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Supplementary

In-silico approaches in comparative genomics, structure prediction and functional characterization of secondary metabolite proteins of Mentha sp

Supplementary Data 1: Contigs and corresponding proteins

Contigs	Organism name	Description(Protein name)	Sequence	Identity
Contig1	*Ocimum basilicum*	gamma-cadinene synthase	>gi|55740199|gb|AAV63787.1| gamma-cadinene synthase [Ocimum basilicum] MDVSILRDVRPPVTSYAPNIWADTFSNISLDEEVQKKYAETIEALKQVVRGML MAAATPIKQMIFIDTLE RLGLAYHFETEIEHKLQKIYDDNVCGDDCDLFTTALRFRLLRQHRHHVSCDVF DKFLYEEGKFKGDAEGL LSLYEASHVRFHNEKILEEAERFTRQELSCWIKLQSPLKDKVKRALERPLHREV PILYARHFISIYEKDE SMDEHLLKLAKFNFNFLQNLYKKELYDLSRWWNKFDLKTKLPYIRDRLAEAY LWGVGYHFEPQYSYVRKG VVLSIKIIGILDDTYDNYATVNEAQLFTEILDRWSMDEIDRLPDYMKIVLHFVM SAYEEYERDAKIVYGK KFASPYFKETIQQLARGYNQELKWVMEKQMPPFKDYLKNSEITSCIYIMFASII PGLKSFTQEAIDWIKN EPNFAVKAGLIGRYWDDIGSHKRESKGGEMLTVMDCYMKQYSVSIQETISEFA KAVEDSWKEVNEGWVYT ISMSKEITVQFLNYSRMCDASYNRNNGDGYTDPSFAKSNITALFVDPIII	64%
Contig1	*Mentha x piperita*	(E)-beta-farnesene synthase	>gi|54969668|emb|CAH10289.1| (E)-beta-farnesene synthase [Mentha x piperita] MATNGVVISCLREVRPPMTKHAPSMWTDTFSNFSLDDKEQQKCSETIEALKQE ARGMLMAATTPLQQMTLIDTLERLGLSFHFETEIEYKIELINAAEDDGFDLFAT ALRFRLLRQHQRHVSCDVFDKFIDKDGKFEESLSNNVEGLLSLYEAAHVGFRE ERILQEAVNFTRHHLEGAELDQSPLLIREKVKRALEHPLHRDFPIVYARLFISIY EKDDSRDELLLKLSKVNFKFMQNLYKEELSQLSRWWNTWNLKSKLPYARDR VVEAYVWGVGYHYEPQYSYVRMGLAKGVLICGIMDDTYDNYATLNEAQLFT QVLDKWDRDEAERLPEYMKIVYRFILSIYENYERDAAKLGKSFAAPYFKETVK QLARAFNEEQKWVMERQLPSFQDYVKNSEKTSCIYTMFASIIPGLKSVTQETID WIKSEPTLATSTAMIGRYWNDTSSQLRESKGGEMLTALDFHMKEYGITKEEA ASKFEGLVEETWKDINKEFIATTNYNVGREIAITFLNYARICEASYSKTDGDAY LDPNVAKANVVALFVDAIVF	99%
Contig2	*Solanum tuberosum*	S-adenosyl-L-homocysteine hydrolase-like	>gi|81075407|gb|ABB55380.1| S-adenosyl-L-homocysteine hydrolase-like [Solanum tuberosum] MALLVEKTTSGREYKVKDMSQADFGRLEIELAEVEMPGLMASRTEFGPSQPF KGAKITGSLHMTIQTAVLIETLTALGAEVRWCSCNIFSTQDHAAAAIARDSAA VFAWKGETLQEYWWCTERALDWGPGGGPDLIVDDGGDATLLIHEGVKAEEE FAKNGTIPDPTSTDNVEFQLVLTIIKESLKTDPLRYTKMKERLVGVSEETTTGV KRLYQMQANGTLLFPAINVNDSVTKSKFDNLYGCRHSLPDGLMRATDVMIAG KVALVAGYGDVGKGCAAAMKQAGARVIVTEIDPICALQATMEGLQVLPLED VVSEVDIFVTTTGNKDIIMVDHMRKMKNNAIVCNIGHFDNEIDMHGLETFPGV KRITISSNDRWVFPDTNSGIIVLAEGRLMNLGCATGHPSFVMSCSFTNQVIAQL ELWNERSSGKYEKKVYVLPKHLDEKVAALHLGKLGAKLTKLTKDQADYISVP VEGPYKPAHYRY	94%
Contig2	*Phaeodactylum tricornutum* CCAP 1055/1	adenosylhomocysteinase	>gi|219112013|ref|XP_002177758.1| adenosylhomocysteinase [Phaeodactylum tricornutum CCAP 1055/1] MSTGDYKVADISLADYGRKDIELAEVEMPGLMACREEYGPAKPFGGARISGSL HMTIQTAVLIETLKDLGGDIRWCSCNIFSTQDHAAAAIARDESAAVFAWKGES LEEYWECTLNAITWPEDDGKGCGPDLIVDDGGDMTLLIHEGKKAEDQFLKDG TVPDPSSTDNAEFKIVLTIIKRLLEGGETDKWNKIASRCKGVSEETTTGVHRLY TMEKTGTLLFTAINVNDSVTKSKFDNLYGCKHSLPDGLMRATDVMLAGKKA VIAGYGDVGKGCAAAMRACGCVVYVTEIDPICALQACMEGYQVVTLEDVVD TADIFITTTGNKGILMCETMSKMKNNAIVGNIGHFDNEIDMDGLMKAAKRINI KPQVDKFVFESGNGIIVLAEGRLLNLGCATGHPSFVMSCSFTNQVLAQLELWN EKDSGKYAHGKVYVLPKTLDEKVALLHLGSLGARLTVLSDEQSEYIGIPVNGP FKPDTYRY	75%
Contig2	*Zea mays*	adenosylhomocysteinase	>gi|226491362|ref|NP_001148534.1| adenosylhomocysteinase [Zea mays] MALSVEKTSSGREYKVKDLSQADFGRLEIELAEVEMPGLMACRAEFGPSKPFA GARISGSLHMTIQTAVLIETLTALGAEVRWCSCNIFSTQDHAAAAIARDSAAVF AWKGETLEEYWWCTERCLDWGEAGGPDLIVDDGGDATLLIHEGVKAEEEYE KTGKIPDPESTDNAEFKIVLTIIRDGLKADPKKYRKMKERLVGVSEETTTGVKR LYQMQETGALLFPAINVNDSVTKSKFDNLYGCRHSLPDGLMRATDVMIAGKV AVVCGYGDVGKGCAAALKQAGARVIVTEIDPICALQALMEGLQVLPLEDVVS EADIFVTTTGNKDIIMVDHMRKMKNNAIVCNIGHFDNEIDMLGLETYPGVKRI TIKPQTDRWVFPETNTGIIVLAEGRLMNLGCATGHPSFVMSCSFTNQVIAQLEL WKEKSSGKYEKKVYVLPKHLDEKVAALHLGKLGAKLTKLTKSQADYISVPIE GPYKPAHYRY	89%
Contig2	*Chlamydomonas reinhardtii*	S-Adenosyl homocysteine hydrolase	>gi|159470383|ref|XP_001693339.1| S-Adenosyl homocysteine hydrolase [Chlamydomonas reinhardtii] MALSVDHVNGREYKVKDIAEADFGRLEIDLAEAEMPGLMACRSEFGPAQPFK GAKITGSLHMTIQTAVLIETLTALGAEVRWCSCNIFSTQDHAAAAIARDSAAVF AWKGETLEEYWWCTEQALTWAGCDGPDLLVDDGGDATLLIHEGLKAEEQY AKDGTLPNPDSTDNAEFKIVLGLIRDSIQKDATKWTRMSKKVMGVSEETTTGV KRLYEMQANGSLLFPAINVNDSVTKSKFDNVYGCRHSLPDGIMRATDVMIAG KTAFIAGYGDVGKGCASAMKAAGARTIVSEIDPICALQAAMEGYQVQPLEDC LETADIFITTTGNKDIIMAEHMAKMKNNAIVGNIGHFDNEVDMAGLYAWPGIK RQNIKPQVDRFIFPDGHGVIVLAEGRLLNLGCATGHPSFVMSCSFTNQVIAQLE LWNERSTGRYEKKVYVLPKHLDEKVAALHLPKLGVKLTKLSADQAAYINVP VDGPYKPAHYRY	86%

Contig3	*Nicotiana tabacum*	S-adenosylmethionine synthase	>gi|33340517|gb|AAQ14854.1|AF321140_1 S-adenosylmethionine synthase [Nicotiana tabacum] METFLFTSESVNEGHPDKLCDQVSDAILDACLEQDPESKVACETCTKTNMVM VFGEITTKAKVDYEKIVRDTCRGIGFTSADVGLDADHCKVLVNIEQQSPDIAQ GVHGHLTKKPEEIGAGDQGHMFGYATDETPELMPLTHVLATQLGAKLTEVRK NKTCPWLRPDGKTQVTVEYKNDNGAMVPIRVHTVLISTQHDEGVTNEQIAQD LKEHVIKPVIPAKYLDENTIFHLNPSGRFVIGGPHGDAGLTGRKIIIDTYGGWGA HGGGAFSGKDPTKVDRSGAYIVRQAAKSVVAAGLARRCIVQVSYAIGVAEPL SVFVDTYKTGTIPDKDILALIKENFDFRPGMIAINLDLLRGGNFRYQKTAAYGH FGRDEADFTWETVKALKPKA	91%
Contig3	*Panax ginseng*	S-adenosylmethionine synthetase	>gi|189345252|gb|ACD92982.1| S-adenosylmethionine synthetase [Panax ginseng] METFLFTSESVNEGHPDKLCDQISDAVLDACLAQDPDSKVACETCTKTNMVM VFGEITTKANVDYEKIVRDTCRSIGFVSDDVGLDADNCKVLVNIEQQSPDIAQG VHGHLTKKPEEIGAGDQGHMFGYATDETPELMPLSHVLATKLGARLTEVRKN GTCAWLRPDGKTQVTVEYYNENGAMVPVRVHTVLISTQHDETVTNDEIAADL KQHVIKPVXPGEYLEEKTIFXLNPSGRXVIGGPHGXAGLTGGKIIIDTYGGWGA HGGGAFSGKDPTKVDRSGAYIVRQAAKSIVASGLARRCMVQVS	87%
Contig3	*Medicago sativa*	S-adenosylmethionine synthase	>gi|48093937|gb|AAT40304.1| S-adenosylmethionine synthase [Medicago sativa] METFLFTSESVNEGHPDKLCDQISDAVLDACLEQDVDSKVACETCTKTNMVM VFGEITTKAKVDYEKIVRDTCRKIGFVSDDVGLDADNCKVLVNIEQQSPDIAQ GVHGHLTKRPEEIGAGDQGHMFGYATDETPELMPLSHVLATKLGARLTEVRK NGTCPWLRPDGKTQVTVEYYNDNGAMVPVRVHTVLISTQHDETVTNDEIAA DLKEHVIKPVIPEKYLDSKTIFHLNPSGRFVIGGPHGDAGLTGRKIIIDTYGGWG AHGGGAFSGKDPTKVDRSGAYIVRQAAKSIVASGLARRCIVQVSYAIGVPEPL SVFVDTYGTGKIPDKEILNIVKQNFDFRPGMISINLDLLRGGNGRFLKTAAYGH FGREDADFTWEVVKPLKWEKA	87%
Contig3	*Ipomoea batatas*	S-adenosyl-L-methionine synthetase	>gi|145049666|gb|ABP35525.1| S-adenosyl-L-methionine synthetase [Ipomoea batatas] METFLFTSESVNEGHPDKLCDQVSDAVLDACLAQDPESKVACETCTKTNMVM VFGEITTKAEIDYEKIVRDTCRAIGFVSDDVGLDADNCKVLVNIEQQSPDIAQG VHGHLTKRPEDIGAGDQGHMFGYATDETPELMPLSHVLATKLGARLTEVRKD GTCAWLRPDGKTQVTVEYYNDNGAMVPVRVHTVLISTQHDETVTNDEIARD LKEHVIKPVIPEKYLDEKTIFHLNPSGRFVIGGPHGDAGLTGRKIIIDTYGGWGA HGGGAFSGKDPTKVDRSGAYVVRQAAKSIVANGLARRCIVQVSYAIGVPEPLS VFVDTYGTGKIPDKEILKIVKEHFDFRPGMIAINLDLKRGGNSRFLKTAAYGHF GRDDPDFTWEVVKPLKWDKPQA	86%
Contig4	*Mentha x piperita*	flavonoid 4'-O-methyltransferase(Q6VMV8)	>gi|38047399|gb|AAR09602.1| flavonoid 4'-O-methyltransferase [Mentha x piperita] MVADEEVRVRAEAWNNAFGYIKPTAVATAVELGLPDILENHDGPMSLLELSA ATDCPAEPLHRLMRFLVFHGIFKKTAKPPLSNEAVYYARTALSRLFTRDELGD FMLLQTGPLSQHPAGLTASSLRTGKPQFIRSVNGEDSWTDPVNGYHMKVFSD AMAAHARETTAAIVRYCPAAFEGIGTVVDVGGRHGVALEKLVAAFPWVRGIS FDLPEIVAKAPPRPGIEFVGGSFFESVPKGDLVLLMWILHDWSDESCIEIMKKC KEAIPTSGKVMIVDAIVDEDGEGDDFAGARLSLDLIMMAVLARGKERTYREW EYLLREAGFTKFVVKNINTVEFVIEAYP	54%
Contig4	*Humulus lupulus*	O-methyltransferase 3	>gi|167613939|gb|ABZ89567.1| O-methyltransferase 3 [Humulus lupulus] MEKLKSFRHLNNNIDLILNEENSTEILGAQAHIWNQIFNFINSMSLKCAIQLGIP DIINNHGKPMTISQL TLALPINRKKSPCVYRLMRILIHSGFFALQKAEVGEEGGGEEEGYVITDASKLL LKDNPMSVTPFLLAMLDPVMTKPWDFLSNWFQNGDPTPFDTANGMAFWDY GSHEPKLARFFNDAMASDARLVTSVVIEKCKGVFEGVESLVDVGGGTGTVAS SIAAAFPHIQCTVFDLPHVVADLQGGNNLNFVGGDMFVDVPATEVVLLKWIL HDWNDEESVKILKKCKEAISKSNKKGGKVIIIDMKVENEKDEDDESYETQLFF DMLMMALVTGRERNEKEWAKLFKDAGFSNYKITPILGLRSLIEVYP	38%
Contig5	*Mentha x piperita*	Isopiperitenone reductase	>gi|158979023|gb|ABW86884.1| isopiperitenone reductase [Mentha x piperita] MAEVQRYALVTGANKGVGFEICRQLAEKGIIVILTSRNEKRGLEARQKLLKEL NVSENRLVFHQLDVTDLASVAAVAVFIKSKFGKLDILVNNAGVSGVEMVGDV SVFNEYIEADFKALQALEAGAKEEPPFKPKANGEMIEKFEGAKDCVVTNYYGP KRLTQALIPLLQLSPSPRIVNVSSSFGSLLLLWNEWAKGVLGDEDRLTEERVDE VVEVFLKDIKEGKLEESQWPPHFAAERVSKAALNAYTKIAAKKYPSFRINAICP GYAKTDITFHAGPLSVAEAAQVPVKLALLPDGGPSGCFFPRDKALALY	89%
Contig5	*Mentha x piperita*	Menthol dehydrogenase	>gi|33950297|gb|AAQ55960.1| menthol dehydrogenase [Mentha x piperita] MADTFTQRYALVTGANKGIGFEICRQLASKGMKVILASRNEKRGIEARERLLK ESRSISDDDVVFHQLDVADPASAVAVAHFIETKFGRLDILVNNAGFTGVAIEGD ISVYQECLEANIIAAQGGQAHPFHPKTTGRLIETLEGSKECIETNYYGTKRITET LIPLLQKSDSPTIVNVSSTFSTLLLQPNEWAKGVFSSNSLNEGKVEEVLHEFLKD FIDGKLQQNHWPPNFAAYKVSKAAVNAYTRIIARKYPSFCINSVCPGFVRTDIC YNLGVLSEAEGAEAPVKLALLPDGGPSGSFFSREEALSLY	56%
Contig6	*Mentha x piperita*	pulegone reductase	>gi|158979025|gb|ABW86885.1| pulegone reductase [Mentha x piperita] MVMNKQIVLNNYINGSLKQSDLALRTSTICMEIPNGCNGAILVKNLYLSVNPY LILRMGKLDIPQFDSIL PGSTIVSYGVSKVLDSTHPSYEKGELIWGSQAGWEEYTLIQNPYNLFKIQDKD VPLSYYVGILGMPGMTAYAGFFEICSPKKGETVFVTAAAGSVGQLVGQFAKM FGCYVVGSAGSKEKVDLLKNKFGFDDAFNYKEESDYDTALKRHFPEGIDIYFD NVGGKMLEAVINNMRVHGRIAVCGMVSQYSLKQPEGVHNLLKLIPKQIRMQ GFVVVDYYHLYPKFLEMVLPCIKEGKVTYVEDISEGLESAPSALLGVYVGRNI GNQVVAVSRE	98%
Contig6	*Ocimum basilicum*	alcohol dehydrogenase-like protein	>gi|62461976|gb|AAX83111.1| alcohol dehydrogenase-like protein [Ocimum basilicum] MFRNENKQVIFNNFVNGSPEESDMSVRTETVDLGIPEGCDDAVLVKNLYLSCG PYMIGRMKNLEGYFFESFKPGSPIVGCGVFKVLDSSHPNYKKGDIISGFTNWEE YSLLTITDATPFFKIQDKDLPLSYYIGILGVPG MTAYTGFFELCCPKKGETVFVSAASGAVGQLVGQFAKLAECYVVGSAGSND KVNLLKNKFGFDEAFNYKDEKDYSAALKRYFPNGIDIYFDNVGGKMLEAAIS NMRAHGRIAICGMVSQYGLEQHEGVHNLFTILTKQIRMQGFLVGEYYHLFPKF LEMILPHIKQGKITYVEDIVEGLENAPSTLVGLLSGRNVGKQVVLVSPE	76%
Contig7	*Picrorhiza kurrooa*	geranyl diphosphate synthase	>gi|58201026|gb|AAW66658.1| geranyl diphosphate synthase [Picrorhiza kurrooa] MSLVNSITWSQTSSILNIQSNISKKLTPFSILPHPLTNNLPISLFPNPKSNISNSNTP LSAILTKDQKPQ NPPTTPTFDFKSYMLQKADSVNKALDDSIPLTEPLKIQESMRYSLLAGGKRIRP MLCIAACELVGGDEST AMPAACAVEMVHTMSLMHDDLPCMDNDDLRRGKPTNHKVFTEDVAVLAGD AMLAFSFEHVASLTKGVCSERIVRVIYELAKCVGCEGLVAGQVVDICSEGMDE VGLEHLEFIHLNKTAALLEGSVVLGAILGGGSDEEVEKLRNFARCIGLLFQVVD	86%

			DILDVTKSSKELGKTAGKDLVADKTTYPKLIGIEKSKEFAERLNREAKEHLAGFDQNKAAPLIALADYIAYRDN	
Contig7	*Jatropha curcas*	geranylgeranyl diphosphate synthase	>gi|291170333|gb|ADD82422.1| geranylgeranyl diphosphate synthase [Jatropha curcas] MAFSATAPACNNILFKKSTFNGLKNRPELPFNHLKFHFRMKMTTTTVQVVSDSSPVTQPLETTQESLSFS PKILLPNFPFEEYMVLKANNVNEALDKAVPLNHPLKIHAAMRYSLLAGGKRVRPILCIAACELVGGDEAAAMPSACAMEMIHTMSLIHDDLPCMDNDDLRRGKPTNHKMFGEETAILAGDAMLSLAFEHIARATKNVSPERVVRVITELGSAVGSEGLVAGQIVDVCSEGKEVNVKDLEYIHIHKTAKLLEAAVVCGAIAGGADDESIERVRKYARCIGLLFQVIDDILDVTKSSEELGKTAGKDLVSDKATYPKLLGIDEARKLAAKLVDEANQELAYFDSAKAAPLYHFANYIASRQN	63%
Contig7	*Carica papaya*	geranylgeranyl pyrophosphate synthase	>gi|77176929|gb|ABA64563.1| geranylgeranyl pyrophosphate synthase [Carica papaya] EMMHTMSLIHDDLPCMDNDDLRRGKPTNHKVFGEDVAVLAGDALLSFSFEHLAVATVGVDPSRIVRAIKELAKSIGTEGLVAGQVVDICSEGMTDVGLEHLEFIHVHKTAALLEAAVVLGAILGGGTDEEIEKLRKFARYIGLLFQVVDDILDVTKSSQELGKTAGKDLVAEKVTYPKLMGIEKSRELAEKLNKDAQEQLRDFDEEKAAPLMAL	74%
Contig7	*Gentiana lutea*	geranylgeranyl pyrophosphate synthase	>gi|18146809|dbj|BAB82463.1| geranylgeranyl pyrophosphate synthase [Gentiana lutea] MVDSWVVQSHSVFHTPISLFRSFLGFLCKPMNYNKIGSNLIEKKKLISSFSVASLITKEEEAMGGPKASN YFDFKAYLIEKANKVNEALDQAVSVKNPPMIHEAMRYSLLAGGKRVRPILCIAACELVGGEESNSVPAACAVEMIHTMSLIHDDLPCYGQRDLRRGKAHETTKSSCEDVAVLAGDSLLAFSFEYIATATKNVSPAKNFSRSRRISKSIGTEGLVAGQVADFVINGENQMFGLDQLEFIHIHKTAALLEAAVVLGAILGGGNPEEVEKLRRFARCIGLLFQVVDDILDVTKSSEELGKTAGKRSCGGKTTYPKLMGLDGAREFADKLNKDAKNQLSEFDREKAAPLLALADYIAYRQN	68%
Contig8	*Oryza sativa* Japonica Group	stress-responsive protein	>gi|33087079|gb|AAP92753.1| stress-responsive protein [Oryza sativa Japonica Group] MAAEAGSGGVVKHILLARFKEDVAPERLDQLMGGYAGLVDLVPSMKAFHWGTDVSIENMHQGFTHVFESTFESTEGVKEYIEHQAHVEFANEFLPVLEKTLIIDYKPTIVNNS	56%
Contig8	*Zea mays*	pop3 peptide	>gi|195623150|gb|ACG33405.1| pop3 peptide [Zea mays] MAGGGVVKHILLASFKEEVTQERLDELIRGYAALVGVVPSMKAFHWGTDVSIENMHQGFTHVYKAF	52%
Contig9	*Vitis vinifera*	Predicted: hypothetical protein	>gi|225425186|ref|XP_002264589.1| PREDICTED: hypothetical protein [Vitis vinifera] MHMKLKLLSSLITVVGAVFCDICSNNTLSRHSYFLPGVEVQIQCKLRVNSARTNEEINFSVNRTTGKHGVYKLEIPSVDGIDCIGGHTMQTLCQAKLIGSSSSACNVPGLKTTTNAISVKSKQDNLCIFNLNALSYRPSKRNTTICGDQTQELPNDLNSAKFFLPCFPPFGFPWPSLPPLPPLPQLPPLPQLPPLPQLPPLPRLPPLPRLPPLPTLPFPFSPLPPFPSLPFPPLPFKTPPSLPFPFPPTPPLSLPPPPPPAFNWGDPRTWIPHIPSLSPPPPPAFNLGDPKTWTPYIPSLTPPPPPAFNLGDPKTWTPYIPSLNPPPPAFNLGDPKTWTPYIPSLNPPPPAFNWEDPRTWIPYYYPPSPPTSPQNQHP	54%
Contig9	*Methanosaeta thermophila*	formate dehydrogenase, alpha subunit	>gi|116754223|ref|YP_843341.1| formate dehydrogenase, alpha subunit [Methanosaeta thermophila PT] MDAIETTCVYCGCGCGLYLHVENSKVIAVTPSLKPPARGRLCAKGWLLHGFVNHPDRLREPLIRRGDRYVQTSWSEALSYIAESFSEIKRDSGPDALAVLTSAKATNEENYLLMKLCRAAFGTNNIDNVARLCHAPTLFALGSSLGSGSMTNPMESLLHSDAIMIIGSNTTEQHPAVAFHIMEARRNGARIIVIDPRRTQIAEIADLHLQLRPGTDIALLNAILNVLVQEGMIDEEFIRSRTEGFDAARDRIAEYTPEVAERICGVPADLIHDAAVLYGGADNAAIVYAMGITQHTHGTDNVQAIVNLALATGNLGRDGSGIYPLRGHQNVQGACDMGALPDYYTGYQRVSEFRGKFEDAWDVKLPTSQGNTAVEIMGSAGSDIRGMYISGENPLLSYPNSSRIRRALESLDLLVVSDIFPTETTRMADVVLPIASFAEKDGTVTSTERKVQLIRKAIDPPGSALPEWVVAAKLLEAFGLSSGYRSSADVMREIASLTPSYGGITHERLEGGGIHWPCPTPDHPGTPVLYRDGFPRGHASFRHVDQCEHQHHKFTLIIGRSQYQFHTGSMTRRVCILEREVPEAFVDINPEDAAALGIRNGTGVILESESGTIRARARLSDNVKRGTLFIPFHFRESPANMLTGWQLDPHSRIPGLKITSVSIRREGA	43%
Contig10	*Zea mays*	dehydrin 13	>gi|195625830|gb|ACG34745.1| dehydrin 13 [Zea mays] MSGIIHKIEEKLHMGGDHKKEDEHHKKAEEHHKKEEGEHHKKDGGEHKEGIVEKIKDKITGEHGDKSGDHKEKKDKKKKKEKKKHGEGHDHDGGHSSSSSDSD	70%
Contig10	*Plantago major*	vascular specific protein 4	>gi|53139488|emb|CAH58741.1| vascular specific protein 4 [Plantago major] MAGIIHKIEEKLGMGGSKDGEHKGEHKPECKPEHKPEHGYGDKKADHSYGEHKPEHGEKKEGLVEKIKDKIHGDGAEECKDGEKKKKKKKEKKHGEGHDGGSSSSSDSD	84%
Contig11	*Mentha arvensis*	menthofuran synthase	>gi|158979036|gb|ABW86890.1| menthofuran synthase [Mentha arvensis] MAALLVFFSLSLILLVVLFHKRSSSLLPSRKRRLPPSPSRLPVIGHLHLIGSLAHRSFHSLSKRYGEVMLLHFGSAPVLVASSAAAAREIMKNQDMIFASRPRLSISDRLLYSGKDVAFAAYGEHWRHARSMCVLQLLSAKRVQSFRRIREEETSAMIEKIRRSQPSVVNLSEMFMALTNGVVHRAALGRKDGGGDDSNLTLNKFIELLGRFNVGDYVPWLAWINRINGVDAEVEKVFRKLDGFIEGILREYRMKNDTHASTNFVDTLLQFQRESKDTNPVEDDVIKALILDMFAAGIDTTSAVLEWTMAELIRNPRTLKTLQNEVREVSRNKGGITEDDVDKMPYLKAVSMEILRLHPPFPSLLPRELTQDANMLGYDVPRGTLVLVNNWAISRDPSLWENPEEFRPERFLETSIDYKGMHFEMLPFGSGRRGCPGITFAMSVYELALSKLVNEFDLRLGNGDRAEDLDMTEAPGIVVHKKSPLLVLATPRQS	86%
Contig11	*Nepeta racemosa*	cytochrome P450	>gi|3582021|emb|CAA70575.1| cytochrome P450 [Nepeta racemosa] MVSLSYFLIALLCTLPFLLFLNKWRRSYSGKTPPPSPPKLPVIGNLHQLGLYPHRYLQSLSRRYGPLMQLHFGSVPVLVASSPEAAREIMKNQDIVFSNRPKMSIANRLFFNNRDVAFTQYGEYWRQIRSICVLQLLSNKRVQSFRRVREEETSIMVEKIMQLGSSSSTPVNLSELLLSLTNDVVCRVTLGKKYGGGNGSEEVDKLKEMLTEIQNLMGISPVWEFIPWLNWTRRFDGVDQRVDRIVKAFDGFLESVIQEHKERDGDKDGDGDGALDFVDILLQFQRENKNRSPVEDDTVKALILDMFVAGTDTTATALEWAVAELIKNPRAMKRLQNEVREVAGSKAEIEEEDLEKMPYLKASIKESLRLHVPVVLLVPRESTRDTNVLGYDIASGTRVLINAWAIARDPSVWENPEEFLPERFLDSSIDYKGLHFELLPFGAGRRGCPGATFAVAIDELALAKLVHKFDFGLPNGARMEELDMSETSGMTVHKKSPLLLLPIPHHAAP	60%
Contig12	*Arabidopsis thaliana*	ATS9 (ARABIDOPSIS NON-ATPASE SUBUNIT 9)	>gi|15218845|ref|NP_174210.1| ATS9 (ARABIDOPSIS NON-ATPASE SUBUNIT 9) [Arabidopsis thaliana] MVSYRATTETISLALEANSSEAITILYQVLEDPSSSPEAIRIKEQAITNLCDRLTE	83%

			EKRGEDLRKLLTKLRPFFSLIPKAKTAKIVRGIIDAVAKIPGTTDLQITLCKEMVEWTRAEKRTFLRQRVEARLAALLMENKEYVEALALLSTLVKEVRRLDDKLLLVDIDLLESKLHFSLRNLPKAKAALTAARTAANAIYVPPAQQGTIDLQSGILHAEEKDYKTGYSYFFEAFESFNALGDPRAVFSLKYMLLCKIMVSQADDVAGIISSKAGLQYVGPDLDAMKAVADAHSKRSLKLFENALRDYKAQLEDDPIVHRHLSSLYDTLLEQNLCRLIEPFSRVEIAHIAELIGLPLDHVEKKLSQMILDKKFAGTLDQGAGCLIIFEDPKADAIYSATLETIANMGKVVDSLYVRSAKIMS	
Contig12	*Danio rerio*	Psmd11a protein	>gi|117167889|gb|AAI24768.1| Psmd11a protein [Danio rerio] RAQSLLSTDRNASIDILHAIVKRDVQDDDEEAVRVKEQSILELGGLLAKTGQAAELGGLLKYVRPFLNSISKAKAARLVRSLLDMFLDMEAATGQEVELCLECIEWAKSEKRTFLRQALEARLVSLYFDTKRYQEALQLGSQLLQELKKMDDKALLVELQLLESKTYHALSNLPKARAALTSARTTANAIYCPPKLQAALDMQSGIIHAAEEKDWKTAYSYFYEAFEGYDSIDSPRAITALKYMLLCKIMLNSPEDVQSLISGKLALRYAGRQTEALKCVAQASKNRSLADFEKALTEYKAELRDDPIISTHLTKLYDNLLEQNLIRVIEPFSRVQIEHISELIKLSKGDVERKLSQMILDQKFHGILDQGEGVLIVFDEPPVDKTYEASLETIQNMSKVVDSLYNKAKKLT	59%
Contig13	*Chelon labrosus*	palmitoyl-CoA oxidase(A9XLN5)	>gi|156144442|gb|ABU52891.1| palmitoyl-CoA oxidase [Chelon labrosus] MNPDITKERENATFXVEKLTNILDGGPEKTKRRRQIESLVFSDPDFKEEDPNFLSRSERYDQAVRKSAQMILKLREYGIADPEEIYYYKNMVKGNQQEAMGLHFAMFLPTLYSQCDPEQSKKWLPLAESFQAIGTYAQTELGHGTHLRGLETTATYDPATQEFVLNSPTVSSIKWWPGGLGKTSNHAIVLAQLYSLGNCHGLHAFIVPIRDMNTHEPLPGIVVGDIGPKFGFNEVDNGFLKLENVRIPRENMLMKYAKVDPDGTYMKPPSAKLTYGTMVFIRSMIVGESARALVKSCTIAIRYSAVRHQSEIRPGEPEPQILDYQTQQYKLFPLLATAYAFTFVGQYMQQTYQRITGDINQGDFSELPELHALSAGLKAFTTWETNSAIEVCRMSCGGHGYSRSSALPDIYVEFTPTCTYEGENTVMMLQTARYLVKSYRQAKAGQQLSGIVSYLNEAGDRRLQPQPVAARPTVVDINDLTSLVEVYKLRAAILVDLAAKSIQQELQRRKSQEDAWNNSAIDLVRASDAHCHYVVVKLFTDKLGEVGDTAIHSVLSNLALLYALNGITKNSGDFLLAGLLSVPQVLQSSVRIKELLSKLRPNAVALVDAFDVHDKKLNSVLGRYDGNVYENMFEWARRSPLNKTQVHESYHKYLKPLRSKL	50%
Contig13	*Homo sapiens*	Acyl-Coenzyme A oxidase 1, palmitoyl	>gi|14714578|gb|AAH10425.1| Acyl-Coenzyme A oxidase 1, palmitoyl [Homo sapiens] MNPDLRRERDSASFNPELLTHILDGSPEKTRRRREIENMILNDPDFQHEDLNFLTRSQRYEVAVRKSAIMVKKMREFGIADPDEIMWFKNFVHRGRPEPLDLHLGMFLPTLLHQATAEQQERFFMPAWNLEIIGTYAQTEMGHGTHLRGLETIATYDPETQEFILNSPTVTSIKWWPGGLGKTSNHAIVLAQLITKGKCYGLHAFIVPIREIGTHKPLPGITVGDIGPKFGYDEIDNGYLKMDNHRIPRENMLMKYAQVKPDGTYVKPLSNKLTYGTMVFVRSFLVGEAARALSKACTIAIRYSAVRHQSEMKPGEPEPQILDFQTQQYKLFPLLATAYAFQFVGAYMKETYHRINEGIGQGDLSELPELHALTAGLKAFTSWTANTGIEACRMACGGHGYSHCSGLPNIYVNFTPSCTFEGENTVMMLQTARFLMKSYDQVHSGKLVCGMVSYLNDLPSQRIQPQQVAVWPTMVDINSPESLTEAYKLRAARLVEIAAKNLQKEVIHRKSKEVAWNLTSVDLVRASEAHCHYVVVKLFSEKLLKIQDKAIQAVLRSLCLLYSLYGISQNAGDFLQGSIMTEPQITQVNQRVKELLTLIRSDAVALVDAFDFQDVTLGSVLGRYDGNVYENLFEWAKNSPLNKAEVHESYKHLKSLQSKL	52%
Contig14	*Zea mays*	axial regulator YABBY2	>gi|195622652|gb|ACG33156.1| axial regulator YABBY2 [Zea mays] MSSAPLQIAPVPEHVCYVHCNFCNTILAVSVPSHSMLNIVTVRCGHCTSLLSVNLRGLIQSLPVQNHHYSQQQENFTVQNMGFTENYPEYAPSYRMPTTLSVKGDLDHMLHVRAPEKRQRVPSAYNRFIKEEIRRIKACNPDISHREAFSTAAKNWAHFPNIHFGLGPCESSNNLDEATGAMCHPQKVQDLY	52%
Contig14	*Lotus japonicus*	YABBY1 protein	>gi|225030810|gb|ACN79518.1| YABBY1 protein [Lotus japonicus] MSSSNSSTTLSLDHQLPPSEQLCYVHCNICDTILAVSVPSTSLFKTVTVRCGHCTNLLPVNMRALLLPSPNQFHLGHSFFSPPHNLLGEMPNPSPNFLMNHTNATSNFSQFSVPARSAADELPRPPIINRPAQEKRQRVPSAYNRFIKDEIQRIKSVNPDITHREAFGAAAKNWAHFPHIHFGLMPDQTMKKTTVCQQEGEEVLMMKDGFYASADVGVSPY	52%
Contig15	*Atriplex nummularia*	lipid transfer protein	>gi|31879432|dbj|BAC77694.1| lipid transfer protein [Atriplex nummularia] MASSVVFKLACAVFMCMLVAAPHAEALTCGQVTSSMTPCMSYLTGGGSPTPACCGGVKSLNSMASTPADRKAACGCLKSAAGAMTNLNMGNAASLPGKCGISLPYPISTSTDCSKVN	44%
Contig15	*Tamarix hispida*	lipid transfer protein 2	>gi|223029865|gb|ACM78614.1| lipid transfer protein 2 [Tamarix hispida] MAGSSALFKLACLVAAFMIVSAPHAEAAISCGTVVSKLAPCLGFLRGGGSPPPACCSGIRNLQSMARSTPDRQAACGCLKSASAGVNMRNAAALPGKCGVNIGYPISRSVDCSRVK	47%
Contig16	*Melastoma malabathricum*	copper/zinc superoxide dismutase	>gi|295979335|dbj|BAJ07302.1| copper/zinc superoxide dismutase MVKAVVVLGNSEGVSGTVYFTQEGDGPTTVTGSLSGLKPGLHGFHVHALGDTTNGCMSTGPHFNPAGKEHGAPEDENRHAGDLGNVTVGDDGTATFTITDKQIPLFGPNSIIGRAVVVHADPDDLGKGGHELSKSTGNAGGRIACGIIGLQG	92%
Contig16	*Fagus sylvatica*	superoxide dismutase	>gi|38228697|emb|CAE54085.1| superoxide dismutase [Fagus sylvatica] SVPTARGVLRSHRTMAKGVAVLSSNEGVCGTIYFAQEGDGPTTVTGNISGLKPGLHGFHVHALGDTTNGCMSTGPHFNPAGKEHGAPEDANRHAGDLGNVNVGDDGTVSFTIIDKQIPLCGPNSIIGRAVVVHGDPDDLGKGGHELSKSTGNAGGRIACGIIGLQG	85%
Contig17	*Medicago truncatula*	FAD-dependent pyridine nucleotide-disulphide oxidoreductase	>gi|87240748|gb|ABD32606.1| FAD-dependent pyridine nucleotide-disulphide oxidoreductase; Calcium-binding EF-hand [Medicago truncatula] MRNFQFFQRFSKNFRDYDSQFKLVLLCTTVSGGGLLAYGEAVATSESAVPEKKKVLVLGTGWAGTSFLRNLNDPRYEVHVVSPRNYFTFTPLLPSVTCGTVEARSIVEPVRNIFRKKHVDSRFSEAECLKIDAVNRKVYCRSNINNNLNEKEEFVVDYDYLIIAVGANVNTFNTPGVTENCHFLKEVEDAQKIRRTVIDSFERASLPSVSDEERKRILHFAIVGGGPTGVEFAAALHDFVSEDLVKLYPGVKDLVKITLLEAGGHILSMFDKRITTFAEDKFKRDGIDVKTGSMVTKVSDREITTKEMKNGGEITTIPYGMAVWSTGIGTRPFIKDFMTQIGQVNRRAIATDEWLRVEGTDNVYALGDCATINQRKVMEDIAAIFKKTDADNSGTLTLKEFQEVMNDICERYPQVELYLKNKQMHGIADLLKESKGDVKKESIELNIEELKTAFSNVDSEMKFLPATAQVASQQGTYLAKCFNRMEECEKNPEGPIRFRGEGRHRFKPFRYKHLGQFAPLGGEQTAAQLPGDWVSIGHSSQWLWYSVYASKQVSWRTRALVVSDWMRRFIFGRDSSQI	51%

Contig17	*Arabidopsis thaliana*	NDB3; NADH dehydrogenase	>gi|240256027|ref|NP_193880.5| NDB3; NADH dehydrogenase [Arabidopsis thaliana] MRPFAYFERLSQAFHDYPSLSKILVVSTISGGGLIVYSEANPSYSNNGVETKTRKRKVVLLGTGWAGASFLKTLNNSSYEVQVISPRNYFAFTPLLPSVTCGTVEARSVVEPIRNIARKQNVEMSFLEAECFKIDPGSKKVYCRSKQGVNSKGKKEFDVDYDYLVIATGAQSNTFNIPGVEENCHFLKEVEDAQRIRSTVIDSFEKASLPGLNEQERKRMLHFVVVGGGPTGVEFASELHDFVNEDLVKLYPKAKNLVQITLLEAADHILTMFDKRITEFAEEKFTRDGIDVKLGSMVVKVNDKEISAKTKAGEVSTIPYGMIVWSTGIGTRPVIKDFMKQIGQGNRRALATDEWLRVEGCDNIYALGDCATINQRKVMEDIAAIFKKADKENSGTLTMKEFHEVMSDICDRYPQVELYLKSKGMHGITDLLKQAQAENGSNKSVELDIEELKSALCQVDSQVKLLPATGQVAAQQGTYLAKCFDRMEVCEKNPEGPIRIRGEGRHRFRPFRYRHLGQFAPLGGEQTAAQLPGDWVSIGHSSQWLWYSVYASKQVSWRTRVLVVSDWMRRFIFGRDSSRI	54%
Contig17	*Solanum tuberosum*	external rotenone-insensitive NADPH dehydrogenase	>gi|5734587|emb|CAB52797.1| external rotenone-insensitive NADPH dehydrogenase [Solanum tuberosum] MRGFTYLSKVLHSHSSYSKLLVLCSVSTGGLLVYAESNVESGKQVVEQNQPESKKKRVVVLGTGWGGTSFLKDVDISSYDVQVVSPRNYFAFTPLLPSVTCGTVEARSIVEPVRNIIKKRSGEIQFWEAECLKIDPVNRTVSCRSGINDNLAGHNDFSLQYDYLVVAVGAQVNTFNTPGVMEHCHFLKEVEDAQRIRRTVIDCFEKSVIPGLSEEERRTNLHFVIVGGGPTGVEFAAELHDYVYEDLVKIYPSVKDFVKITVIQSGDHILNTFDERISSFAEQKFQRDGIEVSTGCRVTSVSDHFINMKVKSTGKHVEVPYGMVVWSTGVGTRPFVKDFMEQVGQEKRRILATDEWLRVKGCSNVYALGDCASVDQHKVMEDISTIFEAADKDDSGTLSVEEFRDVLEDIIIRYPQVDLYLKNKHLLEAKDLFRDSEGNEREEVDIEGFKLALSHVDSQMKSLPATAQVAAQQGTYLARCLNRWDQCKSNPEGPRRFKSSGRHEFLPFEYRHLGQFAPLGGDQAAAELPGDWVSMGHSTQWLWYSVYASKQVSWRTRYLVVGDWVRRYIFGRDSSRI	54%
Contig17	*Ajellomyces capsulatus* H143	alternative NADH-dehydrogenase	>gi|240273875|gb|EER37394.1| alternative NADH-dehydrogenase [Ajellomyces capsulatus H143] MASKFLTTRPNVFSRSAVHLSPAACSSLSILSIRSAHYAGPLRHASLSKPAVQRSFRRTYADLPAPPPSQPPTPKRRFRVFRWMYRLTLMSLLAGAGTLGYSVYLLRNPDEQVQPDASKKTLVILGTGWGSVSLLKRLDTENYNVIVISPRNFFLFTPLLPSCTTGLIEHRSIMEPIRNILRHKKAAVKYYEASATKIDPVRKVVRICDESDIKGDTSTTEVPYDMLVVGVGAENATFGIPGVREHSCFLKEVGDAQEIRKRIMDCVETAIFKDQTKEEVERLLHMVVVGGGPTGVEFAGELQDFFNDDLKKWVPEIKDSFKVTLVEALPN	53%
Contig18	*Populus trichocarpa*]>gb|EEE82447.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]	2-oxoglutarate-dependent dioxygenase	>gi|224052970|ref|XP_002297642.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa] MAPTAAVLINDSSDAITDFVLKQGNGVKGLSEMGLKNLPKQYIQPLEEIISDAKITPQASIPIIDVSKLDGPTVAEAVCRAAERWGFFQIINHGVPIDVLENVKESTHRFFGLPAEEKRKYLKELSPSNNVRFGTSFSPEAEKALEWKDYLSLFYVSEDEASALWPSVCKDQVLDYMRRSEIVIRRLLDVLMKNLKVTEIDETKESLLMGSKRINLNYYPICPNPELTVGIGRHSDVSTLTVLLQDDVGGLYVRGDDDYWIHVPPVNGSLVINVGDALQIMSNGRYKSVEHCVMTDGSKNRISIPIFINPRPSNKISPFHEVLASGEKAAYKEVLYSDYVKHFFRKAHDGKKTIDFAKIRI	60%
Contig18	*Arabidopsis thaliana*	oxidoreductase, 2OG-Fe(II) oxygenase family protein	>gi|18402992|ref|NP_566685.1| oxidoreductase, 2OG-Fe(II) oxygenase family protein [Arabidopsis thaliana] MAPLPISSIRVGKIDDVQELIKSKPNKVPERFIREEYERGVVVSSLKTHHLHHQIPVIDLSKLSKPDNDDFFFEILKLSQACEDWGFFQVINHGIEVEVVEDIEEVASEFFDMPLEEKKKYPMEPGTVQGYGQAFIFSEDQKLDWCNMFALGVHPPQIRNPKLWPSKPARFSESLEGYSKEIRELCKRLLKYIAISLGLKEERFEEMFGEAVQAVRMNYYPPCSSPDLVLGLSPHSDGSALTVLQQSKNSCVGLQILKDNTWVPVKPLPNALVINIGDTIEVLSNGKYKSVEHRAVTNREKERLTIVTFYAPNYEVEIEPMSELVDDETNPCKYRSYNHGDYSYHYVSNKLQGKKSLDFAKILN	41%
Contig18	*Populus trichocarpa*	2-oxoglutarate-dependent dioxygenase	>gi|224103505|ref|XP_002313083.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa] MGEIDPEFIQETEYRPKFKTIEADEEIPVIDLSVSTPSDTKEVVSKIGEACKKWGFFQVINHGVPLELRQKIEKVAKEFFDQPMEEKRKVKRDEVNPMGYHDSEHTKNIRDWKEVFDFLVVDPTLIPASGDPDDKELRAMTNQWPHKPSEFRELCQEYTRQVEKLAFKLLELISLSLGLPADRLNGYFKDQISFARFNHYPPCPAPHLALGVGRHKDGGALTVLSQDDVGGLQIGRRSDGEWIPVKPIPDAFIINIGNCMQVWSNDLYWSAEHRVVVNSQRERFSIPFFFFPSQYVDIKPLDELINEQNLAKYKEFNWGKFFASRNRSDYKKREVENIQIDHFKVPE	32%
Contig18	*Olimarabidopsis pumila*	Fe2+ dioxygenase-like	>gi|38260659|gb|AAR15474.1| Fe2+ dioxygenase-like [Olimarabidopsis pumila] MEKGEDSSTFKMGNSAQERSLPYVPDCYVVPPSCEPCDSNSDVVPTIDVSRLKGVDDDRREVIRELSLACQRLGFFQIVNHGINQNILDDALEVAKGFFELPAKEKKKFMSNDVYAPIRYSTSLKDGLDKIQYWRIFLKHYAHPLHRWIHLWPENPPEYREKMGKFCEEVRKLSIEIMGAITESLGLGRNYMSSRMDENGMQVMAVNCYPPCPDPETALGLPPHSDYSCITILLQNLAGLKIFNPMAHGGSGGWVVVPQVTGALKVHIGDHVEVLSNGLYKSVVHKVTLNEENMRISLASLHSLGMDDKMSVPCELVNHENPVRYRESSFNDFLDFLVKNDISQGDRFIDTLRIKD	42%
Contig19	*Arabidopsis thaliana*	ATMP2; heme binding	>gi|15229044|ref|NP_190458.1| ATMP2; heme binding [Arabidopsis thaliana] MVQQIWETLKETITAYTGLSPAAFFTVLALAFAVYQVVSGFFVSPEVHRPRSLEVQPQSEPLPPPVQLGEITEEELKLYDGSDSKKPLLMAIKGQIYDVSQSRMFYGPGGPYALFAGKDASRALAKMSFEDQDLTGDISGLGAFELEALQDWEYKFMSKYVKVGTIQKKDGEGKESSEPSEAKTASAEGLSTNTGEEASAITHDETSRSTGEKIAETTEKKDVATDDDDAAKE	68%
Contig19	*Zea mays*	membrane steroid-binding protein 1	>gi|195640730|gb|ACG39833.1| membrane steroid-binding protein 1 [Zea mays] MAVVELWETLKQAIVAYTGLSPALLHGCGGGGRSVPREEPETEPLPPPVQMGEVSEEDLRQYDGSDPKKPLLMAIKGQIYDVTQSRMFYGPGGPYALFAGKDASRALAKMSFEPQDLTGDVSGLGPFELDALQDWEYKFMSKYVKVGTVKKSVPVEGGSTASTTEAEKAPTTEEKPSGAVVEKEAVANEGAQEN	58%
Contig20	*Catharanthus roseus*	GCPE protein	>gi|27903511|gb|AAO24774.1| GCPE protein [Catharanthus roseus] MATGTVPASFTGLKSRENGLGFAKSMDFVQVSDLRRVKFRRAKVSVIKNSNPGPETVELQPASQGSQLLVPVQKYCESIHKTVRRKTRTVMVGNVALGSDHPIRIQTMTTTDTKDVAATVEQVMGIADKGADIVRITVQGKKEADACYDIKNTLVQKSYNIPLVADIHFAPAVALRVAECFDKIRVNPGNFADRRAQFEQLEYTDEEYQ	77%

			KELEHIEQVFTPLVEKCKKYGRAMRIGTNHGSLSDRIMSYYGDSPRGMVESAFEFARICRKLDFHNFVFSMKASNPVIMVAAYRLLVAEMYVLGWDYPLHLGVTEAGEGEDGRMKSAIGIGTLLQDGLGDTIRVSLTEPPEEEIDPCRRLANLGARAADLGQGVAPFEEKHRRYFDFQRRTGDLPVQKEGEEVDYRGVLHRDGSVLMSVSLDQLKTPELLYKSLAAKLVVGMPFKDLATVDSILLRELPPIEDKDSRLALKRLIDISMGVITPLSEQLTKPLPNAMVLVTLKELSSGAHKLLPEGTRLVVSVRGDEPYEELDILKNVDVTMILHNLPHTEEKIGRVHAARRLFEYLSENSLNFPVIHHMQFANAIHRDDLVIGAGSDAGALLVDGLGDGVMLEAHDQDFEFLRNTSFNLLQGCRMRNTKTEYVSCPSCGRTLFDLQEISAQIREKTSHLPGVSIAIMGCIVNGPGEMADADFGYVGGAPGKIDLYVGKTVVKRGIDMEHATDALIQLIKDHGRWVDPPAED	
Contig20	*Solanum lycopersicum*	GcpE	>gi|27462474|gb|AAO15447.1|AF435086_1 GcpE [Solanum lycopersicum] MAAGTVPASFTGLKSNENGLGFAKSMNFIRVSDLQRVKFRRTKFSVIRNANPGQETIELQPASEGSPLLVPRQKYCESIYKTVRRQTCTVMVGNVALGSEHPIRIQTMTTTDTKDVAATVEQVMKIADAGADIVRITVQGRKEADACFEIKNTLVQKNYNIPLVADIHFAPSVALRVAECFDKIRVNPGNFADRRAQFEQLEYTEDDYQKELEHIEEVFTPLVEKCKKYGRAMRIGTNHGSLSDRIMSYYGDSPRGMVESAFEFARICRKLDFHNFVFSMKASNPVVMVQAYRLLVAEMYVQGWDYPLHLGVTEAGEGEDGRMKSAIGIGTLLQDGLGDTIRVSLTEAPEEEIDPCRRLADLGKRAAALQQGVAPFEEKHRRYFDFQRRSGELPAQKEGDEVDYRGVLHRDGSVLMSVSLNQLKTPELLYRSLAAKLIVGMPFKDLATVDSILLRELPPLDDIDSRLALKRLVDISMGVIAPLSEQLTKPLPNAMVLVTLKELSGGAHKLLPEGTRLVVSLRGDESHDELEILKSSDVTMILHNLPYTEEKIGRVQAARRLFEYLSENSLNFPVIHHIQFPSNTHRDDLVIGAGTNAGALLVDGLGDGLLLEAPDKDFDFLRNTSFNLLQGCRMRNTKTEYVSCPSCGRTLFDLQEISAQIREKTSHLPGVSIAIMGCIVNGPGEMADADFGYVGGAPGKIDLYVGKTVVKRAIEMEHATDALIQLIKDHDRWVDPPTEE	71%
Contig21	*Oryza sativa* (japonica cultivar-group)] >dbj|BAC83283	Os07g0142300	>gi|115470543|ref|NP_001058870.1| Os07g0142300 [Oryza sativa (japonica cultivar-group)] MASTSGLLATVLAMAVLLAGSSRSCQAARHLADATPPAAVPVPTVPAVTLPPMPAIPAVPAATLPPMPAVPIVPNTALPPMPAVPKVALPPMPAVPAVPTVPAVTVPPMPAVPAVPAATLPPMPAVPAVPAASLPPMPAMPAVPNAALPPMPAVPKVTLPPMPSMPAVPKVTLPPMPSVPMPFLAPPPSA	37%
Contig21	*Oryza sativa* (japonica cultivar-group)] >dbj|BAC21402.1| early nodulin 75 precursor-like protein [Oryza sativa Japonica Group] >dbj|BAF20785.1| Os07g0142500 [Oryza sativa Japonica Group] >gb|EAZ02742.1| hypothetical protein OsI_24861 [Oryza sativa Indica Group]	Os07g0142500	>gi|115470545|ref|NP_001058871.1| Os07g0142500 [Oryza sativa (japonica cultivar-group)] MASTSGLLATVLAMAVLLAGSSSSCQAARHLADATPPAAVPVPTVPAVTLPPMPAIPAVPAATLPPMPAVPTVPNAALPPMPAVPKVALPPMPAVPAVPTVPAVPAVPAASLPPMPAVPAVPNAVLPPMPAVPKVTLPPMPSMPAVPKVTLPPMPSVPMPFLAPPPSA	34%
Contig22	*Daucus carota*	glyceraldehyde 3-phosphate dehydrogenase	>gi|51703306|gb|AAR84410.2| glyceraldehyde 3-phosphate dehydrogenase [Daucus carota] MAPIKIGINGFGRIGRLVARVALQRDDVELVAVNDPFISTDYMTYMFKYDSVHGAWKHHELKVKDEKTLLFGEKPVAVFGCRNPEEIPWASTGAEYIVESTGVFTDKDKAAAHLKGGAKKVIISAPSKDAPMFVVGVNEKEYKSDLHIVSNASCTTNCLAPLAKVINDRFGIVEGLMTTVHSITATQKTVDGPSAKDWRGGRAASFNIIPSSTGAAKAVGKVLPQLNGKLTGMSFRVPTVDVSVVDLTVRLEKKATYDQIKAAIKEESEGKLKGILGYTEDDVVSTDFVGDSRSSIFDAKAGIALNDNFVKLVSWYDNEWGYSTRVVDLIVHMASVQ	90%
Contig22	*Populus maximowiczii x Populus nigra*	glyceraldehyde-3-phosphate dehydrogenase	>gi|74419004|gb|ABA03227.1| glyceraldehyde-3-phosphate dehydrogenase [Populus maximowiczii x Populus nigra] MACDKKIKIGINGFGRIGRLVARVALQRDDVELVAINDPFITTDYMTYMFKYDTVHGRWKHGELKVKDEKTLLFGEKAVAVFGIRNPEEIPWAQAGAEFVVESTGVFTDKDKAAAHLKGGAKKVVISAPSKDAPMFVVGVNEKQYTPDLDIVSNASCTTNCLAPLAKVIHDRFGIVEGLMTTVHAITATQKTVDGPSMKDWRGGRAASFNIIPSSTGAAKAVGKVLPALNGKLTGMSFRVPTVDVSVVDLTVRLEKKATYEAIKSAIKEESENNLKGILGYVEEDVVSTDFIGDSRSSIFDAKAGIALNDNFVKLVSWYDNEWGYSSRVIDLIAHMAKTQA	90%
Contig23	*Tamarix hispida*	lipid transfer protein 2	>gi|223029865|gb|ACM78614.1| lipid transfer protein 2 [Tamarix hispida] MAGSSALFKLACLVAAFMIVSAPHAEAAISCGTVVSKLAPCLGFLRGGGSPPPACCSGIRNLQSMARSTPDRQAACGCLKSASAGVNMRNAAALPGKCGVNIGYPISRSVDCSRVK	47%
Contig23	*Platanus orientalis*	pollen allergen Pla o 3	>gi|162949340|gb|ABY21307.1| pollen allergen Pla o 3 [Platanus orientalis] MAFSRVAKLACLLLACMVATAPHAEAAITCGTVVTRLTPCLTYLRSGGAVAPACCNGVKALNNDAKTTPDRQAACGCLKTASTSISGIQLGNAASLAGKCGVNLPYKISPTIDCSKVK	45%
Contig24	*Salvia fruticosa*	cineole synthase	>gi|111182619|gb|ABH07677.1| cineole synthase [Salvia fruticosa] MSSLIMQVVIPKPAKFFHNNLFSLSSKRHRFSTTTTTRGGRWARCSLQTGNEIQTERRTGGYQPTLWDFSTIQSFDSEYKEEKHLMRAAGMIDQVKMMLQEEVDSIRRLELIDDLRRLGISCHFEREIVEILNSKYYTNNEIDERDLYSTALRFRLLRQYDFSVSQEVFDCFKNAKGTDFKPSLVDDTRGLLQLYEASFLSAQGEETLRLARDFATKFLQKRVLVDKDINLLSSIERALELPTHWRVQMPNARSFIDAYKRRPDMNPTVLELAKLDFNMVQAQFQQELKEASRWWNSTGLVHELPFVRDRIVECYYWTTGVVERRQHGYERIMLTKINALVTTIDDVFDIYGTLEELQLFTTAIQRWDIESMKQLPPYMQICYLALFNFVNEMAYDTLRDKGFDSTPYLRKVWVGLIESYLIEAKWYYKGHKPSLEEYMKNSWISIGGIPILSHLFFRLTDSIEEEAAESMHKYHDIVRASCTILRLADDMGTSLDEVERGDVPKSVQCYMNEKNASEEEAREHVRSLIDQTWKMMNKEMMTSSFSKYFVEVSANLARMAQWIYQHESDGFGMQHSLVNKMLRDLLFHRYE	60%

Contig24	*Ocimum basilicum*	terpinolene synthase	>gi|55740209|gb|AAV63792.1| terpinolene synthase [Ocimum basilicum] MSTFVISNSMHVGISFSFLHKLPQTPPPQVVCCSGGLRLRPSCSLQLQPPPTTRRSGNYEPSAWDFNYLQSLNNYHHKEERYLRRQADLIEKVKMILKEEKMEALQQLELIDDLRNLGLSYCFDDQINHILTTIYNQHSCFHYHEAATSEEANLYFTALGFRLLREHGFKVSQEVFDRFKNEKGTDFRPDLVDDTQGLLQLYEASFLLREGEDTLEFARQFATKFLQKKVEEKMIEEENLLSWTLHSLELPLHWRIQRLEAKWFLDAYASRPDMNPIIFELAKLEFNIAQALQQEELKDLSRWWNDTGIAEKLPFARDRIVESHYWAIGTLEPYQYRYQRSLIAKIIALTTVVDDVYDVYGTLDELQLFTDAIRRWDIESINQLPSYMQLCYLAIYNFVSELAYDIFRDKGFNSLPYLHKSWLDLVEAYFQEAKWYHSGYTPSLEQYLNIAQISVASPAILSQIYFTMAGSIDKPVIESMYKYRHILNLSGILLRLPDDLGTASDELGRGDLAKAMQCYMKERNVSEEEARDHVRFLNREVSKQMNPARAADDCPFTDDFVVAAANLGRVADFMYVEGDGLGLQYPAIHQHMAELLFHPYA	52%
Contig26	*Arabidopsis thaliana*	calcium-binding EF hand family protein	>gi|18406507|ref|NP_566015.1| calcium-binding EF hand family protein [Arabidopsis thaliana] MGVVLIDGSTVRSFVDDEEQFKKSVDERFAALDLNKDGVLSRSELRKAFESMRLLESHFGVDVVTPQDELTNLYDSIFEKFDTDQSGSVDLEEFRSEMKKIVLAIADGLGSCPITMVLDDDDDNFLKKAADLEASKLEKASS	72%
Contig26	*Zea mays*	EF hand family protein	>gi|195627228|gb|ACG35444.1| EF hand family protein [Zea mays] MSVVILDGSTVRGFVADXAXFARSLDARFAALDANGDGVLSRAELRRALESFRLLDGGGFGSAQPAPLPAEVTALYDAVFEQFDADHSGAVDRAEFHDEMRRIMLAVADGLGSQPLQVAVDDEGGSFLLEAAEHEAAGIAAKIEANRKAEAEAEAAK	63%
Contig27	*Nicotiana suaveolens*	S-adenosyl-L-methionine synthase	>gi|115361537|gb|ABI95859.1| S-adenosyl-L-methionine synthase [Nicotiana suaveolens] METFLFTSESVNEGHPDKLCDQVSDAILDACLEQDPESKVACETCTKTNMVMVFGEITTKATVDYEKIVRDTCRGIGFTSADVGLDADNCKVLVNIEQQSPDIAQGVHGHLTKKPKEIGAGDQGHMFGYATDETPELMPLTHVLATKLGAKLTEVRKNKTCPWLKPDGKTQVTVEYKNDNGAMVPIRVHTVLISTQHDETVTNDQIAQDLKEHVIKPVIPAQYLDEKTIFHLNPSGRFVIGGPHGDAGLTGRKIIIDTYGGWGAHGGGAFSGKDPTKVDRSGAYIVRQAAKSVVASGLARRCIVQVSYAIGVAEPLSVFVDTYKTGTIPDKDILALIKENFDFRPGMMSINLDLLRGGNFRYQKTAAYGHFGRDDPDFTWETVKVLKPKA	97%
Contig27	*Arabidopsis thaliana*	MAT3 (methionine adenosyltransferase 3); copper ion binding / methionine adenosyltransferase	>gi|15228048|ref|NP_181225.1| MAT3 (methionine adenosyltransferase 3); copper ion binding / methionine adenosyltransferase [Arabidopsis thaliana] METFLFTSESVNEGHPDKLCDQISDAILDACLEQDPESKVACETCTKTNMVMVFGEITTAAKVDYEKIVRSTCREIGFISADVGLDADKCNVLVNIEQQSPDIAQGVHGHLTKKPEDIGAGDQGHMFGYATDETPELMPLTHVLATKLGAKLTEVRKNKTCPWLRPDGKTQVTVEYKNDGGAMIPIRVHTVLISTQHDETVTNDEIAADLKEHVIKPVIPAKYLDDNTIFHLNPSGRFVIGGPHGDAGLTGRKIIIDTYGGWGAHGGGAFSGKDPTKVDRSGAYIVRQAAKSVVAAGLARRCIVQVSYAIGVPEPLSVFVDTYKTGTIPDKDILVLIKEAFDFRPGMMAINLDLKRGGNFRFQKTAAYGHFGRDDPDFTWEVVKPLKPKA	93%
Contig28	*Mentha x piperita*	isopiperitenone reductase	>gi|158979023|gb|ABW86884.1| isopiperitenone reductase [Mentha x piperita] MAEVQRYALVTGANKGVGFEICRQLAEKGIIVILTSRNEKRGLEARQKLLKELNVSENRLVFHQLDVTDLASVAAVAVFIKSKFGKLDILVNNAGVSGVEMVGDVSVFNEYIEADFKALQALEAGAKEEPPFKPKANGEMIEKFEGAKDCVVTNYYGPKRLTQALIPLLQLSPSPRIVNVSSSFGSLLLLWNEWAKGVLGDEDRLTEERVDEVVEVFLKDIKEGKLEESQWPPHFAAERVSKAALNAYTKIAAKKYPSFRINAICPGYAKTDITFHAGPLSVAEAAQVPVKLALLPDGGPSGCFFPRDKALALY	94%
Contig28	*Artemisia annua*	broad substrate reductase/dehydrogenase	>gi|269308672|gb|ACZ34296.1| broad substrate reductase/dehydrogenase [Artemisia annua] MSYATEKDVSTEKRVALVTGGNKGIGLEICRQLASNDIKVILTARNESRGIEAIEKLKVSGPLDVVFHQLDVKDPSSIARLAKYVELQFKKLDILVNNAGESGIIVREDEFRAFKDGAGYNEVYDENAHLLTEIIEQPPHLGEECIKTNYYGTKGVTEAFLPLLQLSKSLRIVNVSSNYGELKFLPNEKLTQELQDIEHLTNERIDEIIQWXLRDLKANKLLENGWPLTVGAYKISKIAVNAYTRLLARKYQNILVNCVHPGYVITDITSNTGELTSEEGAKAPVMVALLPDDGPSGVYFSRMQITSF	48%
Contig29	*Oryza sativa* Japonica Group	stress-responsive protein	>gi|33087079|gb|AAP92753.1| stress-responsive protein [Oryza sativa Japonica Group] MAAEAGSGGVVKHILLARFKEDVAPERLDQLMGGYAGLVDLVPSMKAFHWGTDVSIENMHQGFTHVFESTFESTEGVKEYIEHQAHVEFANEFLPVLEKTLIIDYKPTIVNNS	51%
Contig29	*Zea mays*	pop3 peptide	>gi|226530706|ref|NP_001152608.1| pop3 peptide [Zea mays] MAGGGVVKHILLASFKEEVTQERLDELIRGYAALVGVVPSMKAFHWGTDVSIENMHQGFTHVFESTFESTEGIKEYIEHPAHVEFASVFLPVLEKVLIIDYKPTSAN	52%
Contig30	*Cylindrospermopsis raciborskii* CS-505]	Phosphoglucose isomerase (PGI)	>gi|282900113|ref|ZP_06308070.1| Phosphoglucose isomerase (PGI) [Cylindrospermopsis raciborskii CS-505] MDAKELWQRYQDWLYYHEGLGLYLDISRMRFDNTFVESLQSKFEQAFREMVDLEKGAIANPDENRMVGHYWLRNPDLAPNSQLRAEIVRTLEEIEVFADQVHTGSIHPPKENRFTDIISIGIGGSALGPQFVAEALAPDLPPLNIHFIDNSDPAGIDRVLSRVGDRLSSTLVLVISKSGGTPEPRNGMIEVKQAYSRRNLDFAQYAIAITSMGSNLDKVAKSENWLGTFPMYDWVGGRTSEMSAVGLVPAALQGINIRAMLDGAKQMDDATRIANIKNNPAALLALSWYFSGNGKGEKDMVVLPYKDSLLLFSRYLQQLVMESLGKERDLDGKTVYQGIAVYGNKGSTDQHAYVQQLREGVPNFFATLIEVLEDRQGASSEIDPGVTAGDYLSGFLLGTRQALYENHRDSITVTIPQVNAQTVGALIALYERAVGLYASLVNVNAYHQPGVEAGKKAAAVILDLQNKVIKVLQSEKKGLTIGEIADKAGASEQVEPIYKILRHLHANNRGVVLTGDLSKPGTLTVSLT	57%
Contig31	*Salvia stenophylla*	3-carene synthase	>gi|22023928|gb|AAM89254.1|AF527416_1 3-carene synthase [Salvia stenophylla] MAFPRNPTKLLHKPHNKSSKLISNSRISSYGHLPLRCSSQQLPTDEFQVERRSGNYSPSKWDVDYIQSLHSDYKEERHTRRASELIMEVKKLLEKEPNPTRQLELIDDLQKLGLSDHFNNEFKEILNSVYLDNKYYRNGAMKEVERDLYSTALAFRLLRQHGFQVAQDVLECFKNTKGEFEPSLSDDTRGLLQLYEASFLLTEGENTLELARDFTTKILEEKLRNDEIDDINLVTWIRHSLEIPIHWRIDRVNTSVWIDVYKRRPDMNPIVLELAVLDSNIVQAQYQEELKLDLQWWRNTCLAEKLPFARDRLVESYFW	66%

			GVGVVQPRQHGIARMAVDRSIALITVIDDVYDVYGTLEELEQFTEAIRRWDISS IDQLPSYMQLCFLALDNFINDIAYDVLKEQGFNIIPYLRKSWTDMIEGFLLEAK WYHNGHKPKLEEYLENGWRSIGSTVVLTHAFFGVTHSLTKENIDQFFGYHEIV RLSSMLLRLADDLGTSTDEVSRGDVPKAIQCYMNDNIGASEAEAREHVKWCI WETWKKMNKVRVARDTPFSQDFIVCAMGMGRMGQYMYHYGDGHGIQHSII HQQMSTCLFHPSSSN	
Contig31	*Perilla citriodora*	monoterpene synthase	>gi|60266126|gb|AAX16078.1| monoterpene synthase [Perilla citriodora] MYTGVMNMAFPMKPANYLHNSGSSNSSKLCGVSSTSTRAATARLRLRLRCSL QLSDQRRSGNYSPSFWNTDYILSLNCDYEDERRMRGAAGELVEQVKMLMEK ETDPIVQLELIDDLQKLALSHYFEKEIKEILFNISTIYDDKNRERDLYSTTLAFRL LRQHGYQVPQELFECFKNDKGEFKESLSNDTKGLLQLYEASFLLTEGETTLEL AREFATKFLQEKEKHNIDDDDDTNLISCVRHSLDMPIYWRIQRQMQGGGFMPI IGELTLIHLCWSFPNLTSILFKHNISKNLNKT	53%
Contig32	*Solanum lycopersicum*	enolase	>gi|1161573|emb|CAA41116.1| enolase [Solanum lycopersicum] LGANAILAVSLAVCKAGAAVKKIPLYKHIANLAGNKKLVLPVPAFNVINGGSH AGNKLAMQEFMILPVGASSFKEAMKMGCEVYHHLKAVIKKKYGQDATNVG DEGGFAPNIQENKEGLELLKTAIEKAGYTGKVVIGMDVAASEFYGKDKTYDL NFKEENNNGSQKISGDQLKDLYKSFVSEYPIVSIEDPFDQDDWETYAKLTAEIG QKVQIVGDDLLVTNPKRVAKAISEKTCNALLLKVNQIGSVTESIEAVKMSKQA GWGVMTSHRSGETEDTFIADLAVGLSTGQIKTGAPCRSERLAKYNQLLRIEEE LGSDAVYAGAS	89%
Contig32	*Penaeus monodon*	phosphopyruvate hydratase	>gi|3885968|gb|AAC78141.1| phosphopyruvate hydratase [Penaeus monodon] MSITKVFARTIFDSRGNPTVEVDLYTHKGLFRAAVPSGASTGVHEALEMRDGD KSKYHGKSVFKAVNNVNSIIAPEIIKSGLKVTQQKECDDFMCKLDGTENKSRL GANAILGVSLAICKAGAAELGIPLYRHIANLANYSDVILPVPAFNVINGGSHAG NKLAMQEFMILPTGATSFTEAMRMGSEVYHHLKAVIKGRFGLDATAVGDEG GFAPNILNNKDALTLIQESIEKAGYTGKIEIGMDVAASEFYKGENIYDLDFKTA NNDGSQKITGDQLRDMYMEFCKEFPIVSIEDPFDQDDWENWTKMTSATNIQIV GDDLTVTNPKRIATAVEKKACNCLLLKVNQIGSVTESIDAHLLAKKNGWGTM VSHRSGETEDCFIADLVVGLCTGQIKTGAPCRSERLAKYNQILRIEEELGGNAK FAGKKFRKPC	67%
Contig33	*Mentha arvensis*	menthofuran synthase	>gi|158979036|gb|ABW86890.1| menthofuran synthase [Mentha arvensis] MAALLVFFSLSLILLVVLFHKRSSSLLPSRKRRLPPSPSRLPVIGHLHLIGSLAHR SFHSLSKRYGEVML LHFGSAPVLVASSAAAAREIMKNQDMIFASRPRLSISDRLLYSGKDVAFAAYG EHWRHARSMCVLQLLSAKRVQSFRRIREEETSAMIEKIRRSQPSVVNLSEMFM ALTNGVVHRAALGRKDGGGDDSNLTLNKFIELLGRFNVGDYVPWLAWINRIN GVDAEVEKVFRKLDGFIEGILREYRMKNDTHASTNFVDTLLQFQRESKDTNPV EDDVIKALILDMFAAGIDTTSAVLEWTMAELIRNPRTLKTLQNEVREVSRNKG GITEDDVDKMPYLKAVSMEILRLHPPFPSLLPRELTQDANMLGYDVPRGTLVL VNNWAISRDPSLWENPEEFRPERFLETSIDYKGMHFEMLPFGSGRRGCPGITFA MSVYELALSKLVNEFDLRLGNGDRAEDLDMTEAPGIVVHKKSPLLVLATPRQ S	86%
Contig33	*Nepeta racemosa*	cytochrome P450	>gi|3582021|emb|CAA70575.1| cytochrome P450 [Nepeta racemosa] MVSLSYFLIALLCTLPFLLFLNKWRRSYSGKTPPPSPPKLPVIGNLHQLGLYPHR YLQSLSRRYGPLMQL HFGSVPVLVASSPEAAREIMKNQDIVFSNRPKMSIANRLFFNNRDVAFTQYGE YWRQIRSICVLQLLSNKRVQSFRRVREEETSIMVEKIMQLGSSSSTPVNLSELLL SLTNDVVCRVTLGKKYGGGNGSEEVDKLKEMLTEIQNLMGISPVWEFIPWLN WTRRFDGVDQRVDRIVKAFDGFLESVIQEHKERDGDKDGDGDGALDFVDILL QFQRENKNRSPVEDDTVKALILDMFVAGTDTTATALEWAVAELIKNPRAMKR LQNEVREVAGSKAEIEEEDLEKMPYLKASIKESLRLHVPVVLLVPRESTRDTN VLGYDIASGTRVLINAWAIARDPSVWENPEEFLPERFLDSSIDYKGLHFELLPF GAGRRGCPGATFAVAIDELALAKLVHKFDFGLPNGARMEELDMSETSGMTVH KKSPLLLLPIPHHAAP	57%
Contig34	*Nicotiana tabacum*	CYP71AT2v2	>gi|85068658|gb|ABC69409.1| CYP71AT2v2 [Nicotiana tabacum] MLFLLFVALPFILIFLLPKFKNGGNNRLPPGPIGLPFIGNLHQYDSITPHIYFWKL SKKYGKIFSLKLASTNVVVVSSAKLAKEVLKKQDLIFCSRPSILGQQKLSYYGR DIAFAPYNDYWREMRKICVLHLFSLKKVQLFSPIREDEVFRMIKKISKQASTSQI INLSNLMISLTSTIICRVAFGVRFEEEAHARKRFDFLLAEAQEMM ASFFVSDFFPFLSWIDKLSGLTYRLERNFKDLDNFYEELIEQHQNPNKPKYMEG DIVDLLLQLKKEKLTPLDLTMEDIKGILMNVLVAGSDTSAAATVWAMTALIK NPKAMEKVQLEIRKSVGKKGIVNEEDVQNIPYFKAVIKEIFRLYPPAPLLVPRE SMEKTILEGYEIRPRTIVHVNAWAIARDPEIWENPDEFIPERFLNSSIDYKGQDF ELLPFGAGRRGCPGIALGVASMELALSNLLYAFDWELPYGVKKEDIDTNVRPG IAMHKKNELCLVPKNYL	58%
Contig34	*Barnadesia spinosa*	germacrene A oxidase	>gi|294845888|gb|ADF43083.1| germacrene A oxidase [Barnadesia spinosa] MELTLTTSLGLAVFVFILFKLLTGSKSTKNSLPEAWRLPIIGHMHHLVGTLPHR GVTDMARKYGSLMHLQLGEVSTIVVSSPRWAKEVLTTYDITFANRPETLTGEI VAYHNTDIVLSPYGEYWRQLRKLCTLELLSAKKVKSFQSLREEECWNLVKEV RSSGSGSPVDLSESIFKLIATILSRAAFGKGIKDQREFTEIVKEILRLTGGFDVADI FPSKKILHHLSGKRAKLTNIHNKLDSLINNIVSEHPGSRTSSSQESLLDVLLRLK DSAELPLTSDNVKAVILDMFGAGTDTSSATIEWAISELIRCPRAMEKVQTELRQ ALNGKERIQEEDIQELSYLKLVIKETLRLHPPLPLVMPRECREPCVLAGYEIPTK TKLIVNVFAINRDPEYWKDAETFMPERFENSPINIMGSEYEYLPFGAGRRMCPG AALGLANVELPLAHILYYFNWKLPNGARLDELDMSECFGATVQRKSELLLVP	49%

			TAYKTANNSA	
Contig35	*Helianthus annuus*	heterotrophic ferredoxin 2	>gi|68137465|gb|AAY85661.1| heterotrophic ferredoxin 2 [Helianthus annuus] MSSFTLPTQTMVRTSPQTMVKTAPQTIVSAFLKYPSTLPTVKSISKTFGLKSGSS FRTTAMATYRVKLVTPDGEHEFDAPDDCYILDSAEAAGIELPYSCRAGACSTC AGKLHTGAVDQSDGSFLDDNQMKEGYLLTCISYPTGDCVVHTHEEGDLY	57%
Contig35	*Citrus sinensis*	non-photosynthetic ferredoxin	>gi|1360725|emb|CAA87068.1| non-photosynthetic ferredoxin [Citrus sinensis] MTTVTLSAPCMVKAAPRNQLSRNLIKSPTSLPSVKGISKTFGLKCSPNFQASMA VYKIKLIGPMGEEHEFEAQEDQYILDAAEEAGVDLPYSCRAGACSTCAGKLVS GSVDQSDGSFLDDNQMEAGYLLTCISYPTSDCVIQSHKEEELC	63%
Contig36	*Mentha arvensis*	limonene hydroxylase	>gi|146386316|gb|ABQ24001.1| limonene hydroxylase [Mentha arvensis] MELQISSAIIILVVTYTISLLIIKQWRKPKPEENLPPGPPKLPLIGHLHLLWGKLP QHALASVAKQYGPV AHVQLGEVFSVVLSSREATKEAMKLVDPACADRFDSIGTKIMWYDNDDIIFSP YSEHWRQMRKICVSGLLSARNVRSFGFIRQDEVSRLLGHLRSSAAAGEAVDLT ERIATLTCSIICRAAFGSVIRDHEELVELVKDALSMASGFELADLFPSSKLLNLL CWNKSKLWRMRRRVDTILEAIVEEHKLKKSGEFGGEDIIDVLFRMQKDSQIKV PITTNAIKAFIFDTFSAGTETSSTTTLWVMAELMRNPEVMAKAQVEVRAALKG KTNWDVDDVQELKYMKSVVKETMRMHPPIPLIPRSCREECEVNGYKIPNKARI MINVWSMGRNPLYWEKPKTFWPERFDQVSRDFMGNDFEFIPFGAGRRICPGL NFGLANVEVPLAQLLYHFDWNLAEGMKPSDMDMSEAEGLTGIRKNNLLLLPT PYDPSS	87%
Contig36	*Perilla frutescens*	(-)-limonene-7-hydroxylase	>gi|289466126|gb|ADC94830.1| (-)-limonene-7-hydroxylase [Perilla frutescens] LIKQWKTTENRGKLLPSPPKLPVIGHLHLMVGRLPQHVLTRAAQKYGPVMHL QLGEIFSVVVSPREATKQVMKGLDPACADRADSIGTKIMWYDNKDLIFSPYNA HWRQMRKICVSELLNARNEKSFGFIREDEMSRLVRFLRSSAGQAVNMTEKITA TTSSIICRAAFGSVVRDDEVLIGLVKTASGMANGFELADLFPSSKLLNLLCLNK YRLWKMRRELDAILEGVVEEHKLKQSGEFGGEDIVDVLLRMQKNSQLQFPITT DTIKGFIFDTFAAGTETSSTTTVWAMAELMKNPRVMANVQAEVREGLKGKKS VDASDVQQLKYLKSVVKETLRLHPPFPLIPRKCREDIEVEGYSIPSNSRIVINVW SLGRDPLYWEEPEIFWPERFDHISTDYVGNNFEFIPFGGGRRICPGLNLGVANV EVPLAQLLYHFDWKLGEPGMSPVHMDMTVAKGLSGPRKTPLFLVPSIYIPTQP N	63%
Contig37	*Thermomonospora curvata* DSM 43183	CDP-glycerol:poly(glycerophosphate)glycerophosph otransferase [Thermomonospora curvata DSM 43183]	>gi|269125463|ref|YP_003298833.1| CDP-glycerol:poly(glycerophosphate)glycerophosph otransferase [Thermomonospora curvata DSM 43183] MRPDVSVIVIAYNDAARLPRAVGSVLAQSLGPVETIIVDDGSTDGTGEVAEQL AAAHPGRVRALHLPRNSGGCGRPRNTGLAQARGAHVMFLDSDDVLDRHACL NLVAAAEETGADLVSGRCVRTRPDRPGDRGHAWYPWLYARRAVYESITQNP DLLYDTLSTNKCYRRDFLTACGLSFAEDVHYEDLLFSTQAYLAARRIALIPHR VYTWHWQQPRPDGGSISSRRAELRNFADRLEVHRRIDAVLRARGAADLKLHK DAKFVNHDLLLYLRELRGRDADYQRRFLELAAAYMAELDERVWQKANPMP AIAAFLLGRGDLEGALAAAEYGRGRVPELLTELTERHGRVYWGRLEGHPAHP VLDVTDLGIHTAPPSRVRPVCTLTRLRRCGPLVLMAGRVHNPLERIPPDAEVQ LTVEFADRRRKGRVLSVPAEVTRRKGWLQWRACFLPSRVLRPWGFIDPVWDL WLRLSVNGERTALRPRPADETVLETELPARPRLTRLAGDRLVPLRTRQDRVAF RLTGRRLRHRLARRAVRWAAATRAGRRLWRRIRAAEQDVRRRLGSQKTKQA VYNRLLVRLPIRKGTAVFESRMGACYAGNPRYIYEELRRSGRPIRVVWSYAGS PRGFPRDARLVRRGSWAYHLALARAEFWVDDHGFPGGLRKRRGTTYLQTWH GSAFKRMGLDHPELKRAGRAEQARFARMTGRFDRFLVRSRHDVDTLARGLG VAPDRLLPVGYPRNDPLVNGGDPAELAALRRALGLAGRQVVLYAPTFRPGRG GKAAPLRLPFDPVRFARELGDTHVMLVRPHYLTRVSLPPEAKAAVRDVGHIPD VTPLLLLADALVTDYSSIMFDYALLDRPMIFYVPDLEEYTGRDRGCYFDLAEH APGPLLREEDALLAALADLPAQRDAHAARRRAFAARFGEYDRGDAAARVVE LIFGGGDRDRT	32%
Contig37	*Drosophila erecta*	GG11745	>gi|194905518|ref|XP_001981213.1| GG11745 [Drosophila erecta] MAPRRNSNISSSGNSTQQQQQHHQQQLQQQQQQHQTQQHQLLQFYAENANS SGVLMAPMQGTGGVGVGVG GVGGVVHCCLPSGDCRKLDSLIPLNELSLADCIRVLCNNENCSAGQYMHRECF EWWEASVLQALKSNGRARSWSERQRLQHLWTKKGYELVQKACSCKCGRGQ LRKDLDWVPPSSQGVIYLNGSGNGRASLGNGSLSEDDDKKKAKKKRNRNNN GGGGGGNGNAKTPLSNNNGNSYAALTPNPNVGVIGSGLPHNNGNTTTSNGSG GNGSSAGLLQPSALATLSNILNPNNVLGLDLRARAGSLSSSGAGSGSTSPSASQ SSGEISVSPVQQLLQQQQQQSLLIQPLGPAFGSNLLQNGLGLSKNLLIAPQQQQ QQQQQQQQQQSNLPALANISNFKPLASYEQQQLVQQQKNKEVELYSERVRST SGCNGIFSRRLDFSSFNLLPKTRLNSYQVKIEDEGNHGNDETRLFILSSLAQSQM SRVACILCEEPLLVFDRYPLVDGSFFLSPKQHSSGCIEVKYEGRTLYLTCVCMS CLDGTSSSRVINCRFCKEPWDGSSLVLGTMYAYDIFAAMPCCAERFKCNNCFK MLMHPQQRLSFYSDYSHGVTCPYCNTQDTHFVKPLSFCYAKSPATRLPTLA	32%
Contig38	*Mus musculus*	mCG145424	>gi|148694049|gb|EDL25996.1| mCG145424 [Mus musculus] HWHFRQTLELSDCSWPVTVIRNTCPLYPVFGLELVAYFIHGTKSSPSDSYVYK HTHKHTYINIYIYIYIH TQTYIHTYIDTHKHSYIYKHTHTCIHRYIYKQIYKHTYVHTSMS	32%
Contig38	*Homo sapiens*	KLHL23 protein	>gi|16877407|gb|AAH16950.1| KLHL23 protein [Homo sapiens] MYMYVYTHIYVFICMRSYIRAYVYIYVYTYVCMYTYMCIHTCVCIHICVYIYM CVYIYTYIRIYVYIYTQLNQWD	31%
Contig39	*Atriplex nummularia*	lipid transfer protein	>gi|31879432|dbj|BAC77694.1| lipid transfer protein [Atriplex nummularia] MASSVVFKLACAVFMCMLVAAPHAEALTCGQVTSSMTPCMSYLTGGGSPTP ACCGGVKSLNSMASTPADRKAACGCLKSAAGAMTNLNMGNAASLPGKCGIS LPYPISTSTDCSKVN	42%
Contig39	*Oryza sativa*	lipid transfer protein precursor	>gi|902058|gb|AAA70046.1| lipid transfer protein precursor [Oryza sativa] AERASAAVSCGDVTSSIAPCLSYVMGRESSPSSSCCSGVRTLNGKASSSADRRT ACSCLKNMASSFRNLNMGNAASIPSKCGVSVAFPISTSVDCSKIN	41%
Contig39	*Tamarix hispida*	lipid transfer protein 2	>gi|223029865|gb|ACM78614.1| lipid transfer protein 2 [Tamarix hispida]	43%

			MAGSSALFKLACLVAAFMIVSAPHAEAAISCGTVVSKLAPCLGFLRGGGSPPP ACCSGIRNLQSMARSTPDRQAACGCLKSASAGVNMRNAAALPGKCGVNIGYP ISRSVDCSRVK	
Contig39	*Vitis aestivalis*	lipid transfer protein	>gi|37625029|gb|AAQ96338.1| lipid transfer protein [Vitis aestivalis] MGSSGAVKLACVMVICMVMAAPAAVEAAITCGQVASALSPCISYLQKGGAVP PACCSGIKSLNSSAKTTA DRQAACKCLKNFSSTVSGINLSLASGLPGKCGVSVPYKISPSTDCTKVT	41%
Contig40	*Ricinus communis*	dehydroquinate dehydratase/ shikimate dehydrogenase	>gi|255542470|ref|XP_002512298.1| shikimate dehydrogenase, putative [Ricinus communis] MGSVGELTSSVMVCTPLMAQSVEQMISDMYNAKTQGADVVEVRLDYIDNFQ PPQDLQAILRNKPLPVIIVYRPKSEGGLYEGDEPTRLEALRLAYVLGADYVDFE LKVASDLIGELKGTHHTGSKVIVSCYVNGDMPTKENLSQLVASMQATGADIIK LVSTANNITELDRIFHLILHCQVPIIAYSVGERGLISQLLSPKFGGSLLYGSMEGS SIPGLPTLDSLREAYKVAYINSDTKVFGLVSKPVSHSKGPLLHNPTFRHANYNG TYVPMFVDDLKEFFSVYSSPDFAGFSVGFPYKEAVVEFCDEVHPLAKSIGAVN TIIRRPGDGKLIGHNTDCEAAITAIEDALKEQGYMDGRTSSNSPLTGRQFVLVG AGGAGRALAFGAKSRGARIVIFDIDLERAKFLADAVSGEAQLFENVVNFEPEN GAILANATPIGMHPNTERIPVAEATLGIYQLVFDAVYTPRKTRLLKEAEAAGAI IVSGVEMFLRQAMGQFSLFTGREAPTEFMREIVLAKF	70%
Contig40	*Populus trichocarpa*	dehydroquinate dehydratase/ shikimate dehydrogenase	>gi|224128592|ref|XP_002320370.1| dehydroquinate dehydratase/ shikimate dehydrogenase [Populus trichocarpa] MAFKNNLLVCTPLECETAGEMLSSMKRAETEGADLTELRLDSLSFSHNSEVEK LIKQRTLPSIVSFRLEP SRISSNKDRKNTCLQVLRLAFDLNVEFVEMDYEVASEDDMAEYVYNRSNTKL IVSSYVNGRKPSAEELGYLIACMQSTGADVLKLVLDVEKITDLAPVFTMLTHC QIPLIALAVGSRGLISQLLGPKFGGFLVYGSLSDKAVPGMPTLLSLRQIYKLEYI NADTKVFGLISNPVGHSKGPVLHNPAFRHTGYNGIYVPMQVDDVKEFFRTYTS SDFAGFSVGIPHKEAAVGCCDEVHPLAKSIGAVNTIVRRPTDGKLVGYNTDCD ASISAIEDALTASPLSGKTFVLIGAGGAGRALAFGAKSRGARVIIFNRNYERAR ALAKAVSGEALPYESLDRFRPVNGMILANASAIGMEPNSDQSPVSKEILKACEL VFDAVYTPRNTRLLREAKEVGAVVVSGVEMFIRQALGQFRLFTGGLAPEAFM RKLVLEQF	56%
Contig41	*Catharanthus roseus*	1-hydroxy-2-methyl-butenyl 4-diphosphate reductase	>gi|113170997|gb|ABI30631.1| 1-hydroxy-2-methyl-butenyl 4-diphosphate reductase [Catharanthus roseus] MAISLQFSGLSTRTADLALPEPRIFRCSKPLSVRCSAAGEAPAVSSSSTESEFDA KKFRHNLARSKNYNR KGFGLKEQSTELMNREYASDIIKKLKENGYEYTWGNVTVKLAEAYGFCWGV ERAVQIAYEARKQFPTERLWLTNEIIHNPTVNQRLEEMKVQEIPIEDGKKQFDV VDKGDVVILPAFGAGVDEMLTVSDKNVQIVDTTCPWVVKVWNVVEKHKKG EYTSVIHGKYGHEETIATASFAGKYIIVKNMKEATYVCGYILGGQLDGSSSTRE AFMEKFKNAVSEGFDPDEDLIKVGIANQTTMLKGETEEIGKLIERTMMRKYGV QNVNDHFMSFNTFCDATQERQDAMYKLVDEPLDLMLVVGGWNSSNTSHLQE IAEERGIPSYWIDSEKRIGPGNKISYKLMHGELVEKENFLPEGPITIGVTSGASTP DKVVEDVLVKVFDIKREEALQLA	83%
Contig41	*Camptotheca acuminata*	hydroxymethylbutenyl diphosphate reductase	>gi|114329246|gb|ABI64152.1| hydroxymethylbutenyl diphosphate reductase [Camptotheca acuminata] MAISLQFCRLSTRVDLSLLESKVFGYRKPLSVRCASGESPSSSVAVDSDFDAKV FRKNLTRSKNYNRKGFGHKEETLEPMNREYTSDIIKTLKENGNEYTWGNVTV KLAESYGFCWGVERAVQIAYEARKQFPDEKIWITNEIIRNPTVNKRLEEMEVE NIPIEDGKKQFDVVDKGDVVILPAFGAGVDEMLVLSDKNVQIVDTTCPWVSK VWNTVEKHKKGEYTSIIHGKYSHEETVATASFAGKFIIVKNMAEATYVCDYIL GGELDGSSSTKEAFLEKFKYAVSKGFDPDSDLAKVGIANQTTMLKGETEEIGK LVERTMMRKYGVENVNEHFISFNTICDATQERQDAMYKLVEENLDLMLVIGG WNSSNTSHLQEISELRGIPSYWIDSEQRVGPGNKISFKLNHGELVEKENWLPQG PVTIGVTSGASTPDKVVEDVLIKVFDIKREEALQLA	81%
Contig42	*Arabidopsis thaliana*	VTE5 (vitamin E pathway gene5); phosphatidate cytidylyltransferase	>gi|15238184|ref|NP_196069.1| VTE5 (vitamin E pathway gene5); phosphatidate cytidylyltransferase/ phytol kinase [Arabidopsis thaliana] MAATLPLSPINHQLCRFGNNSLTTHRFCSPGFLISSPCFIGLTGMGSATQLRARR SLISSAVATNSLLHD VGATVAVLGGAYALVLSFESLTKRNVIQQSLSRKLVHILSGLLFVLAWPIFSGS TEARYFAAFVPLVNGLRLVINGLSISPNSMLIKSVTREGRAEELLKGPLFYVLA LLFSAVFFWRESPIGMISLAMMCGGDGIADIMGRKFGSTKIPYNPRKSWAGSIS MFIFGFFISIALLYYYSSLGYLHMNWETTLQRVAMVSMVATVVESLPITDQLD DNISVPLATILAAYLSFGY	80%
Contig42	*Lactuca sativa*	phytol kinase	>gi|229315933|gb|ACP43458.1| phytol kinase [Lactuca sativa] MAAAAVAAATTATNPKLSLLRPHFCPPRHAFYPTTPYLNLHGLRNASTFIQKQ RRLLLLPPRAFTLDVPGPLLQDAGATIIVVGGAYGLVAGFDYLTQRQIIEQNLS RKLVHILSGLLYMGCWPIFSTSTDARYFAVIAPLLNCTRLLVHGLSLVPNEDLI KSVTREGKPEELLRGPLYYVLMLILSSLLFWRDSPIGVVSLSMMCGGDGIADI MGRRFGLHKIPYNKQKSWVGSISMFMVGFLVSVGMLYYFSKLGYFELDWLK TMERVAMVAIVATLVESLPTKGGLDDNISVPLVSMLTAYLSFGF	76%
Contig43	*Vernicia fordii*	NADH:cytochrome b5 reductase	>gi|55979111|gb|AAV69019.1| NADH:cytochrome b5 reductase [Vernicia fordii] MDLEFLQTLDVQILVGVAVAVLAIGIGAVFLFSSKKPKGCLDPENFKDFKLVN RTQLSHNVAKFSFALPTPTSVLGLPIGQHISCRGKDSQGEEVIKPYTPTTLDSDV GHFELVIKMYPQGRMSHHFREMRVGDYLSVKGPKGRFRYQPGQVRAFGMLA GGSGITPMFQVARAILENPNDKTKVYLIYANVTYEDILLKQELDGLAANYPDR FKVYYVLNQPPEVWDGGVGFVSKEMIENHCPAPASDIQILRCGPPPMNKAMA AHLEALDYTSDMQFQF	88%

Contig43	*Zea mays*	cytochrome b5 reductase	>gi|4336205|gb|AAD17694.1| cytochrome b5 reductase [Zea mays] MDFLQEQSVETTVAVAVAVAAVAAGGAFLLLRSRKPKGCLDPENFRKFKLVEKKQISHNVARFKFALPTPTSVLGLPIGQHISCRGQDATGEEVIKPYTPTTLDSDLGYFELVIKMYPQGRMSHHFREMKVGDYLSVKGPKGRFKYHVGQVRAFGMLAGGSGITPMFQVARAILENPNDNTKVHLIYANVTYEDILLKDELDDMAKTYPGRFKIYYVLNQPPENWNGGVGFVSKEMIQSHCPAPAEDIQILRCGPPPMNKAMAAHLDELNYTKEMQFQF	83%
Contig43	*Zea mays*	ferric-chelate reductase (NADH)2	>gi|162457908|ref|NP_001106072.1| ferric-chelate reductase (NADH)2 [Zea mays] MEFLQGQRLETTLAVAAAVVAVAAGSAYLFLRSRKPRGCLDPENFKEFKLVEKKQLSHNVAKFKFALPTPTSVLGLPIGQHISCRGQDASGEEVIKPYTPTTLDSDIGSFELVIKMYPQGRMSHHFRETKVGDYMSVKGPKGRFKYLPGQVRAFGMVAGGSGITPMFQVTRAILENPKDNTKVHLIYANVTYEDILLKEELDGMAKNYPDRFKIYYVLNQPPEVWDGGVGFVSKEMIQTHCPAPAADIQVLRCGPPPMNKAMAAHLDGLGYTKEMQFQF	82%
Contig44	*Catharanthus roseus*	GCPE protein	>gi|27903511|gb|AAO24774.1| GCPE protein [Catharanthus roseus] MATGTVPASFTGLKSRENGLGFAKSMDFVQVSDLRRVKFRRAKVSVIKNSNPGPETVELQPASQGSQLLVPVQKYCESIHKTVRRKTRTVMVGNVALGSDHPIRIQTMTTTDTKDVAATVEQVMGIADKGADIVRITVQGKKEADACYDIKNTLVQKSYNIPLVADIHFAPAVALRVAECFDKIRVNPGNFADRRAQFEQLEYTDEEYQKELEHIEQVFTPLVEKCKKYGRAMRIGTNHGSLSDRIMSYYGDSPRGMVESAFEFARICRKLDFHNFVFSMKASNPVIMVAAYRLLVAEMYVLGWDYPLHLGVTEAGEGEDGRMKSAIGIGTLLQDGLGDTIRVSLTEPPEEEIDPCRRLANLGARAADLGQGVAPFEEKHRRYFDFQRRTGDLPVQKEGEEVDYRGVLHRDGSVLMSVSLDQLKTPELLYKSLAAKLVVGMPFKDLATVDSILLRELPPIEDKDSRLALKRLIDISMGVITPLSEQLTKPLPNAMVLVTLKELSSGAHKLLPEGTRLVVSVRGDEPYEELDILKNVDVTMILHNLPHTEEKIGRVHAARRLFEYLSENSLNFPVIHHMQFANAIHRDDLVIGAGSDAGALLVDGLGDGVMLEAHDQDFEFLRNTSFNLLQGCRMRNTKTEYVSCPSCGRTLFDLQEISAQIREKTSHLPGVSIAIMGCIVNGPGEMADADFGYVGGAPGKIDLYVGKTVVKRGIDMEHATDALIQLIKDHGRWVDPPAED	88%
Contig44	*Physcomitrella patens* subsp. patens	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	>gi|168028097|ref|XP_001766565.1| 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase [Physcomitrella patens subsp. patens] MAPELVEMKPASEGSQLLAVPRKKYCESIYKPIRRKTRTVNVGGVTVGSEHPIRVQTMTTTDTKDVQRTVEQVMRIADKGCDIVRITVQGKKEADACYSIKNTLVQKGYNIPLVADIHFAPPIAMKVAEFFDKIRINPGNFADRRAQFEKLVYTDADYAEELRHIEEVFTPLVEKCKKYGRAMRIGTNHGSLSDRIMSYHGDSPRGMVESAFQFARICRKNDFHNFVFSMKASNSVVMVQAYRLLVFEMYVNDWDYPLHLGVTEAGEGEDGRMKSAIGIGALLQDGLGDTIRVSLTEAPEEEIDPCSKLANLGMKISAKQKGLPEFQENHRRYFDFERRTGQLPLQKEGDLVDVRNVLHRDGSVLMSVTLDQLKNPEALYRNLATKLIMGMPYKDLATVDTIFLNKLPAAEDRASRLAVKRLTDVGIGVLTPVAEQLVNSLPHAMALATLDEIASGTHKELPTGIRLAVTLRGDEPEEKLEMLKDLDLIMLLQYLPEGDEKSSHVHASRKLFEYLQTNKLDFPVIHHLKFPANTHRDDLVIKAGSEAGAMLVDGLGDGIMLEAADQDFDFIRNTSFGMLQGCRMRHTKTEYVSCPSCGRTLFDLQEISAEIREKTDHLPGVSIAIMGCIVNGPGEMADADFGYVGGAPGKIDLYVGKEVVRRGIAMAMATNELIGLIKEHGRWVDPEPTET	63%
Contig45	*Solanum lycopersicum*	caryophyllene/alpha-humulene synthase	>gi|291337348|gb|ADD96698.1| caryophyllene/alpha-humulene synthase [Solanum lycopersicum] MASSSANKCRPLANFHPTVWGYHFLSYTHEITNQEKVEVDEYKETIRKMLVEAPEGSEQKLVLIDAMQRLGVAYHFDNEIETSIQNIFDASSKQNDNDNNLYVVSLRFRLVRQQGHYMSSDVFKQFINQDGKFKETLTNDVQGLLSLYEASHLRVRDEEILEEALTFTTTHLESTVSNLSNNNSLKAEVTEAFSQPIRMTLPRVGARKYISIYENNDAHNHLLLKFAKLDFNMLQKLHQRELSDLTRWWKDLDFANKYPYARDRLVECYFWILGVYFEPKYSRARKMMTKVIQMASFFDDTFDAYATFDELEPFNNAIQRWDINAIDSVPPYLRHAYQALLDIYSEMEQALAKEFKSDRVYYAKYEMKKLVRAYFKEAQWLNNDNHIPKYEEHMENAMVSAGYMMGATTCLVGVEEFISKETFEWMINEPLIVRASSLIARAMDDIVGHEVEQQREHGASLIECYMKDYGVSKQEAYVKFQKEVTNGWMDINREFFCPDVEVPKFVLERVLNFTRVINTLYKEKDEYTNSKGKFKNMIISLLVESVEI	54%
Contig45	*Solanum lycopersicum*	germacrene C synthase	>gi|2967689|gb|AAC39432.1| germacrene C synthase [Solanum lycopersicum] MAASSADKCRPLANFHPSVWGYHFLSYTHEITNQEKVEVDEYKETIRKMLVETCDNSTQKLVLIDAMQRLGVAYHFDNEIETSIQNIFDASSKQNDNDNNLYVVSLRFRLVRQQGHYMSSDVFKQFTNQDGKFKETLTNDVQGLLSLYEASHLRVRNEEILEEALTFTTTHLESIVSNLSNNNNSLKVEVGEALTQPIRMTLPRMGARKYISIYENNDAHHHLLLKFAKLDFNMLQKFHQRELSDLTRWWKDLDFANKYPYARDRLVECYFWILGVYFEPKYSRARKMMTKVLNLTSIIDDTFDAYATFDELVTFNDAIQRWDANAIDSIQPYMRPAYQALLDIYSEMEQVLSKEGKLDRVYYAKNEMKKLVRAYFKETQWLNDCDHIPKYEEQVENAIVSAGYMMISTTCLVGIEEFISHETFEWLMNESVIVRASALIARAMNDIVGHEDEQERGHVASLIECYMKDYGASKQETYIKFLKEVTNAWKDINKQFSRPTEVPMFVLERVLNLTRVADTLYKEKDTYSTAKGKLKNMINPILIESVKI	53%
Contig46	*Solanum tuberosum*	NADH dehydrogenase	>gi|639834|emb|CAA58823.1| NADH dehydrogenase [Solanum tuberosum] MAPIKGLLSLQRTALAQRSSERWGLYGRLFSTQAASTASTPQPTPPPPPPERTHFGGLKDEDRIFTNLYG LHDPYLKGAMKRGDWYRTKDLVIKGSDWIVNEMKKSGLRGRGGAGFPSGLKWSFMPKTTDGRPSYLVVNADESEPGTCKDREIMRHDPHKLLEGCLIAGVGMR	88%

			AKAAYIYIRGEYVNERKSLQKARQEAYEAGLLGKNACGSGYDFDVYIHFGAG AYICGEETALLESLEGKQGKPRLKPPFPANAGLYGCPTTVTNVETVAVSPTILR RGPEWFASFGRKNNAGTKLFCISGHVNKPCTVEEEMSISLKELIERHCGGVRG GWDNLLAVIPGGSSVPLLPKNICEDVLMDFDALKAVQSGLGTAAVIVMDKST DVVDAIARLSYFYKHESCGQCTPCREGTGWLWMIMERMKVGNAKLEEIDML QEVTKQIEGHTICALGDAAAWPVQGLIRHFRPELERRIREHAERELQQAAAA	
Contig46	*Novosphingobium aromaticivorans* DSM 12444	NADH dehydrogenase I subunit F	>gi|87200309|ref|YP_497566.1| NADH dehydrogenase I subunit F [Novosphingobium aromaticivorans DSM 12444] MALQDKDRIFTNVYGFQPWNLAAARARGDWDNTKALMERGQDAIIEEIKAS GLRGRGGAGFPTGMKWSFMPKESKDGRPSFLVINADESEPGSCKDREIIRHDP HKLIEGALIAGYAMRARAAYIYIRGEYIREADTLFAAVQEAYDAGLIGKNASG SGYDFDVFVHRGAGAYICGEETAMIESLEGKKGQPRLKPPFPAGAGLYGCPTT VNNVESIAVAPTILRRGASWFSSFGRENNKGTKLFQISGHVNRPCVVEEEMSIP FSELIEKHCGGIRGGKDNLLAVIPGGSSVPLVPAAEIWDAPMDFDGLRALGSGL GTAAVIVMDKSTDIVRAISRLSYFYKHESCGQCTPCREGTGWMWRVMERLRT GDADVEEIDMLFNVTKQVEGHTICALGDAAAWPIQGLIRHFRPEIERRIAENAR EAAE	83%
Contig47	*Manihot esculenta*	aldo/keto reductase AKR(**Q52QX9)**	>gi|62526573|gb|AAX84672.1| aldo/keto reductase AKR [Manihot esculenta] MAGAAVKRIKLGSQGLEVSAQGLGCMSMSAFYGPPKPESDMIALIHHAINTG VTFFDTSDVYGPHTNEILLGKALKGDIRKKVELATKFAINLKDGKREIRGDPAY VRAACEASLKRLDVDCIDLYYQHRVDTSVPIEVTVGELKKLVEEGKIKYIGLSE ASASTIRRAHAVHPITAVQLEWSLWSRDVEEEIVPTCRELGIGIVAYSPLGRGFF SSGPKLVETLSEGDFRKYLPRFQPENLEHNKHLFERVNEIAARKQCTPSQLALA WVHHQGDDVCPIPGTTKIENFNQNIGALSVKLTPEDMAELESIASASAVKGGR YGSDMGTYKDSDTPPLSSWKAV	74%
Contig47	*Arabidopsis thaliana*	auxin-induced atb2	>gi|6562980|gb|AAF17106.1|AF057715_1 auxin-induced atb2 [Arabidopsis thaliana] MAEACGVRRMKLGSQGLEVSAQGLGCMGLSAFYGAPKPENEAIALIHHAIHS GVTLLDTSDIYGPETNEVLLGKALKDGVREKVELATKFGISYAEGKREVRGDP EYVRAACEAKFKRLDIACIDLYYQHRVDTRVPIEITMGELKKLVEEGKIKYIGL SEASASTIRRAHAVHPITAVQIEWSLWTRDVEEEIIPTCRELGIGIVAYSPLGRGF FASGPKLVENLEKDDFRKALPRFQEENLDHNKIVYEKVCAISEKKGCTPGQLA LAWVHHQGDDVCPIPGTTKIENLKQNIGALSVKLTPEEMTELEAIAQPGFVKG DRYSNMIPTFKNAETPPLSAWKAA	72%
Contig48	*Manihot esculenta*	aldo/keto reductase AKR	>gi|62526573|gb|AAX84672.1| aldo/keto reductase AKR [Manihot esculenta] MAGAAVKRIKLGSQGLEVSAQGLGCMSMSAFYGPPKPESDMIALIHHAINTG VTFFDTSDVYGPHTNEILLGKALKGDIRKKVELATKFAINLKDGKREIRGDPAY VRAACEASLKRLDVDCIDLYYQHRVDTSVPIEVTVGELKKLVEEGKIKYIGLSE ASASTIRRAHAVHPITAVQLEWSLWSRDVEEEIVPTCRELGIGIVAYSPLGRGFF SSGPKLVETLSEGDFRKYLPRFQPENLEHNKHLFERVNEIAARKQCTPSQLALA WVHHQGDDVCPIPGTTKIENFNQNIGALSVKLTPEDMAELESIASASAVKGGR YGSDMGTYKDSDTPPLSSWKAV	81%
Contig48	*Helianthus annuus*	auxin-induced protein	>gi|2606077|gb|AAB84222.1| auxin-induced protein [Helianthus annuus] MARVPRVKLGSQGLEVSAQGLGCMSMSAFYGPPKPEPDMINLIHHAVNSGVT FVDTSDYYGPKTNEILLGKALKGGMRDKVELATKYGIKLSGSWEVKGDPAYV RAACEASLKRLYVDCIDLYYQHRIDTRVPIEITMGELKELVEEGKIKYVGLSEA SASTIRRAHSVHPITAIQLEWSLWSRDVEEDIIPTCRELGIGIVAYSPLGRGFFAS GSKMMEKLEDGDYRPNFPRFQPENLEHNKILYERVSEIASKKGCTTSQLALAW VHHQGNDVVPIPGTTKIENLEQNIGALSVKITPEEMAELESTTHLVKGARCNA GTPTYLDSETLPLSSWKS	79%
Contig49	*Arabidopsis thaliana*	At1g04290	>gi|164709653|gb|ABY67521.1| At1g04290 [Arabidopsis thaliana] AKEPMVAKLPHRFLERFVTNGLKVDLIEPGRIVCSMKIPPHLLNAGKFLHGGA TATLVDLIGSAVIYTAG ASHSGVSVEINVSYLDAAFLDEDIEIESKALRVGKAVAVVSVELRKKTTGKIIA QGRHTKYFAP	71%
Contig49	*Zea mays*	thioesterase superfamily member 2	>gi|195609384|gb|ACG26522.1| thioesterase superfamily member 2 [Zea mays] MGPEAVRKSLEPTATAEEITGSTPARLHFYDPFVLSGVRIEAAEHGRLLCSFVV TPRLASPVGYLRSGVT ATLADQLGSAVFFCSGIPSSGVSIEISVSFVDSAAVGEEIEVEGKLLRAGKSVGV VSVDFRKKKTGKLMAQARHTKYLVASSKL	57%
Contig50	*Medicago truncatula*	Aldo/keto reductase	>gi|124360844|gb|ABN08816.1| Aldo/keto reductase [Medicago truncatula] MATVGRMKLGSQGMEVSLQGLGCMSMSAFYGPPKPQTDMIALIHHAIQSGVT FLDTSDIYGPHTNELLLGKALKGGVREKVELATKFGAKYTEGKFEICGDPAYV REACEASLKRLDIDCIDLYYQHRIDTRLPIEITIGELKKLVEEGKIKYIGLSEASA STIRRAHAVHPITAVQLEWSLWSRDVEEEIIPTCRELGIGIVAYSPLGRGFFSSGT KIVENFTKDDYRQYMPRFQPENLQQNQTIFERVNELAAKKGCTPSQLALAWL HHQGNDVCPIPGTTKIENFNQNIGALSVKLTQEEMAEIESLADLVEGDRTGKEP TWKESDTPPLSSWKTA	76%
Contig50	*Helianthus annuus*	auxin-induced protein	>gi|2606077|gb|AAB84222.1| auxin-induced protein [Helianthus annuus] MARVPRVKLGSQGLEVSAQGLGCMSMSAFYGPPKPEPDMINLIHHAVNSGVT FVDTSDYYGPKTNEILLG KALKGGMRDKVELATKYGIKLSGSWEVKGDPAYVRAACEASLKRLYVDCID LYYQHRIDTRVPIEITMGELKELVEEGKIKYVGLSEASASTIRRAHSVHPITAIQ LEWSLWSRDVEEDIIPTCRELGIGIVAYSPLGRGFFASGSKMMEKLEDGDYRPN FPRFQPENLEHNKILYERVSEIASKKGCTTSQLALAWVHHQGNDVVPIPGTTKI ENLEQNIGALSVKITPEEMAELESTTHLVKGARCNAGTPTYLDSETLPLSSWKS	76%
Contig51	*Portulaca oleracea*	omega-6 fatty acid desaturase	>gi|239618581|gb|ACR83861.1| omega-6 fatty acid desaturase [Portulaca oleracea] MGAGGRSIAPSVTKDKANALGRSPYAKPPFTLSQLKKAIPPHCFKRSVLRSFSY VVYDFILASIIYYLATTYIDLLPKPLSYFSWAVYGFVQGCVLTGLWVIAHECGH HAFSDHQWLDDTVGLVLHSFLLVPYFSWKYSHRRHHSNTGSMEKDEVFVPK RKSGLQWFSKYLNNPPGRVLTLTITLTLGWPLYLLFNVSGRHYDRYACHYDP YGPIYSDRERLQIYISDAGILAVVYGLYRLTAARGIMWVLCVYGGPLLVVNGF LVLITFLQHTHPSLPHYDSSEWDWLRGALATVDRDYGVLNKVFHNITDTHVG HHLFSTMPHYHAMEATKAIKPILGEYYQFDGTPFYKAMWREAKECLYVEPDE GEQNKGIHWYNNKL	84%

Contig51	*Vernicia montana*	delta-12 oleic acid desaturase	>gi|119655554|gb|ABL86147.1| delta-12 oleic acid desaturase [Vernicia montana] MGAGGRMSVPPPPKKLESEVLKRVPHSKPPFTLGQLKKAIPPHCFQRSVLRSFS YVVYDLTMAFIFYYIATNYFRLLPQPLSYVAWPIYWALQGCVLTGVWVIAHE CGHHAFSGYQLLDDIVGLVLHSCLLVPYFSWKHSHRRHHSNTASLERDEVFVP KKKSSIRWFSKYLNNPPGRLFTLTITLTLGWPLYLAFNVSGRPYDRFACHYDP YGPIYTDRERTEIFISDAGVLAVTFGLYRLAAAKGLAWVICVYGVPLLIVNAFL VMITYLQHTHPSLPHYDSSEWDWLRGALATVDRDYGILNKVFHNITDTHVAH HLFSTMPHYHAMEASKAIKPILGEYYQFDGTPFYKAMWREAKECIYVEADDG DESKGVYWYNKEF	83%
Contig52	*Mentha x piperita*	flavonoid 8-O-methyltransferase	>gi|38047395|gb|AAR09600.1| flavonoid 8-O-methyltransferase [Mentha x piperita] MALPNGISSKQELLEAQAHVWNHIYSYINSMSLKCAIQLGIPDAIHKHGNPITL SQLADALNINKAKSHGLFRLMRILVHSGFFDKVKVKVKVEGEDEEEEEDAYSL TPASRLLLRSEPLSVAPFALAMSDPVYTETWHHLSEWFRNDAVAAFDTKYGM TFPEYAVADDRLNVLFNEAMACDAGFVNSILTTECREIFDGLESMVDVGGGT GATAKGIAAAFPGMECTVLDLPNVVGGLKGSENLSFVSGDMFDFIPHADAIFM KFILHDWNDEECVKILKKCKEAISRSNNSCRKIILVEIVMEDEKETHEATETKLF FDMQMLAIITGKERSEKEWGKLFFDAGFTNYKITRVLGLRSVIEVFP	88%
Contig52	*Rosa hybrid cultivar*	orcinol O-methyltransferase	>gi|27527928|emb|CAD29556.1| orcinol O-methyltransferase [Rosa hybrid cultivar] NQKWSNGEHSNELLHAQAHIWNHIFSFINSMSLKSAIQLGIPDIINKHGYPMTL SELSSALPIHPTKSHS VYRLMRILVHSGFFAKKKLSKIDEEGYTLTDASQLLLKDHPLSLTPFLTAMLDP VLTKPWNYLSTWFQNDDPTPFDTTHGMTFWDYGNHQPNIAHLFNDAMASDA RLVTSVIIDDCKGVFEGLESLVDVGGGTGTVAKAIADAFPHIECTVLDLPHVVG DLQGSKNLKYTGGDMFEAVPPADTVLLKWILHDWNDEECIKILKRSRVAITSK DKKGKVIIIDMMMENQKGDEESIETQLFLDMLMMALVGGKERNEKEWAKLF TDAGFSDYKITPILG	52%
Contig53	*Populus trichocarpa*	unknown	>gi|118484549|gb|ABK94148.1| unknown [Populus trichocarpa] MIYRKWSLLTGPMVILGGIMGTAVAVRVLFFENPYLKPEQKKQDSTPLTK	52%
Contig53	*Vitis vinifera*	unnamed protein product	>gi|270258452|emb|CBI40486.1| unnamed protein product [Vitis vinifera] MIYRKWSLLTGPVAILAAIAVPVTIINYIIVKDDLFPSPEKVKNDQGSTNK	33%
Contig54	*Oryza sativa* (japonica cultivar-group)]	Os01g0652700	>gi|115486127|ref|NP_001068207.1| Os11g0594800 [Oryza sativa (japonica cultivar-group)] MASQIIETNRAGAEIINGDAAGKKKSIELLQELGLPKGLFPLDDIEEFGYNRAN GFMWILHSKKKEHTFK KIKQTVSYATEVTAFVEKGKLKKIAGVKTKELMLWLSVVEVYVEESSAEKITF KTGTGLSDSFDASAFEL GM	57%
Contig55	*Gossypium hirsutum*	ATP synthase delta subunit 2	>gi|242129048|gb|ACS83603.1| ATP synthase delta subunit 2 [Gossypium hirsutum] MFRQASRLLARTTTPWRGSRAFSSDVPATPAQDSSFIESWSKVIPNLDPPKTPS SFMTPRPATPSAIPSK LTVNFVLPYASELSAKEVDMVIVPATTGQMGILPGHVPTIAELKPGILSVHEGN DVTKYFLSSGFALIHANSVADIIAVEAVPVDRLDPALVQKGLADFTQKLVSAT TDLEKAEAQIGVDVHSAMNSAITG	75%
Contig55	*Brassica rapa*	hydrogen-transporting ATP synthase	>gi|119720786|gb|ABL97963.1| hydrogen-transporting ATP synthase [Brassica rapa] MLRQASRLLSRSVTAASSKSVTARAFSTELPSTVDSTFVESWKKVAPNMDPPQ TPSSFMKPRPSTASSIP TKLTVNFVLPYASELSGKEVDMVIIPATTGQMGVLPGHVPTIAELKPGIMSVHE GTDIKKYFVSSGFAFL HANSVADIIAVEAVPLENIDASQVQKGLADFTQKLASASTDLEKAEAQIGVEV HSAMNAALSG	74%
Contig56	*Arabidopsis thaliana*	PKp3 (plastidial pyruvate kinase 3); pyruvate kinase	>gi|18398434|ref|NP_564402.1| PKp3 (plastidial pyruvate kinase 3); pyruvate kinase [Arabidopsis thaliana] MAAYGQISSGMTVDPQVLSSSRNIGVSLSPLRRTLIGAGVRSTSISLRQCSLSVR SIKISEDSRKPKAYA ENGAFDVGVLDSSSYRLADSRTSSNDSRRKTKIVCTIGPSSSSREMIWKLAEAG MNVARLNMSHGDHASHQITIDLVKEYNSLFVDKAIAIMLDTKGPEVRSGDVP QPIFLEEGQEFNFTIKRGVSLKDTVSVNYDDFVNDVEVGDILLVDGGMMSLAV KSKTSDLVKCVVIDGGELQSRRHLNVRGKSATLPSITDKDWEDIKFGVDNQVD FYAVSFVKDAKVVHELKNYLKTCSADISVIVKIESADSIKNLPSIISACDGAMV ARGDLGAELPIEEVPLLQEEIIRRCRSIHKPVIVATNMLESMINHPTPTRAEVSDI AIAVREGADAIMLSGETAHGKFPLKAVNVMHTVALRTEASLPVRTSASRTTA YKGHMGQMFAFHASIMANTLSSPLIVFTRTGSMAVLLSHYRPSATIFAFTNQR RIMQRLALYQGVMPIYMEFSDDAEDTYARSLKLLQDENMLKEGQHVTLVQS GSQPIWREESTHLIQVRKIKIGG	76%
Contig56	*Arabidopsis thaliana*	PKP-BETA1 (PLASTIDIC PYRUVATE KINASE BETA SUBUNIT 1); pyruvate	>gi|15237303|ref|NP_200104.1| PKP-BETA1 (PLASTIDIC PYRUVATE KINASE BETA SUBUNIT 1); pyruvate kinase [Arabidopsis thaliana] MAQVVATRSIQGSMLSPNGGSVSTRSEKLLKPASFAVKVLGNEAKRSGRVSV RSRRVVDTTVRSARVETEVIPVSPEDVPNREEQLERLLEMQQFGDTSVGMWS KPTVRRKTKIVCTVGPSTNTREMIWKLAEAGMNVARMNMSHGDHASHKKVI DLVKEYNAQTKDNTIAIMLDTKGPEVRSGDLPQPIMLDPGQEFTFTIERGVSTP SCVSVNYDDFVNDVEAGDMLLVDGGMMSFMVKSKTKDSVKCEVVDGGELK SRRHLNVRGKSATLPSITEKDWEDIKFGVENKVDFYAVSFVKDAQVVHELKK YLQNSGADIHVIVKIESADSIPNLHSIITASDGAMVARGDLGAELPIEEVPILQEE IINLCRSMGKAVIVATNMLESMIVHPTPTRAEVSDIAIAVREGADAVMLSGETA HGKFPLKAAGVMHTVALRTEATITSGEMPPNLGQAFKNHMSEMFAYHATMM SNTLGTSTVVFTRTGFMAILLSHYRPSGTIYAFTNEKKIQQRLALYQGVCPIYM EFTDDAEETFANALATLLKQGMVKKGEEIAIVQSGTQPIWRSQSTHNIQVRKV	62%
Contig57	*Mentha x piperita*	flavonoid 7-O-methyltransferase	>gi|38047393|gb|AAR09599.1| flavonoid 7-O-methyltransferase [Mentha x piperita] MAPKEDSLALAEAWNHGFGFIKTSIVKTAVELGIPDILESRGAPVSIPELAAAV DCSADRLYRVMRFLAY HGIFKRTEPPPESTGGGSVYYAQTLVSRRLTRENLGPFVLLQGTMREPSGCVTA ETLRMSKRPGLVDDNDSDRLYEDPVFSMKVFRDAMASHARMTTAAVIENYG EGFLGVGSLVDVGGSYGMALSMLVKAFPWLRGICFDLPEVVARASPLKGVEF VAGSMFESIPKADVVMLMFVLHNWSDEECVEILKRCKDAVPKNKGKVIIIDAV	67%

			IDEDGNGDEFTGARLGLDVTMMANMFEGRERTYVEWAHIINEAGFRRHVVKNIKTLESVIEAYP	
Contig57	*Populus trichocarpa*	flavonoid o-methyltransferase predicted protein	>gi|224103121|ref|XP_002312933.1| flavonoid o-methyltransferase predicted protein [Populus trichocarpa] MGSVTKIDEEIREDEEEAQAKVEIWKYIFGFTNMAVVKCAIELGIADAIENNEGPMTLSELSSSLGCAPS SLYRIMRFLVHHNIFKEKPSSQLGTTVYVQTALSRRLLKKGEKSMVDLLLLESSHVMMAPWHNLSSRVLNDNNSPFEGAHGDDIWKYALANPVHSKLIDDAMACDAKLVVPEIVEGFPEVFDGVKTLVDVGGGNGTTLQMLVKAFPWIQGINFDLPHVVSVASESEGVKHVGGDFFESVPKADAAFLMWVLHDWNDEECIQILKNCKEAIQSDKGKVIIVEAVVGEEKGDKLEFVRLMLDMVMMSHTDAGKERTSKEWGYVLKEAGFSSYTIKPIRAVQSVIVASP	51%
Contig58	*Arabidopsis thaliana*	HS1 (HEAT STABLE PROTEIN 1)	>gi|18401423|ref|NP_566569.1| HS1 (HEAT STABLE PROTEIN 1) [Arabidopsis thaliana] MEEAKGPVKHVLLASFKDGVSPEKIEELIKGYANLVNLIEPMKAFHWGKDVSIENLHQGYTHIFESTFESKEAVAEYIAHPAHVEFATIFLGSLDKVLVIDYKPTSVSL	53%
Contig58	*Arabidopsis thaliana*	pop3 peptide	>gi|21554999|gb|AAM63750.1| pop3 peptide [Arabidopsis thaliana] MEEAKGPVKHVLLASFKDGVSPEKIEELIKGYANLVNLIEPMKAFHWGKDVSIENLHQGYTHIFESTFESKEAVAEYIAHPAHVKFATIFLGSLDKVLVIDYKPTSVSL	52%
Contig59	*Nicotiana suaveolens*	S-adenosyl-L-methionine synthase	>gi|115361537|gb|ABI95859.1| S-adenosyl-L-methionine synthase [Nicotiana suaveolens] METFLFTSESVNEGHPDKLCDQVSDAILDACLEQDPESKVACETCTKTNMVMVFGEITTKATVDYEKIVRDTCRGIGFTSADVGLDADNCKVLVNIEQQSPDIAQGVHGHLTKKPKEIGAGDQGHMFGYATDETPELMPLTHVLATKLGAKLTEVRKNKTCPWLKPDGKTQVTVEYKNDNGAMVPIRVHTVLISTQHDETVTNDQIAQDLKEHVIKPVIPAQYLDEKTIFHLNPSGRFVIGGPHGDAGLTGRKIIIDTYGGWGAHGGGAFSGKDPTKVDRSGAYIVRQAAKSVVASGLARRCIVQVSYAIGVAEPLSVFVDTYKTGTIPDKDILALIKENFDFRPGMMSINLDLLRGGNFRYQKTAAYGHFGRDDPDFTWETVKVLKPKA	94%
Contig59	*Arabidopsis thaliana*	MAT3 (methionine adenosyltransferase 3); copper ion binding / methionine adenosyltransferase	>gi|15228048|ref|NP_181225.1| MAT3 (methionine adenosyltransferase 3); copper ion binding / methionine adenosyltransferase [Arabidopsis thaliana] METFLFTSESVNEGHPDKLCDQISDAILDACLEQDPESKVACETCTKTNMVMVFGEITTAAKVDYEKIVRSTCREIGFISADVGLDADKCNVLVNIEQQSPDIAQGVHGHLTKKPEDIGAGDQGHMFGYATDETPELMPLTHVLATKLGAKLTEVRKNKTCPWLRPDGKTQVTVEYKNDGGAMIPIRVHTVLISTQHDETVTNDEIAADLKEHVIKPVIPAKYLDDNTIFHLNPSGRFVIGGPHGDAGLTGRKIIIDTYGGWGAHGGGAFSGKDPTKVDRSGAYIVRQAAKSVVAAGLARRCIVQVSYAIGVPEPLSVFVDTYKTGTIPDKDILVLIKEAFDFRPGMMAINLDLKRGGNFRFQKTAAYGHFGRDDPDFTWEVVKPLKPKA	91%
Contig60	*Ageratina adenophora*	2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	>gi|294769206|gb|ADF36484.1| 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase [Ageratina adenophora] MATSSSCYTSPISTGIFPKHQPTIPTSTSFLTCFTRRSPISLRSVSRPVVVAAAANAVEVEKQAVTKTPS KILPFRVGHGFDLHRLEPGYPLIIGGINIPHERGCEAHSDGDVLLHCVVDAILGALGLPDIGQIFPDNDP KWKGAASSVFIKEAVRLMHEAGYELGNLDATLILQRPKLSPHKEAIRDNLSLLLGADPSVVNLKAKTHEKVDSLGENRSIAAHTVVLLMKK	67%
Contig60	*Citrus jambhiri*	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	>gi|152962682|dbj|BAF73931.1| 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase [Citrus jambhiri] MVLTMAAQSYTTAPLHSKITNKPLCPPPLSLKPRSLTAKHLRTTQSTSLPRISVSAAATSSIEVKESSAS IQPSKSKSLPFRVGHGFDLHRLEPGYPLIIGGINVPHERGCEAHSDGDVLLHCVVDAILGALGLPDIGQI FPDSDPKWKGAPSSVFIKEAVRLMDEAGYEIGNLDATLILQRPKLSPYKETIRTSLSELLGADPAVVNLKAKTHEKVDSLGENRSIAAHTVILLMKK	79%
Contig61	*Ocimum basilicum*	alcohol dehydrogenase-like protein	>gi|62461972|gb|AAX83109.1| alcohol dehydrogenase-like protein [Ocimum basilicum] MANNTNAGVITCKAAAAWKPSEPLVVEEICVEPPKSTEVRIKMLAASMCHTDILLWKGFFPLYPRIPGHEGAGVIESVGEKVANLKVGDTVMPLSIGQCGECSNCATGKTNICFKYPFGISGLMPDGTSRMSAKGQKLYHMFTCSTWSEYTVVDSNFVVKVDPRIPLPHASLLTCGFLTGYGAPWRESRVEKGSTVAVIGLGAVGLGAVSASRILGASKIIGIDVNELKREKATVFGVTEFINPKHSDKTVSQLIQEATGGLGVDCCIECTGVSSLLNEAIASTKVGIGEVVLIGAGEKEKVEISYIPLMLGRSVKGTTLGGVRIHSDLPKIVEKCINKEIDLDELITHEVSLVDVNKGFMEYMNQPDCVKVSVKF	67%
Contig61	*Acinetobacter johnsonii* SH046	glutathione-dependent formaldehyde dehydrogenase	>gi|262368349|ref|ZP_06061678.1| glutathione-dependent formaldehyde dehydrogenase [Acinetobacter johnsonii SH046] MKSRAAVAFGPGQALEIVEIDVAPPQKGEVLVKITHTGVCHTDAFTLSGDDPEGVFPAVLGHEGAGIVVQVGEGVTSVQPGDHVIPLYTAECGECLFCQSGKTNLCVAVRATQGKGLMPDGTTRFSYNGQPIYHYMGCSTFSEYTVVAEVSLAKINPDANPEHVCLLGCGVTTGLGAVKNTAKVQEGDTVAVFGLGGIGLAVVQGAKKAKASRIIAVDTNPDKYKLAAEFGATDFVNPKDHDRPVQEVIVEMTGWGVDHSFECIGNTNVMRSALECAHRGWGQSVIIGVAGAGQEISTRPFQLVTGRTWKGTAFGGVKGRSQLPGMVEEAMTGDIRLAPFVTHTMGLDKINEAFDLMHDGKSIRTVIHFED	43%
Contig62	*Octadecabacter antarcticus* 238	lysine exporter protein	>gi|254453087|ref|ZP_05066524.1| lysine exporter protein [Octadecabacter antarcticus 238] MNGFGVAFSLILAIGAQNAFILKQGLRREHVLAVVLVCALSDAILITVGVSGFAALTESLPSLAPVMLWLGAAFLFGYGAVSFWRSWQGGAALDPATGAGTSLKGAVLFCLAITWLNPHVYLDTLVLIGSIASRFEGAEVGFWAGAVTSSFAFFAALGFGARMLAPVMARPAAWRVLEGVIGCVMWAIALGLIFRG	40%

Contig62	*Metarhizium anisopliae*	carboxylic acid transport protein	>gi|20340159|gb|AAM19667.1|AF500226_1 carboxylic acid transport protein [Metarhizium anisopliae] MSPRENEPADALAKGIIPTAKQSFKDLFIWRQRVVLSNEYGETRCEWRDPDRFVNPISLMAQLSAKNWLFFLVGFLSWTADAFDFHALSIQTKKLAVYYGRSKTDITTAITLTLLLRSIGAAFFGLAGDKWGRKWPMVVNMLVLGLLQIATIYSQTFQQFLAVRSLFGLFMGGVYGNAIAMALEQCPSNARGLMSGILQQGYSFGYVLAACANLGVGGGTDTWKIVFWIAAGFSIAVGLVRILFPESQQFLEAKKNGKKAASPGAFWHDTVKMLKQEWKM RVYCIILMTWFNYYSHTSQDSYTTFMLTQKGLDNAGASRASILMKAGACVGGTILGYMSQFIGRRRTIISSCLMSAVLIPAWILPTGERALSATGFFMQFFVQGAWGVIPIHLNELSPVAFRSTFPGVTYQLGNMISSPS AQIVNAIAEKMFVTTPDGRRAEAYGPVMGIATAIIALGIVFTTMFGPERRGRDFENKVAGMTSEESSTKVMESEDEEKGRVELEERR	51%
Contig63	*Salvia miltiorrhiza*	copalyl diphosphate synthase	>gi|157488863|gb|ABV57835.1| copalyl diphosphate synthase [Salvia miltiorrhiza] MASLSSTILSRSPAARRRITPASAKLHRPECFATSAWMGSSSKNLSLSYQLNHKKISVATVDAPQVHDHDGTTVHQGHDAVKNIEDPIEYIRTLLRTTGDGRISVSPYDTAWVAMIKDVEGRDGPQFPSSLEWIVQNQLEDGSWGDQKLFCVYDRLVNTIACVVALRSWNVHAHKVKRGVTYIKENVDKLMEGNEEHMTCGFEVVFPALLQKAKSLGIEDLPYDSPAVQEVYHVREQKLKRIPLEIMHKIPTSLLFSLEGLENLDWDKLLKLQSADGSFLTSPSSTAFAFMQTKDEKCYQFIKNTIDTFNGGAPHTYPVDVFGRLWAIDRLQRLGISRFFEPEIADCLSHIHKFWTDKGVFSGRESEFCDIDDTSMGMRLMRMHGYDVDPNVLRNFKQKDGKFSCYGGQMIESPSPIYNLYRASQLRFPGEEILEDAKRFAYDFLKEKLANNQILDKWVISKHLPDEIKLGLEMPWLATLPRVEAKYYIQYYAGSGDVWIGKTLYRMPEISNDTYHDLAKTDFKRCQAKHQFEWLYMQEWYESCGIEEFGISRKDLLLSYFLATASIFELERTNERIAWAKSQIIAKMITSFFNKETTSEEDKRALLNELGNINGLNDTNGAGREGGAGSIALATLTQFLEGFDRYTRHQLKNAWSVWLTQLQHGEADDAELLTNTLNICAGHIAFREEILAHNEYKALSNLTSKICRQLSFIQSEKEMGVEGEIAAKSSIKNKELEEDMQMLVKLVLEKYGGIDRNIKKAFLAVAKTYYYRAYHAADTIDTHMFKVLFEPVA	74%
Contig63	*Medicago truncatula*	Terpene synthase-like; Terpenoid synthase	>gi|124360263|gb|ABN08276.1| Terpene synthase-like; Terpenoid synthase [Medicago truncatula] KLGNENEEHMPIGFEVAFPSLLDRARRLNIDVPNDSPILKNIFAKRDEKLKRIPREIMHKVPTTLLHSLE GMLGLDWKQLLKLQSQDGSFLFSPSSTAFALMQTKDENCLKYLNNAVNKFNGGVPNVYPVDLFEHIWLVDRLERLGISRYFQQEIKECMNYVSRYWTEKGICWARNSNVQDIDDTAMAFRLLRLHGYQVSADVFKHFERNGEFFCFAGQCTQAVTGMYNLYRATQVLFPGEKILENAKHFSAKFLKEKREADELIDKWIIMKNLPDEVAYALDVPWYANLGRVETRFYIDQYGGESDVWIGKTLYRMANVNNNNYLELAKLDYNNCQAQHLKEWSMIQKWYSECRLGEFGLSKRDLLMSYFLAAASIFQPERSQERLAWAKTTALLQTFTSYIRDEDLKKDFVNKYNDYINRRDHSIGWRLNRNKTGHDLAETLVATIDQISWDILVSYGHEIGYDMHQCWKKWLSSWQNEGDKCEGEAELLVQIINLSAGHLISEDQIFNPQYKHLLQLTNSICHKLHCYQKDKELKSSSSNLRENTITPEAESKMQELVELVFQQSPNDIDFNIKNTFFTVAKSFYYAAFCDSRTINFHIAKVLFDKVV	44%
Contig64	*Mentha x piperita*	isopiperitenol dehydrogenase	>gi|158979021|gb|ABW86883.1| isopiperitenol dehydrogenase [Mentha x piperita] MASVKKLAGKVAIVTGGASGIGEVIARLFAERGARAVVIADMQPEKGGTVAESIGGRRCSYVHCDITDEEQVRSVVDWTAATYGGVDVMFCNAGTASATAQTVLDLDLAQFDRVMRVNARGTAACVKQAARKMVELGRGGAIICTASATANHAGPNLTDYIMSKRGVLGLVRSASLQLGVHGIRVNSVSPTALATPLTATIGLRTAADVESFYGQVTSLKGVAITAEHVAEAVAFLASDEAAFVTGHDLAVDGGLQCLPFVAVAK	99%
Contig64	*Pisum sativum*	short-chain alcohol dehydrogenase	>gi|6119725|gb|AAF04194.1|AF053639_1 short-chain alcohol dehydrogenase [Pisum sativum] MAESSSTKSSLRLAGKVAIVTGGPKQGARIVVIADIQDKLGIQVAESIGTDKCRFIHCDIRIEDDVKNLV QLTVDCYGQIDIIHCNAGIVSPSDQTLLELDVSQTNGVFATNAIGTALCVKHAARAMVDGKVRGSIVCTASISASYGVTTGTDYSMSKHAVLGLMRSASVQLAKYGIRVNSVSPNGLATPLTEKLLDADAKTVEEIFSKFSMLKGVVLRTNHVADAVLFLASNESDFVTGLDLRVDGNYITSHAVI	56%
Contig64	*Digitalis grandiflora*	3-beta hydroxysteroid dehydrogenase	>gi|55978457|gb|AAV68712.1| 3-beta hydroxysteroid dehydrogenase [Digitalis grandiflora] MSSKPRLEGKVVIITGAASGIGEEAARLFVEHGASVVVADVQDELGHQVVASVNSDDKISYHHCDVRDEKQVAATVRYAVEKYGRLDVMMSNAGVFGALMTNVIDLDMVDFENVLATNVRGVANTIKHAARAMVEGKVKGSIICTASVSASLGGMGPPAYTASKHAVLGLVKAACAELGVHGIRVNSVAPYGVATPMPCSAYGMTPSQMEDANSSRANLKGVVLKAKHVAEAALFLASDESAYVSGQNLAVDGGFTVVR	52%
Contig64	*Eragrostis tef*	short-chain dehydrogenase/reductase	>gi|88175077|gb|ABD39562.1| short-chain dehydrogenase/reductase [Eragrostis tef] GASGIGAAAARLFASSGATVVIADVQDELGETVAASASAAGKCRYMRCDVTDEAQVEATVAAVVAAHGRLDVMLSNAGVLLPTGSVMDMDLRELDRVMAVNFRGAAACVKHAARAMVSQAEAGQGARGGAIVCTASVASVQGGWGPASYTASKHALLGLVRAAAGELGPHGVRVNCVSPGGVATPLSCGFMGVGPEELEAMTVPFNVLQGKVLRAEDVAEAALFLASDQAAFVS	51%
Contig65	*Zea mays*	stachyose synthase	>gi|226508886|ref|NP_001152291.1| stachyose synthase [Zea mays] MPGACQDLSTITPTPRRQSMAQLQRGSVLVGGRELLVRAPPNVNLRPAGAGVADGGAASGAAFLGARAPAASSRHVFSVGNLASGWRWLSLFRFKIWWMIPATGVGAAAVPAETQMLLLEYRSEAGPAAATERGSLYALVLPVLDGGFRASLQGSPEDELQFCFESGDPDVQTMEAVDAVFVNSGDNPFKLLKESIKMLSKIKGTFSHIEDKEIPSNLDWFGWCTWDAFYKAVNPSGIEEGLQSLREGGVPPRFLIIDDGWQETVDEIKEVNEALREQTVFAQRLADLKENHKFRGETCKNLEDLVKTIKGKHGVKCVYMWHALLGYWGGTLATSEVMKKYNPKLVYPVQSRGNVANLRDIAMDSLEKFGVGIVDPDKIYEFYNDQHSYLSSVGVDGVKVDVQNVLETLGRGFGGRVAVTRKYQQALEESIAQNFKTNNLICCMSHNSDSIFSALKGAVARASEDFMPREPTLQTLHIASVAFNSLLLGEIFIPDWDMFHSKHESAEFHGAARALSGGGVYVSDKPGVHDFSVLKKLVLPDGSILRARYAGRPTRDCLFTDPVMDGKSLMKIWNLNNFTGVIGVFNCQGAGQWVWPVKQTAYVPTNINITGQLSPSDVESLEEIAGDD	44%

			WNGETAVYAFGSCSLSRLQKHQSLEVSLSTMTCEIYSISPIKIFSEVVQFTPLGLI DMFNSGGALDNISSVADSSATTVHIRCRGPGRFGAYSDTRPELCRVDEHEVEF TLAEDGLLTFYLPPSSSQDNLRHVEIVYKAS	
Contig65	*Cucumis sativus*	alkaline alpha galactosidase I	>gi|87128422|gb|AAZ81424.2| alkaline alpha galactosidase I [Cucumis sativus] MTVGAGITISDANLTVLGNRVLSDVHNNITLTAAPGGGVMNGAFIGVQSDQIG SRRVFPIGKLIGLRFLC AFRFKLWWMTQRMGCSGQEIPFETQFLVVETRDGSNIAGNGEEGDAVYTVFL PILEGDFRAVLQGNDNNELEICLESGDPSVDGFEGSHLVFVGAGSDPFETITYA VKSVEKHLQTFAHRERKKMPDILNWFGWCTWDAFYTDVTSDGVKKGLESFE NGGIPPKFVIIDDGWQSVAKDAASTDCKADNTANFANRLTHIKENYKFQKDG KEGERIENPALGLQHIVSYMKEKHATKYVYVWHAITGYWGGVSSGVKEMEQ YESKIAYPVASPGVESNEPCDALNSISKTGLGLVNPEKVFNFYNEQHSYLASAG VDGVKVDVQNILETLGAGHGGRVKLARKYHQALEASISRNFQDNGIISCMSH NTDGLYSSKRNAVIRASDDFWPRDPASHTIHIASVAYNSLFLGEFMQPDWDMF HSLHPMAEYHGAARAVGGCAIYVSDKPGQHDFNLLKKLVLHDGSILRAKLPG RPTKDCLFADPARDGKSLLKIWNMNDLSGVVGVFNCQGAGWCKVGKKNLIH DENPDTITGVIRAKDVSYLWKIAGESWTGDAVIFSHLAGEVVYLPQDASMPIT LKSREFDVFTVVPVKELANDIKFAPIGLMKMFNSGGAVKEMNHQPGSSNVSL KVRGSGPFGAYSSSKPKRVAVDSEEVEFIYDEGGLITIDLKVPEKELYLWDIRIE L	60%
Contig65	*Arabidopsis thaliana*	AtSIP2 (Arabidopsis thaliana seed imbibition 2); hydrolase	>gi|15230330|ref|NP_191311.1| AtSIP2 (Arabidopsis thaliana seed imbibition 2); hydrolase, hydrolyzing O-glycosyl compounds MTITSNISVQNDNLVVQGKTILTKIPDNIILTPVTGNGFVSGSFIGATFEQSKSLH VFPIGVLEGLRFMC CFRFKLWWMTQRMGSCGKDIPLETQFMLLESKDEVEGNGDDAPTVYTVFLPL LEGQFRAVLQGNEKNEIEICFESGDKAVETSQGTHLVYVHAGTNPFEVIRQSV KAVERHMQTFHHREKKKLPSFLDWFGWCTWDAFYTDVTAEGVDEGLKSLSE GGTPPKFLIIDDGWQQIENKEKDENCVVQEGAQFATRLVGIKENAKFQKSDQK DTQVSGLKSVVDNAKQRHNVKQVYAWHALAGYWGGVKPAASGMEHYDSA LAYPVQSPGVLGNQPDIVMDSLAVHGLGLVNPKKVFNFYNELHSYLASCGID GVKVDVQNIIETLGAGLGGRVSLTRSYQQALEASIARNFT DNGCISCMCHNTDGLYSAKQTAIVRASDDFYPRDPASHTIHIASVAYNSLFLGE FMQPDWDMFHSLHPTAEYHAAARAVGGCAIYVSDKPGNHNFDLLRKLVLPD GSVLRAKLPGRPTRDCLFADPARDGISLLKIWNMNKFTGIVGVFNCQGAGWC KETKKNQIHDTSPGTLTGSIRADDADLISQVAGEDWSGDSIVYAYRSGEVVRL PKGASIPLTLKVLEYELFHISPLKEITENISFAPIGLVDMFNSSGAIESIDINHVTD KNPEFFDGEISSASPALSDNRSPTALVSVSVRGCGRFGAYSSQRPLKCAVESTE TDFTYDAEVGLVTLNLPVTREEMFRWHVEILV	35%
Contig66	*Mentha x piperita*	flavonoid 7-O-methyltransferase	>gi|38047391|gb|AAR09598.1| flavonoid 7-O-methyltransferase [Mentha x piperita] MAPEEDSLALAEAWNHGFGFIKTSIVKTAVELEIPDILESRGAPVSIPELATAVD CSADRIYRVMRFLAY HGIFKRTKPPPESTEGGSVYYAQTPVSRRLTRENLGPFVLLQGTMREPSGCVTA ETLRTSKRPGVVNENESDHLYEDPVFSMKVFRDAMASHARMTTAAVIENYGE GFQGVGSLVDVGGSYGMALSMLVKAFPWLRGICFDLPEVVARASPLKGVEFV GGTMFESIPKADVVMLMFVLHNWSDEECVEILKRCKDAVSKDKGKVIIIDAVI DEDGDGDEFTGARLGLDVTMMATMFEGRERTYVEWARIINEAGFRRHVVKNI KTLESVIEAYP	96%
Contig66	*Eschscholzia californica*	reticuline-7-O-methyltransferase	>gi|87887871|dbj|BAE79723.1| reticuline-7-O-methyltransferase [Eschscholzia californica] MDEEIILGQADICKYMYGFVDSMTLRCVVELGIPDIIHSHGRPITLTEILNGIPNL SSSFDINYLQGIMT ILVRRRVFAVHKFDPKDGTNLTEIRYGLTPSSKCLLKDSKFNLAPFVLLETHPW ITDPWNYLGKCVQEGGSGFVKAHGSDVFKFGSDHPEFFKLFYDGMECSTKVL VQVVLDKYQQVFKDVKSIVDVGGGTGMMISEIVKNHPHIKGINFDLPHVVAE APDYPGVEHVGGDMFVEIPQADAITMKGILHDWNDDACVKILENCKKAIPKN GKVIIIDCVLNPDGDDLFDDIKVVSDLGMRVHCSDGKERTEAEWEKLLKKGGF PRYKITHVVTVQSMIEA YPE	47%
Contig67	*Solenostemon scutellarioides*	cobalamine-independent methionine synthase	>gi|974782|emb|CAA89019.1| cobalamine-independent methionine synthase [Solenostemon scutellarioides] MALSFFLDTSVSVPLRCQGKMASHIVGYPRMGPKRELKFALESFWDGKSSAE DLEKCQLILGIHLKQMSDAGIKYIPSNTFSYYDQVLDTTAMLGAVPPRYNWTG GEIGFSTYFSMARGNASVPAMEMTKWFDTNYHFIVPELGPDVKFSYASHKAV NEYKEAKALGVDTVPVLVGPVSYLILSKPAKGVEKTFPLLSLLDKILPIYKEVI AELKAAGASWIQFDEPTLVLDLESHQLDAFTKAYAELESSLSGLSTLIETYFAD VPAPAYKTLTSLSGISGFGFDLVRGAQTIELIKGGFPSGKYLFAGVVDGRNIWA NDLASSITTLQALEGIVGKDKLVVSTSSSLLHTAVDLVNEPKLDQEIKSWLAFA AQKIVEVNALAKALTGHKDEAFFSPNAAAQASRKSSPRVNNEAVQKAAAALR GSEHRRVTNVSARLDAQQKKLNLPILPTTTIGSFPQTVELRRVRREFKPTRISEE EYVKAIKEEINKVVKLQEELDIDVLVHGEPERNDMVEYFGEQLSGFAFTANG WVQSYGSRCVKPPIIYGDVSRPKPMTVFWSTAAQSMTQRPMKGMLTGPVTIL NWSFVRNDQPRFETCYQIALAIKDEVEDLEKAGITVIQIDEAALREGLPLRKSE HAFYLDWAVHSFRITNVGVQDTTQIHTHMCYSNFNDIIHSIINMDADVITIENS RSDEKLLSVFREGVKYGAGIGPGVYDIHSPRIPSTEEIADRINKMLAVLETNILW VNPDCGLKTRKYAEVKPALENMVAAAKLLRTQLASAK	87%
Contig67	*Solanum tuberosum*	methionine synthase	>gi|8439545|gb|AAF74983.1|AF082893_1 methionine synthase [Solanum tuberosum] MASHVVGYPRMGPKRELKFALESFWDGKSSAEDLKKVSADLRSSIWKQMSD AGIKYIPSNTFSYYDQVLDTTAMLGAVPSRYNWTGGEIEFGTYFSMARGNASV PAMEMTKWFDTNYHFIVPELGPDVNFSYASHKAVNEYKEAKAQGVDTVPVL VGPVSYLLLSKPAKGVEKSFPLLSLLDKILPIYKEVIAELKAAGASWIQLDEPTL VLDLESHKLEAFTKAYADLESSLSGLNVLVETYFADVPAEAFKTLTALKGVTA FGFDLVRGTQTLELIKSSFPSGKYLFAGVVDGRNIWANDLAASLALLQSLEGV VGKDKLVASTSCSLLHTAVDLINETKLDDEIKSWLAFAAQKVVEVNALAKAL SGAKDEAFFSANAAAQASRKSSPRVTNEAVQKASAALQGSDHRRATNVSARL DAQQKKLNLPILPTTTIGSFPQTVELRRVRREYKAKKISEEEYVKAITEEIKKVV DLQEELDIDVLVHGEPERNDMVEYFGEQLSGFAFTANGWVQSYGSRCVKPPII YGDVSRPKPMTVFWSSKAQEMTKRPMKGMLTGPVTILNWSFVRNDQPRFET CYQIALAIKDEVEDLEKAGITVIQIDEAALREGLPLRKAEHAFYLNWAVHSFRI	90%

			TNVGIEDTTQIHTHMCYSNFNDIIHSIIDMDADVITIENSRSDEKLLSVFREGVK YGAGIGPGVYDIHSPRIPSTEEIADRVNKMLAVLDTNILWVNPDCGLKTRKYT EVKPALQNMVSAAKTIRTQLASAK	
Contig68	*Nicotiana tabacum*	allyl alcohol dehydrogenase	>gi|6692816|dbj|BAA89423.1| allyl alcohol dehydrogenase [Nicotiana tabacum] MAEEVSNKQVILKNYVTGYPKESDMEIKNVTIKLKVPEGSNDVVVKNLYLSC DPYMRSRMRKIEGSYVESFAPGSPITGYGVAKVLESGDPKFQKGDLVWGMTG WEEYSIITPTQTLFKIHDKDVPLSYYTGILGMPGMTAYAGFHEVCSPKKGETVF VSAASGAVGQLVGQFAKMLGCYVVGSAGSKEKVDLLKSKFGFDEAFNYKEE QDLSAALKRYFPDGIDIYFENVGGKMLDAVLVNMKLYGRIAVCGMISQYNLE QTEGVHNLFCLITKRIRMEGFLVFDYYHLYPKYLEMVIPQIKAGKVVYVEDVA HGLESAPTALVGLFSGRNIGKQVVMVSRE	67%
Contig68	*Mentha haplocalyx* var. piperascens	(+)-pulegone reductase	>gi|148887815|gb|ABR15426.1| (+)-pulegone reductase [Mentha haplocalyx var. piperascens] MEVDMVMNKQIVLNNYVNGSLKESDLSLRTSTICMEIPHGCNGAVLVKNLYL SVNPYLILRMGKLDIPQFDSILPGSTIVSYGVSKVLDSTHPSYEKGELIWGSQAG WEEYTLIQNPYNLFKIQDKDVPLSYYVGILGMPGMTAYAGFFEICSPKKGETV FVTAAAGSVGQLVGQFAKMFGCYVVGSAGSKEKVDLLKNKFGFDDAFNYK EESDYDTALKRHFPEGIDIYFDNVGGKMLEAVINNMRVHGRIAVCGMVSQYS LKQPEGVHNLLKLVPKQIRMQGFVVVDYYHLYPKFLEMVLPCIKEGKVIYVE DISEGLESAPSALLGVYVGRNIGNQVVAVSRE	58%
Contig69	*Brassica rapa*	Tat binding protein like protein	>gi|12697589|dbj|BAB21595.1| Tat binding protein like protein [Brassica rapa] MATPMVEDTSSFEEDQLASMSTEDIVRATRLLDNEIRILKEDAQRTNLECDSY KEKIKENQEKIKLNKQLPYLVGNIVEILEMNPEDDAEEDGANIDLDSQRKGKC VVLKTSTRQTIFLPVVGLVDPDSLKPGDLVGVNKDSYLILDTLPSEYDSRVKA MEVDEKPTEDYNDIGGLEKQIQELVEAIVLPMTHKERFEKLGVRPPKGVLLYG PPGTGKTLMARACAAQTNATFLKLAGPQLVQMFIGDGAKLVRDAFQLAKEK APCIIFIDEIDAIGTKRFDSEVSGDREVQRTMLELLNQLDGFSSDERIKVIAATNR ADILDPALMRSGRLDRKIEFPHPTEEARARILQIHSRKMNVHPDVNFEELARST DDFNGAQLKAVCVEAGMLALRRDATEVNHEDFNEGIIQVQAKKKASLNYYA	96%
Contig69	*Equus caballus*	26S protease regulatory subunit 6A	>gi|270358348|gb|ACZ81397.1| 26S protease regulatory subunit 6A [Equus caballus] STEEIIQRTRLLDSEIKIMRSEVLRVTHELQAMKDKIKENSEKIKVDKTLPYLVS NVIELLDVDPNDQEE DGANIDLDSQRKGKCAVIKTSTRQTYFLPVIGLVDAEKLKPGDLVGVNKDSYL ILETLPTEYDSRVKAMEVDERPTEQYSDIGGLDKQIQELVEAIVLPMNHKEKFE NLGIQPPKGVLMYGPPGTGKTLLARACAAQTKATFLKLAGPQLVQMFIGDGA KLVRDAFALAKEKAPSIIFIDELDAIGTKRFDSEKAGDREVQRTMLELLNQLDG FQPNTQVKVIAATNRVDILDPALLRSGRLDRKIEFPMPNEEARARIMQIHSRKM NVSPDVNYEELARCTDDFNGAQCKAVCVEAGMIALRRGATELTHEDYMEGIL EVQAKKKANLQYYA	82%
Contig70	*Gossypium hirsutum*	chalcone isomerase	>gi|295687229|gb|ADG27840.1| chalcone isomerase [Gossypium hirsutum] MTTEMVMVDEVPFPPQITTTKPLSLLGHGITDIEIHFLQIKFTAIGVYLEPEVVG HLQQWKGKPGNVLAE DDDFFEALINAPVEKFLRVVVIKEIKGSQYGVQLESAVRDRLAADDKYEEEEE EALEKVVEFFQSKYFKKDSVITYHFPANSATAEIAFTTEGKEEAKIKVENANVV EMIKKWYLGGTRGVSATTISSLANTLSAELCK	82%
Contig70	*Capsicum annuum*	chalcone isomerase	>gi|224708766|gb|ACN60401.1| chalcone isomerase [Capsicum annuum] VQVDNNVFPPSVVKPPGSNTTLFLAGAGIRGVDIEGKFVKCTAIGVYMEESAV PFLAAKWKGKSSKELTDSVEFFRDIVTGPFEKFFRVTMITPLTGKQYSEKVAEN CVANWKALGTYGDAESEAIEKFLSAFQSENFPPGASILFTQSPAGSLTISFSKDD SVPGTGNAVIENKQLSEAVLESIIGKHGVSPAAKNSLAKRVSELLKSNAEAPVF EKPASDQPAI	35%
Contig71	*Glycine max*	thioredoxin h1	>gi|157781191|gb|ABV71991.1| thioredoxin h1 [Glycine max] MAGSSEEGQVISCHTVEEWNDQLQKGNESKKLIVVDFTASWCGPCRFIAPFLA ELAKKFTSVIFLKVDVDELKSVSQDWAIEAMPTFVFVKEGTLLDKVVGAKKD ELQQKIQKHVASSNA	75%
Contig71	*Ipomoea batatas*	thioredoxin H1	>gi|33621082|gb|AAQ23134.1| thioredoxin H1 [Ipomoea batatas] MESEEGQVIGCHTVDQWKEHFEKARASGKLTVVDFTASWCGPCRFIAPILAD MAKKTPHVIFLKVDVDELKSVAEDYKVEAMPTFVFLKEGNEVDRVVGPRKK NCFVA	71%
Contig72	*Mentha arvensis*	limonene hydroxylase	>gi|146386316|gb|ABQ24001.1| limonene hydroxylase [Mentha arvensis] MELQISSAIIILVVTYTISLLIIKQWRKPKPEENLPPGPPKLPLIGHLHLLWGKLP QHALASVAKQYGPV AHVQLGEVFSVVLSSREATKEAMKLVDPACADRFDSIGTKIMWYDNDDIIFSP YSEHWRQMRKICVSGLLSARNVRSFGFIRQDEVSRLLGHLRSSAAAGEAVDLT ERIATLTCSIICRAAFGSVIRDHEELVELVKDALSMASGFELADLFPSSKLLNLL CWNKSKLWRMRRRVDTILEAIVEEHKLKKSGEFGGEDIIDVLFRMQKDSQIKV PITTNAIKAFIFDTFSAGTETSSTTTLWVMAELMRNPEVMAKAQVEVRAALKG KTNWDVDDVQELKYMKSVVKETMRMHPPIPLIPRSCREECEVNGYKIPNKARI MINVWSMGRNPLYWEKPKTFWPERFDQVSRDFMGNDFEFIPFGAGRRICPGL NFGLANVEVPLAQLLYHFDWNLAEGMKPSDMDMSEAEGLTGIRKNNLLLLPT PYDPSS	95%
Contig72	*Hyoscyamus muticus*	cytochrome P450 hydroxylase(A6YIH8)	>gi|151335776|gb|ABS00393.1| cytochrome P450 hydroxylase [Hyoscyamus muticus] MQFFSLVSIFLFLSFLFLLRKWKNSNSQSKKLPPGPWKLPLLGSMLHMVGGLP HHVLRDLAKKYGPLMHLQLGEVSAVVVTSPDMAKEVLKTHDIAFASRPKLLA PEIVCYNRSDIAFCPYGDYWRQMRKICVLEVLSAKNVRSFSSIRRDEVLRLVNF VRSSTSEPVNFTERLFLFTSSMTCRSAFGKVFKEQETFIQLIKEVIGLAGGFDVA DIFPSLKFLHVLTGMEGKIMKAHHKVDAIVEDVINEHKKNLAMGKTNGALGG EDLIDVLLRLMNDGGLQFPITNDNIKAIIFDMFAAGTETSSSTLVWAMVQMMR NPTILAKAQAEVREAFKGKETFDENDVEELKYLKLVIKETLRLHPPVPLLVPRE CREETEINGYTIPVKTKVMVNVWALGRDPKYWDDADNFKPERFEQCSVDFIG NNFEYLPFGGGRRICPGISFGLANVYLPLAQLLYHFDWKLPTGMEPKDLDLTE LVGVTAARKSDLMLVATPYQPSRE	60%
Contig73	*Prunus persica*	DEAD box RNA helicase	>gi|283049400|gb|ADB07168.1| DEAD-box RNA helicase-like protein [Prunus	98%

			persica] MAGVAPEGSQFDAKQYDTKMSELLSTDGQEFFTSYDEVYESFDSMGLQENLL RGIYAYGFEKPSAIQQRGIVPFCKGLDVIQQAQSGTGKTATFCSGILQQLDYAV VQCQALVLAPTRELAQQIEKVMRALGDYLGVKVHACVGGTSVREDQRILQA GVHVVVGTPGRVFDMLRRQSLRPDYIKMFVLDEADEMLSRGFKDQIYDIFQL LPSKVQVGVFSATMPPEALEITRKFMNKPVRILVKRDELTLEGIKQFYVNVDK EEWKLETLCDLYETLAITQSVIFVNTRRKVDWLTDKMRSRDHTVSATHGDMD QNTRDIIMREFRSGSSRVLITTDLLARGIDVQQVSLVINYDLPTQPENYLHRIGR SGRFGRKGVAINFVTRDDERMLYDIQRFYNVVIEELPSNVADLL	
Contig73	*Pennisetum glaucum*	eukaryotic initiation factor 4A	>gi|63139086|gb|AAY33860.1| eukaryotic initiation factor 4A [Pennisetum glaucum] MAGMAPEGSQFDAKHYDSKMQELLSTGETEEFFTSYDEVFESFDDMGLQENL LRGIYAYGFEKPSAIQQR GIVPFCKGLDVIQQAQSGTGKTATFCSGILQQLDYGLVECQALVLAPTRELAQ QIEKVMRALGDYLGVKV HACVGGTSVREDQRILASGVHVVVGTPGRVFDMLRRQSLRPDHIKMFVLDEA DEMLSRGFKDQIYDIFQL LPAKIQVGVFSATMPPEALEITRKFMNKPVRILVKRDELTLEGIKQFYVNVEKE DWKLDTLCDLYETLAI TQSVIFVNTRRKVDWLTDKMRSRDHTVSATHGDMDQNTRDIIMREFRSGSSR VLITTDLLARGIDVQQVS LVINYDLPTQPENYLHRIGRSGRFGRKGVAINFVTRDDDRMQFDIQRFYSVVIE ELPTNVADLL	95%
Contig74	*Manihot esculenta*	aldo/keto reductase AKR	>gi|62526573|gb|AAX84672.1| aldo/keto reductase AKR [Manihot esculenta] MAGAAVKRIKLGSQGLEVSAQGLGCMSMSAFYGPPKPESDMIALIHHAINTG VTFFDTSDVYGPHTNEILLGKALKGDIRKKVELATKFAINLKDGKREIRGDPAY VRAACEASLKRLDVDCIDLYYQHRVDTSVPIEVTVGELKKLVEEGKIKYIGLSE ASASTIRRAHAVHPITAVQLEWSLWSRDVEEEIVPTCRELGIGIVAYSPLGRGFF SSGPKLVETLSEGDFRKYLPRFQPENLEHNKHLFERVNEIAARKQCTPSQLALA WVHHQGDDVCPIPGTTKIENFNQNIGALSVKLTPEDMAELESIASASAVKGGR YGSDMGTYKDSDTPPLSSWKAV	77%
Contig74	*Rauvolfia serpentina*	perakine reductase	>gi|59896631|gb|AAX11684.1| perakine reductase [Rauvolfia serpentina] MPRVKLGTQGLEVSKLGFGCMGLSGDYNDALPEEQGIAVIKEAFNCGITFFDT SDIYGENGSNEELLGKA LKQLPREKIQVGTKFGIHEIGFSGVKAKGTPDYVRSCCEASLKRLDVDYIDLFY IHRIDTTVPIEITMGE LKKLVEEGKIKYVGLSEASPDTIRRAHAVHPVTALQIEYSLWTRDIEDEIVPLC RQLGIGIVPYSPIGRG LFAGKAIKESLPENSVLTSHPRFVGENLEKNKQIYYRIEALSQKHGCTPVQLAL AWVLHQGEDVVPIPGT TKIKNLHNNVGALKVKLTKEDLKEISDAVPLDEVAGESIHEVIAVTNWKFANT PPLK	57%
Contig75	*Arabidopsis thaliana*	transducin family protein / WD-40 repeat family protein	>gi|30690225|ref|NP_195240.2| transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana] MSEKARRGRSNFNGLHHPVVDFWRREVGGISSRNFSNRFSASENLVLRLEIYK KLEKHKGCVNTVSFNAE GDVLISGSDDRRVVLWDWQLGNVKLSFHSGHANNVFQAKFMPFSDDRTIVTC AADGMVRRASILEGDKVE TSFLGLHQGRAHKLCIEPGNPHIFYTCGEDGLVQRFDLRTEAPTELFTCRSVDP RRRNMDAIQLNAIAID PRNSNLFAVGGMEEYARLYDIRRFQGEGLNGFTRAADHFCPPHLIGNEDVGIT GLAFSEQSELLVSYNDE FIYLFTPGMGLGSNPIPSSPISKSPVSKSESSSSPKDENEHSVSLVYKGHKNCETV KGVNFFGPRSEYVV SGSDCGRIFIWRKKGGELIRVMEADRHVVNCIEPHPHIPVLASSGIESDIKVWTS KAAERATLPENIELR KRTPRGWMYRVSSPHELLAQLFSLQNRSSSSPEREGESSSATGRELLDLILTFN DQSDDENATDDDDGNS HEDFFS	68%
Contig75	*Zea mays*	nucleotide binding protein	>gi|226508452|ref|NP_001150616.1| nucleotide binding protein [Zea mays] MRRPWRHSGPGSAVAARHGAADLCLREVGDLLPRRFARRAAGSEDLVMRLQ IHRKLDRHTGCVNTVGFNE VGDTLISGSDDQKVMLWDWDTGTVKLEFHSGHGGNVFQARFMPCSDDRTIV TCAADGEVRLAKIQDAGDV STTLLGEHEGRAHNLAIEPGSPYIFYSCGEEGFVQHFDLRTNTASKLFLCRNST KSVYSSLVHLNALAID PRNPNLFVVGGSDAYARVYDIRKCKWDGSSDFSHASDCYCPPHLVDNKSVGI TGIAFSHLSELLVSYNEE NIYLFSKDGGLGPDPKKSVRIGAIEGCKSTMLASGHDVSQPAPQTYVGHVNRE TVKRVSFIGPNDEYVAS GSDCGRIFIWRKGDGKFLRAMEGDECIVNCIEPHPHAMAIASCGIDNDVKVWT PSAIERAPMIHVDELQL RPRKRRAKLWRFGIRDLLIQQILVSENRQQSAEEGSSEDHEDNIELLDLVLQAA VEGVSSSSDEEEEDDD DGDNEEAAASDGSE	66%
Contig76	*Medicago sativa*	vestitone reductase	>gi|973249|gb|AAB41550.1| vestitone reductase [Medicago sativa] MAEGKGRVCVTGGTGFLGSWIIKSLLENGYSVNTTIRADPERKRDVSFLTNLP GASEKLHFFNADLSNPD SFAAAIEGCVGIFHTASPIDFAVSEPEEIVTKRTVDGALGILKACVNSKTVKRFI YTSSGSAVSFNGKDK DVLDESDWSDVDLLRSVKPFGWNYAVSKTLAEKAVLEFGEQNGIDVVTLILPF IVGRFVCPKLPDSIEKA LVLVLGKKEQIGVTRFHMVHVDDVARAHIYLLENSVPGGRYNCSPFIVPIEEM SQLLSAKYPEYQILTVD ELKEIKGARLPDLNTKKLVDAGFDFKYTIEDMFDDAIQCCKEKGYL	51%
Contig76	*Pisum sativum*	sophorol reductase	>gi|4336887|gb|AAD17997.1| sophorol reductase [Pisum sativum] MAEGKGRVCVTGGTGFLGSWIIKSLLENGYSVNTTVRPDPKRKRDLSFLTNLP GASERLHFFNADLSDPK	48%

			SFSAAVKGCVGVFHTATPVNFAVSEPEKIVTKRTVDGALGILKACVNSKTLKR FIYTSSGSAVSFNGKNK EVLDETDWSDVGLLKSVKPFGWSYSVSKTLAEKAVLDFGQQNGIDVATLILPF IVGSFICPKLPDSVDKA LVLVLGKKEQIGVTRFHMVHVDDVARAHIYLLENSVPGGRYNCAPFIVTIEEM SQLFSAKYPEFQILSVD ELKEIKGARLAELNSKKLVAAGFEFKYSVDDMFEDAIQCCKEKGYL	
Contig77	*Nicotiana benthamiana*	chalcone synthase	>gi|126211543|gb|ABN80439.1| chalcone synthase [Nicotiana benthamiana] MVTVEEFRRAQRAEGPATVMAIGTATPFNCVDQSTYPDYYFRITNSEHKTELK EKFKRMCEKSMIKKRYM HLTEEILKENPNICAYMAPSLDARQDIVVVEVPKLGKEAAQKAIKEWGQPKSK ITHLVFCTTSGVDMPGC DYQLTKLLGLRPSVKRFMMYQQGCFAGGTVLRMAKDLAENNKGARVLVVC SEITAVTFRGPNDTHLDSLV GQALFGDGAAAVIIGSDPIPEVERPLFQLVSAAQTLLPDSEGAIDGHLREVGLTF HLLKDVPGLISKNIE KSLVEAFQPLGISDWNSLFWIAHPGGPAILDQVELKLGLNQEKLKATRNVLTN YGNMSSACVLFILDEMR KASAKEGLGTTGEGLEWGVLFGFGPGLTVETVVLHSVAT	88%
Contig77	*Rubus idaeus*	aromatic polyketide synthase	>gi|13183377|gb|AAK15174.1|AF292367_1 aromatic polyketide synthase [Rubus idaeus] MVTVDEVRKAQRAEGPATILAIGTATPPNCVDQSTYPDYYFRITKSEHKTELK EKFQRMCDKSMIKKRYM YLTEEILKENPSMCEYMAPSLDARQDMVVVEIPKLGKEAATKAIKEWGQPKS KITHLVFCTTSGVDMPGA DYQLTKLLGLRPSVKRLMMYQQGCFAGGTVLRLAKDLAENNKGARVLVVCS EITAVTFRGPSDTHLDSLV GQALFGDGAAAIIVGSDPLPDIERPLFELVSAAQTILPDSDGAIDGHLREVGLTF HLLKDVPGLISKNIE KSLNEAFKPLDITDWNSLFWIAHPGGPAILDQVEAKLGLKPEKLEATRNILSEY GNMSSACVLFILDEVR RKSVANGHKTTGEGLEWGVLFGFGPGLTVETVVLHSVAAST	83%
Contig78	*Arabidopsis thaliana*	MD-2-related lipid recognition domain-containing protein / ML domain-containing protein	>gi|18399355|ref|NP_566400.1| MD-2-related lipid recognition domain-containing protein / ML domain-containing protein [Arabidopsis thaliana] MSKFTGFSSLAISYFLLVSTIVAATDVHYCDNNEEYEVKVQGVDITPYPIARGE PATFRISANTDTEISS GKLVIEVSYFGWHIHSETHDLCDETSCPVAIGDFLVAHSQVLPGYTPPGSYSLK MKMLDGRKKELTCIKF SFDIGFGSSVADM	63%
Contig78	*Zea mays*	ML domain protein	>gi|195637494|gb|ACG38215.1| ML domain protein [Zea mays] MASKQTRRLFVLAAVAVCFLLLLLPASSVATDVDYCSKKEYPVKVSGVQIVP DPVEPGKPATFKISASTD KTIEKGKLVIDVKYFFFYVHSETRDICGEISCPATGDFVLSHEQTLPGFTPPGSY TIYMKMVGDDDEELS CISFGFSIGFVASS	52%
Contig79	*Cherry rasp leaf virus*	polyprotein	>gi|22002487|gb|AAM82758.1| polyprotein [Cherry rasp leaf virus] MEPDRSQLAPEEVPDSFRVETPAAMLARLRAESAAKKEAARRAAMPYNDDLL VGSELTYLVKDDVFGAGR SALKRLFSRPSAEESVVVSHPLSVKEQVVRYQRPRTDHDPYVAVYTPLPHITEE QARKLMEKGFSNSSNV ALDMAVQSHVGQGTPLLAMCGIMDSRTDDPNEALQVAGYFDLGRDRCDLISL PLINFPLNKEDFDDYMRG LYLCTMFHNVRGFQNNKALCSYSAVGFDQHKETPRCIRSRVKESWEDILARN NENEFSRVQSGQNLLNAI EKERNEAIPDVGAHQFACVPPSKGTPQTSLLTSDGVIKRPNFTLPRSASTRFTM PLNMRYSGRNSVDTAR RSLAANSSDGSTSLRQDPNLLEGQGPSIDFTKIIFPTVIERNFSNPRAEIVNTIQQL YGDTVETLSVNPP ESYSAERLIGKVFSTVYGSFGATDLVEGKVLMSVKIVDLLSSANLGALLLAEV LGGNLTMRVTALVTLNK YTSFALKLVYDELAQLAPDATNFGVASVLPGAIFPSQEKSFSFDFSIFSMGSYT NFRENEGFGRISLVAL SSPNLPDQMPDSANITLEFSVVNVDTSVYNLGQGQCLDLDRFPVHVTSKSKSL SGGAKRAQAEFSLNLYE LGPHFNRFQAICGHLAGYSGDLIVDWMISASALTNGRCYMVPVYDQNTFSEV SEEKLRQCKYVSKELSLN RSGTVHIPFSSSFGSYTKNKHPKLLFVFPGGISGPSGETIHVNIQVRDILNFSGLG HQLLKPILAAEGPD PFSFHLFCLHCGTLKTESLNKGGMWCVPVSPVNLAAMKHGTGSSLVFNESFV SKTHNWLHYMASCTAYWR GTLTYELRVTYNSRVNAVANLVAFYTSQVEDLFGFSDKPVGDTGIASICGDAF SVRISIPFVTPTLWLRT YRNAYDVFTSCNGSLYFHLPTSGVKSVQLFVRAESDFSFERFRALKAEYT	70%
Contig79	*Cherry rasp leaf virus*	coat protein VP24	>gi|52137001|ref|YP_081448.1| coat protein VP24 [Cherry rasp leaf virus] GPDPFSFHLFYLHCGTLKTESLNKGGMWCVPVSPINLAAMKHGTGSSLVFNES FVSKTHNWLHYMASCTA YWRGTLTYELRVTYNSRVNAVANLVAFYTSQVEDLFGFSDKAVGDTGIASIC GDAFSVRISIPFVTPTLW LRTYRNAYDVFTSCNGSLYFHLPTSGVKSVQLFVRAESDFSFERFRALKAEYT	67%
Contig81	*Medicago truncatula*	Short-chain dehydrogenase/reductase SDR	>gi|124359195|gb|ABN05708.1| Short-chain dehydrogenase/reductase SDR [Medicago truncatula] MVGVISLITGMAGPSGFGSASTAEQVTQGIDASNLTAIITGGASGIGLETTRVLA LRKVHVIIAARNIES AEEAKQQITQENKSARVDIMKLDLCSTKSVRSFVDNFIALDLPLNILINNAGIM FCPFKISEEGIEMQFA TNHLGHFLLTNLLLDKMKQTAKTTGIEGRIINLSSIAHRYTYFRKGIKFEKINDK KGYSSKKAYGQSKLA	71%

			NILHANELSRRLQEEGVNITVNSVHPGVIMTPLMRYSSYTMHLLKIFSFYIWKNGAATTCYVALHPSVKGVTGKYFVDCNEFKPSAYAKNKLLAKKLWDFSNKLINSISKA	
Contig81	*Zea mays*	retinol dehydrogenase 11	>gi|195641866|gb|ACG40401.1| retinol dehydrogenase 11 [Zea mays] MGILALITGKAGASGFGSASTAEHVTDGADASRLTVAITGGASGIGLETSRVFALRGAHVVIAARNTEAASEARKTIMEKNPTARIDVLKLDLSSLKSVRAFVDQFNSMKLPLNILINNAGVMFCPFQLSKNGVEMQFATNHLGYFLLTNLLLDTMKATAKSTGIEGRIVNLSSVAHHHTYPKGIDFDNLNDEKIYNDKMAYGQSKLANLLHAKELSRRLKEEGANITVNSVHPGLIMTNLMRHSFVLMKVLQVATYILWKNVPQGAATTCYVGLSPQLKGVTGKYFADCNVEKTSKLARSEELAKQLWDFSEELIKSAK	67%
Contig82	*Rosmarinus officinalis*	cinenol synthase	>gi|112554151|gb|ABI20515.1| cinenol synthase [Rosmarinus officinalis] MSSIIAQVAIPTQTNFLRNNLFHGFSKLRRFSATATTHRGLRARCSLQAANEIQTGRRTGGYQPTLWDFNSIQSFNSKYKEDVHLERAAALIEQVKMLLQEQVDDVRCLELIDDLRRMGISSHFDHEIAQIFNSKYFNNNETGERDLYSTALRFRLLREHGFSVSQEVFDYFKNDNVTDFNPSFAHETKGLLQLYEASFLSAQGEETLEIAREFARKFLEKRVVDHEIDDINLLTSVERALEFPTHWRVQMPNARSFIDAYKRRPDMNPVVLELAKLDINIVQAQFQQELKEASRWWNSTCLVQQLPFVRDRIVECYYWTTGVLERRQHGNERIMLTKIFALVTTIDDVFDIYGTVEELQQFTAAIQRWDIESMNQLPPYMQICYLAVFNFVNETAYDTLKEKGFNSVPFLRKAWVDLVESYLIEADWYYNGHKPSLEEYIENAWISIGGIPILSHLFFQLTDSIEEEAVESMHKYHDIVRASCTILRLPDDLGTSLDEVERGDVPKSVQCYMNEKNASEEEAREHVRSLIEQTWKTMNKEMMMSPFSKYFVEAAANLGRMAQCIYQHERDGFGMQHSLVNKMLRGLLFDSYE	66%
Contig82	*Salvia pomifera*	sabinene synthase	>gi|111182621|gb|ABH07678.1| sabinene synthase [Salvia pomifera] MPLNSLHNLERKPSKAWSTSCTAPAARLQASFSLQQEEPRQIRRSGDYQPSLWDFNYIQSLNTPYKEQRYVNRQAELIMQVRMLLKVKMEAIQQLELIDDLQYLGLSYFFPDEIKQILSSIHNEHRYFHNNDLYLTALGFRILRQHGFNVSEDVFDCFKTEKCSDFNANLAQDTKGMLQLYEASFLLREGEDTLELARRFSTRSLREKLDEDGDEIDEDLSSWIRHSLDLPLHWRIQGLEARWFLDAYARRPDMNPLIFKLAKLNFNIVQATYQEELKDVSRWWNSSCLAEKLPFVRDRIVECFFWAIGAFEPHQYSYQRKMAAIIITFVTIIDDVYDVYGTLEELELFTDMIRRWDNISISQLPYYMQVCYLALYNFVSERAYDILKDQHFNSIPYLQRSWVSLVEGYLKEAYWYYNGYKPSLEEYLNNAKISISAPTIISQLYFTLANSTDETVIESLYEYHNILYLSGTILRLADDLGTSQHELERGDVPKAIQCYMKDTNASEREAVEHVKFLIRETWKEMNTVTTASDCPFTDDLVAVATNLARAAQFIYLDGDGHGVQHSEIHQQMGGLLFQPYV	54%
Contig83	*Perilla frutescens*	cytochrome P450 reductase	>gi|289466128|gb|ADC94831.1| cytochrome P450 reductase [Perilla frutescens] MESTSEKLSPFDFMAAILKGVKLDTSNGSAGAAQPAVVAMLMENRDLMMMLTTSVAVLLGCVVYLIWRRGTGSAKKVVEPPKLVVTKAPAETEEVDDGKKKVTIFFGTQTGTAEGFAKALAEEAKARYPQANFKVVDLDDYAADDEEYEEKMKKESFAFFFLATYGDGEPTDNAARFYKWFAEGKERGDMFKNLHYGVFGLGNRQYEHFNKIAIVVDDILAEQGGKRLVSVGLGDDDQCIEDDFSAWRENVWPELDKMLRDEDDATVSTPYTAAVLEYRVVFHDQSDGLSSENSLANGHANGIAAYDAQHPVVANVAVKKELHTPLSDRSCTHLEFDISGSGLEYETGDHVGVYCENLIETVEEAERLLGMPPQTYFSVHTDKEDGTPLGALPPPFPPCTLRTALSRYADLLNAPKKSALTALAAYASDPSEADRLKHLASPAGKEEYAQYIVAGQRSLLEVMTDFPSTKPPLGVFFAAIAPRLQPRFYSISSSPKIAHSRIHVTCALVYEKTPTGRIHKGVCSTWMKDAVPLEESPNCSSAPIFVRTSNFRLPADPKVPIIMIGPGTGLAPFRGFLQERLALKESGAELGPAILFFGCRNSKMDFIYEDELNHFVKAGVVSELVLAFSREGPTKEYVQHKMAQKALDLWNMISEGGYVYVCGDAKGMARDVHRTLHTIVQEQGSLDSSKTESFVKNLQMNGRYLRDVW	93%
Contig83	*Helianthus tuberosus*	NADPH-ferrihemoprotein reductase	>gi|1359896|emb|CAA81209.1| NADPH-ferrihemoprotein reductase [Helianthus tuberosus] LFEEAKARYEKAVFKVVDLDDYAADDEEYAEKFKKETFAFFFLATYGDGEPTDNAARFYKWFTEGDDKGVWLEKLHYGVFGLGNKQYEHFNKIALVVDEGLTEQGAKRFVPVGLGDDDQSIEDDFSAWKELVWPELDQLLLDEDDKTAATPYTAAIPEYRVVFHDKPDTFSENHSQTNGHTVHDAQHPCRSNVAVKKELHTPESDRSCTHLEFDISHTGLSYETGDHVGVYCENLIEVVEEAEKLIGLPADTYFSLHIDNEDGTPLGGPTLQPPFPPCTLRKALTNYADLLSSPKKSTLLALAAHASDATEADRLQFLASREGKDEYAEWIVANQRSLLEVMEAFPSAKPPLGVFFAAIAPRLQPRYYSISSSPKMVPNRIHVTCALVYEKTPGGRIHKGICSTWMKNAVPLTENQDCSSAPIFVRTSNFRLPADPKVPVIMIGPGTGLAPFRGFLQERLALKESGTELGQSILFFGCRNRKVDFIYENELNNFVENGALSELDMAFSREGASKEYVQHKMSQKASDIWNMLSEGAYLYVCGDAKGMAKDVHRTLHTIVQEQGNLDSSKAELYVKNLQMSGRYLRDVW	78%
Contig84	*Oryza sativa* Japonica Group	Os07g0120500	>gi|255677467|dbj|BAH93754.1| Os07g0120500 [Oryza sativa Japonica Group] MASAPELIDDIAAEILLRIPPDEPAHLVHASLVCKPWRRILTDPAFLRRYRAFHRTPPVLGFLHNVDGNKAISSVPRFVPTTAASPFSPPAIDPPNWWWALDCRHGRVLSHLFNPMELMVWDP	54%

			ITGDQHRFPLPPHPHAY CTGAVLCAASDCHHLDCHQGPFLVVFVGTGRHDHSWACVYSSKTGEWSSQA SIVLDSYVEMLPSVLAENT LYFYCEYGTKILGYDIGKHELSEIDPPLGHDGGILIESEYEGTDIIFMLTDVDLFA IELKSGQVKKVGES RPYYAVIPYMSFYTSVLAARHAVFTGISKGTEGMRLAVKRIKAWKSKRLDPR NEFFDVTSVEPHISSSIT TISQPICTQPKFQTKTSSPETTYPMASQIESHRASAEIVNGDAICRKKSIELLEEL GLPKGLLPLEDIEE FGYNRDTGFMWMVQRKKKIEHTFKKIKQTVSYAGEVTAFVEKGKLKKITGV KTKELLLWLSVVEVYVAEA SPEKVTFKTGTGLSDNFDATAFALGE	
Contig84	*Oryza sativa* Japonica Group	Os07g0118200	>gi|115470331|ref|NP_001058764.1| Os07g0118200 [Oryza sativa (japonica cultivar-group)] MASQIENHRSGAEVVNGDAICRKRSIELLGELGLPKGLLPLEDIEEFGYNRDTG FMWLVQKKKKIEHTFK KIKQTVSYAREVTAFVEKGKLKKITGVKTKELLLWLSVVEVYLADASPEKVTF KTGTGLSDTFDAAAFAL GDKLQVFQSPVANPKPLRISLFDVLIVLEPLCQIRLHPNTNVEEFIHSKTLIKPVF IDHSNLRLGRERLF FSRNTRLIESHRAGAEIVNGDDICRKKSIELLGELGLPMGLLPLEDIEEFGYNRE TGFIWMVQRKKKIEH VFKKIKQNVSYAGEVTAFVEKGKLKKITGVKTKELMLWLSIVEVYAAEASPE KVTFKSGAGICKTFDAAA FAPGE	54%
Contig85	*Zea mays*	hydroxymethylbutenyl 4-diphosphate synthase	>gi|195655961|gb|ACG47448.1| hydroxymethylbutenyl 4-diphosphate synthase [Zea mays] MATGVAPAPLPHVRVHHGGVGFTRSVDFAKVLSAPGAGTMRASSSRGRALV AKSSSTGSETMELEPSSEG SPLLVPRQKYCESTHQTRRRKTRTVMVGNVPLGSDHPIRIQTMTTSDTKDVAK TVEEVMRIADKGADLVRITVQGRKEADACFEIKNTLVQKNYNIPLVADIHCSY GSLRVAECFDKIRVNPGNFADRRAQFEKLEYTDDDYQKELEHIEKVFSPLVEK CKQYGRAMRIGTNHGSLSDRIMSYYGDSPRGMVESALEFARICRKLDFHNFVF SMKASNPVIMVQAYRLLVAEMYNLGWDYPLHLGVTEAGEGEDGRMKSAIGI GTLLMDGLGDTIRVSLTEPPEEEIDPCQRLANLGTQAANLQIGVAPFEEKHRRY FDFQRRSGQLPLQKEGEEVDYRNVLHRDGSVLMSVSLDQLKAPDLLYRSLAA KLVVGMPFKDLATVDSILLRELPPVEDAEARLALKRLVDISMGVLAPLSEQLT KPLPHAIVLVNLDELSSGAHKLLPEGTRLAVTLRGDESYEQLDILKDVDDITML LHNVPYGEEKTGRVHAARRLFEYLQANGLNFPVIHHINFPETIDRDGLVIGAG ANVGALLVDGLGDGVFLEAADQEFEFLRDTSFNLLQGCRMRNTKTEYVSCPS CGRTLFDLQEISAEIREKTSHLPGVSIAIMGCIVNGPGEMADADFGYVGGAPGK IDLYVGKTVVQRAIAMEGATDALIQLIKDHGRWVDPPAEE	90%
Contig85	*Solanum lycopersicum*	GcpE	>gi|27462474|gb|AAO15447.1|AF435086_1 GcpE [Solanum lycopersicum] MAAGTVPASFTGLKSNENGLGFAKSMNFIRVSDLQRVKFRRTKFSVIRNANPG QETIELQPASEGSPLLVPRQKYCESIYKTVRRQTCTVMVGNVALGSEHPIRIQT MTTTDTKDVAATVEQVMKIADAGADIVRITVQGRKEADACFEIKNTLVQKNY NIPLVADIHFAPSVALRVAECFDKIRVNPGNFADRRAQFEQLEYTEDDYQKEL EHIEEVFTPLVEKCKKYGRAMRIGTNHGSLSDRIMSYYGDSPRGMVESAFEFA RICRKLDFHNFVFSMKASNPVVMVQAYRLLVAEMYVQGWDYPLHLGVTEAG EGEDGRMKSAIGIGTLLQDGLGDTIRVSLTEAPEEEIDPCRRLADLGKRAAALQ QGVAPFEEKHRRYFDFQRRSGELPAQKEGDEVDYRGVLHRDGSVLMSVSLNQ LKTPELLYRSLAAKLIVGMPFKDLATVDSILLRELPPLDDIDSRLALKRLVDISM GVIAPLSEQLTKPLPNAMVLVTLKELSGGAHKLLPEGTRLVVSLRGDESHDEL EILKSSDVTMILHNLPYTEEKIGRVQAARRLFEYLSENSLNFPVIHHIQFPSNTH RDDLVIGAGTNAGALLVDGLGDGLLLEAPDKDFDFLRNTSFNLLQGCRMRNT KTEYVSCPSCGRTLFDLQEISAQIREKTSHLPGVSIAIMGCIVNGPGEMADADF GYVGGAPGKIDLYVGKTVVKRAIEMEHATDALIQLIKDHDRWVDPPTEE	88%
Contig86	*Arabidopsis thaliana*	ALIS1 (ALA-INTERACTING SUBUNIT 1); phospholipid transporter	>gi|18399730|ref|NP_566435.1| ALIS1 (ALA-INTERACTING SUBUNIT 1); phospholipid transporter [Arabidopsis thaliana] MSSSNTPSSSAAAAGSIDSSAARRNSKRPKYSKFTQQELPACKPILTPGWVISTF LIISVIFIPLGVISL FASQDVVEIVDRYDSACIPLSDRANKVAYIQGTGNKSCTRTLIVPKRMKQPIYV YYQLENFYQNHRRYVKSRSDSQLRSVKDENQIDACKPEDDFGGQPIVPCGLIA WSLFNDTYVLSRNNQGLTVNKKGIAWKSDKEHKFGKNVFPKNFQKGNLTGG ASLDPNKPLSDQEDLIVWMRTAALPTFRKLYGKIESDLEKGENIQVTLQNNYN TYSFSGKKKLVLSTTSWLGGKNDFLGIAYLTVGGICFVLALAFTVMYLVKPRR LGDPTYLSWNRIPGGR	72%
Contig86	*Zea mays*	cell division control protein 50	>gi|226503181|ref|NP_001149466.1| cell division control protein 50 [Zea mays] MSSHAVGTSNGGSGDAAAGGAARRNTRMPKYSKFTQQELPACKPILTPKWV VSVFLIVGVIFVPIGVVSLLAARDVVEIIDRYDEACVPVNMTENKLAYIQNETIS KECIRNLTVTKYMKQPIFVYYELDNFYQNHRRYVKSRNDAQLRDASKANQTS ACEPEKTTANGQPIVPCGLIAWSLFNDTYNFTRGNENLTVDKKDISWKSDREH KFGKDVYPSNFQNGALKGGATLNPKIPLSEQEDLIVWMRTAALPTFRKLYGRL YFDLKENDTITVRLNNNYNTYSFGGKKKLVLSTATWLGGKNDFLGFAYLIVG GLCIFLAFAFTLLYFVKPRKLGDHNYLSWNRR	83%
Contig87	*Mentha x piperita*	1-deoxyxylulose-5-phosphate synthase	>gi|3114573|gb|AAC33513.1| 1-deoxyxylulose-5-phosphate synthase [Mentha x piperita] MASSCGVIKSSFLPSLHSEDSTFLSRAPTSLPLKNHKLNVVAALQQDSSNDVVP SGDRLSRPKSRALSFT GEKPPIPILDTINYPNHMKNLSVEELANLADELREEIVYTVSKTGGHLSSSLGVS ELTVALHHVFNTPDD KIIWDVGHQAYPHKILTGRRARMHTIRQTFGLAGFPKRDESAHDAFGAGHSST SISAGLGMAVARDLLQKNNHVISVIGDGAMTAGQAYEALNNAGFLDSNLIIVL NDNKQVSLPTATVDGPAPPVGALSKALTKLQASRKFRQLREAAKSMTKQMG APAHEIASKLTQYVKGMMGKPGASLFEELGIYYIGPVDGHNVEDLVYIFKKVK EMPAPGPVLIHIITEKGKGYPPAEIAADKMHGVVKFDAKTGKQMKTKNKTKS	97%

			YTQYFAESLVAEAEHDDKIVAIHAAMGGGTGLNIFQKQFPDRCFDVGIAEQHA VTFAAGMAAEGLKPFCAIYSSFLQRGYDQVVHDVDLQKLPVRFMMDRAGVV GADGPTHCGAFDTTYMACLPNMVVMAPSDEAELMNMIATAAIIDDRPSCVRY PRGNGIGVALPSNNKGTPLEIGKGRILKEGSKVAILGFGTIVQNCMAAANLLEQ HGISVTVADARFCKPLDGDLIKKLVQEHEVLITVEEGSIGGFSAHISHFLSLNGL LDGNLKWRPMVLPDRYIDHGAQSDQIEEAGLSPKHIAGTVVSLIGGGKDSLHL INNL	
Contig87	*Oryza sativa*	CLA1 transketolase-like protein	>gi|2612941|gb|AAB88295.1| CLA1 transketolase-like protein [Oryza sativa] NYPIHMKNLSLKELQQLADELRSDVIFHVSKTGGHLGSSLGVVELTVALHYVF NTPQDKILWDVGHQSYP HKILTGRRDKMPTMRQTNGLSGFTKRSESEYDSFGTGHSSTTISAALGMAVGR DLKGGKNNVVAVIGDGA MTAGQAYEAMNNAGYLDSDMIVILNDNKQVSLPTATLDGPAPPVGALSSALS KLQSSRPLRELREVAKGVTKQIGGSVHELAAKVDEYARGMISGSGSTLFEELG LYYIGPVDGHNIDDLITILREVKSTKTTGPVLIHVVTEKGRGYPYAERAADKYH GVAKFDPATGKQFKSPAKTLSYTNYFAEALIAEAEQDNRVVAIHAAMGGGTG LNYFLRRFPNRCFDVGIAEQHAVTFAAGLACEGLKPFCAIYSSFLQRGYDQVV HDVDLQKLPVRFAMDRAGLVGADGPTHCGAFDVTYMACLPNMVVMAPSDE AELCHMVATAAAIDDRPSCFRYPRGNGIGVPLPPNYKGVPLEVGKGRVLLEGE RVALLGYGSAVQYCLAAASLVERHGLKVTVADARFCKPLDQTLIRRLASSHE VLLTVEEGSIGGFGSHVAQFMALDGLLDGKLKWRP	79%
Contig88	*Zea mays*	fructose-bisphosphate aldolase	>gi|226502756|ref|NP_001152410.1| fructose-bisphosphate aldolase [Zea mays] MAMATAKLNSPATSLVAGGLTRRSAPARCTTVIRAAAGSYSDELISTAKSVAS PGRGILAIDESNATCGKRLSSIGLDNTEVNRQAYRQLLLTTAGLGEYISGAILFE ETLYQSTTDGKKFVDCLKDQNIMPGIKVDKGLVPLPGSNNESWCQGLDGLAS RCAEYYKQGARFAKWRTVVSIPCGPSALAVKEAAWGLARYAAIAQDNGLVPI VEPEILLDGDHGIEGALEVAEKVWSEVFFYLAENNVLFEGILLKPSMVTPGAE HKEKASPEAIAKYTLTMLRRRVPPAVPGIMFLSGGQSEVEATLNLNAMNQSLN PWHVSFSYVRALQNSVLKTWQGRPENVEAAQKALLVRAKANSLAQLGRYTG EGESDDAKKGMFQKGYTY	70%
Contig88	*Triticum aestivum*	aldolase	>gi|32400859|gb|AAP80661.1|AF479042_1 aldolase [Triticum aestivum] GAMVTAKLSSPAAARLAPSAGSARRASRVRVRASGGSYADELVSTAKTVASP GRGILAIDESSATCGKRLASIGLDNTEVNRQAYRQLLLTTAGLGEYISGAILFEE TLYQSTTDGKTFVDVLKDQNIMPGIKVDKGLVPLPGSNNESWCQGLDGLASR CAEYYKQGARFAKWRTVVSIPCGPTALAVKEAAWGLARYAAIAQDNGLVPIV EPEISSTVTM	73%
Contig89	*Artemisia annua*	(E)-4-hydroxy-3-methylbut-2-enyl diphosphate synthase	>gi|254072126|gb|ACT64770.1| (E)-4-hydroxy-3-methylbut-2-enyl diphosphate synthase [Artemisia annua] MQIADRGADIVRITVQGKREADACFEIKNTLVQKNYNIPLVADIHFAPSVALRV AECFDKIRVNPGDFADRRAQFEQLEYTEDDYQQELEHIEKVFTPLVEKCKKYG RAMRIGTNHGSLSDRIMSYYGDSPRGMVESAFEFARICRKLDFHNFVFSMKAS NPVIMVQAYRLLVAEMNVQGWDYPLHLGVTEAGEGEDGRMKSAIGIGTLLQ DGLGDTIRVSLTEPPEEEIDPCRKLANLGMKASQLQQGVAPFEEKHRRYFDFQ RRTGDLPVQKEGEEVDYRGVLHRDGSVIMSVTLDQLKTPELFYRSLAAKLVL GMPFKDLATVDSILLRELPPADDKDARLALKRLIDVSMGIITPLSEQLTKPLPN AIVLVNLNELSTGAHKLLPEGTRLVVSVRGDEPYEELDILKTTDATMILHELPY AEEKTGRVHAARRLFEYLSENSLNFPVLHHIKFPKGIPRDDLVISAGANAGALL VDGLGDGILLEAPDQDFEFIRNTSFNLLQGCRMRNTKTEYVSCPSCGRTLFDLQ VISAEIREKTSHLPGVSIAIMGCIVNGPGEMADADFGYVGGAPGKIDLYVGKTV VQRGIAMEGATDALIQLIKDHGRWVDPPVEE	62%
Contig89	*Catharanthus roseus*	GCPE protein	>gi|27903511|gb|AAO24774.1| GCPE protein [Catharanthus roseus] MATGTVPASFTGLKSRENGLGFAKSMDFVQVSDLRRVKFRRAKVSVIKNSNP GPETVELQPASQGSQLLVPVQKYCESIHKTVRRKTRTVMVGNVALGSDHPIRI QTMTTTDTKDVAATVEQVMGIADKGADIVRITVQGKKEADACYDIKNTLVQ KSYNIPLVADIHFAPAVALRVAECFDKIRVNPGNFADRRAQFEQLEYTDEEYQ KELEHIEQVFTPLVEKCKKYGRAMRIGTNHGSLSDRIMSYYGDSPRGMVESAF EFARICRKLDFHNFVFSMKASNPVIMVAAYRLLVAEMYVLGWDYPLHLGVTE AGEGEDGRMKSAIGIGTLLQDGLGDTIRVSLTEPPEEEIDPCRRLANLGARAAD LGQGVAPFEEKHRRYFDFQRRTGDLPVQKEGEEVDYRGVLHRDGSVLMSVSL DQLKTPELLYKSLAAKLVVGMPFKDLATVDSILLRELPPIEDKDSRLALKRLIDI SMGVITPLSEQLTKPLPNAMVLVTLKELSSGAHKLLPEGTRLVVSVRGDEPYE ELDILKNVDVTMILHNLPHTEEKIGRVHAARRLFEYLSENSLNFPVIHHMQFAN AIHRDDLVIGAGSDAGALLVDGLGDGVMLEAHDQDFEFLRNTSFNLLQGCRM RNTKTEYVSCPSCGRTLFDLQEISAQIREKTSHLPGVSIAIMGCIVNGPGEMAD ADFGYVGGAPGKIDLYVGKTVVKRGIDMEHATDALIQLIKDHGRWVDPPAED	61%
Contig90	*Glycine max*	CYP82C1p	>gi|2739004|gb|AAB94590.1| CYP82C1p [Glycine max] MGMAMDAFQHQTLISIILAMLVGVLIYGLKRTHSGHGKICSAPQAGGAWPIIG HLHLFGGHQHTHKTLGIMAEKHGPIFTIKLGSYKVLVLSSWEMAKECFTVHD KAFSTRPCVAASKLMGYNYAMFGFTPYGPYWREIRKLTTIQLLSNHRLELLKN TRTSESEVAIRELYKLWSREGCPKGGVLVDMKQWFGDLTHNIVLRMVRGKPY YDGASDDYAEGEARRYKKVMGECVSLFGVFVLSDAIPFLGWLDINGYEKAM KRTASELDPLVEGWLEEHKRKRAFNMDAKEEQDNFMDVMLNVLKDAEISGY DSDTIIKATCLNLILAGSDTTMISLTWVLSLLLNHQMELKKVQDELDTYIGKDR KVEESDITKLVYLQAIVKETMRLYPPSPLITLRAAMEDCTFSGGYHIPAGTRLM VNAWKIHRDGRVWSDPHDFKPGRFLTSHKDVDVKGQNYELVPFGSGRRACP GASLALRVVHLTMARLLHS FNVASPSNQVVDMTESIGLTNLKATPLEILLTPRLDTKLYEN	64%
Contig90	*Eschscholzia californica*	(S)-N-methylcoclaurine 3'-hydroxylase	>gi|3127031|gb|AAC39454.1| (S)-N-methylcoclaurine 3'-hydroxylase [Eschscholzia californica] MEKPILLQLQAGILGLLALICFLYYVIKVSLSTRNCNQLVKHPPEAAGSWPIVG HLPQLVGSGKPLFRVL GDMADKFGPIFMVRFGVYPTLVVSTWEMAKECFTSNDKFLASRPPSAASSYM TYDHAMFGFSFYGPYWREIRKISTLHLLSHRRLELLKHVPHTEIHNFIKGLFGI WKDHQKQQQPTGREDRDSVMLEMSQLFGYLTLNVVLSLVVGKRVCNYHAD GHLDDGEEAGQGQKLHQTITDFFKLSGVSVASDALPLLGLFDLGGKKESMKR VAKEMDFFAERWLQDKKLSLSLSSETNNKQNDAGEGDGDDFMDVLMSILPD DDDSLFTKYSRDTVIKATSLSMVVAASDTTSVSLTWALSLLLNNIQVLRKAQD ELDTKVGRDRHVEEKDIDNLVYLQAIVKETLRMYPAGP LSVPHEAIEDCNVGGYHIKTGTRLLVNIWKLQRDPRVWSNPSEFRPERFLDNQ	60%

			SNGTLLDFRGQHFEYIPFGSGRRMCPGVNFATLILHMTLARLLQAFDLSTPSSSPVDMTEGSGLTMPKVTPLKVLLTPRLPLPLYDY	
Contig91	*Mentha x piperita*	geranyl diphosphate synthase small subunit	>gi|6449050|gb|AAF08792.1|AF182827_1 geranyl diphosphate synthase small subunit [Mentha x piperita] MAINLSHINSKTCFPLKTRSDLSRSSSARCMPTAAAAAFPTIATAAQSQPYWAAIEADIERYLKKSITIR PPETVFGPMHHLTFAAPATAASTLCLAACELVGGDRSQAMAAAAAIHLVHAAAYVHEHLPLTDGSRPVSKPAIQHKYGPNVELLTGDGIVPFGFELLAGSVDPARTDDPDRILRVIIEISRAGGPEGMISGLHREEEIVDGNTSLDFIEYVCKKKYGEMHACGAACGAILGGAAEEEIQKLRNFGLYQGTLRGMMEMKNSHQLIDENIIGKLKELALEELGGFHGKNAELMSSLVAEPSLYAA	89%
Contig91	*Arabidopsis thaliana*	GGR (geranylgeranyl reductase); farnesyltranstransferase	>gi|15233848|ref|NP_195558.1| GGR (geranylgeranyl reductase); farnesyltranstransferase [Arabidopsis thaliana] MLFSGSAIPLSSFCSLPEKPHTLPMKLSPAAIRSSSSSAPGSLNFDLRTYWTTLITEINQKLDEAIPVKH PAGIYEAMRYSVLAQGAKRAPPVMCVAACELFGGDRLAAFPTACALEMVHAASLIHDDLPCMDDDPVRRGKPSNHTVYGSGMAILAGDALFPLAFQHIVSHTPPDLVPRATILRLITEIARTVGSTGMAAGQYVDLEGGPFPLSFVQEKKFGAMGECSAVCGGLLGGATEDELQSLRRYGRAVGMLYQVVDDITEDKKKSYDGGAEKGMMEMAEELKEKAKKELQVFDNKYGGGDTLVPLYTFVDYAAHRHFLLPL	31%
Contig92	*Mentha x piperita*	flavonoid 8-O-methyltransferase	>gi|38047395|gb|AAR09600.1| flavonoid 8-O-methyltransferase [Mentha x piperita] MALPNGISSKQELLEAQAHVWNHIYSYINSMSLKCAIQLGIPDAIHKHGNPITLSQLADALNINKAKSHGLFRLMRILVHSGFFDKVKVKVKVEGEDEEEEEDAYSLTPASRLLLRSEPLSVAPFALAMSDPVYTETWHHLSEWFRNDAVAAFDTKYGMTFPEYAVADDRLNVLFNEAMACDAGFVNSILTTECREIFDGLESMVDVGGGTGATAKGIAAAFPGMECTVLDLPNVVGGLKGSENLSFVSGDMFDFIPHADAIFMKFILHDWNDEECVKILKKCKEAISRSNNSCRKIILVEIVMEDEKETHEATETKLFFDMQMLAIITGKERSEKEWGKLFFDAGFTNYKITRVLGLRSVIEVFP	99%
Contig92	*Vitis vinifera*	resveratrol O-methyltransferase	>gi|212290116|emb|CAQ76879.1| resveratrol O-methyltransferase [Vitis vinifera] MDLANGVISAELLHAQAHVWNHIFNFIKSMSLKCAIQLGIPDIIHNHGKPMTLPELVAKLPVHPKRSQCVYRLMRILVHSGFLAAQRVQQGKEEEGYVLTDASRLLLMDDSLSIRPLVLAMLDPILTKPWHYLSAWFQNDDPTPFHTAHERSFWDYAGHEPQLNNSFNEAMASDARLLTSVLLKEGQGVFAGLNSLVDVGGGTGKVAKAIANAFPHLNCTVLDLPHVVAGLQGSKNLNYFAGDMFEAIPPADAILLKWILHDWSDEECVKILKRCREAIPSKENGGKVIIIDMIMMKNQGDYKSTETQLFFDMTMMIFAPGRERDENEWEKLFLDAGFSHYKITPILGLRSLIEVYP	58%
Contig93	*Enterococcus faecalis* HH22	cell wall surface anchor family protein	>gi|227555773|ref|ZP_03985820.1| cell wall surface anchor family protein [Enterococcus faecalis HH22] MKRGKHMKKTMLILLFGLLTVVGLPMVTEAVEPVNATDTTIFGAQAMVPNSTEDQTDKLQTLLSQTAKEGRALFLPQGSYALSKDIAISSNYQLIGDTTGATILHNATGAPIQLTDTTYGTKTNVRLQNIAFDGINVTLKLTNQLTLANNIFYNPLKGFVVNLNADIGVKISGNIFMRDTAHMQSGGDFNRAIYIGGYSTPSRFQYMSDVDIVDNLFGLKVTELDAIKSTSRSDLAATITRLQTAIEAGAISVPNEQNYLSTGVNSFNMLKDVTVQHNFFYSPYDNENLNGLVGDHAIYFRGAQNITVVGNHLRGLQNGPAGGFKFKSGRNITIMNNYLRNTGLIMYGTPEIGLAETQAEGAISELSNWLVANNIFDWKYWDNQYAIGMEYNRHTGNNNVFNGVFINNQFVNYHNIPQNRRRELLIASGGGFRPETSFVKDNTRDDGLKNGQLLVENWTEADYRLMPATWESLISPTLYEQYKNTPIPVRNTLATPVATTIVQGQSIDPQQLVANTNDADEAVPAAKIVNPEVLNEIGQQKVTVQLTYETGSLVTVNVPVTVEAPAKKLDLSQLQTVYASIGEANQYTVYSWQLFTAIGPKTIVPSYYQQATQLLAEGQESQDKTQEQVDQLTSNLQSAMKVLVKKADITLERTEAENELASVHKLDESVYTKNSWQAMQEALIDTTTGEGSSKQLQQLLAWSDEELLEPTLGGFKTPADAQKRINQLTQTIKTALLLLVEKSTETTSNTSESSTSSTTSETSNTSESSTSSTTSETSNTNESNTPSTTSKTSNTSESSTSSTTSETSNTNESNTPSTTSETSNTSESSTSSTTSESSSTSESSTPSTTSESSSTSESSTSSTTSETSNTSESSTPSTTSESSSTSESNTPSTTSETSSTSESSTSSTTSETSNTNESNTPSTTSKTSSTSESSASSTTSATNNTSESSTPSTVNESSQSKGQNSVIYAVESNQDPNDAQSNSKPSAKASQTKESVAENQATKQIQTNQESSGTVKKADNTTKIAKKKFPKTGEQSSAVGSFLGLSFLSLAIATYCFKVKR	58%
Contig93	*Toxoplasma gondii* ME49	PHD-finger domain-containing protein	>gi|237837385|ref|XP_002367990.1| PHD-finger domain-containing protein [Toxoplasma gondii ME49] MEASDAEEARSVSSRESNDSICFCCRGGGEVVCCEGCPNSFHVGCLDTARRPQLTEEEWFCPECVARSAESKGDLASAFFSGVLPSPGSSRFRPPSPLYPAKDANFKDSQSSLRAKKRSLRASQLLASEASSSSLATAGGELREKATEEREGAREAQRGERGEQTAEMEERGEQRAEREAREEREETETERAVKNEGGEAAKEDPFREPANAAASLGKLEVSSETENGGSQPVLDSRHRRMPEQENEEKGDRRMQSALLNCEKENDREDRDKREGDAGADGEASRGRPCSVSSSPSTAASSRDLCPPLSSHPSLSSSSLSSSLSSSSLSSSFSSSSLSSSSLSSSSSPSSSSSPSSSSSSLSSSSSLSSSSFSSSSLSSSSLSSSSLSSSSLSSSSLSSSSLSSSSLSSSSLSSASSSSLSSSSLSSSFHPSSCSSPQSSSPQPPSALPSSFHSPLSAFSSFASCRPGRWGNTAGGAGSSSKKRRRRGDETRINVGPDYQPSAASSFSFQERLYSQAAPCAAFRDAAQAEGLRGRSQAQTAGEEKKRFRAFPGCSLASPCGGYFLPPVFCSGDSAAALGAAGNFGAPPGSAFEDSRHSALEPRLVYSPRCLEEKRQQCLATGRMQHCIRTQGELADFVETCSRCWHARPGWQPFSAEFAYQLLHRAGYDPQRALRMLDDPGFCFNDICDPPLRKYDNKWKRRDKRGTFPNSPYPPPLVVQSFLQEKSRACRPSLSGTGSYAIR	43%
Contig94	*Populus trichocarpa*	AP2 domain-containing transcription factor	>gi|224072757|ref|XP_002303866.1| AP2 domain-containing transcription factor [Populus trichocarpa] MGKTSKQSLKNSANTSINPATKVKRTRKSVPRDSPPQRSSIYRGVTRHRWTGRYEAHLWDKNCWNESQNKKGRQGAYDDEEAAGHAYDLAALKYWGQDTILNFPLSTYEEEFKEMEGHSKEEYIGSLRRKSSGFSRGVSKYRGVARHHHNGRWEARIGRVFGNKYLYLGTYATQEEAATAYDMAAIEYRGLNAVTNFDLSRYSSKFKEMLERTSASDCPLTPPESDRDPPRRSFPDDIQTYFDCQDSSSYTDGDDIIFGDLHSFASPIFHCELDG	47%
Contig94	*Oryza sativa* Japonica Group	WRINKLED1-like protein	>gi|50725899|dbj|BAD33427.1| WRINKLED1-like protein [Oryza sativa Japonica Group] MEGQSREEYIGSLRRKSSGFSRGVSKYRGVARHHHNGRWEARIGRVFGNKYL	82%

			YLGTYATQEEAAMAYDMAAIEYRGLNAVTNFDLSRYIKWLRPGADGAGAPQ NPHPMLGALSAQDLPAIDLDAMASSFQHDGHGAAAAAAQLIPARHSLGHTPT TSALSLLLQSPKFKEMIERTSAAETTTTSSTTTSSSSPSPPQATKDDGASPQCSFP EDIQTYFGCAAEDGAAGAGYADVDGLFFGDLAAYASPAFHFELDL	
Contig95	*Populus trichocarpa*	ATP/ADP transporter	>gi|224070859|ref|XP_002303268.1| ATP/ADP transporter [Populus trichocarpa] MEAVLQTRGLLSLPPNPKGRVLYPSQGLKQRLFATKPKTFSGFSLSSNGVPKFP TSVSKPNGFFPKDRNL HICRAEAAAAADGQPLFGEETDKPKFLGIELATFKKIIPLGLMFFCILFNYTILR DTKDVLVVTAKGSSA EIIPFLKTWVNLPMAIGFMLLYTKLANVLSKQALFYTVILPFIAFFGAFGFVLYP LSSYIHPEAFADKLL NVLGPRFLGPLAIMRIWTFCLFYVMAELWGSVVVSVLFWGFANQITTVDEAK RFYPLFGLGANVALIFSGRTVKYFSNLRKNLGPGVDGWAVSLKGMMSIVVLM GLAICLCYWWVNTFVPLPTRSLKKKEKPKMSTMESLKFLVSSRYIRDLATLVV AYGISINLVEVTWKSKLKAQFPSPNEYSAFMGDFSTATGIATFSMMLLSQFIFD KYGWGVAAKITPTVLLLTGVGFFSLILFGGPLAPTLTQFGMTPLLAAVYVGAM QNIFSKSAKYSLFDPCKEMAYIPLDEDTKVKGKAAIDVVCNPLGKSGGALIQQ FMILTFGSLANSTPYLGGILLVIVFAWLGAAKSLDTQFTALRQEEELEKEMERA AVKIPVVSQEGGNGALSSGTALNPTTGDPSSSSSEPSSPRNI	87%
Contig95	*Arabidopsis thaliana*	NTT1 (NUCLEOTIDE TRANSPORTER 1); ATP:ADP antiporter	>gi|15220099|ref|NP_178146.1| NTT1 (NUCLEOTIDE TRANSPORTER 1); ATP:ADP antiporter [Arabidopsis thaliana] MEAVIQTRGLLSLPTKPIGVRSQLQPSHGLKQRLFAAKPRNLHGLSLSFNGHK KFQTFEPTLHGISISHK ERSTEFICKAEAAAAGDGAVFGEGDSAAVVASPKIFGVEVATLKKIIPLGLMFF CILFNYTILRDTKDVL VVTAKGSSAEIIPFLKTWVNLPMAIGFMLLYTKLSNVLSKKALFYTVIVPFIIYF GAFGFVMYPLSNYIH PEALADKLLTTLGPRFMGPIAILRIWSFCLFYVMAELWGSVVVSVLFWGFANQ ITTVDEAKKFYPLFGLGANVALIFSGRTVKYFSNLRKNLGPGVDGWAVSLKA MMSIVVGMGLAICLLYWWVNRYVPLPTRSKNKKEKPKMGTMESLKFLVSSP YIRDLATLVVAYGISINLVEVTWKSKLKAQFPSPNEYSAFMGDFSTCTGVATFT MMLLSQYVFNKYGWGVAAKITPTVLLLTGVAFFSLILFGGPFAPLVAKLGMTP LLAAVYVGALQNIFSKSAKYSLFDPCKEMAYIPLDEDTKVKGKAAIDVVCNPL GKSGGALIQQFMILSFGSLANSTPYLGMILLVIVTAWLAAAKSLEGQFNSLRSE EELEKEMERASSVKIPVVSQDESGNGSLGESPSSSPEKSAPTNL	87%
Contig96	*Nicotiana tabacum*	glucose-6-phosphate dehydrogenase	>gi|3021510|emb|CAA04993.1| glucose-6-phosphate dehydrogenase [Nicotiana tabacum] MAASWCIEKRGSIRLDSFRDNDNIPETGCLSIIVLGASGDLAKKKTFPALFNLY RQGFLQSNEVHIFGYA RTKISDDDLRGRIRGYLSQGKENEEEVSEFLQLIKYVSGSYDSGEGFSLLDKAI AEHEIAKNSTEGSSRR LFYFALPPSVYPSVCRMIKNYCMNKSDLGGWTRIVVEKPFGKDLASAEQLSSQ IGELFDEPQIYRIDHYL GKELVQNLLVLRFANRFFLPLWNRDNIDNIQIVFREDFGTEGRCGYFDEYGIIR DIIQNQLLQVLCLVAM EKPVSQKPEHIRDEKVKVLQSMLPIKDEEVVLGQYEGYKDDPTVPDNSNTPTF ATMVLRIHNERWEGVPFIMKAGKALNSRKAEIRVQFKDVPGDIFRCKKQGRN EFVIRLQPSEAMYMKLTVKKPGLEMSTVQSELDLSYRQRYQGVVIPEAYERLI LDTIRGDQQHFVRRDELKAAWEIFTPLLHRIDDGEVKPIPYKPGSRGPAEADEL LQNVGYVQTHGYICIPPTL	72%
Contig96	*Saccharomyces cerevisiae*	YNL241C	>gi|51013447|gb|AAT93017.1| YNL241C [Saccharomyces cerevisiae] MSEGPVKFEKNTVISVFGASGDLAKKKTFPALFGLFREGYLDPSTKIFGYARSK LSMEEDLKSRVLPHLKKPHGEADDSNVEQFFKMVSYISGNYDTDEGFDELRT QIEKFEKSANVDVPHRLFYLALPPSVFLTVAKQIKSRVYAENGITRVIVEKPFG HDLASARELQKNLGPLFKEEELYRIDHYLGKELVKNLLVLRFGNQFLNASWN RDNIQSVQISFKERFGTEGRGGYFDSIGIIRDVMQNHLLQIMTLLTMERPVSFDP ESIRDEKVKVLKAVAPIDTDDVLLGQYGKSEDGSKPAYVDDDTVDKDSKCVT FAAMTFNIENERWEGVPIMMRAGKALNESKVEIRLQYKAVASGVFKDIPNNE LVIRVQPDAAVYLKFNAKTPGLSNATQVTDLNLTYASRYQDFWIPEAYEVLIR DALLGDHSNFVRDDELDISWGIFTPLLKHIERPDGPTPEIYPYGSRGPKGLKEY MQKHKYVMPEKHPYAWPVTKPEDTKDN	47%
Contig97	*Nicotiana tabacum*	epoxide hydrolase	>gi|1354849|gb|AAB02006.1| epoxide hydrolase [Nicotiana tabacum] MEKIQHNYVDVRGLKLHIAEIGTGPAVFFLHGFPEIWYSWRHQMIAVADAGF RGIAPDFRGYGLSELPAEPEKTTFRDLVDDLLDMLDSLGIHQVFLVGKDFGAR VAYHFALVHPDRVSTVVTLGVPFLLTGPETFPRDLIPNGFYMLRWQEPGRAEK DFGRFDTKTVVKNIYTMFSGSELPIAKDDEEIMDLVDPSAPVPDWFTGEDLAN YASLYEKSSFRTALQVPYRAWLEEYGVKDIKVKVPCLLVMGEKDYALKFGGL EQYVKSGMVKEYVPNLETIFLPEGSHFVQEQFPEQVNQLIITFLKKLI	62%
Contig97	*Medicago truncatula*	Epoxide hydrolase	>gi|124360008|gb|ABN08024.1| Epoxide hydrolase [Medicago truncatula] MEGIEHRTVEVNGIKMHIAEKGKEGPVVLFLHGFPELWYSWRHQIVALGSLG YRAVAPDLRGYGDTEAPSSISSYTGFHIVGDLVALIDLLGVDQVFLVAHDWGA IIGWYLCMFRPERIKAYVCLSVPLLRRNPKIKTVDAMRAAYGDDYYISRFQEP GKMEAEMAEVGTAYVMKNILTTRQTGPPIFPKGEYGTGFNPDTPDTLPSWLTE	35%

			EDLAYFVSKFEKTGFTGALNYYRNFNVNWELMAPWNGVKIKVPVKFITGDLD MVYTSLNMKEYIHGGGFKEDVPNLEEVIIQKGVAHFNNQEAAEEISNHIYEFIK KF	
Contig98	*Hevea brasiliensis*	geranyl-diphosphate synthase	>gi|164605008|dbj|BAF98300.1| geranyl-diphosphate synthase [Hevea brasiliensis] MAGALSSTIHGNLIARAVSSSNPKHPLFSHRPMVVAMSTDQSYWSSVNADLD THLKQAIPIRQPLAVFEPMRHLILSAPQTSAPALCIAACELVGGHRNQAMAAAS ALRLVHASASTHENLPLTDRPRPMPRTRPTLYGPNIELLIADGIIPYGFELLARD DDAAENNSNRVLRAIIEISRAMGSQGVIEGQYNESQYEESEGEEIFHVG WLQNVCRKKEGTLHACAGACGAILGGGSEDEIEKLRRYGLYVGMVQGILSKV DERKEWPVKEVNKLRDLALKELKDFNQAKVKTISILVETRFCNL	45%
Contig98	*Drosophila grimshawi*	GH14822	>gi|195018605|ref|XP_001984814.1| GH14822 [Drosophila grimshawi] MESALDVLSRAATMVQNNASETRLTSKELPTAKWRRERRQRAAAAEYQVHD AGSDRERERERERDREPDM DSPIDMSVTSSTVKHQRASPPPPYREPQGGAASSHCYAASRPSVITQAPPKREQ PEHVHHHHHSHSSREH DNRSTESVSICDIDEHFRRSLGPDYAALLKSPTSSSPTSSPQPQPQPQQQQQPSQ PVVVASSGTPMQQIS PQGYRQHQPTTYQQQHHSPLPLPLPLSKLGLSIVHSPTLHSAPVSPQHELPPPQE EPLSLTPPPVRAASA SALTASSPPPQQLLHPSPLSATTSGASLILDMPVAKKERALDTPHHTPPRYNTPP PAYGSVLAPSTPTPT PPTMPAIIRVKAEPGLAAASSTHTPPASPTSSTNISIFTKTEASVDDHFAKALGD TWKKLQGQGKE	26%
Contig99	*Ipomoea batatas*	S-adenosyl-L-methionine synthetase	>gi|145049666|gb|ABP35525.1| S-adenosyl-L-methionine synthetase [Ipomoea batatas] METFLFTSESVNEGHPDKLCDQVSDAVLDACLAQDPESKVACETCTKTNMVM VFGEITTKAEIDYEKIVR DTCRAIGFVSDDVGLDADNCKVLVNIEQQSPDIAQGVHGHLTKRPEDIGAGDQ GHMFGYATDETPELMPLSHVLATKLGARLTEVRKDGTCAWLRPDGKTQVTV EYYNDNGAMVPVRVHTVLISTQHDETVTNDEIARDLKEHVIKPVIPEKYLDEK TIFHLNPSGRFVIGGPHGDAGLTGRKIIIDTYGGWGAHGGGAFSGKDPTKVDRS GAYVVRQAAKSIVANGLARRCIVQVSYAIGVPEPLSVFVDTYGTGKIPDKEILK IVKEHFDFRPGMIAI NLDLKRGGNSRFLKTAAYGHFGRDDPDFTWEVVKPLKWDKPQA	84%
Contig99	*Zea mays*	S-adenosylmethionine synthetase 1	>gi|195645456|gb|ACG42196.1| S-adenosylmethionine synthetase 1 [Zea mays] MAALDTFLFTSESVNEGHPDKLCDQVSDAVLDACLAEDPDSKVACETCTKTN MVMVFGEITTKANVDYEKIVRETCRNIGFVSNDVGLDADHCKVLVNIEQQSP DIAQGVHGHFTKRPEEIGAGDQGHMFGYATDETPELMPLSHVLATKLGARLT EVRKNGTCPWLRPDGKTQVTVEYRNEGGAMVPIRVHTVLISTQHDETVTNDE IAADLKEHVIKPIIPEQYLDEKTIFHLNPSGRFVIGGPHGDAGLTGRKIIIDTYGG WGAHGGGAFSGKDPTKVDRSGAYVARQAAKSIVASGLARRAIVQVSYAIGVP EPLSVFVDTYGTGAIPDKEILKIVKENFDFRPGMIIINLDLKKGGNGRYLKTAA YGHFGRDDPDFTWEVVKPLKSEKPSA	82%
Contig100	*Mentha x piperita*	flavonoid 4'-O-methyltransferase	>gi|38047399|gb|AAR09602.1| flavonoid 4'-O-methyltransferase [Mentha x piperita] MVADEEVRVRAEAWNNAFGYIKPTAVATAVELGLPDILENHDGPMSLLELSA ATDCPAEPLHRLMRFLVF HGIFKKTAKPPLSNEAVYYARTALSRLFTRDELGDFMLLQTGPLSQHPAGLTA SSLRTGKPQFIRSVNGE DSWTDPVNGYHMKVFSDAMAAHARETTAAIVRYCPAAFEGIGTVVDVGGRH GVALEKLVAAFPWVRGISF DLPEIVAKAPPRPGIEFVGGSFFESVPKGDLVLLMWILHDWSDESCIEIMKKCK EAIPTSGKVMIVDAIV DEDGEGDDFAGARLSLDLIMMAVLARGKERTYREWEYLLREAGFTKFVVKNI NTVEFVIEAYP	90%
Contig 100	*Mentha x piperita*	flavonoid 7-O-methyltransferase	>gi|38047391|gb|AAR09598.1| flavonoid 7-O-methyltransferase [Mentha x piperita] MAPEEDSLALAEAWNHGFGFIKTSIVKTAVELEIPDILESRGAPVSIPELATAVD CSADRIYRVMRFLAY HGIFKRTKPPPESTEGGSVYYAQTPVSRRLTRENLGPFVLLQGTMREPSGCVTA ETLRTSKRPGVVNENESDHLYEDPVFSMKVFRDAMASHARMTTAAVIENYGE GFQGVGSLVDVGGSYGMALSMLVKAFPWLRGICFDLPEVVARASPLKGVEFV GGTMFESIPKADVVMLMFVLHNWSDEECVEILKRCKDAVSKDKGKVIIIDAVI DEDGDGDEFTGARLGLDVTMMATMFEGRERTYVEWARIINEAGFRRHVVKNI KTLESVIEAYP	55%
Contig102	*Arabidopsis thaliana*	hydroxymethyltransferase	>gi|21592544|gb|AAM64493.1| hydroxymethyltransferase [Arabidopsis thaliana] MEPVSSWGNTSLVSVDPEIHDLIEKEKRRQCRGIELIASENFTSFAVIEALGSAL TNKYSEGIPGNRYYG GNEFIDEIENLCRSRALEAFHCDPAAWGVNVQPYSGSPANFAAYTALLQPHDR IMGLDLPSGGHLTHGYYTSGGKKTSATSIYFESLPYKVNFTTGYIDYDKLEEKA LDFRPKLLICGGSAYPRDWDYARFRAIADKVGALLLCDMAHISGLVAAQEAA NPFEYCDVVTTTTHKSLRGPRAGMIFYRKGPKPPKKGQPEGAVYDFEDKINFA VFPALQGGPHNHQIGALAVALKQANTPGFKVYAKQVKANAVALGNYLMSKG YQIVTNGTENHLVLWDLRPLGLTGNKVEKLCDLCSITLNKNAVFGDSSALAPG GVRIGAPAMTSRGLVEKDFEQIGEFLSRAVTLTLDIQKTYGKLLKDFNKGLVN NKDLDQLKADVEKFSASYEMPGFLMSEMKYQD	92%
Contig102	*Arabidopsis thaliana*	EDA36 (EMBRYO SAC DEVELOPMENT ARREST 37); catalytic/ glycine hydroxymethyltransferase/ pyridoxal phosphate binding	>gi|15236371|ref|NP_193125.1| EDA36 (EMBRYO SAC DEVELOPMENT ARREST 37); catalytic/ glycine hydroxymethyltransferase/ pyridoxal phosphate binding [Arabidopsis thaliana] MEPVYSWGNTHLDFVDPEIYDLIEKEKHRQCRGIELIAAENFTSVAVMEALGS CLTNKYSEGMPGNRYYGGTEFIDEIESLCRSRSLEAFHCNPEKWGVNVQPYSG SPANFAAYTALLQPHDRIMGLDLPSGGHITHGYYSSGGKNISATSIYFENLPYK VDSKTGYIDYDKLEEKAMDFRPKLIICGGTSYPREWDYARFRAVADKVGAFL LCDMAHNSALVAAQEAADPFEYCDVVTTSTHKSLRGPRAGMIFYRKGPKPAK KGQPEGEVYDFDAKINSAVFPALQSGPHNNKIGALAVALKQVMAPSFKVYAK QVKANAACLASYLINKGYTLVTDGTDNHLILWDLRPLGLTGNKVEKVCELCY ITLNRNAVFGDTSFLAPGGVRIGTPAMTSRGLVEKDFEKIGEFLHRAVTITLDIQ	81%

			EQYGKVMKDFNKGLVNNKEIDEIKADVEEFTYDFDMPGFFISESRND	
Contig103	*Mentha haplocalyx* var. piperascens	(-)P450 limonene-3-hydroxylase	>gi|148887809|gb|ABR15423.1| (-)P450 limonene-3-hydroxylase [Mentha haplocalyx var. piperascens] MELLQLWSALIILVVTYAISLLINQWRKPEPQEKFPPGPPKLPLIGHLHLLWGK LPQHALASVAKEYGPVAHVQLGEVFSVVLSSREATKEAMKLVDPACANRFES IGTRIMWYDNEDIIFSPYSEHWRQMRKICVSELLSSRNGRSFGFIRQDEVSRLLR HLRSSAGAAVDMTERIETLTCSIICRAAFGSVIRDNAELVGLVKDALSMASGFE LADMFPSSKLLNLLSWNKSKLWRMRGRVDTILEAIVDEHKLKKSGEFGGEDII DVLFRMQKDTQIKVPITTNSIKAFIFDTFSAGTETSSTTTLWVLAELMRNPAVM AKVQAEVRAALKGKTNWDVDDVQELKYMKSVVKETMRMHPPIPLIPRSCRE ECVVNGYTIPNKARIMINVWSMGRNPLYWEKPETFWPERFDDVSKDFMGNDF EFVPFGAGRRICPGLNFGLANVEVPLAQLLYHFDWKLAEGMKPSDMDMSEAE GLTGIRKNNLLLVPTPYDPSS	65%
Contig103	*Mentha arvensis*	limonene hydroxylase	>gi|146386316|gb|ABQ24001.1| limonene hydroxylase [Mentha arvensis] MELQISSAIIILVVTYTISLLIIKQWRKPKPEENLPPGPPKLPLIGHLHLLWGKLP QHALASVAKQYGPV AHVQLGEVFSVVLSSREATKEAMKLVDPACADRFDSIGTKIMWYDNDDIIFSP YSEHWRQMRKICVSGLLSARNVRSFGFIRQDEVSRLLGHLRSSAAAGEAVDLT ERIATLTCSIICRAAFGSVIRDHEELVELVKDAL SMASGFELADLFPSSKLLNLLCWNKSKLWRMRRRVDTILEAIVEEHKLKKSGE FGGEDIIDVLFRMQKDSQIKVPITTNAIKAFIFDTFSAGTETSSTTTLWVMAELM RNPEVMAKAQVEVRAALKGKTNWDVDDVQELKYMKSVVKETMRMHPPIPLI PRSCREECEVNGYKIPNKARIMINVWSMGRNPLYWEKPKTFWPERFDQVSRD FMGNDFEFIPFGAGRRICPGLNFGLANVEVPLAQLLYHFDWNLAEGMKPSDM DMSEAEGLTGIRKNNLLLLPTPYDPSS	63%
Contig103	*Barnadesia spinosa*	germacrene A oxidase	>gi|294845888|gb|ADF43083.1| germacrene A oxidase [Barnadesia spinosa] MELTLTTSLGLAVFVFILFKLLTGSKSTKNSLPEAWRLPIIGHMHHLVGTLPHR GVTDMARKYGSLMHLQ LGEVSTIVVSSPRWAKEVLTTYDITFANRPETLTGEIVAYHNTDIVLSPYGEYW RQLRKLCTLELLSAKK VKSFQSLREEECWNLVKEVRSSGSGSPVDLSESIFKLIATILSRAAFGKGIKDQR EFTEIVKEILRLTGG FDVADIFPSKKILHHLSGKRAKLTNIHNKLDSLINNIVSEHPGSRTSSSQESLLD VLLRLKDSAELPLTS DNVKAVILDMFGAGTDTSSATIEWAISELIRCPRAMEKVQTELRQALNGKERI QEEDIQELSYLKLVIKE TLRLHPPLPLVMPRECREPCVLAGYEIPTKTKLIVNVFAINRDPEYWKDAETFM PERFENSPINIMGSEY EYLPFGAGRRMCPGAALGLANVELPLAHILYYFNWKLPNGARLDELDMSECF GATVQRKSELLLVPTAYKTANNSA	42%
Contig104	*Helianthus annuus*	heterotrophic ferredoxin 2	>gi|68137465|gb|AAY85661.1| heterotrophic ferredoxin 2 [Helianthus annuus] MSSFTLPTQTMVRTSPQTMVKTAPQTIVSAFLKYPSTLPTVKSISKTFGLKSGSS FRTTAMATYRVKLVT PDGEHEFDAPDDCYILDSAEAAGIELPYSCRAGACSTCAGKLHTGAVDQSDGS FLDDNQMKEGYLLTCISYPTGDCVVHTHEEGDLY	65%
Contig104	*Citrus sinensis*	non-photosynthetic ferredoxin	>gi|1360725|emb|CAA87068.1| non-photosynthetic ferredoxin [Citrus sinensis] MTTVTLSAPCMVKAAPRNQLSRNLIKSPTSLPSVKGISKTFGLKCSPNFQASMA VYKIKLIGPMGEEHEF EAQEDQYILDAAEEAGVDLPYSCRAGACSTCAGKLVSGSVDQSDGSFLDDNQ MEAGYLLTCISYPTSDCVIQSHKEEELC	65%
Contig105	*Olea europaea*	acyl carrier protein	>gi|16518983|gb|AAL25091.1|AF428256_1 acyl carrier protein [Olea europaea] MASITASSVSFSASCPLKQNQASNLKKVSLSFSGKSFPSLRLQPSRFRIACAAKP ETVEKVCEIVRKQLA LPADSAVTGESKFASLGADSLDTVEIVMGLEEEFGISVEEESAQTITTVQEAAD MIENLKAKKA	76%
Contig105	*Brassica napus*	ACP preprotein	>gi|17767|emb|CAA31519.1| ACP preprotein [Brassica napus] MSTTFCSSVSMQATSLAATTRISFQKPALVSRTNLSFNLSRSIPTRLSVSCAAKP ETVEKVSKIVKKQLS LKDDQNVVAETKFADLGADSLDTVEIVMGLDEEFDIEMAEEKAQKITTVEEA AELIDELVQAKK	51%
Contig106	*Zea mays*	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	>gi|195657063|gb|ACG47999.1| 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase [Zea mays] MATSTSQHALSSIKLLSTGCLHPDKRNCRVLSVSVGRRCPSARNLGLLCASNS QSSVIEPVQLPRSPKSG VTPKKSGESALILIRHGESLWNEKNLFTGCVDVPLTPKGVDEAIEAGKRICNIP VDVIYTSSLIRAQMTA MLAMMQHRRKKVPIILHNESEQAHMWSQIYSEETKKQSIPVITAWQLNERMY GELQGLNKQETADRFGKEQVHEWRRSYDIPPPNGESLEMCAERAVAYFKDQII PKLVDGKHVMIAAHGNSLRSIIMHLDKLTSQEVISLELSTGIPMLYIFKEGKFIR RGSPAGPSEAGVYAYTKNLAQYRQKLDGIVQ	79%
Contig106	*Arabidopsis thaliana*	PGM (PHOSPHOGLYCERATE/BISPHOSPHOGLYCERATE MUTASE); catalytic/ intramolecular transferase, phosphotransferases	>gi|42563306|ref|NP_177928.2| PGM (PHOSPHOGLYCERATE/BISPHOSPHOGLYCERATE MUTASE); catalytic/ intramolecular transferase, phosphotransferases [Arabidopsis thaliana] MATSTTMSHQAIGSVVSQRPFKASQFLKEPLNNVPMKFRQKRFKIEATASQIS VVDNTFLSPSPSKNKPHESKKKSNEAALILIRHGESLWNEKNLFTGCVDVPLTQ KGVGEAIEAGKKISNIPVDLIFTSSLIRAQMTAMLAMTQHRRKKVPIILHNESV KAKTWSHVFSEETRKQSIPVIAAWQLNERMYGELQGLNKKETAERYGTQQVH EWRRSYEIPPPKGESLEMCAERAVAYFEDNIKPELASGNNVMIAAHGNSLRSII MYLDDLTSQEVTTLDLSTGVPLLYIFKEGKFMKRGSPVGSTEAGVYAYTKRL AQYREKLDAAATI	88%
Contig107	*Mentha arvensis*	limonene hydroxylase	>gi|146386316|gb|ABQ24001.1| limonene hydroxylase [Mentha arvensis] MELQISSAIIILVVTYTISLLIIKQWRKPKPEENLPPGPPKLPLIGHLHLLWGKLP QHALASVAKQYGPV	93%

			AHVQLGEVFSVVLSSREATKEAMKLVDPACADRFDSIGTKIMWYDNDDIIFSPYSEHWRQMRKICVSGLL SARNVRSFGFIRQDEVSRLLGHLRSSAAAGEAVDLTERIATLTCSIICRAAFGSVIRDHEELVELVKDAL SMASGFELADLFPSSKLLNLLCWNKSKLWRMRRRVDTILEAIVEEHKLKKSGEFGGEDIIDVLFRMQKDSQIKVPITTNAIKAFIFDTFSAGTETSSTTTLWVMAELMRNPEVMAKAQVEVRAALKGKTNWDVDDVQELKYMKSVVKETMRMHPPIPLIPRSCREECEVNGYKIPNKARIMINVWSMGRNPLYWEKPKTFWPERFDQVSRDFMGNDFEFIPFGAGRRICPGLNFGLANVEVPLAQLLYHFDWNLAEGMKPSDMDMSEAEGLTGIRKNNLLLLPTPYDPSS	
Contig107	*Solanum tuberosum*	cytochrome P450	>gi|12331298|emb|CAC24711.1| cytochrome P450 [Solanum tuberosum] MQFLSLASIFLFLSFLFLLRKWKNSNSQSKKLPPGPWKLPLLGSMLHMAGGLPHHVLRDLAKKYGPLMHL QLGEVSAVVVTSPDMAKEVLKTHDIAFASRPKLLAPEIVCYNRSDIAFCPYGDYWRQMRKICVLELLSAKNVRSYGSIRRDEVDRLVNFIRSSSGEPVNFTERLFLFTSSMTCRSAFGKVFKEQDKFIQLIKEVIGLAGGFDVADIFPSLKFLHVLSGMKGKIMNAHHKVDAIVEDVINEHKKKFAIGKTNGALGGEDLIDVLIRLMNDGGLQFPITNDNIKAIIFDMFAAGTETSSSTLVWAMVQMMKNPSVIAKAQAEVREAFKDKETFDENDVEELKYLKLVIKETLRLHPPVPLLVPRECREETDINGYTIPVKTKVMVNVWALGRDPKYWDDAESFKPERFEQRSVDFVGNNFEYLPFGGGRRICPGISFGLANVYLPLAHLLYHFDWKLPIGMEPKDLNLTELVGVTAARKDDLILVATPYEPPRQ	56%
Contig108	*Zea mays*	glyceraldehyde-3-phosphate dehydrogenase, cytosolic 3	>gi|195628558|gb|ACG36109.1| glyceraldehyde-3-phosphate dehydrogenase, cytosolic 3 [Zea mays] MAKIKIGINGFGRIGRLVARVALQSDDVELVAVNDPFISTDYMTYMFKYDTVHGQWKHHEVKVKDSKTLLFGEKEVTVFGCRNPEEIPWGSVGAEYVVESTGVFTDQEKAAAHLKGGAKKVVISAPSKDAPMFVVGVNEKEYKSDINIVSNASCTTNCLAPLAKVINDKFGIVEGLMTTVHAITATQKTVDGPSSKDWRGGRAASFNIIPSSTGAAKAVGKVLPVLNGKLTGMSFRVPTVDVSVVDLTVRLEKSATYDEIKAAVKAESEGSLKGILGYVEEDLVSTDFQGDSRSSIFDAKAGIALNGNFVKLVSWYDNEWGYSTRVVDLIRHMNSTK	86%
Contig108	*Selaginella lepidophylla*	glyceraldehyde-3-phosphate-dehydrogenase	>gi|2078386|gb|AAB59010.1| glyceraldehyde-3-phosphate-dehydrogenase [Selaginella lepidophylla] MGSEAKIKIGINGFGRIGRLVARVVLERDDVELVAVNDPFISTEYMAYMFKYDSVHGKWKKADVEVKDHETLIFGGKPVGCFACKDPSEIPWGKFGAEFVVESTGVFTDRDKASAHLKAGAKKVVISAPSSNAPMFVMGVNENDYKPDIDIVSNASCTTNCLAPLSKVINDRFAIIEGLMTTVHSLTATQKTVDGPSSKDWRGGRGAGFNIIPSSTGAAKAVGKVLPALNGKLTGMAFRVPTADVSVVDLTVRLEKPASYEEIKKAVKEESEGKLKGIMGYTEDAVVSSDFIGDSRSSIFDAAAGIALNDSFVKLVSWYDNEWGYSNRVVDLIVHMAKTK	77%
Contig109	*Mentha x piperita*	pulegone reductase	>gi|158979025|gb|ABW86885.1| pulegone reductase [Mentha x piperita] MVMNKQIVLNNYINGSLKQSDLALRTSTICMEIPNGCNGAILVKNLYLSVNPYLILRMGKLDIPQFDSIL PGSTIVSYGVSKVLDSTHPSYEKGELIWGSQAGWEEYTLIQNPYNLFKIQDKDVPLSYYVGILGMPGMTAYAGFFEICSPKKGETVFVTAAAGSVGQLVGQFAKMFGCYVVGSAGSKEKVDLLKNKFGFDDAFNYKEESDYDTALKRHFPEGIDIYFDNVGGKMLEAVINNMRVHGRIAVCGMVSQYSLKQPEGVHNLLKLIPKQIRMQGFVVVDYYHLYPKFLEMVLPCIKEGKVTYVEDISEGLESAPSALLGVYVGRNIGNQVVAVSRE	97%
Contig109	*Nicotiana tabacum*	allyl alcohol dehydrogenase	>gi|6692816|dbj|BAA89423.1| allyl alcohol dehydrogenase [Nicotiana tabacum] MAEEVSNKQVILKNYVTGYPKESDMEIKNVTIKLKVPEGSNDVVVKNLYLSCDPYMRSRMRKIEGSYVESFAPGSPITGYGVAKVLESGDPKFQKGDLVWGMTGWEEYSIITPTQTLFKIHDKDVPLSYYTGILGMPGMTAYAGFHEVCSPKKGETVFVSAASGAVGQLVGQFAKMLGCYVVGSAGSKEKVDLLKSKFGFDEAFNYKEEQDLSAALKRYFPDGIDIYFENVGGKMLDAVLVNMKLYGRIAVCGMISQYNLEQTEGVHNLFCLITKRIRMEGFLVFDYYHLYPKYLEMVIPQIKAGKVVYVEDVAHGLESAPTALVGLFSGRNIGKQVVMVSRE	63%
Contig110	*Vitis vinifera*	farnesyl diphosphate synthase	>gi|62199628|gb|AAX76910.1| farnesyl diphosphate synthase [Vitis vinifera] MSETKSKFLEVYSVLKSELLNDPAFEFTDDSRQWVERMLDYNVPGGKLNRGLSVVDSYKLLQGRQLTDDEVFLACVLGLCIEWLQAYFLVLDDIMDNSHTRRGQPCWFRVPKVGMIAANDGVILRNQIPRILKNHFKGKPYYVDLLDLFNEVEFQTASGQMIDLITTIEGEKDLSKYSLPLHRRIVQYKTAYYSFHLPVACALLMAGENLDNHTSVKDILVQMGIYFQVQDDYLDCFGDPQVIGKIGTDIEDFKCSWLIVKALEICNEEQKKTLYGNYGKADPANVAKVKALYKDLDLQGVFLEYESKSYETLVSSIEAHPSKAVQAVLKSFLGKIYKRQK	83%
Contig110	*Gossypium arboreum*	farnesyl pyrophosphate synthase	>gi|1922251|emb|CAA72793.1| farnesyl pyrophosphate synthase [Gossypium arboreum] MADLRSAFLNVYSQLKSELLQDPSFELTDESRQWVERMLDYNVPGGKLNRGLSVIDSYRLLKDGKELTQD EIFLTSALGWCIEWLQAYFLVLDDIMDSSHTRRGQPCWFRLPKVGMIAVNDGVILRNHITRILKNHFRGK PYYVDLLDLFNEVEFQTASGQMIDLITTLEGEKDLSKYSLQQHRRIVQYKTAYYSFYLPVACALVMCGEN LDNHIDVKNILVDMGIYFQVQDDYLDCFGNPETIGKIGTDIENFKCSWLVVKALEFCNEEHNKVLYENYG ETRPANVAKVKALYNELNLKGVFEDYESKSYERLVTSIEAHPSKPVQAVLKSFLGKIYKRQK	80%
Contig111	*Salvia fruticosa*	1,8 cineole synthase 2	>gi|223468790|gb|ACM89961.1| 1,8 cineole synthase 2 [Salvia fruticosa] MCSVVIQMAIPSKPTNHLHNSRTKSSKLSSNSITSVGARLRSPRCSVQLSAGQLQTERRSGNYSPSLWDV DYIQSLHSDYKEERHMRRASELIMQVKMMLEEEADPVRQLELIDDLQRLGLGDHFQNEFKEILKSIYLDH KCFKNHGEMDLYSTALAFRLLRQHCFQVAQDVFDCFKNEKGELKASLSDDTRGVLQLYEASFLTMEGEKT LDLGREFAAKILEDKLKEESSDDLYLLLSIRYALDIPIHWRIGRGNASMWIDAYKRRSDMNPIVLELAIL	71%

			DSNIVQAQYQEELKQDLQWWRNTCIVEKLPFARDRLVECYFWTTGIVQPRQH ANARITVGKVNALITTID DVYDVYGTLEELEQFTDVIRRWDMSSIEQLPGYMQLCFLALDNFVKDTAYEV LKEQGFNAIPYLQKSWRD LVEAYLVEAKWYHSGHKPNLEEYLNTSWISIGGTVILTHAFFRVTESLTKEAS DALYGYHDLVRWSSVIL RLADDLGTSVDEVSRGDVPKSIQCYMNDHNASEAQARDHVKWMIAETWKKI NQERVAMDPPFCQDFIACA VDMGRKTQYMYHYGDGHGIQHPIIHQQMTTCLFNPF	
Contig111	*Ocimum basilicum*	fenchol synthase	>gi|55740205|gb|AAV63790.1| fenchol synthase [Ocimum basilicum] MWSTISISMNVAILKKPLNFLHNSNNKASNPRCVSSTRRRPSCPLQLDVEPRRS GNYQPSAWDFNYIQSL NNNHSKEERHLQGKAKLIEEVKMLLEQEMAAVQQLEFIEDLKNLGLSYLFQD EIKIILNSIYNHHKCFHN NHQQRTDENADLYFVALGFRLFRQHGFKVSQEVFDCFKNEEGSDFIPNLAEDT KGLLQLYEASYLVRQDE DTLEMARQFSTKILQKKVEEKMIEENLLSWTCHSLELPLHWRVQRIEAKWFLD AYASKPDMNPIIFELAK LEFNIAQALQQGELKDLSRWWNDTGIAEKLPFARDRIVEAHYWAIGTLEPYQY RYQRSLIAKIIALTTVV DDVYDVYGTLDEPQLFTDAIRRWDIESINQLPHYLQLCYLAIYNFVSELAYDIF RDKGFNSLPYLHKSWL DLVEAYFLEAKWFHSGYTPTLEEYLNNSKMTITCPAIVSEIYFAFANSIDKTEV ESVYKYHDILYLSGML LRLPDDLGTTTFEMKRGDVAKAIQCYMKEHNASEEEAREHIRFLMREAWKQ MNTAAAANNCPFVNDFVVG AASLGRVANFVYVEGDGFGVQHSKIHQQMAELLFYPYQ	49%
Contig112	*Ipomoea batatas*	S-adenosyl-L-methionine synthetase	>gi|145049666|gb|ABP35525.1| S-adenosyl-L-methionine synthetase [Ipomoea batatas] METFLFTSESVNEGHPDKLCDQVSDAVLDACLAQDPESKVACETCTKTNMVM VFGEITTKAEIDYEKIVR DTCRAIGFVSDDVGLDADNCKVLVNIEQQSPDIAQGVHGHLTKRPEDIGAGDQ GHMFGYATDETPELMPL SHVLATKLGARLTEVRKDGTCAWLRPDGKTQVTVEYYNDNGAMVPVRVHT VLISTQHDETVTNDEIARDL KEHVIKPVIPEKYLDEKTIFHLNPSGRFVIGGPHGDAGLTGRKIIIDTYGGWGAH GGGAFSGKDPTKVDR SGAYVVRQAAKSIVANGLARRCIVQVSYAIGVPEPLSVFVDTYGTGKIPDKEIL KIVKEHFDFRPGMIAI NLDLKRGGNSRFLKTAAYGHFGRDDPDFTWEVVKPLKWDKPQA	94%
Contig112	*Pisum sativum*	S-adenosylmethionine synthase	>gi|609557|gb|AAA58772.1| S-adenosylmethionine synthase [Pisum sativum] VAVDACLEQDSDSKVACETCTKTNLVMVFGEITTKANVDYEKIVRNTCRNIGF VSADVGLDADNCKVLVN IEQQSPDIAQGVHGHFTKRPEEIGAGDQGHMFGYATDETPELMPLSHVLATKL GARLTEVRKNGTCAWLR PDGNTQVTVEYYNDKGAMVPIRVHTVLISTQHDETVTNDEIAADLKGHVIKPV IPEKYLDSKTIFHLNPS GRFVIGGPHGDAGLTGRKIIIDTYGCTRCSGKDPTKVDRRGAYIVRQAAKSIVA SGLARRAIVQVSYAIG VPEPLSVFVDTYGTGKIPDREILKIVKETFDFRPGMISINLDLLRGGNGRFLKTA AYGHFGREDPDFTWE VVKPLKWEKA	87%
Contig113	*Mentha x piperita*	limonene synthase	>gi|158979017|gb|ABW86881.1| limonene synthase [Mentha x piperita] MALKVFSGAMQMPIPSKLTTYLQPSHLNSSPKLLSNTKGTSRSRLRVSCSSSQL TTERRSGNYNPSRWDV DFIQTLHSDYKDEKHARRASELVTLVKMELEKETDQIRQLELIDDLQRMGLSD HFQNEFKEILSSVYLDH GYYKNPDPKEERDLYSTSLAFRLLREHGFQVAQEVFDSFKNEEGEFKESLSDD TRGLLQLYEASFLLTEG ETTLESAREFATKFLEERVNEGGGDENLLTRIAYSLEIPLHWRIKRPNAPVWID SYRKRPNMNPVVLDLA ILDLNIVQAHFQQELKESFRWWRNTGFVEKLPFARDRLVECYFWNTGIIEPRQ HASARIMMGKVNALITV IDDIYDVYGTLEELEHFTDLIRRWDIDSIDQLPDYMQLCFLALNNFVDETSYDV MKEKGVNVIPYLRQSW VDLADKYMVEARWFYGGHKPSLEEYLENSWMSISGPCMLTHIFFRVTDSFTK ETVDSLYKYHDLVRWSSF VLRLADDLGTSVEEVSRGDVPKSLQCYMSDYNASEAEARKHVKWLIAEVWK KMNAERVSKDSPFGKDFIG CAVDLGRMAQLMYHNGDGHGTQHPIIHQQMTATLFEPFA	94%
Contig113	*Lavandula latifolia*	linalool synthase	>gi|89574406|gb|ABD77417.1| linalool synthase [Lavandula latifolia] MSIISMHVGILNRPAAYNHLRNLDRRASKPRHVSSTAAATRLRVSCATQLEIKS VDETRRSGNYNPTAWD FNYIQSLDNQYKKERYSTRHAELTVQVKKLLEEEMEAVQKLELIEDLKNLGIS YPFKDNIQQILNQIYNE HKCCHNSEVEEKDLYFTALRFRLLRQQGFEVSQEVFDHFKNEKGTDFKPNLA DDTKGLLQLYEASFLLRE AEDTLESARQFSTKLLQKKVDENGDDKIEDNLLLWIRRSLELPLHWRVQRLEA RGFLDAYVRRPDMNPIV FELAKLDFNITQATQQEELKDLSRWWNSTGLAEKLPFARDRVVESYFWAMGT FEPHQYGYQRELVAKIIA LATVVDDVYDVYGTLEELELFTDAIRRWDRESIDQLPYYMQLCFLTVNNFVFE LAHDVLKDKSFNCLPHL QRSWLDLAEAYLVEAKWYHSRYTPSLEEYLNIARVSVTCPTIVSQMYFALPIPI GKPVIEIMYKYHDILY LSGMLLRLTDDLGTASFELKRGDVPKAVQCYMKERNVPENEAREHVKFLIRE ASKQMNTAMATDCPFTED FAVAAANLGRVANFVYVDGDGFGVQHSKIYEQIGTLMFEPYP	53%

Contig114	*Lavatera thuringiaca*	annexin	>gi|2459926|gb|AAB71830.1| annexin [Lavatera thuringiaca] MATLTVPSTLPSVSEDCEQLRKAFSGWGTNEDLIINILGHRNADERNSIRKAYT ETHGEDLLKALDKELS NDFERLVLLWTLDPPERDALLANEATKRWTSSNQVIMEIACRSSSDQLLRARQ AYHVRYKKSLEEDVAHH TTGDFRKLLLPLVSSYRYEGDEVNMTLAKTEAKLLHEKISNKAYSDDDVIRVL ATRSKSQINERLNHYKN EYATDINKDLKADPKDEFLALLRSTVKCLVYPEKYFEKVLRLAINKRGTDEGA LTRVVSTRAEVDLKIIA DEYQRRNSVPLTRAIVKDTNGDYEKLLLVLAGEVEA	72%
Contig114	*Arabidopsis thaliana*	calcium-binding protein annexin 7	>gi|12667522|gb|AAG61156.1| calcium-binding protein annexin 7 [Arabidopsis thaliana] MASLKVPATVPLPEEDAEQLYKSFKGWGTNERMIISILAHRNATQRSFIRAVY AANYNKDLLKELDRELS GDFERAVMLWTFEPAERYAYLAKESTKMFTKNNWVLVEIACTRSALELFNAR QAYQARYKTSLEEDVAYH TSGDIRKLLVPLVSTFRYDGDEVNMTLARSEAKILHEKIKEKAYADDDLIRILT TRSKAQISATLNHYKN NFGTSMSKYLKEDSENEYIQLLKAVIKCLTYPEKYFEKVLRQAINKLGTDEWG LTRVVTTRAEFVMERIK EEYIRRNSVPLDRAIAKDTHGDYEDILLALLGHDHA	70%
Contig115	*Drosophila yakuba*	GE20234	>gi|195493344|ref|XP_002094376.1| GE20234 [Drosophila yakuba] MAATTTTTTTLATTTGNSSSTNNNSSSNNNNNNSIASSNNNNIVTVHAVLNN PPTNTAGGGVADAATVA IAKDMLQLHHGAAAAATAALNNNNNNSSSNNNNSSADQLTSNNSANHLPATSS TNNSSSNSSANTTTPSGN AASTLTSSAPPYGELRFNQEVLPITDAVTVIGRNSSTSLVHFNVAENNLVSRKH FQVLYDVELRAFFVQC LSKNGIFVDDFLQRRNVDPLRLPQRCYFRFPSTEIRIEFESYVPATSSDAIAGHSP SLVVGGGGGGVAGG GAHVIITPPPRDELHQQQLHHHQQQQQQLQQHPHHPPAHHLPLQQQQPAHH QLPHTPHHPLHHTALHQQ QQRSGSIVVAPPAGAAAHLIAGDGPGIYSPLKISIPKKEQKSPYLSPTGNCPASP RQGFIQNQPNNYNNY GNNNTQDLFQTPSTASYNHNEKPPYSYAQLIVQAISAAPDKQLTLSGIYSFIVK HYPYYRKETNKGWQNS IRHNLSLNRYFIKVARSQDEPGKGSFWRIDPDSGAKLIDHSYKKRRQRSSQGFR PPYGMPRSAPVSPSHM DNSRESSPLQDIVLQSAPGSPGMSLEQRAADAEIIYNSQNAHQQQHQQQQQ QTLSNNSNQYSSGSPYY VTNQSSGVSAQQSHAEGNAASGGGGVGALIALKRNHVMGGGASHTLHQQQA VAQQQHSEIIYEELPTDYS GHIEASEEECVTTATDATVAKRPKYVSEVL	36%
Contig115	*Polysphondylium pallidum* PN500	leucine carboxyl methyltransferase	>gi|281209564|gb|EFA83732.1| leucine carboxyl methyltransferase [Polysphondylium pallidum PN500] MIYYEVDYSKVIVNKLKIIKSCKELNQLIGDNAKWDDENHSLQTSDYRVAPID LTAGTECFDSVFSALNI DFEAPTMFLSECVIIYIPTEAGNSLINWTSNRFKESVFITYEQIKPYDEFGSMMIK NIENKGCPLLSINS FPEIKDQRERYLGFGWKRVDVLDMLDVYNYFIEKERVKETERLEIFDEFEEWY LIQGHYCYVLAINSQDP TKIKQYHFEDKKPLTKSSGTIPIYNKFMS	33%
Contig116	*Arabidopsis thaliana*	ACD1-LIKE (ACD1-LIKE); 2 iron, 2 sulfur cluster binding / electron carrier/ oxidoreductase	>gi|18416592|ref|NP_567725.1| ACD1-LIKE (ACD1-LIKE); 2 iron, 2 sulfur cluster binding / electron carrier/ oxidoreductase [Arabidopsis thaliana] MEAALAACALPSLRILNTKPRFRCSFSNPSLPISPNSLITRKSSRFTTAVSSPPSSS AATSTNSPPEPEA LFEPGSDKFDWYANWYPVMPICDLDKKVPHGKKVMGIDLVVWWDRNEKQW KVMDDTCPHRLAPLSDGRID QWGRLQCVYHGWCFNGSGDCKLIPQAPPDGPPVHTFKQACVAVYPSTVQHEI IWFWPNSDPKYKNIIETN KPPYIPELEDPSFTKLMGNRDIPYGYDVLVENLMDPAHVPYAHYGLMRFPKPK EKIDREGGKPLEINVKK LDNKGFFSKQEWGYSNFIAPCVYRSSTDPLPEQEHEYPAPAASDKAALSKRRL SLIFICIPVSPGRSRLI WTFPRNFGVFIDKIVPRWVFHIGQNTILDSDLHLLHVEERKILERGPENWQKAC FIPTKSDANVVTFRRW FNKYSEARVDWRGKFDPFLLPPTPPREQLFDRYWSHVENCSSCKKAHKYLNA LEVILQIASVAMIGVMAV LKQTTMSNVARIAVLVAAVLSFAASKWLSHFIYKTFHYHDYNHAVV	53%
Contig116	*Acaryochloris marina* MBIC11017	pheophorbide A oxygenase	>gi|158336046|ref|YP_001517220.1| pheophorbide A oxygenase [Acaryochloris marina MBIC11017] METQTSSNPSNLDIQFNFWQQWYPVAPLEDLDPQRPTPITLLGQHFVIWQPKD SGQYLVFQDLCPHRLAP LSEGRIDDQTGQLMCSYHGWQFDQQGLCTHIPQAEAVTSQQSQLYCVTVIPTQ AHSGLLWVWPDPDTQDV AATQPLPLSPLVDADQNFVYSSFMRDLAYDWQTLVENLSDPSHVPFAHHGVQ GNRNQAAPIPMEVLTSTP ELIEVQTTGKFSTNITFQPPCRMEYQFSIGDGKQATMVTYCIPIAPGRSRIVALF ARNFATGLMKVIPRW VEHMLNRNPVLDGDMILLRSQEKQLLQHTQTQNWQTTYKLPTSADRLVIEYR RWFEKYSHGQIPWGSADG QIPVASNNYAYLQPLGEQRPQLLDRYHQHTLICSSCRGALSRIKQLQKMLVAV FAIAISGAAILPDDLRA TWGIPLVITALLGLGGCYWLKYWLEPKFYFVDYIHADH	40%
Contig117	*Capsicum annuum*	MADS box protein	>gi|14518447|gb|AAF22139.2|AF130118_1 MADS box protein [Capsicum annuum] MGRGRVQLRRIENKINRQVTFSKRRSGLLKKAHEISVLCDAEVGLIVFSSKGKL FEYSTDSCMERILERY ERYSYAERQLNATDVETPGSWTLEHAKLKARLEVLQRNQRHYAGEDLDSLS MKELQNLEQQLDSALKHIR	65%

			SRKNQLMHESISELQKKDKALQEQNNNLSKQMKEREKQLAQQHTPWEQQNH DHLNSSSFGLPHPFNNNHL GEVYPTAGDNGEVEGSSRQQQQNAAVMPPWMLRHLNG	
Contig117	*Misopates orontium*	squamosa protein	>gi|82734203|emb|CAJ44135.1| squamosa protein [Misopates orontium] MGRGKVQLKRIENKINRQVTFSKRRGGLLKKAHEISVLCDAEVALIVFSNKGK LFEYSTDSCMDRILEKY ERYSFAERQLVSNEPQSPANWTLEYSKLKARIELLQRNHRHYMGEDLDSMSL KELQSLEQQLDTALKNIR SRKNQLLYDSISDLQRKEKAIQEQNTMLAKKIKEKEKELAQQPQWEHHRHHT NASIMPPPPQYSMAPQFP CINVGNTYEGEGANEDRRNELDLTLDSLYSCHLGCFAA	71%
Contig118	*Perkinsus chesapeaki*	ubiquinol-cytochrome c reductase hinge protein	>gi|163636564|gb|ABY27174.1| ubiquinol-cytochrome c reductase hinge protein [Perkinsus chesapeaki] MARAYCGRFAFMLDYPKSYHPPRKNEDGEFVDPRTDMLPKCAAECSEWLTE YNACVQRIKMRTDGRGNCQGQYEEFGMCQDHCIAHELFHYLK	40%
Contig118	*Trypanosoma brucei* TREU927	mitochondrial hinge protein	>gi|72393543|ref|XP_847572.1| mitochondrial hinge protein [Trypanosoma brucei TREU927] MADEEPRDIKLDLEKDCLANNCQHKVLAYSACLERIKDIPSEKEPHCYHQYFD IVHCVDVCVDPKLWPTLV	44%
Contig119	*Zea mays*	stachyose synthase	>gi|226508886|ref|NP_001152291.1| stachyose synthase [Zea mays] MPGACQDLSTITPTPRRQSMAQLQRGSVLVGGRELLVRAPPNVNLRPAGAGV ADGGAASGAAFLGARAPA ASSRHVFSVGNLASGWRWLSLFRFKIWWMIPATGVGAAAVPAETQMLLLEY RSEAGPAAATERGSLYALV LPVLDGGFRASLQGSPEDELQFCFESGDPDVQTMEAVDAVFVNSGDNPFKLLK ESIKMLSKIKGTFSHIE DKEIPSNLDWFGWCTWDAFYKAVNPSGIEEGLQSLREGGVPPRFLIIDDGWQE TVDEIKEVNEALREQTV FAQRLADLKENHKFRGETCKNLEDLVKTIKGKHGVKCVYMWHALLGYWGG TLATSEVMKKYNPKLVYPVQ SRGNVANLRDIAMDSLEKFGVGIVDPDKIYEFYNDQHSYLSSVGVDGVKVDV QNVLETLGRGFGGRVAVT RKYQQALEESIAQNFKTNNLICCMSHNSDSIFSALKGAVARASEDFMPREPTLQ TLHIASVAFNSLLLGE IFIPDWDMFHSKHESAEFHGAARALSGGGVYVSDKPGVHDFSVLKKLVLPDG SILRARYAGRPTRDCLFT DPVMDGKSLMKIWNLNNFTGVIGVFNCQGAGQWVWPVKQTAYVPTNINITG QLSPSDVESLEEIAGDDWN GETAVYAFGSCSLSRLQKHQSLEVSLSTMTCEIYSISPIKIFSEVVQFTPLGLIDM FNSGGALDNISSVA DSSATTVHIRCRGPGRFGAYSDTRPELCRVDEHEVEFTLAEDGLLTFYLPPSSS QDNLRHVEIVYKAS	53%
Contig119	*Glycine max*	raffionse synthase 3	>gi|187610416|gb|ACD13462.1| raffionse synthase 3 [Glycine max] MGPSSKKASPKSGVTKHMKGFSLCNSTLKVNGQVILSQVPKNVTLTPCTYDT HTTGCFLGFHATSPKSRH VAPLGQLKNISFTSIFRFKVWWTTLWTGSNGRDLETETQFLMLQSHPYVLFLPI LQPPFRASLQPHSDDN VAVCVESGSSHVTASSFDTVVYLHAGDNPFTLVKEAMRVVRAHLGSFKLLEE KTVPGMVDKFGWCTWDAF YLTVHPEGVREGVKGLVDGGCPPGFVLIDDGWQCISHDSDPEKEGMNQTVAG EQMPCRLISYEENYKFRS YKEGKGLKGFVRELKEEFGSVEYVYVWHALCGYWGGVRPGVAGMAEAAVE KPKLTEGLKGTMEDLAVDKI VNNGVGVVPPELVGEMYERLHAHLESAGIDGVKVDVIHLLEMVCEKYGGRV DMAKAYYKALTASVRKHFK GNGVIASMEHCNDFMLLGTEAISLGRVGDDFWCTDPYGDPNGTFWLQGCHM VHCAYNSLWMGNFIHPDWD MFQSTHPCAAFHAASRAISGGPIYISDTVGNHNFELLKTLALPDGSILRCEHYA LPTRDCLFADPLHDGK TMLKIWNLNKYTGVLGVFNCQGGGWFREIRSNKCAAEFSHRVSTKTNIKDIE WDSGKNPISIEGVQLFAS YFSQAKKLILSAPSDDSEEISLEPFNFELITVSPVTVLPGKSVKFAPIGLVNMLNT GGAVQSLAFDEGQN LVEVGLRGTGEMRVYASEKPRTCRIDGKEVDFEYEGSMVNIQVPWPGSSKLST VQYVF	36%
Contig120	*Mentha x piperita*	O-methyltransferase	>gi|38047401|gb|AAR09603.1| O-methyltransferase [Mentha x piperita] MALPNLEESTVEELLDAEAHVWNHIFSYINSMSLKSALQLGIPDIIHKHGNPITL SQLADALNINKAKTD GLFRLMRLLEHSKFFDKVKVEGEGEEEAYSLTRASRLLLRDEPSSLAPYIRAML DPNFMDPFHHLSEWLG SECPSPFEFKHGRSLWEYAGIEERWNQLFNQAMANDAKLVTSILVKECRHIFQ GLESLVDVGGGAGTVAK VVADAFPGLKAVVLDLPHVVADLATSENLRYVSGDMFEDIPRADAVLLKWIL HNWSDEECIKILEKCKEA ITPSKNNNGGKVIVIDMILKDEKQHHKGTETQLLFDVLMMTALTGKERTEKE WANLFFAAGFKTYKIHPV LRLRSVIEIFP	67%
Contig120	*Prunus armeniaca*	methyltransferase	>gi|2282586|gb|AAB71213.1| methyltransferase [Prunus armeniaca] MGSVRASHELLQAQAHIWNHIFSFINSLSLKCAVQLDIPDVIQKHGQPMTLSEL VSALPISPTKAHFIPR LMRILVHSGFFAKESLSGCGEQGYILTDASALLLKDNPMSARPFLLAMLSPILT DPYQYLTTWFQNDNPT PFHVVNGMTCWDYVNQDPTLAHFFNDAMASDAQLISSLVIDDCKEVFQGVDS LVDVGGGTGTVAKSIADA FPHMKCTVLDLPHVVADLKGSKNLEYVAGDMFEAVPAADAIFLKWILHDWS DEECVKILERCKAAVTREG	54%

			KKGKVIIVEMTVENKNTDKESGETQLFFDMHMMVMSTGKERNEKEWAKLFS DAGFSQYKITPLFGFKSLI EVYP	
Contig121	*Ocimum basilicum*	selinene synthase	>gi|55740195|gb|AAV63785.1| selinene synthase [Ocimum basilicum] MSANCVSAAPTSPKNSDVEEIRKSATYHSSVWGNHFLSYTSDVTEITAAEKEQ LEKLKEKVKNLLAQTPD ESTGKMELIDAIQRLGVGYHFTTEIQESLRQIHEGQIRNDDDDVRVVALRFRLL RQGGYRAPCDVFEKFM DDGGNFKESLKKDVEGMLSLYEASYYGIDGEEIMDKALEFSSSHLESMLHNIS TKTNKSLLRRLQEALDT PISKAAIRLGATKFISTYREDESHNEDILNFAKLDFNILQKMHQEEANYLTRWW EDLDLASKLDFARDRM VESYFWSLGVYFQPQYRTSRIYLTKIISIVAVIDDIYDVYGSFDDLRSFTDVIQS WKISNADELPPYMRI CFEALLGIYEDMGDRIGAPYAIDTMKELVDTYMQEAEWCYTEYVPTVDEYM KVALVTGGYLMVATTFLTG INNITKKDFDWIRNRPRLLQVAEVLTRLMDDIAGHGTEKKTTAVSCYMKEYE CSEMEASRELSKQVKKAW KDLNDEWMEPRSSSAEIIGCIVNMSRVLHIMYSTGDDGFSDSSTRTTQAVKTLL VDHPMN	66%
Contig121	*Ocimum basilicum*	germacrene D synthase	>gi|55740197|gb|AAV63786.1| germacrene D synthase [Ocimum basilicum] MTNMFASAAPISTNNTTVEDMRRSVTYHPSVWKDHFLDYASGITEVEMEQLQ KQKERIKTLLAQTLDDFV LKIELIDAIQRLGVGYHFEKEINHSLRQIYDTFQISSKDNDIRVVALRFRLLRQH GYPVPSDVFKKFIDN QGRLDESVMNNVEGMLSLYEASNYGMEGEDILDKALEISTSHLEPLASRSRRI NEALEMPISKTLVRLGA RKFISIYEEDESRDEDLLKFAKLDFNILQKIHQEELTHIARWWKELDLGNKLPF ARDRVVECYFWILGVY FEPQYNIARRFMTKVIAMTSIIDDIYDVHGTLEELQRFTDAIRSWDIRAIDELPP YMRLCYEALLGMYAE MENEMVKQNQSYRIEYARQEMIKLVTTYMEEAKWCYSKYIPNMDEYMKLAL VSGAYMMLATTSLVGILGD PITKQDFDWITNEPPILRAASVICRLMDDVVGHGIEQKISSVDCYMKENGCSK MEAVGEFSKRVKKAWKN LNEEWVEPRAASMVILVRVVNLARVINLLYVGEDSYGNSSVKTKELIKGVLV HPIK	59%
Contig121	*Cucumis melo*	terpene synthase	>gi|162285971|gb|ABX83200.1| terpene synthase [Cucumis melo] MSSQVSNFPASIMKTNDIPDVKRSLANFHPNIWKEHFLSFTFDDALKIDEGMKE RTEKLKEEIRMMMIAY VENQLIKLNLVDSIQRLGVSYHFEDEVDEFLEHIYVSYNNSLLLSNKNSNGEDL HITALLFRLLRQQGYR ISCDIFLKFMDDNGKFKESLVEDERGLLSLYEASHMMGHGEALLEEALEFTTT HLQTYIHRYSNINPSFA SEVSNALKLPIRKSVPRIKAREYLEIYQQHPSHNETLLEFSKLDFNILQKLHQKE LSEICRWWKDLDVPT KFPFARDRIVECYFWTLGAYFEPQYSVGRKMLTKVIAIASILDDIYDAYGTFEE LQVLTPAIQRWDRSMV HTLPLYMKPFYVAMLELYEEIGKEIDKDQNSLHLQVAIGGIKRLSESYFEEAK WLNKEYKPSFKEYMELA LKTTGYTMLISISFLGLGDHIVTNEVLQWLSNGPQIIKASTIICRLMDDIASHKFE QEREHVASAVECYM KQYDCSEEEACIELHKEVVDAWKDTNEAFYRPFNVPVPVLMRVLNFSRVINLL YLDEDGYTNAKSGTKFL IKSLLVDPLPC	40%
Contig122	*Glycine max*	BURP domain protein	>gi|222160332|gb|ACM47360.1| BURP domain protein [Glycine max] MEYRLLPIFTLLNLALVAIHAALPPEVYWKSVLPTTPMPKAITDILYPDWVEEK STSVNVGGKGVNVHAG KGGGGTNVNVGGKGSGGGVNVHAGHKGKPVHVSVGSKSPFNYIYASTETQL HDDPNVALFFLEKDLHPGT KLNLHFTTSSNIQATFLPRQVADSIPFSSSKVEVVFNKFSVKPGSEEAQIMKNTL SECEEGGIKGEEKYC ATSLESMIDFSTSKLGKNVEVVSTEVVEDKETGLQKYTVAPGVNKLSGDKAV VCHKQNYPYAVFYCHKTE TTRAYSVPLEGTNGVRVKAVAVCHTHTSEWNPKHLAFQVLKVKPGTVPVCH FLPEDHVVWVPK	61%
Contig122	*Vigna radiata*	resistant specific protein-2	>gi|24416618|dbj|BAC22500.1| resistant specific protein-2 [Vigna radiata] MEFQCLALFFSLIVILMAAQASLPSEVYWERKLPNTPIPKVIRQFSKQDGGKDI ASKDEFLLFGSGDKKN KDKLLRFGCGDKENKLQDDVQDISPEDENLLLIYDRYAKNKLQDDLQDISPED ENFLLFYDRYAKNKLQD DVQDISPEDENLLLFYDRYAKNKLQDNVQDISPEDENLLDYEKSKLQDDVQDI SPEDENLSGYKKNGVVL RGIGPIANHHHHDHLKPSSYFSEEGLRRGAKLVMLFHKRKFSTPLLTREIAEHL PFSSEKINEILEILAV KPDSKNAKNVEKTLNNCEEPALKGEEKHCATSVESMVDFVTSKLGNNARVTS TELEIESKFQKFIVKDGV KILAEEEIIACHPMSYPYVVFYCHKMSNSTAHVVPLEGEDGTRVKAIVICHKDT SQWDPDHVAFQVLKVK PGTSPVCHFFPNGHLLWYAK	45%
Contig123	*Mentha x piperita*	isopiperitenone reductase	>gi|158979023|gb|ABW86884.1| isopiperitenone reductase [Mentha x piperita] MAEVQRYALVTGANKGVGFEICRQLAEKGIIVILTSRNEKRGLEARQKLLKEL NVSENRLVFHQLDVTDL ASVAAVAVFIKSKFGKLDILVNNAGVSGVEMVGDVSVFNEYIEADFKALQAL EAGAKEEPPFKPKANGEM IEKFEGAKDCVVTNYYGPKRLTQALIPLLQLSPSPRIVNVSSSFGSLLLLWNEW AKGVLGDEDRLTEERV	96%

			DEVVEVFLKDIKEGKLEESQWPPHFAAERVSKAALNAYTKIAAKKYPSFRINAICPGYAKTDITFHAGPL SVAEAAQVPVKLALLPDGGPSGCFFPRDKALALY	
Contig123	*Capsicum annuum*	short-chain dehydrogenase/reductase	>gi|121483692|gb|ABM54181.1| short-chain dehydrogenase/reductase [Capsicum annuum] MAEKTTSTRYAVVTGGNKGIGYETCRQLASKGVVVVLTSRDKKKGIEAIERLKEESNFTDEHILFHQLDI MDPASISSLVNLIKTKFGRLDILINNAGISGVMVEGDVQVLKEILERYISIVFTEDENGEEGGWTKSVPG SVTNYELTKECIETNYYGAKRMTEAFIPLLQLSNSPRIVNVASSMGKLKLLCNKWATEVLRDADSLTEEK VDQVVNEFLXDFTEKSTESKGWPSYFTAYKVSKASLIAYTRVLATKYSNFRINSVCPGYCKTDVNANTGS LTAGEGAESLVNLALLPNDGPSGLFFYRKEVTFF	54%
Contig123	*Zea mays*	carbonyl reductase 1	>gi|195650645|gb|ACG44790.1| carbonyl reductase 1 [Zea mays] MAAATPSPHSARVAVVTGGNKGIGLEVCRQLASNGITVVLTARDEKRGAAAVEELADAGLSGVVFHQLEV TDAQSIARLAGFLKAWFGKLDILVNNAAIGGVQSLPVENVGEKIKGMDASQMAELMWKSCRETNDAAKAG VQTNYYGVKNVTEALLPLLLQASSSGGGRVVNVSSDFGLLRYLRNEEVKRELDDIEGLTEERLDELLSTF LRDFEAGALESRGWPTEFAAYKVAKAALNSYSRVLARRHPELRVNCAHPGYVKTDMTRQTGLLTPAQGAA NVVKVALLPEGGPTGAFFALGKEAPFV	47%
Contig123	*Papaver somniferum*	salutaridine reductase	>gi|83817206|gb|ABC47654.1| salutaridine reductase [Papaver somniferum] MPETCPNTVTKRRCAVVTGGNKGIGFEICKQLSSNGIMVVLTCRDVTKGHEAVEKLKNSNHENVVFHQLD VTDPIATMSSLADFIKTHFGKLDILVNNAGVAGFSVDADRFKAMISDIGEDSEELVKIYEKPEAQELMSE TYELAEECLKINYNGVKSVTEVLIPLLQLSDSPRIVNVSSSTGSLKYVSNETALEILGDGDALTEERIDM VVNMLLKDFKENLIETNGWPSFGAAYTTSKACLNAYTRVLANKIPKFQVNCVCPGLVKTEMNYGIGNYTA EEGAEHVVRIALFPDDGPSGFFYDCSELSAF	50%
Contig124	*Phelipanche ramosa*	methionine synthase	>gi|113473614|gb|ABI35986.1| methionine synthase [Phelipanche ramosa] MASHIVGYPRMGPKRELKFALESFWDGKSSAEDLEKVAADLKASIWKQMSEAGIKYIPSNTFSYYDQVLD TTAMLGAVPPRYNWTGGEIGFATYFSMARGNASVPAMEMTKWFDTNYHFIVPELGPDVKFSYASHKAVNE YNEAKALGVNTVPVLVGPVTYLLLSKPAKGVEKTFPLLSLLDKILPIYKEVIAELKAAGASWIQFDEPTL VLDLESHQLEAFTKAYAELESSLSGLNVLIETYFADVPAAAYKALTSLSAVSGFGFDLVRGTQTLDLIKG GFPSGKYLFAGVVDGRNIWANDLSASLCTLQSLEGIIGKDKLVVSTSCSLLHTAVDLVNEPKLDQEIKSW LAFAAQKVVEVNALAKALAGEKDEAFFSANAAAQASRKSSPRVTNEAVQKAAAALKGSDHRRATNVSARL DAQQKKLNLPILPTTTIGSFPQTIELRRVRREYKAKKISEEEYIKAIKEEINKVVKLQEELDIDVLVHGE PERNDMVEYFGEQLSGFAFTANGWVQSYGSRCVKPPIIYGDVSRPKPMTVFWSTAAQSMTKRPMKGMLTG PVTILNWSFVRNDQPRFETCYQIALAIKDEVEDLEKAGITVIQIDEAALREGLPLRKSEHAFYLDWAVHS FRITNVGVEDTTQIHTHMCYSNFNDIIHSIINMDADVITIENSRSDEKLLSVFREGVKYGAGIGPGVYDI HSPRIPSSEEIADRINKMLAVLETNILWVNPDCGLKTRKYSEVKPALENMVSAAKLLRTQLASAK	97%
Contig124	*Zea mays*	methionine synthase	>gi|17017263|gb|AAL33589.1| methionine synthase [Zea mays] MASHIVGYPRMGPKRELKFALESFWDGKSTAEDLEKVATDLRASIWKQMADAGIKYIPSNTFSYYDQVLD TTAMLGAVPERYSWTGGEIGFDTYFSMARGNATVPAMEMTKWFDTNYHFIVPELGPNTKFSYASHKAVNE YKEAKALGVDTVPVLVGPVSYLLLSKPAKGVEKGFPLLSLLSSILPVYKEVIAELKAAGASWIQFDEPTL VLDLDSDKLAAFSAAYAELESVLSGLNVLVETYFADVPAESYKTLTSLSSVTAYGFDLVRGTQTLGLVTS AGFPAGKYLFAGVVDGRNIWADDLATSLSTLQSLEAVVGKDKLVVSTSCSLMHTAVDLVNETKLDSEIKS WLAFAAQKVVEVDALAKALAGQKDEAYFAANAAAQASRKSSPRVTNEEVQKAAAALKGSDHRRGTNVSAR LDAQQKKLNLPILPTTTIGSFPQTVELRRVRREYKAKKISEEEYVTAIKEEINKVVKLQEELDIDVLVHG EPERNDMVEYFGEQLSGFAFTANGWVQSYGSRCVKPPIIYGDVSRPNPMTVFWSKTAQSMTSRPMKGMLT GPVTILNWSFVRNDQPRFETCYQIALAIKKEVGDLKAGGIQVIQIDEAALREGLPLRKAEHAFYLDWAVH SFRITNCEIQDTTQIHTHMCYSNFNDIIHSIIDMDADVITIENSRSDEKLLSVFREGVKYGAGIGPGVYD IHSPRIPSAEEIADRIDKMLAVLDTNILWVNPDCGLKTRKYTEVKPALTNMVSAAKLIRTQFASAK	90%
Contig125	*Jatropha curcas*	DSBA oxidoreductase family protein	>gi|284520982|gb|ADB93066.1| DSBA oxidoreductase family protein [Jatropha curcas] MSQSVSNSSGKKQIRIDISSDTICIWCFVGKRNLDKAIATAKDRFDFEIRWHPFLIDPSAPKEGTKLMPL FQQRFGSRTDAVLNQLREALRGVGLEFNICELFGNSLESHRLIHFAGQQGLDKQHNLAEELFLGYFTKAK YIGDREFLLECAEKVGVEGAAEFLQDPNNGVKEVYEDLHKYSAGLTGVPNYVINGKKKLNGAQPPEVFLR AFEAAAN	39%

Contig125	Agrobacterium radiobacter K84	dithiol-disulfide isomerase protein	>gi|222085975|ref|YP_002544507.1| dithiol-disulfide isomerase protein [Agrobacterium radiobacter K84] MERITIDIVSDVVCPWCYLGKARLELAIAEVQDEMGVDLNWRPYRLNPEYPPEGVDQKKALAQKLGGEER VAQAHKMLSDLGRDVGIKFDFDAIKIGPNTLDAHRLIHWAGTENREKQEKVVNALFKANFEEGRNVGDHA VLLDIAEGAGLDRSVIAALLSSDADRDLIIGEIEAAQKIGVTGVPFFIFDQQYAVSGAQTPDVLVEALRD IAKMKAEARAGMN	37%
Contig126	*Arabidopsis thaliana*	MUB2 (MEMBRANE-ANCHORED UBIQUITIN-FOLD PROTEIN 2)	>gi|18417680|ref|NP_568315.1| MUB2 (MEMBRANE-ANCHORED UBIQUITIN-FOLD PROTEIN 2) [Arabidopsis thaliana] MAEVKDQLEIKFRLNDGSDIGPKLFPDATTVATLKETVVAQWPRDKENGPKTVKDVKLISAGRILENNKT VGDCRSPVGNFSGAVTTMHVIIQHQVTEKEKKKKKPKGDLKQNKCVCLCFGARC	62%
Contig126	*Zea mays*	ubiquitin-fusion protein	>gi|195624124|gb|ACG33892.1| ubiquitin-fusion protein [Zea mays] MSGVQEQFEIKFRLPDGTDIGPRRFPPASTVATLKETIIAQWPKDKEKGPRTVNDLKLINAGKILENNKT LSECKSPICDFSAMTTMHVVIRAPTSSKQSDKRAEKKAKNFRCGCAIM	55%
Contig127	*Zea mays*	dehydrin 13	>gi|195625830|gb|ACG34745.1| dehydrin 13 [Zea mays] MSGIIHKIEEKLHMGGDHKKEDEHHKKAEEHHKKEEGEHHKKDGGEHKEGIVEKIKDKITGEHGDKSGDH KEKKDKKKKKEKKKHGEGHDHDGGHSSSSSDSD	43%
Contig127	*Medicago truncatula*	cold-acclimation specific protein 15	>gi|161897791|gb|ABX80065.1| cold-acclimation specific protein 15 [Medicago truncatula] MAGIMNKIGDALHIGGDKKEGEHKGEQHGHVGGEHHGEYKGEQHGFVGGHGGEHKGEQHGFGHGDHKEGH HGEEHKEGFVDKIKDKIHGEGADGEKKKKKEKKKHGEGHEHGHDSSSSDSD	45%
Contig128	*Zea mays*	pop3 peptide	>gi|226530706|ref|NP_001152608.1| pop3 peptide [Zea mays] MAGGGVVKHILLASFKEEVTQERLDELIRGYAALVGVVPSMKAFHWGTDVSIENMHQGFTHVFESTFEST EGIKEYIEHPAHVEFASVFLPVLEKVLIIDYKPTSAN	51%
Contig128	*Arabidopsis thaliana*	HS1 (HEAT STABLE PROTEIN 1)	>gi|18401423|ref|NP_566569.1| HS1 (HEAT STABLE PROTEIN 1) [Arabidopsis thaliana] MEEAKGPVKHVLLASFKDGVSPEKIEELIKGYANLVNLIEPMKAFHWGKDVSIENLHQGYTHIFESTFES KEAVAEYIAHPAHVEFATIFLGSLDKVLVIDYKPTSVSL	50%
Contig129	*Mentha arvensis*	limonene hydroxylase	>gi|146386316|gb|ABQ24001.1| limonene hydroxylase [Mentha arvensis] MELQISSAIIILVVTYTISLLIIKQWRKPKPEENLPPGPPKLPLIGHLHLLWGKLPQHALASVAKQYGPV AHVQLGEVFSVVLSSREATKEAMKLVDPACADRFDSIGTKIMWYDNDDIIFSPYSEHWRQMRKICVSGLL SARNVRSFGFIRQDEVSRLLGHLRSSAAAGEAVDLTERIATLTCSIICRAAFGSVIRDHEELVELVKDAL SMASGFELADLFPSSKLLNLLCWNKSKLWRMRRRVDTILEAIVEEHKLKKSGEFGGEDIIDVLFRMQKDS QIKVPITTNAIKAFIFDTFSAGTETSSTTTLWVMAELMRNPEVMAKAQVEVRAALKGKTNWDVDDVQELK YMKSVVKETMRMHPPIPLIPRSCREECEVNGYKIPNKARIMINVWSMGRNPLYWEKPKTFWPERFDQVSR DFMGNDFEFIPFGAGRRICPGLNFGLANVEVPLAQLLYHFDWNLAEGMKPSDMDMSEAEGLTGIRKNNLL LLPTPYDPSS	92%
Contig129	*Barnadesia spinosa*	germacrene A oxidase	>gi|294845888|gb|ADF43083.1| germacrene A oxidase [Barnadesia spinosa] MELTLTTSLGLAVFVFILFKLLTGSKSTKNSLPEAWRLPIIGHMHHLVGTLPHRGVTDMARKYGSLMHLQ LGEVSTIVVSSPRWAKEVLTTYDITFANRPETLTGEIVAYHNTDIVLSPYGEYWRQLRKLCTLELLSAKK VKSFQSLREEECWNLVKEVRSSGSGSPVDLSESIFKLIATILSRAAFGKGIKDQREFTEIVKEILRLTGG FDVADIFPSKKILHHLSGKRAKLTNIHNKLDSLINNIVSEHPGSRTSSSQESLLDVLLRLKDSAELPLTS DNVKAVILDMFGAGTDTSSATIEWAISELIRCPRAMEKVQTELRQALNGKERIQEEDIQELSYLKLVIKE TLRLHPPLPLVMPRECREPCVLAGYEIPTKTKLIVNVFAINRDPEYWKDAETFMPERFENSPINIMGSEY EYLPFGAGRRMCPGAALGLANVELPLAHILYYFNWKLPNGARLDELDMSECFGATVQRKSELLLVPTAYK TANNSA	56%
Contig130	*Mentha arvensis*	limonene hydroxylase	>gi|146386316|gb|ABQ24001.1| limonene hydroxylase [Mentha arvensis] MELQISSAIIILVVTYTISLLIIKQWRKPKPEENLPPGPPKLPLIGHLHLLWGKLPQHALASVAKQYGPV AHVQLGEVFSVVLSSREATKEAMKLVDPACADRFDSIGTKIMWYDNDDIIFSPYSEHWRQMRKICVSGLL SARNVRSFGFIRQDEVSRLLGHLRSSAAAGEAVDLTERIATLTCSIICRAAFGSVIRDHEELVELVKDAL SMASGFELADLFPSSKLLNLLCWNKSKLWRMRRRVDTILEAIVEEHKLKKSGEFGGEDIIDVLFRMQKDS QIKVPITTNAIKAFIFDTFSAGTETSSTTTLWVMAELMRNPEVMAKAQVEVRAALKGKTNWDVDDVQELK YMKSVVKETMRMHPPIPLIPRSCREECEVNGYKIPNKARIMINVWSMGRNPLYWEKPKTFWPERFDQVSR DFMGNDFEFIPFGAGRRICPGLNFGLANVEVPLAQLLYHFDWNLAEGMKPSDMDMSEAEGLTGIRKNNLL	93%

			LLPTPYDPSS	
Contig130	*Nicotiana tabacum*	elicitor-inducible cytochrome P450	>gi|18644953|gb|AAK62343.2| elicitor-inducible cytochrome P450 [Nicotiana tabacum] MEFFSLVSIFLFLSFLFLLRKCKNSNSQTKQLPPGPWKIPILGSMLHMLGGEPHHILRDLAKKYGPIMHL QFGEISAVVVTSREMAKEVLKTHDVVFASRPKIVAMDIICYNQSDIAFSPYGDHWRQMRKICVMELLNAK NVRSFSSIRRDEVVRLIDSIRSDSSSGELVNFTQRIIWFASSMTCRSAFGQVLKGQDVFAKKIREVIGLA EGFDVADIFPSYKFLHVLSGMKRKLLNAHLKVDAIVEDVINEHKKNLATGKTNGALGDMFAAGTETSSTT TVWAMAEMMKNPNVFNKAQAEVRETFKDKVTFDEIDAEELEYLKLVIKETLRLHPPSPLLVPRECREDTD INGYTIPAKTKVMVNVWALGRDPKYWDDAESFKPERFEQCSVDFFGNNFEFLPFGGGRRICPGMSFGLAN LYLPLAQLLYHFDWKLPSGMMPGDLDLTELAGITIARKGDLYLMATPYQPSRE	62%
Contig131	*Arabidopsis thaliana*	transferase/ transferase, transferring acyl groups other than amino-acyl groups	>gi|240254146|ref|NP_173852.4| transferase/ transferase, transferring acyl groups other than amino-acyl groups [Arabidopsis thaliana] MGLEITVTSQELVKPSPRNLNHPPCHHHLSFLDQLAPPIFMPFLFFYHNKTNLSDKERSDHIKSSLSEIL NLYYPLAGRIKNSGDVVVCNDVGVSFVEAKADCNMSQILENPNPNELNKLHPFEFHEVSDVPLTVQLTFF ECGGLALGIGLSHKLCDALSGLIFVNSWAAFARGQTDEIITPSFDLAKMFPPCDIENLNMATGITKENIV TRRFVFLRSSVESLRERFSGNKKIRATRVEVLSVFIWSRFMASTNHDDKTGKIYTLIHPVNLRRQADPDI PDNMFGNIMRFSVTVPMMIINENDEEKASLVDQMREEIRKIDAVYVKKLQEDNRGHLEFLNKQASGFVNG EIVSFSFTSLCKFPVYEADFGWGKPLWVASARMSYKNLVAFIDTKEGDGIEAWINLDQNDMSRFEADEEL LRYVSSNPSVMVSVS	34%
Contig131	*Actaea racemosa*	BAHD-type acyltransferase	>gi|291059157|gb|ADD71922.1| BAHD-type acyltransferase [Actaea racemosa] MEVVVSSREIIKPSSPTPNHLKKLNFSLNDQYSTHYVSVLLFYSAQGDVDRFKQTNTSDRLKKSLSEILT QFYPLAGRIINNECIDCNDDGLEYLEARVPCPLSQLLGCPKADELNQLIPFSQKLSAVQVSLFDCGGIAI GVTISHTAGDASSLTAFINSWAATAKGANEIVPPKFGFDYLFPPRDVPTVSFGGGAVDYTQLPRFVGKRF IFDSSKLAALKSACADVERPTRVEVVTAFIYKCFLNTIRSRSSKPSVLSMPINLRGRMNPPLPPHSFGNL AIRLTSQPWPAEKEPELNCLVKQLRETIRKVNGGFVEKLQADNAELLFEHWKDWKKGIELSLTGDLNVLM VLICCRFPFYEADFGWGKPAWATRVNLYPSVSLVDTKDGEGVEAWVTLAEGDMTRFCSEPDLLDFSIENP PIHE	31%
Contig132	*Picrorhiza kurrooa*	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	>gi|124054083|gb|ABM89226.1| 4-hydroxy-3-methylbut-2-enyl diphosphate reductase [Picrorhiza kurrooa] MAISLQFSRICTRTELSLPDTRIFRQRKPSSFRCSSAGENAASSSVSGESSEFDAKVFRHNLTRSKNYNR KGFGRKEITLEQISKEYTSDIIKKLKDNGYEYTWGNITVKLAESYGFCWGVERAVQIAYEARKQFPTENI WITNEIIHNPTVNQRLEDMDVKNIPLDNGQKQFDVINKGDVVVLPAFGAAVDEMLTLSEKNVQIVDTTCP WVSKVWNSVEKHKKGEHTSIIHGKYSHEETMATASFAGKYIVVKNMAEATYVRDYILGGKLDGSSSTKEA FLEKFKYALSKGFDPDTDLVKVGIANQTTMLKGETEAIGKLAERTMMQKYGVENVNNHFMSFNTICDATQ ERQDAMYKLVDEKVDLIIVVGGWNSSNTSHLQEIAEDRGIPSYWVDSDVRIGPGNKISCKLMHGELVEKE NWLPEGPITIGVTSGASTPDKAVEDVLTKIFDIKREELLQLA	80%
Contig132	*Solanum lycopersicum*	ISPH protein	>gi|262176919|gb|ACY27516.1| ISPH protein [Solanum lycopersicum] MAIPLQFSSISTRTDLSLPETRTFRLPKPFSVIRCSAGEPVPSSSATAESEFDAKVFRKNLTRSANYNRK GFGHKEATLELMNREYTSDIIKKLKENEFEYTWGNVTVKLAESYGFCWGVERAVQIAYEARKQFPTERIW ITNEIIHNPTVNKRLEDMDVKNIPLEEGKKNFDVVDKDDVVVLPAFGAAVDEMLVLSDKNVQIVDTTCPW VTKVWNTVEKHKKGEYTSIIHGKYAHEETVATASFAGKYIIVKNMAEATYVCDYILGGKLDGSSSTKEAF MQKFKYAVSEGFDPDVDLVKAGIANQTTMLKGETEDIGKLVERTMMQKYGVENVNNHFVSFNTICDATQE RQDAMYKLVEQKLDLMLVIGGWNSSNTSHLQEIAEERGIPSYWIDSEQRVGPGNKISYKLMHGELVEKEN FLPEGPITVGVTSGASTPDKVVEDVLIKVFDIKREEALQLA	69%
Contig133	*Elaeis guineensis*	ribosomal protein S14	>gi|192913024|gb|ACF06620.1| ribosomal protein S14 [Elaeis guineensis] MSRRKTREPKEENVTLGPTVREGEHVFGVAHIFASFNDTFIHVTDLSGRETMVRITGGMKVKADRDESSP YAAMLAAQDVAQRCKELGITALHIKLRATGGNKTKTPGPGAQSALRALARSGMKIGRIEDVTPIPTDSTR RKGGRRGRRL	94%
Contig133	Coccidioides immitis RS	40S ribosomal protein S14	>gi|119188601|ref|XP_001244907.1| 40S ribosomal protein S14 [Coccidioides immitis RS] MPPKKKTDRPANENVSLGPLSGDGSLVFGVARIFASFNDTFVHVTDLSGRETICRVTGGMKVKADRDESS PYAAMLAAQDVAARCKELGINALHIKIRATGGNGTKTPGPGAQSALRALARSGMRIGRIEDVTPTPSDST	83%

			RRKGGRRGRRL	
Contig134	*Mentha x piperita*	flavonoid 3'-O-methyltransferase	>gi|38047397|gb|AAR09601.1| flavonoid 3'-O-methyltransferase [Mentha x piperita] MEASFENGRKRSSSSSSEEESAFSFAMELAAGSVLPMVIKSAIDLNLLELIKRGG EEGASAYELAAQINA ENPKAAAEMIDRILQLLAAHSVLTCRVETPPSRRRRYSLAAVCKFLTRDEDGA SLAPLSLLVQDRVFMEP WYHLKDVIVEGGVAFERAYGVHAFEYHAKDPKFNKIFNQAMHNQSIIFMKRI LEIYKGFEGVKSLVDVGG GTGASSKMIVSKYPLIKAINFDLPHVIQDASPHPEVEHVGGDMFVSVPKADAIF LKWICHDWSDEHCRKL LKNCYDAILGNGKVIIAESTLPEDPNSGPDTIHAIRGDVIMLTVNPGGKERTEKE FRTLALQAGFKRLVK VCAAFHTCIMECHK	79%
Contig134	*Coffea canephora*	caffeic acid O-methyltransferase	>gi|22652500|gb|AAN03726.1| caffeic acid O-methyltransferase [Coffea canephora] MAEEEACLFAMSLASASVLPMVLKSAIELDLLELIAKAGPGAYVSPSELAAQL PTHNPEAPIMLDRILRL LATYSVLDCKLNNLADGGVERLYGLAPVCKFLTKNADGVSMAPLLLMNQDK VLMESWYHLKDAVLDGGIP FNKAYGMTAFEYHGTDPRFNKVFNQGMSNHSTITMKKILEVYRGFEGLKTVV DVGGGTGATLNMIISKYP TIKGINFELPHVVEDAPSHPGVEHVGGDMFVSVPKGDAIFMKWICHDWSDDH CRKLLRNCYQALPDNGKV ILAECVLPEAPDTSLATQNVVHVDVVMLAHNPGGKERTEKEFEALAKGAGFK EFRKVCSAVNTWIMELCK	56%
Contig135	*Antirrhinum majus*	1-deoxy-D-xylulose-5-phosphate synthase	>gi|56785668|gb|AAW28999.1| 1-deoxy-D-xylulose-5-phosphate synthase [Antirrhinum majus] MASCGVNMRSSFFSLLKSHDSSSWWLSSSTTTLPSKRQKFSGISAVQQERDTSE KSEIINVNKENLNGKN GRVARTLNFTGEKPSTPILDTINYPIHMKNLSLEELEILADELREELVYSVSKTG GHLSSSLGVAELTVA LHHVFSTPEDKIIWDVGHQAYPHKILTGRRSKMHTMRKTFGLAGFPKREESVH DAFGAGHSSTSISAGLG MAVARDLLGNNNHVISVIGDGAMTAGQAYEAMNNAGYLDSNLIIILNDNKQV SLPTATVDGPAPPVGALT KALTRLQTSRKFRQLREVAKELTKQIGTEAHEVAAKVDSFVRGVAGSPGACLF EELGIYYIGPVDGHSIE DLVFIFKKIKEMPAPGPVMIHIITEKGKGYPPAEVAADKMHGVVKFDPRTGQQ KKSKSETLSYTQYFAES LIAEAEQDDKVVAIHAAMGGGTGLNIFQKRFPGRTFDVGIAEQHAVTFAAGLA TEGLKPFCAIYSSFLQR GYDQVAHDVDLQKLPVRFIMDRAGLVGADGPTHCGAFDTTYMACLPNMVV MAPSDEAELMHMIATAAIID DRPSCLRYPRGNGIGAVLPPNNKGTPMEIGKGRILREGSRVAILGFGTIIQNCLA AADLLQEHRVSITVA DARFCKPLDGDLIRQLVKEHEVLITIEEGSIGGFSSHVSHFLCLNGLLDGNLKW RAMVLPDRYIDHGAQS DQIEEAGLSPRHIAATVLSLIGEGKDSLHLMDL	86%
Contig135	*Tagetes erecta*	1-deoxy-D-xylulose-5-phosphate synthase	>gi|9971824|gb|AAG10432.1| 1-deoxy-D-xylulose-5-phosphate synthase [Tagetes erecta] MALCGALKGGFVPIAQNGYTSSSLLNPSANAIMPSNKRKFLGIVAVSKEHATN EHEDLTTMDKTTSTTLK YSGDKPKTPILDTINYPIHMKNLCVEELVKLADELREEIVYTVSKTGGHLSSSL GVVELTVSLHHVFNTP EDKIIWDVGHQAYPHKILTGRRSRMRTIRQTFGLAGFPKRDESNHDAFGAGHS STSISAGLGMAVGRDLL GKNNHVIAVIGDGAMTAGQAYEAMNNAGYLDSNLIIVLNDNRQVSLPTATID GPAPPVGALSRSLTRLQT SQKFRQLREAAKEVTKQLGDKTHEVAAKMDSLVKGMVGGQGASMFEELGL YYVGPVDGHNLEDLVYVFDK IKSMTAPGPVLVHIVTEKGKGYPPAEVAADKMHGVVKFDTQTGKQKKNKTK TLSYTQYFVDSLVAEAKED DKIVAIHAAMGGGTGLNTFQKEFPARCFDVGIAEQHAITFAAGLATEGLKPFC AIYSSFLQRGYDQVVHD VDLQKLPVRFAMDRAGLVGADGPTHCGAFDTTFMACLPNMVVMAPSCEAEL MNMVATAVAIDDRPSCFRY PRGNGIGSILPANNKGTLIEVGTGRVIKEGNRVALLGYGTIVQSCLAASEVLKK IGISVTVADARFCKPL DGNLIKQLANEHEVLITVEEGSIGGFSSHVSHFLALNGLLDGHLKWRAMMLPD RYIEHGAQSDQIEEAGL SSKHIAATVLSLIGGSKETLHALNV	78%
Contig135	*Gossypium barbadense*	1-deoxy-D-xylulose 5-phosphate synthase	>gi|124558735|gb|ABN13970.1| 1-deoxy-D-xylulose 5-phosphate synthase [Gossypium barbadense] MALCASSFPAIINWGAASDPQKSTPFASHFLGGSDLVLQPLKKLNQVKKRPGG AYASLSEGAEYHSQRPA TPLLDTINYLIHMKNLSVKELKQLSEELRSDVVFNVSKTGGHLGSSLGVVELT VALHYVFNAPRDKILWD VGHQSYPHKILTGRRHKMHTMRQTNGLAGFTKRSESEYDCFGTGHSSTTISAG LGMAVGRDLKGERNHVV AVIGDGAMTAGQAYEAMNNAGYLDSDMIVILNDNKQVSLPTANLDGPIPPVG ALSSALSRLQSNRPLREL REVAKGVTKQIGGPMHELAAKVDEYARGMISGSGSTLFEELGLYYIGPVDGH NIDDLVSILKEVKTTKTT GPVLIHVVTEKGRGYPYAERAADKYHGVVKFDPATGKQFKGNSATQSYTTYF AEALIAEAEADKNIVAIH AAMGGGTGLNLFLRRFPQRCFDVGIAEQHAVTFAAGLACEGLKPFCAIYSSFM QRAYDQVVHDVDLQKLP VRFAMDRAGLVGADGPTHCGAFDVTFMACLPNMVVMAPSDEAELFHMVAT AAAIDDRPSCFRYPRGNGIG VQLPPGKKGVPLEVGKGRVLIEGERVALLGYGSAVQSCLAAASLLESHGLRLT VADARFCKPLDHALIRK	70%

			LAKSHEVLITVEEGSIGGFGSHVAQFLALDGLLDGKVKWRPLVLPDRYIDHGS PVDQLAEAGLTPSHIAA TVFNVLEQKREALEVMSSRN	
Contig136	*Rehmannia glutinosa*	ascorbate peroxidase	>gi|42558486|gb|AAS19934.1| ascorbate peroxidase [Rehmannia glutinosa] MVKNYPTVSEEYLNAVEKCKKKLRGLIAEKNCAPIMLRLAWHSAGTFDQCSK TGGPFGTMRFKAEQGHAA NNGLDIALRLLQPIREQFPILSHADFYQLAGVVAVEVTGGPEVPFHPGRPDKEE PPVEGRLPDATKGSDH LRDVFTKQMGLSDQDIVALSGAHTLGRCHKERSGFEGPWTANPLIFDNSYFKE LLSGEKEGLLQLPSDKA LLADPSFRPLVEKYAADEDAFFADYAEAHLKLSELGFADA	85%
Contig136	*Mesembryanthemum crystallinum*	cytosolic ascorbate peroxidase	>gi|4835909|gb|AAD30294.1|AF139190_1 cytosolic ascorbate peroxidase [Mesembryanthemum crystallinum] MAMPPVVDSVYLKEIDKARRDLRALISNRSCAPIMLRLAWHDAGTYCAKTKT GGANGSIRNEEEYAHGAN NGLKKAIDWCEEVKAKYPKITYADLYQLAGVVAVEVTGGPTIEFVPGRKDSK VSTNEGRLPDAKKGPPHL RDIFYRMGLTDKDIVALSGAHTLGRAHPERSGFDGPWTQEPLKFDNSYFVELL KGESEGLLQLPTDKALV EDPAFRPYVELYAKDEDAFFRDYAVSHKKLSELGFTPSGSKSGPKDSTILAQG AVGVAVAAAVVILSYIF EVRKRLK	63%
Contig136	*Suaeda salsa*	cytosolic ascorbate peroxidase	>gi|14324146|gb|AAK58449.1| cytosolic ascorbate peroxidase [Suaeda salsa] MGKSYPTVSEENQKSIEKAKKKLRGLISEKHCAPIMLRLAWHSAGTFDVQSKT PGPFGTMRHQAELAHGA NNGLDIALRLLEPIKEQFPEISFADFYQLAGVVAVEVTGGPEIPFHPGREDKPEP PQEGRLPDATKGCDH LRDVFIKQMGLTDQDIVALSGGHTLGRCHKDRSGFEGPWTPNPLVFDNSLLKE LLSGEKDGLLQLPSDKA LLADPVFRPLVEKYAADEDAFFADYSDAHLKLSELGFADA	73%
Contig136	*Citrus maxima*	ascorbate peroxidase 2	>gi|221327589|gb|ACM17464.1| ascorbate peroxidase 2 [Citrus maxima] MTKNYPTVSEDYKKAVEKCKRKLRGFIAEKNCAPLMLRIAWHSAGTYDVKT KTGGPFGTMRLAAEQAHSA NNGLDIAVRLLEPFKEQFPTISYADLYQLAGVVGVEVTGGPDIPFHPGRDDKA EPPQEGRLPDAKQGNDH LRQVFGAQMGLSDKDIVALSGGHTLGRCHKERSGFEGPWTRNPLIFDNSYFTE LLTGEKDGLLQLPSDKA LLDDPVFRPLVEKYAADEDAFFADYAEAHLKLSELGFAEA	72%
Contig137	*Nicotiana tabacum*	jasmonate ZIM-domain protein 2	>gi|196259696|dbj|BAG68656.1| jasmonate ZIM-domain protein 2 [Nicotiana tabacum] MERDFMGLNSKDSVVVVKEEPVETCKDSGFRWQLSSKVGIPHFMSLSSAQDE KPTKALSSADGVDSCLKR QSGEIQISAAATMKQQLLGGIPVTAPHSILPSSGSVAGITEPWFNSKGSAAPAQL TIFYGGTVNVFDDIS PEKAQAIMFLAGNGCVPPNVVQPRFQVQASTPKLAAVDGTCVNQTPNMLPAS GHSSPMSVSSHPIGQSAG NSGNKDDMKISKTANISVETPKIVTSLGPVGATTIMPAAVPQARKASLARFLEK RKERVMNAAPYGLSKK SGECSTPESIGVGFSATSSVGTSPLIAGKET	52%
Contig137	*Arabidopsis thaliana*	JAZ3 (JASMONATE-ZIM-DOMAIN PROTEIN 3)	>gi|18401669|ref|NP_566590.1| JAZ3 (JASMONATE-ZIM-DOMAIN PROTEIN 3) MERDFLGLGSKNSPITVKEETSESSRDSAPNRGMNWSFSNKVSASSSQFLSFRP TQEDRHRKSGNYHLPH SGSFMPSSVADVYDSTRKAPYSSVQGVRMFPNSNQHEETNAVSMSMPGFQSH HYAPGGRSFMNNNNNSQP LVGVPIMAPPISILPPPGSIVGTTDIRSSSKPIGSPAQLTIFYAGSVCVYDDISPEK AKAIMLLAGNGSS MPQVFSPPQTHQQVVHHTRASVDSSAMPPSFMPTISYLSPEAGSSTNGLGATK ATRGLTSTYHNNQANGS NINCPVPVSCSTNVMAPTVALPLARKASLARFLEKRKERVTSVSPYCLDKKSS TDCRRSMSECISSSLSS AT	37%
Contig137	*Medicago truncatula*	cytochrome P450 monooxygenase CYP78A29	>gi|84514161|gb|ABC59089.1| cytochrome P450 monooxygenase CYP78A29 [Medicago truncatula] MSTNIDNLWIFALASKCTQENIAYSLLIMALLWITMTFFYWSHPGGPAWGKYY YSSNYSTTKTNNKNNLN SSTKPSTTTSSSIFIPGPKGYPLFGSMNLMSSSLAHHRIASTAKTCKATRLMAFS LGDTRAMVTCNPDVA KEILHSSVFADRPIKESAYSLMFNRAIGFAPYGVYWRTLRKISTNHLFSPMQIKS SGPQRSEIATQMIDL FRNRHLHGGFCVRDVLKKASLNNMMCSVFGQRFKIDEVNERMMELSGLVEQ GYDLLGGLNWGDHLPFLKD FDVQKIRFSCSELVPKVNRFVGSIISDHRADKNQTNKDFVHVLLSLQEPDKLSD SDMIAVLWEMIFRGTD TVAVLIEWILARLVIHPDVQKKVQTELDEVASGESCAITEEDVAAMVYLPAVI KEVLRLHPPGPLLSWAR LAITDTTIDGYHVPAGTTAMVNMWAISRDPDVWRNPLEFNPERFVSEGAEFSV LGSDLRLAPFGSGRRSC PGKNLGLATVTFWVAKLLHEFEWLPLDEVNGVDLTEVLRLSCEMANPLTVQV RPRR	37%
Contig137	*Solanum lycopersicum*	jasmonate ZIM-domain protein 3	>gi|164472579|gb|ABY58971.1| jasmonate ZIM-domain protein 3 [Solanum lycopersicum] MERDFMGLNIKDSLLVVKDEPVESSKDSGFRWPMSSKVGVPHFMSLNSAQDE NTFKALSATDGVDAGLKR QPGELQMKQVLGGIPVTAPHSMLPSRGSVAGTTEPWFNSKGSAAPAQLTIFYG GMVNVFEDISPEKAQAI	39%

			MFLAGHGCAPPNVVQPRFQLQASASKPAAADGVCVNQTPNMLPASGLSSPMS VSSHPIGQSDGSSGNKDD MKMSKTANISVTPHVKLDTSKIVTSLGPVGATTIMTAAVPQARKASLARFLEK RKERVMNLAPYGLSKKS PECSTPESNGVGFSATSTPLLAGKET	
Contig138	*Arabidopsis thaliana*	sec34-like family protein	>gi|30698937|ref|NP_177485.2| sec34-like family protein [Arabidopsis thaliana] MATKAASSSSLPKSGAISKGYNFASTWEQSAPLTEQQQAAIVSLSHAVAERPFP ANLVHEHVHRPENGLS VSVEDTHLGDSGAIEAVLVNTNQFYKWFTDLESAMKSETEEKYRHYVSTLTE RIQTCDNILHQVDETLDL FNELQLQHQGVTTKTKTLHDACDRLLMEKQKLMEFAEALRSKLNYFDELENV SSNFYSPNMNVSNSNFLP LLKRLDECISYIEDNPQYAESSVYLLKFRQLQSRALGMIRTYILAVLKTAASQV QAAFRGTGGNKTSVSE GVEASVIYVRFKAAANELKPVLEEIESRSARKEYVQILAECHRLYCEQRLSLVK GIVHQRVSDFAKKEAL PSLTRSGCAYLMQVCHMEHQLFTHFFPASSEEVSSLAPLVDPLSTYLYDILRPK LIHEANIDLLCELVHI LKVEVLGDQSARQSEPLAGLRPTLQRILADVNERLTFRARTYIRDEIANYTPSD EDLDYPAKLEGSPNTT SETDLRDDENADVFKTWYPPLEKTLSCLSKLYRCLEQAVFTGLAQEAVEVCSL SIQKASKLIIKRSTTMD GQLFLIKHLLILREQIAPFDIEFSVTHKELDFSHLLEHLRRILRGQASLFDWSRST SLARTLSPRVLESQ IDAKKELEKCLKTTCEEFIMSVTKLVVDPMLSFVTKVTAIKVALSSGTQNHKV DSVMAKPLKEQAFATPD KVVELVQKVYAAIQQELLPILAKMKLYLQNPSTRTILFKPIKTNIVEAHTQVES LLKAEYSAEEQANINM ISIQDLQTQLDNFL	85%
Contig138	Laccaria bicolor S238N-H82	cis-Golgi transport vesicle tethering complex subunit	>gi|170115140|ref|XP_001888765.1| cis-Golgi transport vesicle tethering complex subunit [Laccaria bicolor S238N-H82] SASKQVISVEEWEAKAPLGDLEIRSINAIKAATEKVPYPLKFAEEDDSSASGSV TPITQQQRNKLVASAS GSGSRPSTPSGRSNAHALHPKQPIQTPQQFYDWFALIDRSVAHSQESHFRTHVA SVSEHLETCDLLLDRI AEIDREVDGMMEGWTGVEEGGKNLKDACERLLEERDRLLELTDDIDSYLEYF QELEPATRMLNHPGESLI FQSDFLYMVERVDICIDFLKSHRHFKESEVYLLRYQQCMTRAMTLIKMNFVGS LRALSSDVSTRLSEKDV SPTAQMHLLYTRFRTVSKKVAPLLGELERRALAYPDELSALLSECHSAYFYAR KQLLVPRILEEIKGLNP SRSELVELTRAGCSYLKQLCTDEFNLYREFFSTAEDQLYQYLETLCDFLYDDL RPRILHEPRLTALCEVC TVLQALMVLDAPSSSSSSMVFSANDDDDESGDDDDADRSEDDEDGDVDELTI DLDNPHPKGKGKVGRRLH ISHLLQMVLQDAQTRLFFKAQSVIQSDIRYYVPKAEDLAYPDILICQKPQSGNEI REKESVSEIFQLPSL DKQDTWYPTMRKMVWVLSQLHDFVKPAIFEDIAQEAANLCRQSLVAASEAIK TRSGLDGHLFLVRNLLIL KEITRNLDLDQRNTIEPSSSKSTTDFETFANLLSRTTSMLPDGLFASLGMTRGED GIRGGIDHDLRRACE NVISVSVDSICEPLQSWAERIHAYKSIPPSLEKQDDEHPPSGPLSEQVWASRSAA ETLNLRFREACERDM RSSVARLRLYLEDDRTVRVLVEHMQDRIMDAYAAYREVVWGMY	34%
Contig138	*Homo sapiens*	conserved oligomeric Golgi complex subunit 3	>gi|13899251|ref|NP_113619.1| conserved oligomeric Golgi complex subunit 3 [Homo sapiens] MAEAALLLLPEAAAERDAREKLALWDRRPDTTAPLTDRQTDSVLELKAAAEN LPVPAELPIEDLCSLTSQ SLPIELTSVVPESTEDILLKGFTSLGMEEERIETAQQFFSWFAKLQTQMDQDEG TKYRQMRDYLSGFQEQ CDAILNDVNSALQHLESLQKQYLFVSNKTGTLHEACEQLLKEQSELVDLAENI QQKLSYFNELETINTKL NSPTLSVNSDGFIPMLAKLDDCITYISSHPNFKDYPIYLLKFKQCLSKALHLMK TYTVNTLQTLTSQLLK RDPSSVPNADNAFTLFYVKFRAAAPKVRTLIEQIELRSEKIPEYQQLLNDIHQC YLDQRELLLGPSIACT VAELTSQNNRDHCALVRSGCAFMVHVCQDEHQLYNEFFTKPTSKLDELLEKL CVSLYDVFRPLIIHVIHL ETLSELCGILKNEVLEDHVQNNAEQLGAFAAGVKQMLEDVQERLVYRTHIYI QTDITGYKPAPGDLAYPD KLVMMEQIAQSLKDEQKKVPSEASFSDVHLEEGESNSLTKSGSTESLNPRPQTT ISPADLHGMWYPTVRR TLVCLSKLYRCIDRAVFQGLSQEALSACIQSLLGASESISKNKTQIDGQLFLIKH LLILREQIAPFHTEF TIKEISLDLKKTRDAAFKILNPMTVPRFFRLNSNNALIEFLLEGTPEIREHYLDSK KDVDRHLKSACEQF IQQQTKLFVEQLEEFMTKVSALKTMASQGGPKYTLSQQPWAQPAKVSDLAAT AYKTIKTKLPVTLRSMSL YLSNKDTEFILFKPVRNNIQQVFQKFHALLKEEFSPEDIQIIACPSMEQLSLLLSV SK	33%
Contig138	*Chlamydomonas reinhardtii*	component of oligomeric golgi complex 3	>gi|159470393|ref|XP_001693344.1| component of oligomeric golgi complex 3 [Chlamydomonas reinhardtii] MSVAGPRSGSKLAGAASKSYNVAAIWEKTAALSEGQLRAIESLGQCCSQRPLP SHVTRPETPVALTVAPA AGYVGTLEDAVLHNTSQFHKWHSELEAACASETEEKYKRYADLLNCHVQSC ETILHRVDLTLEAFDALLA QHRDVVGRSRSLHSSCEQLVREKEALMEFAEAMRAKLRFFDEFETVAAQFAA LSVAQSSGFLALLRKLDD CMAYVANNPQYADAAQYSAKFKQLQGRALGAVRTKVQQVLRAAVQQAAA	45%

			AGAVPQLAEGAEVPMLYVRFR AAAEPNIKGLLREVESRSGRPEYLRLLQELHTLYGQARLALIGPYVCQLEVQLF EHFFPGQQQAAAAADG AAAAGGGKPAGARSAGHGAGAGAGPVLPSSAEALSPLLEPLATMLYDHLRPA VVVMQDLDELCELVDILK HEVMGEQLARRGPGGEALKPLLGRCLADVQGRLIFRVQAYIRDEISGYHHHSH SADDVPDGNGAAVASSS SDAAAAATAARPPPSADPYASLFPPLRATLLVLSKLYRAVDSKIFGGLAQEAV SACTVAVQNASRAVAKR AAGSAPALAAATSAAAATGAGAALFMIRNLLFLREQIVPFDVDFAVTDIDLDF SHMRDHLRRIMVGQESL FTLGPSNAMVRMLGASGPRVLTYQLDSKKELEKALKSVCEALIMALTKVAVE PMLSFITKVTAVRLAGQS SGAAAQATKPMREQAFASTAKLGEMVGRVNAAMAAGGPLAAAVSKMRLYL PNPATHAILLKPVKSNIAEA HGQIAKLLQTDYTPEEAAEVPLHNPQQLQAVLEAL	
Contig139	*Mentha arvensis*	limonene hydroxylase	>gi|146386316|gb|ABQ24001.1| limonene hydroxylase [Mentha arvensis] MELQISSAIIILVVTYTISLLIIKQWRKPKPEENLPPGPPKLPLIGHLHLLWGKLP QHALASVAKQYGPV AHVQLGEVFSVVLSSREATKEAMKLVDPACADRFDSIGTKIMWYDNDDIIFSP YSEHWRQMRKICVSGLL SARNVRSFGFIRQDEVSRLLGHLRSSAAAGEAVDLTERIATLTCSIICRAAFGSV IRDHEELVELVKDAL SMASGFELADLFPSSKLLNLLCWNKSKLWRMRRRVDTILEAIVEEHKLKKSGE FGGEDIIDVLFRMQKDS QIKVPITTNAIKAFIFDTFSAGTETSSTTTLWVMAELMRNPEVMAKAQVEVRA ALKGKTNWDVDDVQELK YMKSVVKETMRMHPPIPLIPRSCREECEVNGYKIPNKARIMINVWSMGRNPLY WEKPKTFWPERFDQVSR DFMGNDFEFIPFGAGRRICPGLNFGLANVEVPLAQLLYHFDWNLAEGMKPSD MDMSEAEGLTGIRKNNLL LLPTPYDPSS	96%
Contig139	*Ammi majus*	cytochrome P450-dependent monooxygenase-like protein	>gi|130845569|gb|ABO32531.1| cytochrome P450-dependent monooxygenase-like protein [Ammi majus] MELPSPFAVASSLLVITFLLFHIVKKSKQQSKSNLPPGLWKLPVFGNLFQVAGK IPHRGLRKLADKFGPL MHLQLGEISAIVISDPRVAKEVLRTHDLAFADRPVVLLGNIILANCRDIVLALY GDYWRQMRKICTLELL SANKVRSFRSIREDETWKLIQSIKLSSGSSLVDVSHKVSALANAVTCRATIGQA CKYQDELIELVEEIAY LGSGFFLADLFPSIFFLPTLSGMKPALKKIRKKLDVIFDNIIKEHNDKLSRRKKG SEIDAEEEDLVDVLL RINDSQRLEFPISSGDIQGLVLDMLTAGTDTSSAVLEWAMSELMRNPKVMKK VQSEVREVVKGKEKIEEA DIQNMSYLKLVVKETLRLHAPVPLLLPRECRKECEINGYTIPVGTKVMVNVW AIARDPECWDDAESFIPE RFENSSVDYIGANFEFLPFGAGRRMCAGISFGIATVELPLAQLLHSFDWKLPNE MKPEDLDMDETNAATC KRKNNLMLIATDCSHTIESVTEVS	51%
Contig140	*Medicago sativa*	vestitone reductase	>gi|973249|gb|AAB41550.1| vestitone reductase [Medicago sativa] MAEGKGRVCVTGGTGFLGSWIIKSLLENGYSVNTTIRADPERKRDVSFLTNLP GASEKLHFFNADLSNPD SFAAAIEGCVGIFHTASPIDFAVSEPEEIVTKRTVDGALGILKACVNSKTVKRFI YTSSGSAVSFNGKDK DVLDESDWSDVDLLRSVKPFGWNYAVSKTLAEKAVLEFGEQNGIDVVTLILPF IVGRFVCPKLPDSIEKA LVLVLGKKEQIGVTRFHMVHVDDVARAHIYLLENSVPGGRYNCSPFIVPIEEM SQLLSAKYPEYQILTVD ELKEIKGARLPDLNTKKLVDAGFDFKYTIEDMFDDAIQCCKEKGYL	44%
Contig140	*Lotus corniculatus*	dihydroflavanol reductase 3	>gi|31324464|gb|AAF23884.2|AF117263_1 dihydroflavanol reductase 3 [Lotus corniculatus] MGSVPETVCVTGAAGFIGSWLVMRLMERGYMVRATVRDPANMKKVKHLLE LPEAKTKPTLWKADLAEEGS FDEAIKGCTGVFHVATPMDFESKNPENEVIKPTINGVLDIMKACQKAKTVRRL VFTSSAGTLNVIEHQKQ MFDESCWSDVEFCRRVKMTGWMYFVSKTLAEQEAWKFAKEHGIDFITIIPPLV VGSFLMPTMPPSLITAL SPITGNEAHYSIIKQGQYVHLDDLCLAHIFLFEHPESEGRYICSASEATIHDIAKL INSKYPEYNIPTKF KNIPDELELVRFSSKKIKDMGFEFKYSLEDMYTGAIDTCKEKGLLPKAAENPSN GK	40%
Contig141	*Arabidopsis thaliana*	lactate dehydrogenase	>gi|110740557|dbj|BAE98384.1| lactate dehydrogenase [Arabidopsis thaliana] MEKNASTSSLKDLGPSGLDLTSAFFKPIHNSDPPLPSNRRTKVSVVGVGNVGM AIAQTILTQDLADEIALVDAKPDKLRGEMLDLQHAAAFLPRTKITASVDYEVT AGSDLCIVTAGARQNPGESRLNLLQRNVALFRHIIPPLAKASPDSILIIVSNPVD VLTYVAWKLSGFPVNRVLGSGTNLDSSRFRFLIADHLDVNAQDVQAFIVGEH GDSSVALWSSISVGGIPVLSFLEKNQIAYEKQTLEDIHQAVVGSAYEVIGLKGY TSWAIGYSVANLARTILRDQRKIHPVTVLARGFYGVDGGDVFLSLPALLGRNG VVAVTNVHMTDEEAEKLQKSAKTILEMQSQLGL	73%
Contig141	*Mus musculus*	Ldha protein	>gi|13529599|gb|AAH05509.1| Ldha protein [Mus musculus] APQNKITVVGVGAVGMACAISILMKDLADELALVDVMEDKLKGEMMDLQH GSLFLKTPKIVSSKDYCVTANSKLVIITAGARQQEGESRLNLVQRSVNIFKFIIPN IVKYSPHCKLLIVSNPVDILTYVAWKISGFPKNRVIGSGCNLDSARFRYLMGER LGVHALSCHGWVLGEHGDSSVPVWSGVNVAGVSLKSLNPELGTDADKEQW KEVHKQVVDSAYEVIKLKGYTSWAIGLSVADLAESIMKNLRRVHPISTMIKGL YGINEDVFLSVPCILGQNGISDVVKVTLTPEEEARLKKSADTLWGIQKELQF	70%
Contig141	*Gillichthys mirabilis*	muscle-type lactate dehydrogenase	>gi|10121703|gb|AAG13331.1|AF266211_1 muscle-type lactate dehydrogenase	64%

			[Gillichthys mirabilis] MSTKEKLISHVSKEEAVGSRNKVTVVGVGMVGMASAISILLKDLCDELALVDVMEDKLKGEVMDLQHGSLFLKTHKIVADKDYSVTANSKVVVVTAGARQQEGETRLNLVQRNVNIFKFIIPNIVKYSPNCILMVVSNPVDS	
Contig141	*Apalone ferox*	L-lactate dehydrogenase A	>gi|39545696|gb|AAR27951.1| L-lactate dehydrogenase A [Apalone ferox]MSVKELLIQNVHKEEHSHAHNKITVVGVGAVGMACAISILMKDLADELALVDVIEDKLRGEMLDLQHGSLFLRTPKIVSGKDYSVTAHSKLVIITAGARQQEGESRLNLVQRNVNIFKFIIPNIVKYSPDCMLLVVSNPVDILTYVAWKISGFPKHRVIGSGCNLDSARFRYLMGERLGIHSLSCHGWIIGEHGDSSVPVWSGVNVAGVSLKALQPDLGTDADKEHWKEVHKQVVNSAYEVIKLKGYTSWAIGLSVADLAETVMKNLRRVHPVSTMVKGMYGVSSDVFLSVPCVLGYAGITDVVKMTLKSEEEEKLRKSADTLWGIQKELQF	69%
Contig143	*Mentha x piperita*	flavonoid 4'-O-methyltransferase	>gi|38047399|gb|AAR09602.1| flavonoid 4'-O-methyltransferase [Mentha x piperita] MVADEEVRVRAEAWNNAFGYIKPTAVATAVELGLPDILENHDGPMSLLELSAATDCPAEPLHRLMRFLVFHGIFKKTAKPPLSNEAVYYARTALSRLFTRDELGDFMLLQTGPLSQHPAGLTASSLRTGKPQFIRSVNGEDSWTDPVNGYHMKVFSDAMAAHARETTAAIVRYCPAAFEGIGTVVDVGGRHGVALEKLVAAFPWVRGISFDLPEIVAKAPPRPGIEFVGGSFFESVPKGDLVLLMWILHDWSDESCIEIMKKCKEAIPTSGKVMIVDAIVDEDGEGDDFAGARLSLDLIMMAVLARGKERTYREWEYLLREAGFTKFVVKNINTVEFVIEAYP	61%
Contig143	*Eschscholzia californica*	reticuline-7-O-methyltransferase	>gi|87887871|dbj|BAE79723.1| reticuline-7-O-methyltransferase [Eschscholzia californica] MDEEIILGQADICKYMYGFVDSMTLRCVVELGIPDIIHSHGRPITLTEILNGIPNLSSSFDINYLQGIMTILVRRRVFAVHKFDPKDGTNLTEIRYGLTPSSKCLLKDSKFNLAPFVLLETHPWITDPWNYLGKCVQEGGSGFVKAHGSDVFKFGSDHPEFFKLFYDGMECSTKVLVQVVLDKYQQVFKDVKSIVDVGGGTGMMISEIVKNHPHIKGINFDLPHVVAEAPDYPGVEHVGGDMFVEIPQADAITMKGILHDWNDDACVKILENCKKAIPKNGKVIIIDCVLNPDGDDLFDDIKVVSDLGMRVHCSDGKERTEAEWEKLLKKGGFPRYKITHVVTVQSMIEAYPE	45%
Contig144	*Atriplex nummularia*	lipid transfer protein	>gi|31879432|dbj|BAC77694.1| lipid transfer protein [Atriplex nummularia] MASSVVFKLACAVFMCMLVAAPHAEALTCGQVTSSMTPCMSYLTGGGSPTPACCGGVKSLNSMASTPADRKAACGCLKSAAGAMTNLNMGNAASLPGKCGISLPYPISTSTDCSKVN	43%
Contig144	*Platanus orientalis*	pollen allergen Pla o 3	>gi|162949340|gb|ABY21307.1| pollen allergen Pla o 3 [Platanus orientalis] MAFSRVAKLACLLLACMVATAPHAEAAITCGTVVTRLTPCLTYLRSGGAVAPACCNGVKALNNDAKTTPDRQAACGCLKTASTSISGIQLGNAASLAGKCGVNLPYKISPTIDCSKVK	44%
Contig145	*Arabidopsis thaliana*	histone H3.2	>gi|145334271|ref|NP_001078516.1| histone H3.2 [Arabidopsis thaliana] MFFLLLSPRSDFTTIEFRVLSHSSLKIKMARTKQTARKSTGGKAPRKQLATKAARKSAPTTGGVKKPHRYRPGTVALREIRKYQKSTELLIRKLPFQRLVREIAQDFKTDLRFQSHAVLALQEAAEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	95%
Contig145	*Oryza sativa*	disease-resistent-related protein	>gi|18698662|gb|AAL78367.1|AF467728_1 disease-resistent-related protein [Oryza sativa] MARTKQTARKSTGGKAPRKQLATKAARKSAPTTGGVKKPHRYRPGTVALREIRKYQKSTELLIRKLPFQRLVREIAQDFKTDLRFQSHAVLALQEAAEAYLVGLFEDTNLCAIHAKRVTIMPKDIKLARRIRGERA	97%

Supplementary Data 2: Contigs and their homologous proteins in *A. thaliana*

Contig number	Homologous proteins in *A.thaliana*	Percentage identity	Coding gene with locus	Protein function
Contig2	S-adenosyl-L-homocystein hydrolase	89%	AAP92453	catalyzes the hydrolysis of S-adenosyl-L-homocysteine(AdoHyc) to form adenosine (Ado) and homocysteine (Hcy)
Contig3	MAT3 (methionine adenosyltransferase 3)copper ion binding / methionine adenosyltransferase	88%	MAT3 at locus AT2G36880	copper ion binding, methionine adenosyltransferase activity, one-carbon compound metabolic process, S-adenosylmethionine biosynthetic process
Contig6	quinone oxidoreductase-like protein	75%	AAM63201	Zinc-binding dehydrogenase
Contig7	geranylgeranyl pyrophosphate synthase	77%	AAA32797	isoprenyl diphosphate synthases which synthesis various chain length
Contig12	26S proteasome subunit RPN6a	83%	RPN6a at locus AAP86661	Posttranslational modification, protein turnover,chaperones
Contig13	ACX5 (ACYL-COA OXIDASE 5); FAD binding / acyl-CoA dehydrogenase	80%	ACX5 at locus AT2G35690	Both mitochondrial acyl-CoA dehydrogenases (ACAD) and peroxisomal acyl-CoA oxidases (AXO) catalyze the alpha,beta dehydrogenation of the corresponding trans-enoyl-CoA by FAD, which becomes reduced.
Contig14	YAB5 (YABBY5)	70%	YAB5 at	transcription factor activity,regulation

			locus AT2G26580	of transcription
Contig16	CSD1 (COPPER/ZINC SUPEROXIDE DISMUTASE 1) superoxide dismutase	84%	CSD1 at locus AT1G08830	Superoxide dismutases catalyse the conversion of superoxide radicals to molecular oxygen
Contig22	GAPC1 (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE C SUBUNIT)	90%	GAPC1 at locus AT3G04120	glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity
Contig26	calcium-binding EF hand family protein	72%	AT2G44310	calcium ion binding
Contig27	MAT3 (methionine adenosyltransferase 3)copper ion binding / methionine adenosyltransferase	93%	MAT3 at locus AT2G36880	copper ion binding, methionine adenosyltransferase activity,one-carbon compound metabolic process, S-adenosylmethionine biosynthetic process
Contig30	PGI1 (PHOSPHOGLUCOSE ISOMERASE 1)	74%	PGI1 at locus AT4G24620	glucose-6-phosphate isomerase activity, positive regulation of flower development, starch metabolic process
Contig32	enolase (2-phospho-D-glycerate hydroylase)	86%	AAM12985	catalyse the reversible dehydration of 2-phospho-D-glycerate to phosphoenolpyruvate as part of the glycolytic and gluconeogenesis pathways
Contig41	AT4G34350	76%	AT4G34350	(E)-4-hydroxy-3-methyl-but-2-enyl pyrophosphate reductase
Contig42	VTE5 (vitamin E pathway gene5); phosphatidate cytidylyltransferase/ phytol kinase.	80%	VTE5 at locus AT5G04490	phytol kinase activity, phosphatidate cytidylyltransferase activity; vitamin E biosynthetic process, phospholipid biosynthetic process
Contig43	ATCBR (ARABIDOPSIS THALIANA NADH:CYTOCHROME B5 REDUCTASE 1)	83%	ATCBR at locus AT5G17770	Cytochrome b5 reductase catalyzes the reduction of 2 molecules of cytochrome b5 using NADH as an electron donor.
Contig44	HDS (4-HYDROXY-3-METHYLBUT-2-ENYL DIPHOSPHATE SYNTHASE)	83%	HDS at locus AT5G60600	4 iron, 4 sulfur cluster binding, 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase activity; response to light stimulus,isoprenoid biosynthetic process, isopentenyl diphosphate biosynthetic process, mevalonate-independent pathway, response to bacterium, systemic acquired resistance,salicylic acid mediated signaling pathway
Contig46	NADH dehydrogenase	90%	AAM65274	NADH-ubiquinone oxidoreductase-F iron-sulfur binding
Contig47	ATB2; oxidoreductase	72%	ATB2 at locus AT1G60710	oxidoreductase activity
Contig48	ATB2; oxidoreductase	72%	ATB2 at locus AT1G60710	oxidoreductase activity
Contig49	thioesterase family protein	70%	AT1G04290	hydrolase activity, acting on ester bonds, acyl-CoA thioesterase activity
Contig50	aldo/keto reductase family protein	73%	AT1G60730	oxidoreductase activity, aldo-keto reductase activity, oxidation reduction
Contig51	FAD2 (FATTY ACID DESATURASE 2)	80%	FAD2 at locus AT3G12120	omega-6 fatty acid desaturase activity, delta12-fatty acid dehydrogenase activity; lipid metabolic process
Contig55	ATP synthase delta chain(mitochondrial)	75%	AT5G47030	hydrogen ion transporting ATP synthase activity, response to salt stress
Contig56	PKp3 (plastidial pyruvate kinase 3)	76%	PKp3 at locus AT1G32440	pyruvate kinase activity, glycolysis, fatty acid biosynthetic process
Contig59	MAT3 (methionine adenosyltransferase 3)	91%	MAT3 at locus AT2G36880	copper ion binding, methionine adenosyltransferas activity; one-carbon compound metabolic

				process, S-adenosylmethionine biosynthetic process
Contig60	2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	82%	AAM62786	catalyzes the formation of 2-C-methyl-D-erythritol 2,4-cyclodiphosphate (MEC) in the non-mevalonate deoxyxylulose (DOXP) pathway for isoprenoid
Contig67	ATMS1(5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase/ copper ion binding / methionine synthase)	90%	ATMS1 at locus AT5G17920	response to cadmium ion, response to salt stress, methionine biosynthetic process; 5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity, copper ion binding, methionine synthase activity
Contig69	19S proteasome regulatory complex subunit S6A	96%	AAD46145	ATPases Associated with a wide variety of cellular Activities) superfamily represents an ancient group of ATPases belonging to the ASCE (for additional strand, catalytic E) division of the P-loop NTPase fold
Contig70	chalcone-flavanone isomerase family protein	72%	AT5G05270	chalcone isomerase activity;,flavonoid biosynthetic process
Contig71	ATTRX1(oxidoreductase, acting on sulfur group of donors, disulfide)	81%	ATTRX1 at locus AT3G51030	oxidoreductase activity, acting on sulfur group of donors, disulfide as acceptor, cell redox homeostasis
Contig73	EIF4A1 (Eukaryotic translation initiation factor 4A1);	97%	EIF4A1 at locus AT3G13920	translation initiation factor activity, ATP-dependent helicase activity,translational initiation
Contig74	ATB2(oxidoreductase)	74%	ATB2 at locus AT1G60710	oxidoreductase activity
Contig77	chalcone synthase	81%	AAT96388	plant-specific polyketide synthases (PKS) and related enzymes
Contig83	ATR2(ARABIDOPSIS P450 REDUCTASE 2)	81%	ATR2 at locus AT4G30210	NADPH-hemoprotein reductase activity, phenylpropanoid metabolic process
Contig84		56%(unknown protein)		
Contig85	HDS (4-HYDROXY-3-METHYLBUT-2-ENYL DIPHOSPHATE SYNTHASE); 4 iron, 4 sulfur cluster binding / 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	88%	HDS at locus AT5G60600	4 iron, 4 sulfur cluster binding, 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase activity, response to light stimulus,isoprenoid biosynthetic process, isopentenyl diphosphate biosynthetic process, mevalonate-independent pathway, response to bacterium, systemic acquired resistance,salicylic acid mediated signaling pathway
Contig86	ALIS1 (ALA-INTERACTING SUBUNIT 1); phospholipid transporter	72%	ALIS1 at locus AT3G12740	phospholipid transporter activity
Contig87	transketolase	89%	CAA74713	TPP-binding module; 1-Deoxy-D-xylulose-5-phosphate synthase (DXS) is a regulatory enzyme of the mevalonate-independent pathway involved in terpenoid biosynthesis
Contig95	adenine nucleotide translocase	87%	BAD95278	ATP/ADP transporter
Contig96	G6PD6 (GLUCOSE-6-PHOSPHATE DEHYDROGENASE 6)	70%	G6PD6 at locus AT5G40760	glucose-6-phosphate dehydrogenase activity, pentose-phosphate shunt, oxidative branch,glucose metabolic process
Contig99	SAM1 (S-ADENOSYLMETHIONINE SYNTHETASE 1)	83%	SAM1 at locus AT1G02500	methionine adenosyltransferase activity
Contig102	hydroxymethyltransferase	92%	AAM64493	carries out interconversion of serine and glycine

Contig106	PGM (PHOSPHOGLYCERATE/BISPHOSPHOGLYCERATE MUTASE)	88%	PGM at locus AT1G78050	intramolecular transferase activity, phosphotransferases, catalytic activity,response to nitrate, metabolic process
Contig108	GAPC1(glyceraldehyde-3-phosphate dehydrogenase)	84%	GAPC1 at locus AT3G04120	glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity,glyceraldehyde-3-phosphate dehydrogenase activity
Contig110	FPS1(FARNESYL DIPHOSPHATE SYNTHASE 1(dimethylallyltranstransferase/ geranyltranstransferase ase)	77%	FPS1 at locus AT5G47770	geranyltranstransferase activity,dimethylallyltranstransferase activity
Contig112	SAM-2 (S-ADENOSYLMETHIONINE SYNTHETASE 2); copper ion binding / methionine adenosyltransferase	92%	SAM-2 at locus AT4G01850	copper ion binding, methionine adenosyltransferase activity
Contig114	ANNAT1 (Annexin Arabidopsis 1)	76%	ANNAT1 at locus AT1G35720	response to oxidative stress,response to cadmium ion, response to abscisic acid stimulus, response to osmotic stress
Contig117	AP1 (APETALA1)	71%	AP1 at locus AT1G69120	protein binding,transcription factor activity, protein heterodimerization activity, transcription activator activity, DNA binding,flower development, meristem structural organization, maintenance of floral meristem identity,positive regulation of transcription
Contig124	ATMS3 (methionine synthase 3)	88%	ATMS3 at locus AT5G20980	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity, methionine synthase activity
Contig128	ATFYPP3 (FLOWER-SPECIFIC, PHYTOCHROME-ASSOCIATED PROTEIN PHOSPHATASE 3)	88%	ATFYPP3 at locus AT3G19980	protein binding,protein serine/threonine kinase activity, protein serine/threonine phosphatase activity
Contig129	CYP71B38	88%	CYP71B38 at locus AT3G44250	electron carrier activity,monooxygenase activity, iron ion binding, oxygen binding, heme binding
Contig133	40S ribosomal protein S14	90%	AT3G52580	structural constituent of ribosome,involved in translation
Contig135	CLA1 (CLOROPLASTOS ALTERADOS 1)	72%	CLA1 at locus AT4G15560	1-deoxy-D-xylulose-5-phosphate synthase activity, chlorophyll biosynthetic process, response to light stimulus, isopentenyl diphosphate biosynthetic process, mevalonate-independent pathway
Contig136	APX1 (ascorbate peroxidase 1)	70%	APX1 at locus AT1G07890	L-ascorbate peroxidase activity; embryonic development ending in seed dormancy, response to reactive oxygen species, response to salt stress, response to heat
Contig138	sec34-like family protein	85%	AT1G73430	Intracellular protein transport
Contig141	lactate dehydrogenase	73%	BAE98384	lactate dehydrogenase
Contig145	histone H3.2	95%	AT4G40030	DNA binding, nucleosome assembly

Supplementary Data 3: PMID of modeled proteins as assigned by PMDB database

S.No	PROTEIN NAME	PMID
1.	(-)-limonene-7-hydroxylase	PM0076930
2.	(-)P450 limonene-3-hydroxylase	PM0076702
3.	(+)-pulegone reductase	PM0077020
4.	1-hydroxy-2-methyl-butenyl 4-diphosphate reductase	PM0076939
5.	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	PM0077125
6.	26S protease regulatory subunit 6A	PM0077022
7.	2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	PM0076998
8.	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	PM0076999

9.	2-oxoglutarate-dependent dioxygenase	PM0076890
10.	3-carene synthase	PM0076913
11.	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	PM0076951
12.	ACP preprotein	PM0077122
13.	acyl carrier protein	PM0077121
14.	alcohol dehydrogenase-like protein	PM0077002
15.	aldo/keto reductase AKR	PM0076694
16.	aldolase	PM0077069
17.	alkaline alpha galactosidase I	PM0077011
18.	allyl alcohol dehydrogenase	PM0076716
19.	annexin	PM0076730
20.	aromatic polyketide synthase	PM0077039
21.	At1g04290	PM0076682
22.	ATP synthase delta subunit 2	PM0076984
23.	AtSIP2	PM0077012
24.	auxin-induced atb2	PM0076695
25.	auxin-induced protein	PM0076957
26.	axial regulator YABBY2	PM0076889
27.	caffeic acid O-methyltransferase	PM0077015
28.	calcium-binding EF hand family protein	PM0076902
29.	calcium-binding protein annexin 7	PM0076732
30.	carbonyl reductase 1	PM0076908
31.	caryophyllene/alpha-humulene synthase	PM0076954
32.	CDP-glycerol:poly(glycerophosphate)glycerophosph	PM0076933
33.	chalcone isomerase	PM0077026
34.	chalcone isomerase	PM00770251
35.	chalcone synthase	PM0076975
36.	cinenol synthase	PM0076976
37.	CLA1 transketolase-like protein	PM0077055
38.	cobalamine-independent methionine synthase	PM0077016
39.	copalyl diphosphate synthase	PM0077006
40.	copper/zinc superoxide dismutase	PM0076663
41.	CYP71AT2v2	PM0076917
42.	CYP82C1p	PM0077076
43.	cytochrome b5 reductase	PM0076945
44.	cytochrome P450 reductase	PM0077050
45.	delta-12 oleic acid desaturase	PM0076960
46.	dihydroflavanol reductase 3	PM0076983
47.	dithiol-disulfide isomerase protein	PM0077165
48.	DSBA oxidoreductase family protein	PM0077164
49.	EDA36 (EMBRYO SAC DEVELOPMENT ARREST 37)	PM0077117
50.	Epoxide hydrolase	PM00771101
51.	epoxide hydrolase	PM0077109
52.	eukaryotic initiation factor 4A	PM0076691
53.	farnesyl diphosphate synthase	PM0076719
54.	ferric-chelate reductase (NADH)2	PM0077179
55.	flagellar associated protein	PM0077170
56.	flavonoid 8-O-methyltransferase	PM0077004
57.	flavonoid o-methyltransferase predicted protein	PM0076993
58.	fructose-bisphosphate aldolase	PM0077068
59.	GCPE protein	PM0077073
60.	GE20234	PM0077142
61.	geranyl-diphosphate synthase	PM0077078
62.	germacrene A oxidase	PM0076918
63.	germacrene C synthase	PM0076956
64.	germacrene D synthase	PM0076953
65.	GG11745	PM0076934
66.	GGR (geranylgeranyl reductase) farnesyltranstransferase	PM0077079
67.	glucose-6-phosphate dehydrogenase	PM0077105
68.	glyceraldehyde 3-phosphate dehydrogenase	PM0076897
69.	glyceraldehyde-3-phosphate dehydrogenase, cytosolic 3	PM0077130
70.	glyceraldehyde-3-phosphate-dehydrogenase	PM0077131
71.	heterotrophic ferredoxin 2	PM0076920
72.	heterotrophic ferredoxin 2	PM0076706

73.	hydrogen-transporting ATP synthase	PM0076985
74.	hydroxymethylbutenyl 4-diphosphate synthase	PM0077074
75.	isopiperitenol dehydrogenase	PM0076686
76.	isopiperitenone reductase	PM0076673
77.	ISPH protein	PM0076940
78.	leucine carboxyl methyltransferase	PM0077143
79.	limonene hydroxylase	PM0076704
80.	lipid transfer protein	PM0076659
81.	lipid transfer protein	PM0076681
82.	lipid transfer protein 2	PM0076660
83.	lipid transfer protein 2	PM0076680
84.	lipid transfer protein precursor	PM0076671
85.	MADS box protein	PM0077148
86.	MAT3 (methionine adenosyltransferase 3); copper ion binding / methionine adenosyltransferase	PM0076905
87.	membrane steroid-binding protein 1	PM0076894
88.	methionine synthase	PM0077018
89.	methionine synthase	PM0077161
90.	methionine synthase	PM0077162
91.	mitochondrial hinge protein	PM0077153
92.	MUB2 (MEMBRANE-ANCHORED UBIQUITIN-FOLD PROTEIN 2)	PM0077168
93.	NADH:cytochrome b5 reductase	PM0076944
94.	NADPH-ferrihemoprotein reductase	PM0077051
95.	non-photosynthetic ferredoxin	PM0076927
96.	non-photosynthetic ferredoxin	PM0076707
97.	nucleotide binding protein	PM0077033
98.	orcinol O-methyltransferase	PM0076963
99.	oxidoreductase, 2OG-Fe(II) oxygenase family protein	PM0076891
100.	perakine reductase	
101.	PGM (PHOSPHOGLYCERATE/BISPHOSPHOGLYCERATE MUTASE); catalytic/ intramolecular transferase, phosphotransferases	PM0077126
102.	pheophorbide A oxygenase	PM0077145
103.	Phosphoglucose isomerase (PGI)	PM0077177
104.	phytol kinase	PM0076943
105.	PKp3 (plastidial pyruvate kinase 3) pyruvate kinase	PM0076988
106.	PKP-BETA1 (PLASTIDIC PYRUVATE KINASE BETA SUBUNIT 1) pyruvat	PM0076989
107.	pollen allergen Pla o 3	PM0076899
108.	polyprotein	PM0077045
109.	pop3 peptide	PM0076677
110.	pop3 peptide	PM0076652
111.	pop3 peptide	PM0076676
112.	Psmd11a protein	PM0076885
113.	Pulegone reductase	PM0076609
114.	resveratrol O-methyltransferase(	PM0076965
115.	reticuline-7-O-methyltransferase	PM0076967
116.	retinol dehydrogenase 11	PM0077047
117.	sabinene synthase	PM0076977
118.	S-adenosyl-L-methionine synthase	PM0076904
119.	S-adenosyl-L-methionine synthetase	PM0076726
120.	S-adenosylmethionine synthase	PM0076597
121.	S-adenosylmethionine synthetase 1	PM0076729
122.	salutaridine reductase	PM0077160
123.	selinene synthase	PM0077156
124.	short-chain alcohol dehydrogenase	PM0076687
125.	Short-chain dehydrogenase/reductase SDR	PM0076880
126.	sophorol reductase	PM0077038
127.	squamosa protein	PM0077149
128.	stachyose synthase	PM0077009

129.	stress-responsive protein	PM0076651
130.	superoxide dismutase	PM0076664
131.	Tat binding protein like protein	PM0077021
132.	terpene synthase	PM0076982
133.	Terpene synthase-like Terpenoid synthase	PM0077005
134.	Terpene synthase-like Terpenoid synthase	PM0076966
135.	thioesterase superfamily member 2	PM0076683
136.	thioredoxin H1	PM0077029
137.	transducin family protein / WD-40 repeat family protein	PM0077032
138.	ubiquinol-cytochrome c reductase hinge protein	PM0077152
139.	ubiquitin-fusion protein	PM0077169
140.	vestitone reductase	PM0077037
141.	YABBY1 protein	PM0076658
142.	YNL241C	PM0077106
143.	Gamma-cadinene_synthase	PM0076874
144.	(E)-beta-farnesene_synthase	PM0076875
145.	Menthol dehydrogenase	PM0076879
146.	d-limonene synthase	PM0076901
147.	Vestitone reductase	PM0076973
148.	Chalcone_isomerase	PM0076971
149.	Sophorol reductase	PM0076974
150.	Chalcone synthase	PM0076975
151.	Cinenol synthase	PM0076976
152.	Sabinene synthase	PM0076977
153.	1-deoxyxylulose-5-phosphate_synthase	PM0076979
154.	GGR_geranylgeranyl_reductase_farnesyltranstransferase	PM0076981
155.	Flavonoid 8-O-methyltransferase	PM0077004
156.	Terpene synthase-like Terpenoid synthase	PM0077005
157	Limonene synthase	PM0077138
158	1,8_cineole_synthase_2	PM0077139
159	3-carene synthase	PM0077140

Supplementary Data 4: Result of TM Align

Sl. No	**SMP**	**ORGANISM**	**AMINO ACID MAKING CLASHES**	**RMSD**	**TM SCORE**
1	(E)-beta-farnesene synthase	*Mentha x piperita*	NO	0.97	0.4536
2	Isopiperitenone reductase	*Mentha x piperita*	NO	0.71	0.88314
3	Menthol dehydrogenase	*Mentha x piperita*	NO	0.66	0.8765
4	Pulegone reductase	*Mentha x piperita*	NO	1.70	0.79650
5	Geranyl diphosphate synthase	*Picrorhiza kurrooa*	NO	0.44	0.88314
6	Geranylgeranyl diphosphate synthase	*Jatropha curcas*	NO	1.64	0.9725
7	Geranylgeranyl pyrophosphate synthase	*Gentiana lutea*	NO	0.71	0.79650
8	Menthofuran synthase	*Mentha arvensis*	NO	0.69	0.97751
9	d-Limonene synthase	*Mentha longifolia*	NO	0.54	0.88314
10	3-Carene synthase	*Salvia stenophylla*	NO	0.59	0.87727
11	Monoterpene synthase	*Perilla citriodora*	NO	1.76	0.53839
12	Germacrene A oxidase	*Barnadesia spinosa*	NO	0.66	0.96550
13	Shikimate dehydrogenase	*Zea mays*	NO	1.23	0.95200
14	Germacrene D synthase	*Ocimum basilicum*	NO	0.39	0.97164
15	Caryophyllene/alpha-humulene synthase	*Solanum lycopersicum*	NO	0.39	0.99024
16	Germacrene C synthase	*Solanum lycopersicum*	NO	0.32	0.96575
17	Flavonoid 8-O-methyltransferase	*Mentha x piperita*	NO	1.48	0.91185
18	Orcinol O-methyltransferase	*Rosa hybrid cultivar*	NO	0.78	0.95570
19	Resveratrol O-methyltransferase	*Vitis vinifera*	NO	1.57	0.91214
20	Flavonoid 7-O-methyltransferase	*Mentha x piperita*	NO	1.34	0.94920

21	Terpene synthase-like; Terpenoid synthase	*Medicago truncatula*	NO	1.02	0.91496
22	Reticuline-7-O-methyltransferase	*Eschscholzia californica*	NO	1.53	0.90161
23	(+)-Pulegone reductase	*Mentha haplocalyx var. piperascens*	NO	0.75	0.393
24	Chalcone isomerase	*Gossypium hirsutum*	NO	0.45	0.97911
25	Cytochrome P450 hydroxylase	*Hyoscyamus muticus*	NO	0.50	0.89894
26	Perakine reductase	*Rauvolfia serpentina*	NO	0.64	0.92063
27	Vestitone reductase	*Medicago sativa*	NO	0.43	0.97716
28	Sophorol reductase	*Pisum sativum*	NO	0.40	0.95978
29	Chalcone synthase	*Nicotiana benthamiana*	NO	0.29	0.97365,
30	Cinenol synthase	*Rosmarinus officinalis*	NO	0.51	0.89238
31	Sabinene synthase	*Salvia pomifera*	NO	0.57	0.89116
32	Fenchol synthase	*Ocimum basilicum*	NO	0.43	0.89107
33	1-deoxyxylulose-5-phosphate synthase	*Mentha x piperita*	NO	0.62	0.79375
34	(S)-N-methylcoclaurine 3'-hydroxylase	*Eschscholzia californica*	NO	0.56	0.82676
35	Geranyl-diphosphate synthase	*Hevea brasiliensis*	NO	1.44	0.76661
36	GGR (geranylgeranyl reductase); farnesyltranstransferase	*Arabidopsis thaliana*	NO	0.80	0.80437
37	Resveratrol O-methyltransferase	*Vitis vinifera*	NO	1.36	0.90990
38	(-)P450 limonene-3-hydroxylase	*Mentha haplocalyx var. piperascens*	NO	0.59	0.90684

39	1,8 cineole synthase 2	*Salvia fruticosa*	NO	0.80	0.85757
40	Selinene synthase	*Ocimum basilicum*	NO	0.76	0.91787
41	Terpene synthase	*Cucumis melo*	NO	0.39	0.92970
42	Salutaridine reductase	*Papaver somniferum*	NO	0.61	0.84201

Supplementary Data 5: Result of Molecular Threading

Protein name	**Fold ID(given by Biosuite)**	**Score**	**Fold name**
dehydrin 13	1.1ACC- 2. 1EGUA 3. 1EPUA 4. 1I50A 5.1IN5A	1.6334.5 2. 6292 3.6279.5 4.6298.5 5.6578	5. DNA/RNA-binding 3-helical bundle
vascular specific protein 4	1.1BJT- 2.1EGUA 3.1IN5A 4.1QL0A 5.2BTVA	1.6852 2.6846 3.7014 4.6870 5.6836.5	3. DNA/RNA-binding 3-helical bundle
Acyl-Coenzyme A oxidase 1, palmitoyl	1.1HLRA 2.1JNRB 3.1KCQA 4.2A0B- 5.2BTVA	1.35694 2.31779.5 3.31486.5 4.35079.5 5.35309	1. CO dehydrogenase ISP C-domain like
FAD-dependent pyridine nucleotide-disulphide oxidoreductase; Calcium-binding EF-hand	1.1EGUA 2.1G8KA 3.1HLRA 4.1I50A 5.1JNRB	1.29933 2.31534 3.32683.5 4.36197 5.29360	4. beta and beta-prime subunits of DNA dependent RNA- polymerase
alternative NADH-dehydrogenase	1.1EGUA 2.1HLRA 3.1HWWA 4.1JK3A 5.1JNRB	1.20575.5 2.21773 3.21885 4.20070.5 5.20052.5	3..immunoglobulin/albumin-binding domain-like
Os07g0142300 [Oryza sativa (japonica cultivar-group)]	1.1G8KA 2.1HLRA 3.1I50A 4.2A0B- 5.2BDVA	1.11000.5 2.11003.5 3.10879.5 4.11006 5.10884	4.. Four-helical up-and-down bundle
Os07g0142500 [Oryza sativa (japonica cultivar-group)]	1.1EGUA 2.1G8KA 3.1HLRA 4.2A0B- 5.2BDVA	1.12071.5 2.12410 3.12456.5 4.12369 5.12237	1.. CO dehydrogenase ISP C-domain like
mCG145424	1.1AMUA 2.1BL2A 3.1G5AA 4.1G8KA 5.1I1QA	1.9048 2.9004.5 3.9030.5 4.9055.5 5.9027	1. Acetyl-CoA synthetase-like
KLHL23 protein	1.1DL2A 2.1G8KA 3.1G0IA 4.1HLRA 5.2BTVA	1.7015.5 2.6991.5 3.6991 4.7003 5.6991.5	2. ISP domain
lysine exporter protein	1.1CY9A	1.1.88867e+21	1. Prokaryotic type I DNA topoisomerase

[Octadecabacter	2.1G8KA 3.1HWWA 4.1I50A 5.2A0B-	2.15385.5 3.15595 4.15579.5 5.15316 4.28045 5.30741	

Supplementary Data 6: Comparison of properties of SMPs of *Mentha piperita* as predicted by ProtParam program

S.no	Protein	Molecular weight	-N*	+N*	Theoretical pI	Extinction coefficients **(M^{-1} cm$^{-)}$ ^{at} 260nm	Instability index	Aliphatic index	Grand average of hydropathicity (GRAVY)
1	(E)-beta-farnesene synthase	63855.6	85	67	5.27	94115-93740	32.70	83.20	-0.391
2	Flavonoid 4'-O-methyltransferase	37820.5	47	35	5.22	45170-44920	26.82	91.02	0.024
3	Isopiperitenone reductase	34395.7	40	39	6.39	28670- 28420	28.78	98.79	-0.047
4	Menthol dehydrogenase	34070.7	37	32	5.77	24785- 24410	39.89	90.35	-0.126
5	Pulegone reductase	37874.8	34	32	6.25	41175- 40800	31.71	95.67	0.023
6	Geranyl diphosphate synthase	40391.4	48	38	5.38	14940-14440	39.43	96.50	-0.076
7	Geranylgeranyl diphosphate synthase	40373.5	47	41	6.03	12420-11920	46.67	93.41	-0.064
8	Geranylgeranyl pyrophosphate synthase	23322.8	38	24	4.90	3105- 2980	36.35	104.81	-0.027
9	Menthofuran synthase	55769.4	59	64	9.02	46535-46410	49.53	96.32	-0.158
10	d-Limonene synthase	71422.8	93	67	5.07	105490-104740	51.07	85.07	-0.403
11	Cineole synthase	69613.4	85	75	5.93	103625- 103250	53.23	81.66	-0.440
12	Terpinolene synthase	69999.5	85	60	5.24	103180- 102680	55.51	89.47	-0.334
13	4S-Limonene synthase	69905.1	92	70	5.36	113135- 112760	51.52	82.35	-0.458
14	3-Carene synthase	69714.0	87	69	5.65	113260-112760	43.71	87.19	-0.468
15	Monoterpene synthase	34431.1	41	36	5.87	33265- 32890	48.02	83.10	-0.491
16	Germacrene A oxidase	55699.4	59	59	7.19	58245- 57870	49.49	99.68	-0.132
17	Shikimate dehydrogenase	54964.3	56	55	6.69	22850-22350	32.44	95.20	0.025
18	Germacrene D synthase	63395.0	82	68	5.46	87125- 86750	45.07	94.08	-0.272
19	Caryophyllene/alpha-humulene synthase	64321.0	82	64	5.42	87460-87210	37.72	80.42	-0.455
20	Germacrene C synthase	64037.8	79	65	5.63	86095-85720	36.18	84.87	-0.431
21	Flavonoid 8-O-methyltransferase	40848.8	54	36	5.07	38305- 37930	45.97	89.56	-0.052
22	Orcinol O-methyltransferase	38982.7	45	32	5.56	54555- 54430	28.89	90.80	-0.182
23	Resveratrol O-methyltransferase	40085.4	41	33	6.00	50670- 50420	34.20	97.56	-0.043
24	Flavonoid 7-O-methyltransferase	37895.6	47	38	5.33	35660-35410	38.34	88.98	-0.003
25	Terpene synthase-like; Terpenoid synthase	71391.3	80	74	6.32	121990-121240	42.59	84.29	-0.445
26	Isopiperitenol	27206.1	24	24	6.95	11835- 11460	26.15	97.25	0.326

	dehydrogenase								
27	Monoterpene synthase	84113.4	90	72	5.46	111560-110810	41.89	85.07	-0.141
28	Reticuline-7-O-methyltransferase	39505.6	50	37	5.46	37400- 36900	30.30	93.48	-0.082
29	(+)-Pulegone reductase	38359.3	37	32	5.77	41175- 40800	30.09	95.38	31
30	Chalcone isomerase	23376.7	34	22	4.86	19940- 19940	35.39	91.87	-0.153
31	Cytochrome P450 hydroxylase	56788.2	58	61	8.30	55265- 54890	33.58	95.12	-0.038
32	Perakine reductase	37159.7	45	39	5.91	31775- 31400	32.41	98.90	-0.178
33	Vestitone reductase	35918.2	45	37	5.31	30285- 29910	30.79	94.45	-0.035
34	Sophorol reductase	35696.1	37	40	8.34	28795- 28420	19.58	91.75	-0.005
35	Chalcone synthase	42663.3	45	42	6.28	34420- 33920	37.94	91.23	-0.070
36	Sabinene synthase	68132.1	82	57	5.08	117160- 116660	48.09	89.50	-0.360
37	Fenchol synthase	69865.4	81	62	5.52	111200-100345	47.33	87.29	-0.367
38	1-deoxyxylulose-5-phosphate synthase	77782.2	75	72	6.85	35340- 34840	38.26	90.03	-0.109
39	(S)-N-methylcoclaurine 3'-hydroxylase	63003.5	64	60	6.50	68215- 67840	38.62	92.23	-0.168
40	Geranyl diphosphate synthase small subunit	33465.3	36	28	5.84	17795- 17420	56.60	89.97	-0.020
41	GGR (geranylgeranyl reductase); farnesyltranstransferase	35188.5	38	31	5.74	22265- 21890	45.39	85.06	-0.034
42	(-)P450 limonene-3-hydroxylase	56383.4	60	60	7.12	85285- 84910	35.83	91.43	-0.135
43	1,8 cineole synthase 2	69013.4	84	66	5.60	109500- 108750	42.74	86.88	-0.387
44	Linalool synthase	70237.9	89	73	5.54	93210- 92710	43.14	88.29	-0.410
45	Gamma-cadinene synthase	83708.5	84	71	6.07	123520- 122270	29.27	78.77	-0.161
46	O-methyltransferase	40746.9	52	39	5.56	47690-47440	45.11	98.09	-0.139
47	Selinene synthase	63125.3	90	63	4.92	88615- 88240	41.89	81.56	-0.417
48	Terpene synthase	66633.4	85	63	5.35	84730- 84230	42.36	93.40	-0.273
49	Salutaridine reductase	34049.7	44	28	4.78	19410-18910	32.74	89.29	-0.093
50	Flavonoid 3'-O-methyltransferase	40263.3	47	43	6.37	28920- 28420	41.37	90.08	-0.103
51	Dihydroflavanol reductase 3	37745.7	43	40	6.33	41410- 40910	37.42	80.98	-0.187

*- N: Total number of negative residues; + Total number of positive residues
**: First value is based on the assumption both cysteine from cystines and the second assumes that both cysteine residues are reduced.
Same conditions apply for Table 8.

Supplementary Data 7: Comparison of properties of SMP of *Mentha arvensis* as predicted by Protparam program

S.no	**Protein**	**Molecular weight**	**-N***	**+N***	**Theoretical pI**	**Extinction coefficients **(M^{-1} cm$^{-)}$ ^{at} 260nm**	**Instability index**	**Aliphatic index**	**Grand average of hydropathicity (GRAVY)**
1	stress-associated protein 1	9889.4	12	20	9.44	4470-4845	24.66	62.76	-0.741

2	stress-associated protein 10	17600.0	20	28	9.34	This protein does not contain any Trp residues. Experience shows that this could result in more than 10% error in the computed extinction coefficient	71.80	63.38	-0.677

Supplementary Data 8: Predicted secondary and super secondary structures for SMPs of *M. piperita* by Promotif.

S.No	Protein	Alpha Helix	β-sheets	β Bulge	β Turns	Gamma Turns	β Hairpins	3-10 Helix	β -α – β Motif
1.	Geranyl diphosphate synthase small subunit	16	0	0	17	1	0	3	0
2.	(-)P450 limonene-3-hydroxylase	22	3	1	41	7	3	10	0
3.	(+)-pulegone reductase	14	3	5	29	4	3	12	5
4.	Isopiperitenone dehydrogenase	13	2	0	21	3	0	17	5
5.	Isopiperitenone reductase	11	1	0	25	5	0	0	0
6.	Menthofuran synthase	22	3	1	47	5	3	11	0
7.	Menthol dehydrogenase	12	1	0	27	2	1	2	5
8.	4S Limonene synthase	32	0	0	43	14	0	25	0
9.	Flavonoid 4'-O-methyltransferase	1	0	0	3	6	0	0	0
10.	Flavonoid 7 '-O-methyltransferase	17	3	0	28	23	0	7	4
11	Flavonoid 8 '-O-methyltransferase	19	3	0	22	9	2	3	4
12	Flavonoid 3 '-O-methyltransferase	21	3	0	20	6	0	2	2
13	Pulegone reductase	16	3	4	26	3	3	11	5
14.	Geranylgeranyl diphosphate synthase	17	1	0	24	4	1	3	0
15.	Geranylgeranyl pyrophosphate synthase	15	1	0	9	1	1	5	0
16.	Terpinolene synthase	31	0	0	26	10	0	35	0
17	Monoterpene synthase	24	0	0	21	11	0	19	0
18	Limonene hydroxylase	21	3	1	43	4	3	6	0
19	Shikimate dehydrogenase	12	2	0	52	9	1	0	4
20	Germacrene D synthase	32	0	0	25	12	0	34	0
21	Caryophyllene/alpha-humulene synthase	32	0	0	27	11	0	36	0
22	Orcinol O-methyltransferase	21	3	1	19	1	1	9	4
23	Resveratrol O-methyltransferase	20	3	2	29	2	2	9	4
24	Reticuline-7-O-methyltransferase	20	3	0	31	3	2	7	4
25	Chalcone isomerase	9	3	4	14	0	7	5	0
26	Cytochrome P450 hydroxylase	23	4	1	51	1	3	16	0
27	Perakine reductase	16	3	2	26	4	2	22	5
28	Vestitone reductase	16	3	0	21	6	0	8	4
29	Sophorol reductase	16	3	0	21	5	0	10	4
30	Cinenol synthase	30	0	0	39	10	0	27	0
31	Sabinene synthase	33	0	0	40	12	0	27	0
32	Fenchol synthase	32	0	0	17	6	0	24	0
33	(S)-N-methylcoclaurine 3'-hydroxylas	23	4	1	65	5	4	7	0
34	GGR (geranylgeranyl reductase)	14	1	0	20	4	1	0	0
35	Dihydroflavanol reductase 3	16	3	1	26	4	0	5	4

36	1-deoxyxylulose-5-phosphate synthase	33	3	3	53	16	0	16	8
37	Gamma cadinene synthase	29	0	0	25	12	0	16	0
38	O-methyltransferase	19	2	1	100	29	2	5	3
39	Terpene synthase-like Terpenoid synthase	34	0	0	45	13	0	28	0
40	(E)-beta-farnesene synthase	31	0	0	23	5	0	22	0
41	Terpene synthase	31	0	0	27	9	0	37	0
42	Chalcone synthase	18	4	4	29	2	4	14	2
43	Salutaridine reductase	13	1	0	22	4	1	2	5
44	d-Limonene synthase	29	0	0	28	7	0	22	0
45	Selinene synthase	18	4	4	29	2	4	0	2
46	Geranyl-diphosphate synthase	13	0	0	22	5	0	0	0
47	Germacrene A oxidase	24	4	1	53	8	2	17	0
48	Germacrene C synthase	33	0	0	26	10	0	35	0
49	1-8 cineole synthase2	31	0	0	36	6	0	22	0
50	Linalool synthase	24	0	0	24	50	0	14	0
51	3-Carene synthase	18	1	0	19	4	0	12	0