

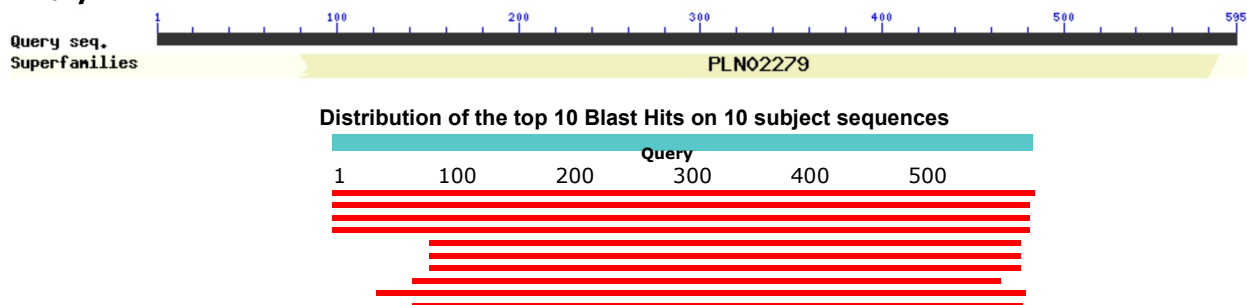
BLAST® >> blastp suite >> results for RID-NWB01UZH016

Job Title ST0001 ...
RID NWB01UZH016 Search expires on 09-14 22:26 pm
Program BLASTP
Database swissprot
Query ID lcl|Query_31394
Description None ...
Molecule type amino acid
Query Length 595

Descriptions

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
RecName: Full=Miltiradiene synthase KSL1, chloroplastic; AltName: Full=Kaurene synthase-like 1; Short=SmKSL; Short=SmKSL1; Flags: Precursor [Salvia miltiorrhiza]	1233	1233	100%	0.0	99.16%	C8XPS0.1
RecName: Full=Class I diterpene synthase 2, chloroplastic; Short=VacTPS2; AltName: Full=(13S)-vitexifolin A synthase; AltName: Full=9,13-epoxylabda-14-ene synthase; AltName: Full=Vitexagrusin D synthase; Flags: Precursor [Vitex agnus-castus]	826	826	99%	0.0	67.23%	A0A2K9RFZ2.1
RecName: Full=Class I diterpene synthase TPS6, chloroplastic; AltName: Full=Labd-13(16),14-diene-9-ol synthase; AltName: Full=Syn-isopimara-7,15-diene synthase; AltName: Full=Terpene synthase 6; Short=VacTPS6 [Vitex agnus-castus]	795	795	99%	0.0	63.41%	A0A2K9RFZ9.1
RecName: Full=9,13-epoxylabda-14-ene synthase, chloroplastic; AltName: Full=Manoyl oxide synthase; AltName: Full=Miltiradiene synthase; Flags: Precursor [Marrubium vulgare]	766	766	99%	0.0	64.37%	A0A075FBG7.1
RecName: Full=Cis-abienol synthase, chloroplastic; Short=NtABS; Flags: Precursor [Nicotiana tabacum]	371	371	84%	6e-118	37.40%	G3CCC1.1
RecName: Full=Santalene and bergamotene synthase, chloroplastic; AltName: Full=(+)-alpha-santalene synthase ((2Z,6Z)-farnesyl diphosphate cyclizing); AltName: Full=(+)-endo-beta-bergamotene synthase ((2Z,6Z)-farnesyl diphosphate cyclizing); AltName: Full=(-)-endo-alpha-bergamotene synthase ((2Z,6Z)-farnesyl diphosphate cyclizing); Flags: Precursor [Solanum habrochaites]	351	351	84%	2e-110	37.20%	B8XA41.1
RecName: Full=Beta-phellandrene synthase (neryl-diphosphate-cyclizing), chloroplastic; Flags: Precursor [Solanum lycopersicum]	346	346	84%	1e-108	37.01%	C1K5M3.1
RecName: Full=Ent-kaurene synthase-like 2; Short=OsKSL2 [Oryza sativa Japonica Group]	316	316	83%	8e-96	34.13%	Q0JA81.2
RecName: Full=Ent-kaur-16-ene synthase, chloroplastic; AltName: Full=Ent-kaurene synthase; AltName: Full=Ent-kaurene synthase B; Short=KSB; Flags: Precursor [Cucurbita maxima]	309	309	92%	3e-94	33.27%	Q39548.1
RecName: Full=Ent-kaur-16-ene synthase, chloroplastic; AltName: Full=Ent-kaurene synthase; Short=AtKS; AltName: Full=Ent-kaurene synthase B; Short=KSB; AltName: Full=Protein GA REQUIRING 2; Flags: Precursor [Arabidopsis thaliana]	305	305	86%	8e-93	35.23%	Q9SAK2.1

Graphic Summary



Alignments

Alignment view ☒ Pairwise ☐ CDS feature

RecName: Full=Miltiradiene synthase KSL1, chloroplastic; AltName: Full=Kaurene synthase-like 1; Short=SmKSL; Short=SmKSL1;
Flags: Precursor [Salvia miltiorrhiza]
Sequence ID: **C8XPS0.1** Length: 595 Number of Matches: 1
Range 1: 1 to 595

Score	Expect	Method	Identities	Positives	Gaps	Frame
1233 bits(3190)	0.0()	Compositional matrix adjust.	590/595(99%)	592/595(99%)	0/595(0%)	
Query 1	MSLAFNPAATAFSGNGARSRENFPVKHVTVRGFPMTNKSSFAVKCNLTITDLMGKIAE					60
Sbjct 1	MSLAFNPAATAFSGNGARSRENFPVKHVTVRGFPMTNKSSFAVKCNLTITDLMGKIAE					60
Query 61	KFKGEDSNFPAAAVQPAADMPSNLCIIDLTLQRLGVDRYFRSEIDTILEDTYRLWQRKER					120

Sbjct	61	KFKGEDSNFPAAAVQPAADMPSNLCIIDTLQRLGVDRYFRSEIDTILEDITYRLWQRRER	120
Query	121	AIFSDTTIHAMAFRLLRVKGYEVSSEELAPYADQEHVDLQTIIEVATVIELYRAAQERTGE	180
Sbjct	121	AIFSDT IHAMAFRLLRVKGYEVSSEELAPYADQEHVDLQTIIEVATVIELYRAAQERTGE	180
Query	181	DESSLKKLHAWTTTFLKQKLLTNSIPDKKLHKLVEYYLKNYHGILDRMGVRQNLDLYDIS	240
Sbjct	181	DESSLKKLHAWTTTFLKQKLLTNSIPDKKLHKLVEYYLKN HGILDRMGVRQNLDLYDIS	240
Query	241	YYRTAKAANRFSNLCSEDFLAFARQDFNICQAQHQKELQQLQRWYADCKLDTLKYGRDVV	300
Sbjct	241	YYRT+KAANRFSNLCSEDFLAFARQDFNICQAQHQKELQQLQRWYADCKLDTLKYGRDVV	300
Query	301	RVANFLTSAIIGDPELSDVRIVFAQHIVLVTRIDFFDHRGSREESYKILELIKEWKEKP	360
Sbjct	301	RVANFLTSAIIGDPELSDVRIVFAQHIVLVTRIDFFDHRGSREESYKILELIKEWKEKP	360
Query	361	AAEYGSEEEVILFTAVYNTVNELAERAHVEHGRSVKDFLIKLVQILSIFKRELDTWSD	420
Sbjct	361	AAEYGSEEEVILFTAVYNTVNELAERAHVE GRSVKDFLIKLVQILSIFKRELDTWSD	420
Query	421	TALTLDLYLSASWVSIGCRICILMSMQFIGIKLSDEMLLSEECIDLCRHVSMVDRLLNDV	480
Sbjct	421	TALTLDLYLSASWVSIGCRICILMSMQFIGIKLSDEMLLSEECIDLCRHVSMVDRLLNDV	480
Query	481	QTFEKERKENTGNSVTLLLAANKDDSSFTEEEAIRIAKEMAECNRRQLMQIVYKTGTIFP	540
Sbjct	481	QTFEKERKENTGNSVTLLLAANKDDSSFTEEEAIRIAKEMAECNRRQLMQIVYKTGTIFP	540
Query	541	RQCKDMFLKVCRIGCYLYASGDEFTSPQQMMEDMKS LVYEPLTIHPLVANNVRGE	595
Sbjct	541	RQCKDMFLKVCRIGCYLYASGDEFTSPQQMMEDMKS LVYEPLTIHPLVANNVRG+	595

RecName: Full=Class I diterpene synthase 2, chloroplastic; Short=VacTPS2; AltName: Full=(13S)-vitexifolin A synthase; AltName: Full=9,13-epoxylabda-14-ene synthase; AltName: Full=Viteagnusin D synthase; Flags: Precursor [Vitex agnus-castus]
Sequence ID: **A0A2K9RFZ2.1** Length: 589 Number of Matches: 1
Range 1: 1 to 584

Score	Expect	Method	Identities	Positives	Gaps	Frame
826 bits(2133)	0.0()	Compositional matrix adjust.	398/592(67%)	487/592(82%)	9/592(1%)	
Query	1	MSLAFNPAATAFSGNGARSRENFFVKHVTVRGFFMITNKKSSFAVKCNL-TTDLMGKIA				59
Sbjct	1	MSL FN T FS + R+RRE FP + FP+ T+KS+ VKCNL T+TDL+GK+ MSLRFNLIVTFPSNHRIRNRRETFFPAQE-----FPVATSKSAVKVKCNLITSTDLVGKVR				55
Query	60	EKFKGEDSNFPAAAVQPAADMPSNLCIIDTLQRLGVDRYFRSEIDTILEDITYRLWQRKE				119
Sbjct	56	EK G+ N A+ P D+PSNLC+IDTL+RLGVDRYF+SEID +LE+TYRLWQ+KE EKINGKVDNSLEVPAIHPV-DIPSNLCMIDTLERLGVDRYFQSEIDGVLEETTYRLWQQKE				114
Query	120	RAIFSDTTIHAMAFRLLRVKGYEVSSEELAPYADQEHVDLQTIIEVATVIELYRAAQERTG				179
Sbjct	115	+ IF+D T AMAFRLLRVKGYEVSS+ELAPYADQ HV+LQ +V VIELYRA+QER KDIFADVTCRAMAFRLLRVKGYEVSSDELAPYADQAHVNLQISDVTAVIELYRASQERIY				174
Query	180	EDESSLKKLHAWTTTFLKQKLLTNSIPDKKLHKLVEYYLKNYHGILDRMGVRQNLDLYDI				239
Sbjct	175	E+ES+L+KLHAWT+T+LKQ+L++ +I DKKLHK VEYYLKNYHGILD +G+R++LDLYDI EEESTLEKLHAWTSTYLKQQVLVSGTISDKKLHKQVEYYLKNYHGILDVLGIRRLSDLYDI				234
Query	240	SYRTAKAANRFSNLCSEDFLAFARQDFNICQAQHQKELQQLQRWYADCKLDTLKYGRDV				299
Sbjct	235	+Y+ KAA+RF +C +D LAF+RQDFN CQAQ+Q+ELQ LQRWY DC+LD L YGRDV DHYQILKAADRFRFTIC-KDLLAFSRQDFNNCQAQYQRELQQLQRWYEDCRLDKLYNGRDV				293
Query	300	RVANFLTSAIIGDPELSDVRIVFAQHIVLVTRIDFFDHRGSREESYKILELIKEWKEK				359
Sbjct	294	+R++ F++SAIIGDPELSD R+ FA++ VL T IDDDFDH GSREESY+ILEL+KEWKEK LRISYFVSSAIIGDPELSDARLAFAKYCVLTTCIDDDFDHAGSREESYRILELVKEWKEK				353
Query	360	PAAEYGSEEEVILFTAVYNTVNELAERAHVEHGRSVKDFLIKLVQILSIFKRELDTWSD				419
Sbjct	354	PA +YGS+EVE LFTAVYNTVNELAE A+VE GR VK LIKLWV++L+ FK+ELD+W+D PAEDYGSKEVEFLFTAVYNTVNELAEMAYVEQGRCVKSLIKLWVELLTSFKKELDSWTD				413
Query	420	DTALTLDLYLSASWVSIGCRICILMSMQFIGIKLSDEMMLSEECIDLCRHVSMVDRLLND				479
Sbjct	414	DTAL+LD+YLS+SWVSI RI IL S+QF+G+KLS+EML S+EC DLCRH S+V RLLND DTALSLDEYLLSSWVSITSRINILTSIQFLGLKLEEMLSSQECTDLCRHGSLVVRLND				473
Query	480	VQTFEKERKENTGNSVTLLLAANKDDSSFTEEEAIRIAKEMAECNRRQLMQIVYKTGTIF				539
Sbjct	474	+QTFEKER+ENT NSV++LL A K + + TEEE I KE+ E NRR+LMQ+VY+ GTIF MQTFEKERRENTKNSVSTLLEAPKHEGAITEEEVISKIKEIVEQNRRKLMQMVYQRGTIF				533
Query	540	PRQCKDMFLKVCRIGCYLYASGDEFTSPQQMMEDMKS LVYEPLTIHPLVANN				591
Sbjct	534	PR+CKD+FLK CR G YLY++GDEFTSP Q+MEDMK L YEPLT HPL ANN PRKCKDVLKSCRGGYIYLSNGDEFTSPVQIMEDMK-LCYEPLTFHPLEANN				584

RecName: Full=Class I diterpene synthase TPS6, chloroplastic; AltName: Full=Labd-13(16),14-diene-9-ol synthase; AltName: Full=Syn-isopimara-7,15-diene synthase; AltName: Full=Terpene synthase 6; Short=VacTPS6 [Vitex agnus-castus]
Sequence ID: **A0A2K9RFZ9.1** Length: 594 Number of Matches: 1
Range 1: 1 to 588

Score	Expect	Method	Identities	Positives	Gaps	Frame
795 bits(2053)	0.0()	Compositional matrix adjust.	376/593(63%)	478/593(80%)	6/593(1%)	
Query	1	MSLAFNPAATAFSGNGARSRENFFVKHVTVRGFFMITNKKSSFAVKCNL-TTDLMGKIA				59
Sbjct	1	MSL FN T FS R+RRE FPV+ F M T+KS+ VKC+L T+ DL+GKI MSLRFNLIVTFPSNYEIRNRRETFFVQ-----KFLMTTSKSAIKVKCSLKTSIDLVGKIR				55
Query	60	EKFKGEDSNFPAAAVQPAADMPSNLCIIDTLQRLGVDRYFRSEIDTILEDITYRLWQRKE				119
Sbjct	56	EK G+ N + D+PSNLC+ID+L+RLGV RYF+SEID +LE TYRLWQ++E EKINGKVDNSLEVPTINYLVDIPSNLCMIDSLERLGVARYFQSEIDGVLEKTYRLWQQRE				115
Query	120	RAIFSDTTIHAMAFRLLRVKGYEVSSEELAPYADQEHVDLQTIIEVATVIELYRAAQERTG				179
Sbjct	116	+ IF+D T AMAFR LRVKGYEVSS+ELAPYADQ HV+ Q +V TV+ELYRA+Q R KDIFADVTCRAMAFRLRVKGYEVSSDELAPYADQVHVNPQISDVTTVVELYRASQVRIY				175
Query	180	EDESSLKKLHAWTTTFLKQKLLTNSIPDKKLHKLVEYYLKNYHGILDRMGVRQNLDLYDI				239
Sbjct	176	E++S L+KLHAWT+TFLKQ+L + +I DKKLH+ VEYYLKNYHGI +++ VR++LDLYDI EEDSILEKLHAWTSTFLKQQLSKTSIDKKLHKEQVEYYLKNYHGIQNQVAVRRSLDLYDI				235
Query	240	SYRTAKAANRFSNLCSEDFLAFARQDFNICQAQHQKELQQLQRWYADCKLDTLKYGRDV				299
		+Y K A+RF + +EDF F RQDFN+CQAQHQKELQQLQRWY DC+LDTL YGR+V				

Sbjct	236	DHPILKVADRFRIIYNEDFFVFLRQDFNLCQAQHQKELQQQLQRWYEDCRLDTLNYGRNV	295
Query	300	VRVANFLTSAIIGDPELSDVRIVFAQHIVLVTRIDDDFDHGRSREESYKILELIKEWKEK V V+ FL +A GDPELS+ R+ FA+ IVLVTRIDDDFD GSREESYKILEL+KEWKEK	359
Sbjct	296	VHVSCFLAAANFGDPELSNARLAFAKTIVLVTRIDDDFDLAGSREESYKILELVKEWKEK	355
Query	360	PAAEYGSSEVEILFTAVYNTVNELAERAHVEHGRSVKDFLIKLVWQILSIFKRELDTSWD P +YGS+EVEILFTA+Y+TVNE AE A++E GR VK LIKLWV++L+ FK+ELD+W+D	419
Sbjct	356	PTEDYGSKEVEILFTALYDVTNEFAETIAYIEQGRCVKPLLIKLVWVELLTSFKKELDSWTD	415
Query	420	DTALTLDYYLSASWVSIGCRICILMSMQFIGIKLSDEMLLSEECIDLCRHVSMVDRLLND DTALTLD+YLS++W+SI CR+C L ++QF+G+KLS+EML S+EC DLCRH+S V+RLND	479
Sbjct	416	DTALTLDDEYLSASWMSIACRVCTLTALQFLGVKLSSEMLSSQECTDLCRHLSFVNRLND	475
Query	480	VQTFEKERKENTGNSVTLLLAANKDDSSFTEEEAIRIAKEMAECNRRQLMQIVYKTGTIF VQTFE+ERKENT N+V++LLAA++ + + TEEEA I +E+ E NRR+LM++VY+ ++F	539
Sbjct	476	VQTFEREKENTINAVSVLLAAHRHERAITEEEAISKIQEIVEQNRRKLMRMVYQRESVF	535
Query	540	PRQCKDMFLKVCRIGCYLYASGDEFTSPQOMMEDMKSILVYEPLTIHPLVANNV	592
Sbjct	536	PR+C+++FL+V ++G YLYASGDE T+PQQ+MEDMKSIV+EPL +HPL NNV PRKCRNVPLEVSKMGHYLYASGDELTPPQQLMEDMKSIVFEPLALHPLETNNV	588

RecName: Full=9,13-epoxylabda-14-ene synthase, chloroplastic; AltName: Full=Manoyl oxide synthase; AltName: Full=Miltiradiene synthase; Flags: Precursor [Marrubium vulgare]

Sequence ID: **A0A075FBG7.1** Length: 580 Number of Matches: 1
Range 1: 1 to 580

Score	Expect	Method	Identities	Positives	Gaps	Frame
766 bits(1978) 0.0() Compositional matrix adjust. 383/595(64%) 471/595(79%) 18/595(3%)						
Query	1	MSLAFNPAAATAFSGNGARSRENFPVKHVTVRGFFMITNKSSFAVKCNLT-TTDLMGKIA				59
Sbjct	1	MS+ FN FSG G + +E FP + + + KS+ KC+ +TD MGK+ MSITFNLKIAPFSGPGIQRSKETFPATEIQITA----STKSTMTTKCSFNASTDFMGKLR				56
Query	60	EKFKGEDSNFPAAAAVQPAADMPSNLCIIDTLQRLGVDRYFRSEIDTILEDTYRLW-QRK				118
Sbjct	57	EK G+ P + P D+ SNLC+IDTLQ LGVDRYF+SEI+T+LE TYRLW ++K EKVGGKADKPPVV--IHPV-DISSNLCMIDTLQSLGVDRYFQSEINTLLEHTYRLWKEKK				113
Query	119	ERAFISDTTIHAMAFRLLRVKGYESSEELAPYADQEHVDLQTIEVATVIELYRAAQERT				178
Sbjct	114	+ IF D + A+AFRLLR KGY+VSS++LAP+AD D VAT++EELYRA+Q R KNII FKDVSCCAIAFRLLREKGYQVSSDKLAPFADYRIRD----VATILELYRASQARL				168
Query	179	GEDESSLKKLHAWTTTFLKQKLLTNSIPDKKLHLKVEYYLKNYHGILDRMGVRQNLDLYD				238
Sbjct	169	EDE +L+KLH W++ LKQ LL SIPD KLHK VEY+LKNYHGILDR+ VR++LDLY+ YEDEHTLEKLDHWDSSNLLKQHLLNGSIPDHKLHKQVEYFLKNYHGILDRVAVRRSLDLYN				228
Query	239	ISYY-RTAKAANRFSNLCSEDFLAFARQDFNICQAQHQKELQQQLQRWYADCKLDTLKYGR				297
Sbjct	229	I+++ R A+ F EDFL ++ QDFNICQAQ Q+EL QLQRWYADC+LDTL YGR INHHHRIPDVADGFPK---EDFLEYSMQDFNICQAQQQEELHQLQRWYADCRRLDTLNYGR				285
Query	298	DVVRVANFLTSAIIGDPELSDVRIVFAQHIVLVTRIDDDFDHGRSREESYKILELIKEWK				357
Sbjct	286	DVVR+ANFLTSAI G+PE SD R+ FA+HI+LVTRIDDDFDH GSREESYKIL+L++EWK DVVRIANFLTSAIFGEPEFS DARLAFAKHII LVTRIDDDFDHGG SREESYKILDLVQEWK				345
Query	358	EKPAAEYGSSEVEILFTAVYNTVNELAERAHVEHGRSVKDFLIKLVWQILSIFKRELDTW				417
Sbjct	346	EKPA EYGS+EVEILFTAVYNTVN+LAE+AH+E GR VK LIKLWV+IL+ FK+ELD+W EKPAEEYGSKEVEILFTAVYNTVNDLAEKAHIEQGRVCVKPLLIKLVWEILTSFKKELDSW				405
Query	418	SDDTALTLDYYLSASWVSIGCRICILMSMQFIGIKLSDEMLLSEECIDLCRHVSMVDRLL				477
Sbjct	406	+++TALTLD+YLS+SWVSIGCRICIL S+Q++GIKLS+EML S+EC DLCRHVS VDRLL TEETALTLDDEYLSSSWVSIGCRICILNSLQYLGIKLSSEMLSSQECTDLCRHVSSVDRLL				465
Query	478	NDVQTFEKERKENTGNSVTLLLAANKDDSSFTEEEAIRIAKEMAECNRRQLMQIVYKTGT				537
Sbjct	466	NDVQTF+KER ENT NSV L LAA+K + + TEE+A+ KEMA+ +RR+LMQIVYK GT NDVQTFKKERLENTINSVGLQLAAHKGERAMTEEDAMSKIKEMADYHRRKLMQIVYKEGT				525
Query	538	IFPRQCKDMFLKVCRIGCYLYASGDEFTSPQOMMEDMKSILVYEPLTIHPLVANNV				592
Sbjct	526	+FPR+CKD+FL+VCRIG YLY+SGDEFTSPQQM EDMKSIVY+P+ IHPL A NV VFPRECKDVFLRVCRIGYYLYSSGDEFTSPQQMKEDMKSIVYQPVKIHPLEAINV				580

RecName: Full=Cis-abienol synthase, chloroplastic; Short=NtABS; Flags: Precursor [Nicotiana tabacum]
Sequence ID: **G3CCC1.1** Length: 792 Number of Matches: 1
Range 1: 284 to 788

Score	Expect	Method	Identities	Positives	Gaps	Frame
371 bits(952) 6e-118() Compositional matrix adjust. 190/508(37%) 309/508(60%) 10/508(1%)						
Query	83	SNLCIIDTLQRLGVDRYFRSEIDTILEDTYRLWQRKERAIFSDTTIHAMAFRLLRVKGYE	142			
Sbjct	284	SNL ++D LQ LGVDRYF++E+ +L++ YRLW K IFSD AMAFRLLR+ YE SNLFLVDALQNLGVDRYFKTEVKRVLDEIYRLWLEKNEEIFSDVAHCAMAFRLLRMNNYE	343			
Query	143	VSSEELAPYADQEHV---DLQTIEVATVIELYRAAQERTGEDESS-LKKLHAWTTTFLK	197			
Sbjct	344	VSSEEL + DQEH + + ++EL+RA+Q E + L K+ WT F++ VSSELEGFVDQEHFFTSSGKLMNHVAILELHRASQVAIHERKDHILDKISTWTRNFME	403			
Query	198	QKLLTNSIPDKKLHLKVEYYLKNYHGILDRMGVRQNLDLYDISYYRTAKAANRFSNLCSE	257			
Sbjct	404	QKLL IPD+ K +E+ ++ ++G DR+ R+ ++ Y + ++ KAA R S + + QKLLDKHIPDRS--KKEMEFAMRKFGYGTFRVETRRIIESYKMDSFKILKAAAYRSSGINNI	462			
Query	258	DFLAFARQDFNICQAQHQKELQQQLQRWYADCKLDTLKYGRDVVRVANFLTSAIIGDPELS	317			
Sbjct	463	D L F+ DFN+CQ +H++ELQQ++RW+ DCKL+ + + + + F+ +AI+ +PE + DLLKFESEHDFNLCTRHKELQMKRWFTDCKLEQVGLSQQYLYTSYFIIAAILFEPEYA	522			
Query	318	DVRIVFAQHIVLVTRIDDDFDHGRSREESYKILELIKEWKEKPAAEYGSSEVEILFTAVY	377			
Sbjct	523	D R+ +A++ +++T +DDFFD +EE I+EL++ W+ + SE V I F A+Y DARLAYAKYAIITITAVDDFFDCFICKEELQNIIELVVERWEGYSTVGFRSERVRIFFLALY	582			
Query	378	NTVNELAERAHVEHGRSVKDFLIKLVWQILSIFKRELDTWS-DDTALTLDYYLSASWVSI	436			
Sbjct	583	V E+A +A + GR VKD LI LW+ +L ELD W T ++++YLS + V+I KMVEEIIAAKAETKQGRVCVKDHLINLWIDMLKCMLVELDLWKIKSTTPSIEEYLSVACVTI	642			
Query	437	GCRICILMSMQFIGIKLSDEMLLSEECIDLCRHVSMVDRLLNDVQTFEKERKENTGNSVT	496			
Sbjct	643	G +L S+ +G KLS +++ S E LC + V RL+ND+ ++++E+ E++ N V+ GVPCFVLTSLYLLGPKLSKDVIESSEVSALCNCTAAVARLINDHSYKREQAESSTNMVS	702			
Query	497	LLLAANKDDSSFTEEEAIRIAKEMAECNRRQLMQIVYKTG-TIFPRQCKDMFLKVCRIGC	555			
Sbjct	703	+L+ ++ + +EEEEAIR KEM E RR+L+ +V + + P+ CKD+F ILITQSQ--GTISEEEAIRQIKEMMESKRRELLGMVLQNKESQLPQVCKDLFWTTINAAY	760			

Query 556 YLYASGDEFTSPQQMEDMKSLVYEPLT 583
++ GD + P++ + ++Y+PL
Sbjct 761 SIHTHGDGYRFPPEEFKNHINDVIYKPLN 788

RecName: Full=Santalene and bergamotene synthase, chloroplastic; AltName: Full=(+)-alpha-santalene synthase ((2Z,6Z)-farnesyl diphosphate cyclizing); AltName: Full=(+)-endo-beta-bergamotene synthase ((2Z,6Z)-farnesyl diphosphate cyclizing); AltName: Full=(-)-endo-alpha-bergamotene synthase ((2Z,6Z)-farnesyl diphosphate cyclizing); Flags: Precursor [Solanum habrochaites]

Sequence ID: **B8XA41.1** Length: 777 Number of Matches: 1
Range 1: 275 to 776

Score	Expect	Method	Identities	Positives	Gaps	Frame
351 bits(900) 2e-110() Compositional matrix adjust. 189/508(37%) 310/508(61%) 13/508(2%)						
Query 83	SNLCIIDTLQRLGVDRYFRSEIDTILED	TYRLWQRKERAIFSDTTIHAMAFRLLRVKGYE	142			
Sbjct 275	S LC++DTLQ LGV R+F+SEI L++ YRLWQ+K IFS+ T AMAFRLLR+ Y+ SLLCLVDTLQNLGVHRHFKSEIKKALDEIYRLWQQKNEQIFSNVTHCAMAFRLLRMSYD		334			
Query 143	VSSEELAPYADQEH---VDLQTIEVATVIELYRAAQERTG-EDESSLKKLHAWTTTFLKQ	VSS+ELA + D+EH + + ++EL++A+Q E + L K++ WT TF++Q	198			
Sbjct 335	VSSDELAEFVDEEHFFAISGKYTSHVEILELHKASQLAIDHEKDDILDKINNWTRTFMEQ		394			
Query 199	KLLTNSIPDKLHKLVEYYLKNYHGILDRMGVVRQNLDLYDISYYRTAKAANRFSNLCSED	KLL N D+ K VE L+ ++ I D R+ + Y+ + ++ KAA R N+ ++D	258			
Sbjct 395	KLLNNGFIDRMSKEVELALRKFYTISDLAENRRCIKSYEENNFKILKAAYRSPNIYNKD		454			
Query 259	FLAFARQDFNICQAQHKELOQLQRWYADCKLDTLKYGRDVVRVANFLTSAIIGDPELSD	F+ ++F +CQAQHQ+ELQQ +RW+ D +LD L + ++ +PELSD	318			
Sbjct 455	LFIFISIRNFELCQAQHQEELQQFKRWFEYRLDQLGIAERYIHDTYLCAVIVVPEPELSD		514			
Query 319	VRIVFAQHIVLVTRIDDDFFDHRSREESYKILELIKEWKEKPAAEYGSSEEVEILFTAVYN	R+++A++++L+T +DD FD S +E I+EL++ W + + Y SE+V++ F+ +Y	378			
Sbjct 515	ARLLYAKVLLLTIVDDQFDSFASTDECLNIIELVERWDDYASVGKSEKVKVFFSTLYK		574			
Query 379	TVNELAERAAHVEHGRSVKDFLIKLWVQILSIFKRELDTW-SDDTALTDDYLSASVWSIG	++ EL A ++ GRSVK+ L+ LW++++ + E W S T ++++YL + ++G	437			
Sbjct 575	SIEELVTIAEIKQGRSVKNHLLNLWLELVKMLMERVEWFGSGKTIPSEIEYLYVTSITFG		634			
Query 438	CRICILMSMQFIGIKLSDEMLLSEECIDLCRHVSMVDRLRLNDVQTFEKERKENTGNSVTL	R+ L + F+GIK+S+++L S+E LC V R+LND+Q +KE+KE++ VTL	497			
Sbjct 635	ARLIPLTTQYFLGIKISEDILESDEIYGLCNCTGRVLRILNDLQDSKKEQKEDSVTIIVTL		694			
Query 498	LLAANKDDSSFTTEEEAIRIAKEMAECNRRQLMQIVY--KTGTIFPRQCKDMFLKVCIRIGC	L+ S +EEEEAI KE+ E NRR+L+++V K G+ P+ CKD+F +	555			
Sbjct 695	LM-----KSMSEEEAIMKIKEILEMNRRELLKMVLVQKKSQLPQICKDFWRTSNWAD		748			
Query 556	YLYASGDEFTSPQQMEDMKSLVYEPLT 583	++Y D + ++M + + Y+PL				
Sbjct 749	FIYLTQDGYRIAEEEMKNHIDEVIFYKPLN 776					

RecName: Full=Beta-phellandrene synthase (neryl-diphosphate-cyclizing), chloroplastic; Flags: Precursor [Solanum lycopersicum]
Sequence ID: **C1K5M3.1** Length: 778 Number of Matches: 1
Range 1: 276 to 777

Score	Expect	Method	Identities	Positives	Gaps	Frame
346 bits(888) 1e-108() Compositional matrix adjust. 188/508(37%) 310/508(61%) 13/508(2%)						
Query 83	SNLCIIDTLQRLGVDRYFRSEIDTILED	TYRLWQRKERAIFSDTTIHAMAFRLLRVKGYE	142			
Sbjct 276	S LC++DTLQ LGV R+F+SEI L++ YRLWQ+K IFS+ T AMAFRLLR+ Y+ SLLCLVDTLQNLGVHRHFKSEIKKALDEIYRLWQQKNEQIFSNVTHCAMAFRLLRMSYD		335			
Query 143	VSSEELAPYADQEH---VDLQTIEVATVIELYRAAQERTG-EDESSLKKLHAWTTTFLKQ	VSS+ELA + D+EH + + ++EL++A+Q E + L K++ WT F++Q	198			
Sbjct 336	VSSDELAEFVDEEHFFATNGKYKSHVEILELHKASQLAIDHEKDDILDKINNWTRAFMEQ		395			
Query 199	KLLTNSIPDKLHKLVEYYLKNYHGILDRMGVVRQNLDLYDISYYRTAKAANRFSNLCSED	KLL N D+ K VE L+ ++ R+ + Y+ + ++ KAA R N+ ++D	258			
Sbjct 396	KLLNNGFIDRMSKEVELALRKFYTTSHLAENRRYIKSYEENNFKILKAAYRSPNINNKD		455			
Query 259	FLAFARQDFNICQAQHKELOQLQRWYADCKLDTLKYGRDVVRVANFLTSAIIGDPELSD	LAF+ DF +CQAQH++ELQQL+RW+ D +LD L + + +I +PELSD	318			
Sbjct 456	LLAFSIIHDFELCQAQHREELQQLKRWFEYRLDQLGIAERYIHASYLFGVTVIPEPELSD		515			
Query 319	VRIVFAQHIVLVTRIDDDFFDHRSREESYKILELIKEWKEKPAAEYGSSEEVEILFTAVYN	R+++A++++L+T +DD F+ S++E + I+EL++ W + + Y SE+V++ F+ Y	378			
Sbjct 516	ARLMYAKVVMLLTIVDDHFESFASKDECFNIIELVERWDDYASVGKSEKVKVFFSVFYK		575			
Query 379	TVNELAERAAHVEHGRSVKDFLIKLWVQILSIFKRELDTW-SDDTALTDDYLSASVWSIG	++ ELA A ++ GRSVK+ LI LW++++ + E W S T ++++YL + ++	437			
Sbjct 576	SIEELATIAEIKQGRSVKNHLLNLWLELMKMLMERVEWCSGKTIPSEIEYLYVTSITFC		635			
Query 438	CRICILMSMQFIGIKLSDEMLLSEECIDLCRHVSMVDRLRLNDVQTFEKERKENTGNSVTL	++ L + F+GIK+S ++L S+E L V R+LND+Q ++E+KE + N VTL	497			
Sbjct 636	AKLIPLSTQYFLGIKISKDLLESDEICGLWNCSGRVMRILNDLQDSKREQKEVSINLVTL		695			
Query 498	LLAANKDDSSFTTEEEAIRIAKEMAECNRRQLMQIVY--KTGTIFPRQCKDMFLKVCIRIGC	L+ S +EEEEAI KE+ E NRR+L+++V K G+ P+ CKD+F +	555			
Sbjct 696	LM-----KSMSEEEAIMKIKEILEMNRRELLKMVLVQKKSQLPQLCKDFWRTSKWAH		749			
Query 556	YLYASGDEFTSPQQMEDMKSLVYEPLT 583	+ Y+ D + ++M + + Y+PL				
Sbjct 750	FTYSQTDGYRIAEEEMKNHIDEVIFYKPLN 777					

RecName: Full=Ent-kaurene synthase-like 2; Short=OsKSL2 [Oryza sativa Japonica Group]
Sequence ID: **Q0JA81.2** Length: 937 Number of Matches: 1
Range 1: 198 to 698

Score	Expect	Method	Identities	Positives	Gaps	Frame
316 bits(810) 8e-96() Compositional matrix adjust. 172/504(34%) 299/504(59%) 8/504(1%)						
Query 69	FPAAAAVQPAADMPNSNLCIIDTLQRLGVDRYFRSEIDTILED	TYRLWQRKERAIFSDTTI	128			
Sbjct 198	F +A A++ S L ++D L+++G+ R+F EI +IL+ TY W++++ I D FGSEAVPAAYPANIQSOLYXVVLVEKMGISRHFVGEIKSILBMTYSCWKQRDEEIVLDMQT		257			

Query	129	HAMAFRLLRVKGYEVSSEELAPYADQE--HVDLQTI--EVATVIELYRAAQERTGEDESS	184
Sbjct	258	MAFR+LR+ GY+VSS+EL+ +++ H LQ + +++EL++A++ E E	317
Query	185	LKKLHAWTTTFLKQKLLTNSIPDKKLHLKLV EYYL--NYHGILDRMGVRQNL DLYDISYR	243
Sbjct	318	L + +WT LK++LL++++ L + V EY L+ ++ ILDR+ ++N++ +DI+ +	377
Query	244	TAKAANRFSNLCSEDFLAFARQDFNICQAQHQKELQQLQRWYADCKLDTLKYGRDVVRVA	303
Sbjct	378	+ A +E+ +A +DF+ Q Q+ELQQL W + +LD L++ R +	436
Query	304	NFLTSAIIGDPELSDVRIVFAQHIVLVTRIDDDFDHGRSREESYKILELIKWEKPAAE	363
Sbjct	437	F +A I PELSDVRI++A++ VL T +DDFFD GS+EE ++ L+++W + E	496
Query	364	YGSEEVEILFTA VYNTVNELAERAHVEHGRSVKDFLIKLVQILSIFKRELD TWSDDTAL	423
Sbjct	497	Y SE+VEI+F+A+Y + N+L A V GR V L+++W ++L E++	556
Query	424	Y YSEQVEIVFSAIYTSTNQ LGSMA SVVQGRDVTKHLVEIWQELLRSMTEVEWRQSRYP	561
Query	424	TLDYLSASWVSIGCRICILMSMQFIGIKLSDEMILLSEECIDLCRHVSMVDRLLNDVQTF	483
Sbjct	557	T ++Y+ + V+ +L ++ +G K+ D ++ S+EC +L R +S RLLNDVQ++	616
Query	484	TAEYEMENAVVTFALGPVVLPALYLVGPKMPDSVIRSQECSELFRLMSKCGRLNDVQSY	543
Sbjct	617	EREGSQGKLN SVSL--ALHSGG SVSMEEAVKQIRPTEKCRRELLKLVVSRGGAVPRPC	674
Query	544	KDMFLKVCIRIGCYLYASGDEFTSP	567
Sbjct	675	+++F +C++ + Y+ GD F+SP	698
		RELFWSMCKVCHFFYSGGDGFSSP	

RecName: Full=Ent-kaur-16-ene synthase, chloroplastic; AltName: Full=Ent-kaurene synthase; AltName: Full=Ent-kaurene synthase B; Short=KSB; Flags: Precursor [Cucurbita maxima]

Sequence ID: **Q39548.1** Length: 789 Number of Matches: 1
Range 1: 239 to 787

Score	Expect	Method	Identities	Positives	Gaps	Frame
309 bits(791) 3e-94() Compositional matrix adjust. 186/559(33%) 315/559(56%) 18/559(3%)						
Query	38	TNKSFFAVKCNLT	TTDLMGKIAEKFKGEDSNFPAAAAVQPAADMPSNLCI	IDTLQRLGVD		97
Sbjct	239	T	++F ++ D + + +KF G + + P D+ + L ++D+LQ+ G+			291
Query	98	TTAAAFMRNRDDGCGFDYLRSL	LQKFDG-----SVPTIYPL-DIYARLHMVDSLQKFGIA			154
Sbjct	292	RYFRSEIDTILED	TYRLWQRKERAIFSDTTIHAMAFRLLRVKGYEVSSEELAPYADQ---			351
Query	155	RHFKEEIRSVLDETYRCWMQGEENIFLDASTCAMA	FRMLRVEGYDVSSDQLTQFSEDIFP			214
Sbjct	352		+ + +ELY+A+Q T DES L+ +++WT+ FLK L ++S+ + +V			411
Query	215	EYYLKN-----YHGILDRMGVRQNL	DLYDISYYRTAKAANRFSNLCSEDFLAFARQDFNI			269
Sbjct	412		+ N Y+ L+R+ ++ ++ Y R +K+ N +DFL A +DEN			471
Query	270	KQEA	VNALEFPYNATLERLISKRAMESYSGDIVRISKSPYACLNFGHQDFLELAVEDFNT			531
Sbjct	472	CQAQHQKELQQLQRWYADCKLDTLKYGRDVVRVANFLTSAIIGDPELSDVRIVFAQHIVL				329
Query	330	Q H KEL++LQRW + KLD LK+ R + F +A + DP EL D RI +AQ+ VL				531
Sbjct	472	LQRH LKLEELQRWVENKLDL KFFRLHLGYCYFAAAATLTDP ELHDARIAWAQNGVL				389
Query	330	VTRIDDDFDHGRSREESYKILELIKWEKPAAEYGS	EEVEILFTA VYNTVNELAERAHV			591
Sbjct	532	T +DDF+D GS EE ++EL+++W Y S++VEI+F A+++TV E+ RA V				449
Query	390	TTVVDDFYDGGGSEELDNLI	ELVEKWDPDGEVGYCSKDVEIVFLALHSTVCEIGRRALV			651
Sbjct	592	EHGRSVKDFLIKLVQILSIFKRELD TWSDDTALTLDYLSASWVSIGCRICILMSMQFI				509
Query	450	GRSV +I Wt +L + ++E + ++ ++ +Y+ + VS IL + F+				709
Sbjct	652	WQGRSVMRNRV DGLWALLKVMRKEAWSTNKVVPSMGEYMQAHVSFALGP I I L PMLFFV				569
Query	510	GIKLSDEMILLSEECIDLCRHVSMVDRLLNDVQTFE	K E R K E N T G N S V T L L A A N K D S S F T			768
Sbjct	652	GPKLSEEMIGSCEYQKLYKLMSTAGRLKNDIRS YDRECKEGKLNILSLWMIDGG--GNVT				
Query	510	EEEAIRIAKEMAECNRQLMQIVYKTGTIFPRQCKDMFLKVCIRIGCYLYASGDEFTSPQQ				569
Sbjct	710	+EEAI K E R+L+ +V + T PR CKD+F K+ I Y D +TS +				768
Query	570	KEEAIEAIKGD FERAIRELLGLVLQENTTIPRACKDLFWKLMSIVNLFYMEDDGYTS-NR				
Query	570	MMEDMKSLVYEPLTIHPLV	588			
Sbjct	769	+M +K++ +P+ + L+ LMNTVKAMFEQPMOLDALL	787			

RecName: Full=Ent-kaur-16-ene synthase, chloroplastic; AltName: Full=Ent-kaurene synthase; Short=AtKS; AltName: Full=Ent-kaurene synthase B; Short=KSB; AltName: Full=Protein GA REQUIRING 2; Flags: Precursor [Arabidopsis thaliana]

Sequence ID: **Q9SAK2.1** Length: 785 Number of Matches: 1
Range 1: 259 to 780

Score	Expect	Method	Identities	Positives	Gaps	Frame
305 bits(781) 8e-93() Compositional matrix adjust. 186/528(35%) 299/528(56%) 17/528(3%)						
Query	69	FPA AAAVQPAADMPSNLCIIDTLQRLGVDRYFRSEIDTILED TYRLWQRKERAIFSDTTI	128			
Sbjct	259	F + AA D + L II TL+ LG+DR F++EI +IL++TYR W R + I D	318			
Query	129	FEAAVPSVYPFDQYARLSIIIVTLES LGIDRDFKTEIKSILDETYRYWLRGDDEEICLDLAT	183			
Sbjct	319	HAMAFRLLRVKGYEVSSEELAPYADQE HVDLQTI E----VATVIELYRAAQERTGEDES	375			
Query	184	A+AFRLL GY+VS + L P+A++ T+E +V+EL++AAQ + ES	238			
Sbjct	376	CALAFRLLLAHGYDVSYDPLKPF AEESGFS-DTLEGYVKNTFSVLELFKAAQ--SYPHES	435			
Query	239	SLKKLHAWTTTFLKQKL---LTNSIPDKKLHLKLV EYYL--KNYHGILDRMGVRQNL DLYD	298			
Sbjct	436	+LKK WT L+ +L + S+ DK L K VE L +Y + R+ L+	495			
Query	299	ALKKQCCWTKQYLEMELSSWKT SVRD KYLKKEVEDALAFPSYASLERSDHRRKILNGSA	358			
Sbjct	496	ISYYRTAKAANRFSNLCSEDFLAFARQDFNICQAQHQKELQQLQRWYADCKLDTLKYGRD	555			
Query	239	+ R K + R N+C+ D L A DEN CQ+ H++E+++L RW + +L LK+ R				
Sbjct	436	VENTRVTKTSYRLHNICTSDILKLAVDDFNFCQSIHREEMERLDRWIVENRLQELKFARQ				
Query	299	VVRVANFLTSAIIGDPELSDVRIVFAQHIVLVTRIDDDFDHGRSREESYKILELIKWEK	358			
Sbjct	496	+ F +A + PELSD RI +A+ VL T +DDFFD GS+EE ++ L+++W	555			
		KLAYCYFSGAATLFSPELSDARISWAKGGVLT TVVDDFFDVGGSKEELENLHLVEKWDL				

Query	359	KPAAEYGS EEVILFTAVYNTV NELAERAHVEHGRSVKDFLIKLVQILSIFKRELDTWS	418
		BY SE VEI+F+ + +T+ E ++A GR+V ++K+W+ +L RE + S	
Sbjct	556	NGVPEYSESHVEIIFSVLRDTILETGDKAFTYQGRNVTHHIVKIWL DLLKSM LREA EWSS	615
Query	419	DDTALTLDYLSASWVSIGCRICILMSMQFIGIKLSDEMILLSEECIDLCRHVSMVDRLLN	478
		D + +L+DY+ +++S +L + IG L ++ + S + L + VS + RLLN	
Sbjct	616	DKSTPSLEDYMENAYISFALGP IVL PATY LIGPPLPEKTVDSHQYNQLYKLVSTMGRLLN	675
Query	479	DVQTFEKERKENTGNSVTLLLAANKDDSSFTEEEAIRIAKEMAECNRRQLMQIVY-KTGT	537
		D+Q F++E E N+V+L + +D+ S +E I K +AE R +L ++V + G+	
Sbjct	676	DIQGFKRESAEGK LNAVSLHMKHERDNRS--KEV IESMKGLAERKREELHKLVL EEKGS	733
Query	538	IFPRQCKDMFLKVC RIGCYLYASGDEFTSPQQMMEDMKS L VYEPLTIH	585
		+ PR+CK+ FLK+ ++ Y D FTS +M +KS++YEP+++	
Sbjct	734	VVPRECKEAF LKMSKVLNLFYRKDDGFTS-NDLMSLVKSVIYEPVSLQ	780

Taxonomy

Reports

Lineage

o	Organism	Blast Name	Score	Number of Hits	Description
	Mesangiospermae	flowering plants		<u>10</u>	
	.Pentapetalae	eudicots		<u>9</u>	
	.Lamiids	eudicots		<u>7</u>	
	...Lamiaceae	eudicots		<u>4</u>	
	Salvia miltiorrhiza	eudicots	1233	<u>1</u>	Salvia miltiorrhiza hits
	Vitex agnus-castus	eudicots	826	<u>2</u>	Vitex agnus-castus hits
	Marrubium vulgare	eudicots	766	<u>1</u>	Marrubium vulgare hits
	...Nicotiana tabacum	eudicots	371	<u>1</u>	Nicotiana tabacum hits
	...Solanum habrochaites	eudicots	351	<u>1</u>	Solanum habrochaites hits
	...Solanum lycopersicum	eudicots	346	<u>1</u>	Solanum lycopersicum hits
	..Cucurbita maxima	eudicots	309	<u>1</u>	Cucurbita maxima hits
	..Arabidopsis thaliana	eudicots	305	<u>1</u>	Arabidopsis thaliana hits
	.Oryza sativa Japonica Group	monocots	316	<u>1</u>	Oryza sativa Japonica Group hits

Organism

o	Description	Score	E value	Accession
	Salvia miltiorrhiza [eudicots]			
	RecName: Full=Miltiradiene synthase KSL1, chloroplastic; AltName: Full=Kaurene synthase-like 1; Short=SmKSL; Short=SmKSL1; Flags: Precursor [Salvia miltiorrhiza]	1233	0.0	C8XPS0
	Vitex agnus-castus [eudicots]			
	RecName: Full=Class I diterpene synthase 2, chloroplastic; Short=VacTPS2; AltName: Full=(13S)-vitexifolin A synthase; AltName: Full=9,13-epoxylabda-14-ene synthase; AltName: Full=Viteagnusin D synthase; Flags: Precursor [Vitex agnus-castus]	826	0.0	A0A2K9RFZ2
	RecName: Full=Class I diterpene synthase TPS6, chloroplastic; AltName: Full=Labd-13(16),14-diene-9-ol synthase; AltName: Full=Syn-isopimara-7,15-diene synthase; AltName: Full=Terpene synthase 6; Short=VacTPS6 [Vitex agnus-castus]	795	0.0	A0A2K9RFZ9
	Marrubium vulgare (white horehound) [eudicots]			
	RecName: Full=9,13-epoxylabda-14-ene synthase, chloroplastic; AltName: Full=Manoyl oxide synthase; AltName: Full=Miltiradiene synthase; Flags: Precursor [Marrubium vulgare]	766	0.0	A0A075FBG7
	Nicotiana tabacum (common tobacco) [eudicots]			
	RecName: Full=Cis-abienol synthase, chloroplastic; Short=NtABS; Flags: Precursor [Nicotiana tabacum]	371	6e-118	G3CCC1
	Solanum habrochaites [eudicots]			
	RecName: Full=Santalene and bergamotene synthase, chloroplastic; AltName: Full=(+)-alpha-santalene synthase ((2Z,6Z)-farnesyl diphosphate cyclizing); AltName: Full=(+)-endo-beta-bergamotene synthase ((2Z,6Z)-farnesyl diphosphate cyclizing); AltName: Full=(-)-endo-alpha-bergamotene synthase ((2Z,6Z)-farnesyl diphosphate cyclizing); Flags: Precursor [Solanum habrochaites]	351	2e-110	B8XA41
	Solanum lycopersicum (tomato) [eudicots]			
	RecName: Full=Beta-phellandrene synthase (neryl-diphosphate-cyclizing), chloroplastic; Flags: Precursor [Solanum lycopersicum]	346	1e-108	C1K5M3
	Oryza sativa Japonica Group (Japanese rice) [monocots]			
	RecName: Full=Ent-kaurene synthase-like 2; Short=OsKSL2 [Oryza sativa Japonica Group]	316	8e-96	Q0JA81
	Cucurbita maxima (winter squash) [eudicots]			
	RecName: Full=Ent-kaur-16-ene synthase, chloroplastic; AltName: Full=Ent-kaurene synthase; AltName: Full=Ent-kaurene synthase B; Short=KSB; Flags: Precursor [Cucurbita maxima]	309	3e-94	Q39548
	Arabidopsis thaliana (thale cress) [eudicots]			
	RecName: Full=Ent-kaur-16-ene synthase, chloroplastic; AltName: Full=Ent-kaurene synthase; Short=AtKS; AltName: Full=Ent-kaurene synthase B; Short=KSB; AltName: Full=Protein GA REQUIRING 2; Flags: Precursor [Arabidopsis thaliana]	305	8e-93	Q9SAK2

Taxonomy