2010	2010-03-30	난지농업연구소 감귤시험장	11	×
진귤 성숙과실 유전자정보	2010	2010-03-26	제주특별자치도농업기술원	8	×
진귤 성숙과실 DNA Clone	2010	2010-03-26	제주특별자치도농업기술원	1	×
진귤 성숙과실 유전자정보	2010	2010-03-26	아열대원예산업연구센터	6	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
진귤 성숙과실 DNA Clone	2010	2010-03-23	난지농업연구소 감귤시험장	8	×
진귤 성숙과실 DNA Clone	2010	2010-03-19	자연과학대학	18	×
진귤 성숙과실 유전자정보	2010	2010-03-19	자연과학대학	3	×
한라봉 미숙과실 과피 DNA Clone	2005	2010-03-17	아열대원예산업연구센터	14	×
한라봉 미숙과실 과피 유전자정보	2005	2010-03-15	제주대학교	1	×
진귤 미숙과실 유전자정보	2006	2010-03-15	제주대학교	4	×
진귤 성숙과실 DNA Clone	2010	2010-03-12	바이오스펙트럼(주)	15	×
진귤 성숙과실 DNA Clone	2010	2010-03-12	제주대학교	14	×
진귤 성숙과실 DNA Clone	2010	2010-03-12	제주대학교	13	×
진귤 성숙과실 유전자정보	2010	2010-03-12	제주대학교	1	×
진귤 성숙과실 DNA Clone	2010	2010-03-12	제주대학교	14	×
진귤 성숙과실 DNA Clone	2010	2010-03-12	제주생물종다양성연구소	14	×
진귤 성숙과실 DNA Clone	2010	2010-03-09	제주대학교	16	×
진귤 성숙과실 DNA Clone	2010	2010-03-09	난지농업연구소	15	×
진귤 성숙과실 DNA Clone	2010	2010-03-09	제주생물종다양성연구소	14	×
진귤 성숙과실 DNA Clone	2010	2010-02-25	제주대학교	10	×
진귤 성숙과실 DNA Clone	2010	2010-02-24	난지농업연구소	14	×
진귤 성숙과실 유전자정보	2010	2010-02-24	난지농업연구소 감귤시험장	9	×
진귤 성숙과실 DNA Clone	2010	2010-02-24	난지농업연구소 감귤시험장	6	×
진귤 성숙과실 DNA Clone	2010	2010-02-24	아열대원예산업연구센터	12	×
진귤 미숙과실 유전자정보	2006	2010-02-17	제주대학교	15	×
온주밀감 미숙과실 유전자정보	2002	2010-02-17	제주대학교	14	×
한라봉 성숙과실 과피 유전자정보	2004	2010-02-17	제주아열대원예산업연구소	15	×
온주밀감 성숙과실 유전자정보	2003	2010-02-17	아열대원예산업연구소	15	×
한라봉 성숙과실 과피 유전자정보	2004	2010-02-16	생명공학부	15	×
온주밀감 미숙과실 유전자정보	2002	2010-02-16	제주대학교	15	×
온주밀감 성숙과실 유전자정보	2003	2010-02-16	제주대학교	15	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
온주밀감 성숙과실 유전자정보	2003	2010-02-10	제주대학교	16	×
온주밀감 성숙과실 유전자정보	2003	2010-02-10	제주대학교	15	×
한라봉 성숙과실 병반과피 유전자정보	2006	2010-02-08	생명공학부	15	×
온주밀감 성숙과실 유전자정보	2003	2010-01-29	제주대학교	15	×
진귤 성숙과실 DNA Clone	2010	2010-01-27	생명공학부	15	×
진귤 성숙과실 DNA Clone	2010	2010-01-26	제주대학교	15	×
한라봉 성숙과실 과피 유전자정보	2004	2010-01-26	아열대원예산업연구센터	11	×
진귤 성숙과실 유전자정보	2010	2010-01-18	제주대학교	11	×
온주밀감 미숙과실 유전자정보	2002	2010-01-18	아열대원예산업연구소	20	×
진귤 성숙과실 유전자정보	2010	2010-01-13	제주대학교	1	×
진귤 미숙과실 유전자정보	2006	2010-01-13	제주대학교	1	×
한라봉 성숙과실 과피 유전자정보	2004	2009-12-29	제주대학교	50	×
한라봉 성숙과실 병반과피 유전자정보	2006	2009-12-29	제주대학교	100	×
한라봉 미숙과실 과피 유전자정보	2005	2009-12-29	아열대원예산업연구소	50	×
한라봉 미숙과실 과피 유전자정보	2005	2009-12-28	아열대원예산업연구센터	4	×
한라봉 미숙과실 과피 DNA Clone	2005	2009-12-28	아열대원예산업연구센터	10	×
한라봉 성숙과실 병반과피 유전자정보	2006	2009-12-28	난지농업연구소	8	×
한라봉 미숙과실 과피 유전자정보	2005	2009-12-23	제주특별자치도농업기술원	9	×
진귤 미숙과실 유전자정보	2006	2009-12-11	제주특별자치도농업기술원	2	×
온주밀감 미숙과실 유전자정보	2002	2009-12-11	제주특별자치도농업기술원	4	×
한라봉 미숙과실 과피 유전자정보	2005	2009-12-04	제주생물종다양성연구소	6	×
온주밀감 미숙과실 유전자정보	2002	2009-12-04	난지농업연구소 감귤시험장	2	×
온주밀감 미숙과실 DNA Clone	2002	2009-12-04	난지농업연구소 감귤시험장	5	×
진귤 미숙과실 DNA Clone	2006	2009-12-01	아열대원예산업연구소	8	×
온주밀감 미숙과실 유전자정보	2002	2009-11-27	제주대학교	1	×
진귤 미숙과실 유전자정보	2006	2009-11-27	제주대학교	1	×
한라봉 미숙과실 과피 유전자정보	2005	2009-11-27	제주대학교	1	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
한라봉 미숙과실 과피 유전자정보	2005	2009-11-21	난지농업연구소 감귤시험장	7	×
온주밀감 성숙과실 유전자정보	2003	2009-11-21	제주생물종다양성연구소	4	×
온주밀감 성숙과실 DNA Clone	2003	2009-11-21	제주생물종다양성연구소	6	×
온주밀감 미숙과실 DNA Clone	2002	2009-11-19	아열대원예산업연구소	8	×
한라봉 성숙과실 병반과피 유전자정보	2006	2009-11-16	바이오스펙트럼(주)	4	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2009-11-16	바이오스펙트럼(주)	14	×
한라봉 미숙과실 과피 유전자정보	2005	2009-11-13	제주대학교	13	×
한라봉 성숙과실 병반과피 유전자정보	2006	2009-11-11	(주)바이오애그젠엔텍	3	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2009-11-11	(주)바이오애그젠엔텍	3	×
한라봉 미숙과실 과피 DNA Clone	2005	2009-11-11	제주특별자치도농업기술원	3	×
한라봉 미숙과실 과피 유전자정보	2005	2009-11-11	제주특별자치도농업기술원	5	×
한라봉 미숙과실 과피 유전자정보	2005	2009-11-06	난지농업연구소 감귤시험장	5	×
한라봉 미숙과실 과피 DNA Clone	2005	2009-11-06	난지농업연구소 감귤시험장	7	×
온주밀감 성숙과실 DNA Clone	2003	2009-11-06	아열대원예산업연구소	3	×
온주밀감 미숙과실 유전자정보	2002	2009-11-06	아열대원예산업연구소	10	×
한라봉 미숙과실 과피 유전자정보	2005	2009-10-29	난지농업연구소	8	×
한라봉 성숙과실 과피 유전자정보	2004	2009-10-28	(주)바이오애그젠엔텍	6	×
온주밀감 미숙과실 DNA Clone	2002	2009-10-28	제주생물종다양성연구소	3	×
온주밀감 미숙과실 유전자정보	2002	2009-10-28	제주생물종다양성연구소	1	×
온주밀감 미숙과실 DNA Clone	2002	2009-10-24	제주대학교	5	×
한라봉 미숙과실 과피 DNA Clone	2005	2009-10-20	난지농업연구소	4	×
진귤 미숙과실 DNA Clone	2006	2009-10-20	난지농업연구소	2	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2009-10-19	제주특별자치도농업기술원	5	×
한라봉 성숙과실 병반과피 유전자정보	2006	2009-10-13	아열대원예산업연구소	79	×
한라봉 성숙과실 과피 DNA Clone	2004	2009-10-09	자연과학대학	69	×
진귤 미숙과실 유전자정보	2006	2009-10-07	제주대학교	100	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2009-10-06	아열대원예산업연구소	39	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
한라봉 성숙과실 병반과피 유전자정보	2006	2009-10-06	아열대원예산업연구소	40	×
한라봉 미숙과실 과피 DNA Clone	2005	2009-10-06	제주대학교	20	×
한라봉 미숙과실 과피 유전자정보	2005	2009-10-06	제주대학교	25	×
온주밀감 미숙과실 DNA Clone	2002	2009-10-05	생명공학부	30	×
온주밀감 미숙과실 유전자정보	2002	2009-10-05	생명공학부	30	×
온주밀감 미숙과실 DNA Clone	2002	2009-10-01	제주대학교	20	×
온주밀감 미숙과실 유전자정보	2002	2009-10-01	제주대학교	18	×
온주밀감 성숙과실 DNA Clone	2003	2009-09-30	아열대원예산업연구센터	17	×
온주밀감 성숙과실 유전자정보	2003	2009-09-30	아열대원예산업연구센터	12	×
한라봉 성숙과실 과피 유전자정보	2004	2009-09-30	아열대원예산업연구센터	5	×
한라봉 성숙과실 과피 DNA Clone	2004	2009-09-29	제주대학교	21	×
한라봉 성숙과실 과피 유전자정보	2004	2009-09-29	제주대학교	20	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2009-09-22	아열대원예산업연구소	20	×
한라봉 성숙과실 병반과피 유전자정보	2006	2009-09-22	아열대원예산업연구소	14	×
한라봉 미숙과실 과피 DNA Clone	2005	2009-09-22	제주대학교	17	×
한라봉 미숙과실 과피 유전자정보	2005	2009-09-22	제주대학교	20	×
진귤 미숙과실 DNA Clone	2006	2009-09-21	아열대원예산업연구소	20	×
진귤 미숙과실 유전자정보	2006	2009-09-21	아열대원예산업연구소	20	×
한라봉 성숙과실 병반과피 유전자정보	2006	2009-09-14	제주대학교	2	×
진귤 미숙과실 유전자정보	2006	2009-09-14	제주대학교	1	×
한라봉 미숙과실 과피 유전자정보	2005	2009-09-14	제주대학교	1	×
한라봉 성숙과실 과피 유전자정보	2004	2009-09-14	제주대학교	1	×
한라봉성숙과실 Library	2004	2009-09-11	감귤시험장	1	×
진귤 미숙과실 DNA Clone	2006	2009-09-11	제주대학교	37	×
온주밀감 미숙과실 유전자정보	2002	2009-09-08	생명공학부	18	×
한라봉 성숙과실 과피 DNA Clone	2004	2009-09-08	아열대원예산업연구소	4	×
한라봉 성숙과실 과피 유전자정보	2004	2009-09-08	아열대원예산업연구소	30	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
온주밀감 미숙과실 DNA Clone	2002	2009-09-04	아열대원예산업연구센터	17	×
온주밀감 미숙과실 유전자정보	2002	2009-09-04	아열대원예산업연구센터	14	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2009-09-04	제주대학교	15	×
한라봉 성숙과실 병반과피 유전자정보	2006	2009-09-04	제주대학교	15	×
한라봉 미숙과실 과피 DNA Clone	2005	2009-09-03	아열대원예산업연구소	11	×
한라봉 미숙과실 과피 유전자정보	2005	2009-09-03	아열대원예산업연구소	17	×
진귤 미숙과실 DNA Clone	2006	2009-09-03	생명공학부	18	×
진귤 미숙과실 유전자정보	2006	2009-09-03	생명공학부	14	×
한라봉 성숙과실 과피 유전자정보	2004	2009-08-31	제주특별자치도농업기술원	4	×
한라봉 성숙과실 과피 DNA Clone	2004	2009-08-31	제주특별자치도농업기술원	9	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2009-08-28	난지농업연구소 감귤시험장	12	×
진귤 미숙과실 DNA Clone	2006	2009-08-28	제주대학교	9	×
한라봉 성숙과실 과피 유전자정보	2004	2009-08-26	제주대학교 생명공학부	6	×
한라봉 성숙과실 과피 DNA Clone	2004	2009-08-26	제주대학교 생명공학부	3	×
한라봉 미숙과실 과피 유전자정보	2005	2009-08-26	바이오스펙트럼(주)	14	×
한라봉 미숙과실 과피 DNA Clone	2005	2009-08-26	바이오스펙트럼(주)	13	×
진귤 미숙과실 DNA Clone	2006	2009-08-26	아열대원예산업연구센터	14	×
진귤 미숙과실 유전자정보	2006	2009-08-26	아열대원예산업연구센터	9	×
한라봉 미숙과실 과피 DNA Clone	2005	2009-08-25	제주대학교	20	×
온주밀감 미숙과실 DNA Clone	2002	2009-08-24	바이오애그진엔텍	8	×
온주밀감 미숙과실 유전자정보	2002	2009-08-24	바이오애그진엔텍	13	×
온주밀감 성숙과실 Library	2003	2009-08-19	제주대학교	1	×
한라봉 미숙과실 과피 DNA Clone	2005	2009-08-17	바이오스펙트럼(주)	2	×
한라봉 미숙과실 과피 유전자정보	2005	2009-08-17	바이오스펙트럼(주)	7	×
한라봉 성숙과실 과피 DNA Clone	2004	2009-08-17	제주생물종다양성연구소	2	×
한라봉 성숙과실 과피 유전자정보	2004	2009-08-17	제주생물종다양성연구소	1	×
한라봉 미숙과실 과피 DNA Clone	2005	2009-08-17	제주생물종다양성연구소	5	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
한라봉 미숙과실 과피 유전자정보	2005	2009-08-17	제주생물종다양성연구소	7	×
진귤 미숙과실 유전자정보	2006	2009-08-17	자연과학대학	3	×
진귤 미숙과실 DNA Clone	2006	2009-08-17	자연과학대학	8	×
한라봉 성숙과실 병반과피 유전자정보	2006	2009-08-14	제주대학교	2	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2009-08-14	제주대학교	5	×
진귤 미숙과실 유전자정보	2006	2009-08-14	제주대학교	3	×
진귤 미숙과실 DNA Clone	2006	2009-08-14	제주대학교	6	×
온주밀감 미숙과실 DNA Clone	2002	2009-07-30	제주대학교	7	×
온주밀감 미숙과실 유전자정보	2002	2009-07-30	제주대학교	5	×
진귤 미숙과실 DNA Clone	2006	2009-07-30	난지농업연구소 감귤시험장	19	×
온주밀감 성숙과실 DNA Clone	2003	2009-07-29	제주대학교	7	×
온주밀감 성숙과실 유전자정보	2003	2009-07-29	제주대학교	1	×
한라봉 성숙과실 과피 유전자정보	2004	2009-07-23	아열대원예산업연구센터	4	×
한라봉 성숙과실 과피 DNA Clone	2004	2009-07-23	아열대원예산업연구센터	11	×
진귤 미숙과실 DNA Clone	2006	2009-07-22	제주대학교	11	×
한라봉 미숙과실 과피 DNA Clone	2005	2009-07-21	바이오애그진엔텍	3	×
한라봉 미숙과실 과피 유전자정보	2005	2009-07-21	바이오애그진엔텍	11	×
한라봉 성숙과실 병반과피 유전자정보	2006	2009-07-20	제주대학교	8	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2009-07-20	제주대학교	8	×
진귤 미숙과실 DNA Clone	2006	2009-07-17	제주대학교	17	×
진귤 미숙과실 DNA Clone	2006	2009-07-17	바이오스펙트럼(주)	5	×
진귤 미숙과실 유전자정보	2006	2009-07-17	바이오스펙트럼(주)	10	×
한라봉 성숙과실 과피 유전자정보	2004	2009-07-16	제주특별자치도농업기술원	5	×
한라봉 성숙과실 과피 DNA Clone	2004	2009-07-16	제주특별자치도농업기술원	10	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2009-07-15	제주생물종다양성연구소	17	×
온주밀감 미숙과실 DNA Clone	2002	2009-07-02	제주대학교	5	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2009-06-25	제주대학교	50	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
한라봉 성숙과실 과피 DNA Clone	2004	2009-06-22	아열대원예산업연구소	30	×
온주밀감 성숙과실 DNA Clone	2003	2009-06-22	제주대학교	20	×
한라봉 성숙과실 과피 DNA Clone	2004	2009-06-22	(주)바이오애그젠엔텍	25	×
두릅 DNA Clone	2005	2009-06-19	아열대원예산업연구센터	20	×
진귤 미숙과실 DNA Clone	2006	2009-06-19	아열대원예산업연구센터	5	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2009-06-08	아열대원예산업연구센터	26	×
한라봉 미숙과실 과피 DNA Clone	2005	2009-06-08	제주대학교	25	×
한라봉 성숙과실 과피 DNA Clone	2004	2009-06-05	농촌진흥청 감귤시험장	42	×
한라봉 성숙과실 과피 DNA Clone	2004	2009-06-05	제주대학교	33	×
온주밀감 성숙과실 DNA Clone	2003	2009-06-03	생명공학부	39	×
진귤 미숙과실 DNA Clone	2006	2009-06-02	제주대학교	38	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2009-05-29	바이오스퀙트럼(주)	36	×
두릅 DNA Clone	2005	2009-05-27	제주대학교	1	×
한라봉 성숙과실 과피 DNA Clone	2004	2009-05-27	제주대학교	40	×
한라봉 미숙과실 과피 DNA Clone	2005	2009-05-25	난지농업연구소	18	×
온주밀감 미숙과실 DNA Clone	2002	2009-05-22	제주생물종다양성연구소	33	×
진귤 미숙과실 DNA Clone	2006	2009-05-21	제주특별자치도농업기술원	12	×
진귤 미숙과실 유전자정보	2006	2009-05-21	제주특별자치도농업기술원	2	×
온주밀감 미숙과실 유전자정보	2002	2009-05-20	바이오애그진엔텍	15	×
온주밀감 미숙과실 DNA Clone	2002	2009-05-20	바이오애그진엔텍	23	×
한라봉 미숙과실 과피 유전자정보	2005	2009-05-19	생명자원과학대학	9	×
한라봉 미숙과실 과피 DNA Clone	2005	2009-05-19	생명자원과학대학	8	×
온주밀감 미숙과실 유전자정보	2002	2009-05-12	제주생물종다양성연구소	13	×
온주밀감 미숙과실 DNA Clone	2002	2009-05-12	제주생물종다양성연구소	20	×
한라봉 미숙과실 과피 DNA Clone	2005	2009-05-12	난지농업연구소	23	×
온주밀감 미숙과실 유전자정보	2002	2009-05-08	난지농업연구소 감귤시험장	10	×
온주밀감 미숙과실 DNA Clone	2002	2009-05-08	난지농업연구소 감귤시험장	11	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
한라봉 성숙과실 병반과피 DNA Clone	2006	2009-05-04	제주생물종다양성연구소	19	×
한라봉 성숙과실 과피 DNA Clone	2004	2009-04-27	제주대학교	17	×
진귤 미숙과실 DNA Clone	2006	2009-04-27	제주대학교	20	×
온주밀감 성숙과실 DNA Clone	2003	2009-04-22	제주대학교	15	×
온주밀감 미숙과실 DNA Clone	2002	2009-04-17	아열대원예산업연구소	18	×
온주밀감 미숙과실 DNA Clone	2002	2009-04-17	제주아열대원예산업연구소	19	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2009-04-15	제주대학교	16	×
한라봉 성숙과실 과피 DNA Clone	2004	2009-04-15	생명공학부	17	×
한라봉 미숙과실 과피 DNA Clone	2005	2009-04-14	아열대원예산업연구센터	31	×
한라봉 미숙과실 과피 DNA Clone	2005	2009-04-10	제주특별자치도농업기술원	12	×
한라봉 미숙과실 과피 DNA Clone	2005	2009-04-10	제주생물종다양성연구소	15	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2009-04-07	바이오스펙트럼(주)	38	×
한라봉 미숙과실 과피 DNA Clone	2005	2009-04-02	난지농업연구소 감귤시험장	23	×
진귤 미숙과실 DNA Clone	2006	2009-04-01	제주대학교	22	×
진귤 미숙과실 DNA Clone	2006	2009-03-30	제주대학교	25	×
진귤 미숙과실 유전자정보	2006	2009-03-30	제주대학교	25	×
진귤 미숙과실 유전자정보	2006	2009-03-30	제주대학교	23	×
진귤 미숙과실 DNA Clone	2006	2009-03-30	제주대학교	27	×
한라봉 미숙과실 과피 DNA Clone	2005	2009-03-25	제주대학교	41	×
한라봉 미숙과실 과피 유전자정보	2005	2009-03-25	제주대학교	9	×
한라봉 미숙과실 과피 유전자정보	2005	2009-03-23	제주대학교	23	×
한라봉 미숙과실 과피 DNA Clone	2005	2009-03-23	제주대학교	26	×
온주밀감 성숙과실 유전자정보	2003	2009-03-23	아열대원예산업연구소	25	×
온주밀감 성숙과실 DNA Clone	2003	2009-03-23	아열대원예산업연구소	25	×
한라봉 성숙과실 과피 유전자정보	2004	2009-03-20	제주대학교	27	×
한라봉 성숙과실 과피 DNA Clone	2004	2009-03-20	제주대학교	23	×
한라봉 미숙과실 과피 유전자정보	2005	2009-03-19	제주대학교 생명공학부	23	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
한라봉 미숙과실 과피 DNA Clone	2005	2009-03-19	제주대학교 생명공학부	25	×
진귤 미숙과실 유전자정보	2006	2009-03-19	제주대학교	22	×
진귤 미숙과실 DNA Clone	2006	2009-03-19	제주대학교	28	×
한라봉 성숙과실 병반과피 유전자정보	2006	2009-03-17	제주대학교	29	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2009-03-17	제주대학교	26	×
한라봉 미숙과실 과피 유전자정보	2005	2009-03-17	아열대원예산업연구센터	26	×
한라봉 미숙과실 과피 DNA Clone	2005	2009-03-17	아열대원예산업연구센터	26	×
온주밀감 미숙과실 유전자정보	2002	2009-03-16	제주대학교	23	×
온주밀감 미숙과실 DNA Clone	2002	2009-03-16	제주대학교	26	×
진귤 미숙과실 DNA Clone	2006	2009-03-12	제주대학교	7	×
온주밀감 성숙과실 DNA Clone	2003	2009-03-12	제주대학교	13	×
온주밀감 성숙과실 유전자정보	2003	2009-03-12	제주대학교	20	×
온주밀감 미숙과실 DNA Clone	2002	2009-03-12	아열대원예산업연구소	20	×
온주밀감 미숙과실 유전자정보	2002	2009-03-12	아열대원예산업연구소	20	×
두릅 유전자정보	2005	2009-03-09	제주대학교	4	×
한라봉 성숙과실 병반과피 유전자정보	2006	2009-03-09	제주대학교	1	×
한라봉 성숙과실 과피 유전자정보	2004	2009-03-09	제주대학교	2	×
한라봉 미숙과실 과피 유전자정보	2005	2009-03-09	제주대학교	1	×
진귤 미숙과실 유전자정보	2006	2009-03-09	제주대학교	2	×
온주밀감 성숙과실 유전자정보	2003	2009-03-09	제주대학교	1	×
온주밀감 미숙과실 유전자정보	2002	2009-03-09	제주대학교	2	×
온주밀감 성숙과실 DNA Clone	2003	2009-03-05	제주대학교	24	×
두릅 DNA Clone	2005	2009-03-05	제주대학교	12	×
진귤 미숙과실 DNA Clone	2006	2009-03-05	생명공학부	38	×
온주밀감 성숙과실 DNA Clone	2003	2009-03-04	제주대학교	36	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2009-03-04	제주대학교 생명공학부	29	×
두릅 DNA Clone	2005	2009-03-04	제주대학교	27	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
한라봉 성숙과실 과피 DNA Clone	2004	2009-03-04	제주대학교	5	×
한라봉 미숙과실 과피 DNA Clone	2005	2009-03-04	생명자원과학대학	30	×
온주밀감 미숙과실 DNA Clone	2002	2009-03-04	제주대학교	28	×
두릅 유전자정보	2005	2009-02-27	제주대학교	2	×
한라봉 성숙과실 병반과피 유전자정보	2006	2009-02-27	제주대학교	1	×
한라봉 성숙과실 과피 유전자정보	2004	2009-02-27	제주대학교	1	×
한라봉 미숙과실 과피 유전자정보	2005	2009-02-27	제주대학교	1	×
진귤 미숙과실 유전자정보	2006	2009-02-27	제주대학교	1	×
진귤 미숙과실 DNA Clone	2006	2009-02-26	제주대학교	24	×
한라봉 미숙과실 과피 DNA Clone	2005	2009-02-26	바이오애그진엔텍	12	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2009-02-23	제주대학교	1	×
한라봉 성숙과실 과피 DNA Clone	2004	2009-02-23	제주대학교	3	×
진귤 미숙과실 DNA Clone	2006	2009-02-23	제주대학교	2	×
진귤 미숙과실 DNA Clone	2006	2009-02-23	바이오스펙트럼(주)	19	×
한라봉 미숙과실 과피 유전자정보	2005	2009-02-19	제주대학교 생명공학부	20	×
진귤 미숙과실 유전자정보	2006	2009-02-19	제주대학교 생명공학부	20	×
한라봉 미숙과실 과피 DNA Clone	2005	2009-02-18	바이오애그진엔텍	25	×
한라봉 성숙과실 과피 DNA Clone	2004	2009-02-16	생명공학부	20	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2009-02-16	제주대학교	50	×
한라봉 미숙과실 과피 DNA Clone	2005	2009-02-13	자연과학대학	3	×
진귤 미숙과실 DNA Clone	2006	2009-02-13	자연과학대학	3	×
한라봉 성숙과실 과피 DNA Clone	2004	2009-02-13	자연과학대학	1	×
온주밀감 미숙과실 DNA Clone	2002	2009-02-13	자연과학대학	7	×
진귤 미숙과실 Library	2006	2009-01-30	제주대학교	1	×
온주밀감 미숙과실 유전자정보	2002	2009-01-29	(주)바이오애그젠엔텍	30	×
두릅 유전자정보	2005	2009-01-22	제주대학교	1	×
쇠무릎 유전자정보	2002	2009-01-22	제주대학교	2	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
온주밀감 성숙과실 유전자정보	2003	2009-01-22	제주대학교	1	×
한라봉 성숙과실 과피 유전자정보	2004	2009-01-22	제주대학교	1	×
온주밀감 미숙과실 유전자정보	2002	2009-01-22	제주대학교	3	×
참취 유전자정보	2004	2009-01-22	제주대학교	2	×
한라봉 성숙과실 과피 유전자정보	2004	2009-01-21	제주특별자치도농업기술원	10	×
진귤 성숙과실 Library	2009	2009-01-20	제주생물종다양성연구소	1	×
진귤 성숙과실 Library	2009	2009-01-20	바이오스펙트럼(주)	1	×
한라봉 성숙과실 과피 유전자정보	2004	2009-01-20	제주특별자치도농업기술원	10	×
참취 유전자정보	2004	2009-01-20	제주특별자치도농업기술원	15	×
쇠무릎 유전자정보	2002	2009-01-19	제주대학교	2	×
한라봉 성숙과실 과피 유전자정보	2004	2009-01-19	제주대학교	1	×
온주밀감 성숙과실 유전자정보	2003	2009-01-19	제주대학교	1	×
온주밀감 미숙과실 유전자정보	2002	2009-01-19	제주대학교	3	×
참취 유전자정보	2004	2009-01-19	제주대학교	2	×
진귤 미숙과실 유전자정보	2006	2009-01-19	제주대학교	1	×
두릅 유전자정보	2005	2009-01-19	제주대학교	5	×
한라봉 미숙과실 과피 유전자정보	2005	2009-01-19	제주대학교	4	×
한라봉 성숙과실 병반과피 유전자정보	2006	2009-01-19	제주대학교	2	×
두릅 유전자정보	2005	2009-01-16	바이오애그진엔텍	1	×
쇠무릎 유전자정보	2002	2009-01-16	바이오애그진엔텍	2	×
온주밀감 성숙과실 유전자정보	2003	2009-01-16	바이오애그진엔텍	1	×
한라봉 성숙과실 과피 유전자정보	2004	2009-01-16	바이오애그진엔텍	1	×
온주밀감 미숙과실 유전자정보	2002	2009-01-16	바이오애그진엔텍	3	×
참취 유전자정보	2004	2009-01-16	바이오애그진엔텍	2	×
한라봉 미숙과실 과피 유전자정보	2005	2009-01-16	제주대학교	1	×
온주밀감 미숙과실 DNA Clone	2002	2009-01-16	제주대학교	1	×
두릅 DNA Clone	2005	2009-01-16	제주대학교	2	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
쇠무릎 DNA Clone	2002	2009-01-16	제주대학교	1	×
온주밀감 성숙과실 DNA Clone	2003	2009-01-16	제주대학교	2	×
진귤 미숙과실 DNA Clone	2006	2009-01-16	제주대학교	2	×
참취 DNA Clone	2004	2009-01-16	제주대학교	3	×
한라봉 미숙과실 과피 DNA Clone	2005	2009-01-16	제주대학교	2	×
한라봉 성숙과실 과피 DNA Clone	2004	2009-01-16	제주대학교	2	×
한라봉 성숙과실 과피 유전자정보	2004	2009-01-16	제주특별자치도농업기술원	10	×
두릅 DNA Clone	2005	2009-01-15	제주대학교	2	×
진귤 미숙과실 DNA Clone	2006	2009-01-15	제주대학교	3	×
참취 DNA Clone	2004	2009-01-15	제주대학교	1	×
한라봉 성숙과실 과피 DNA Clone	2004	2009-01-15	제주대학교	5	×
온주밀감 미숙과실 유전자정보	2002	2009-01-14	제주대학교	11	×
진귤 미숙과실 유전자정보	2006	2009-01-13	난지농업연구소	1	×
온주밀감 성숙과실 유전자정보	2003	2009-01-13	난지농업연구소	2	×
쇠무릎 유전자정보	2002	2009-01-13	난지농업연구소	2	×
두릅 유전자정보	2005	2009-01-13	난지농업연구소	2	×
한라봉 미숙과실 과피 유전자정보	2005	2009-01-13	난지농업연구소	1	×
한라봉 성숙과실 과피 유전자정보	2004	2009-01-13	난지농업연구소	2	×
온주밀감 미숙과실 유전자정보	2002	2009-01-13	난지농업연구소	4	×
참취 유전자정보	2004	2009-01-13	난지농업연구소	2	×
두릅 DNA Clone	2005	2009-01-13	난지농업연구소 감귤시험장	5	×
진귤 미숙과실 DNA Clone	2006	2009-01-13	난지농업연구소 감귤시험장	3	×
한라봉 성숙과실 과피 DNA Clone	2004	2009-01-13	난지농업연구소 감귤시험장	1	×
한라봉 미숙과실 과피 DNA Clone	2005	2009-01-13	난지농업연구소 감귤시험장	4	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2009-01-13	난지농업연구소 감귤시험장	4	×
한라봉 성숙과실 과피 유전자정보	2004	2009-01-13	제주특별자치도농업기술원	10	×
진귤 미숙과실 유전자정보	2006	2009-01-13	제주특별자치도농업기술원	30	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
온주밀감 성숙과실 유전자정보	2003	2009-01-12	(주)바이오애그젠엔텍	10	×
한라봉 성숙과실 과피 유전자정보	2004	2009-01-09	농촌진흥청 감귤시험장	5	×
한라봉 성숙과실 병반과피 유전자정보	2006	2009-01-09	농촌진흥청 감귤시험장	1	×
참취 유전자정보	2004	2009-01-09	농촌진흥청 감귤시험장	1	×
진귤 미숙과실 유전자정보	2006	2009-01-09	농촌진흥청 감귤시험장	3	×
두릅 유전자정보	2005	2009-01-09	농촌진흥청 감귤시험장	2	×
두릅 유전자정보	2005	2009-01-09	제주특별자치도농업기술원	7	×
진귤 미숙과실 유전자정보	2006	2009-01-09	제주특별자치도농업기술원	5	×
온주밀감 미숙과실 유전자정보	2002	2009-01-09	제주특별자치도농업기술원	4	×
한라봉 미숙과실 과피 유전자정보	2005	2009-01-09	제주특별자치도농업기술원	1	×
온주밀감 미숙과실 DNA Clone	2002	2009-01-09	제주대학교	6	×
두릅 DNA Clone	2005	2009-01-09	제주대학교	5	×
진귤 성숙과실 Library		2009-01-08	제주대학교	1	×
진귤 미숙과실 유전자정보	2006	2009-01-08	제주생물종다양성연구소	4	×
한라봉 미숙과실 과피 유전자정보	2005	2009-01-08	제주생물종다양성연구소	4	×
한라봉 성숙과실 병반과피 유전자정보	2006	2009-01-08	제주생물종다양성연구소	3	×
쇠무릎 유전자정보	2002	2009-01-08	제주생물종다양성연구소	1	×
두릅 유전자정보	2005	2009-01-08	제주생물종다양성연구소	4	×
한라봉 성숙과실 병반과피 유전자정보	2006	2009-01-08	(주)바이오애그젠엔텍	20	×
한라봉 성숙과실 과피 유전자정보	2004	2009-01-07	난지농업연구소 감귤시험장	129	×
한라봉 미숙과실 과피 DNA Clone	2005	2009-01-07	난지농업연구소 감귤시험장	1	×
한라봉 미숙과실 과피 유전자정보	2005	2009-01-07	난지농업연구소 감귤시험장	131	×
한라봉 성숙과실 병반과피 유전자정보	2006	2009-01-06	제주대학교	3	×
두릅 유전자정보	2005	2009-01-06	제주대학교	3	×
한라봉 미숙과실 과피 유전자정보	2005	2009-01-06	제주대학교	4	×
진귤 미숙과실 유전자정보	2006	2009-01-06	제주대학교	1	×
진귤 미숙과실 유전자정보	2006	2009-01-06	(주)바이오애그젠엔텍	20	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
한라봉 미숙과실 과피 DNA Clone	2005	2009-01-06	바이오스펙트럼(주)	50	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2009-01-06	제주생물종다양성연구소	102	×
한라봉 성숙과실 병반과피 유전자정보	2006	2009-01-05	제주특별자치도농업기술원	20	×
한라봉 성숙과실 과피 유전자정보	2004	2009-01-02	(주)바이오애그젠엔텍	20	×
온주밀감 미숙과실 DNA Clone	2002	2009-01-02	제주아열대원예산업연구소	56	×
한라봉 성숙과실 과피 유전자정보	2004	2008-12-26	제주생물종다양성연구소	1	×
한라봉 미숙과실 과피 유전자정보	2005	2008-12-26	제주생물종다양성연구소	2	×
진귤 미숙과실 유전자정보	2006	2008-12-26	제주생물종다양성연구소	2	×
온주밀감 미숙과실 유전자정보	2002	2008-12-26	제주생물종다양성연구소	7	×
쇠무릎 유전자정보	2002	2008-12-26	제주생물종다양성연구소	1	×
한라봉 성숙과실 병반과피 유전자정보	2006	2008-12-26	제주대학교	1	×
한라봉 성숙과실 과피 유전자정보	2004	2008-12-26	제주대학교	1	×
한라봉 미숙과실 과피 DNA Clone	2005	2008-12-26	제주대학교	1	×
진귤 미숙과실 유전자정보	2006	2008-12-26	제주대학교	1	×
한라봉 미숙과실 과피 유전자정보	2005	2008-12-17	난지농업연구소	2	×
참취 유전자정보	2004	2008-12-17	난지농업연구소	3	×
진귤 미숙과실 유전자정보	2006	2008-12-17	난지농업연구소	2	×
온주밀감 성숙과실 유전자정보	2003	2008-12-17	난지농업연구소	2	×
쇠무릎 유전자정보	2002	2008-12-17	난지농업연구소	1	×
두릅 유전자정보	2005	2008-12-17	난지농업연구소	2	×
한라봉 성숙과실 과피 유전자정보	2004	2008-12-17	난지농업연구소	1	×
온주밀감 미숙과실 유전자정보	2002	2008-12-17	난지농업연구소	1	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2008-12-11	제주생물종다양성연구소	2	×
한라봉 미숙과실 과피 DNA Clone	2005	2008-12-11	제주생물종다양성연구소	1	×
참취 DNA Clone	2004	2008-12-11	제주생물종다양성연구소	2	×
두릅 DNA Clone	2005	2008-12-11	제주생물종다양성연구소	2	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2008-12-11	생명공학부	2	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
한라봉 성숙과실 과피 DNA Clone	2004	2008-12-11	생명공학부	1	×
한라봉 미숙과실 과피 DNA Clone	2005	2008-12-11	생명공학부	2	×
쇠무릎 DNA Clone	2002	2008-12-11	생명공학부	2	×
두릅 DNA Clone	2005	2008-12-11	생명공학부	3	×
참취 DNA Clone	2004	2008-12-11	생명공학부	1	×
진귤 미숙과실 DNA Clone	2006	2008-12-11	생명공학부	1	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2008-12-09	제주대학교	2	×
한라봉 미숙과실 과피 DNA Clone	2005	2008-12-09	제주대학교	4	×
두릅 DNA Clone	2005	2008-12-09	제주대학교	3	×
진귤 미숙과실 DNA Clone	2006	2008-12-09	제주대학교	1	×
한라봉 미숙과실 과피 DNA Clone	2005	2008-12-09	아열대원예산업연구소	3	×
진귤 미숙과실 DNA Clone	2006	2008-12-09	아열대원예산업연구소	2	×
두릅 DNA Clone	2005	2008-12-09	아열대원예산업연구소	2	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2008-12-09	아열대원예산업연구소	2	×
한라봉 성숙과실 과피 DNA Clone	2004	2008-12-09	아열대원예산업연구소	4	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2008-12-05	제주대학교	2	×
한라봉 성숙과실 과피 DNA Clone	2004	2008-12-05	제주대학교	2	×
한라봉 미숙과실 과피 DNA Clone	2005	2008-12-05	제주대학교	2	×
쇠무릎 DNA Clone	2002	2008-12-05	제주대학교	1	×
두릅 DNA Clone	2005	2008-12-05	제주대학교	5	×
진귤 미숙과실 DNA Clone	2006	2008-12-05	제주대학교	2	×
한라봉 미숙과실 과피 DNA Clone	2005	2008-12-05	바이오스펙트럼(주)	3	×
참취 DNA Clone	2004	2008-12-05	바이오스펙트럼(주)	3	×
진귤 미숙과실 DNA Clone	2006	2008-12-05	바이오스펙트럼(주)	1	×
쇠무릎 DNA Clone	2002	2008-12-05	바이오스펙트럼(주)	3	×
두릅 DNA Clone	2005	2008-12-05	바이오스펙트럼(주)	2	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2008-12-05	바이오스펙트럼(주)	2	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
한라봉 성숙과실 과피 DNA Clone	2004	2008-12-05	바이오스펙트럼(주)	3	×
온주밀감 미숙과실 DNA Clone	2002	2008-12-05	바이오스펙트럼(주)	3	×
온주밀감 성숙과실 DNA Clone	2003	2008-12-02	아열대원예산업연구센터	5	×
온주밀감 미숙과실 DNA Clone	2002	2008-12-02	아열대원예산업연구센터	1	×
두릅 DNA Clone	2005	2008-12-02	아열대원예산업연구센터	2	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2008-12-02	아열대원예산업연구센터	3	×
한라봉 성숙과실 과피 DNA Clone	2004	2008-12-02	아열대원예산업연구센터	3	×
한라봉 미숙과실 과피 DNA Clone	2005	2008-12-02	아열대원예산업연구센터	2	×
쇠무릎 DNA Clone	2002	2008-12-02	아열대원예산업연구센터	3	×
한라봉 성숙과실 병반과피 유전자정보	2006	2008-12-02	하이테크산업진흥원	5	×
한라봉 성숙과실 과피 유전자정보	2004	2008-12-02	하이테크산업진흥원	7	×
한라봉 미숙과실 과피 유전자정보	2005	2008-12-02	하이테크산업진흥원	7	×
온주밀감 성숙과실 유전자정보	2003	2008-12-02	하이테크산업진흥원	3	×
쇠무릎 유전자정보	2002	2008-12-02	하이테크산업진흥원	3	×
진귤 미숙과실 유전자정보	2006	2008-12-02	하이테크산업진흥원	7	×
온주밀감 미숙과실 유전자정보	2002	2008-12-02	하이테크산업진흥원	8	×
참취 유전자정보	2004	2008-12-02	하이테크산업진흥원	3	×
두릅 유전자정보	2005	2008-12-02	하이테크산업진흥원	5	×
한라봉 미숙과실 과피 DNA Clone	2005	2008-12-01	(주)바이오애그젠엔텍	1	×
참취 DNA Clone	2004	2008-12-01	(주)바이오애그젠엔텍	3	×
진귤 미숙과실 DNA Clone	2006	2008-12-01	(주)바이오애그젠엔텍	3	×
쇠무릎 DNA Clone	2002	2008-12-01	(주)바이오애그젠엔텍	2	×
두릅 DNA Clone	2005	2008-12-01	(주)바이오애그젠엔텍	8	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2008-12-01	(주)바이오애그젠엔텍	1	×
한라봉 성숙과실 과피 DNA Clone	2004	2008-12-01	(주)바이오애그젠엔텍	1	×
한라봉 미숙과실 과피 유전자정보	2005	2008-12-01	(주)바이오애그젠엔텍	1	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2008-12-01	제주특별자치도농업기술원	3	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
한라봉 성숙과실 과피 DNA Clone	2004	2008-12-01	제주특별자치도농업기술원	2	×
한라봉 미숙과실 과피 DNA Clone	2005	2008-12-01	제주특별자치도농업기술원	4	×
쇠무릎 DNA Clone	2002	2008-12-01	제주특별자치도농업기술원	4	×
한라봉 미숙과실 과피 유전자정보	2005	2008-12-01	제주특별자치도농업기술원	1	×
진귤 미숙과실 DNA Clone	2006	2008-12-01	제주특별자치도농업기술원	2	×
두릅 DNA Clone	2005	2008-12-01	제주특별자치도농업기술원	2	×
참취 DNA Clone	2004	2008-12-01	제주특별자치도농업기술원	1	×
한라봉 성숙과실 과피 유전자정보	2004	2008-12-01	제주특별자치도농업기술원	1	×
쇠무릎 유전자정보	2002	2008-12-01	제주특별자치도농업기술원	1	×
두릅 유전자정보	2005	2008-12-01	제주특별자치도농업기술원	4	×
참취 유전자정보	2004	2008-12-01	제주특별자치도농업기술원	2	×
진귤 미숙과실 유전자정보	2006	2008-12-01	제주특별자치도농업기술원	1	×
한라봉 성숙과실 병반과피 유전자정보	2006	2008-12-01	난지농업연구소 감귤시험장	2	×
한라봉 성숙과실 과피 유전자정보	2004	2008-12-01	난지농업연구소 감귤시험장	3	×
한라봉 미숙과실 과피 유전자정보	2005	2008-12-01	난지농업연구소 감귤시험장	7	×
진귤 미숙과실 유전자정보	2006	2008-12-01	난지농업연구소 감귤시험장	6	×
쇠무릎 유전자정보	2002	2008-12-01	난지농업연구소 감귤시험장	3	×
두릅 유전자정보	2005	2008-12-01	난지농업연구소 감귤시험장	10	×
참취 유전자정보	2004	2008-12-01	난지농업연구소 감귤시험장	6	×
온주밀감 성숙과실 유전자정보	2003	2008-12-01	난지농업연구소 감귤시험장	2	×
온주밀감 미숙과실 유전자정보	2002	2008-12-01	난지농업연구소 감귤시험장	1	×
한라봉 성숙과실 병반과피 유전자정보	2006	2008-11-29	농촌진흥청 감귤시험장	1	×
한라봉 성숙과실 과피 유전자정보	2004	2008-11-29	농촌진흥청 감귤시험장	2	×
한라봉 미숙과실 과피 유전자정보	2005	2008-11-29	농촌진흥청 감귤시험장	2	×
진귤 미숙과실 유전자정보	2006	2008-11-29	농촌진흥청 감귤시험장	3	×
두릅 유전자정보	2005	2008-11-29	농촌진흥청 감귤시험장	2	×
참취 유전자정보	2004	2008-11-29	농촌진흥청 감귤시험장	3	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
쇠무릎 유전자정보	2002	2008-11-29	농촌진흥청 감귤시험장	1	×
한라봉 성숙과실 과피 유전자정보	2004	2008-11-28	제주대학교	2	×
한라봉 미숙과실 과피 유전자정보	2005	2008-11-28	제주대학교	1	×
참취 유전자정보	2004	2008-11-28	제주대학교	1	×
진귤 미숙과실 유전자정보	2006	2008-11-28	제주대학교	1	×
쇠무릎 유전자정보	2002	2008-11-28	제주대학교	1	×
두릅 유전자정보	2005	2008-11-28	제주대학교	1	×
온주밀감 성숙과실 유전자정보	2003	2008-11-28	제주대학교	1	×
온주밀감 미숙과실 유전자정보	2002	2008-11-28	제주대학교	1	×
한라봉 성숙과실 과피 유전자정보	2004	2008-11-28	아열대원예산업연구센터	5	×
한라봉 미숙과실 과피 유전자정보	2005	2008-11-28	아열대원예산업연구센터	5	×
참취 유전자정보	2004	2008-11-28	아열대원예산업연구센터	5	×
진귤 미숙과실 유전자정보	2006	2008-11-28	아열대원예산업연구센터	3	×
온주밀감 성숙과실 유전자정보	2003	2008-11-28	아열대원예산업연구센터	2	×
두릅 유전자정보	2005	2008-11-28	아열대원예산업연구센터	3	×
온주밀감 미숙과실 유전자정보	2002	2008-11-28	아열대원예산업연구센터	4	×
쇠무릎 유전자정보	2002	2008-11-28	아열대원예산업연구센터	3	×
한라봉 성숙과실 병반과피 유전자정보	2006	2008-11-28	아열대원예산업연구센터	2	×
한라봉 성숙과실 병반과피 유전자정보	2006	2008-11-27	제주대학교	2	×
한라봉 성숙과실 과피 유전자정보	2004	2008-11-27	제주대학교	3	×
한라봉 미숙과실 과피 유전자정보	2005	2008-11-27	제주대학교	5	×
진귤 미숙과실 유전자정보	2006	2008-11-27	제주대학교	5	×
쇠무릎 유전자정보	2002	2008-11-27	제주대학교	3	×
두릅 유전자정보	2005	2008-11-27	제주대학교	5	×
참취 유전자정보	2004	2008-11-27	제주대학교	4	×
한라봉 성숙과실 과피 유전자정보	2004	2008-11-26	제주대학교	10	×
참취 유전자정보	2004	2008-11-26	제주대학교	8	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
진귤 미숙과실 유전자정보	2006	2008-11-26	제주대학교	8	×
두릅 유전자정보	2005	2008-11-26	제주대학교	8	×
한라봉 성숙과실 병반과피 유전자정보	2006	2008-11-26	제주대학교	5	×
한라봉 미숙과실 과피 유전자정보	2005	2008-11-26	제주대학교	7	×
온주밀감 미숙과실 유전자정보	2002	2008-11-26	제주대학교	3	×
쇠무릎 유전자정보	2002	2008-11-26	제주대학교	4	×
한라봉 성숙과실 과피 DNA Clone	2004	2008-11-26	아열대원예산업연구소	2	×
한라봉 미숙과실 과피 DNA Clone	2005	2008-11-26	아열대원예산업연구소	3	×
진귤 미숙과실 DNA Clone	2006	2008-11-26	아열대원예산업연구소	2	×
온주밀감 미숙과실 DNA Clone	2002	2008-11-26	아열대원예산업연구소	7	×
쇠무릎 DNA Clone	2002	2008-11-26	아열대원예산업연구소	2	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2008-11-26	아열대원예산업연구소	1	×
온주밀감 미숙과실 유전자정보	2002	2008-11-26	제주대학교	5	×
쇠무릎 유전자정보	2002	2008-11-26	제주대학교	3	×
두릅 유전자정보	2005	2008-11-26	제주대학교	4	×
진귤 미숙과실 유전자정보	2006	2008-11-26	제주대학교	1	×
한라봉 성숙과실 병반과피 유전자정보	2006	2008-11-26	제주대학교	2	×
한라봉 성숙과실 과피 유전자정보	2004	2008-11-26	제주대학교	3	×
한라봉 미숙과실 과피 유전자정보	2005	2008-11-26	제주대학교	2	×
한라봉 미숙과실 과피 DNA Clone	2005	2008-11-26	제주대학교	7	×
진귤 미숙과실 DNA Clone	2006	2008-11-26	제주대학교	7	×
쇠무릎 DNA Clone	2002	2008-11-26	제주대학교	5	×
두릅 DNA Clone	2005	2008-11-26	제주대학교	5	×
참취 DNA Clone	2004	2008-11-26	제주대학교	5	×
한라봉 성숙과실 과피 유전자정보	2004	2008-11-26	제주대학교	2	×
온주밀감 미숙과실 DNA Clone	2002	2008-11-26	제주대학교	7	×
한라봉 성숙과실 과피 DNA Clone	2004	2008-11-26	제주대학교	1	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
한라봉 성숙과실 병반과피 DNA Clone	2006	2008-11-26	제주대학교	2	×
쇠무릎 유전자정보	2002	2008-11-26	제주대학교	1	×
한라봉 미숙과실 과피 유전자정보	2005	2008-11-26	제주대학교	1	×
한라봉 성숙과실 병반과피 유전자정보	2006	2008-11-26	제주대학교	4	×
한라봉 성숙과실 과피 유전자정보	2004	2008-11-26	제주대학교	2	×
한라봉 미숙과실 과피 유전자정보	2005	2008-11-26	제주대학교	3	×
참취 유전자정보	2004	2008-11-26	제주대학교	2	×
진귤 미숙과실 유전자정보	2006	2008-11-26	제주대학교	4	×
쇠무릎 유전자정보	2002	2008-11-26	제주대학교	1	×
두릅 유전자정보	2005	2008-11-26	제주대학교	3	×
쇠무릎 유전자정보	2002	2008-11-26	바이오스펙트럼(주)	3	×
두릅 유전자정보	2005	2008-11-26	바이오스펙트럼(주)	4	×
한라봉 성숙과실 병반과피 유전자정보	2006	2008-11-26	바이오스펙트럼(주)	4	×
한라봉 성숙과실 과피 유전자정보	2004	2008-11-26	바이오스펙트럼(주)	9	×
한라봉 미숙과실 과피 유전자정보	2005	2008-11-26	바이오스펙트럼(주)	6	×
참취 유전자정보	2004	2008-11-26	바이오스펙트럼(주)	3	×
진귤 미숙과실 유전자정보	2006	2008-11-26	바이오스펙트럼(주)	12	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2008-11-26	바이오스펙트럼(주)	1	×
한라봉 성숙과실 과피 DNA Clone	2004	2008-11-26	바이오스펙트럼(주)	1	×
한라봉 미숙과실 과피 DNA Clone	2005	2008-11-26	바이오스펙트럼(주)	1	×
진귤 미숙과실 DNA Clone	2006	2008-11-26	바이오스펙트럼(주)	2	×
두릅 DNA Clone	2005	2008-11-26	바이오스펙트럼(주)	1	×
두릅 DNA Clone	2005	2008-11-26	바이오애그진엔텍	5	×
참취 DNA Clone	2004	2008-11-26	바이오애그진엔텍	4	×
진귤 미숙과실 DNA Clone	2006	2008-11-26	바이오애그진엔텍	2	×
한라봉 미숙과실 과피 DNA Clone	2005	2008-11-26	바이오애그진엔텍	1	×
쇠무릎 DNA Clone	2002	2008-11-26	바이오애그진엔텍	1	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
진귤 미숙과실 유전자정보	2006	2008-11-26	바이오애그진엔텍	3	×
두릅 유전자정보	2005	2008-11-26	바이오애그진엔텍	4	×
한라봉 미숙과실 과피 유전자정보	2005	2008-11-26	바이오애그진엔텍	3	×
한라봉 성숙과실 병반과피 유전자정보	2006	2008-11-26	바이오애그진엔텍	1	×
한라봉 성숙과실 과피 유전자정보	2004	2008-11-26	바이오애그진엔텍	1	×
온주밀감 미숙과실 유전자정보	2002	2008-11-25	농촌진흥청	7	×
쇠무릎 유전자정보	2002	2008-11-25	농촌진흥청	3	×
한라봉 성숙과실 병반과피 유전자정보	2006	2008-11-25	농촌진흥청	3	×
한라봉 성숙과실 과피 유전자정보	2004	2008-11-25	농촌진흥청	5	×
한라봉 미숙과실 과피 유전자정보	2005	2008-11-25	농촌진흥청	4	×
진귤 미숙과실 유전자정보	2006	2008-11-25	농촌진흥청	2	×
두릅 유전자정보	2005	2008-11-25	농촌진흥청	1	×
한라봉 미숙과실 과피 DNA Clone	2005	2008-11-24	(주)바이오애그젠엔텍	2	×
참취 DNA Clone	2004	2008-11-24	(주)바이오애그젠엔텍	2	×
진귤 미숙과실 DNA Clone	2006	2008-11-24	(주)바이오애그젠엔텍	3	×
두릅 DNA Clone	2005	2008-11-24	(주)바이오애그젠엔텍	3	×
쇠무릎 DNA Clone	2002	2008-11-24	(주)바이오애그젠엔텍	1	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2008-11-24	(주)바이오애그젠엔텍	1	×
한라봉 성숙과실 과피 DNA Clone	2004	2008-11-24	(주)바이오애그젠엔텍	1	×
한라봉 미숙과실 과피 유전자정보	2005	2008-11-24	난지농업연구소	2	×
참취 유전자정보	2004	2008-11-24	난지농업연구소	3	×
두릅 유전자정보	2005	2008-11-24	난지농업연구소	3	×
진귤 미숙과실 유전자정보	2006	2008-11-24	난지농업연구소	3	×
쇠무릎 유전자정보	2002	2008-11-24	난지농업연구소	1	×
한라봉 성숙과실 병반과피 유전자정보	2006	2008-11-24	난지농업연구소	1	×
한라봉 성숙과실 과피 유전자정보	2004	2008-11-24	난지농업연구소	1	×
한라봉 미숙과실 과피 유전자정보	2005	2008-11-24	제주대학교	1	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
참취 유전자정보	2004	2008-11-24	제주대학교	3	×
진귤 미숙과실 유전자정보	2006	2008-11-24	제주대학교	1	×
쇠무릎 유전자정보	2002	2008-11-24	제주대학교	1	×
두릅 유전자정보	2005	2008-11-24	제주대학교	2	×
한라봉 성숙과실 병반과피 유전자정보	2006	2008-11-22	제주대학교	1	×
한라봉 성숙과실 과피 유전자정보	2004	2008-11-22	제주대학교	1	×
한라봉 미숙과실 과피 유전자정보	2005	2008-11-22	제주대학교	1	×
진귤 미숙과실 유전자정보	2006	2008-11-22	제주대학교	2	×
두릅 유전자정보	2005	2008-11-22	제주대학교	1	×
참취 유전자정보	2004	2008-11-21	농촌진흥청 감귤시험장	1	×
두릅 유전자정보	2005	2008-11-21	농촌진흥청 감귤시험장	1	×
한라봉 성숙과실 과피 유전자정보	2004	2008-11-21	농촌진흥청 감귤시험장	3	×
한라봉 성숙과실 병반과피 유전자정보	2006	2008-11-21	농촌진흥청 감귤시험장	2	×
한라봉 미숙과실 과피 유전자정보	2005	2008-11-21	농촌진흥청 감귤시험장	2	×
온주밀감 미숙과실 유전자정보	2002	2008-11-21	농촌진흥청 감귤시험장	3	×
쇠무릎 유전자정보	2002	2008-11-21	농촌진흥청 감귤시험장	2	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2008-11-18	난지농업연구소	2	×
한라봉 성숙과실 과피 DNA Clone	2004	2008-11-18	난지농업연구소	3	×
한라봉 미숙과실 과피 DNA Clone	2005	2008-11-18	난지농업연구소	2	×
온주밀감 미숙과실 DNA Clone	2002	2008-11-18	난지농업연구소	3	×
쇠무릎 DNA Clone	2002	2008-11-18	난지농업연구소	2	×
진귤 미숙과실 DNA Clone	2006	2008-11-18	제주특별자치도농업기술원	4	×
쇠무릎 DNA Clone	2002	2008-11-18	제주특별자치도농업기술원	1	×
두릅 DNA Clone	2005	2008-11-18	제주특별자치도농업기술원	1	×
한라봉 성숙과실 병반과피 유전자정보	2006	2008-11-18	제주특별자치도농업기술원	4	×
진귤 미숙과실 유전자정보	2006	2008-11-18	제주특별자치도농업기술원	1	×
두릅 유전자정보	2005	2008-11-18	제주특별자치도농업기술원	2	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
한라봉 성숙과실 과피 유전자정보	2004	2008-11-18	제주특별자치도농업기술원	3	×
한라봉 미숙과실 과피 유전자정보	2005	2008-11-18	제주특별자치도농업기술원	2	×
참취 DNA Clone	2004	2008-11-18	제주특별자치도농업기술원	2	×
한라봉 미숙과실 과피 DNA Clone	2005	2008-11-18	제주특별자치도농업기술원	3	×
한라봉 성숙과실 과피 DNA Clone	2004	2008-11-18	제주특별자치도농업기술원	2	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2008-11-18	제주특별자치도농업기술원	1	×
온주밀감 미숙과실 유전자정보	2002	2008-11-17	제주대학교 생명공학과	2	×
쇠무릎 DNA Clone	2002	2008-11-15	제주대학교	3	×
진귤 미숙과실 DNA Clone	2006	2008-11-14	제주아열대원예산업연구소	4	×
진귤 미숙과실 DNA Clone	2006	2008-11-14	제주특별자치도농업기술원	2	×
한라봉 미숙과실 과피 유전자정보	2005	2008-11-14	제주특별자치도농업기술원	1	×
한라봉 미숙과실 과피 DNA Clone	2005	2008-11-14	제주특별자치도농업기술원	1	×
한라봉 성숙과실 과피 유전자정보	2004	2008-11-14	제주특별자치도농업기술원	1	×
온주밀감 미숙과실 DNA Clone	2002	2008-11-14	제주특별자치도농업기술원	6	×
두릅 DNA Clone	2005	2008-11-14	제주특별자치도농업기술원	1	×
쇠무릎 DNA Clone	2002	2008-11-14	제주특별자치도농업기술원	1	×
한라봉 성숙과실 병반과피 유전자정보	2006	2008-11-13	난지농업연구소 감귤시험장	2	×
진귤 미숙과실 유전자정보	2006	2008-11-13	난지농업연구소 감귤시험장	3	×
한라봉 미숙과실 과피 유전자정보	2005	2008-11-13	난지농업연구소 감귤시험장	3	×
쇠무릎 유전자정보	2002	2008-11-13	난지농업연구소 감귤시험장	1	×
두릅 유전자정보	2005	2008-11-13	난지농업연구소 감귤시험장	4	×
두릅 유전자정보	2005	2008-11-11	제주특별자치도농업기술원	6	×
참취 유전자정보	2004	2008-11-11	제주특별자치도농업기술원	1	×
한라봉 성숙과실 병반과피 유전자정보	2006	2008-11-11	제주특별자치도농업기술원	1	×
진귤 미숙과실 유전자정보	2006	2008-11-11	제주특별자치도농업기술원	2	×
한라봉 미숙과실 과피 유전자정보	2005	2008-11-11	제주특별자치도농업기술원	2	×
진귤 미숙과실 유전자정보	2006	2008-11-07	농촌진흥청 감귤시험장	2	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
한라봉 미숙과실 과피 유전자정보	2005	2008-11-07	농촌진흥청 감귤시험장	2	×
한라봉 성숙과실 과피 유전자정보	2004	2008-11-07	농촌진흥청 감귤시험장	1	×
온주밀감 미숙과실 유전자정보	2002	2008-11-07	농촌진흥청 감귤시험장	7	×
쇠무릎 유전자정보	2002	2008-11-07	농촌진흥청 감귤시험장	1	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2008-11-07	(주)바이오애그젠엔텍	3	×
온주밀감 미숙과실 유전자정보	2002	2008-11-07	생명공학과	2	×
한라봉 성숙과실 과피 DNA Clone	2004	2008-11-06	아열대원예산업연구센터	2	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2008-11-06	아열대원예산업연구센터	1	×
한라봉 성숙과실 과피 DNA Clone	2004	2008-11-06	제주대학교	5	×
한라봉 성숙과실 과피 유전자정보	2004	2008-11-06	제주대학교	1	×
두릅 DNA Clone	2005	2008-11-05	제주아열대원예산업연구소	3	×
진귤 미숙과실 DNA Clone	2006	2008-11-05	제주아열대원예산업연구소	1	×
쇠무릎 DNA Clone	2002	2008-11-04	(주)바이오애그젠엔텍	1	×
두릅 DNA Clone	2005	2008-11-04	(주)바이오애그젠엔텍	6	×
두릅 DNA Clone	2005	2008-11-03	제주대학교	5	×
진귤 미숙과실 DNA Clone	2006	2008-11-03	제주대학교	1	×
진귤 미숙과실 DNA Clone	2006	2008-11-03	제주아열대원예산업연구소	3	×
두릅 유전자정보	2005	2008-10-27	제주대학교	1	×
두릅 유전자정보	2005	2008-10-27	제주대학교	1	×
두릅 유전자정보	2005	2008-10-22	제주대학교	1	×
두릅 유전자정보	2005	2008-10-22	제주대학교	1	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2008-10-21	생명공학부	3	×
쇠무릎 DNA Clone	2002	2008-10-20	제주대학교	4	×
온주밀감 미숙과실 DNA Clone	2002	2008-10-15	제주대학교	3	×
진귤 미숙과실 DNA Clone	2006	2008-10-15	제주대학교	3	×
쇠무릎 DNA Clone	2002	2008-10-14	제주대학교	3	×
쇠무릎 유전자정보	2002	2008-10-14	제주대학교	1	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
온주밀감 미숙과실 유전자정보	2002	2008-10-08	아열대원예산업연구센터	4	×
쇠무릎 유전자정보	2002	2008-10-03	제주대학교	4	×
온주밀감 성숙과실 유전자정보	2003	2008-10-02	아열대원예산업연구센터	3	×
진귤 미숙과실 DNA Clone	2006	2008-10-01	제주대학교	3	×
한라봉 미숙과실 과피 유전자정보	2005	2008-09-29	제주대학교	3	×
두릅 유전자정보	2005	2008-09-29	제주대학교	2	×
진귤 미숙과실 유전자정보	2006	2008-09-19	생명공학부	5	×
두릅 유전자정보	2005	2008-09-19	생명공학부	1	×
온주밀감 성숙과실 유전자정보	2003	2008-09-19	생명공학부	1	×
두릅 유전자정보	2005	2008-09-18	제주대학교	4	×
쇠무릎 유전자정보	2002	2008-09-18	제주대학교	1	×
한라봉 성숙과실 과피 유전자정보	2004	2008-09-17	아열대원예산업연구센터	1	×
진귤 미숙과실 DNA Clone	2006	2008-09-03	제주대학교	4	×
진귤 미숙과실 유전자정보	2006	2008-09-03	제주대학교	1	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2008-09-03	생명공학부	2	×
한라봉 미숙과실 과피 유전자정보	2005	2008-09-03	생명공학부	4	×
두릅 DNA Clone	2005	2008-09-03	생명공학부	1	×
온주밀감 미숙과실 유전자정보	2002	2008-09-03	생명공학부	1	×
온주밀감 미숙과실 유전자정보	2002	2008-09-02	아열대원예산업연구센터	6	×
한라봉 미숙과실 과피 유전자정보	2005	2008-08-30	제주대학교	1	×
온주밀감 미숙과실 유전자정보	2002	2008-08-30	제주대학교	3	×
진귤 미숙과실 유전자정보	2006	2008-08-30	제주대학교	2	×
진귤 미숙과실 유전자정보	2006	2008-08-29	농촌진흥청	2	×
온주밀감 미숙과실 유전자정보	2002	2008-08-29	농촌진흥청	8	×
한라봉 미숙과실 과피 유전자정보	2005	2008-08-29	난지농업연구소 감귤시험장	1	×
한라봉 미숙과실 과피 DNA Clone	2005	2008-08-29	난지농업연구소 감귤시험장	3	×
두릅 유전자정보	2005	2008-08-29	난지농업연구소 감귤시험장	6	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
두릅 DNA Clone	2005	2008-08-29	난지농업연구소 감귤시험장	1	×
진귤 미숙과실 유전자정보	2006	2008-08-29	난지농업연구소 감귤시험장	1	×
온주밀감 성숙과실 유전자정보	2003	2008-08-29	난지농업연구소 감귤시험장	1	×
온주밀감 미숙과실 유전자정보	2002	2008-08-29	난지농업연구소 감귤시험장	1	×
한라봉 미숙과실 과피 유전자정보	2005	2008-08-27	제주대학교	2	×
진귤 미숙과실 DNA Clone	2006	2008-08-27	제주대학교	1	×
진귤 미숙과실 유전자정보	2006	2008-08-27	제주대학교	5	×
온주밀감 성숙과실 DNA Clone	2003	2008-08-27	제주대학교	1	×
온주밀감 미숙과실 DNA Clone	2002	2008-08-27	제주대학교	1	×
쇠무릎 유전자정보	2002	2008-08-27	제주대학교	1	×
두릅 DNA Clone	2005	2008-08-26	바이오스펙트럼(주)	1	×
온주밀감 성숙과실 유전자정보	2003	2008-08-26	바이오스펙트럼(주)	2	×
온주밀감 미숙과실 DNA Clone	2002	2008-08-26	바이오스펙트럼(주)	1	×
온주밀감 미숙과실 유전자정보	2002	2008-08-26	바이오스펙트럼(주)	5	×
한라봉 성숙과실 병반과피 DNA Clone	2006	2008-08-25	(주)바이오애그젠엔텍	1	×
한라봉 성숙과실 병반과피 유전자정보	2006	2008-08-25	(주)바이오애그젠엔텍	1	×
한라봉 성숙과실 과피 유전자정보	2004	2008-08-25	(주)바이오애그젠엔텍	1	×
한라봉 미숙과실 과피 유전자정보	2005	2008-08-25	(주)바이오애그젠엔텍	2	×
온주밀감 미숙과실 DNA Clone	2002	2008-08-25	(주)바이오애그젠엔텍	1	×
두릅 유전자정보	2005	2008-08-25	(주)바이오애그젠엔텍	2	×
쇠무릎 유전자정보	2002	2008-08-25	(주)바이오애그젠엔텍	1	×
참취 유전자정보	2004	2008-08-21	제주대학교	2	×
두릅 유전자정보	2005	2008-08-21	제주대학교	4	×
쇠무릎 유전자정보	2002	2008-08-21	제주대학교	1	×
한라봉 성숙과실 과피 유전자정보	2004	2008-08-21	제주대학교	1	×
온주밀감 미숙과실 유전자정보	2002	2008-08-21	제주대학교	3	×
진귤 미숙과실 유전자정보	2006	2008-08-21	제주대학교	1	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
온주밀감 성숙과실 유전자정보	2003	2008-08-21	제주대학교	1	×
한라봉 미숙과실 과피 유전자정보	2005	2008-08-21	대학교	6	×
두릅 유전자정보	2005	2008-08-21	대학교	1	×
진귤 미숙과실 DNA Clone	2006	2008-08-18	제주특별자치도농업기술원	1	×
온주밀감 미숙과실 DNA Clone	2002	2008-08-18	제주특별자치도농업기술원	1	×
한라봉 성숙과실 병반과피 유전자정보	2006	2008-08-18	제주특별자치도농업기술원	4	×
한라봉 성숙과실 과피 유전자정보	2004	2008-08-18	제주특별자치도농업기술원	1	×
한라봉 미숙과실 과피 유전자정보	2005	2008-08-18	제주특별자치도농업기술원	2	×
참취 DNA Clone	2004	2008-08-14	제주대학교	2	×
쇠무릎 DNA Clone	2002	2008-08-14	제주대학교	3	×
온주밀감 미숙과실 유전자정보	2002	2008-08-12	제주대학교	1	×
두릅 유전자정보	2005	2008-08-11	아열대원예산업연구소	16	×
한라봉 성숙과실 과피 DNA Clone	2004	2008-08-05	제주대학교	1	×
온주밀감 미숙과실 유전자정보	2002	2008-08-04	제주대학교	1	×
온주밀감 미숙과실 유전자정보	2002	2008-07-29	제주대학교	1	×
온주밀감 미숙과실 유전자정보	2002	2008-07-28	아열대원예산업연구소	1	×
온주밀감 미숙과실 유전자정보	2002	2008-07-18	제주대학교	1	×
온주밀감 미숙과실 유전자정보	2002	2008-07-16	제주대학교	1	×
한라봉 성숙과실 과피 DNA Clone	2004	2008-07-14	아열대원예산업연구소	2	×
진귤 미숙과실 DNA Clone	2006	2008-07-14	아열대원예산업연구소	1	×
한라봉 미숙과실 과피 DNA Clone	2005	2008-07-14	아열대원예산업연구소	2	×
두릅 DNA Clone	2005	2008-07-14	아열대원예산업연구소	4	×
온주밀감 미숙과실 DNA Clone	2002	2008-07-14	아열대원예산업연구소	1	×
쇠무릎 DNA Clone	2002	2008-07-14	아열대원예산업연구소	1	×
참취 DNA Clone	2004	2008-07-14	아열대원예산업연구소	1	×
진귤 미숙과실 DNA Clone	2006	2008-07-10	제주대학교 생명공학부	3	×
온주밀감 성숙과실 DNA Clone	2003	2008-07-10	제주대학교 생명공학부	1	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
진귤 미숙과실 유전자정보	2006	2008-07-02	제주대학교 생명공학부	1	×
한라봉 성숙과실 병반과피 유전자정보	2006	2008-07-02	제주대학교 생명공학부	1	×
참취 유전자정보	2004	2008-07-02	제주대학교 생명공학부	2	×
온주밀감 미숙과실 유전자정보	2002	2008-07-02	제주대학교 생명공학부	1	×
한라봉 미숙과실 과피 유전자정보	2005	2008-06-30	제주아열대원예산업연구소	4	×
한라봉 성숙과실 병반과피 유전자정보	2006	2008-06-30	제주아열대원예산업연구소	2	×
두릅 유전자정보	2005	2008-06-30	제주아열대원예산업연구소	3	×
진귤 미숙과실 유전자정보	2006	2008-06-30	제주아열대원예산업연구소	1	×
온주밀감 미숙과실 유전자정보	2002	2008-06-27	난지농업연구소	2	×
참취 DNA Clone	2004	2008-06-18	난지농업연구소	1	×
두릅 DNA Clone	2005	2008-06-18	난지농업연구소	2	×
한라봉 성숙과실 과피 DNA Clone	2004	2008-06-18	제주대학교	1	×
한라봉 미숙과실 과피 DNA Clone	2005	2008-06-18	제주대학교	1	×
진귤 미숙과실 DNA Clone	2006	2008-06-11	제주대학교	1	×
한라봉 미숙과실 과피 DNA Clone	2005	2008-06-11	제주대학교	1	×
한라봉 성숙과실 병반과피 유전자정보	2006	2008-06-10	제주대학교	1	×
한라봉 성숙과실 과피 유전자정보	2004	2008-06-10	제주대학교	1	×
한라봉 미숙과실 과피 유전자정보	2005	2008-06-10	제주대학교	1	×
진귤 미숙과실 유전자정보	2006	2008-06-10	제주대학교	1	×
한라봉 미숙과실 과피 DNA Clone	2005	2008-06-09	자연과학대학	2	×
진귤 미숙과실 DNA Clone	2006	2008-06-05	자연과학대학	1	×
진귤 미숙과실 유전자정보	2006	2008-06-05	자연과학대학	1	×
쇠무릎 유전자정보	2002	2008-06-05	아열대원예산업연구센터	1	×
진귤 미숙과실 유전자정보	2006	2008-06-02	제주대학교	1	×
한라봉 성숙과실 과피 DNA Clone	2004	2008-06-02	제주대학교	1	×
한라봉 성숙과실 과피 DNA Clone	2004	2008-05-27	바이오애그진엔텍	1	×
참취 DNA Clone	2004	2008-05-27	바이오애그진엔텍	1	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
진귤 미숙과실 유전자정보	2006	2008-05-27	바이오애그진엔텍	1	×
두릅 DNA Clone	2005	2008-05-27	바이오애그진엔텍	1	×
온주밀감 미숙과실 DNA Clone	2002	2008-05-27	바이오애그진엔텍	1	×
두릅 유전자정보	2005	2008-05-18	제주대학	3	×
한라봉 성숙과실 병반과피 유전자정보	2006	2008-05-18	제주대학	1	×
한라봉 성숙과실 과피 유전자정보	2004	2008-05-18	제주대학	1	×
한라봉 미숙과실 과피 유전자정보	2005	2008-05-18	제주대학	1	×
진귤 미숙과실 유전자정보	2006	2008-05-18	제주대학	1	×
온주밀감 미숙과실 유전자정보	2002	2008-05-18	제주대학	2	×
한라봉 성숙과실 과피 유전자정보	2004	2008-05-09	제주아열대원예산업연구소	1	×
한라봉 미숙과실 과피 유전자정보	2005	2008-05-09	제주아열대원예산업연구소	1	×
쇠무릎 유전자정보	2002	2008-05-09	제주아열대원예산업연구소	1	×
두릅 유전자정보	2005	2008-05-09	제주아열대원예산업연구소	4	×
한라봉 성숙과실 병반과피 유전자정보	2006	2008-04-27	아열대원예산업연구소	1	×
한라봉 성숙과실 과피 유전자정보	2004	2008-04-27	아열대원예산업연구소	1	×
온주밀감 성숙과실 유전자정보	2003	2008-04-27	아열대원예산업연구소	1	×
두릅 유전자정보	2005	2008-04-27	아열대원예산업연구소	2	×
참취 유전자정보	2004	2008-04-27	아열대원예산업연구소	1	×
쇠무릎 유전자정보	2002	2008-04-27	아열대원예산업연구소	1	×
한라봉 성숙과실 과피 유전자정보	2004	2008-04-21	제주아열대원예산업연구소	1	×
쇠무릎 유전자정보	2002	2008-04-21	제주아열대원예산업연구소	2	×
두릅 유전자정보	2005	2008-04-21	제주아열대원예산업연구소	1	×
온주밀감 성숙과실 유전자정보	2003	2008-04-21	제주아열대원예산업연구소	1	×
두릅 DNA Clone	2005	2008-04-17	(주)바이오애그젠엔텍	1	×
쇠무릎 DNA Clone	2002	2008-04-17	(주)바이오애그젠엔텍	1	×
한라봉 성숙과실 과피 DNA Clone	2004	2008-04-07	제주대학교	2	×
한라봉 성숙과실 과피 DNA Clone	2004	2008-04-02	제주아열대원예산업연구소	1	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
참취 DNA Clone	2004	2008-04-02	제주아열대원예산업연구소	2	×
두릅 DNA Clone	2005	2008-04-02	제주아열대원예산업연구소	1	×
진귤 미숙과실 DNA Clone	2006	2008-04-02	제주아열대원예산업연구소	2	×
쇠무릎 DNA Clone	2002	2008-03-28	아열대원예산업연구소	3	×
두릅 DNA Clone	2005	2008-03-28	아열대원예산업연구소	4	×
두릅 DNA Clone	2005	2008-03-19	제주대학교	3	×
진귤 미숙과실 DNA Clone	2006	2008-03-19	제주대학교	1	×
두릅 DNA Clone	2005	2008-03-15	제주대학교	1	×
진귤 미숙과실 DNA Clone	2006	2008-03-15	제주대학교	1	×
두릅 유전자정보	2005	2008-03-07	(주)바이오애그젠엔텍	1	×
진귤 미숙과실 유전자정보	2006	2008-02-28	(주)바이오애그젠엔텍	1	×
진귤 미숙과실 DNA Clone	2006	2008-02-20	제주대학교	3	×
참취 유전자정보	2004	2008-02-15	(주)바이오애그젠엔텍	1	×
한라봉 성숙과실 병반과피 유전자정보	2006	2008-02-11	(주)바이오애그젠엔텍	1	×
한라봉 성숙과실 과피 유전자정보	2004	2008-02-04	(주)바이오애그젠엔텍	1	×
진귤 미숙과실 DNA Clone	2006	2008-01-30	제주대학교	1	×
진귤 미숙과실 유전자정보	2006	2008-01-22	(주)바이오애그젠엔텍	1	×
참취 유전자정보	2004	2008-01-17	제주대학교생명공학부	745	×
참취 염기서열정보 유전자정보	2004	2008-01-17	Gene&Tech	2306	×
두릅 DNA Clone	2005	2008-01-14	제주대학교생명공학부	30	×
일남1호 성숙과실 DNA Clone	2003	2008-01-14	제주대학교 생명공학부 식물화학연구실	6	×
참취 DNA Clone	2004	2008-01-11	제주대학교생명공학부	10	×
참취 DNA Clone	2004	2007-12-20	제주대학교생명공학부	20	×
한라봉 흑변발생과피 유전자정보	2004	2007-12-13	난지농업연구소감귤연구센터	780	×
쇠무릎 DNA Clone	2002	2007-11-21	제주대학교 생명공학부 식물화학연구실	20	×
참취 DNA Clone	2004	2007-11-09	제주대학교생명공학부	17	×
진귤 미숙과실 유전자정보	2006	2007-10-24	바이오애그	936	×

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
쇠무릎 DNA Clone	2002	2007-10-19	제주대학교 생명공학부 식물화학연구실	19	×
한라봉 성숙과피 라이브러리	2004	2007-09-07	난지농업연구소감귤연구센터	5	×
진귤 미숙과실 DNA Clone	2006	2007-08-28	제주대학교아열대원예산업연구센터	20	×
한라봉 미숙과피 DNA Clone	2005	2007-08-17	바이오스펙트럼	3	×
진귤 미숙과실 DNA Clone	2006	2007-08-17	바이오스펙트럼	5	×
한라봉 미숙과피 DNA Clone	2005	2007-08-09	제주대학교 생명공학부 허미주	10	×
진귤 미숙과실 DNA Clone	2006	2007-08-09	제주대학교아열대원예산업연구센터	12	×
한라봉 미숙과피 DNA Clone	2005	2007-07-11	제주대학교생명공학부	10	×
한라봉 미숙과피 DNA Clone	2005	2007-07-11	제주대학교생명공학부	6	×
진귤 미숙과실 DNA Clone	2006	2007-07-11	제주대학교아열대원예산업연구센터	10	×
한라봉 흑변발생과피 DNA Clone	2004	2007-07-10	제주대학교아열대원예산업연구센터	15	×
진귤 미숙과실 DNA Clone	2006	2007-06-26	Gene&Tech	4	×
한라봉 성숙과피 DNA Clone	2004	2007-06-26	제주대학교생명공학부	12	×
한라봉 미숙과피 라이브러리	2005	2007-06-21	난지농업연구소감귤연구센터	5ml	×
한라봉 성숙과피 DNA Clone	2004	2007-06-15	생물종다양성연구소	16	×
두릅 DNA Clone	2005	2007-06-15	생물종다양성연구소	9	×
한라봉 미숙과피 DNA Clone	2005	2007-06-15	생물종다양성연구소	5	×
일남1호 미숙과실 DNA Clone	2002	2007-06-15	생물종다양성연구소	9	×
한라봉 흑변발생과피 DNA Clone	2004	2007-06-15	생물종다양성연구소	6	×
일남1호 성숙과피 DNA Clone	2003	2007-06-15	생물종다양성연구소	2	×
쇠무릎 DNA Clone	2002	2007-06-15	생물종다양성연구소	1	×
한라봉 성숙과피 DNA Clone	2004	2007-06-12	제주대학교생명공학부	10	×
한라봉 성숙과피 유전자정보	2004	2007-06-07	난지농업연구소감귤연구센터	109	×
한라봉 미숙과피 유전자정보	2005	2007-06-07	난지농업연구소감귤연구센터	534	×
쇠무릎 라이브러리	2002	2007-05-02	제주대학교생명공학부	10ml	×
일남1호 성숙과실 유전자정보	2003	2007-04-24	제주대학교 생명공학부 식물화학연구실	69	×
일남1호 미숙과실 유전자정보	2002	2007-04-17	제주대학교 생명공학부 식물화학연구실	2350	○

IP : 14.49.138.138, 2017-11-03 13:30:33

보유 소재명	최초 보유연도	분양 실적			
		분양 년도	분양 기관	분양 건수	논문 발표 여부 (○/×)
일남1호 미숙과실 DNA Clone	2002	2007-04-03	제주대학교 생명공학부 식물화학연구실	18	○

IP : 14.49.138.138, 2017-11-03 13:30:33

첨부자료 9. 《학술지 발표 논문 내역서》

년 도	활용 소재명	발표 학술지명,호,면,년도	발표자 (자체,외부)	발표학술지 (SCI,비SCI)	소재은행표시 여부 (○/×)
2007	온주밀감 미숙과실 유전자	Journal of Plant Biology, 50(4), 2007	자체	SCI	○
2007	식물의 Essential Oils 생합성 관련 유전자	J. Appl. Biol. Chem. 50(3), 2007	외부	비SCI	×
2007	감귤 과피 Essential Oils 생합성 관련 유전자	J. Appl. Biol. Chem. 50(3), 2007	외부	비SCI	×
2007	감귤 limonoid 생합성 관련 유전자	J. Korean Soc. Appl. Biol. Chem. 50(3), 2007	내부	비SCI	×
2007	Protein phosphatase 관련 유전자	J. Appl. Biol. Chem. 50(2), 2007	내부	비SCI	○
2007	Protein phosphatase 관련 유전자	J. Appl. Biol. Chem. 50(4), 2007	내부	비SCI	○
2010	온주밀감 캘러스세포	J. Korean Soc. Appl. Biol. Chem. 53(6), 2010	내부	SCI	○
2010	우슬 20-Hydroxyecdysone	Biosci. Biotechnol. Biochem, 74(11), 2010	외부	SCI	○
2010	식물세포내 glycosylation	Molecular Medicine REPORTS 3: 115-119 2010	외부	SCI	○
2011	감귤의 limonoid UDP-glucosyltransferase	Korean J Food Preserv 18(2), 2011	자체	비SCI	○
2011	Bacillus에서 분리된 항암제	J. Korean Soc. Appl. Biol. Chem. 54(1), 2011	외부	SCI	○
2011	Bacillus에서 분리된 항암제	. J. Korean Soc. Appl. Biol. Chem. 54(2), 2011	외부	SCI	○
2011	상황버섯	. J. Korean Soc. Appl. Biol. Chem. 54(3), 2011	외부	SCI	○

IP : 14.49.138.138, 2017-11-03 13:30:33

년 도	활용 소재명	발표 학술지명,호,면,년도	발표자 (자체,외부)	발표학술지 (SCI,비SCI)	소재은행표시 여부 (○/×)
2011	온주밀감 과피의 flavonoid	Food Chemistry 128 49- 5, 2011	외부	SCI	○
2011	Paeonia lactiflora 뿌리	J. Korea Soc. Appl. Biol. Chem. 54(1), 2011	외부	SCI	×
2011	가자나무추출물	J. Korean Soc. Appl. Biol. Chem. 54(2), 2011	외부	SCI	○
2011	온주밀감 궁천조생 캘러스	. Hort. Environ. Biotechnol. 52(2), 2011	내부	SCI	○
2011	온주밀감 궁천조생 캘러스	J. Korean Soc. Appl. Biol. Chem. 54(1), 2011	내부	SCI	○
2011	항균활성 물질(Methylelaiophylin)	. J. Microbiol. Biotechnol. 21(3), 2011	외부	SCI	×
2011	감귤의 limonoid UDP-glucosyltransferase	Korean J Food Preserv 18(2), 2011	외부	비 SCI	×
2012	재래감귤3품종	Biomedical Chromatography, 26(4) 464-470 2012	외부	SCI	○
2012	Citrus leaf	Gene 494, 2012	외부	SCI	○

IP : 14.49.138.138, 2017-11-03 13:30:33