

Seq File S1: Full length amino acid sequence details for the genes and gene families used in this study for *in silico* analysis.

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>SiFabD1 Malonyltransferase [Sesamum indicum] XP_011080770
MHALVLHHNHRLLPLYLVRFNLPSSAKSSSLSRAMSSSVLPSISLTKPALGSSESFRSSTCLGFKNEIRRV
RLGLGKSRVFMVAVGSEAVVDDALFKDYKPSSAFLFPGQGAQAVGMGVEAQKVPAAAELYKRANDILGF
DLLDICINGPKEKLDSTVLSQPAIYVTS�AAVEVLRARDGGQIIIDSVDVTCGLSLGEY TALAFAGAFSFE
DGLKLVKLRGEAMQDAADAASAMVSIIGLDSAKVQQLCDAANEEVDEANKVQIANFLCPGNYAVSGGLKG
IEAVEAKAKSFKARMTVRLAVAGAFHTGFM EPAVSRL EAA LASTVIRSPRIPVISNVDAEPHADPNTIKKI
LARQVTSVPVQWETT VKTLLNRGLKKS YELGPGKVIAGIVKRM DKGADIENICA
>SiSAD6 Palmitoyl-ACP Δ9 desaturase (PAD) [Sesamum indicum] XP_011100275.1
MKTLLFSTTIIPLACGGATTFRRPQSISAISKQPVSTLHQRRITHMPPEKLEVFKSLESWASDYVLP LL
KPVNKCWQPSDFLPDPTQPTDDFMDEVRLRERTMGLPDEYFVVVLVGDMITEEALPTYQSTINACDGIRD
ESGASRSPWATWLRSWTAEENRHGDLLRTYLYLSGRVDMSMIEKTIHQ LIGAGMDVGW DNNPYLTFVYTS
FQERATFIAHGNTARLAKEGGDPVLARICGTIAADEKRHEHAYVRIKKLLEIDPNETMLAISKMMRKRV
IMP SHLMCDGRDPHLFQH FSSVTERIGVYTAIDYIEILEFLIEEWNLEKLEGLKGDGRHAQEHVCDIPT R
MRKVLEQAVERVGKMEAKGQNF SWIFNREVTM
>SiSAD7 Palmitoyl-ACP Δ9 desaturase (PAD) [Sesamum indicum] XP_011100276.1
MEILAFSNIIPATALASMP CGGATTFRRPKPISAAANAKQPPSRSRHQKLTHQMPPEKVEVFKSLESWAS
RFVLPLVKPVDKWCQPS EFLPNPAKPADDFMDEVKALRDRTIGLPDEYFVVVLVGDMITEEALPTYQSMIN
TCDGVREESGASPCQWAAWVRSWAAEENRHGDLLRTYLYLSGRVDM LMVERTTQH LIRAGADIGLDNNPY
LTFVYTSFQERATFVSHGNTARLAKKAGDPILASICGTIATDEKRHENAYVRIVEKLL EVDPNDTMLAIG
NMMRKRITMPGHL MCDGQDPILFQHFSVVAEQIGVYTID DYEILEFLIGRWRLEKLDGLKGDGRREQEY
VC SLPTRMRKLQEQAVERGRKMEPHEQKFSWIFNREVTIQV
>SiLPAAT1 1-acyl-sn-glycerol-3-phosphate acyltransferase 1 [Sesamum indicum] XP_011084281.2
MAASIARSILT VRSTGATASLLLHRRFFSSTVSKPPSLPGLARLRISTRSVTPALSHAVRFSSSTRINQ
VRCRVNRSGSAYSPLNSESNFSDLPPT EMAPLFPGCDYERWLVLMDKPGGEGATKQQMIDCYIQT LAKVV
GSEEEAKKRIYNVSSEMYFGFVCEIDEETSNNLEGLPGVLCVLPDSYVDPENKDCGGIQEQRH LIGLSSR
PLASHDGFHLGCFPHKHPIQRKSKYGLPHETVFGSRTHQYPTLGSSNHKGEFCGT FNGSGSCRRGKFSRD
VVVRSELT SAGSTGASYPLLEIWLNSKVRGICFYAVTACAAIILFVPM LLEHPFVLMFDRYRRQAHYLV A
KTWAFLT VAPFVKIEYEGLENLPPTNTPAVYVANHQSF LDIYTLTLGRSFKFISKTSIFLYPIIGWAMF
LLGVIPLKRMDSRSQ LDC LKQCMALIKKGASVFFFPEGTRSKDGKLGPFKKGAFSVA AKTGVPVIPITLI
GTGEIMPAGMEGR LNP GS VKV IHP SLVGNKPDALCNEARNIIAQDLIHQS
>SiLPAATB B-class lysophosphatidate acyltransferase [Sesamum indicum] XP_020554192.1
METSGLGGLRNRRFGSYFDASTGPNTEPPPRAMVDGQQKRAGGHEYYTDDDDTGWF PVLISWVRIVVCF
VSMMLTTFIWGVIMVLLPWPYQRIRQGN IYGHVTGKMLMWILGNPITI QGAEYSNERAIYISNHASPID
IFLIMWLTPTGT VGI AKKEIIFYPLFGQLYVLANHLRIDRSNP KAAIESMKEAADAVVRNNLSLIIFPEG
TRSKNGRLLPFKKG FVHLALQTRRPVPIILTGT HRAWRKGS LHVRPAPLTVRYLPPIRTDDWTPDKVED
YVKLVHDVYAKNLP HSQRPTPPALSENGGSCRTVAS
>SiaccB1 Biotin carboxyl carrier protein of acetyl-CoA carboxylase 1 [Sesamum indicum] XP_011077154.1
MATTFGAAATAASLTGNANKSSTYLPLASRHFFLRANSNKVSFRLTPRPKLRLFSKGLQSGWKCSAMVKA
QLNDVATDGSSKAEASTPATSEVSPAKSKDTPIALASEESIS EFITQVASLVKLVD AKDIVELELKQLDC
EVLIRKKEALAAPPPVAYVQSQPQPAVLPPVSTPSPAPTAAPT PPPAPALSPPKAQPAKSSHPPLKSPM
AGTFYRSPAPGEPFVKVGDKVQKGQVLCIIEAMKLMNEIEADQSGKIVEILLEDGKPVSVDTPLFVIEP
>SiaccB-2 Biotin carboxyl carrier protein of acetyl-CoA carboxylase 2 [Sesamum indicum] XP_011072841.1
MASFSVPCPKVSPTLVASSQSTQKLQPIASFPRSDRSNRALATVAQFQGC SRRQSDVFKVCAQLNQVA
VEKISNATPALETVP MNKSENQHEIPDESSILTFMTQVKDLVKLVDSKDIAEELKQMDCELIIRKKEAL
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SQPSIAAHYSTPPPTHQALLPPQLPPASAPAPASLPSAPASVSPPAPSKPKSSHPPFKCPMAGNFYRSPA
PGAPPFVKVGDKVQKGQVICIIEAMKLMNEIEADQSGTVVEILVDDGKPVSVDMPLFIIEP
>SiaccC Biotin carboxylase 2 [*Sesamum indicum*] XP_011070473.1
MDSATMNFCSKSVCSPPGLFMGRITGIRSSQCSFMAGSRVNFPRQRVQASRVGHKSGKRGGALAATCRDD
KILVANRGEIAVRVIRTAHEMGIPCAVAVYSTIDKDALHVKLADESVCIGEAPSNQSYLVIIPNVLSAAISR
GCTMLHPGYGFLSENAVVFVEMCREHGINFIGNPESIRIMGDKSTARDTMKNAGVPTVPGSDGLLKSTEE
AVRLADEIGYPVMIKATAGGGGRGMLAKEPDEFVKLLQQAkteAAAAFGNDGVYLEKFIQNPRHIEFQV
LADKYGNVVHFGERDCSIQRRNQKLEEEASPALTPELKRKAMGDAVAAAAASIGYIGVGTIEFLLDERGS
FYFMEMNTRIQVEHPVTEMISSVDLIEEQIRVARGEKLRYTQEDIVLRGHSIECRINAEDAFKNFRPGPG
RITAYLPAGGPFVRMDSHVYPDYVPPSYDSLLGKLIVWGPTRERAIERMKRALNDTIITGVPTTIDYHK
LILDIEDFKNGKVDATAFIPKHEEELAAPQPTQPATTQKQLISTSA

>SiaccA-1 Acetyl-coenzyme A carboxylase carboxyl transferase subunit
alpha [*Sesamum indicum*] XP_011077598.1
MSSMTQTPASFTGNLAPKPTASDLLRSSNGVSGVPLKALGRAQLGARMNFSITARVRKVKKHEYPWPE
DPDLNVKGGVLSHLSPFKPLKEKPKPVTLDFEKPLMDLQKKIIDVQKMANETGLDFSDQIISLENKYQQA
LKDLYTHLTPIQVRNIARHPNRPTFLDHVFNITEKFVELHGDRAgyDDPAVVTGLGTINGRSYMFMGHQK
GRNTKENIKRNFgmptPHGYRKALRMMYYADHHGFPIITFIDTPGAYADLKSEELGQGEAIAQNLRMTMG
LKVPIVSIVMGEGSGGALAIGCANKLLMLENAVFIYASPEACAAILWKSASPKAAEKLKITAKELTK
LQIADGIIPEPLGGAHADPYWTSQQIKTAILESMDLVKMDTETLLKHRAQKFRKLGGFQEGVPIDPKRK
VNMKKKDKSIVPISKtSESELrDEVEKLKTQILEASKSSVEHPGTGLKEMMEKLKREIDYEYDEAAKALG
MQDKILMLREEVAKARNHNDQLAHPALKEKIDHLKDEFDKNLPSAPNYPNLKYKLGMLKELSKASNLTKK
STTRDELKLEINKRFSEFMDRPDVQKQIETLKAIEASSGVSNIIDSKPELKEKVSQMSGELESEFKAVLNS
MGLQVVPDSEALAKINAFDEEVNMTIDDLVNSSYLKERIELLKTEVEKAGSRPDEDSKSKIQVLQAEIK
QAITEAISFPPELKEKYERLAAEILETTKPSVGSNGSSGDENTEDSQVNVNLEANRSFV

>SiaccA-2 Acetyl-coenzyme A carboxylase carboxyl transferase subunit
alpha [*Sesamum indicum*] XP_020551382.1
MTTSLISGNCGRGRGEDTGSGYGLTSHFANEFLSSDTNGRLFRNFNGIRLKDLEGLRKRNGNGFRVFAR
VRKGKKHDYPWPDDINPNSKAPLTYLSYFKPLKEKPKPVTLAFEKPLVDLEQKIIIEVQRMADDTGLDFTD
QINALELKYQQALKDLYTHLTPIQRLNIARHPNRPTVLDHILNITEKWVELHGDRAgyDDPAIVTGIGSM
EGRSYMFIGHQKGRNTKENIMRNFAMPTPHGYRKALRMMKYADHHGFPIVTFVDTPGAFADLKSEELGQG
EAIAHNLramfGLRPVITIVTGEggSGGALAIACANKLLMLENSAFIYASPEACAAILWKSskaAPKAA
EKLKITAQEHYKRRIADGIIPEPLGGAHADPVWTSLQIKDAILRQMEELTRMNAEELIRHRMLKFRMIGV
GAYREGSEVEPVRKRNMRASEVNAPKFADIESALDDLKILKAKGPSDPITYKKIEKLEEDLDQEMTKA
FISMGLIDQIKSLNLELARSNPNDQASNRRLKEKADKIVQEFKRNLSQPGAYIGLKQKLQMLNMVSRLL
LKESEKLSELNQLSADIKAKMETWKLAREKSSSTGDPDENLAREVEVAKEELDQVLRSANLHVGGTT
KKENINPLPELREEMLNINRAIKQEIKKVIDEKGLSWKINELKAEAVKDSSEKAKKLEAELKEVIAAAL
SASPLKDRLDNLRVQHESVNVKVVEGNVGTDNGRW

>SiaccA-3 Acetyl-coenzyme A carboxylase carboxyl transferase subunit
alpha [*Sesamum indicum*] XP_011094964.1
MASVAQSPVSFTGNLASKSTASDLLKSSINGACGLPLRALGKAQLGAKRRDFAISARVRKVKKHDYPWPE
DPDPNVKGGVLTSLSPFKPLKEKQKPVTLDFEKPLMDLQKKIIDVQKMANETGLDFSDQIISLENKYQKA
LKDLYTHLTPIQVRNIARHPNRPTFLDHIFNITEKFVELHGDRAgyDDPAVVTGLGTINGRSYMFMGHQK
GRNTKENIKRNFgmptPHGYRKALRMMYYADHHGFPIVTFIDTPGAYADVKSEELGQGEAIAHNLRTMG
LKVPIVSIVIGEGSGGALAIGCANKLLMLENAVFIYASPEACAAILWKSASPKAAEKLKITATELTK
LQIADGVIPEPLGGAHADPYWTSQQIKTAIVESMDLVKMDTETLLKHRAQKFRKLGGFQEGIPIDPKRK
VNMKKKEQPLVPISKtSEVELRNEVERVKQQILEASKSSSTGAPATRLKEVIEKLKRELDYEYDEAAKALG
MDGKILMMREEIAKARNVNDQLAHPALKEKIEQLKDEFDKNLPTAPNYSSLKSKLNMLKALSKALNLRKK
STPKDELKIEINKRFNELVDRPDVKQIETLKAIEVNSGVSGIGANPELKEKVQKLSRELDSEFMDVLKS
FGLQVVPsAPAAmVKIDAFEEGVSMIIDDfVNSSDLKDKIETLKAIEVGKAGNTPDGDSKSKIQALETEIK
QAIIIEGISSPELKEKHERLATEVLEATKSSVESTTDDQSKLDESrvNVNSLEANRSFI

>SiaccD Acetyl-CoA carboxylase beta subunit [*Sesamum indicum*]
YP_004935675.1
MTIHLLYFDANRGQENSMERWWFNSMVFKKELERRYGIKKSTDNLGPTSESEDpNRKGRakNIHswRGRD
NSSYSNVdHLFGVKDIRNFSSDDTFLVRDSNGDYYSIYDFDfENHIFEIDNDHSFLSELESSFSYRNSSS
MNNGSSSEDSLYNRYMYDTQSSWNNHITSCVDSYLSQSIIDTSIVSDSSDSYISRCVFDKRTSSesGR

SSIETHAKSSDLTLGERSNDLDATQNYRDLWVQCENCYGLNYKKFLKSKMNICEQCGYHLKMSSSERIEV
SIDPGTWDPMDEDMVSLDPIEFHSEEEPKDRIDSYQSKTGLTEAVQTGVGQLNGIPVAIAVMDFEFMGG
SMGSVVGEKITRLIEYATNQFLPLIIVCASGGARMQEGSLSLMQMAKISSALYDYQSNKKLFYVSILTSP
TTGGVTASFGLGDI IIAEPNSYIAFAGKRVEQTLNKTVPEGLQAAEYLFEGKGLFDLIVPRNLLKSVLS
ELFNLHAFFPLNSNSSRAH

>SiFabH-1 3-oxoacyl-[acyl-carrier-protein] synthase 3 [*Sesamum indicum*]
XP_011069912.1

MANASGLLSPAVAPSVRRRLNPPIGVFQSGSWFSEGVSRRIVCSSTVQGAEKLSPSKSGVPRLVSRGCKLV
GCGSAVPRQLQISNDDLKIVDTSDEWISVRTGIRNRRILSGKDSLTDLAAEAAKKALQMAEVDPPDDVLDVL
LCTSTPEDLFGSAPQIQKALGCKNNPLAYDITAACSGFILGLVSASCIIRGGGFNNVLVIGADALSRYVDW
TDRGSCILFGDAAGAVLVQACDSEEDGLFAFDLHSDGEGQRHLRATMNENEKDHGTLGTNGSLLGLLPKGSS
YSCIQMNGKEVFRFAVRVVPQSIELALEKAGLPGSSIDWLLLHQANQRIIDAVAARLELPSERVISNLANY
GNTSAASIPLALDEAVRKGKVKAGHKIATAGFGAGLTWGSAILRWG

>SiFabH-2 3-oxoacyl-[acyl-carrier-protein] synthase 3 [*Sesamum indicum*]
XP_011079297

MANASGLFTPTVPTVRRRFSPPLGIYRSGFWFSDGVSRRIVCSSTVQGAEKLSPSGSRVPRLAGKGCKLVG
CGSAVPTVQISNDDLKIVDTSDEWISVRTGIRNRRILSRKDSLIDLAAEAAKKALQMAEVDPPDDVLDVLL
CTSTPEDLFGSAPQIQKALGCKNNPLAYDITAACSGFILGLVSAACHIRGGGFNNVLVIGADALSRYVDWT
DRGSCILFGDAAGAVLVQACNSEEDGLFAFDMHSDGEGQRHLKAGIKENETDKEPGTNGSLVGLLPKGSAY
SCIQMNGKEVFRFAVRVVPQSIESALEKAGLTGSSIDWLLLHQANQRIIDAVATRLDVPYERVISNLANYG
NTSAASIPLALDEAVRSGKVQAGHTIATAGFGAGLTWGSAILRWG

>SiFabB-1 3-oxoacyl-[acyl-carrier-protein] synthase I [*Sesamum indicum*]
XP_011085258.1

MQSLHSTSLRPSPLDRLRRPRRSTIFPGNNAKPPPQRLPFKVSSSAVTAAPKRETDPKKRVVITGMGLVSV
FGNDVDVYYEKLKSGESGITLIDRFDASKFPTFRGGQIRGFKAEGYIDGKNDRRLDDCLRYCIVAGKKALE
GADLGDKDLKIDKIRAGVLIGTGMGGLTVFSDGVQALIEKGHRKITPFFIPYAITNMASALLAIDLGFMG
PNYSISTACATSNYCFYAAANHIRRGEADLMIAGGTEAAIIPIGLGGFVACRALSQRNDDPQTASRPWDKD
RDGFVMGEGAGVLVLESLEHAMKRGAPIIAEYLGAVNCDAYHMTDPRSDGLGVSSCIQSALEDAGVSP
VNYINAHATSTIVGDLAEVNAIKKVFKNTSEIKINATKSMIGHCLGAAGGLEAIATVKAITTGWLHPTINQ
FSAEPSVEFDTVANKKQHEVNVAISNSFGFGGHNSVVAFAFAFKP

>SiFabB-2 3-oxoacyl-[acyl-carrier-protein] synthase I [*Sesamum indicum*]
XP_011096538.1

MQALQSAALRPSPLDPLRKPYPTSLPSNNAKPPVKRLPFTISASASTVSSPKRETDPKKRVVITGMGLVS
VFGNDVDAYYEKLKLAGESGITPIDRFDASKFPTFRGGQIRGFKSEGYIDGKNDRRLDDCLRYCIVAGKKAL
EDADLGGDRLGKIDKIRAGVLVGTGMGGLTVFSDGVQALIEKGYRKITPFFIPYAITNMGSALLAIDLGLM
GPNYSISTACATSNYCFYAAANHIRRGEADLMIAGGTEAAIIPIGLGGFVACRALSQRNDDPKTASRPWDK
DRDGFVMGEGAGVLVMELEHAMKRDAPIIAEYLGAVNCDAYHMTDPRADGLGVSSCIQSALEDAGVSPE
EVNYINAHATSTVVGDLAEVNAIKKVFKNTSGIKINATKSMIGHCLGAAGGLEAIATVKAITTGWLHPTIN
QFNPEPSVEFDTVANKKQHEVNVAISNSFGFGGHNSVVAFAFAFKP

>SiFabB-3 3-oxoacyl-[acyl-carrier-protein] synthase I [*Sesamum indicum*]
XP_011082304.1

MAAIIASASSSGLILEKSGKSSARNGVSMFQYNGLRVETMHVGSTGIRTTGFISTSSKWGRKAMASPTVS
APKRETDPKKRIVITGMGLVSVFGSDVDTFYKNLLDGVSGITPIDRFDASEYSVRFSGQIRDFTSKGYIDG
KSDRRLLDDVWRYCLVSGKRALDDASLSKDVLKMDKTRIGVLVSGMGGISAFSNGVEALVLKGYKKITPF
FIPYSITNMGSALLAIDTGLMGPNYSISTACATANYCFFAAANHIRRGDADIMVAGGAESAITPAGVGGFI
ACRALSSRNNDNPQEASRPWDKNRDGFVIGEGAGVLIMESLEHAVKRGANIIAEYLGAVTCDAAHMTDPRK
DGLGVSSCIKSLQDAGVAPEEVNYVNAHATSTLAGDLAEVNAIKKVFKDTSEIKMNGTKSMIGHGLGAAG
GLEAIATIKAITTGWLHPTINQYELEPEVTIDTPVNVKKQHEVNVAISNSFGFGGHNSVVVFAPFKP

>SiFabF-1 3-oxoacyl-[acyl-carrier-protein] synthase II, [*Sesamum indicum*]
XP_011093876.1

MAASSVVCSWLMAACMSVACEKDSSISMLSTPSSNSSRISKWAARRRKRALAKCAPQLSGTRNLMTSCLAF
EPCDRFYESSDASEFFFFGFSRNALLHRRRRKFQRPRTARSGEAMAIAVHPAMEVTPKKKPSTKQRRVVVTG
MGVETPLGHDPDTFYNNLLEGVSGISEIEAFDCSQYPTRIAGEIKSFSTDGWVAPKLSKRMDRFMLYMLTA

GKKALADAGITEDVMDLNNKARCGVLIGSAMGGMKVFNDIAEALRISYRKMNPFCVPPFATTNMGSAAMLAMD
LGWMGPNYSISTACATSNFCILNAAHIIIRGEADMMLCGGSDAVIIPIGLGGFVACRALSQNRNTDPTKASR
PWDSSRDGFVMGEGAGVLLLEELEHAKKRGATIYAEFLGGSFTCDAYHMTPEHPPEGTGVILCIEKALAQSG
VSKEDVNYINAHATSTPAGDLKEYKALIHCFGENPELRVNSTKSMIGHLLGAAGAVEAVATVQAIRTGWIH
PNINLENPDDGVDTNVLVGPTKERLAIKVALSNSFGFGGHNS
ILFAPFQ

>SiFabF-2 3-oxoacyl-[acyl-carrier-protein] synthase II [*Sesamum indicum*]
XP_011078136.1

MAATSVVCSWLMAACMSVAYEKESSVSMLSSTSLCRLSKWAARRRKRVLAKCAPDFSSSFSSLASSCFAFEP
CDDFYKSSHASSGCLFGFASRNPLLLRRRRKLLRSSPHCGEIMATAVSPAMEVTPKQKPPTPQRRVVVTGM
GVETPLGHDPDVFYNNLLQGVSGISEIEAFDCSQYPTRIAGEIKSFSADGWVAPKFSKRMDRFLMYLMTAG
KKALADGGITEDVMEELNKAACMSVAYEKESSVSMLSSTSLCRLSKWAARRRKRVLAKCAPDFSSSFSSLASSCFAFEP
GWMGPNYSISTACATSNFCILNAAHIIIRGEADMMLCGGSDAAIIPIGLGGFIACGALSQRNADPTKASRP
WDTNRDGFVMGEGAGVLLLEELEHAKKRGATIYAEFLGGSFTCDAYHMTPEHPPEGTGVILCIEKALSQSGV
SKEDVNYINAHATSTLSGDLKEYQALIHCFGQNPPELRVNSTKSMIGHLLGAAGAVEAVATVQAIRTGWIHP
NVNLENPDDGVNTNLLVGPTKERLDIKVALSNTFGFGGHNSILFAPYK

>SiFabF-3 3-oxoacyl-[acyl-carrier-protein] synthase II [*Sesamum indicum*]
XP_011072620.1

MVVASSVASPLCTWLVAACMTAPSEKGTFCCKPSEFIKCPKLSRSARRKSMVAQKSGSLVSSLYGCGINSL
MSFCFPFEEYNSQGLSPCFALFGENGFSLLFGSKTLPNMRKQRRNLQASNSGKTMVVGQPEKQVSMK
KKLVTKRRRVVTGLGVVSPLGHDAADVFGNLLLEGISGVSQIEAFDCTEFPTRIAGEIKNFSPDGWSVKL
SKRADKFMLYLLTAGKKALADGGITDDVMAELDKTRCGIIIGSALGGMKVFSDAIEALRISHKKMNPFCIP
FATSNMGSAVLALDLGWMGPNYSISAACATSNFCILDAANHIIIRGETDMMLCGGSDAAIIPIGLGGFAACQ
ALSQRNDEPTKASRPWDVHCDGFVMGEGAAVLLLEELEHAKKRGATIYAEFLGGSSTCDAYHTTEPHPDGR
GIVLCIEKALAESGVAREDINYINAHATSTPLADLIECQAINHCFGQNTLRMNSTKSMIGHLLGAAGAVE
AVATVKAIQTGWIHPNVNLERPDDEVDANILVGCKRERLDVKVALSNSLGFGGHNSIVFAAYKDCKATA

>SiKASmt 3-oxoacyl-[acyl-carrier-protein] synthase mitochondrial
[*Sesamum indicum*] XP_011077001.1

MAMARRYSNRLVSSIIQFTRFYSSGPFDPFPLPRRVVVTGLGMVTPLCGGEVETWKRLIEGECGIRAVT
IEDLKMNGFDRETQLHTFDQLTSKVAGIVPCGANPGEFNEELWLNKSKDHKSTARFISYALCAADEALRDAN
YMPTTQDEKERTGVSIGAGTGSISDILDASKMICEKKLRLSPFFIPRILINMASGHVSMKYGFQGNHAA
VTACATGAHSIGDAARMIQFGDQVDMVAGGTEASIDALSIAFGCRSRALTTKYNAVPEEASRPDCARDGF
VIGEGSGILVLEELEHAKKRGAKVYAEVRGYGMSGDAYHITQPHADGRGAVLAMTRALKQSGNLNPNQVDYV
NAHATSTPLGDAVEAKAIQSLFSDHAASGALAFSSTKGAIGHLLGAAGAVEALFSILAIHHGIAPLTLNLS
KPDVPVFSGNFMPLSASKKMTIKAALSNSFGFGGTNSSLFASID

>SiSAD1 Acyl-[acyl-carrier-protein] desaturase [*Sesamum indicum*]
NP_001291335.1

MALKLNAINFQSPKCPSPFALPPVASVRSKPFVASTLRSGSKEVETVKRPFNPPREVHVQVTHSMPPQKI
EIFKALEDWADNNILVHLKPVEKWCQPPQDFLPDPSSDGFDDQVKELRERAKEIPDDYFVVLVGDMITEEA
LPTYQTMLNTLDGVRDETGAISPTSWAIWTRAWTAENRHGDLNLYLYLSGRVDMRPNGKTFRYLIGSGM
DPRTEENPYLGFYIYTSFQERATFISHGNTARLAREHGDLLKLAQICGTIAADEKRHETAYTKIVEKLFEID
PNDTVLAFADMMRKKISMPAHLMYDGRDDNLFDFHSSVAQRLGVYTAADYADILEHLVARWKVANLTGLS
ADGQKAQDYVCGLPPIRRLEERAQGRAKQAPKIPFSWVHDREVQL

>SiSAD2 Stearoyl-[acyl-carrier-protein] 9-desaturase [*Sesamum indicum*]
XP_011091536.1

MALKLNASNQYQPKCASFPALPPVATIRSPKFFMASTLRSGSKEVDTVKKPFSPPREVHVQVTHSMPPQKI
EIFKAMEDWAENNILVHLKPVEKWCQPPQDFLPDPASDGFYDQVKELRERAREIPDDYFVVLVGDMITEEA
LPTYQTMLNTLDGVRDETGAISPTSWAIWTRAWTAENRHGDLNLYLYLSGRVDMKQIEKTIQYLIGSGM
DPRTEENPYLGFYIYTSFQERATFISHGNTARLAREHGDLLKLAQICGTIASDEKRHETAYTKIVEKLFEID
PDGTVLAFADMMRKKISMPAHLMYDGHDDNLFDFHSSVAQRLGVYTARDYADILEHLVGRWKVENLTGLS
AEGQKAQDYVCGLPPIRRLEERAQGRARAKEVPRIPFSWIYDREVQL

>SiSAD3 Stearoyl-[acyl-carrier-protein] 9-desaturase [*Sesamum indicum*]
XP_011084689.1

MALRVSFVPHRIPAFPASQLRSHRVSMASLTLSHSPSAEVGNVRKPFSPPREVHVQVTHSMPPQKQEIFNSL
HDWAEENILVLLKDVCKWCQPSDFLPNPPSPGFHDQVKELRERSMELPEDYFVVLVGDMITEEALPTYQT
MINTLDAVRDETGAISLTPWAIWTRAWTAENRHGDLNLYLYLSGRVDMKQIEKTIQYLIGSGMDPRTEEN

NPYLGFIYTSFQERATFISHGNTARLAKDHGDKLAQICGTIAADEKRHETAYTKIVEKLFEIDPDDTVL
SLADMMRKKISMPAHLMYDGKDDNLFHFSAVAQRLGVYTAKDYADILEFLVARWEVEKLTGLSSEGRKA
QDYVCGLPPRIRLRLEERAQARAKKRSAPFWSWIYGGKIMI

>SiSAD4 Stearoyl-[acyl-carrier-protein] 9-desaturase [*Sesamum indicum*]
XP_011077116.1

MALKLSVAAHKMPSFAGYNLRSHRVSMASLHSTSIENGKVKKPFTPPREVHGQVTHPMPPEKREIFHSL
NSWAEDNILVLLKPVEKWCQPNDFLPDSSSEGFDEQVKELRERTKEIPDDYFVVLVGDMMITEEALPTYQT
MLNTLDAVRDETGASLTPWAIWTRAWTAENRHGDLNLYLSGRVDMKQIEKTIQYILIGSGMDPRTDK
NPYLGFIYTSFQERATFISHGNTARLAKEHGDLLKLAQICGTIAADEKRHETAYTKIVEKLFEIDPDGTVL
ALADMMRKKVSMAPHLMYDGRDENLFDHFSAVAQRLGVYTAKDYADILEFLVARWEVEKLTGLSSEGRKA
QDYVCGLPPRIRLRLEERAHARAKQASPVFPFSWIYGREVKL

>SiSAD5 Stearoyl-[acyl-carrier-protein] 9-desaturase [*Sesamum indicum*]
XP_011074783.1

MQSSAFTHIATAQLAWAPRGGGAAATRRVPPSSAVAAPLRHRQITHSMPEKVEVFKSLESWASKSVLPL
LKPVDKWCQPTFLPDPTRPISDFMDEVRLDRASELPDEYFVVLVGDMMITEDALPTYQTMINTLDGVR
DETGASPNPWASWTRGWTAENRHGDLRLTYLYLSGRVDMLEIERTVQYILIGAGMDPGTENNPLYGFVYT
SFQERATAVSHGNTARLAKEGGDPVLAQICGTIAADEKRHENAYARIVEKLLEVDPNGAMIAVGDMMRKK
ITMPAHLMYDGQDPLHFEHFSAVAQRMGVYTADDYADILEFLIGRWRLKLDGLKGDGRQAQEFVCGLPQ
RIRKLQERADERAKKMKPKGQRFWSWIFNREVVV

>SiFatB1-1 Fatty acyl-ACP thioesterase B [*Sesamum indicum*] (XP_011073093)
MALMQNAALHFPKDLCHAERNDDFVATFVRVGGTTRRRAGVKMKASSTNVDTVNGKKVNGVHVDGRIPFLDQRSADLLK
DGESVYGSVEPNHEYLLGRFVEDRFVYRQSFVIRSYEIGDPKTATMETLMNLLQETALNHVASAGVAGNGFGATREMSI
RKLIWVVTRIHVQVEKYSSWGDVVEIDTWVDAAGKNGMRDWIIRDYNTQKII TRATSTWVIMNRETRRLSKIPEEVKN
EVQPFYLNRAAIATENTDSEKIEKLTDETAEI IRTGLAPRWSMDMDANQHVN NVKY IGWLLSV PINVLEDYNMTRLTLE
YRRECRQSNVLESLSMKAKTGEEEDKQFTEKSGAEDLECTHLLRMEADQAEIVRARSVWQIKQHDNQMT

>SiFatB1-2 Fatty acyl-ACP thioesterase B [*Sesamum indicum*] (XP_011078334)
MVTTAATSAPLPIASPDSSGKTLGKVGGSIPANVDARGTSAKSKSSSSGKLRVNANAQAPPKVNGTKVGVIDGPKAE
DEVAVSPPPRTFINQLPDWSMLLAITTI FLAAEQWMLLDWKPKRPDMLVDPFGLGRIVQDGLVFRQNFSIRS YEIGA
DRTASVETLMNHLQETALNHVKNAAGLLADGFGSTPEMCKRNLIWVVTMQLVLDVRYPTWGDVVDVQDVTWVAASGKNGMR
DWLVRDNTGDLTRATSLWMMNKETRRLSKIPEVREEIGGYFVDSPIVDDDSRKLPLKDDNTADYIRTGLTPRWS
DLDVNQHVNNVKYVGWVLESAPLPILETHELAGMTLEYRRECMRDSVLQSLTAVVDKGVGDLANSGFVEQCQHLRLLEGG
GEIVKGRQTQWRPKYADRIGSWGELPAESA

>SiFatA Fatty acyl-ACP thioesterase A [*Sesamum indicum*] (XP_011089673)
MLLRGAFSACNAAGEHQGQGNCRFSGLI RRPTRGVATVWCSRTRRGNLLRVASVATGEPKSKPQESSYQPSVADRLR
LGSLTEDGLSYKEKFIVRCYEVGINKTATVETIANLLQEVGCNHAQSVGFSTDGFATTLTMRKMHLI WVTARMHIEIYK
YPAWSDVVEIETWCQSEGRIGTRRDWILKDYATGEVIGRATSKWVMNQDTRRLQKVTEDEVREYLVFCPKKLRLAFPE
ENNASLKKISKLDDPAEYYKVGLVPRADLDMNQHVNNVTYIGWVLESMPQEIIDSYELQITITLDYRRECQHDVVDLSL
TTPEPILNDSVSQLHGTNGSPTAAKDESDYLQFLHLLRISNDGSEINRGRTEWRKKPAKR

>SiFAD2-1 Oleic acid desaturase [*Sesamum indicum*] AAX11454.1
MGAGGRMSDPTTKDEQKKNPLQRPYAKPPFTLGDIKKAIPPHCFERSVSRFSYVVDLVIVFLLYYIA
TSYFHLPLSPYCYLAWPIYWAVQGCVCCTGIWVIAHECGHHA FSDYQWLDDTVGLILHSALLVPYFSWKYS
HRRHHSNTGSLERDEVFVPKPKSRVSWYSKYLNNPLGRVITLVVTLTLGWPLYLLFNVSGRPYNRFACHF
DPYGPYIYNDRELQIFISDAGIIAAVCVLYRVALVKGLAWLVGVYGVPLLVNGFLVLITFLQHTHPSLP
HYDSSEWDWLRLGALATVDRDYGVNLKVFNITDTHVTHHLFSTMPHYHAMEATKA IKPILGQYYQFDGTP
FYKAMWREAKECLYVEPDESTPKGVFWYKNKF

>SiFAD2-2 Delta(12)-fatty-acid desaturase [*Sesamum indicum*]
XP_011075145.1

MGAGGRMSVPPEGKSKSDAFQRPVPHSKPPFTLGELKKAIPPHCFQRSIPRSFSYVIYDLAIASLFYYVA
TNYFHLPLPSLSCLAWPLYWICQGCVLTVGVVIAHECGHHA FSDYQWLDDTVGLILHSALLVPYFSWKYS
HRRHHSNTGSLERDEVFVPKVKSGIRWFAKYMNNPPGRVLM LIVQFTLGWPLYLLFNVSGRHYDRFACHY
DPKSPIYSDRELQILISDAGVLAVTYGHLRLAIAGLAWLVGVYGGPLL VVNAFLVLITYLQHTHPALP
HYDSSEWDWLRLGALATVDRDYGILNTVFHNITDTHVAHHLFSTMPHYHAMEATKA IKPILGNYYQFDGTP
IFKAVWREAKECIYVEPDEGDKNKGVFWYNNKL

>SiFAD3 Acyl-lipid omega-3 desaturase [*Sesamum indicum*] XP_011080789.1
MAVISGLRHSSFLNTTAAEEINGGPEEKERMKQNTPAAATVTPGGEAFDPAAPPPFRIADIRAAIPAHCW

VKDPWRSFSYVVQDVAADVGLLSAAVYFDSWAFWPVYVWAQGTFLFWAIFVLGHDCGHGSFSDNPVLNNVV
GHFLHSSILVPYHGWRISHKTHHQNHGHVENDESWVPLPEKLYKKLDYSTKFLRYKIPFPMFAYPIYLWS
RSPGKSGSHFNPYSALFRADERKLVMTSTICWAAMVAFLFCASTIIGPLSLFKLYGVPYLIFVMWLDTVT
YLHHHGHEQKLPWYRGKEWSYLRGGLTTVDRDYGLFNKIHHDIGTHVIHHLFPQIPHYHLVEATREAKRV
LGKYYREPRKSGPIPFHLIPSLVNSIQSDHYVSDTGDVVYYQTDTSHFSSLPSSKLHTN

>SiFAD6 Omega-6 fatty acid desaturase [*Sesamum indicum*] XP_011079423.1
MACRIAHSSFLFLGPQKRPTGEGNRIFPQSSASSGAYLLKWEGLPQRRSKQNQSLISFRKHKVVKAVAVSV
APPPADSAEHRQQLCQEYGFQIGETLPDNTLNRNIIDTLPKKVFEIDDVKAWSVLVSVTSYALGIFMI
AKVPWYLLPLAWAWTGTAVTGFFVIGHDCAHKSFSRNKLVEDIVGTLAFLPLIYPYEPWRYKHDRHAKT
NMLVEDTAWQPVDPEEFDS SPVLRAIIYGYGPFPRPMSIAHWLICHFDLKKFRPNEVNRVKISLACVFA
FMAIGWPLIIYKTGIMGWIKFWLMPWLGYHFWMSTFTMVHHTAPHIPFKSSEEWNAQAQLNGTVHCDYP
SWIEVLCHDINVHIPHHISPRIPSYNLRAAHQSLQENWGKYMNEATWNWRLMKTILTVCVHYHKEQNYIA
FDELAPEDSQPITFLKRVMPDYA

>SiFAD7 Omega-3 fatty acid desaturase [*Sesamum indicum*] NP_001306619.1
MASWVLSECGLRPLRPVYPKPTGHPHLLNSNPTKLRFSRTDLGNGSSFCLSSGILREKNWALRVSAPLRV
LQVEEEENKEGERVINGGEEFDGAPPPFKLS DIREAIPKHCWVKDPWRSMGYVVRDVAVVFGLAAVAA
YFNWVWVWPLYWFAQSTMFWALFVLGHDCGHGSFSDPKLNSVVGHILHSSILVPYHGWRISHRTHHQNH
GHVENDESWHPLSEKIYKNLDTATKKLRFTLPFPLLAYPIYLWSRSPGKQGSFHDPDSDLFVPNEKKDVI
TSTVCWTAMLALLVGLSFVIGPVQLLKLYGIPYLGVMWLDLVTYLHHHGHEQKLPWYRGKEWSYLRGGL
TTLDRDYGWNNIHHDIGTHVIHHLFPQIPHYHLIEATEAAKPVLGKYYREP KKSAPLPFHLLGDLTRSL
KRDHYVSDVGDVVYYQTDPQLTGAEKS

>SiFAD8 Omega-3 fatty acid desaturase [*Sesamum indicum*] XP_011076709.1
MASWVLSECGVSPLRPLYPKPTGHAQAFNLPPNPSKLRISRTDFGNSFSFCLVNHKERNWALRVSAPLT
VGQVEEESKENGGEFDGAPPPFKLS DIRAAIPNHCWVKDPWRSMGYVVRDVVVVFGLAAVAAYFNWVA
VWPLYWFAQSTMFWALFVLGHDCGHGSFSDPKLNSVVGHLLHSSILVPYHGWRISHRTHHQNHGHVEND
ESWHPLEKIYKNLNDNVTKKLRFTLPFPMLAYPIYLWSRSPGKTGSHFHPDSDLFVPSEKDKVITSTVCW
TAMVALLVGLSFLMGPLQLLKLYGIPYLGFTWLDLVTYLHHHGHEQKLPWYRGEEWSYLRGGLTTLDRD
YGWNNIHHDIGTHVIHHLFPQIPHYHLIEATEAAKPVLGKYYREPQKSGPLPFYLLGVLLRSMKKDHYV
SDTGDVVYYQTDPPELN

>SiLACS1 Long chain acyl-CoA synthetase 1 [*Sesamum indicum*]
XP_011079524.1

MKKFAVKVEEGKKGRDGKPSVGPVYRNLLAGNAYPPVDPNLSTAWEIFRASAETHSGNRMLGWRELNVNGK
WGPYVWKSYSYKEVYEETLHAGSALRAHGSEPGARVGIYSSNCPQWIVAMEACNAHSLICVPLYDTLGTGAV
DYILDHAEIDVVFVQDKKVKELLNPECTHARRLKLIVCFTSLTEEQQGKAASIGIKTCSWTEFLNMGREN
PVEISPPEPSSICTIMYTSGTSGAPKGVILTHENISTNIRGVDLFMDQFEDKMTVDDVYISFLPLAHILD
RMIEEYFFHKGASVGYHGDINEIRDLMELKPTFLAGVPRVFERVHEGVKALEELNWRRRKIFHMLYK
YKLYWMNRGYKQKQDASPLADLLAFGKVNRLGGRIRLIVSGGAPLSSEVEEFLRVTSFAFVVQGYGLTES
CGLSTIGFPDEMCMIGTVGASFVYNEICLEEVPEMGYDPLADPPRGEICLRGKTTFAGYKNPETLQEA
KDGWFHTGDIGEMLPNGVVKIIDRKKNLIKLSQGEYVALEYLEKVYGITPIVEDIWWYVGSFYSMLVSVV
VPNEENTKKWAQQNGQKGSFMDLCSLDQLKDHILLELKSTAERNKLKGFEHIKGVIVEPKLFELSEKELV
TATLKKRRDRLLKNYKVEIDALYQTLRAAKP

>SiLACS2 Long chain acyl-CoA synthetase 2 [*Sesamum indicum*]
XP_011088325.1

MGDYVVKVEDGRGASDGKPSAGPVYRCIYAKDGLLDIPTHFDSPWNFFSASVKKPNPNQMLGRRQIKDGK
AGAYTWLTYQQVYDATLKIGSAMRRRGVNPBGDKGIYGANCPWEIIGMEACIGQSVTYVPLYDTLGNANAV
EFIINHAEVSIQVQESKLVPIILCLPKCVSHLKTIVSFGKVS DKKHETAEEELGVACFSWEEFALLGDLD
ENLPPKKKTDTCTIMYTSGTGEPKGVILSSAAFMAEVLSMDQLLLETDKVGTEEDVYFSFLPLAHIFDQ
IMETYCIYRGSSIGFWQGDIFLIEDLIVLKPTIFCGVPRVYDRIYTGIMDKISASGALRKSFLQIAYNY
KLRNLEKGLRQEEASPFDFKLVFDKIKQFGGRVRLMLSGAAPLPKHIEEFLRVTTCCCVLSQGYGLTESC
SGCFTSIANVYPMMGTVGVPMTTIEARLESVPPEMGYDALSSVPRGEICLRGSTLFSGYHKRPDLTAEVVV
DGWFHTGDVGEWQPSGALKIIDRKKNIFKLSQGEYVAVESIESVYSRCPLITSIWVYGNFSFESFLVAVVV
PEKKALEEWAANNQEKGDFQSLCSNIKARKYMLDELNSTAKTHNLRGFEMLRGVHLEPAPFGIDRDLVTP
TFKLKRPQLLKYYKDCIDQLYSEAKETKA

>SiLACS4 Long chain acyl-CoA synthetase 4 [*Sesamum indicum*]
XP_011101042.1

MAKERYTVEVEPGKPAKDGKPSVGPVYRSKFAKDGFPPEPIPGLDSCWDIFRLSVEKFPPNNRMLGRREIVD
GKPGKYSWMTYKEVYDIVLKVGNSIRSCGIEEGGRCGIYGANSPEWIMSMEACNAHGLYCVPLYDTLGAG
AVEFIICHAEVALAFVEEKKISELLKTFPGATKCLRTIVSFGKVTSQQKDEVEKFGVAIYSWDEFLSLGE
NKDYDLPVKKKTDICTIMYTSGETGDPKGMISNNSIVTLIAGVKRLLESVNESLTVNDVYLSYLPLAHI
FDRVIEECFINHGASIGFWRGDKLLVEDIGELKPTIFCAVPRVLDRIYSGLQQKVSSGGFIKHTMFNLA
YSLKLRSRMRKGRKHTEASPLCDKIVFSKVQGLGNNVRLILSGAAPLASHVEEFLRVVSGSYVLQGYGLT
ETCAGTFVSIPELSMLGTVGPPVNVNVCLESVPPEMGYDALSSTPRGEVVCVRGDTLFSGYKRDLLTKE
VFVDGWFTGDVGEWQANGSLKIIDRKKNIFKLSQGEYVAVENLENIYGLVPAIDSIWIYGNFSFESFLVA
IINPNKQVVEQWAEENGVSQDFNLCENPKVKEYFLGELSRIAKEKKLKGFEFIKAVHLDPVFPFDMERDL
ITPTFKKKRPQLLKYQGVIDSMYKSGK

>SiLACS6 Long chain acyl-CoA synthetase 6 [*Sesamum indicum*] XP_011090746.1

MDSRAERRLQAVRNHLVGSTTWEQSPVLRPQPTVGDDFFSVEQGYISIVLPEKLQTKGNVYRNRRSPLKLV
SRFVDHPEIATLHDNFMHAEKTFRDYKYLGRVREDGTGVEYKWITYGEAGASRAAIGSLIRYGIQKGS
CIGLYFVNRPEWLVDHACSAYSFISVPLYDTLGPDAVKYIVNHAAVQAIFCAPETLKILLRFLSEIPSV
HLIVVVGGVEEQPLSLPSTTGVEFISYSKLHTEGLGSLQPFCSPTADDVATICYTSGETGTPKGVVLTHG
NLIANVAGASLGKLYPSDLIISYLPLAHIYERANQILVVYFGGASGFYQGDNMKLLDMLAVLKPTVFC
VPRLYNRIYAGVMNAVKTSGVLRERLFNAAYKAKKQSFSGKKSSPMWDKLVFNKIKEKLGGRVRYMVSG
ASPLSPEVMDFLRVCFCGIVVEGYGMESSCVISNMDETDLVSGHVGAPNAACEIKLVDVPEMNYTSEDQ
PHPRGEICVRGPVIFVQGYKDEVQTRVIDDDGWLHTGDIGLWLPGGRLKIIDRKKNIFKLAQGEYIAPE
KIENVYAKCKFVAQCFIHGDSLNSFLVAVVAVDHDMLKAWAAAEGIKYQDLKQLCADPRARGAVLADMDA
VAREAQLRGFEFAKAVTLVVEPFTVENGLLTPTFKIKRPQAKAYFANAISDMYNQLSASHASAQKLV

>SiLACS8 Long chain acyl-CoA synthetase 8 [*Sesamum indicum*]
XP_011085413.1

MMSESAESNLNTNTMKNVGISDYLSIFKDNNGTYGVTCVIVAVITPILLSLVLQGRKKLKQRGVPVQVGG
EAGFAVRNARFPKLVEVPWEGATTMAALFEQSCKRYSQQNLGTRKVIADLVTSSDGRKFEKLHLGEYQ
WETYRQIFDRACNFASGLLKLGHVDVTRAAIFSETRAEWLIAFQACFRQNTVVTIYASLGDDALIHSNL
ETQVTTLICDSKQLKKLALSSSLTTLRNIIYFDEDDSSSGSTVTQESGNWQVSSVFSEVEKLGRNNPAQP
NLPIKTDIAVIMYTSGSTGLPKGVMMTHGNIVATAAAVMTVIPSIGRKDVYLAYLPLAHVFEAAETVML
TAGAAIGYGSALTTLTDTSNKIKKGTGKGDASVLKPTLMAAVPAILDVRDGVVKKVEEKGKGVKKLFKIA
SRRLVAIEGWSWFGAWGVEALLWDIVVFKKIRSILGGEIRFMLCGGAPLSGDTQRFINICMGAPIGQGYGL
TETCAGAAFSEWDDISVGRVGPPLPSCYIKLVSWEEGGYTISDKPMRGEVVVGGASVTAGYFSNDAKTA
EVYKVDEKGMHWFYTGDIRFHPDGCLEIIDRKKDIVKLQHGEYISLGKVEAALVSSKYVENIMVYADPY
HNFCAVALVVPARQTLEGWAKESGIKYNDFPELCEKAEAKNEVQQSLLKEAKAAKLDKFEIPAKIKLLPDP
WTPESGLVTAALKLKREQLKAKFKDELDKLYK

>SiLACS9 Long chain acyl-CoA synthetase 9 [*Sesamum indicum*]
XP_011069534.1

MGPIYVGVIIPLVVTLLRGTKGKKRGLPVNVGGEPGYAIRNYRFSSPVQSAWEGVTTTAELEFELSCKKH
SDMRLLGTRKLIASEVEISDGRSFEKLHLGDYEWLSYGQVFEAVCNFASGLVQLGHQKGERAAIFADTRE
EWFIALQACFRNVSVVTIYASLGEEALCHSFNETEVTTVICGYKELKKIANVSGQLDVTVKRIICMDDF
QSDASLVPGSSSWTITSFSDVEKLGRENVPDPLPLSADIAVIMYTSGSTGMPKGVMMTHGNVLATVSAV
MTIVPGLGNQDVYLAYLPLAHILELAAENLIAAIGSSIGYGSPLTLTDTSNKIKRGTGKDATVLRPTLMA
AVPAILDVRDGVRRKKIDATGGLPKKFLDLAYARRLSAINGSWFGAWGLERLLWNLLVFRKVQAILGGRI
RFILSGGAPLSGDTQRFINICLGSPIGQGYGLTETCAGGTFSEYDDTSVGRVGAPLPCSI IKLVDPWEGG
YLISDSPKARGEIVIGGPNVTLG YFKNDDKTKEVYKVDERGTRWFYTGDIGQFHADGCLEIIDRKKDIVK
LQHGEYVSLGKVEAALIVSPYVDNIMLHADSFHSYCVLVASQASLEAWASKQGITYSDFSGLCGKEET
LKEVSTSLKAAKAAKLEKFEIPAKIKLLSEPWTPESGLVTAALKLKREVIRKTFSDDLGKLYSS

>SiGPAT1 Glycerol-3-phosphate acyltransferase [*Sesamum indicum*]
XP_011069706.1

MIFSTTSSTTLFTCNTTPRVASASPSTSRACLLKSSCGGASRRSRSSFLVLCASKLSEAIDGKKSSTST
VAAAPVFASSAYDQDEISAPRTFLDARTEQDLLLGIQKEAEAGRLPINVAQGMEELYHNYRNAVFHSGH
PKAHEIVLSNMAVALDRIFMDVRDPFQFSPHKAIREPFDYLLFGQKYISPLLDNRNSFLGNSSFLDEME
KKLQQGENVILISNHQTEADPAIISLLESTNPFIAENMICVAGDRVVTDPCKPFSMGRNLLCVYSKKH
MNDDPELIDMKRRANTKSLKEMAMLLRVGSKVIWIAPSGGRDRPDVTKEWYPAPFDASSVDNMRRLEH
AGVPGHIYPLAILCYDVMPPPAQVEKEIGEKRVISFHGVGLSVAPKISYQEITATLEDPEEAKNAFSELL

YSSVCEQYDVLRSIAIHGKQGLAASTPTVSLSQPWE

>SiGPAT2 Glycerol-3-phosphate acyltransferase 1 [*Sesamum indicum*]
XP_011082911.1

MTASVKTMFEFPMVLLRLADWFLYQFLANSCYRAAMKIKNHGFSFFLKNPSIRSSSSSHQFPLYPSLTKCNL
HGRKYQTLVCDIHGCLLRSHSFFPYFMLVAFEGGSIFRAFLLLSCPFLILIDYELKLRAMIFLTFCGLR
LKDMESVSRAVLPKFYLENLNFHAYEAVCSAGSKVVFSTVPRVMVEGFLKEYLSVDSVVGTELQTKGKFF
TGLVSSSGLLVKHRAKELFGDKRPDIGIGSSSLHDHLLISLCKEAYVVSKEEAKSNPSSVMPRDKYPKP
LVFHDGRLAFLPTPFATLSMFMWLPFIGILLAVFRLFVGICLPYNLAILLGIASGVNLKVKGCPPMKSQNG
KGVLYVCTHRTLLDPVFLSTSLGKPLTAVTYLSKMSSEILAPIRTVRLTRDRKRDGETMQKLLSEGDLVV
CPEGTTCREPYLLRFSSLFAELADEIVPVAMNTDVTMFYGT TASGLKCLDPIFFLMNPRPSYSVEILGKV
PRELTCAGGKSSYEYVANYIQKELGMALGFECTSLTRRD KYLMLAGNEG VVQEKRRKP

>SiGPAT3 probable glycerol-3-phosphate acyltransferase 3 [*Sesamum indicum*]
XP_011094070.1

MAPKAFPF SKLALLFSAFLDNFRDTRRN LGNHWSPRSPFEFQNL EFLGQRPHLENQVLV FHAETVLLRSS
SLFPYFMLVAFEAGSLIRALILFVLYPFICLCHQDLALEVMVFICFLGLKKERFTEGRAVL PKFFLEDVG
RESFEVLRRGKLIV AISDLPQVMVESFLKDFLDVDFVVG RDLKACRGYFVGLMEERRDYNAFQVVKLSPH
VIGVGCFRKCFEHEWFSNCKE IYLVDEQERRNWHQLPRDLYPKPLIFHDGRLAFRPTFWATLAMFMWLP
GFTLGIIRTIVLSSLPFEIKFPILHLTGVRIKISNSELATMSNVNGALYVCNHRTLFDPLMLSCLRTP
LTAVVYSLSRVSEILSPIKTVRLTRNRGQDAELMSKVLSQGNLVVCEP GTTCREPYLLRFSP LFTEISDN
IFPVAIDCHVSMFYGTTARGFKSLDPLFFSMNPRSTYSARFLNMVHRGAGDENGDDARTSNYKMANLVQS
MIAEELGF SCKLTKRKDY LILAA NEG VVRKG GELKTETETKMK

>SiGPAT4 Probable Glycerol-3-phosphate acyltransferase 3 [*Sesamum indicum*]
XP_011077903.1

MALMKPLSVQKLPLLFSILILKHFRNPKRTHQGNFYTADSVEYHKFQVLGQRQDLEDQFLIFNVETSL
RSSSLFPYFLLVAFEAGSPIRAFIFLILYPFITVCRDGLALKLMVMICFFGISKDRFREGRAVL PKFFLE
NVGRESFEVLRRGKKT VGVSNLPHVMVESFLRDHLDIDYVVGKDLKVFCGYFVGLMEERRKLIVPDNLVH
NAIGISGCKKDFDCPWF AHCKE IYLVNEQERRNWHQLPRNSYKPLIFHDGRLAFQPSFLAALAMFMWLP
LGFTLAIIRTIALTL PFEIAIPLMHFIGIRIVSKPHSFSNRKHGEAKRRLYVSNHKTLLDPIVVSYAT
RNTTLTAVTYLSLRMSEIISPIKTVRLTRHRDQDAELMHKLLSQNDLVVCEP GTTCRESYLLRFSP LFSE
ISNEVFPVAVNCHISMFYGTTARGLKFLDPFFFLMNPWPSYSARFLGVIHRAGGS RFEAADLVQSEIGKA
LGFTCTKLTRKDY LILAGNDGVVRDGSRR

>SiGPAT5 Glycerol-3-phosphate acyltransferase 3-like [*Sesamum indicum*]
XP_011088689.1

MSKLNKSSSEL DLRPNIEDYLPSGSLQDSHPKLRRLRDL DISPTLTEAAGAI VDDSFTRCFKSNPPEPW
NWNVYLFPLWCLGVVVRYGVL FPLRAIVLT TGWII FLSCYFPVHFLLKGHDKLRKRLERSLVELICSFFV
ASWTGVVRYHGPRPSMRPKQVFVANHTSMIDFII LEQMTAFAVIMQKH PGWVGLLQSTILES LGCIWFNR
SESKDREIVARKLREHVNGADNNPLLIFPEGTCVNNHYTVMFKKGAFELGCTVCPIAIKYNKIFVDAFWN
SRKQSF TTHLLQLMTSWAVVCDVWYLEPQNLKPGETPIEFAERVRNII SVRAGLKKVPWDGYLKYSRSP
KLRELKQQSFAESVLRHLEQK

>SiGPAT6 Glycerol-3-phosphate acyltransferase 3-like [*Sesamum indicum*]
XP_011092934.1

MSKLN TSSSELDFDRPNIEDYLPSGSIQEPHGKLRRLRDL DISPTLTEAAGAI VDDSFTRCFKSNPPEPW
NWNIIYLFPLWCLGVVIRYGLL FPLRVIVLT TGWII FLSCYFPVHFLLRGHDKLRKRLERGLVELICSFFV
ASWTGVVKYHGPRPSMRPKQVFVANHTSMIDFIVLEQMTAFAVIMQKH PGWVGLLQSTILES LGCIWFNR
SESKDREIVAKKLREHVHDADNNPLLIFPEGTCVNNHYTVMFKKGAFELGCTVCPIAIKYNKIFVDAFWN
SRKQSF TTHLLQLMTSWAVVCDVWYLEPQNLKPGETPIEFAERVRDII SVRAGLRKVPWDGYLKYSRSP
KHRERKQQSFAESILRRLEEK

>SiGPAT7 Probable glycerol-3-phosphate acyltransferase 3 [*Sesamum indicum*]
XP_011094147.2

MLVAFEAGGLIRALILFLLYPMISLCRQELALKVMVFVCFLGLKKERFVEGRAVL PKFFLEDVGRESFEV
LRRGKMTVGVS DLPQVMVESFLRDYLEVDVVGRELKVFRGYFVGLMEERRERGFQVVKMAPDVIGIGCF
RKCLDREWF LNCKE IYLVSEQERRNWHQLPRDLYPKPLIFHDGRLAFRPTFWATLSMFMWLPFIGFTLGI
RAIVALSSLPFEIKFPILHLTGAQIKISNPELATNNANGALYVCNHRTLLDPLMLS YCLRTPLTAVVYS
LSRVSEIISPIKTARLTRNRGQDAELMHKLLSQGNLVVCEP GTTCREPYLLRFSP LFTEISDRIFPAID
YDVSMFYGTTARGFKSLDSLFLLMNPQPSCSVRFLNMVRGGADETGDDVETSKYKTANLVQAMIAEELGF
TCTKLTRKDY LILAGNEGIVGDGKKV

>SiGPAT8 Glycerol-3-phosphate acyltransferase 5-like [*Sesamum indicum*]
XP_011085137.1

MEYCVVSELEGTLLKDHDPFSYFMLIAFEASGLIRFALLLALWPFIRLLEALGRGDDGLKLMIFVATAGV
PFSEIEAVARAVLPKFYLDINMDAWRVFSSYPKRVVVTKMPKIMVERFVMEHLRADHVVGSDLSMNRFG
FATGFLKDDFGSVAKRVAQLFGDDEKPCGLGLGRPDSCSSFLPLCKEECHPPFITNHNHQQHIIIRP
LPVIFHDGRLAKRPTPSTALLIILWVPLGIILAAIRIAVGLMLPMWATRHIAPLLGGRVVVKGNPPPPPS
RRSSTSGVLFVCTHRTLMDPVVLSTVLRRIIPAVTYSISRLSEILSPIPTIRLTRIRDVDATKIKQELEK
GDLVVCPEGTTCREPFLLRFSALFAELTDQIVPVAMNYRVGLFHATTARGWKAMDPIFFFMNPRPVYEV
FLNQLPVEATCSAGKSPHDVANYVQRILAATLGFECTNFTRKDKYRVLAGNDGNVSSTDGGGAAGLVDAF
KKIVPSFIILH

>SiGPAT9 Glycerol-3-phosphate acyltransferase 5-like [*Sesamum indicum*]
XP_011076807.1

MESVVSELEGTLLKDPHVFSYFMLIAFEASGLVRFALLALWPLIRLLEVCGRGDDGLRLTVFAATVGV
VSEIEAVARAVLPKFYLDINMDAWRVFSSYDRRVVTRMPRIMVERFGKEHLMAGDVVGTELSVNRFG
ATGFIKSGIGSIGKKVTELFGEKPRGLGRPKCGFSSFLMPLCQEECHPPFPNRKPMHENHIIIRPLPVI
FHDGRLVKRPTPSAALVILLWIPLGILLAAIRIAVGLMLPMWAIIPRVAPAFGGRVVVKGTTPPPASASNS
GVLFVCTHRTLMDPVVLAALAIQRRIPAVTYSISRLSEILSPIPTVRLTRNRDVAQKIKRELEKGDVVC
PEGTTCREPFLLRFSALFAELTDRIVPVAMNYSVGFFHPTTARGWKAMDPIFFFMNPRPIYEVTF
VEATCSAGKSPHDVANYVQRILAAALGFECTNFTRKDKYRVLAGNDGTVSQTSEPDTKMVNAFKKVVASF
MLH

>SiGPAT10 Glycerol-3-phosphate 2-O-acyltransferase 6-like [*Sesamum indicum*]
XP_011073520.1

MAVPKTNTPNRIPTIFQCDSKGRENHTVVADLDGTLIGRSSFPYFALIAFDVGGILRLLLLLLASPLAG
FLYYFVSEAAGIRVLIFATFAGVKVSAIKSAASAVLPKHYSEDMPETWRVFSSCGRKCVLTANPRIMVE
PFLKNYLGVDDVLGTEISSYKGIATGFVASAGVLVGRNKAIALRRAFGAESMPDIGIGDRKTDFFPMRLC
KERYIVPSRPEVRPVRHDALPKPVI FHDGRLVQKPTPLMALLIILWFPIGIIILSVLVLGSLSPISLTY
YIVNFMGCPITVKGTPPRGAKSSSTRGVVFCVSHRTVLDAVFVSASLGRMTTTSISVSASFTEFLSPIK
TSRLTRERTKDAQILINDILDQGRYLMCPEGTTCREPYLLRFSSFLFAELTDQIVPVAIVVKTSMFHGTTA
RGHKWLDPPFFFFMNPVPAYEVTFLNKLSPDQTCAGKSSHEVANSVQEMIAKTLNLYKCTNLTRKDKYRAL
AGTDGLVGQQPVRAATKVIGG

>SiGPAT11 Glycerol-3-phosphate 2-O-acyltransferase 6-like [*Sesamum indicum*]
XP_011086432.1

MAAGEFPTVDVCPISIGREKDTVVADMDGTLLRGRSSFPYFALVAFEVGGVLRLLFLLLLAPLAGVLYYFV
SESAGIRVLIFATFAGMRVSDIESVARAVLPKFYSGDLHSESWRVFSSCGKRCVLTANPRIMVEAFLKEF
LGADMVLGTEVSTYGGGRATGFVKEPGVLVGKNKAELKAAFGAPPEIALGDRHTDFFPMSLCKEGYIVP
PKPEVKAVTIEKLPKPIIFHDGRLVQKPTPFLALLTILWIPVGFLACLRIAAGSLLPMLPVYAFWALG
VRVTVKGTPPPPVHKSSTQSGVLFICSHRTLLDPIFLSTALGRPIPAVTYSVSRLEIISPIKTVRLSRD
RATDAAMIKLLQEGDLAICPEGTTCREPFLLRFSFLFAELTDELVPVAMVNRMSMFHGTTARGWKGMDF
FYFFMNPSPAYEVTFLNKLPRELTCGAGKSSHEVANYIQRVIAATLSYECTTFTTRKDKYRALAGNDGTV
EKPRRQVMGC

>SiGPAT12 Glycerol-3-phosphate 2-O-acyltransferase 6-like [*Sesamum indicum*]
XP_011091226.1

MAVRSTHSPSKIPTIYQCDSKGRENQTIAADMHGTLLIDRSLFPYFALIAFDVGGILRLLLLLLTAPLAW
FLHHFVSESAGIRVLVFAFAGVKVSEIESAANAVLPKHYSEDLHPETWRVLSSCGRKCVLTESPRIMVE
PFLKNYLGVDDLVLGTEISSWGVATGFMARGGVLVGEQKAMALRKAFESSLAPEIGIGDSEADFAMNLC
KEYIIVPSEQRVRPVKQVELPKPVI FHDGRLVQKPSPLIALLIIVWFPIGVLLSVSRVLIGNSPISLFY
YIIQLTGCKILVKGTTPPNKNSRRTGVAFICSHKTVMDPLFVSAVLGRNTTCISYSVSRLEFLSPIRN
CRLTRERSKDAKIIKDILEEGWDLVLCPEGTTCREPYLLRFSSFLFAELTDEIVPVAINIRTSMFHGSTAR
GRKWLDIFFFFMNPVPVEITFLDKLSPDQTCAGKSSFDVANNVQEMIGTVLKFCKTKFTRKDKYRMLA
GTDGLVGKPGAVAADKLS

>SiGPAT13 Glycerol-3-phosphate 2-O-acyltransferase 4 [*Sesamum indicum*]
XP_011092551.1

MASAAVAARFPSIEKCDTSGENRRSIAADLDGTLISRSSFPYFMLVAIEAGSLLRGLILLLSFPLIAV
AYIFVSESLAIQMLIYISYGLKVRDIELVSRAVLPRFYANDVRPESYEVFDKCDRKVIITANPTIMVEP
FVKEYLGGDKVVGTEIEVDPKTKKATGFVKKPGVLVGKWKGLVKEFGEEKPDIGIGDRESHDHFMSCIC
KEGYMVHPSKSAKPLPLDRLKSRLIFHDGRLVQCPTPLNALITYIWLPGFILSLIRVYFNLPLPERIVR
YTYPMLGINLVKGNPPPPPSAGSPGNLYVCNHRTALDPIVIAIALGRKVSCVTYSVSKLSRFLSPIAV

ALTRDREADAARIKALLQKGD LVVCP EGTTCREPYLLRFSALFAELSDRIVP VAVNLKQNM FHGTTVRGV
KFWDAYFYFMNPRPTYEITFLERLPEEMTCKGGGKSSIEVANHVQRILAGALGFECTQLTRKDKYM LLLGG
NDGKVESIYSKK

>SiGPAT14 Glycerol-3-phosphate 2-O-acyltransferase 4-like [*Sesamum indicum*] XP_011093132.1

MAKTATAAVRFPSIEKCDASGENRQAIAADLDGTLLISRSSFYFMLVAIEAGSLLRGLILLLSFPPIIAI
AYVVFVSEALAIQMLIYISFSGIKVRDIELVSRVLPFRFYARDVRAESYEVFDKCKRKVIITANPTIMVEP
FVKEFLGGDKVIGTEIEVDPKTRKATGYVKKPGVLVGKWKKLGLVKEFGEEKPDIGIGDRASDHDFMSIC
KEGYMVPPSKTAKPLPLDRLKSRLIFHDGRLVQRPTPLNALITYIWL PFGFLLSLIRVYFNLPLPERIVR
YTYPMLGINLVIKGNPPPPSPGSPGNLYVCNHR TALDPIVIAIALGRKVSCVTYSVSKLSRFLSPIPAV
ALTRDREADAAMIKALLQKGD LVVCP EGTTCREPYLLRFSALFAELSDRIVP VAVNIKQNM FYGTTVRGV
KFWDAYFYFMNPRPTYELTFLERLPEEMTCKAGGKSSIEVANHVQRILAGTLGFECTQLTRKDKYM LLLGG
NDGKVESMYSKK

>SiGPAT15 Glycerol-3-phosphate 2-O-acyltransferase 6-like [*Sesamum indicum*] XP_011077573.2

MGahrhFHPITKCTTQGRSNQTVAADLDGTLLVSRSAFPYFMLVALEAGSLIRALLLLSSVPFVYLVYLF
VSESLAIQSFIFISFSGLKIRDIELVSRSVLPKFYSEDVHPETWKVFNSFGKRYIVTANPRIMVEHFAKS
YLGADKVLGTELEVTKSGRATGFVKKPGVLVGEHKKMAIVKEFGSNVPDLGLGDRET DHDFMSICKEGYM
VPRTATEPLPRNKLLSPIIFHEGRLVQRPTPLVALVTFLWMPIGFVLSVIRIYLDIPLPERIVRYTYMML
GIKLIVKGTPPPPSPGRGGVLFVCNHR TILDPVVTAV ALGRKISCVTYSISKFSELISPIKAVALSRER
EKDAANIKRLL EEGDLVICPEGTT CREPFLLRFSALFAELSDRIVPVAINTKQSVFYGTTARGYKVLDPY
FVFMNPRPTYEITFLNQLPEELTVKGGKSAIEVANYIQRVLAGTLGFECTNLTRKDKYIMMAGTDGRVQP
NKDKDDREHKK

>SiGPAT16 Glycerol-3-phosphate 2-O-acyltransferase 6-like [*Sesamum indicum*] XP_011094988.1

MGahREFEPITKCKSSEGRSNQTVAADLDGTLLVSSNAFPYMLVALEAGSLIRALLLASVPFVYFLYL
FLSESLAVQILIFIAFSGLKIRDVELVAKSVLPKFYAEDVHPETWRVFNSFGKRYIVTANPRIMVEHFVK
NYLGVDKVLGTELQVTKSGRATGFVKKPGVLVGDHKKMAIVNEFGTNVPDLGLGDRET DYDFMSICKEGL
IVPRTRTEPLPRNKLLSPIIFHEGRLVHKPTPLVAF LTF LWMPIAITLSFVRVFLHIPLPERIVRYTSM
LGIKLIVKGTPPPPPRPGQGGRLLVCNHR TVLDPLVTAVALGRKITCVTYSISKFSESISPIKTVGLSRE
TEKDAATIKRLL EEGDLVICPEGTT CREPFLLRFSALFAELSDRIVP VAVNTKQCVFYGTTTRGYKFLDP
FFVFMNPRPTYEITFLNEVPREFSVRGGKSGIEVANYVQSAIAGKLG FQCTNLTRKDKYAMMAGTDGRVH
SKYSGLIMPAK

>SiGPAT17 Glycerol-3-phosphate 2-O-acyltransferase 6-like [*Sesamum indicum*] XP_011098557.1

MAESKLHSSVTFPSISKCESHGREKHTVVADMDGTLLIGRSSFHYFALVAFEVGGMLRLLFLLLASPLAG
ILYYFISESAGIRVLIFATFAGMKVSDIESVGRAVL PKFYSGDLHPETWRVFSSCGMKCVLTANPRIMVE
AFLKEYLGADLIIGTEISTYKGRATGLVTSPGILVGKNKA EGLRKAFGNTTPEIGIGDRKTDYPFMNLCK
ESYMVHRTPKVQPVSQDRLLKPIVFHDGRLVQKPSPLMALLIILWIPIGFILACIRIAAGALLPMPMVYY
AFRALGVRVTIKGTPPPRPEKSLGQTGVLFVCSHRSLDPIFLSTALGRAIPAVTYSLSR LSEIISPIKT
VRLNRDRADADM IKLLKEGDLVICPEGTT CREPFLLRFSALFAELTDELVPVAMS NRMSMFHGTTARG
WKGMDPFYFFMNPSPAYEVTFLNKLPGDLTCGAGKSSHEVANYIQRMIAATLSYECTSFTRKDKYRALAG
NDGNVVEKPRKIAADKVMGS

>SiLPAAT2-1 1-acyl-sn-glycerol-3-phosphate acyltransferase 2 [*Sesamum indicum*] XP_011075205.1

MAIAAAIVIVPLGLVFFVSGLVINFIQAVCFLLIRPLSKKTYRRINREVAGLLWLGLVWLIDWWAGVKIE
LYTDSETFKLMGKEHALVICNHKSDIDWLVGWVLAERSGCLGSTLAVMKSSRFLPVIGWSMWFSEYLF
ERSWAKDESTLKSGLQRLRDFPRPFWLALFVEGTRFTQAKLLAAQEYASSAGLPVPRNVLI PRTKGFVTA
VSHLRSFAPAIYDVTVAIPKTSPAPTMLRLFKGQSSVVHVHLKRHLMKDLPETDEAIAQWCRDAFVAKDK
LLDKHNDEDSFGEQLQDTSRPVKSLLVCCWAILLILGLTKVIQHYSLSSRKGAALSAIALAVVTILMQ
ILIQFSQSERSTPAKVVP SKSRNGVEPSRAN

>SiLPAAT2-2 1-acyl-sn-glycerol-3-phosphate acyltransferase 2-like [*Sesamum indicum*] XP_011078878.1

MAFPAAVVIVPLGLVFFMSGLVVNLIQAICYVLIRPLSKNTYRRINREVAELLWLELVWLVDWWAGVKIE

IYTDAETFKLMGKEHALVICNHRSDIDWLVGWILAQRSGCLGSTLAVMKSSKFLPVIGWSMWFSEYLFL
 ERSWAKDENTLKTGLQRLRDFPRPFWLALFVEGTRFTQAKLLAAQEYASSTGLPIPRNVLIPTKGFVTA
 VSHMRSFVPAIYDATVAIPKTSPTPTMLRLFKGQSSVIHVHLKRHLMNLDLPETDEAVAQWCRDAFVAKDK
 LLDRHIAEGTFGEQLQNTGRPVKSLLVSSWAILLILGTMKVIQWFSLFSSWKGIIFSAVALAVITILMQ
 ILIQFSQSERSTPAKVAPAKHKSVTESASRLDKHQ
 >SiLPAAT3 1-acyl-sn-glycerol-3-phosphate acyltransferase 2 [*Sesamum indicum*] XP_011080283.1
 MAIAAAVFLPLGLFLLSGFIVNLIQAVLFVLIRPVSKSAYRRINKEIIELLWLELIWLFDDWWANIKVEL
 FVDQETFDLLGKERALLICNHRSDIDWLVGWVLAQRAGCLGSSLAMIKKSSLFLPVIGWSMWFSDYIFLE
 RSWAKDENTLKSGLVALNDYPLPFWLALFVEGTRFTQAKLEAAQEYAAAGLPVPRNVLIPTKGFVAAV
 THLRSFVPVIYNITVAIPKNEPRPTLLKIFRGRSSAVHVHIERHIMRDLPETSSGISQWCKDMFVAKDAL
 LERHLATNTFGDEIRHDIGRPKSSLLVLTWSSILILAIKVLECFPFSWGEIVFCVVFALVTTLMQIL
 IVFSQSEHSTPPKVS KPDHLRQVLLQS
 >SiLPAAT4 Probable 1-acyl-sn-glycerol-3-phosphate acyltransferase 4 [*Sesamum indicum*] XP_011074489.1
 MSMEISQPLQSTKGLKHFLTPFRFFRGLLCLAVYLSTAFMFLVYFVPLVAVVLR LISVHYSRKSVSFLF
 GLWLGLWPFLFEKINKTRVIFSGDRVPVEQVRVLI IANHRTEVDWMYLWNLALRKGCLGYIKYILKSSLMK
 LPVFGWGFHILEFIPVERKWEVDEPVMRQMLSTFTNREDPLWLAVFPEGTDYTEQKCLKSQKFANENGLP
 VLKNVLLPKTRGFNVCL EILRGSLDAVYDVTIAYKNQCPSFLDNAFGIDPSEVHMHVRRIPLEEIPVSKD
 EAAAWLMNAFVLKDQLLTDFIVNGHFRQESTENQLSTVKCVANCIVVIVFTGIFTYLTFFSSHWFKVYVG
 >SiLPAAT5 Probable 1-acyl-sn-glycerol-3-phosphate acyltransferase 5 [*Sesamum indicum*] XP_011088344.1
 MESDSVLKLRGQRHRPLTPFRVIRGVLCILVVLTA FVLLVYFGFWTAIPLRFFSMHHSRKATAFIFGS
 WIALWPFWF EKINRTKVVFSGDCVPAEERVLLIANHRTEVDWMYLWDLALRKGCEGYIKYILKSSLMKLP
 VFGWVFHVM EFIPVVRKWEADELMMRQMLSSFRDPRDPLWLAVFPEGTDFT EQKCVRSQKYASENGLPIL
 KNVLLPKTKGFHACLENLKDSDAVYDITIGYRQNCPSFLDNAFGVDPSEVHIHVRRISLKEIPTSEDQT
 SSWLMNTFSLKDQMLSDFYTQGHFPNEGTTETSLSTVKCVNFILVMILTGTCTFLTFFSSIWFKIYVSLV
 CAYMASATYFDVRPSPIVH

>SiPAH1-1 Phosphatidate phosphatase 1 [*Sesamum indicum*] XP_011077414.2
 MNVVGKVSSFITQGVYSVATPFHPFGGAVDIIVVQQNDGTFRSTPWYVRF GKFGVLKGA EKVVRIEVNG
 VEANFHMFLDNSGEAYFVREVD PDKDSENLEDGREDNSTDFSNSDGGSKENDFSGQDASEFNNDVEDEIE
 VRDERVTLGMDRLERVESDSGIFYELHDEQSSIEGSVEFSEYDSSGFNSLESVEHALESQDSNSEVVLVS
 VDGHVLTAPISASERNAENVELGTPQFHLGPGEGETENFN RVEDPWNADYLRELDASAHEVTTENICKGNS
 ETRSSEQQLELSSGDGEHLCHVEETQDSADQDKELCTESSEYTTTRFKRREVF KSCVELLELELQSPTNN
 QENVGSSVEILEAANDLNEKSPLSPSINETEEGNVEISRDSNELSTHDTGDPGSVSSPELQVEAATNERN
 TSHMNHDGSDSMVPQSVSNQELQKQLEAHPTAKRVHNDQESHTDECSKSESHADASIEDGKSDLLAKLE
 ISLCGNLLHAGMGLNAAEDAFNANCVSLEEFKLSASSIVKNENLIVRLQGKYL PWCKAAHIVLGMAAYGL
 DLPVDVHDIIPVEQEVP GAKEDDSATTPTQSGGWRLWRPFRRVKTLEHNVSNSSNFVDSDSVSQGQVRVSS
 PLARSVSSPVARAVSTPTARAAADSPRKKIIRTNPVTTDEIASLNLKEGQNMVNFVFSTRVLGSQKVEAH
 IYLWKWNTRIVISDVGDTITKSDVLGQFMPLVGKDWTHSGIARLFCAIKENGYQLLFLSARAIVQSYLTK
 SFLFNLKQDGKSLPSGPVVISPDGLFPSLFREVIRRAPHEFKIACLEDIKALFPDPYNPFYAGFGNRD TD
 ELSYRKIGIPKGKIFIINPKGEVA INNRVDVKSYSLSLHTLVNDMFPTSLVEQEDYNSWNYWKMLPDDID
 >SiPAH1-2 Phosphatidate phosphatase 1 [*Sesamum indicum*] XP_011094787.1
 MDVVGKVSSFITQGMYSVATPFHPFGGAVDIIVVKQDGTFRSTPWYVRF GKFGVLKGTEKVVRIEVNG
 VEANFNMYLDNSGEAYFVREVYPGKDDDECLTNSENIDVNSIGSSNIDDLKESDLYGQEVNDFNNGELE
 VQNKHLNLGRGRLQRVESDTGYVFEYFQDEPSLEGSVELPEYGSNTCDTLETVEDALESENSNSEVVLVS
 VDGHILTAPISSSETDAEDVELDTPQFHLGPAGATEEYDTGETTWTSDYLSDLHSSAHNIDTEETCDANS
 GTLPPKHPSEPCEGDQEHLFHTQETQATTDN GKEVCINSSSGSTSSALKRDDVFKSCLELSELAVQSANT
 NKVDVGSSDEIHEATEDPHKKS PGSPGNPETEKRNEILTKDGLSPTDSGYPI SISLPEVQVEAAIHER
 NTLDMDDDGSDSKHLQFVSSNQEPQDQTDVDLAVESKPSGEEVHASDDGYCKSELAEPHKAAPAPNEDTK
 SDASTRPEISLSENVQHAGMESRTVEDAFDPNHTSIKPHDIIPGNVETAERKIDSSMTSARWRLWPIPF
 RRVKTLEHSDTISSCDEVFVDSECVSPRQPPTTPIARVATDSPRKQIIRTNPVTTDQIASLNLKEGQNMV
 NFVFSTRVLGSQKVEAH IYLWKWNARIVISDVGDTITKSDVLGQFMPLVGKDWTHSGIARFFSAIKENGY
 QLLFLSARAIVQAYLTKNFLFNLKQDGKSLPDGPVVISPDGLFPSLYREVIRRAPHEFKIACLEDIKALF
 PDPYNPFYAGFGNRD TDELSYRKIGIPKGKIFIINPKGEVA INHRVEVKAYTSFHTLVNDMFPTSLVEQ

EDYNSWNYWKMLPDVE

>SiPAH2 Phosphatidate phosphatase 2 [*Sesamum indicum*] XP_020550995.1
MQAVGKLGSIYSRVSIVTVSGPFHPFGGAVDIIVVEQPDGSYKSSPWYVRFQGVLTKEKVVSIISVNG
VEADFHMYLDHKGEAFFLKEVDIDAGESPGSPSSSLGEDMDKQPQSRLPLKSKSCNYNSDFPDSIGNERN
GNCVAVGRSTSRRSQILSLVFGRRMTKEEGGQEEKNAYDMVRTDSLERAIEAADLLDLKWSNKLASSRNR
KDNASRFSAVDTSKDEANINLQVGSSSYDETGLISHTSYQELKSTLEENVVEMKCLSTECLVQTPTKAES
VGYTNLSDADALMTDKRGLAESSVITVSEFAKAGSRIEDSVEKLNGLADTSFSESNNPRDRTRSLYHCQAS
GTSRVVLDASIERKTNLICHGGCEEVCVQCEAVQDMALKSEPERDMIHAQEKSLTIQHGLRKGDGLSFVQ
EEKTTMNRGTIYGASESTVTECYPVLVPLHQSNQYIKDVDSQSVATASSLSYSTCSPAEEQITILAKGEIN
KHSTSVGPVCDTHISVSNFVPPCIQASRISEEEQLLFGIPDNNGYIDGKQMGSLSHADLEGENADSSFPSPG
VAGVNESNDATGCSVFSLDHSHVIDDYINDANLERRKLRSISGDVCLNKTGHVQSKELMRMVRSLPLSLPLR
NNLEVSDDLGHASNPISLYPGMEGGANRNNHQLPCAQTMAEDVNVLENKENKEEHTNPSIGNSPRFVDSLGRSR
RGWPFSSFKRSRSMKVS HVDTNSSEIPSAVKFLNDSSELEGKDVANGKVNKKIVRTLTPTEQLASLKLK
EGKNIVIFTFTSTAMLGKQVVDARIFLWRWDARIVISDVGDTITRSDLLGQVMPLVGMDSQSGVAHLFSA
IKENGYQLLFLSARAISSQSFHTRQFLFNKQDGKALPDGPVVISPDLFPPLFREVVRAPHEFKIACLE
DIKALFPGDRNPFYAGFGNRDTDEFSYLVKVGIPKGKIFIINPKGEIVVNRVDTKSYLSLHALVHGMFPT
MLSSEQEDFNSWNYWKLPPPAIDV

>SiDGAT1 Diacylglycerol O-acyltransferase 1 [*Sesamum indicum*]
NP_001291334.1

MAILDSPESFDTTSSSAGNDGDHRSTLRRRPSARAAEVLLDSNSNSLEADTVVNGAESDRNDGNSTGNLC
GRVVESLNEEQRSESAGEGLSYVKEKEEEKGKENGEGIGEGKGGEALAVKFAYRPSAPAHRKIKESPLSSD
AIFKQSHAGLFNLICIVVLVAVNGRLIIENLMKYGWLKSGFWFSSTSLRDWPLLCCCLSLPVFPLAAFLV
EKSQVQNYISEWVAVFLHVIITTEILYPVVILRCGSAVLSGVTLMLFACIVWLKLVSYAHTNYDLRVL
SKSLDKWEALSSYWNVDYSYDVSFKSLVYFMVAPTLCYQPSYPRTACIRKGWVVRQLVKLVIFTGLMGFI
VEQYINPIVQNSQHPLKGDLLYAIERVLKLSVPNLYVWLCMFYCFHFLWLNILAEELLCFGDREFYKDWNN
ARTVEEYWRMWNMPVHKWVRHIYFPCLRNGIPKGVAVLVAFFVSAIFHELCAIAPCHIFKFWAFLGIMF
QVPLVIVTNFLQDKFKNSMVGNNMFWCFFCILGQPMVSVLLYYHDLNMRKASAR

>SiDGAT2 Diacylglycerol O-acyltransferase 2D [*Sesamum indicum*]
XP_011098009.1

MALEADGDVGQRKSPSAEAAAPSTPAEFRGSQGPVLHTILALVLWLGSVHFNVVVVLVSFIFLPPFQKALG
VIGLLLILMVIPIDERSKLGRKLSRYICKHAVGYFPVNLYVEDIKAFDPNEAYVFGYEPHSVWPIGVVAL
ADHTGFMPLPKMKVLASTAVFYTPLLRHVWSWLGLAPATRKNTSLLLSGYSCIIIPGGVQEAIFYMERGS
EIAFLQKRKGFVRIAIETGKPLVPVFCFGQSDVYKWWKPSWKLYREFARAIFAPIVFWGVLGSPLPFRR
PLHVVVGRPILLKKNPQPTREEVAEVHSQFVEGLEGLFERHKTRVGCTDVQLRIL

>SiDGAT3 Diacylglycerol O-acyltransferase 3, [*Sesamum indicum*]
XP_011086024.1

MDSAAVVLKQPLRISSSCYSASPSKELRTFSESVMVGRRRRPRPGILSSGFCDDQGHLLQYNSNSGPPSSSRG
MTMMTVMSGKQDKTTTEKAPKKMKKKKQLKLLKGLSRDLSTFSQMGFGLSDVALLDQVKGNMISEAAEL
LLEQLQKLRADEKKLKRKMKEEKARLKAANKQSAHMDCERSSSSSSSESDSECGEVIDMTDLKRAQAKQS
IMQQVIEEATSSYSTPVMPLESNVSEARLVVPVFPISITIPESQLRSPHNVENECSSGTSSSFINTGNLV
EENVSSPSCSKKIEVCMGGKCKKSGAGALLEEFQRVVVGIEGAVSGCKCMGKCRDGNPVKVLRGFDGGVAD
ADAAPRAPANSLCIGVGLEDVNMIVANFLGENHNQLGLAAS

>AtaccB1 Acetyl-CoA Carboxylase biotin-containing subunit [*Arabidopsis thaliana*] AAC49114.1

MASSSFVSTSPAAAASVYAVTQTSSHFPIQNRSRVSRFLSAKPKLRFLSKPSRSSYPVVKAQSNKVSTG
ASSNAAKVDGPSSAEGKEKNSLKESSASSPELATEESISEFLTQVTTLVKLVDSRDIVELQLKQLDCELV
IRKKEALPQPAPASYVMMQQPNQPSYAQQMAPPAAPAAAAPAPSTPASLPPSPPTPAKSSLPTVKSPM
AGTFYRSPAPGEPFFIKVGDKVQKGQVLCIVEAMKLMNEIESDHTGTVVDDIVAEDGKPVSLDTPLFVVQP
VESAP

>AtaccB2 Biotin carboxyl carrier protein 2 [*Arabidopsis thaliana*] NP_568316.1

MASLSVPCVKICALNRRVGSPLGISTQRWQPQPNGISFSPSDVSNHSAFWRLRATTNEVVSNSPTMTNGG
YMNGKAKTNVPEPAELSEFMAKVSGLLKLVDSDKDIVELKQLDCEIVIRKKEALQAVPPAPVYHSMPP
VMADFSMPPAQPVLPSPPTPTSTPATAKPTSAPSSSHPLKSPMAGTFYRSPGPGEPFFVKVGDKVQKG
QIVCIIIEAMKLMNEIEAEKSGTIMELLAEDGKPVSVDTPLFVIAP

>BnaccB1 Biotin carboxyl carrier protein of acetyl-CoA carboxylase 1, [*Brassica napus*] XP_013649844.1

MASSSFSLTSPAASVYGATQASSQRPLPTTSSRLPRSVSRFLSAKPKLRFLSKPSRSSYPVVKAQSNQVG
GNASSKASAPVKIDESSAEKDSNTSSSAELATEESISEFLTQVTTLVKLVDSRDIVELQLKQLDCELV
RKKEALPQAQTPAPYVMMQQPNQPSYVQATAPPPPSAPAPSTPASSPPSPSPPAKSSLPTVKSPMAGTF
YRSPGPGEPFFIKVGDKVQKGQVLCIVEAMKLMNEIESDQTGTVVDDIVAEDGKPVSLDTPLFVVQP

>BnaccB2 Biotin carboxyl carrier protein of acetyl-CoA carboxylase 2, [*Brassica napus*] XP_013728269.1

MASLSVPYAKISASNRRVGSIPGIRRPQLNAVSRFSPSDVSQTQSTTWKLRATTNEVVSNSPTVTNGGCLN
GNVKSNPESAELSDFMAKVSGLLKLVDSDKDIVELKQLDCEIVIRKKEALAAPPAPVYHSMPPPMAGF
PMAPSHPVAPPFPSPSSAPETAKPVTTPSSSHPLKSPMAGTFYRSPGPGEPFFVKVGDKVQKGQVVC
IIEAMKLMNEIEAEKSGTITELLAEDGKPVSVDTPLFTIVP

>GmaccB2 Biotin carboxyl carrier protein subunit [*Glycine max*] AAG44776.1

MASFTIPCPCVVPFAHLGLNSQTQQRNALGLKKSLSFGSLSSDSAPNGIQCLNKKQSSVWKLQAQPK
AVTVENSAPVQVNGPKIAPPEEKDDHNGKPSGPSTADASSISAFMNQVSDLVKLVDSKDIMELQLKQAN
CELVIRKKEALLPPPATFVAPVSQPFYPTNSLPAAPPSVATSTPASSPSSKAAPALPPAKASKSSHPAL
KCPMAGTFYRSPAPGEPFFVKVGDKVQKGQVICIIEAMKLMNEIEADQSGTVAEVVAEDGKPVSVDTPLF
VIVP

>GmaccB1 Biotin carboxyl carrier protein subunit [*Glycine max*] AAG44776.1

MASSLAPATKAATNLRLTHSLRFSPKPNLRFATKPGNTLLCTRVKAQLNEVALDSSSNATSPPMKAKSK
EEPPAKPLAEPSSSVLATQESVSQFITQVASLVKLVDSRDIVELKQLKQHDVEVTIRKKEAMPQPPAPQP
SVVYSPPPALPPPPVAPSTPAPTLARATPTPTSAPAVKSAKSSLPLKSPMAGTFYRSPAPGEPSFVKV
GDKVKKGQVVCIIEAMKLMNEIEADQSGTIVEIVAEDAKSVSVDTPLFVIQ

>AhaccB1 Biotin carboxyl carrier protein of acetyl-CoA carboxylase, [*Arachis hypogaea*] XP_025649626.1

MASSFASTASSASSSLPTPSKPKPKINHFRFSHNSLFRSLSPKPNLPFLTSGSPQCIVCPRVKAQLNEV
SLDGSSNAVAPTTANSEAEATAKPSSTSSGVLASQESISQFITQVASLVKLVDSRDIVELQLKQHDCEV
MIRKREAMPQPQPPAQPAMYPPPSLAAPPVAPASSPAPAPTATRAASAPPAKSTKSSLPLKCPMA
GTFYRSPGPGEPFFVKVGDKVKKGQVLCIIEAMKLMNEIEADQSGTIVEILAEDGKPVSDMPLFVIEP

>AhaccB2 Biotin carboxyl carrier protein of acetyl-CoA carboxylase 2, [*Arachis hypogaea*] XP_025681786.1

MASFTVPCPCPSPSLGLNSQKLLKPSLSFGSLAAESASSGIRCLNGKQFSVQKLQAQRREAVTTIENSA
PVLVSGPKVAAPNEKEDQNGKPGGTTTDPSSLVSAFMAQVADLVKLVDSRDIVELQLKQSDCELMIRKKEA
LEPPPQVIAPASAPMHYAAYSPPPPPPPVAASSTPASSPPAKAAPALPSPGKASTSGHPPLKCPMAGTF
YRSPAPGEPFFVKVGDKVQKGQVICIIEAMKLMNEIEADQGTITEILAEDGKPVSVDTPLLVIA

>AhaccB1-1 Biotin carboxyl carrier protein 1-1 [*Arachis hypogaea*] ACO53609.1

MASSFASTASSASSSLPTPSKPKPKINHFRFSHNSLFRSLSPKPNLPFLTSGSPQCIVCPRVKAQLDEV
SLDGSSNAVAPTTANSEAEATAKPSSTSSGVLASQESISQFITQVASLVKLVDSRDIVELQLKQHDCEV

MIRKREAMPQPQPPAQPAMYPPPSLAAPPAAPASSPAPAPTPATRAASASPPAAKSTKSSLPPLKCPMA
 GTFYRSPGPGEPPFVKVGDKVKKGVLCIIEAMKLMNEIEADQSGTIVEILAEDGKPVSVDMPLFVIEP
 >AhaccB2-1 Biotin carboxyl carrier protein 2-1 [*Arachis hypogaea*]
 ACO53611.1
 MASFTVPCPKCPSPLGLNSQKLLKPSLSFGSLAAESASSGIRCLNGKQFSVQKLQAQRREAVTTIENSA
 PVLVSGPKVAAPNEKEDQNGKPGGTTTDPSSLVSAFMAQVADLVKLVDSRDIVELQLKQSDCELMIRKKEA
 LEPPSQVIAPASAPMHYAAYPSLPPPPPPAAASSTPASSPPAKAAPALPSPGKTSTSGHPPLKCPMAGTF
 YRSPAPGEPPFVKVGDKVQKGQVICIIEAMKLMNEIEADQGTITEILAEDGKPVSVDTPLLVIAPI
 >GhaccB1 Biotin carboxyl carrier protein of acetyl-CoA carboxylase
 [*Gossypium hirsutum*] ABU41516.1.
 MASSLSTTSSAAFTSVAKTTTALPNSTNLQLSIVSFRFSSRRNLRFSSKSLQHGQNSKTVVKAQLNEVAI
 DGSSNAAAPTIKSGAPTAEKDAKTSSDVSLAMATEESIAEFLNQVSSLVKLVDSRGIVELQLKQLDC
 ELVIRKKEALPQPPSAAPVVMQSPSQLPVMPPPPSPALPAGQASAAPTPAPSLAASKSAKSSLPPLKC
 PMARTFYRSPAPGEPPFVKVGDKVQKGQVLCIIEAMKLMNEIEADQSGTMVEILAEDGKAVSVDMPFLVIEP
 >AtaccC Acetyl Co-enzyme a carboxylase biotin carboxylase subunit
 [*Arabidopsis thaliana*] NP_198386.1
 MDASMITNSKSITSPPSLALGKSGGGVIRSSLCNLMMPSKVNFPRQRTQTLKVSQKKLKRATSGGLGVT
 CSGGDKILVANRGEIAVRVIRTAHEMGIPCVAVYSTIDKDALHVKLADAVCIGEAPSNQSYLVI PNVL
 AAISRGTMLHPGYGFLSENALFVEMCRDHGINFIGNPDSIRVMGDKATARETMKNAGVPTVPGSDGLL
 QSTEEAVRVANEIGFPVMIKATAGGGGRGMRLAKEPGEFVKLLQQAQSEAAAAFGNDGCYLEKFVQNPRI
 IEFQVLADKFGNVVHFGERDCSIQRRNQKLLLEEAPSPALTAELRKAMGDAAVAAAASIGYIGVGTVEFLL
 DERGSFYFMEMNTRIQVEHPVTEMIYSVDLIEEQIRVAMGEKLRKQEDIVLRGHSIECRINAEDPFKGF
 RPPGGRITSYLPSSGGPFVRMDSHVYSDYVPPSYDSLLGKLIVWAPTREKAIERMKRALNDTIITGVPTT
 INYHKLILDVEDFKNGKVDTAFIGVKEHEELAEPEIVAVKDLTNATV
 >CoaccC Biotin carboxylase [*Camellia oleifera*] ACS14663.1
 MDSALTFCKSVHSPGLFVGRSRGIQSPQCSVMVGSRVNFRQSVRVAQISRKSEKRGALCATCRDEKI
 LVINRGEIAVRIIRTAHEMGIPCVAVYSTIDKDALHVKLADAVCIGEAPSSQSYLVI PNVL
 TMLHPGYGFLAENAVFVEMCREHGINFIGNPDSIRVMGDKATARETMKNAGVPTVPGSEGLLQNTTEAV
 RLSEEIGFPVMIKATAGGGGRGMRLAKEPDEFVKLLQQAQSEAAAAFGNDGVYLEKYIQNPRIEFQVLA
 DKFGNVVHFGERDCSIQRRNQKLLLEEAPSPALTPELRKAMGDAAVAAAASIGYIGVGTVEFLLDERGSFY
 FMEMNTRIQVEHPVTEMISSVDLIEEQIRVAMGEKLRKQEDIVLRGHSIECRINAEDAFKNFRPPGGRIT
 TAYLPSSGGPFVRMDSHVYPDYVPPSYDSLLGKLIVWAPTREKAIERMKRALNDTIIGVPTTIDYHKLIL
 LDVEDFKNGKVDTAFIGVKEHEELAEPEIVAVKDLTNATV
 >AhaccC2 Biotin carboxylase 2, [*Arachis hypogaea*] XP_025636875.1
 MEATMAACNSLSSPSVPIPGLYAGTSRGIKNSQCSFLGATKVNFPSTMPGTCQLNHKHKTRSGALHATC
 QGDKILVANRGEIAVRVIRTAHELGI PCVAVYSTIDKDALHVKLADAVCIGEAPSSQSYLLIPNVL
 ISRRCTMLHPGYGFLAENAVFVEMCREHGINFIGNPDSIRVMGDKSTARDTMKNAGVPTVPGSDGLLQ
 TEEAIRLANEIGFPVMIKATAGGGGRGMRLAKEPGEFVKLLQQAQSEAAAAFGNDGVYLEKYIQNPRIE
 FQVLADKYGNVVHFGERDCSIQRRNQKLLLEEAPSPALTPELRKAMGDAAVAAAASIGYIGVGTVEFLLDE
 RGSFYFMEMNTRIQVEHPVTEMISSVDLIEEQIRVAMGAKLRKQEDII LRGHSIECRINAEDAFKGF
 RPPGGRITAYLPSSGGPFVRMDSHVYPDYVPPSYDSLLGKLIVWAPTREKAIERMKRALDDTIITGVPTTIE
 YHKLILDIEDFRNGKVDTAFIGVKEHEELAEPEIVAVKDLTNATV
 >AhaccC1 Biotin carboxylase 1 [*Arachis hypogaea*] XP_025700754.1
 MESRIMAALNSVTSPHLPSPGLYAVENSISQCSFSAGSKKVSFPRQCSHVTKTTRAARDGGAGGAL
 GATCQAEKILVANRGEIAVRVIRTAHEMGIPCVAVYSTIDKDALHVKLADAVCIGEAPSSQSYLLIPNVL
 LSAAISRCTMLHPGYGFLAENAVFVEMCREHGINFIGNPDSIRVMGDKSTARDTMKNAGVPTVPGSDG
 LLQTTEEAIRLANEIGFPVMIKATAGGGGRGMRLAKEPDEFVKLLQQAQSEAAAAFGNDGVYLEKYVQNP
 RHIEFQVLADKYGNVVHFGERDCSIQRRNQKLLLEEAPSPALTPELRKAMGDAAVAAAASIGYIGVGTVEF
 LLDERGSFYFMEMNTRIQVEHPVTEMISSVDLIEEQIRVAMGEKLRKQEDIVLRGHSIECRINAEDAFK
 GFRPPGGRITAYLPSSGGPFVRMDSHVYPDYVPPSYDSLLGKLIVWAPTREKAIERMKRALDDTIITGVPT
 TIDYHKLILDIEDFRNGKVDTAFIGVKEHEELAEPEIVAVKDLTNATV
 >AhaccC4 Biotin carboxylase 4 [*Arachis hypogaea*] ACO53619.1
 MEATMAACNSLSSPSVPIPGLYAGTSRGIKNSQCSFLGATKVNFPSTMSRTCQLNHKHKTRSGALHATC
 QGDKILVANRGEIAVRVIRTAHELGI PCVAVYSTIDKDALHVKLADAVCIGEAPSSQSYLLIPNVL
 ISRRCTMLHPGYGFLAENAVFVEMCREHGINFIGNPDSIRVMGDKSTARDTMKNAGVPTVPGSDGLLH
 TEEAIRLANEIGFPVMIKATAGGGGRGMRLAKEPGEFVKLLQQAQSEAAAAFGNDGVYLEKYIQNPRIE

FQVLADKYGNVVHFGERDCSIQRRNQKLLLEAPSPALTPELRKAMGDAAVAAAASIGYIGVGTVEFLLDE
RGSFYFMEMNTRIQVEHPVTEMISSVDLIEEQIRVAMGAKLRYKQEDIILRGHSIECRINAEDAFKGF
PGGRITAYLPSGGPFVVRMDSHVYPDYVPPSYDSLLGKLIVWAPTREKAIERMKRALDDTIITGVPTTIE
YHKLILDIEDFRNGKVDTAFIGKHEEELTMPPQKMVPAINKAKEFVGATV

>AhaccC3 Biotin carboxylase 3 [*Arachis hypogaea*] AC053618.1

MGATMAACNSLSSPSVPIPGLYAGTSRGIKNSQCSFLGATKVNFPSTMSRTCQLNHKHKTRSGALHATC
QGDKILVANRGEIAVRVIRTAHELGI PCVAVYSTIDKDALHVKLADESVCIGEAPSSQSYLLIPNVLSAA
ISRRCTMLHPGYGFLAENAVFVEMCREHGINFIGPNPDSIRVMGDKSTARDTMKNAGVPTVPGSDGLLQS
TEEAIRLANEIGFPVMIKATAGGGGRGMRLAKEPGEFVKLLQQA KSEAAAAFGNDGVYLEKYIQNPRHIE
FQVLADKYGNVVHFGERDCSIQRRNQKLLLEAPSPALTPELRKAMGDAAVAAAASIGYIGVGTVEFLLDE
RGSFYFMEMNTRIQVEHPVTEMISSVDLIEEQIRVAMGAKLRYKQEDIILRGHSIECRINAEDAFKGF
PGGRITAYLPSGGPFVVRMDSHVYPDYVPPSYDSLLGKLIVWAPTREKAIERMKRALDDTIITGVPTTIE
YHKLILDIEDFRNGKVDTAFIGKHEEELTMPPQKMVPAINKAKEFVGATV

>BnaccC Biotin carboxylase [*Brassica napus*] ADI79335.1

MDASMITNPKSIVSLPSLFMGRSGGSIRSSQCNVTMGQAVSFPSQKTKTLKVS RNVKRRSGGGGAFAATC
SSGDKILVANRGEIAVRVIRTAHEMGI PCVAVYSTIDKDALHVKLADEAVCIGEAPSNQSYLLIPNVLSA
AISRGCTMLHPGYGFLAENALFVEMCREHRINFIGPNPDSIRVMGDKSTARETMKNAGVPTVPGSDGLLQ
STEEGVRLANEIGYPVMIKATAGGGGRGMRLANEPSEFVKLLQQA KSEAAAAFGNDGVYLEKYVQNPRHI
EFQILADKFGNVVHFGERDCSIQRRNQKLLLEAPSPALTPELRKAMGDAAVAAAASIGYIGVGTVEFLLD
ERGSFYFMEMNTRIQVEHPVTEMIYSDV LIEEQIRVAMGEKLRYTQDEIVLRGHSIECRINAEDPFKGF
PGGRITSYLPSSGGPFVVRMDSHVYPDYVAPPSYDSLLGKLIVWAPTREKAIERMKRALNDTIITGVPTTIE
EYHKLILEVEDFKNGKVDTAFIGKHEEELAE PHEIVPVKDLTNVAA

>HaaccC Biotin carboxylase 2 [*Helianthus annuus*] XP_021986207.1

MDSAAVTFC SKPITSPPGVFIGRSSGIKSSQCNFLVGKNLNF PKQRFQASEKAHRS AKREGALGVT CRAE
KILVANRGEIAVRVIRTAHELGI PCVAVYSTIDKDALHVKLADESVCIGEAPSNQSYLLIPNVLSAAISR
GCTMLHPGYGFLAENAVFVEMCREHGINFIGPNPDSIRVMGDKATARDTMKNAGVPTVPGSDGLLQSTEE
GIRLADEIGFPVMIKATAGGGGRGMRLAKERDEFVKLLQQA KSEAAAAFGNDGVYLEKCI LNPRHIEFQV
LADKYGNVVHFGERDCSIQRRNQKLLLEAPSPALTPELRKAMGDAAVAAAASIGYIGVGTIEFLLDERGD
FYFMEMNTRIQVEHPVTEMISSVDLIEEQIRVAMGEKLRYTQDDIVLRGHSIECRINAEDAFKNFRPGPG
RITSYLPSSGGPFVVRMDSHVYTDYVPPSYDSLLGKLIVWAPTREKAIERMKRALDDTIITGVPTTIEYHK
LILDIEDFKNGKVDTAFIGKHEDELAEPQKPSTSNAAKEVAKAVA

>AtaccA Carboxyltransferase alpha subunit [*Arabidopsis thaliana*]
BAD93727.1

MASISHSSALGGASASASDYLRSSSNGVNGVPLKTLGRAVFTTIRRKDLAVTSRLKKGKKFEHPWPAN
PDPNVKGGVLSYLAEFKPLGDTQKPVTLDFEKPLVELEKKIVDVRKMANETGLDFTEQIITLENKYRQAL
KDLYTHLTPIQRVNIARHPNRPTFLDHIHNITDKFMELHGDRAGYDDPAIVTGIGTIDGKRYIFIGHQKG
RNTKENIMRNFGMPTPHGYRKALRMYYADHHGFPIVTFIDTPGAYADLKSEELGQGEAIANNLR TMFGL
KVPILSIVIGEGSGGALAIGCANKMLMLENAVFYVASPEACAA ILWKTSKAAPEAAEKL RITSKELVKL
NVADGIIPEPLGGAHADPSWTSQQIKIAINENMNEFGKMSGEELLKHMAKYRKIGVFIEGEP IEP SRKI
NMKKREAVFSDSRKLQGEVDKLKEQILKAKETSTEAPSSSEVLNEMIEKLKSEIDDEYTEAAI AVGLEER
LTAMREEFSKASSEHLMHPV LIEKIEKLKEEFNTRLT DAPNYESLSKSKLNMLRDFSRAKAASEATSLKK
EINKRFQEAVDRPEIREKVEA IKA EVASSGASSFDEL PDALKEKVLKTKGEVEAEMAGVLKSMGLELDAV
KQNQKDTAEQIYAANENLQEKLEKL NQEITSKIEEVVRTPEIKSMVELLKVETAKASKTPGVTEAYQKIE
ALEQQIKQKIAEALNTSGLQEKQDELEKELAAARELAAEESDGSVKEDDDDDDEDSS ESGKSEM VNPSFA

>BnaccA Carboxyltransferase alpha subunit isoform 2 [*Brassica napus*]
ACN65504.1

MASMSHSSIALGGASASASDYLRSSANGVTGVSLRALGRRTMVTATTRSSNLYVTARLKKGKKFDHPWPA
NPDPNVKGGLSYLSEFKPLGNAQKPVTLDFERPLVELEKKIVDVRKMAEETGLDFTEQIITLET KYRQA
LKDLYTHLTPIQRVNIARHPNRPTFLDHIHNITDKFMELHGDRAGYDDPAIVTGIGTIDGKRYMFI GHQK
GRNTKENIMRNFGMPTPHGYRKALRMYYADHHGFPIVTFIDTPGAYADLKSEEKGQGEAIANNLR TMFG
LKVPILSIVIGEGSGGALAIGCANKMLMLENAVFYVASPEACAA ILWQTSKAAPEAAEKLRIASKELVN
LNVADGIIPEPLGGAHADPSWTSQQIKIAINENMNEFGKMSGEELLKHMAKYRKIGVFIEGEPVEPEKK
INMKRRDAVASTSRNLEGEVEKLREQILKAKEASPESEGEELSSQVLKEMIEKLKSDIDE EYTKAAKAM
GLEERLAATREEFSKANAEEHLMHPV LIEKIEKLKEEFNARLSEAPNYESLKAKLDMLKDFSRAKAASDA
ASVKKEINKRFQEAVRPEVREKVEAVKA EVASSGASSFEELSDELKEKVLKTKREVEAEMAVVLKSMGL
ELEAVKPNLKEVVAESPENIQEKIEKL NREITEKIEEVVRTPEIKSMVELLKVETAKASQMPDQGSQKI

EALEMQIKQKIADALSMGLQEKQEELEKELAAARELAGEESDESVKDDDDDEDGSGSGRSEIINPHFA
>GmaccA-1 Carboxyl transferase alpha subunit [*Glycine max*] AAF80496.1
MAASSASLSGASASDLLRSSTSGFNGVPLRTMGKGKLVLRNRFTVAARLRKVKKHEYWPWPNDPNVKG
GVLSHLSLKFPLKEKPKPVTLDFERPLVDLQKKIIDVQKMANETGLDFSDQILSLETKYHQALKDLYTHL
TPIQRVNIARHPNRPTFLDHVFNITEKFVELHGDRAGYDDPAIVTGLGTIDGRSYMFIGHQKGRNTKENI
QRNFGMPTPHGYRKALRLMEYADHHGFPIVTFIDTPGAYADLKSEELGQGEAIAHNLRSMFGLKVPVISI
VIGEGSGGALAIGCANKLLMLENAVFYVASPEACAAILWKTAKASPKAAEKLKITATELCKLQIADGVI
PEPLGGAHADPEWTSQQIKKAIKETMDELTKMNTTEELLKHRMLKFRKIGGFQEGIPIDPKRKANMKKRDL
SIAKIPDAELEVEVEKLEKQVLEAKESSPVPPKLDLDEMLKQLAREVDLEYSEAVKATGLTDSLLKLREE
VSKANADNQIVDPLLEGKIEKLRVEFEQQLRAAPNYGRLQNKLNLYSELCKVKLLSDGKKDNEAVTFKQE
LKKKIDNALS DPKIRETFEALKAIEKGVGASSASDLDELKKKIIIEFIKEVKEVKEVKEVIENQIESLVN
SSDDIKSKILQLKLEVPKAGETPDSEPKNRIGALVQLIKPSLVEAVDSSGLKDLFENLVNSDGLSLTHGDP
ARDSLTDDQ

>GmaccA-3 Carboxyl transferase alpha subunit [*Glycine max*] AAF89549.1
MAASSASLSGASASDLLRSSTSGFNGVPLRTLKGKGKLVLRNRDFTVAAKLRKVKKHEYWPWPNDPNVKG
GVLSHLSLKFPLKEKPKPVTLDFEKPLVDLQKKIIDVQKMANETGLDFSDQILSLENKYQQALKDLYTHL
TPIQRVNIARHPNRPTFLDHVFNITEKFVELHGDRAGYDDPAIVTGLGTIDGRSYMFIGHQKGRNTKENI
QRNFGMPTPHGYRKALRLMEYADHHGFPIVTFIDTPGAYADLKSEELGQGEAIAHNLRSMFGLKVPVISI
VIGEGSGGALAIGCANKLLMLENAVFYVASPEACAAILWKTAKASPKAAEKLKITATELCKLQIADGVI
PEPLGGAHADPEWTSQQIKKAIKETMDELTKMNTTEELLKHRMLKFRKIGGFQEGIPIDPKRKANMKKRDL
SIAKIPDAELEVEVEKLEKQVLEAKESSPVPPKLDLDEMLKQLAREVGLEYSEAVKATGLTDSLLKLREE
VSKANADSQIVDPLLKDKIEKLRVEFEQQLRAAPNYGRLQNKFKYLSSELCKVKLLSDANKDNQAVTFKQE
LEKKVDNALNDPKIRETFEALKAIEKGAGASSASDLDELKKKIVGFMIELKEVKEVKEVIENQIESLVN
SSDDIKSKILQLKLELPKAGETPDSESNNRIGDFIFKSSKIIIMAILLRDMFGNFKEIPC

>AhaccA-1 Acetyl-coenzyme A carboxylase carboxyl transferase subunit
alpha, [*Arachis hypogaea*] XP_025695444.1

MASSSAAASLAGGSASDLLRGSTSGFSGVPLRTLGRARLPLKQRDFSVSCKMRKVKKHEHPWPNDPNV
KGGVLSHLSLSPFKPLKEKPKPVTLDFEKPLIALQKKIIDVRKMANETGLDFSDQILSLETKYQQALKDLYT
HLTPIQRVNIARHPNRPTFLDHIYNITDKFVELHGDRAGYDDPAIVTGIGTIDGRYMFIGQQKGRNTKE
NIQRNFGMPTPHGYRKALRLMEYADHHGFPIVTFIDTPGAYADLKSEELGQGEAIAHNLRSMFGLKVPVI
SIVIGEGSGGALAIGCGNKLLMLENAVFYVASPEACAAILWKSAKAAPKAAEKLKITASELCRLEIADG
VIPEPLGGAHADPSWTSQQIKKAVNEAMDELTKMNTTEELLRHRMLKFRKIGGFQEGIPVEPKKKINMKKK
DIPIANKISDAELEVEVEKLEKQILDSKESSVEPRDLDDMIKQLQIEVDQEYSEAVNAIGLSDRMSKLK
EEVVKANTDNQFIDPLLKSKIEKLKEEFDQKLSTAPNFGRLNKNVNLKELSKVKRLQDQNKRTSALEQE
LKTTFDGMKNPRIKEYEALKSEIQAAGASSRDLDDDLKQKIVEFNKEFDSLLAESLKSAGMEVKIAP
ARPRDSSGESAEELGYESKIEELREGISKEIEKLANSSNIKSKIELLLKLEVAKAGETPDTESKNRIAALVQ
QIKQSLEEAVDSSSLKEEYENLVSKISSRDSEVEDGLTNDQLREKVGANRSFS

>AhaccA-2 Acetyl-coenzyme A carboxylase carboxyl transferase subunit
alpha [*Arachis hypogaea*] XP_025649321.1

MNTMSLTRGNYMDGRLIIIEHGIESANQCVGKDFLGGSRAICIWPKYLTSSRNNTNTNPNNGKWQRFN
VAAKIRKGGKHDYPWPKMDPNISSGYLTYLSHFKPLAEKPKPVTLDFEKPLVDLEKKIIIEVRSMADDTG
LDFSNQIEALESKYQQALKDLYTHLTPFQRLMIARHPNRPTVLDHILNITEKWVELHGDRAGYDDPAIVT
GLGTMDGKSYMFIGHQKGRNTKENITRNFAMPTPHGYRKALRMMKYADHHKFPITFVDTGAYADLKSE
ELGQGEAIAHNLRMTMFLKVPILTIVVTGEGSGGALAIACANKLFMLENSAFYVASPEACAAILWKSSKA
APKAAEKLKITAQEHYRLGIADGVIPEPLGGAHVDPWTWTSQQIKLTLTQAMEELTKMNEELFRHRHLKF
RSIGGFQEGIPVEPERKRNMPKPSDVNSSTLT DIESELQTLRKQILES KGPDPITNESIQKLKVEVDEEI
TKAII SMGLAEKVQSVRMELSKNSNQPLSTNMEEKVDRIMEEINMKMAQPGAYLGLKQKLKLDLTINSFI
EMKVKQEKLRNELNEKLSADTKAKIASLMDAQERMPDHELVEKAMEVQRELEEVLKSANLEIVGVMMKNV
ETPPADIKQKIVELNNEIIGEIDRVVNAEEGLKDQIKELNMIAQGLDSKDVEKMEAGIKERILAAALDAA
GVKEKIERMKKEEVESLSMAGFEDKIGEENGRC

>BnaccA2 Carboxyltransferase alpha subunit [*Brassica napus*] ACT83681.1
MASMSH2IALGGASASADYLRSANGVTGVSRLALGRRTMTVATTSSNNLYVTARLKKGKKFDHPWP
ANPDPNVKGGVLSYLSDFKPLGNAQKPVTLDFERPLVELEKKIVDVRKMAEETGLDFTEQIITLETYRQ
ALKDLYTHLTPIQRVNIARHPNRPTFLDHIHNITDKFMELHGDRAGYDDPAIVTGIGTIDGKRYMFIGHQ
KGRNTKENIMRNF GMPTPHGYRKALRMMYADHHGFPIVTFIDTPGAYADLKSEEKGQGEAIAANNLRMTL
GLKVPILSIVIGEGSGGALAIGRANKMLMLENAVFYVASPEACAAILWQTSKAAPEAAEKLKITSKELV

NLNVDAGI IPEPLGGAHADPSWTSQQIKIAINENMNEFGKMSGEELLKHRMAKYRKIGAFIEGEPVEPEK
KINMKRRDAVASTSRNLEGEVEKLREQILKAKEASPESEVELSSEVLNEMIEKLKSDIDEEYTKAAKAMG
LEERLAATREEFSKANAEHLMPVLIERIEKLKEEFNARLSEAPNYESLKAKLMDLKDFSRAKAASEAA
SVKKEIDKRFREAVERPVEKVEAVKAEVASSGASSFEELSDELKEKVLKTKREAAEMAVVLKSMGLG
LEAVKPNLKEVVAESPENIQEKLEKLNREINEKIEEVVRTPEIKSMVELLKVETAKASRMPDQGSQKIE
ALEMQIKQKIADALSMSGLQEQEELKEKELAAARELAGEESESVKEDDDDDDEDGSGSGRSEIINPHFA
>HaaccA-1 Acetyl-coenzyme A carboxylase carboxyl transferase subunit
alpha [*Helianthus annuus*] QGZ98789.1
MASVSQSPVNFSGSLSSATSASDLLRSSINGVNGVPLQTLGKGHVGP RRKGLNIVAKVRKVKKHEYWPWQ
DPDPNVKGGVLSHLSFPFKPLKEKPKPVTLEFEKPLMDLQKKIIDVQKMANETGLDFSDQIIISLENKYQQA
LKDLYTHLTPIQVRNIARHPNRPTFLDHVFNITDKFVELHGDRAGYDDPAVVTGIGTIDGRRFMFMGHQK
GRNTKENIQRNFGMPTPHGYRKALRMMYYADHHGFPIVTFIDTPGAFADLKSEELGQGEAIAHNLRTMFG
LKVPIVSIVMGEGGSGGALAIGCANKLLMLENAVIFYVASPEACAAILWKTAKASPKAAEKLKITANELCK
LQIADGIIPEPLGGAHADPHWTSEQIKKAILESMDLQTMGTEELLRHRMLKFRKIGGFQEGLPVEPEKK
VNMKRKEEPRPGLISDKVLQGEVNKLKEQIMKAKESSIDMDQNGLIEKLQREINYEFSAAKALGIEEK
LSQMREEFAKVENGQLTSGQIENLERLKNEFNEKLETAPNYGRLKYKLSLLKEITEAKVFAENYKKTLP
KAKVNEKFKEVLEKSTLKQKIENLKA EVEKSDVSSIEEFDQDLKEKVLEVREEVESEFINALESSGVHVT
SKIGQSSMSLVKAKVDELNAEINQIIQDVIESTPDLKSKIEMLKLEVVKDKNTPSKESKEKIEALQQQIK
EGVADVMSAAIKEKYEQLQAELAEELSGSGDGLIKESSYA
>HaaccA-2 Acetyl-coenzyme A carboxylase carboxyl transferase subunit
alpha, [*Helianthus annuus*] XP_022010319.1
MASVSQSPVTFSGSLSSATSASDLLRSSMNGVNGVPLKTLGKGHVGHGRKGLNIVAKVRKVKKHEYWPWQ
DPDPNVKGGVLSHLSFPFKPLKEKPKPVTLEFEKPLMDLQKKIIDVQKMANETGLDFSDQIIISLENKYQQA
LKDLYTHLTPIQVRNIARHPNRPTFLDHVFNITDKFVELHGDRAGYDDPAVVTGIGTIDGRRFMFMGHQK
GRNTKENIQRNFGMPTPHGYRKALRMMYYADHHGFPIVTFIDTPGAFADLKSEELGQGEAIAHNLRTMFG
LKVPIVSIVMGEGGSGGALAIGCANKLLMLENAVIFYVASPEACAAILWKTAKASPKAAEKLKITANELCK
LQIADGIIPEPLGGAHADPQWTSMQIKNAILDSDMLEKMGTEELLRHRMLKFRKIGGFQEGLPVDPEKK
VNMKRKEEPRPGLISDKALQGEVNKLKEQILKAKETSSINMDQNGLIEKLQREINYEFSAAKALGIEEK
LSKMREEFAKAENEQLTPGQIKNLENLKNFENENLATAPNYGRLKYKLSLLKEITEAKTFAENYKKA
LPLKAKVNEKFKEVLEKPTLKQNIENIKAEIEKSGVSNIEEFDQELKEKVLEVREQVESEFVNALESSGVHVT
SKVDQTSMSMIKAKVDELNAEINQIIQDVIESTPDLKNKIEILKLEIVKDKNAPSKESKEKIESLQQQIK
QGVGDVMSYAAVKEKYEELQAELAEELSGVSGDGLIKEPIYA

>AtaccD Acetyl-CoA carboxylase beta subunit [*Arabidopsis thaliana*]
NP_051068.1
MEKSWFNFMFSGKELEYRGELSKAMDSFAPGEKTTISQDRFIYDMKNFYGWDERSSSYSSSYNNVDLLV
SSKDIRNFISDDTFFVRDSNKNSYSIFFDKKKKIFEIDNDFSDEKFFYSYCSSSYLNNRSKGDNDLHYD
PYIKDTKYNCTNHINSCIDSYFRSYICIDNNFLIDSNNFNESYIYNFICSESGKIRESKNYKIRTNRRS
NLISSKDFDITQNYNQLWIQCDCNYGLMYKKVKMNVCQCGHYLKMSSSERIELSIDPGTWNPMDEDMVS
ADPIKFHSKEEPEYKNRIDSQKTTGLTDAVQTGTGQLNGIPVALGVMDFRFMGGSMGSSVGEKITRLIEY
ATNQCLPLILVCSSGGARMQEGSLSLMQMAKISSVLCDYQSSKKLFYISILTSPTTGGVTASFGLGDI
IAEPYAYIAFAGKRVIEQTLKAVPEGSQAESLLRKGLLDAIVPRNLLKGVLSSELFQLHAFFPLNTN
>GmaccD Beta-carboxyltransferase subunit [*Glycine max*] AAA80643.1
MEKWWFNSMLFNRKLEYRCELSKSMDSLGPIENTSLREDPKILTIEKKIHRDLDYLEMEGFFSSDLNTV
SKNDDDHMYETQFSFNNNITSFIDSCIESFNLGIDKYNDIYFNYSYIFLGRNCSESNNSTSIITSTN
DTNDSSTIGESSNNLDESQYKHLWLECENCYGLNYKKFFKSKMNICEYCGYHLKMSSDRIELSIDSG
TWNPMDEDMVSLDPIEFHSEEEPYKDRIDSQYRKTGLTEAVQTGTGQLNGIPVAIGIMDFQFMGGSMGSA
VGEKITRLVEYATNQLPLILVCASGGARMQEGSLSLIQMAKISSALYDYQKNKKLFYVILTSPTTGGV
TASFGLGDI IIAEPNAYIAFAGKRVIEQTLNKA VPEGSQAAYLFHKGFLFDSIVPRNLLKGVLSSELFQF
HNSFSLTKNDKA
>AhaccD Beta-carboxyltransferase 1 [*Arachis hypogaea*] AC053622.1
MEKGWFNSMLFYRQLEYRCGLSNSMDSFGPVENTSASEDPILIDMEKDFPSWNDSNSSYSNVLYGV
NIRNFLSDKILLVRDNNQRNRYSIYFDIENQFLEISNDPSFLSEPESLFDSYNKNSSYLNNVSKRHENH
YMYDTKSSWKNGIHNCIESYLSQICIVSHILGESDKYNDYSYFYSICGKGGNSSESEGSSIKTTITNEN
LTKREDSKDLDETQYKHLWIECENCYGLNYRKF FFSKMNICEHCGYHLKMSSSDRIELLIDPGTWNPM
EDMVSMDDPIEFHSEEESESYKNRMSYQYRKTGLTEAVQTGTGQLNGIPVAIGIMDFQFMGGSMGSSVGEK

ITRLVEHAGNQLLPLILVCASGGARMQEGSLSLMQMAKISSALYEQKNKRLFYVSILTSPTTGGVTASF
GMLGDIIIAEPDAYIAFAGKRVIEQTLNNTIPEGSQVAEYLFQKGLFDSIVPRNLLKGVLSLSELFQLHAFF
PL
>BnaccD Acetyl CoA carboxylase carboxyltransferase (beta subunit)
[*Brassica napus*] CAA90747.1
MEKSWFNLMSKGELEYRGELSKAMDSFAPIEKTTISKDRFIYDMDKNFYGWGERSSSYYNNVDLLVNSKD
IRNFISDDTFFVRDSNKSYSIYFDIEKKKFEINNDLSLEIFFYSYCSSSYLNNRSKGDNDLHYDPYIK
DTKYNCNNHINSCIDSYFRSHICINSHFLSDSNNSNESYIYNFICSESGSGKIRESKNDKIRTNSNRNLL
MSSKDFDITKNYNQLWIQCDNCYGLKYKKVEMNVCEECGHYLMKMTSSERIELSIDPGSWNGMDEDMVSAD
PIKFHSREEPYKKRIASAQKKTGLTDAIQGTGTGQLNGIPVALGVMDQFMGGSMGSSVVGDKITRLIEYAT
NQCLPLILVCSSGGARMQEGSLSLMQMAKISSVLCQYSSKKLFYISILTSPTTGGVTASLGMGLGDIIIA
EPYAYIAFAGKRVIEQTLKKAVPEGSQAESLLRKGLLDAIVPRNPLKGVVSELFLHAFFPLNKNEIK
>NtaccD Acetyl-CoA carboxylase beta subunit [*Nicotiana tabacum*]
MTIHLLYFHANRGQENSMERWWFNSMLFKKEFERRCGLNKSMSGLGPIENTNEDPNRKVKNIHWRNRDN
SSCSNVLDYLFVGKDIRNFISDDTFLVSDRNGDSYSIYFDIENHIFEIDNDHSFLSELESSFYRNSNYR
NNGFRGEDPYNSYMYDTQYSWNNHINSCIDSYLQSQICIDTSIISGSENYGDSYIYRAVCGGESRNSSE
NEGSSRRTRTKGSDLTIRESSNDLEVTQKYRHLVWCENCYGLNYKKFLKSKMNICEQCGYHLKMSSSDR
IELLIDPGTWDPMDEDMVSLDPIEFHSEEPYKDRIDSYQRKTGLTEAVQTGIGQLNGIPVAIGVMDQF
MGGSMGSSVVGKITRLIEYAANQILPLIIVCASGGARMQEGSLSLMQMAKISSALYDYLNNKKLFYVSIL
TSPTTGGVTASFGMLGDIIIAEPNAYIAFAGKRVIEQTLNKTVPESQAAYELFQKGLFDLIVPRNLLKS
VLSELFKLHAFFPLNQKSSKIK

>AhFabD1-1 Malonyl-CoA:ACP transacylase 1-1 [*Arachis hypogaea*] ACJ07137.1
MQALLHHSPLIRTSHTSSFPAMASSSLTLPSLSLNNFPSSPSNAHSRTFNLPLLRSRVFMVSVASGSQVSVL
NDALFSDYKPSNAFLFPGQGAQAVGMGKEAQNVPAAVLYKKANEILGYDLLDICINGPKDKLDSTVLSQ
PAIYVTSLAARELLRARDGGQQIIDSVDVTCGLSLGEYALAFAGAFSFDGLKLVLKLRGEAMQDAADAA
KSAMVSVIGLDSEKVQQLCDAANQEVPEAEKVQIANYLCPGNYAVSGGLKGVEVLESKAKSFKARMTVRL
AVAGAFHTSFMEPAVSRLEAALAATEIRTPRIPVISNVDAQPHADPDTIKKILARQVTSPVQWETTVKTL
LNKGLKKSSELGPGKVIAGIIRVDDKGADIENTIGA

>AhFabD1-2 Malonyl-CoA:ACP transacylase 1-2 [*Arachis hypogaea*] ACJ07138.1
MQALLHHSPLIRTSHTSSFPAMASSSLTLPSLSLNNFPSSPSNAHSRTFNLPLLRSRVFMVSVASGSQVSVL
NDALFSDYKPSNAFLFPGQGAQAVGMGKEAQNVPAAVLYKKANEILGYDLLDICINGPKDKLDSTVLSQ
PAIYVTSLAARELLRARDGGQQIIDSVDVTCGLSLGEYALAFAGAFSFDGLKLVLKLRGEAMQDAADAA
KSAMVSVIGLDSEKVQQLCDAANQEVPEAEKVQIANYLCPGNYAVSGGLKGVEVLESKAKSFKARMTVRL
AVAGAFHTSFMEPAVSRLEAALAATEIRTPRIPVISNVDAQPHADPDTIKKILARQVTSPVQWETTVKTL
LNKGLKKSSELGPGKVIAGIIRVDDKGADIENTIGA

>GmFabD Malonyltransferase [*Glycine max*] NP_001238312.2
MSSSLALPSTPFFANGTRIFALKHSLPRSRVMSVSAGSQASVHQALFADYKASTSFLFPGQGAQAVGMG
KEAQNVPAAVLNFNKANDILGFDLLDICINGPKDKLDSTVISQPAIYVTSLAARELLRAREGGQQIIDS
VDVTCGLSLGEYALAFAGAFSFDGLKLVLKLRGEAMQDAADAARSAMVSVIGLDSEKVQQLCDAANQEV
EAEKVQIANYLCPGNYAVSGGLKGVEVLESKAKSFKARMTVRLAVAGAFHTSFMEPAVSRLEAALATTEI
RTPRIPVISNVNAQPHDTPNTIKKILARQVTSPVQWETTVKTLTKGLKKSSELGPGKVIAGIVKRMDDG
ADIENIGA

>AtFabD Malonyltransferase [*Arabidopsis thaliana*] CAA0373481.1
MRSLHRTILLTSPSHSLIRRTSLSAMATTASSLLLPISLNNLSSSKNASFGFAAKNLSRSRISMSVS
AGSQSTTVHDSLFADYKPTSAFLFPGQGAQAVGMGKEAQSVGAAGELYKKANDILGYDLLDICVNGPK
LDSTVISQPAIYVTSLAARELLRVREGGEQIINSVDVTCGLSLGEYALAFAGAFSFDGLKLVLKLRGEA
MQAAADAASAMVSIIGLDSEKVQQLCDAANQEVDEADKVQIANYLCPGNYAVSGGLKGIEVEAKAKSF
KARMTVRLAVAGAFHTSFMEPAVSRLEAALAATEIRSPRIPVISNVDAQPHADPDTIKKILARQVTSPVQ
WETTVKTLTKGLKKSSELGPGKVIAGIFKRVDDKSASFENISA

>AhFabH 3-oxoacyl-[acyl-carrier-protein] synthase 3 A, [*Arachis hypogaea*]
XP_025611200.1
MANASAFFTPSPVKFGETVPPLNLIAIHRFQRFSAKVVCFGTIEGAGKHASAASPSQSQLPRLVGKGCKL

VGCGSAVPTLQISNDDLKSMVDTSDEWISVRTGIRRRRVLSGRDNLIALGVDA SRKALEMANVDPDDLIL
 ILMCTSTPEDLFGSAPQIQKQLGCKANPLAYDITAACSGFVLGLISAACHIRGGGFNRVLVIGADALSRY
 VDWTDRGSCILFGDAAGAVLVQACDTEEDGLFGFDLHSDGSGQRHLNASIKEHETNTALDSNGSVLDFPP
 RKSSYSFIQMNGKEVFRFAVRCVPQSIESALQKAGLPASSIDWLLLHQANQRIIDAVARLEVPSEVIS
 NLANYGNTSAASIPLALDEAVRSGKVKAGQTIAAAGFGAGLTWGS AIIIRWG
 >GmFabH Beta-ketoacyl-acyl carrier protein synthase III [*Glycine max*]
 NP_001237735.1
 MANASGFFSPSPVPHFKVRVKPLTTAIGFSAKVVVCVGNIEGAEKHASTVSPSSQSPIPRLVSKGCKLVGCG
 SAVPALQISNDDLKSMVDTNDEWISVRTGIRRRRVLSGKDNLTGLAVEAARKALEMAKVDPPDDLILMC
 TSTPEDLFGSAPQIQKQLGCKANPLSYDITAACSGFVLGLISAACHIRGGGFNNVLVIGADALSRYVDWT
 DRGTCILFGDAAGAVLVQACNSEEDGLFGFDLHSDGSGQRHLNASIKENESNNALDSNGSVFGFPPKQSS
 YSCIQMNGKEVFRFAVRCVPQSIESALEKAGLPASSIDWLLLHQANQRIIDAVATRLLELPSEVISNLN
 YGNTSAASIPLALDEAVRSGKVKAGQTIATAGFGAGLTWGS AIIIRWG
 >BnFabH 3-oxoacyl-[acyl-carrier-protein] synthase III, [*Brassica napus*]
 XP_013732147.1
 MANASGFFAHPSISSMRSRTHLPIAVSGSGFCVSKRFSKRVLCSLSSLDNNASPSQYRPPRLVPSGC
 KLIGSGSAVPSLLISNDDLAKIVDTNDEWIATRTGIRNRRVVS GKDSLVLGLAVEAATKALEMAEVAPEDI
 DLVLMCTSTPDDLFGAAPQIQKALGCTKNPLAYDITAACSGFVLGLVSAACHIRGGGFKNVLVIGADSL
 RFVDWTDRTGTCILFGDAAGAVVVQACDIEDDGLYSFVHSDGDGRRHLNASVKESQTDGALSSNGSALGD
 FPPKQSSYSYSCIQMNGQEVFRFAVRCVPQSLETALQKAGLPASSIDWLLLHQANQRILDSVATRLQFPPER
 VISNLANYGNTSAASIPLALDEAVRSGKVKPGHTIATSGFGAGLTWGS AIVRWRTSAASIPLALDEAVRSG
 KVKPGHTIATSGFGAGLTWGS AIMRWR
 >AtFabH-1 3-ketoacyl-acyl carrier protein synthase III, [*Arabidopsis*
thaliana] OAP12004.1
 MANASGFFTHPSIPNLSRIHVPVRVSGSGFCVSNRFSKRVLCSVSSVVDKDASSSPSQYQRPRLVPSGC
 KLIGCGSAVPSLLISNDDLAKIVDTNDEWIATRTGIRNRRVVS GKDSLVLGLAVEAATKALEMAEVPEDI
 DLVLMCTSTPDDLFGAAPQIQKALGCTKNPLAYDITAACSGFVLGLVSAACHIRGGGFKNVLVIGADSL
 RFVDWTDRTGTCILFGDAAGAVVVQACDIEDDGLFSFVHSDGDGRRHLNASVKESENDGESSNGSVFGD
 FPPKQSSYSYSCIQMNGKEVFRFAVKCV PQSIESALQKAGLPAS AIDWLLLHQANQRIIDS VATRLHFPPER
 VISNLANYGNTSAASIPLALDEAVRSGKVKPGHTIATSGFGAGLTWGS AIVRWR
 >AtFabH-2 3-ketoacyl-acyl carrier protein synthase III [*Arabidopsis*
thaliana] CAA72385.1
 MANASGFFTHPSIPNLSRIHVPVRVSGSGFCVSNRFSKRVLCSVSSVVDKDASSSPSQYQRPRLVPSGC
 KLIGCGSAVPSLLISNDDLAKIVDTNDEWIATRTGIRNRRVVS GKDSLVLGLAVEAATKALEMAEVPEDI
 DLVLMCTSTPDDLFGAAPQIQKALGCTKNPLAYDITAACSGFVLGLVSAACHIRGGGFKNVLVIGADSL
 RFVDWTDRTGTCILFGDAAGAVVVQACDIEDDGLFSFVHSDGDGRRHLNASVKEQN DGESSNGSVFGD
 FPPKQSSYSYSCIQMNGKEVFRFAVKCV PQSIESALQKAGLPAS AIDWLLLHQANQRIIDS VATRLHFPPER
 VISNLANYGNTSAASIPLALDEAVRSGKVKPGHTIATSGFGAGLTWGS AIMRWR

>GmFabB-1 3-oxoacyl-[acyl-carrier-protein] synthase I, [*Glycine max*]
 XP_006584769.1
 MAGIAGTCPLGALLRNSVSENNKGISVVHYEGLRLQQRMQMPSPSQYISASSSAAPRCRTIKAMASPTVG
 APKREKDPKKRVVITGMGLVSVFGSDVDAFYNKLLLEGESGISLIDRFDASNFSVRFGGQIRDFSSEGYID
 GKNDRRLDNCWRYCIVAGKRALDDANLGKQVLDTQMDKTRIGVLVSGMGGITAFSNGVEALVQKGYKKI
 TPFFIPIYSITNMGSALLAIDTGLMGPNYSISTACATANYCFCAAANHIRKGEADIMVVGTEAAIMPSGL
 GGFIAACRALSHRNEDPKKASRPWDKDRDGFVMGEGSGVLVMESLESATKRGAKIIAEYLGGAITCDAHMM
 TDPRADGLGVSSCISKSLDAGVSPPEVNVYNAHATSTLAGDLAEVNAIKKVKFDTSELKMNATKSMIGH
 GLGAAGGLEAIATIKAITTGWLHPSINLDNLEASVTIDTPNVKKKHEVNVGISNSFGFGGHNSVVVFAP
 FRP
 >GmFabB-2 Beta-ketoacyl-ACP synthetase I [*Glycine max*] NP_001238610.1
 MQALHSPTLRASPLDPLRGPNNAAANRRSSSAKRVFFVSATVAPKVSAPQRQKDPKKRVVITGMGLASV
 GNDVEGYEYKLLAGESGITAIIDRFDASKFPTRFGGQIRGFS AEGYIDGKNDRRLDDCLRYCIVAGKKALE
 NADLAPDNHSHKIDKERAGVLVSGMGGLTVFSDGVQALIEKGHRKITPFFIPIYAITNMGSALLGIDLGM
 GPNYSISTACATSNYCFYAAANHIRRGEADLMIAGGTEAAIIPIGLGGFVACRALSQNRNDPKTASRPWD
 KERDGFVMGEGAGVLVMESLEHAMKRGAPIIAEYLGGAVNCDAYHMTDPRSDGLGVSTCIQSSLEDAGVS

PEEVNYINAHATSTLAGDLAEINAIKKVFKDTSGIKINATKSMIGHCLGAAGGLEAIATVKAITTGWLHP
TINQFNPEPAVDFTVANVKQQHEINVAINSNSFGFGGHNSVVAFAFKP
>BnFabB 3-oxoacyl-[acyl-carrier-protein] synthase I [*Brassica napus*]
XP_013662893.1
MQALQSSSLRASPPNPLIKPSNRQSHQITNARQPTRRRTFISASAAVSAPKRETDPKKRVVITGMGLVSV
FGNDVDAYYEKLLSGESGISLIDRFDASKFPTRFGGQIRGFSSEGYIDGKNERRLDDCLKYCIVAGKKAL
ESANLGGDKLNTIDKQRAGVLVGTGMGGLTVFSDGVQALIEKGHRRISPFFIPYAITNMGSALLAIDLGL
MGPNYSTACATSNYCFYAAANHIRRGEADMMIAGGTEAAIIPIGLGGFVACRALSQRNDDPKTASRPW
DKQRDGFVMGEGAGVLVMELEHAMKRGAPIIAEYLGGAVNCDAAHMTDPRADGLGVSSCIESCLEDAGV
SPEEVNYINAHATSTLAGDLAEINAIKKVFKSTAGIKINATKSMIGHCLGAAGGLEAIATVKAIN TGWLH
PSINQFNPEPAVDFTVANQKQHEVNVAISNSFGFGGHNSVVAFAFTP
>HaFabB-1 3-oxoacyl-[acyl-carrier-protein] synthase I [*Helianthus annuus*]
XP_022025436.1
MQAQALLQSPHLRVSPDLPLRTRPKPTNFKPRTTVIASATAPKREKDPKKRVVITGMGLVSVFGNDVDTY
YEKLLAGESGIGLIDRFDASKFPTRFGGQIRGFKSDGYIDGKNDRRLDDCLRYCIVAGKKALEADLGGD
KLSKIDKERAGVLVGTGMGGLTVFSDGVQNLIEKGYRKITPFFIPYAITNMGSALLAIDVGFMGPNYSIS
TACATSNYCFYAAANHIRRGEADMMIAGGTEAAIIPIGLGGFVACRALSQRNDDPQTASRPWDKDRDGFV
MGEGAGVLVMELEHAMKRGAPIIAEYLGGAVNCDAYHMTDPRSDGLGVSSCIQSSLEDAGVSPEEVNYI
NAHATSTLVGD LAEVNAVKKVFKSTDG IKMNSTKSMIGHCLGAAGGLEAIATVKAIQTGWLHPTINQFNP
EPAVEFDTVANQKQQHEVNVAISNSFGFGGHNSVVAFAFKP
>HaFabB-2 3-keto-acyl-ACP synthase I [*Helianthus annuus*] ABM53471.1
MQAQALLQSPHLRVSPDLPLRTRPKPTNFKPRTTVIASATAPKREKDPKKRVVITGMGLVSVFGNDVDTY
YEKLLAGESGIGLIDRFDASKFPTRFGGQIRGFKSDGYIDGKNDRRLDDCLRYCIVAGKKALEADLGGD
KLSKIDKERAGVLVGTGMGGLTVFSDGVQNLIEKGYRKITPFFIPYAITNMGSALLAIDVGFMGPNYSIS
TACATSNYCFYAAANHIRRGEADMMIAGGTEAAIIPIGLGGFVACRALSQRNDDPQTASRPWDKDRDGFV
MGEGAGVLVMELEHAMKRGAPIIAEYLGGAVNCDAYHMTDPRSDGLGVSSCIQSSLEDAGVSPEEVNYI
NAHATSTLVGD LAEVNAVKKVFKSTDG IKMNSTKSMIGHCLGAAGGLEAIATVKAIQTGWLHPTINQFNP
EPAVEFDTVANQKQQHEVNVAISNSFGFGGHNSVVAFAFKP
>AhFabB 3-oxoacyl-[acyl-carrier-protein] synthase I [*Arachis hypogaea*]
XP_025639780.1
MQAIHTPTLRVSPDLPLRKSTNPPISTRASKRVSFTVSAAAVSPKVSAPQRQKDPKKRVVITGMGLASV
FGNDVDTFYDRLLAGESGITTIDRFDASKFPTRFGGQIRGFSSEGYIDGKNDRRLDDCLRYCIVAGKKAL
ENADLGGEKLNKLDKEKAGVLVGSGMGGLTVFSDGVQALIEKGHRKITPFFIPYAITNMGSALLGIDLGF
MGPNYSTACATSNYCFYAAANHIRRGEADLMIAGGTEAAIIPIGLGGFVACRALSQRNDDPKTASRPW
DKDRDGFVMGEGSGVLVMELEHAMRRGAPIIAEYLGGAVNCDAYHMTDPRSDGLGVSSCIQSSLEDAGV
SPEEVNYINCHATSTLAGDLAEINAIKKIFKKTG IKINATKSMIGHCLGAAGGLEAIATVKAITTGWLH
PSINQFNPEPAVDFTVANVKKQHEINVGISNSFGFGGHNSVVAFAFKP
>NtFabB 3-ketoacyl-acyl-carrier protein synthase I [*Nicotiana tabacum*]
ANT48295.1
MQSIQSPSFRPSPLDPLKKTVPQLTNVRPLSHAKRVPFISASATTVSAPKREKDPKKRVVITGMGLVSVF
GNDVDTTYDRLLAGESGISLIDRFDASKFPTRFGGQIRGFTSDGYIDGKNDRRLDDCLRYAIVAGKKALE
NADLGGDRLGKIDKERAGVLVGTGMGGLTVFSDGVQNLIEKGHRKITPFFIPYAITNMGSALLGIDLGM
GPNYSTACATSNYCFYAAANHIRRGEADLMLAGGTEAAIIPIGLEVLWHVXLLSQRNDDPQTASRPWD
KERDGFVMGEGSGVLVMELEHAMKRGAPIIAEYLGGAVNCDAAHMTDPRADGLGVSSCIQSSLEDAGVS
PEEVNYINAHATSTIVGDIAEVNAIKKVFKN TSGIKMNATKSMIGHCLGAAGGMEAIATVKAITTGWVHP
SINQFNPEPSVEFDTVPNKKQQHEVNVGISNSFGFGGHNSVVAFAFKP
>AtFabB-I 3-ketoacyl-acyl carrier protein synthase I [*Arabidopsis thaliana*]
NP_199441.1
MQALQSSSLRASPPNPLRLPSNRQSHQLITNARPLRRQQRSFISASASTVSAPKRETDPKKRVVITGMGL
VSVFGNDVDAYYEKLLSGESGISLIDRFDASKFPTRFGGQIRGFSSEGYIDGKNERRLDDCLKYCIVAGK
KALESANLGGDKLNTIDKRKAGVLVGTGMGGLTVFSEGVQNLIEKGHRRISPFFIPYAITNMGSALLAID
LGLMGPNYSTACATSNYCFYAAANHIRRGEADMMIAGGTEAAIIPIGLGGFVACRALSQRNDDPQTAS
RPWDKARDGFVMGEGAGVLVMELEHAMKRGAPIIAEYLGGAVNCDAAHMTDPRADGLGVSSCIERCLED
AGVSPPEEVNYINAHATSTLAGDLAEINAIKKVFKSTSGIKINATKSMIGHCLGAAGGLEAIATVKAIN TG
WLHPSINQFNPEQAVDFTVPNEKKQHEVDVAISNSFGFGGHNSVVAFAFKP

>HaFabF-1 3-oxoacyl-[acyl-carrier-protein] synthase II [*Helianthus annuus*] XP_022013627.1

MVASAVATWLVAACMSFSGDTRLKPSPPAALPLPSKRLSRSARRKLQAMTKCNHFS AAGGLMSSIIYSGI
MNLLEPCEEYKSKPLSSSSLSIFGYENRRVKQTGKAMAIQVPAKEPTTKKKPVTKRRVVVTGLGVVS
PVGDVVDVFYENLLDGVSGISEIESFDCQHFPPTKIAGEIKSFSADGWIAPKLSKRVDKFMLYLLTAGKKA
LEDGGVTDEVMKELDITCKGVIIGSALGGMKIFQDAIEALRVSYKKMNPFCVPFATTNMGSAIAMD LGW
MGPNYSISTACATSNYCILNANHIIIRGETDMMLSGGSDSAIPIGLGGFVACNSLSQRND DPTKASRPW
DVSRDGFVMGEGAGVLLLEELEHAKARGAKIYAEFMGGSFTCDAYHMT EPHPDGTGIALCIEKALAQSGV
AREDVNYINAHATSTPSGDLNEYEAIIRCFGDNSQLKINSTKSMVGHL LGAAGAVEAVATVKAIQTGWLH
PNINLENPDVGVDKNVLVGAKKERFDVKVALSNSFGFGGHNSSILFAPYKDQ

>HaFabF-2 3-keto-acyl-ACP synthase II [*Helianthus annuus*] ABI18155.1

MAASMVCTWIVAACMSVSSSSSSNSLFSSKRKRRLDRFSLSSRCRRGGRVAMAIQIPSSIEMEEETTLT
KRKQPPTKQRRVVVTGMGVETPIGNPDQFYNNLLQGVSGITQIEAFDCSSYPTRIAGEIKNFSTDGWVA
PKLSKRMDRFMLYMLTAGKKALADAGISPSDSDEIDKSRGVLIGSAMGGMKVFND AIEALRVSYRKMNP
FCVPFATTNMGSAIAMD LGWMGPNYSISTACATSNFCILNANHIIIRGEADMMLCGGSDAVIPIGLGG
FVACRALSERNTDPAKASRPWD SGRDGFVMGEGAGVLLLEELEHAKKRGAKIYAEFLGGSFTCDAYHMT E
PHPEGAGVILCIEKALSQAGVRREDVNYINAHATSTPAGDLKEYHALLHCFGN NQELRVNSTKSMIGHLL
GAAGAVEAVATVQAIRTGWIHPNINLENPDQGVDTKVLVGSKKERLNVKVGLSNSFGFGGHNSSILFAPF
Q

>AhFabF-1 3-oxoacyl-[acyl-carrier-protein] synthase II [*Arachis hypogaea*]
XP_025644592.1

MAFSSAFAASSPLCTWLVAACMSLTSHSDHSPSLTCSRRTHTVTRSSFTPRSTSAFNRTTRTRTNRMPLSR
KIMAIALQPAQEATTVSKKPPTKERRVVVTGMGVVTPLGHDADVFYKNLLDGVSGISEINAFDCAEFPTR
IAGEIKSVSADGWVAPKLSKR LDKFMLYMLIAGKKALVDGGITEDIMNELNKQKCGVLIGSAMGGMKVFS
DAIEALRISYKKMNPFCVPFATTNMGSAIAMD LGWMGPNYSISTACATSNFCILNANHIIIRGEADMML
CGGSDSAIPIGLGGFVACRALSQRNSDPTKASRPWDSNRDGFVMGEGAGVLLLEELEHAKRGAEIYAE
FRGGSFTCDAYHMT EPHPDGAGVILCIEKALTHSGLSKEDVNYINAHATSTPAGDLKEYQALMHCFGRNP
ELKVNSTKSMIGHLLGAAGGVEAVATVQAIRTGWIHPNINLESPDKGVDANVLVGPKKERLEVKAALSNS
FGFGGHNSSIIIFSPFK

>AhFabF-2 3-oxoacyl-[acyl-carrier-protein] synthase II [*Arachis hypogaea*]
XP_025645142.1

MIHSAASSMASPLCTWLVAACMSVTCHTDRA GTPKAALRSSKRSRRTKALPANTSQ LNMRLISSLYGSSI
QGLISSFEPCDDYCNTHNAFSSLFRSTTPNRRHTRLNKL SHSGKTM A VAVEPAHEVTATKKPPTKQRRVV
VTGLGVVTPLGHEPDVYYNNLLDGVSGISEIETFDCAEYPTRIAGEIKSFSTDGWVAPKLSKRMDKFMLY
LLTAGKKALVDGGITEDVMD ELNKEKCGVLIGSAMGGMKVFND AIEALRVSYKKMNPFCVPFATTNMGSA
IAMD LGWMGPNYSISTACATSNFCILNANHIIIRGEADVMLCGGSDAAIPIGLGGFVACRALSQRNTD
PTKASRPWDINRDGFVMGEGAGVLLLEDLEHAKKRGATIYAEFLGGSFTCDAYHVTEPRPDGAGVILCIE
KALAQSGVSKEDVNYINAHATSTPAGDLKEFQALLHCFGQNP ELRVNSTKSMIGHLLGAAGGVEAVATVQ

>GmFabF Beta-ketoacyl-ACP synthetase 2 [*Glycine max*], AAF61737.1

MASTTTSSLCTWLVAACMSVTCHADRTKTPHAMFRSSKKSRYSQFNVCRSTHSGKTM AVALQPTQGITT I
KKPPTKQRRVVVTGLGVVTPLGHEPDIFYNNLLDGASGISEIETFDCADIPTRIAGEIKSFSTDGWVAPK
LSKRMDKFMLYMLTAGKKALVDGGITDDVMD ELYKDKRGVLIGSAMGGMKVFND AIEALRISYKKMNPFC
VPFATTNMGSAIAMD LGWMGPNYSISTACATSNFCILNANHIIIRGEADVMLCGGSDAAIPIGLGGFV
ACRALSQRNTDPTKASRPWDINRDGFVMGEGAGVLLLEELEHAKERGATI LAEFLGGSFTCDAYDVT EPR
PDGAGVILCIEKALAQSGVSKEDVNYINAHATSTPAGDLKEYQALMHCFGQNP ELRVNLT KSMIGHLLGA
AGGVEAVATIQAIRTGWVHPNINLENPDNGVD AKVLVGSKKERLDVKAALSNSFGFGGHNSSIIIFAPY

>JrFabF Beta-ketoacyl-ACP synthase II [*Jatropha curcas*] ABJ90469.2

MMGSASFASPLCTWLVAACMSVTCAKENRTAPHA FHSSQPSNRLSRWARRRKT LHAQYNSDSSNSIAAGG
GGGGGGGYSTEFLSNSLVSTLCGSSFQGLMSSCLA FEPCSQYYSSNGLFRSRNLNRKQRRNLRLALSGEA
MAIAVQPEKEVATKKKPKTKQRRVVVTGMGVVSPLGHEPDVFYNNLLEGVSGISQIEAFECAQFPTRIAG
EIKSFSTDGWIAPKLSKRMDKFMLYMLTAGKKALADGGITEDIMDEL DKA KCGVLIGSAMGGMKVFND AI
EALRVSYRKMNPFCVPFATTNMGSAIAMD LGWMGPNYSISTACATSNFCILNANHIIIRGEADIMLCGG
SDAAIPIGLGGFVACRALSQRND DPAKASRPWDMNRDGFVMGEGAGVLLLEELEHAKKRGANIYAEFLG
GSFTCDAYHMT EPRPGGIGVILCIEKALAQSGVSREDVNYINAHATSTPAGDIKEFGALMHCFGQNPGLR
VNSTKSMIGHLLGAAGAVEAIAAIQAIRTGWVHPNINLENPD EGVDTNVLVGPKKERLDVKVALSNSFGF

GGHNSSIVFAPHK

>AhKASmt 3-oxoacyl-[acyl-carrier-protein] synthase mitochondrial
[*Arachis hypogaea*] XP_025632626.1

MAMRASRRVFGSRGLGFYQSISSSSSVGRAIMDPPPVVSSRRVVVTGLGMVTPLGCGVDKTRHLLIDGKC
GVRSLCLEDLQMSSFDKETQLSTFDQLTSKVAAVVPTGTNLGEFNEEIWLNSKDHRSIARFIAYALCAAD
EALKDSNWFPTQEHRERTGVSIGGGIGSISDVLDQAQLLCEKRLRRLSPFFIPRILVNMAAGHVSVMKYG
FQGPNHAAVTACATGAHSIGDAVRMIQFGDADVMVAGGTESSIDALSIAAGFCRSRALTTKYNSSPQEASR
PFDSGRDGFVIGEGCGVLVLEEFNHAKNRGAKVYAEVRGYGMSGDAHHITQPPNDGRGAILAMTHALRQS
GLHPSEVDYINAHATSTPLGDVIEANAIAKTIFSGHANSSALAFSSTKGAIGHLLGAAGAVEAIFSVLAIR
HGIAPLTLNLTKPDPVFADGFMPLTASKEMPIRVAMSNFSGFGGTNASLLFASVGS DR

>BrSAD1 Stearoyl-[acyl-carrier-protein] 9-desaturase [*Brassica rapa*]
XP_009133630.1

MALKLNPLASQPYNFPSSARPPVSTFRSPKFLCLASSSPALSSKEVESLKKPFTPPKEVHVQVLHSMPPQ
KIEIFKSMEDWAEQNLLTQLKDVEKSWQPQDFLPDPASDGFEDQVRELRRERARELPDDYFVVLVGD MITE
EALPTYQTMLNTLDGVRDET GASPTSWAIWTRAWTA EENRHGDLLNKYLYLSGRVDMRQIEKTIQYLIGS
GMDPRTENNPYLGFIYTSFQERATFISHGNTARQAKEHGD LKLAQICGTIAADEKRHETAYTKIVEKLFE
IDPDGTVMAFADMMRKKISMPAHLMYDGRDESLFDNFSSVAQRLGVYTAKDYADILEFLVGRWKIESLTG
LSGEGNKAQEYLCGLTPRIRRLDERAQARAKKGPKVPF SWIHDREVQL

>BrSAD2 stearoyl-[acyl-carrier-protein] 9-desaturase [*Brassica rapa*]
XP_009142970.1

MALKLNPLASQPYKLHTSARPPISTFRSPKFLCLASSSPALSSSTKEVESLKKPFTPPKEVHVQVLHSM
PPQKIEIFKSMEDWAEHNLLPHLKDVEKSWQPQDFLPDPASDGFEDQVKELRRERARELPDDYFVVLVGD M
ITEEALPTYQTMLNTLDGVRDET GASPTSWAVWTRAWTA EENRHGDLLNKYLYLSGRVDMRQIEKTIQYL
IGSGMDPRTENNPYLGFIYTSFQERATFVSHGNTARQAKEHGD LKLAQICGTIAADEKRHETAYTKIVEK
LLEIDPDGTVVAFADMMRKKISMPAHLMYDGRDDKLF DNFSVAQRLGVYTAKDYADILEFLVGRWKIES
LSGLSGEGNKAQEYLCGLTPRIRRLDERAQARAKKGPKIPF SWIHDREVQL

> BrSAD3A Stearoyl-[acyl-carrier-protein] 9-desaturase [*Brassica rapa*]
XP_018513314.1

MAMSMDRIVVSPSSYVCRPSQARGSRSSVSMAS TIRSASTYREVTNGKKLYIPPREVHVQVKHSMPPQK
LEIFKSLEGWADETLTLYLKPVKSWQPTDFLPEAESEGFYDQVKELRRERCKELPDEYFVVLVGD MITEE
ALPTYQTMLNTLDGVRDET GASPTPWAVWTRAWTA EENRHGDLLNKYLYLSGRVDMRQIEKTIQYLIGSG
MDPKTENNPYLGFIYTSFQERATFISHGNTARLAKDRGDLKLAQICGTIAADEKRHETAYTKIVEKLFEI
DADGTILGLADMMKKKISMPAHLMYDGQDDNLF EHFSTVAQRLGVYTAKDYADILEFLVERWNVETLSGL
SSEGHMAQDFVCGLPARIRRIEERAQGRAKEAAKNVPF SWIFGREIRA

> BrSAD4 Stearoyl-[acyl-carrier-protein] 9-desaturase [*Brassica rapa*]
XP_009118393.2

MAMAMAMNRIVVLPSSYAYRPHQARGSRSP IASSIRSATTEVTNGRKLYIPPREVHVQVKHSMPPQKLEI
FKSLEGWADETLTLYLKPVKSWQPTDFLPEAESEGFYDQVKELRRERCKELPDEYFVVLVGD MITEEALP
TYQTMLNTLDGVRDET GASPTPWAVWTRAWTA EENRHGDLLNKYLYLSGRVDMRQIEKTIQYLIGSGMDP
KTENNPYLGFIYTSFQERATFISHGNTARHAKDLGDLKLAQICGTIAADEKRHETAYTKIVEKLFEIDAD
GTILGLADMMKKKISMPAHLMYDGQDDNLF EHFSTVAQRLGVYTAKDYADILEFLVERWNVETLSGLSSE
GHKAQDFVCGLPARIRKIEERAQGRAKEAAKNVPF SWIFGREIRA

> BrSAD5 Stearoyl-[acyl-carrier-protein] 9-desaturase [*Brassica rapa*]
XP_009121502.1

MVMAMDRIAFTSSPSAYQRSYHPHYRSSRVFMS STIRPASTEVTNGRKPYLPPREVQLQVKYSMP PQKL
EIFKSLEEWANDNLLPYLKPVKSWQPTDFLPEPESEGFYDQVKELRRERCKELSDDYFVVLIGD MITEEA
LPTYQTMINTLDGVRDET GASPTPWAVWTRAWTA EENRHGDLLNKYLYLSGRVDMRQIEKTIQYLIGSGM
DPKTENNPYLGFIYTSFQERATFISHGNTAGLAKKLGS SKLAQICGTIAADEKRHETAYTKIVEKLFEID
PDTTVVG FADMMKKKIAMP AHLMYDGCDDNLF EHFSSVAQRLGVYTARDYADILEFLVRRWNVENLVGLS
GDGHKAQDYLCGLPARIRKLEERAQGRNKDAARNIPF SWIFGREIRA

> BrSAD6 Stearoyl-[acyl-carrier-protein] 9-desaturase [*Brassica rapa*]
XP_009147347.1

MTMTLPLNSTKTPMKQNPFVAVSSPSLFLGPSFPRRLRVSCVATSPRKTSEQTHKKTFRPIKEVPNQI

THTITQEKLEIFKSMENWAQENLLSYLKPVETSWQPQDLLPQTNDEDQFYEQVKELRDRTREIPDDYFVV
 LVGDMITEEALPTYQTTLNTLDGVKDETTGGSLTPWAVVWRAWTAENRHGDLLNKYLYLSGRVDMQHV
 TIQYLIGSGMDSKFENNPNYNGFIYTSFQERATFISHANTAKLATTYGDTTLAKICGTIAADEKRHETAYT
 RIVEKLFEIDPDGTVQALASMMRKRTMPAHLMDHGRDDNLFHDHYGAVAQIRIGVYTAMDYAGILEFLLRR
 WKVESLGVLGTGEGRRAQEYLCSLPQRITRLEERANDRVKLGSRPSVAFSWIYGREVGL
 >BrSAD7 Stearoyl-[acyl-carrier-protein] 9-desaturase [*Brassica rapa*]
 XP_009121503.1
 MSIALLLPSPVMTQKPSSITSPPRGFGSSSSRLLQVSCVTKNPARNNNVTCNNFRPIKEVNNQITHTIPO
 EKLEIFKSMENWAETTLPLYLKPVEDSWQPQDFLPAPETDDAFYDQVREIRERTKEIPDDYFVVVLVGDM
 TEEALPTYQTTLNTLDGVKDETTGGSLSPWAVWIRAWTAENRHGDLLNKYLYLCGRVDMRHVERTIQYLI
 GSGMDSKFENNPNYNGFIYTSFQERATFISHGNTARLATTYGDTTLAKICGTIAADEKRHETAYTKIVEKL
 FELDPDGTQVQALASMMKKRTMPAHLMDHGRDDQLFDHYAAVAQIRIGVYTAADYAGILEFLLRRWKVESL
 GSGLSGEGRRAQEYLCSTLPQRIKRLEERANDRVKRQSKGSVSFSWVFGRDVEL
 >RcSAD1 Stearoyl-[acyl-carrier-protein] 9-desaturase [*Ricinus communis*]
 NP_001310659.1
 MALKLNPFSLQTKLPSPFALPPMASTRSPKPYMASTLKSGSKEVENLKKPFMPPREVHVQVTHSMPPQKI
 EIFKSLDNWAEENILVHLKPVKWCWQPQDFLPDPASDGFDEQVRELRRERAKEIPDDYFVVVLVGDMITEEA
 LPTYQTMLNTLDGVRDETGA SPTSWAIWTRAWTAENRHGDLLNKYLYLSGRVDMRQIEKTIQYLIGSGM
 DPRTENSPYLGFIYTSFQERATFISHGNTARQAKEHGDIKLAQICGTIAADEKRHETAYTKIVEKLFEID
 PDGTVLAFADMMRKKISMPAHLMDHGRDDNLFHDHSAVAQRLGVYTAKDYADILEFLVGRWKVDKLTGLS
 AEGQKAQDYVCRLPPRIRLEERAQGRAKEAPTMPFSWIFDRQVKL
 >AhSAD1 Stearoyl-[acyl-carrier-protein] 9-desaturase [*Arachis hypogaea*]
 ACI45450.1
 MALRLNPNPSQKLFLSPSSSSSSSSSSSFLPQMASLRSPRFRMASTLRTGSKEVENLKKPFTPPREVHVQ
 VTHSMPPQKIEIFKSLEGWAEENILTLLKPVGKCWQPQDYLPPESEDGFEEQVRELRRERAKEIPDDYFVV
 LVGDMITEEALPTYQTMLNTLDGVRDETGA SLSWAVWTRAWTAENRHGDLLNKYLYLSGRVDLRQIEK
 TIQYLIGSGMDPRTENSPYLGFIYTSFQERATFISHGNTARLAKEHGDMLKLAQICGMIA SDEKRHETAYT
 KIVEKLFEIDPDGTVMAFADMMRKKIAMP AHLMDHGRDDNLFENYSAVAQIRIGVYTAKDYADILEFLVGR
 WKVADLTGLSGEGRKAQDYVCGLPPRIRLEERAQGRAKESPRLKFSWIYDREVQL
 >AhSAD2 Stearoyl-[acyl-carrier-protein] 9-desaturase [*Arachis hypogaea*]
 AID51207.1
 MQMQISSLRQTFLHFSPAQKYGRHIMPLPRAAIAAPPLKSQKTHSMAPEKIEIFKSLENWASECVLP
 MLKPVEQCWQPQNLPDSSSQPFDEFTDEVKNLRQRTAEIPDDYFVVVLVGDMITEEALPTYQSMINNLG
 GDEIGSSPNPWAVWTRAWTAENRHGDLLRTYLYLSGRVDMMLIEKTVQYLIGAGMDPGTENNPYLG
 FVYTSFQERATFVSHGNTARLAKEGGDPVLARICGTIAADEKRHENAYQKIVEKLLEVDPSDAVVAIGDMMQK
 KITMPAHLMDGSDPKLFEHFSAVAQRLGVYTANDYADILEFLVGRWRLEKLEGLTAEGKRAQDYVCGLS
 QMIRRLQERADERARNMKKSHSVKFSWIFNKEVLL
 >AhSAD3 Stearoyl-[acyl-carrier-protein] 9-desaturase [*Arachis hypogaea*]
 AID51208.1
 MILLGWFLPIPEEEMAMQLQTRMMFTPKRASLAHAWTPSGIHISMLHAHARSSSSSSTLPPEKIEIFKSL
 EGWASQCILPLVPKPEKSWQPHDLLPDSSLSLDEFIYQVKALRDRTAELPDDYLVVLVGDMITEEALPSY
 QTWFNQLDGVGDKLGSSPNPWAVWSRAWTSEENRHGDLLKTYLYLSGRVDMFMIEKTIHYLIGAGVDVKT
 ENNPYMGFVYTSFQERATFISHGNTARLATKSGDPVLARICGTIAADEKRHENVYSKIVEKLLEVDPTGT
 MIAISEMMRKKITMPAYLMHDGRDPLFDHFSAVAQRLGVYTAADYADILEYLI GRWRLGELQGLTPEGR
 HAQDFVCGLAPRIRRLQERADKQVCKMKSRSVKFSWIFSREVPII
 >AtFAB2 Stearoyl-acyl-carrier-protein desaturase [*Arabidopsis thaliana*]
 AT2G43710.1
 MALKFNPLVASQPYKFPSSSTRPPTPSFRSPKFLCLASSPALSSGPKEVESLKKPFTPPR
 EVHVQVLHSMPPQKIEIFKSMENWAEENLLIHLKDVEKSWQPQDFLPDPASDGFEDQVRE
 LRERARELPDDYFVVVLVGDMITEEALPTYQTMLNTLDGVRDETGA SPTSWAIWTRAWTAE
 ENRHGDLLNKYLYLSGRVDMRQIEKTIQYLIGSGMDPRTENNPYLGFIYTSFQERATFIS
 HGNTARQAKEHGDIKLAQICGTIAADEKRHETAYTKIVEKLFEIDPDGTVMAFADMMRKK
 ISMPAHLMDGRNDNLFDFNSSVAQRLGVYTAKDYADILEFLVGRWKIQDLTGLSGEGNK
 AQDYLCGLAPRIKRLDERAQARAKKGPKIPFSWIHDREVQL
 >AtAAD2 Stearoyl-acyl-carrier-protein desaturase [*Arabidopsis thaliana*]
 AT3G02610.1
 MALLNSTITVAMKQNPLVAVSFPRTTCLGSSSFSPRLLRVSCVATNPSKTSEETDKKKFRPIKEVPNQV

THTITQEKLEIFKSMENWAQENLLSYLKPVEASWQPQDFLPETNDEDRFYEQVKELRDRTKEIPDDYFVV
LVGDMITEEALPTYQTTLNTLDGVKDETGGSLSWAVVWRAWTAENRHGDLLNKYLYLSGRVDMRHVEK
TIQYLIGFGMDSKFENNPNYNGFIYTSFQERATFISHGNTAKLATTYGDITLAKICGTIAADEKRHETAYT
RIVEKLF EIDPDGTVQALASMMRK RITMPAHLMDGRDDDLFDHYA AQAQRIGVYTATDYAGILEFLLRR
WEVEKLG MGLSGEGRR AQDY LCTLPQRI RRL EERANDRVK LASKSKPSVSFSWIYGREVEL

>AtAAD3 Stearoyl-acyl-carrier-protein desaturase [*Arabidopsis thaliana*]
AT5G16230.1

MSMALLLTSPAMKQKPAVITSPRRGSSPSRRLRVSCVTTNPARKKNETCNHFRPIKEVNNQLTHTIPQEK
LEIFKSMENWAEQKLLPYLKPVEDSWQPQDFLPAPENDDEFYDRVKEIRERTKEIPDDYFVVVLVGDMITE
EALPTYQTTLNTLDGVKDETGGSLSWAVVWRAWTAENRHGDLLNKYLYLTGRVDMRHVEKTIQYLGIS
GMDSKFENNPNYNGFIYTSFQERATFISHGNTARLATTYGDVTLAKICGTIAADEKRHETAYTKIVEKLF E
IDPDGTVQALASMMRK RITMPAHLMDGRDDDLFDHYA AQAQRIGVYTADYAGILEFLLRRWKVESLGL
GLSGEGRR AQEYLCTLPQRI RKL EERANDRVK LVS KPSVSFSWVFGRDVKL

>AtSAD4 Stearoyl-acyl-carrier-protein desaturase [*Arabidopsis thaliana*]
AT3G02620.1

MALLLNSTMTVAMKQNPATAVSFMQTTCLGSSFSPPRHLQVSCVATNPSKTFRPIKEVSNQVTHITQEK
LEIFKSMENWAQENLLSYLKPVETSWQPQDFLPETKDEDRFYEQVKELRDRTKEIPDDYFVVVLVGDMITE
EALPTYQTVMTNTLDGAKDETGVS LTPWAVVWRAWTAENRHGDLLNKYLYLSGRVDTRHVEKTIQYLGIS
GMDTKYENNPYNGYIYTSFQERATFISHANTAKLATTYGDITLAKICGTIAADEKRHEMAYTRIVEKLF E
IDPDGTVQALASMMRK RITMPAQLMDGRDDDLFDHYA AQAQRIGVYTATDYAGILEFLLRRWEVEKLG M
GLSGEGRR AQDY LCTLPQRI RRL EERADDRVK RASKSKPSVSFSWIYGREVEL

>AtSAD5 Stearoyl-acyl-carrier-protein desaturase [*Arabidopsis thaliana*]
AT3G02630.1

MAMAMDRIVFSPSSYVYRQCARGSRSSRVSMASTIRSATTEVTNGRKLYIPPREVHVQVKHSMPPQKLE
IFKSLEGWADETLLTYLKPVEKSWQPTDFLPEPESEGFDYQVKELRERCKELPDDYFVVVLVGDMITEEAL
PTYQTMNTLDGVRDET GASPTPWAIWTRAWTAENRHGDLLNKYLYLSGRVDMRQIEKTIQYLGISGMD
PKTENNPYLGFIYTSFQERATFISHGNTARLAKDRGDLKLAQICGTIAADERRHETAYTKIVEKLF EIDP
DGTILGLADMMKKKISMPAHLMYDGQDDNLF EHFSTVAQRLGVYTAKDYADILEFLVERWNVETLTDLSS
EGHRAQDFVCGLPARIRKIEERAQGRAKEAAKNIPFSWIFGRNIRA

>AtSAD6 Stearoyl-acyl-carrier-protein desaturase [*Arabidopsis thaliana*]
AT5G16240.1

MVMAMDRIALFSSSSSVYHHGSSSHSGSKSSRVFTIRSDSTAVGRKLYIPPREVHLQVKYSMPQKLEIF
KSLEGWANDNLLAYLKPVEKSWQPTDFLPEPESEGFDYQVKELRERCKELSDDYLVVLVGDMITEEALPT
YQTMINTLDGVRDET GASPTPWAVWTRAWTAENRHGDLLNKYLYLSGRVDMRQIEKTIQYLGISGMDPK
TENNPYLGFIYTSFQERATFISHGNTARLAKDLGDLTLGKICGTIAADERRHEHAYTKIVEKLF EIDPDT
TVVGFADMMRK KISMPAHLMYDGRDDNLFDFHSSVAQRLGVYTAKDYADILQHLVERWNVEKLS DLSSEG
NRAQDYLCGLPARIRKLEERAQGRTEAAKNIPFSWIFGREVRA

>AtSAD7 Stearoyl-acyl-carrier-protein desaturase [*Arabidopsis thaliana*]
AT1G43800.1

MLAHKSLLSFTTQWATLMPSPSTFLASRPRGPAKISAVAAPVRPALKHQNKIHTMPPEKMEIFKSLDGWA
KDQILPLLKPVDQCWQPASFLPDPALPFSEFTDQVREL RERTASLPDEYFVVVLVGDMITEDALPTYQTM I
NTLDGVRDET GASESAWASWTRAWTAENRHGDLLR TYLYLSGRVDM LMVERTVQH LIGSGMDPGTENNP
YLG FVYTSFQERATFVSRGNTARLAKSAGDPVLARICGTIAADEKRHENAYVRIVEKLL EIDPNGAVSAV
ADMMRKKITMPAHLMTDGRDPMLFEHFSAVAQRLEVYTADYADILEFLVGRWRLEKLEGLTGEGQRAQE
FVCGLAQRIRRLQERADERAKKLKKTHEVCFSWIFDKQISV

>Muc-PAD Acyl-ACP desaturase, [Macfadyena unguis-cati] AAC05293.1

MALKLNAINFQSPKCSSFGLPPVSLRSPKLSVAATLRSGLRDVETVKKTFSPAREVHVQVTHSMAPQKI
EIFKAMEDWAENNILVHLKNVEKCPQPDFLPDPASDEFHDQIKELRERAKEIPDDYFVVVLVGDMITEEA
LPTYQTMNTWDGVRDET GASPTSWAIWTRAWTAENRHGDPLNKYLYLSGRVDMKQIEKTIQYLGISGM
DPRTENSPYLGFIYTSFQERATFISHGNTARLARDHGDFKLAQICGTIASDEKRHETAYTKIVEKLF EID
PDGTVLAFGDMKKKISMPDHFMYDGRDDNLFDFHSSVAQRLGVYTAKDYADILEHLVGRWKVEKLTGLS
AEGQKAQDYVCGLP PPRIRRL EERAQIRAKQAPRLPFSWIYDREVQL

>AtFatA-1 Acyl-ACP thioesterase A, [*Arabidopsis thaliana*], NP_189147.1
MLKLSCNVTD SKLQSRLLFFSHSYRSDPVNFIRRRIVSCSQT KKTGLVPLRAVVSADQGSVVQGLATLAD
QLRLGSLTEDGLSYKEKFVVRSYEVGSNKTATVETIANLLQEVGCNHAQSVGFSTDG FATTMTMRKLHLI
WVTARMHIEIYKPAWGDVVEIETWCQSEGRIGTRRDWILKDSVTGEVTGRATSKWVMNQDTRRLQKVS

DDVRDEYLVFCPQEPRLAFPEENNRSLLKKIPKLEDPAQYSMIGLKPRRADLDMNQHVNNVTYIGWVLESIP
PQEIVDTHELQVITLDYRRECQDDVVDLSLTTTSEIGGTNGSATSGTQGHNDSQFLHLLRLSGDGQEIN
RGTTLWRKKPSS

>AtFatA-2 Acyl-ACP thioesterase A [*Arabidopsis thaliana*] NP_189147.1
MLKLSCNVTDHIIHNFNSRRIFVPVHRQTRPISCFQLKKEPLRAILSADHGNSSVRVADTVSGTSPADR
LRFGRLMEDGFSYKEKFIVRSYEVGINKTATIIETIANLLQEVACNHVQNVGFSTDGFAATLTMRKLHLI
VTARMHIEIYKYPAWSVDVVEIETWCQSEGRIGTRRDWILKDCATGEVIGRATSKWVMNQDTRRLQRVTD
EVRDEYLVFCPPEPRLAFPEENNSSLKKIPKLEDPAQYSMLGLKPRRADLDMNQHVNNVTYIGWVLESIP
QEIIDTHELKVITLDYRRECQDDIVDSLTTSETPNEVVSKLTGTNGSTTSSKREHNESHFLHILRLSEN
GQEINRGRTQWRKKSSR

>CsFatA-1 Acyl-ACP thioesterase A [*Camelina sativa*] AFQ60948.1
MLKLSCNVTDSKQLRSLLFFSHSHRSDPVNCIRRRIVSSSVSCSQTKKTGLVDPLRAVVSADQGSVIRA
EQGLGTADQLRLGSLTEDGLSYKEKFVRSYEVGSNKTATIIETIANLLQEVGCNHAQSVGFSTDGFAAT
PTMRKLHLIIVVTARMHIEIYNYPAGNVVEIETWCQSEGRIGTRRDWILKDCATGEVTGRATSKWVMNQ
DTRRLQKVSDDVRDEYLVFCPQEPRLAFPEENNRSLLKKIPKLEDPAQYSMIGLKPRRADLDMNQHVNNVT
YIGWVLESVPQEIVDTHELQVITLDYRRECQDDVVDLSLTTSEIGGTNGSATSGTQGHNDSQFLHLLRLS
GDGQEINRGTTLWRKKSSR

>CsFatA-2 Acyl-ACP thioesterase A [*Camelina sativa*] AFQ60947.1
MLKLSCNVTDSKQLRSLLFFSHSHRSDPVNCIRRRIVASSVSCSQTKKTGLVDPLRAVVSADQGSVIRA
EQGLGTADQLRLGSLTEDGLSYKEKFVRSYEVGSNKTATIIETIANLLQEVGCNHAQSVGFSTDGFAAT
PTMRKLHLIIVVTARMHIEIYNYPAGNVVEIETWCQSEGRIGTRRDWILKDCATGEVTGRATSKWVMNQ
DTRRLQKVSDDVRDEYLVFCPQEPRLAFPEENNRSLLKKIPKLEDPAQYSMIGLKPRRADLDMNQHVNNVT
YIGWVLESVPQEIVDTHELQVITLDYRRECQDDVVDLSLTTSEIGGTNGSATSGTQGHNDSQFLHLLRLS
GDGQEINRGTTLWRKKSSR

>CsFatA-3 Acyl-ACP thioesterase A [*Camelina sativa*], AFQ60948.1
MLKLSCNVTDSKQLRSLLFFSHSHRSDPVNCIRRRIVSSSVSCSQTKKTGLVDPLRAVVSADQGSVIRA
EQGLGTADQLRLGSLTEDGLSYKEKFVRSYEVGSNKTATIIETIANLLQEVGCNHAQSVGFSTDGFAAT
PTMRKLHLIIVVTARMHIEIYNYPAGNVVEIETWCQSEGRIGTRRDWILKDCATGEVTGRATSKWVMNQ
DTRRLQKVSDDVRDEYLVFCPQEPRLAFPEENNRSLLKKIPKLEDPAQYSMIGLKPRRADLDMNQHVNNVT
YIGWVLESVPQEIVDTHELQVITLDYRRECQDDVVDLSLTTSEIGGTNGSATSGTQGHNDSQFLHLLRLS
GDGQEINRGTTLWRKKSSR

>HaFatB Fatty acyl-ACP thioesterase B [*Helianthus annuus*] CAC80370.1
MVAMSATASLFPVSSPKPHSGAKTSDKLGGEPSVAVRGIKTKSVNSGGMKVKANAAQAPTEVNGSRSRIT
HGFKTDDYSTSPAPRTFINXLPDWXMLLAAITTIFLAAEKQWMMLEWKTKRPDMIADMDPFGLGRIVQDG
LVFRQNFIRSIEIGADRTASIEITLMNHLQETALNHVKSAGLLGDGFGSTPEMCKKNLFVWVTMKNQVIVD
RYPTWGDVVQVDTWVAPNGKNGMRRDWLLRDYKTGEILTRASSNWMMNKETRRLSKIPEVGEIEHYF
VDAPPVVEDDSRKLSKLDDESTADYVRDGLIPRWSLDVNQHVNNVKYIGWILESAPQVVEKYELARITL
YRRECRKDSVVKSLTSVLGGGDDNGGIGDSGRVDCQHVLLFAGGGDGTGGEIVKGRTQWRPKYEKQDG
SVDHFSAGNV

>AhFatB Fatty acyl-ACP thioesterase B [*Arachis hypogaea*] ABO38555.1
MATAATASIFVPSPSPDAGADGNKLVGGSVKLQGLKSKHASSGGLQVKAHAQAPPKINGSTVESLKHDD
DLPSPPPRTFINQLPDWSMLLAAITTIFLAAEKQWMMLDWKPRRSMDLIDPFGIGRIVQDGLVFRQNFISI
RSYIEIGADRTASIEITVMNHLQETALNHVKTAGLLGDGFGSTPEMCKKSLIWWVTRMQVVVDYPTWGDVV
QVDTWVSASGKNGMRRDWLLRDCKTGEILTRASSVWMMNKLTRRLSKIPEEVRAEIASYFVNSAPILEE
DNRKLSKLDNDTADYIRTGLSPRWNDLDVNQHVNNVKYIGWILESAPQPILESHELAMTLEYRRECRD
SVLQSLTAVSAADVGNLAHRGQLECKHLLRLEDGAEIVRGRTEWRPKPVSNFDIVNQVPAESI

>GmFata acyl-ACP thioesterase A [*Glycine max*] XP_006602508.1
MLKLSCNGLDRAHSLAQCGFAGRPACAVPRRRSGVSGFRLPEGRSIRVSAAVSAKDGAATRVADPGTL
ADRLRVGSLTEDGLSYKEKFIVRSYEVGINKTATVETIANLLQEVGCNHAQSVGYSTDGFAATPTMRKLRL
IIVVTARMHIEIYKYPAWSDIVEIETWCQGEGRVGTTRDFILKDYATDEVIGRATSKWVMNQDTRRLQKVS
DDVKEEYLVFCPREPRLAIPEDNSLKKIPKLEDPAQYSRLGLVPRRADLDMNQHVNNVTYIGWVLESMP
QEIIDSHELQSITLDYRRECQHDIVDSLTSVEAIQGGAEAVPELKGTNGSATAREDKHEHQFLHLLRLS
TEGLEINRGRTTEWRKKAPR

>RcFatA acyl-ACP thioesterase A [*Ricinus communis*] NP_001310680.1
MLKVPCCNATDPIQLSSQCRFLTHFNNRPYFTRRPSIPTFFSSKNSSASLQAVVSDISS
VESAACDSLNRRLRLGKLTEDGFSYKEKFIVRSYEVGINKTATVETIANLLQEVGCNHAQ
SVGFSTDGFAATTSMRKMHLIIVVTARMHIEIYKYPAWSDVVEVETWCQSEGRIGTRRDWI

LTDYATGQIIIGRATSKWVMNQDTRRLQKVTDVREEYLVFCPRELRLAFPEENNRRSSKK
ISKLEDPAQYSKLGVPFRADLDMNQHVNNVTYIGWVLESIPQEIIDTHELQTITLDYRR
ECQHDDIVDSLTSVEPSENLEAVSELRGTTNGSATTAGDEDCRNFLHLLRLSGDGLEINR
GRTEWRKKSAR

>HaFatB-1 Fatty acyl-ACP thioesterase B [*Helianthus annuus*]
XP_022024086.1

MTTSLSYVPSFRTTSFNDNDIRSMVWGYKIFGASNTMKMGRTTMYATPVTKGVNGKPAV
VERTMIPTQKQFVDPFRQGIILDGVGVRQTVVVRSYEVGPDKAVTLQSI LNLQETALN
HVWMSGLLGDGFGATHGMMKNLIWVVSVMQVQVDQYPIWGEILEIDTWVGASGKNGMRR
DWEIRSHTTGIVFARATSTWVMNQKTRRLSKMPDEVRAEISPFINKQAIKEESVEKID
KLDDNAKYINSGLQPKRSDLDMNHVNNVKYVGWMLEAIPPEECLENYQLSNIILEYRREC
GSSDVVESLCEPEQVGIIEDVNYMSRCPIGAGFLNCLVNQCIRFTHVLQVKEDSKCQEI
VGKTTWKKNRNNHYPYCG

>HaFatB-2 Fatty acyl-ACP thioesterase B [*Helianthus annuus*] XP_021989855.1

MVMAASTYFFLNSSSYHDMTRNNLRRTPGPKDAHGIKKNKGSSRSLAKDLTKVNATE
VRANRASFLKPIMMLGQNKNYLDMIPDLGFGSMLSDGFVFRQNFQIRSYEVGSDQAVTTE
TLMNLQETSINHLKAIGVWGDGLGLTREMCKKNLIWVMSKLQVAVDRYPIWDDVIQIDT
WKGAYGKIGMCSNWKFCDAKTGEILLTASCIWLMNEETRRLSKFPDEVRSSELDEHFTNA
TLPVIARKWSPHDEMSIVDHRNGIMPRWSDLDINHVN NVKYIGWILESVPHSIVENYE
IASLTLEYRQECKMESVVSHTYVMVSNNKGKGDNDHVDCKHALQLETGGGEIMKGWTIW
RPKQYENRLGLE

>AtFAD2 Fatty acid desaturase 2 [*Arabidopsis thaliana*] NP_187819.1

MGAGGRMPVPTSSKKSETDTTKRVPCEKPPFSVGDLKKAIPPHCFKRSIPRSFSYLI SDII IASCFYYVA
TNYFSLLPQPLSYLAWPLYWACQGCVLGTGIWVIAHECGHAFSDYQWLDDTVGLIFHSFLLVPYFSWKYS
HRRHNSNTGSLERDEVFVPKQKSAIKWYGKYLNNPLGRIMMLTVQFVLGWPLYLAFNVSGRPYDGFACHF
FPNAPIYNDRELRQIYLS DAGILAVCFGLYRYAAQGMASMICLYGVPLLIVNAFLVLITYLQHTHPSLP
HYDSSEWDWLRGALATVDRDYGILNKVFHNITDTHVAHHLFSTMPHYNAMEATKAIKPILGDYYQFDGTP
WYVAMYREAKECIYVEPDREGDKKGVYWYNNKL

>AtFAD3 Omega-3 fatty acid desaturase [*Arabidopsis thaliana*] AAA61778.1

MVVAMDQRTNVNGDPGAGDRKKEERFDPSAQPPFKIGDIRAAIPKHCWVKSPLRSMYSVV RDII IAVAALA
IAAVYVDSWFLWPLYWAAQGT LFWAIFVLGHDCGHGSFSDIPLLSVVGHILHSFILVPYHGWRISHRTH
HQNHGHVENDESWVPLPERVYKKLPHSTRMLRYTVPLMLAYPLYLCYRSPGKEGSHFNPYSSLFAPSER
KLIATSTTCWSIMFVSLIALSFVFGPLAVLVYGVPIIFVMWLDVATY LHHHGHDEKLPWYRGKEWSYL
RGGLTTIDRDY GIFNNIHHDIGTHVIHHLFPQIPHYHLVDATKA AKHVLGRYYREPKTSGAIP IHLVESL
VASIKKDHYVSDTGDIVFYETDPDLVYASDKSKIN

>AtFAD6 Fatty acid desaturase 6 [*Arabidopsis thaliana*] NP_194824.1

MASRIADSLFAFTGPQQLPRVPKLAASSARVSPGVYAVKPIDLLLKGRTHRSRRCVAPVKRRIGCIKAV
AAPVAPPSADSAEDREQLAESYGFRRQIGEDLPENVT LKDIMDTLPKEVFEIDDLKALKSVLISVTSYTLG
LFMIAKSPWYLLPLAWAWTGTAITGFFVIGHDCAHKSFSKNKLVEDIVGT LAFPLPVYPYEPWRFKHDRH
HAKTNMLVHDTAWQPVPPEEFESSPVMRKAIIFGYGPIRPWLSIAHWVNW HFNLLKFRASEVNRVKISLA
CVFAFMAVGWPLIVYKVGILGWVKFWLMPWLGYHFWMSTFTMVHHTAPHIPFKPADEWNAAQAQLNGTVH
CDYPSWIEILCHDINVHIPHHISPRIPSYNLRAAHESI QENWGKYTNLATWNWRLMKTIMTVCHVYDKEE
NYIPFDRLAPEESQPITFLKKAMPNYTA

>AtFAD7 Fatty acid desaturase 7 [*Arabidopsis thaliana*] NP_187727.1

MANLVLSECGIRPLPRIYTT PRSNFLSNNKFRPSLSSSYKTSSSPLSFG LNSRDGFTRNWALNVSTPL
TTPIFEESPLEEDNKQRFDPGAPPPFN LADIRAAIPKHCWVKNPWKSLSYVVRDVAIVFALAAGAA YLNN
WIVWPLYWLAQGTMFALFVLGHDCGHGSFSNDPKLNSVVGHLHSSILVPYHGWRISHRTHHQNHGHVE
NDESWHPMSEKIYNTLDKPTRFFRFTLPLVMLAYPFY LWARSPGKKGSHYHPDSDFLPKERKDVLTSTA
CWTAMAALLVCLNFTIGPIQMLKLYGIPYWINVMWLD FVTYLHHHGHEDKLPWYRGKEWSYLRGGLTTLD
RDYGLINNIHHDIGTHVIHHLFPQIPHYHLVEATEAAKPV LGKYYREPDKSGPLPLHLEILAKSIKEDH
YVSDEGEVYVYKADPNLYGEVKVRAD

>AtFAD8 Omega-3 fatty acid desaturase [*Arabidopsis thaliana*] AAA65621.1

MASSVLSECGFRPLPRFYPKHTTSFASNPKPTFKFNPPLKPPSSLLNSRYGFYSKTRN WALNVATPLTTL

QSPSEEDTERFDPGAPPPFNLAIRAAIPKHCWVKNPWMSMSYVVRDVAIVFGLAAVAAYFNNWLLWPLY
WFAQGTMFWALFVLGHDCGHGSFSNDPRLNSVAGHLLHSSILVPYHGWRI SHRTHHQNHGHVENDES WHF
LPESIYKNLEKTTQMFRFTLPFPMLAYPFYLWNRSPGKQGSYHPDSDLFLPKKKDVLSTACWTAMAA
LLVCLNFVMGPIQMLKLYGIPYWIFVMWLDVFTYLHHHGHDKLPWYRGKEWSYLRGGLTTLDRDYGWIN
NIHHDIGTHVIHHLFPQIPHYHLVEATEAAKPVLGKYYREPKNSGPLPLHLLGSLIKSMKQDHFVSDTGD
VVYYEADPKLNGQRT

>AhFAD2-1A Omega-6 desaturase [*Arachis hypogaea*] AAB84262.1

MGAGGRVTKIEAQKKPLSRVPHSNPPFSVGQLKKAIPPHCFERSLFISFSYVVYDLLVAYLLFYIATTYF
HKLPYPFSFLAWPIYWAIQGCILTGVWVIAHECGHHAFFSKYQLVDDMVGLTLHSCLLVPYFSWKISHRRH
HSNTGSLDRNEVFVPKPKSKVSWYNKYMNPPGRAISLFITLTGLWPLYLAFNVSGRPYDRFASHYDPYA
PIYSNRERLLIYVSDSSVFAVTYLLYHIATLKG LGWVVCVYGVP LLIVNGFLVTITITYLQHTHASLPHYDS
SEWDWLRGALATVDRDYGILNKAFHHITDTHVAHHLFSTMPHYHAMEATNAIKPILGDYYQFDGTPFYKA
LWREAKECLYVEPDDGASKKGVYWKNF

>AhFAD2-1B Oleate desaturase [*Arachis hypogaea*] AAF82293.1

MGAGGRVTKIEAQKKPLSRVPHSNPPFSVGQLKKAIPPHCFERSLFISFSYVVYDLLMAYLLFYIATTYF
HKLPYPFSFLAWPIYWAIQGCILTGVWVIAHECGHHAFFSKYQLVDDMVGLTLHSCLLVPYFSWKISHRRH
HSNTGSLDRDEVFVPKPKSKVSWYNKYMNPPGRAISLFITLTGLWPLYLAFNVSGRPYDRFASHYDPYA
PIYSNRERLLIYVSDSSVFAVTYLLYHIATLKG LGWVVCVYGVP LLIVNGFLVTITITYLQHTHASLPHYDS
SEWDWLRGALATVDRDYGILNKAFHHITDTHVAHHLFSTMPHYHAMEATNAIKPILGDYYQFDGTPVYKA
LWREAKECLYVEPDDGASQKGVYWKNF

>AhFAD2-2 Omega-6 fatty acid desaturase [*Arachis hypogaea*] ACZ06072.1

MGAGGRVTSVPPSNRTVEADYAKRVPHEKPPFSLSQVKKAIPPHCFQRSVIRSFYSYVVYDLTIAFCLYYAA
TNYFHKLSSPLFYLAWLLYGAVQGCILTGVWVIAHECGHHAFFSDYQWLDDTVGLVLHSGLLVPYFSWKYS
HRRHSNTGSLDRDEVFVPKPKSSIAWWSKYLNPLGRVLTITLTGLWPLYLAFNVSGRPYDRFACHY
DPYGPISDRERLQIYISDAGVLAVSYGLIRLVMAKGLAWVAVYGVPLLVVNGFLVLITITYLQHTHPALP
HYDSSEWDWLRGALATVDRDYGILNKVFHNITDTHVAHHLFSTMPHYHAMEATNAIKPILGEYYRFDGTP
FYKAMWREAKECLYVESDQGAQNKG VFWYNNKL

>AhFAD3-4 Omega-3 fatty acid desaturase [*Arachis hypogaea*] QFR98376.1

MAVSHVYVTNGHKKKENDEFDASAPPPFKIADIRAAIPRHCWVKNPWRSLSYVLRDLVLVATLLASAIHFN
SWFFFWPIYWPLQGTMFWALFVLGHDCGHGSFSNNAKLSIVGHILHSSILVPYHGWRI SHKTHHQNHGHV
ENDES WVP LPEKIYKSLDNVTCLMRFTVPFPIFAYPFYLWRRSPGKEGSHFNPYGKLFSPNERKDVMI ST
MCWVAMFSLLLFLSFIVTPLSILKLYGIPYLIFIMWLDVFTYLHHHGKQKLPWYRGKEWSYLRGGLTTV
DRDYG LVNNIHHDIGTHVIHHLFPQIPHYHLLATEAAKPVLGKYYREPEKSGPLPSHLIKYLLQSIGQD
HYVSDNGDIVYYQSDPYLLNNNNKSN

>AhFAD6 Omega-6 fatty acid desaturase [*Arachis hypogaea*] ACZ06070.1

MACRLADSFILFKGSHQKPLQSKRAIVAQYSPRVCNLKECGLIQKGRHRLNFPVPRKKVTVIQAVAVPLE
PFPVESAERYKQLAESYGRQIGELPDDITLKDVIDSLPKKVFEIDDTKAWKTVLISVASYALGLFMIS
KAPWYLLPLAWAWTGTAVTGFFVIGHDCAHKSFSKNKLVEDIVGTLAFLPLIYPYEPWRFKHRRHAKTN
MLYEDTAWHPVWKDEFDSSPALRNAI IYGYGPFRTWMSIAHWLMWHFDLKKFRTNEVKRVKISLACVFAF
MAIGWPLI IYKTGIMGWIKFWFMPWLGYHFWMSTFTMVHHTAPHI PFKYSENWNAQAQLNGTVHCDYPQ
WIEILCHDINVHIPHHISPRIPSYNLRAAHKSLQENWGKYLNEASWNWRLMKTIMTVCHVYDKQQNYVAF
DELAPEDSRPITFLKEVMPDYA

>AhFAD7-1A Delta 15 desaturase [*Arachis hypogaea*] AID51460.1

MATWVLSEGLRPLPPMFPRPRTGSISCTKSSSINSTFLSSDLKS FQQQTRFQCCSFKERRRSWEIKVSV
PLRVGTIEEEEEEEEG IINGVVEKREVCEFDPGAPPPFKLSDIRAAIPKHCWVKDPWRMSYVVRD VVVV
LG LAAAAAHLNNWIVWPLYWAAQGTMFWALFVLGHDCGHGSFSNNPKLNSVVGHLHSSILVPYHGWRI S
HRTHHQNHGHVENDES WHPLPEKIFKSLDNVTRTLRFTIPFPMLAYPIYLWSRSPGKTGSHFHPDSDLFV
SNERKDVITSTICWAAMASLLVGLGFVMGPIQLLKLKLYGIPYVLFVMWLDVFTYLHHHGHDKLPWYRGEE
WSYLRGGLTTLDRDYGWINNIHHDIGTHVIHHLFPQIPHYHLIEATEAAKPVLGKYYREPKKS LPLPFHL
IGDLMRSMKKDHYVSDTGDVYYYQTDPTLGGSSTSI

>AhFAD8 Omega-3 fatty acid desaturase [*Arachis hypogaea*] AFD93985.1

MATWVLSEGLRPLPPMFPRPRTGSISCTKSSSINSTFLSSDLKS FQQQTRFQCCSFKERRRSWEIKVSV
PLRVGTIEEEEEEEEG IINGVVEKREVCEFDPGAPPPFKLSDIRAAIPKHCWVKDPWRMSYVVRD VVVV
LG LAAAAAHLNNWIVWPLYWAAQGTMFWALFVLGHDCGHGSFSNNPKLNSVVGHLHSSILVPYHGWRI S
HRTHHQNHGHVENDES WHPLPEKIFKSLDNVTRTLRFTIPFPMLAYPIYLWSRSPGKTGSHFHPDSDLFV
SNERKDVITSTICWAAMASLLVGLGFVMGPIQLLKLKLYGIPYVLFVMWLDVFTYLHHHGHDKLPWYRGEE
WSYLRGGLTTLDRDYGWINNIHHDIGTHVIHHLFPQIPHYHLIEATEAAKPVLGKYYREPKKS LPLPFHL

IGDLMRSMKKDHYVSDTGDVYYYQTDPTLGGSSSTSI
>GmFAD2-1A Omega-6-desaturase [*Glycine max*] AAX29989.1
MGGRGRVAKVEVQRKKPLSRVPNTKPPFTVGQLKKAIPPHCFQRSLLTSFSYVVYDLSFAFIFYIATTFY
HLLPQPFSLIAWPIYWVLQGCLLTGVWVIAHECGHHAFSKYQWVDDVVGTLHSTLLVPYFSWKISHRRH
HSNTGSLDRDEVFVFKPKSKVAWFSKYLNPLGRAVSLVLTITIGWPMYLAFNVSGRPYDSFASHYHPYA
PIYSNRERLLIYVSDVALFSVTYSLYRVATLKGLVWLLCVYGVPLLVNGFLVTITYLQHTHFALPHYDS
SEWDWLK GALATMDRDYGILNKVFHHTDTHVAHHLFSTMPHYHAMEATNAIKPILGEYYQFDDTPFYKA
LWREARECLYVEPDDEGTSEKGVYWRNKY
>GmFAD2-2 Omega-6 fatty acid desaturase [*Glycine max*] BAD89862.1
MGAGGRDTPPANRSEVDPLKRVPFKEKPPFSLSQIKKVIPPHCFQRSVFRSFSYVVYDLTIAFCLYYVA
THYFHLLPSPLSFLAWPIYWAVQGCILTGVWVIAHECGHHAFSDYQLLDDIVGLVLHSGLLVPYFSWKYS
HRRHHSNTGSLERDEVFVFKQKSCIKWYSKYLNPPGRVLTAVTLTLGWPLYLALNVSGRPYDRFACHY
DPYGPISDRERLQIYISDAGVLAVCYGLFRLAMAKGLAWVVCVYGVPLLVNGFLVLITFLQHTHPALP
HYTSSEWDWLRGALATVDRDYGILDKVFHNITDTHVAHHLFSTMPHYHAMEATKAIKPILGEYYRFDET
FVKAMWREARECIYVEPDQSTESKGVFWYNNKL
>GmFAD3A Omega-3 fatty acid desaturase A [*Glycine max*] AMY60543.1
MVKDTKPLAYAANNQYQKEAFDPSAPPPFKIAEIRVAIPKHCWVKNPWRSLSYVLRDVLVIAALMAAASH
FNNWLLWLIYWPIQGTMFWALFVLGHDCGHGSFSDSPFLNSLVGHILHSSILVPYHGWRISHRTHQNHG
HIEKDES WVPLTEKIYKNLDMTRLVRFTVPFPLFVYPIYLFSSRSPGKEGSHFNYPYNSLPSPERKGI
STLCWVTMFMSLIYLSFITSFVLLKLYGIPYIWFVMWLDFTYLLHHGHGKLPWYRGKEWSYLRGGLT
TVDRDYGWINNIHHDIGTHVIHHLFPQIPHYHLVEATQAASVVLGEYYREPERSAPLPFHLIKYLIQSMR
QDHFVSDTGDVYYYQTDLSLHLSHRD
>GmFAD6C Omega-6 fatty acid desaturase [*Glycine max*] P48628.1
MACTLADSLLLFKGSYQKPVLRRDIAARYSPGIFSLNSNGLIQKRFRQRNFVTRNKVTVIHAVAIPVQP
APVESAEYRKQLAEDYGRQVGEPLSDDVTLKDVINPLPKEVFEIDDVKAWSVLISVTSYALGLFMISK
APWYLLPLAWVWTGTAITGFFVIGHDCAHRSFSSNKLVEDIVGTAFMPLIYPYEPWRFKHDRHAKTNM
LREDTAWHPVWKDEFESTPLLRKAIYGYGPFRCWMSIAHWLMWHFDLKKFRPSEVPRVKISLACVFAFI
AIGWPLIIYKTGIMGWIKFWLMPWLGYHFWMSTFTMVHHTAPYIPFKYSEWNRAQAQLNGTVHCDYPKW
IEILCHDINVHIPHHISPRIPSYNLRAAHKSLQENWGQYLNESWNWRLMKTIMTVCQYVDKEKSLCCL
RTCP
>GmFAD7 Omega 3 fatty acid desaturase [*Glycine max*] ACF19424.1
MATWVLSECSLKPLAPVIPRPTGAVLSSTSKVGFLTNKVLEGSKFQPLRCNLRERNWGLKVSVPLRIA
SIEEEEQKSVDVINGSNGVEHEKLPEFDPGAPPPFNADIRAAIPKHCWVKDPLKSMSYVVRDVIAVFG
ASAAAYLNNWLVWPLYWAAQGTMFWALFVLGHDCGHGSFSSNPKLNSVVGHLHSSILVPYHGWRISHRT
HHQHGHGVENDES WHPLPEKLFRLSDTVTRMLRFTAPFPLLAYPVYLWGRSPGKTGSHFDPSSDLFVPNE
RKDVITSTACWAAMLGLLVGLGFVMGPVQLLKLYGVPIYFVMWLDLVTYLHHGHGHDKLPWYRGKEWSY
LRGGLTTLD RDYGLINNIHHDIGTHVIHHLFPQIPHYHLVEATEAAKPVFGKYREPKKSSPLPFHLIGE
LIKSFKTDHFVSDKGDVYYYQTDSEINGSSKSE
>GmFAD8-2 Omega-3 fatty acid desaturase [*Glycine max*] NP_001239777.1
MATWVLSECGLRPLPPVPRSTRPISQKPSKSRFLSTNKGVPDLNLQARGLTCCSFDRDKWELGVSA
PLKFATNEGEEEEERTNGANNVGEEVSEFDPSAPPPFKLADIRAAIPKHCWVKDPWKSMSYVVRDVIVVFG
AAAAAYLNNWVWPLYWAAQGTMFWALFVLGHDCGHGSFSSNPKLNSVAGHLHSSILVPYHGWRISHRT
HHQNHGHGVENDES WHPLPEKIFKSLDNVTRILRFTLPFPLLAYPIYLWSRSPGKTGSHFNPDSDLFVPSE
RKDVITSTICWTAMAALLVGLGFVMGPVQLLKLYGIPYAFVMWLDLVTYLHHGHGHDKLPWYRGEESY
LRGGLTTID RDYGLINNIHHDIGTHVIHHLFPQIPHYHLIEATEAAKPVLGQYYREPKKSSPLPIYLI
GELLRSMKKDHFVSDSGDIVYYYQTDPTLSSSSTSQ
>CsFAD2 Omega-6 fatty acid desaturase [*Camelina sativa*] XP_019096117.1
MGAGGRMPVPSSSSKKSETDAIKRVPCEKPPFTLGELKKAIPPQCFKRSIPRSFSYLITDIIIVASCFYYV
ATNYFSLLPQPLSYLAWPLYWACQGCVLTVGVVIAHECGHHAFSDYQWLDDTVGLIFHSFLLVPYFSWKY
SHRRHHSNTGSLERDEVFVFKQKSAIKWYGKYLNNPAGRIMMLTVQFVLGWPLYLAFNVSGRPYDGFACH
FFPNAPIYNDRELRQIYLS DAGILAVCFGLYRYAAAQGLASMICLYGVPLLVNAFLVLITYLQHTHPAL
PHYDSSEWDWLRGALATVDRDYGILNKVFHNITDTHVAHHLFSTMPHYNAMEATKAIKPILGDYQYQFDGT
PWYVAMYREAKECIYVEPDREGDKKGVYWYNNKL
>CsFAD2-2 Omega-6 fatty acid desaturase [*Camelina sativa*] NP_001291954.1
MGAGGRMPVPSSSSKKSETDAIKRVPCEKPPFTLGDLKKAIPPQCFKRSIPRSFSYLITDIIIVASCFYYV
ATNYFSLLPQPLSYLAWPLYWACQGCVLTVGVVIAHECGHHAFSDYQWLDDTVGLIFHSFLLVPYFSWKY

SHRRHHSNTGSLERDEVFVVPKQKSAIKWYGKYLNNPAGRIMMLTVQFVLGWPLYLAFNVSGRPYDGFACH
FFPNAPIYNDRERLQIYLS DAGILAVCFGLYRYAAAQGLSMICLYGVPLLIVNAFLVLITYLQHTHPAL
PHYDSSEWDWLRGALATVDRDYGILNKVFHNITDTHVAHHLFSTMPHYNAMEATKAIKPILGDYYQFDGT
PWYVAMYREAKECIYVEPDREGDKKGVYWYNNKL

>BnFAD2-4 Omega-6 fatty acid desaturase [*Brassica napus*] XP_022570693.1
MGAGGRMQVSPSSSPETKTLKRVPCETPPFTLGDLLKKAIPPHCFKRSIPRSFSYLLFDILVSSSLYHLS
TAYFPLLPHPLPYLAWPLYWACQGCVLTLGLWVIAHECGHAFSDHQWLDDAVGLVFHSFLLVPYFSWKYS
HRRHHSNTGSLERDEVFVPPKKSDIKWYGKYLNNPLGRTVMLTVQFTLGLWPLYLAFNVSGRPYSDGFACH
FHPNAPIYNDRERLQIYISDAGVLSVCYGLYRYAGSRGVASMVCVYGVPLMIVNCFVLITYLQHTHPSL
PHYDSSEWDWLRGALATVDRDYGILNKVFHNITDTHVAHHLFSTMPHYNAMEATKAIKPILGEYYQFDGT
PVVKAMWREAKECIYVEPDROGEKKGVFWYNNKL

>BnFAD3 Omega-3 fatty acid desaturase [*Brassica napus*] NP_001302953.1
MVMAMDQRSNVNGDSGARKEEGFDPSEQPPFKIGDIRAAIPKHCWKSPLRSMYSVARDIFAVAALAMAA
VYFDSWFLWPLYWVAQGTFLWAI FVLGHDCGHSFSDIPLLNSVVGHIHLSFILVPYHGWRISHRTHQN
HGHVENDES WVPLPEKLYKNLPHSTRMLRYTVPLPMLAYPIYLWHRSPGKEGSHFNYPYSSLFAPSERKLI
ATSTTCWSIMLATLVYLSFLVGPVTVLKVYGVPIIIFVMWLDVAVTYLHHHGHDEKLPWYRGKEWSYLRGG
LTTIDRDYGIFNNIHHDIGTHVIHHLFPQIPHYHLVDATRAAKHVLGRYYRVPKTS GAIP IHLVESLVA
IKKDHYVSDTGDIVFYETDPDLYVYASDKSKIN

>BnFAD6 Omega-6 desaturase [*Brassica napus*] AAA50157.1
MASRIADSLFAFTGPQQCLPRAPKLASARLSPGVYAVRPIDLLLKGTRRTFLVPAKKRIGCIKAVFVPVA
PPSADNAEDREQLAESYGFKQIGQDLDPDNTLKDIMDTLPKEVFEIDDVKAWKSVLISVTSYALGLFMIA
KAPWYLLPLAWAWTGTAVTGFFVIGHDCAHKSFSKNKLVEDIVGTLAFLPLVYPYEPWRFKHDRHHAKTN
MLVHDTAWQPVPPEEFDSSPVLRKAIIFGYGPIRPWLSIAHWVNWVFNLRKFRPSEVNRVKISLACVFAF
MAVGWPLIIYKVGVLGWVKFWLMPWLGYHFWMSTFTMVHHTAPHIPFKPADEWNAAQAQLNGTVHCDYPS
WIEILCHDINVHIPHHISPRIPSYNLRAAHQSIQENWGKYTNLATWNWRLMKTIMTVCHVYDKEENYIPF
DRLAPEESQPITFLKKAMPDYAA

>HaFAD2 Delta(12) fatty acid desaturase, [*Helianthus annuus*]
XP_021972383.1
MGAGGRMSNPVNGEEKPNPDPLQRPVYQKPPFTVGDVKAIPPHCFNRSVIRSFYSYVYDLTIASIFYYL
ANNYIALLPSPLAYVAVPVYIWICQGCVLTVGVVIAHECGHAFSDYQWLDDTVGLVLHSALLVPYFSWKY
SHRRHHSNTGSLIEHDEVFVPKLKS GVRSTARLLNNPPGRILTLLVTLTMGWPLYLMFNVSGRYDRFACH
FDPNSPIYSNRERAQIFISDAGILTVLFLVFRVAMTKGLTWVLTMYAGPLL VVNGFLVLITFLQHTHPSL
PHYDSTEDWDLRGALATIDRDYGVNLKVFNITDTHVTHHLFSTMPHYHAMEATKAIKPILGEYYQFDGT
SVFKAMYRETKECIYVDKDEEVKDG VYWRNKI

>BnLACS1 Long-chain acyl-CoA synthetase 1 [*Brassica napus*] CDY27501.1
MKSFAAKVEDGVRGENGKPSVGPVYRNLLSEKGFPPIDSDITTAWDIFSKSVKKFPDNKMLGWRRIVDEK
VGPYMWKTYKEAYDEVLQIGSALRAIGAEPGCRVGIYGVNCPQWIIITMEACAAHTLICVPLYDTLGS GAV
DYIVDQAEIDFVVFQETKIKGLLEPDCKCARRLKAIVSFTNVSEEHNKLGSEVGVKTYSWLDFLQMGCGK
PEETTPPKPFNICTIMYTS GTSGDPKGVVLTHEAVATYIVGMDLFMDQFEDKMTHEDEVYLSFLPLAHILD
RMNEEYFFRK GASVGYHGDNLVLRDDIQELKPTYLAGVPRVFERIHEGIQKALQELNPRRRFIFNALYK
HKLAWLNRGYSHSKASPMADFI AFGKIRDKLGGRI RLLVSGGAPLSTEIEEFLRV TCCCFFVVG YGLTET
LGGTAMGFDPDEMCLGTVGIPAVYNEIRLEEVAEMGYDPLGENPAGEICIRGKCLFSGYYKNPKLTQEVM
KDGWFHTGDIGEIQSNGLVKI I DRKKNLIKLSQGEYVALENLENIYGQNSLVQDIWVYGDSFKSMLVAVI
VPNQETIKRWAKELGFTKPFEE LCSELQEHII SELKSTAEKNKL RKF EYI KAVTVETKPF DVARDLVT
ATLKNRRNNLLKYYQVQVDEMYRKLASKKI

>BnLACS2 Long-chain acyl-CoA synthetase 2 [*Brassica napus*] CDY29350.1
MAAAADHVVIIMEEGRQATAEHPSAGPVYRCKYAKDGLLDLPADLDSWQLFSEAVKQYPNEQMLGRRVTV
DSKVGPYTWITYREAHDAALRIGSAIRS RGVNPGNCCGIYGSNCP EWI IAMEACMSQGITYVPLYDSLGV
NAVEFIINHAEVSLV FVQEKALSSILACRKGCSNLKTIVSFGEVSITQKEEAENQCVSLFSWHEFLLMG
NSDETTLP RKQKT DICTIMYTS GTTGEPKGVILSNAAIMVEVLSIDKMLQVTRSCDTS DLFFSYLPLAH
CYDQVMEIYFLSRGSSVGYWRGDIRYLMDDVHALKPTVFCGVPRVYDKLYAGVMQKISAGGLIRKKLFDL
AYNYKLG NMRKGLS QEEASPRLDRLMFDKIKDALGGRAHMLLSGAAPLPRHVEEFLRIIPASNLSQGYGL
TESCGGSFTTLAGVFSMVGTVGVPMPTVEARLVSPPEMGYEA FSGDVARGEICLRGNSMFSGYHQRQDLT
DQVVINGWFHTGDIGEWQEDGSMKII DRKKNIFKLSQGEYVALENLENTY SRCPLIAQIWIYGN SFESFL
VAVVVPERKAIEDWAKLNNQSSPNDFESLCQNLKAQKYFLDELNSTAKQYQLKGFEMLKAVHLEPNLFDI

ERDLITPTFKLRPQLLKHYKSIIDQLYTEAKASRA

>BnLACS3 Long chain acyl-CoA synthetase 3 [*Brassica napus*] XP_013664517.1
MATDRFIVEVEKGEKGVGGSPSVGSVYRSIYAKDGFPEPADLLSCWDIFRLSAEKSPDNPMGLGRREIV
DGKAGKYVWQTYKEVYDIVIKLGNISIRTIGVGKGEKCGIYGANSPEWIIISMEACNAHGLYCVPLYDTLGA
GAIEFIICHAKVSLAFSEEKKISELLKTAPNSTKYLNIVSFGEVSNVQRAEAERHGLSIYSWDQFLKLG
EGKHYELPEKKRSDICTIMYTS GTTGD PKGVLLT NESIIYLLEGVKLLKTINEELTSKDVLYSYLPLAH
IFDRVIEELFIYEASIGFWRGDKILVEDIAALKPTIFCAVPRVLERIYNGLQQKLS DGGFLKKT LFN
AFNYKHNNMVKGKAHEQAAPIFDKIVFKKVKEGLGGRVRLILSGAAPLAHIESFLRVVACAHVLQGYGL
TESCGGT FVSIPNELQMLGTVGPPVPNVDIRLESVP EGMGYDALARKPRGEICIRGKTLFSGYYKREDLTQ
EVFIDGWLHTGDVGWQPDGAMKIIDRKKNIFKLSQGEYVAVENLENIYSHVAAIESVWVYGNSSYESYLV
AVVCPSKIQIEHWAKEHNVSGDFETIGQNQKTEFILGEFNRVAKDKKLKGFELIKGVHLDTPVDFMERD
LITPSYKKKR PQLLKYYQKEIDEMYNKTKN

>BnLACS4 Long chain acyl-CoA synthetase 4 [*Brassica napus*] NP_001302548.1
MTQQLEKFIFQVEEGREGSDGRPSVGPVYRSVFAKDGFPEPIEGMDS CWDVFRMSVEKYPNNPMLGRREI
VDGKPGKYVWQTYQEVYDIVIKLGNLSRSCGVVEQAKCGIYGANSPEWIIISMEACNAHGLYCVPLYDTLGA
AGAVEFIITHSEVSIVFVEEKKISELFKTCPKATEYMKTVVSFGGV TREQKEAAET FGLVIYAWDEFLKL
GEGKQFDLP IKKKSDICTIMYTS GTTGD PKGVMISNESIVTLIAGVIRLLKSANEALTVKDVLYSYLPLA
HIFDRVIEECFIQHGAAGFWRGDKLLIEDLGELKPTIFCAVPRVLD RVSGLQQKLAAGGF FKKFMFD
SAFSFKYGHMKKGQSHVEASPLCDKLVFSKVKQGLGGNVRIILSGAAPLASHVESFLRVVACCHVLQGYG
LTESCAGTFVSLPDRLDMLGTVGPPVPNVDIRLESVP EMEYDALASTPRGEICIRGKTLFSGYYKREDLS
KEVLIDGWLHTGDVGWQPNGSMKIIDRKKNIFKLSQGEYVAVENLENIYGEVQAVDSVWVYGNSSFESFL
IAVANPNQHILEKWAAENGVS GDYNALCQNAKAKEFILGELVKMGKEKKMKGF EIIKAVHLDPVDFMER
DLLTPTYKKKR PQLLKHYQCVIDEMYKTTNESLASRK

>BnLACS5 Long chain acyl-CoA synthetase 5 [*Brassica napus*] XP_013669542.1
MTSQKRFIIEVEAAKEATDGKPSIGPVYRSTFAKDGFNPIDGIDSCWDIFRTAVEKYPNNRMLGRREIV
NNKAGKYEWKTYKEVYDIVLKLGNLSRSCGIEEGGKCGIYGANCP EWIIISMEACNAHGLYCVPFYDTLGS
GAVEFIISHAEVSI AFVEEKKIPELFKTCPNSTKYMKT VVSFGGVKSEQKEEA EKLGLVIHAWDEFLKLG
EGKQYDLPVKKKSDICTIMYTS GTTGD PKGVLM SNESIVTITAGVRHFLAIFNESL TEKDVYISYLPLAH
VFDRAVEECIIQVGGSIGFWRGDKLLIEDLGELKPSIFCAVPRVLERVYTG LQQKLSVGGFFKKKVFNV
AFSYKFGNMKKGQSHVEAAPFCDKLVFNKVQGLGGNVRIILSGAAPLASHIESFLRVVACCHVLQGYGL
TESCAGTFVTFPDELDMLGTVGPPVPNVDIRLESVP DMEYDALGSI PRGEICIRGKTLFSGYHKREDLTK
EVLIDGW FHTGDIGEWQPDGSMKIIDRKKNIFKLSQGEYVAVENLE NVYGQVEAIDSIWVYGNSSFESFLI
AVANPSQQT LERWAAENG VNGDFDSICQNTKARAFLLGELVKTAKERKLKGFEIIRAVHLEPVAFDIERD
LLTPTYKKKR PQLLKYYQNVIDDMYKTAKEGQASVQ

>BnLACS9 Long chain acyl-CoA synthetase 9 [*Brassica napus*] NP_001303207.1
MIPYAAGVIVPLALTL LVRNAKKDKKRGVVVDVGGE PGHTVRNHRFKDPVSSHWE DISTLP ELFEISCK
SHSDRFFLGTRRLIAREVETSEDGKVFEKLHLGDYEWKTFGETLEAVCSFASGLVQIGHKSEERVAIFAD
TREEWFIALQGC FRNRVT VVTIYSSLGEEALCHSLNETEVTTVICGNKELKKLMDISQQL ETVKRVICMD
DEFPSEASSTWTTTSLADVQKLGRESPVDPSPFLSADVAVIMYTS GSTGLPKGVMMTHGNVLATVSAVMT
IVPDLGKRDTY MAYLPLAHILELAAESVMATIGSAIGYGSPLT LTDTSNKIKKGT KGDVTALKPTIMTAV
PAILDRVRDGV RKKVDAKGGA AKKLFDFAYARRLSAINGSWFGAWGLEKLLWDVLVFGKIRAVLGGLQRY
LLSGGAPLSGDTQRFINICVGAPIGQGYGLTETCAGGTFSEFDDTSVGRVGA PLPCSFVKLIDWPEGGYL
ISDKPMPRGEIVIGGSNITLGYFKNEEKTKEVYKVDEKGMRFYTG DIGQFHPDGCLEIIDRKKDIVKLQ
HGEYVSLGKVEAALSISPYVENIMVHADPFYSYCVALVVA AQQTLEGWASKQGIEFTNFEELCAKEQPVK
EVYASLVKAAKQSRLEKFEIPAKIKVLAAPWTPESGLVTAALKLKR DVIRKEFS EDLTKLYAS

>AtLACS1 Long chain acyl-CoA synthetase 1 [*Arabidopsis thaliana*]
AT2G47240

MKSFAAKVEEGVKGIDGKPSVGPVYRNLLSEKGFPPIDSEITTAWDIFSKSVEKFPDNNMLGWRRIVDEK
VGPYMWKTYKEVYEEVLQIGSALRAAGAEPGSRVGIYGVNCPQWIIAMEACAAHTLICVPLYDTLGS GAV
DYIVEHAEIDFV FVQDTKIKGLLEP DCKCAKRLKAIVSFTNVSD ELSHKASEIGVKTYSWIDFLHMGREK
PEDTNPPKAFNICTIMYTS GTSGDPKGVLTHQAVATFVVGMDLYMDQFEDKMT HDDVLYSFLPLAHILD
RMNEEYFFRK GASVGYHGNLNVLRDDIQELKPTYLAGVPRVFERIHEGIQKALQELNPRRRFIFNALYK
HKLAWLNRGYSHSKASPMADFI AFRKIRD KLGGRI RLLVSGGAPLSPEIEEFLRV TCCCFFVQGYGLTET
LGGTALGF PD EMCMLGTVGIPAVYNEIRLEEVSEMGYDPLGENPAGEICIRGQCMFSGYYKNPELTEEVM
KDGWFHTGDIG EILPNGVLKIIDRKKNLIKLSQGEYVALEHLENIFGQNSVVQDIWVYGDSFKSMLVAVV
VPNPETVNRWAKDLGFTKPFEE LCSFP ELKEHII SELKSTAEKNKL RKF EYIKAVTVETKPF DVERDLVT
ATLKNRRNNLLKYYQVQIDEMYRKLASKKI

>AtLACS2 Long chain acyl-CoA synthetase 2 [*Arabidopsis thaliana*]
AT1G49430

MSLAADNVLLVEEGRPATAEHPSAGPVYRCKYAKDGLLDLPTDIDSPWQFFSEAVKKYPNEQMLGQRVTT
DSKVGPYTWITYKEAHDAAIRIGSAIRSRGVDPGHCCGIYGANCPewIIAMEACMSQGITYVPLYDSLGV
NAVEFIINHAEVSLVVFVQEKTVSSILSCQKGCSSNLKTIVSFGEVSSTQKEEAKNQCVSLFSWNEFSLMG
NLDEANLPRKRKTIDICTIMYTS GTTGEPKGVILNNAAISVQVLSIDKMLEVTD RSCDTSDFVFSYLPLAH
CYDQVMEIYFLSRGSSVGYWRGDIRYLMDDVQALKPTVFCGVP RVYDKLYAGIMQKISASGLIRKKLDFD
AYNYKLG NMRKGFSQEEASPRLDRLMFDKIKEALGGRAHMLLSGAAPLPRHVEEFLRIIPASNLSQGYGL
TESCGGSFTTLAGVFSMVGTVGVPMP TVEARLVSVPEMGYDAFSADVPRGEICLRGNSMFSGYHQRDLT
DQVLIDGWFHTGDIGEWQEDGSMKIIDRKKNIFKLSQGEYVAVENLENTYSRCPLIAQI WVYGN SFESFL
VGVVVPDRKAIEDWAKLNYQSPNDFESLCQNLKAQKYFLDELNSTAKQYQLKGFEMLKAIHLEPNPFDIE
RDLITPTFKLRPQLLQHYKGIVDQLYSEAKRSMa

>AtLACS3 Long chain acyl-CoA synthetase 3 [*Arabidopsis thaliana*]
AT1G64400

MATGRIIVEVEKKGQGV DGGSPSVGPVYRSIYAKDGFPEPPDDLVS AWDFRLSVEKSPNNPMLGRREIV
DGKAGKYVWQTYKEVHNVIKLGNSIRTIGVGKDKCGIYGANSPEWII SMEACNAHGLYCVPLYDTLGA
GAIEFII CHAEVSLAF AEENKISELLKTAPKSTKYLYIVSFGEVTNNQRVEAERHRLTIYSWDQFLKLG
EGKHYELPEKRSDVCTIMYTS GTTGDPKGVLLTNESIIHLLEGVKLLKTIDEELTSKDVLYSYLPLAH
IFDRVIEELCIYEAASIGFWRGDVKILIEDIAALKPTVFC AVPRVLERIYTGLQQLSDGGFVKKKLFNF
AFKYKHKNMEKGQPHEQASPIADKIVFKKVKEGLGGNVRLILSGAAPLAHIESFLRVVACAHVLQGYGL
TESCGGT FVSIPNELSMLGTVGPPV PNVDIRLESVP EMGYDALASNPRGEICIRGKTLFSGYYKREDLTQ
EVFIDGWLHTGDVGEWQPDGAMKIIDRKKNIFKLSQGEYVAVENLENIYSHVAAIESIWVYGN SYESYLV
AVVCPSKIQIEHWAKEHKVSGDFESICRNQKTKEFVLGEFNRVAKDKKLKGFELIKGVHLDTPPFDMERD
LITPSYKMKRPQLLKYYQKEIDEMYKKNREVQLRV

>AtLACS4 Long chain acyl-CoA synthetase 4 [*Arabidopsis thaliana*]
AT4G23850

MSQKKYIFQVEEGKEGSDGRPSVGPVYRSIFAKDGFDPDIEGMDSCWDVFRMSVEKYPNNPMLGRREIV
DGKPGKYVWQTYQEVYDIVMKLGNSLR SVGVKDEAKCGIYGANSPEWII SMEACNAHGLYCVPLYDTLGA
DAVEFII SHSEVSIVFVEEKKISELFKTCPNSTEYMKTVVSFGGVSREQKEEAETFGLVIYAWDEFLKLG
EGKQYDLPIKKKSDICTIMYTS GTTGDPKGV MISNESIVTLIAGVIRLLKSANEALT VKDVLYSYLPLAH
IFDRVIEECFIQHGA AIGFWRGDVKLLIEDLAELKPTIFCAVPRVLD RVYSGLQKKLS DGGFLLKKFIFDS
AFSYKFGYMKKGQSHVEASPLFDKLVFSKVKQGLGGNVRIILSGAAPLASHVESFLRVVACCHVLQGYGL
TESCAGTFVSLPDELGM LGTVGPPV PNVDIRLESVP EMEYDALASTARGEICIRGKTLFSGYYKREDLT
EVLIDGWLHTGDVGEWQPDGSMKIIDRKKNIFKLSQGEYVAVENIENIYGEVQAVDSVWVYGN SFESFLI
AIANPNQHILERWAAENGVS GDYDALCQNEKAKEFILGELVKMAKEKKMKGF EIIKAIHLDPVPFDMERD
LLTPTFKKKRPQLLKYYQSV IDEMYKTINAKFASRG

>AtLACS5 Long chain acyl-CoA synthetase 5 [*Arabidopsis thaliana*]
AAM28872.1

MTSQKR FIFEVEAAKEATDGNPSVGPVYRSTFAQNGFPNPIDGIQSCWDIFRTAVEKYPNNRMLGRREIS
NGKAGKYVWKTYKEVYDIVIKLGNSLR SCGIKEGEKCGIYGINCCEWII SMEACNAHGLYCVPLYDTLGA
GAVEFII SHAEVSI AFVEEKKIPELFKTCPNSTKYMKTVVSFGGVKPEQKEEA EKLGLVIHSWDEFLKLG
EGKQYELPIKKPSDICTIMYTS GTTGDPKGV MISNESIVTIT TGMHFLGNVNASLSEKDVYISYLPLAH
VFDRAIEECIIQVGGSIGFWRGDVKLLIEDLGELKPSIFCAVPRVLD RYVTGLQQLSGGGFFKKKVF DV
AFSYKFGNMKKGQSHVAASPFCDKLVFNKVKQGLGGNVRIILSGAAPLASHIESFLRVVACCNVLQGYGL
TESCAGTFATFPDEL DMLGTVGPPV PNVDIRLESVP EMNYDALGSTPRGEICIRGKTLFSGYYKREDLT
EVFIDGWLHTGDVGEWQPNGSMKIIDRKKNIFKLAQGEYVAVENLENVYSQVEVIESIWVYGN SFESFLV
AIANPAQQTLERWAVENG VNGDFNSICQNAKAKAFILGELVK TAKENKLKGF EIIKDVHLEPVAFDMERD
LLTPTYKKKRPQLLKYYQNV IHEMYKTTKETLASGQ

>AtLACS6 Long-chain acyl-CoA synthetase 6 [*Arabidopsis thaliana*]
NP_566265.1

MDSSSSSSSSAAARRRINAIHSHLVTSSRSSPLLRSNPTAGEFCLDN GYSVVLPEKLNTGSWNVYRS AKSP
FKLVSRFPDHPDIATLHDNFEHAVHDFRDYKYLGTRVRVDGT VGDYKWM TYGEAGTARTALGSGLVHHGI
PMGSSVGIYFINRPEWLIVDHACSSYSYVS VPLYDTLGPDAVKFIVNHATVQAIFCVAETLNSLLSCLSE
MPSVRLVVVVGG LIESLPSLPSSSGVKVVSYSVLLNQGRSNPQRFFPPKPDDVATICYTS GTTGTPKGVV
LTHANLIANVAGSSFSVKFFSSDVYISYLPLAH IYERANQILT VYFGVAVGFYQGDNMKLLDDLAALRPT
VFSSVPRLYNRIYAGI INAVKTS GGLKERLFNAAYNAKKQALLNGKSASPIWDRLVFNKIKDRLGGRVRF
MTSGASPLSPEVMEFLKVCFGGRVTEGYGMTETSCVISGMDEGDNLTGHVGS PNPACEVKLVDPPEMNYT

SADQPHPRGEICVRGPPIIFTGYYKDEIQTKVEIDEDGWLHTGDIGLWLPGGRLKIIDRKKNIFKLAQGEY
 IAPEKIENVYAKCKFVGQCFIYGDSFNSSLVAVVSVDPDLKSWAASEGIGGDLRELCNNPRVKA AVL
 DMDTVGREAQLRGFEFAKAVTLVLEPFTLENGLLTPTFKIKRPQAKAYFAEAITNMYKELGASDPSANR
 L

>AtLACS7 Long-chain acyl-CoA synthetase 7 [*Arabidopsis thaliana*]
 NP_198112.2
 MEFASPEQRRLLETIRSHIDTSPTNDQSSSLFLNATASSASPFKEDSYSVVLPEKLDTGKWNVYRSKRSP
 TKLVSRFPDHPEIGTLHDNFVHAVETYAENKYLGTRVRSDDGTIGEYSWMTYGEAASERQAIGSGLLFHGV
 NQGDVGLYFINRPEWLVDHACAAYSFVSVPLYDTLGPDAVKFVVNHNALQAIFCVPQTLNILLSFLAE
 IPSIRLIVVVGGADEHLPSLRGTGVTIVSYQKLLSQGRSSLHPFSPKPEDIATICYTS GTTGT PKGV
 LTHGNLIANVAGSSVEAEFFPSDVYISYLPLAHIYERANQIMGVYGGVAVGFYQGDVFKLMDDFAVLRPT
 IFCSVPRLYNRIYDGITSAVKSSGVVKKRLFEIAYNSKKQAIINGRTPSAFWDKLVFNKIKEKLGGRVF
 MGSGASPLSPDVMDFLRICFGCSVREGYGMTETSCVISAMDDGDNLSGHVGSNPACEVKLVDPPEMNYT
 SDDQPYPRGEICVRGPPIIFKGYKDEEQTREILDGDGWLHTGDIGLWLPGGRLKIIDRKKNIFKLAQGEY
 IAPEKIENVYTKCRFVSQCFIHGDSFNSSLVAIVSVDPPEVMKDWAASEGIKYEHGLQCLNDPRVRKTVLA
 EMDDLGREAQLRGFEFAKAVTLVPEPFTLENGLLTPTFKIKRPQAKAYFAEAISKMYAEIAASNPIPSKL
 >AtLACS8 Long-chain acyl-CoA synthetase 8 [*Arabidopsis thaliana*]
 AT2G04350
 MEDSGVNPMDSPSKGSDFGVYGIIGGGIVALLVPVLLSVVLNGTKKGKKRGVPIKVGGEEGYTMHRARAP
 ELVDVPWEGAATMPALFEQSCCKYSKDRLLGTREFIDKEFITASDGRKFEKLHLGEYKWQSYGEVFERVC
 NFASGLVNVGHNVDDRVAIFSDTRAEFIAFQGCFRQSITVVTIYASLGEEALIYSLNETRVSTLICDSK
 QLKKLSAIQSSLKTVKNI IYIEEDGVDVASSDVNSMGDITVSSI SEVEKLGQKNAVQPIPSKNGVAVIM
 FTSGSTGLPKGVMITHGNLVATAAGVMKVVPKLDKNDTYIAYLPLAHVFELEAEIVVFTSGSAIGYGSAM
 TLTDTSNKVKKGTGKDVSAKPTIMTAVPAILDRVREGVLKKVEEKGGMAKTLDFDAYKRRLA AVDGSWF
 GAWGLEKMLWDALVFKKIRAVLGGHIRFMLVGGAPLSPDSQRFINICMGSPIGQGYGLTETCAGATFSEW
 DDPVAVGRVGPPPCGYVKLVSWEEGGYRISDKPMRGEIVVGGNSVTAGYFNNQEKTEDEVYKVDEKGT
 RWFYTGDIGRFHPDGCLEVIDRKKDIVKLQHGEYVSLGKVEAALGSSNYVDNIMVHADPINSYCVLVVPSR
 GALEKWAEEAGVKHSEFAELCEKGEAVKEVQQSLTKAGKAAKLEKLELPAKIKLLSEPWTPESGLVTAAL
 KIKREQIKSKFKDELKLYA

>AtLACS9 Long-chain acyl-CoA synthetase 9 [*Arabidopsis thaliana*]
 AT1G77590
 MIPYAAGVIVPLALTFLVQKSKKEKRGVVVDVGGEPGYAIRNHRFTEPVSSHWEHISTLPELFEISCNA
 HSDRVFLGTRKLISREIETSEDGKTFEKLHLGDYEWLTFGKTEAVCDFASGLVQIGHKTEERVAIFADT
 REEWFISLQGCFRNVTVVTIYSSLGEEALCHSLNETEVTTVICGSKELKKLMDISQQLETVKRVICMDD
 EFPDVSNSNMATSFTDVQKLGRENVPDPNPLSADVAVIMYTSGSTGLPKGVMTHGNVLATVSAVMTI
 VPDLGKRDIY MAYLPLAHILELAAESVMATIGSAIGYGSPLTLTDTSNKIKKGTGKDV TALKPTIMTAVP
 AILDRVDRGVRKKVDAKGLSKKLDFDAYARRLSAINGSWFGAWGLEKLLWDVLVFRKIRAVLGGQIRYL
 LSGGAPLSGDTQRFINICVGAFIGQGYGLTETCAGGTFSEFEDTSVGRVGAPLPCSFVKLVDAEGGYLT
 SDKPMRGEIVIGGSNITLGYFKNEEKTKEVYKVDEKGMRFYTGDIGRFHPDGCLEIIDRKKDIVKLQH
 GEYVSLGKVEAALSISPYVENIMVHADSFYSYCVLVVASQHTVEGWASKQGIDFANFEELCTKEQAVKE
 VYASLVKAAKQSRLEKFEIPAKIKLLASPWTPESGLVTAALKLRDVIRREFSEDLTCLYA

>BnGPAT1 Glycerol-3-phosphate acyltransferase 1 [*Brassica napus*]
 XP_013696751.1
 MVFPELLVILAEWVLYRLLANS CYRAARKLRGYGFQLKNFLNLSKSQSQQNTSHLLNNQQQQQONQDSL
 NPLFPSITKYEDTGCSVPDDTLVCDIDGVLLRQLSSKHFFHAFFPYFMLVAFEGGSIIRAIILLFSCSFLW
 ALPQETKLKVLTFITFSGLVKMDNVSRSVLSKFFLES LNFQVYNVWARTEYSKVVFSTSLPQVMVERFL
 REHLNADDVIGTKLQQIEVMGRKVYTGLTSGSLVKHRAAKDYFDNNNKKKPVLGIGSSSSVQDHTLISIC
 KEVYVCNEEDSMNTLPRERYPKPLIFHDGRLAFLPTPSATLAMFTWLPIGFFLAVFRILIGVLLPYHVAN
 FLAAISGVRITFKTHNLYNGPPEKKGSGVLYVCNHR TLLDPVFLT TSLGKPLTAVTYSLSKFSELIAPLK
 TVSLKRDRKKDGEAMQRLLSKGD LVVCP EGTTCREPYLLRFSPLFAELTEDIVPVAVDARVSMFYGT TAS
 GLKCLDPIFFLMNRPVYICIEVLKKLPKEMTCAGGKSSFEVANFIQGELARVLGFECTNLTRKD KYLVLA
 GNEGIVK

>BnGPAT2 Glycerol-3-phosphate acyltransferase 2 [*Brassica napus*]
 CDY15240.1

MLVAFETGGIIRSFLLFILYPPFISLMSYELGMKTMVMVSFFGIKKEKFLLGTSVLPKYFLEDVGLMEFEV
LKRGGKRVGVSDLPQVMIDGFLEDYLGIEVVVGREMKGIGYYSGILEDKKKHEFYLGELVQEEKLSSGH
VIGITSYNLPSHRSLSQFCQEIYFVRNSDKSWQTLPRNQYRPLIFHDGRLAIKPTPTNTLALFMWAP
FAAVLATARTVAGLNLPYSLAIPFLAFSGFRLTLTVNNDLISPQKEGCLFVCNHRITLLDPLYISYALRK
TNIKAVTYSLSRSELLAPIKTVRLTRDRVQDGQAMKRLLRQGDVVCPGTTTCREPYLLRFSPLFAEVS
DAIVPVAIDSHVTFHGTASGLKAFDPIFFLLNPYPTYTVRLLDPVFGGSSSTCRDPDDGKSKFEVANH
VQHEIGKALGFECTNLTRDKYLILAGNNGVVDKK

>BnGPAT3 Glycerol-3-phosphate acyltransferase 3 [*Brassica napus*]
CDY22016.1

MLVAFEAGGVIRSFILFILYPLITLMLSHEMGVKVMVMVSFFGIKKDGFRAGGAVLPKHFLLEDVGLMEFK
VLRGGKRVVSYDLPQVMIEGFLRDYLEVEVVVGREMKVGGYYLGIMEDKTKHDLVFDELVRKERLNT
GRVIGITSYNTSLHRYLFSQFCQEIYFVKRSDKRTWQTLPKSQYPKPLIFHDGRLAIRPTLMNTLALFMW
GPFVLAARLFVSLCIPYTLSSIPILSFFGCRLTVKIDDVSSQKLNSSERKGCLFACNHRITLLDPLYVG
FALKKKNIKTVTYSLSRVSEILAPIKTVRLTRDRVSDGQAMKLLAEGDLVVCPEGTTTCREPYLLRFSPL
FAEISDVIVPVAVTSPATFFYGTASGLKAFDPLFFLMDPYPTYTVQFLDPVPGVTCQDPEGKCLKFEVAN
HVQSAIGKALDFECTYLTRDKYLILAGNNGVVKKN

>AhGPAT1 Glycerol-3-phosphate acyltransferase 1 [*Arachis hypogaea*]
AER51964.1

MVFPMLLLRLLDWVLYQLLANSFYRAARKMKSYPWFNFYNIISSKPQHLQPCLSFSPSVTKCDLEALRAS
QPTLAFCDVHKVLLNTHSFFPFFMLVAFEGGSILRALLLLSCPLLLILNHDMLKLMTFITFCGLRIKD
MECVSRVAVLPKFYLENLNLHAYEVMASSSSKVFTSVPRVMVEGFLKEYLSVCNVIQTELQTFGTFTGTF
VSDSGLLVKHRALKEYFGDRKPDIGIGSSSFDDHIFMSLCKEGYVNNPSPMLGREKYPKPLIFHDGRLA
FLPTPSATLLMFMWLPIGILLAIYRILVGILLPYKWAMILGVWSGINLVKGIMRSQSSEQKKGVLYVCT
HRTLLDPVFLSTSLAKPLTAVTYSLSKVSEFIAPIRTVRLTRDRKQDAQTMQRLLSEGDLVVCPEGTTTCT
EPYLLRFSSSLFAELADEIVPVAMNAHVSMFYGTAAAGLKCLDPIFFFMNPRPCYHIHILGKVPKELTCAG
GRSSCEVANYIQSQLALALGFQCTTLTRDKYLMLAGNEGIVNQQRNTKINHHCTNNNKGETLLS

>AhGPAT2 Glycerol-3-phosphate acyltransferase 2 [*Arachis hypogaea*]
AER42344.1

MAKMFRAFFFKSLFFFWYRFLFRQLKSLTGLRRNILSTQFKYQKFSSFLHQHRSSELGDHTLVFDVENA
LLKSSSLFPYFMLVAFEAGGLIRAIVLVLLYPVACAPDIVGQELGLKMMVMICFFGIKVDSFRVGRSVLP
KFLLEDVKGEMFDVLKRSSGKKVGVNMPRIMVESFLREYLEIDVVVGRELKVFCGYFVGLMEEKKSALH
ALEQVQEGKGCSDMIGITRFNKVVDHQLFSHCKEVYAVSEAEKRSWQRLSKDKYPKPLIFHDGRLALRPT
LFDSIAILMWLPYALILAIIRISLALSPLYNFSTPLLVTGHIHLLTSEIPKMPPNNNNKTGTLYVCNHR
LLDPLYISFTLQRLNLIQVAVTYSLSRMSEILAPIKTVRLTRNRDQDANMMKHLLAQGDVVCPGTTTCT
LLRFSPLFSEMCDIAPVAVNSHVTMFHGTAGGLKCLDPVFFLMNPSPVYTVDLLQHVQSRSCVDRAV
TEKEHQARFKVANHVQSQIGSALGFECTKLTRDKYLILAGNEGVINRACGKS

>AhGPAT6 Glycerol-3-phosphate acyltransferase 6 [*Arachis hypogaea*]
AER42345.1

MVMGAFSHFEQVSKCNTEGRSNQTVASDLTGTLVSRSAFPYYMLVAIEAGSLLRALILLISVPFVYFTY
IFISETIAIKTLIFVTFAGLKIRDVEMVARSVLPKFYAEDVHPVTWKVFNSFGKRYIVTASPRLMVEPFV
KTLLGADKVLGTELEATKSGRLTGFKVKEPGVLVGEHKKTVLVKEFQSNLPDLGLGDSETDHDHFMISCKEG
YMVPRTKCEALARNKLISPIIFHEGRFVQRPTPLASLLTFLWLPIGIIILSVLYLNIPLPERIAWYNYK
LLGIRVTVKGTPPPPPKKGQSGVLVFCNHRITVLDPVVTAVALGRKISCVTYSISKFTEIISPIKAVALSR
EREKDAENIKRLLEEGDLVICPEGTTTCTREPFLLRFSALFAELTDRIVPVAINTKQSVFYGTTVRGHKL
LDPYFVFMNPMPTYEITFLNQLPKELTCSSGKSAIEVANYIQRVLAGTLGFECTNLTRDKYAMLAGTDGRV
ASSNKENKA

>AhGPAT4 Glycerol-3-phosphate acyltransferase 4 [*Arachis hypogaea*]
AGR66149.1

MAAPKPKRTFPVTECNGNSPSSPRESVAADLDGTLISRSSFPYFMLVAVEAGSLLRGFILLISVPFVI
IAYLFISEAIGIQILIFISFAGLKIRDIELASRAVLPRFYASDVRKESFEVFDCKRKVVVTANPTVMVE
PFVKDFLGGDKVLGTEIEVNPKTKKATGFVKKPGVLVGLKRLAILKEFGETTSPDIGLDRESHDHFM
ACKEGYMPVPSKSAKPVPRDLKSRILFHDGRFVQRPDPLNALFTFLWIPFGFALSIFRVYFNLPLPERI
VRYTYELLGHIHLVISGHRPPPPSPGTPGNLYVCNHRITLDPVIAIALGRKVCVTYSVSKLSRFLSPIP
AVALTRDRAADAARIKDLLQKGDVVCPGTTTCTREPFLLRFNALFAELSDRIVPVAVDCKQSMFFGTTVR
GVKFWDPYFFFMNPRPVYIEIRFLDRLPEEMSCKAGGKSSIEVANHVQKVLGDVLGFECAGLTRDKYMLL
GGNDGKVESMYSSKK

>AhGPAT9 Glycerol-3-phosphate acyltransferase 9 [*Arachis hypogaea*]
AGR66148.1

MMRKTNPKSQSTELELDQPNIEDYLPSGHTIHQEPHGKLRLCDLLDISPTLSEAAGAIVDDSFRLRCFKSI
RSEPNWNVYLFPLWCFGVVIRYLILFPAVLLLSFGWMIFLSAFIPVHLLLRDNSVRKNIERCLVEMI
CGFFVASWTGVVKYHGPRPSMRPKQVFVANHTSMIDFIIILEQMTAFVIMQKHPGWVGLLQNTILESVC
IWFNRTEAKDREIVARKLREHVQGADNNPLLIFPEGTCVNNHYSVMFKKGAFELGCTVCPVAIKYNKIFV
DAFWNSRKQSFTKHLQLMTSWAVVCDVWYLEPQNQKPGETSIEFAERVREIISQRAGLKMVPWDGYLKY
SRPSPKLREGKQRNFVESVLRLEEK

>AtATS1 Phospholipid/glycerol acyltransferase family protein [*Arabidopsis thaliana*]
AT1G32200

MTLTFSSAATVAVAAATVTSSARVPVYPLASSTLRGLVSFRLTAKKLFLPPLRSRGGVSVRAMSELVQD
KESSVAASIAFNEAAGETPSELSSHRTFLDARSEQDLLSGIKKEAEAGRLPANVAAGMEELYWNYKNAVL
SSGASRADETIVSNMSVAFDRMLLGVEDPYTFNPYHKAVREPFDDYMFVHTYIRPLIDFKNSYVGNASIF
SELEDKIRQGHNVILISNHQSEADPAVISLLEAQSPFIVENIKCVAGDRVITDPLCKPFSMGRNLICVY
SKKHMNDDELVDMMRKANTRSLKEMATMLRSGQLIWIAPSGGRDRPNPSTGEWFPAPFDASSVDNMRR
LVEHSGAPGHIYPMSLLCYDIMPPPPQVEKEIGEKLRLVGFHGTGLSIAPEINFSDVTADCESPNEAKEAY
SQALYKSVNEQYEILNSAIKHRRGVEASTSRVLSQPWN

>AtGPAT1 Glycerol-3-phosphate acyltransferase 1 [*Arabidopsis thaliana*]
NP_563768.1

MVLPELLVILAEWVLYRLLAKSCYRAARKLRGYGFQKLNLLSLSKTQSLHNNSQHHLHNNHQQNHPNQT
QDSDLPLFPLSLTKYQELLLDKNRACSVSSDHYRDTFFCDIDGVLLRQHSSSKHFHTFFFPYFMLVAFEGGSI
IRAILLLLSCSFLWTLQQETKLRVLSFITFSGLRVKMDMNVSRSVLPKFFLENLNIQVYDIWARTEYSKV
VFTSLPQVLVERFLREHLNADDVIGTKLQEIKMGRKFYTGGLASGSGFVLKHKSAEDYFFDSKKKPALGI
GSSSSPDHIFISICKEAYFWNEEESMSKNNALPRERYPKPLIFHDGRLAFLPTPLATLAMFIWLPIGFL
LAVFRISVGVLPHYVANFLASMSGVRITFKTHNLNNGRPEKGNVGVLYVCNHRLLDPLVFLTTSLGKPL
TAVTYSLSKFSEFIAPLKTVSLKRDRKKDGEAMQRLLSKGDLVVCPGTTTREPYPYLLRFSPLFAELTEDI
VPVAVDARVSMFYGTASGLKCLDPIFFLMNPRPVYCLEILKKLPKEMTCAGGKSSFEVANFIQGELARV
LGFECTNLTRDKYLVLAGNEGIVR

>AtGPAT2 Glycerol-3-phosphate acyltransferase 2 [*Arabidopsis thaliana*]
AT1G02390

MSGNKISTLQALVFFLYRFFILRRWCHRSKPQKYQKCPSHGLHQYQDLSNHTLIFNVEGALLKSNLSFPY
FMVVAFEAGGVIRSLFLLVLYPFISLSYEMGLKTMVMLSFFGVKKESFRVGKSVLPKYFLEDVGLMEFQ
VLKRGGKRVAVSDLPQVMIDVFLRDYLEIEVVVGRDMKMGVGYLGLIVEDKKNLEIAFDKVVQEERLGS
RRLIGITSFNSPSHRSLSQFCQEIYFVRNSDKSWQTLQDQYKPLIFHDGRLAVKPTPLNTLVLFMW
APFAAVLAAARLVFGLNLPYSLANPFLAFSGIHLTLTVNNHNDLISADRKRGLFVCNHRLLDPLYISY
ALRKKNMKAVTYSLSRSELLAPIKTVRLTRDRVKGQAMEKLLSQGDLVVCPEGTTTREPYPYLLRFSPLF
SEVCDVIVPVAIDSHVTFYGTASGLKAFDPIFFLLNPFPSYTVKLLDPVSGSSSTCRGVPDNGKVN
EVANHVQHEIGNALGFECTNLTRDKYLILAGNNGVVKKK

>AtGPAT3 Glycerol-3-phosphate acyltransferase 3 [*Arabidopsis thaliana*]
AT4G01950

MHCLKPNKENTRRKEKSKKKSFLQNPMSAKISIFQALVFLFYRFILRRYRNSKPKYQNGPSSLLQSDL
SRHTLIFNVEGALLKSDSLFPYFMLVAFEAGGVIRSLFLLFILIPLISLSHEMGVKVMVMVSFFGIKKEG
FRAGRAVLPHYFLEDVGLMEFVLKRGGKKIGVSDDLQVMIEGFLRDYLEIDVVGREMKVVGYYLGI
MEDKTKHDLVDFELVRKERLNTGRVIGITSFNTSLHRYLFSQFCQEIYFVKKSDKRSWQTLPRSQYKPL
IFHDGRLAIKPTLMNTLVLFMWGPFAAAAAARLFVSLCIPYSLIPILAFSGCRLTVTNDYVSSQKQKP
SQRKGCLFVCNHRLLDPLYVAFALRKKNIKTVTYLSRVSEILAPIKTVRLTRDRVSDGQAMEKLLTEG
DLVVCPEGTTTREPYPYLLRFSPLFTEVSDVIVPVAVTVHVTFYGTASGLKALDPLFLLDPYPTYTIQF
LDPVSGATCQDPDGKLKFEVANVQSDIGKALDFECTSLTRDKYLILAGNNGVVKKN

>AtGPAT4 Glycerol-3-phosphate acyltransferase 4 [*Arabidopsis thaliana*]
AT1G01610

MSPAKKSRSFPPISECKSREYDSIAADLDGTLTLLSRSSFYFMLVAIEAGSLFRGLILLLSLPVIVIIAYL
FVSESLGIQILIFISFAGIKIKNIELVSRVLTFRYAADVRRKDSFEVFDKCKKRKVVTANPIVMVEPFV
KDYLGDKVLGTEIEVNPKTMKATGFVKKPGVLVGLKRLAILKEFGDDSPDLGLGDRTSDHDFMSICKE
GYMVHETKSATTVPISLKNRIIFHDGRLVQRPTPLNALIIYLWLPFGFMLSFRVYFNLPLPERFVRYT
YEILGIHLTIRGHRPPPPSPGKPGNLYVLNHRALTDPPIIAIALGRKITCVTYSVSRLSLMLSPIPAVAL
TRDRVADAARMRQLLEKGLVICPEGTTTREPYPYLLRFSALFAELSDRIVPAMNCKQGMFNGTTVRGVKF
WDPYFFFMNPRPSYEATFLDRLPEEMTVNGGGKTPFEVANYVQKVIGGVLGFECTELTRDKYLLLGND

GKVESINKTKSME

>AtGPAT5 Glycerol-3-phosphate acyltransferase 5 [*Arabidopsis thaliana*]
NP_187750.1

MVMEQAGTTSYSVSEFEGTILKNADSFSYFMLVAFEAAGLIRFAILLFLWPVITLLDVFSYKNAALKLK
IFVATVGLREPEIESVARAVLPKFYMDVSM DTRVVFSSCKKRVVVTMRPRVMVERFAKEHLRADEVIGT
ELIVNRFGEFVTGLIRETDVDQ SALNRVANLFVGRRPQLGLGKPALTASTNFLSLCEEHIHAPIPENYNHG
DQQLQLRPLPVIFHDGRLVKRPTATALIILLWIPFGIILAVIRIFLGAVLPLWATPYVSQIFGGHIIVK
GKPPQPPAAGKSGVLFVCTHRTLM DFPVLSYVLGRSIPAVTYSISRLSEILSPIPTVRLTRIRDVDAAKI
KQQLSKGDLVVCPEGTT CREPFLRFSALFAELTD RIVPVAMNYRVGFFHATTARGWKGLDPIFFFMNPR
PVYEITFLNQLPMEATCSSGKSPHDVANYVQRILAATLGFECTNFTRKDKYRVLAGNDGTVSYLSLLDQL
KKVVSTFEPCLH

>AtGPAT6 Glycerol-3-phosphate acyltransferase 6 [*Arabidopsis thaliana*]
NP_181346.1

MGAQEKRRRFEQISKCDVKDRSNHTVAADLDGTL LISRSAPFYFLVALEAGSLLRALILLVSPFVYLT
YLTISETLAINVFVITFAGLKIRDVELVRSVLPRFYAEDVRPDTRIFNTFGKRYIITASPRIMVEPF
VKTFGLGVDKVLGTELEVSKSGRATGFTRKPGILVGQYKRDVVLREFGGLASDLPDLGLGDSKTDHDFMSI
CKEGYMPVPTKCEPLPRNKLLSPIIFHEGRLVQRPTPLVALLTFLWLPVGFVLSIIRVYTNIPLERIAR
YNYKLTGIKLVVNGHPPPPKPGQPGHLLVCNHRTVLDPVVTAVALGRKISCVTYSISKFSELISPIKAV
ALTRQREKDAANIKRLL EGD LVICPEGTT CREPFLRFSALFAELTD RIVPVAINTKQSMFNGTTTTRGY
KLLDPYFAFMNPRPTYEITFLKQIPAELTCKGGKSPIEVANYIQRVLG GTLGFECTNFTRKDKYAML AGT
DGRVPVKKEKT

>AtGPAT7 Glycerol-3-phosphate acyltransferase 7 [*Arabidopsis thaliana*]
NP_196227.1

MESSTTTSYSVSELEGTL LKNPKPFAYFMLVAFEASGLIRFATLLFLWP IIALLDVLGYRNGSLKLMIF
VATAGLHESEIESVARAVLPKFFMDDISMDAWRAFGSCDKRVVVTMRPRVMVERFAKDHL SADEVIGTEI
VVNRFGYATGLIQETNVDQSVFNSVANLFVDRRPQLGLGRH IISDSPTFLSLCEEQVHAPVPSNYNGHNQ
RLHVQPLPVIFHDGRLVKLPTPATALIILLWIPFGIILAMIRIFVGFLPLWAIIPVSRIFNTRFIVKGK
PPAQATTGNPGVLFVCTHRTLM DFPVLSYVLGRSIPAVTYSISRLSEILSPIPTFRLTRIRDVD AEMIKK
ELSNGLDVVYPEGTT CREPFLRFSALFAELTD NIVPVAMNYRVGFFHATTARGWKGLDPIFFFMNPRPV
YEVTFNLQLEVEATCSSGKSPYDVANYVQRILAATLGFECTNFTRKDKYRVLAGNDGTVSYLSFLDQVKK
VVTTFKPFLH

>AtGPAT8 Glycerol-3-phosphate acyltransferase 8 [*Arabidopsis thaliana*]
NP_191950.2

MSPEKKSQNFPPI TECDGEYDSIAADLDGTL LLSRSSFPYFMLVAVEAGSLLRGLILL LSLPFV IISYL
FVSESLGIQILIFISFAGLKIRDIELVSR AVLPRFYAADVRKDSFEVFDKCKRKVVVTANPIVMVEAFVK
DYLGGDKVLGTEIEVNPKNRATGFVKKPGVLVGD LKRLAILKEFGNESPD LGLGDRTSDHDFMSLCKKG
YMVHATKSATTIPKERLKNRIVFHDGRLAQRPTPLNAIITYLWLPFGFILSIIRVYFNLPLPERFVRYTY
EMLGIHLTIRGHRPPPPSPGTLGNLYVLNHR TALDPIIVAIALGRKICCVTYSVSRLSLMLSPIPAVALT
RDRATDAANMRK LLEKGD LVICPEGTT CREEYLLRFSALFAELSD RIVPVAMNCKQGMFNGTTVRGVKFW
DPYFFFMNPRPSYEATFLDRLPEEMTVNGGGKTPIEVANYVQKVIGAVLGFECTELTRKDKYLL LGGNDG
KVESINNTKK

>AtGPAT9 Glycerol-3-phosphate acyltransferase 9 [*Arabidopsis thaliana*]
At5g60620

MSSTAGRLVTSKSEL DLDHPNIEDYLP SGSSINEPRGKLSLRD LLDISPTLTEAAGAI VDDSFTRCFKSN
PPEPWNWNIYLFPLYCFGVVRYCILFPLRCFTLAFGW IIFLSLFI PVNALLKGQDRLRKKIERVLVEMI
CSFFVASWTGVVKYHGPRPSIRPKQVYVANHTSMIDFIVLEQMTAF AVIMQKHPGWVGLLQSTILESVC
IWFNRSEAKDREIVAKKLRDHVQGADSNPL LIFPEGTCVNNNYTVMFKKGAFEL DCTVCPIAIKYNKIFV
DAFWNSRKQSFTMHLLQLMTSWAVVCEVWYLEPQTIRPGETGIEFAERVRDMISLRAGLKKVPWDGYLKY
SRSPKHSERKQQSFAESILARLEEK

>BnLPAAT1 1-acyl-sn-glycerol-3-phosphate acyltransferase 1 [*Brassica napus*]
Q9LLY4.2

MDVASAPGVSSHPPYYSK PICSSQSSLIRIPINKGCCFARSSNLITSLHAASRGVTRRTSGVQWCYRSIR
FDPFKVNDKNSRTVTVRSDLSGAATPESTYPEPEIKLSSRLRGICFCLVAGVSAIVLIVL MITGHPFVLL
FDRYRRKFHHFIAKLWASIS IYPFYKTDIQGLENLPSSDTPCVYVSNHQSF LDIYTLLSLGQSYKFISK T
GIFVIPVIGWAMSMGMVPLK RMDPRSQVDCLKRCMELVKKGASVFFFPEGTRSKDGRLGPFKKGAFTIA

AKTGPVVPVITLMGTGKIMPTGSEGILNHGDVVRVIIHKPIYGSKADLLCDEARNKIAESMNLVS
>BnLPAAT2-1 1-acyl-sn-glycerol-3-phosphate acyltransferase 2 [*Brassica napus*] Q9XFW4.1
MAMAAAVIVPLGILFFISGLVNVNLLQAVCYVLVRPMSKNTYRKINRVVAETLWLELVWIVDWWAGVKIQV
FADDETFNRMGKEHALVVCNHRSDIDWLVGWILAQRSGCLGSALAVMKSSKFLPVIGWSMWFSEYLFLE
RNWAKDESTLQSGQLQRLNDFPRPFWLALFVEGTRFTEAKLKAAQEYAASSELVPRNVLIIPRTKGFVSAV
SNMRSFVPAIYDMTVAIPKTSPPPTMLRLFLKGQPSVVHVHIKCHSMKDLPEPEDEIAQWCRDQFVAKDAL
LDKHIAADTFPGQKEQNIGRPIKSLAVVSVWACLLTLGAMKFLHWSNLFSSWKGIASAFGLGIITLCMQ
ILIRSSQSERSTPAKVAPAKPKDNHQSGPSSQTEVEEKQK
>BnLPAAT2-2 1-acyl-sn-glycerol-3-phosphate acyltransferase 2-like
[*Brassica napus*] NP_001302981.1
MAMAAAVIVPLGILFFISGLVNVNLLQAICYVLIRPLSKNTYRKINRVVAETLWLELVWIVDWWAGVKIQV
FADNETFNRMGKEHALVVCNHRSDIDWLVGWILAQRSGCLGSALAVMKSSKFLPVIGWSMWFSEYLFLE
RNWAKDESTLQSGQLQRLNDFPRPFWLALFVEGTRFTEAKLKAAQEYAASSELVPRNVLIIPRTKGFVSAV
SNMRSFVPAIYDMTVAIPKTSPPPTMLRLFLKGQPSVVHVHIKCHSMKDLPESDDAIAQWCRDQFVAKDAL
LDKHIAADTFPGQKEQNIGRPIKSLAVVLSWSCLLILGAMKFLHWSNLFSSWKGIASAFGLGIITLCMQ
ILIRSSQSERSTPAKVVPAPAKPKDNHNSGSSSQTEVEEKQK
>BnLPAAT2-3 1-acyl-sn-glycerol-3-phosphate acyltransferase 2 [*Brassica napus*] AX75484.1
MAMAAAVIVPLGILFFISGLVNVNLLQAVCYVLVRPMSKNTYRKINRVVAETLWLELVWIVDWWAGVKIQV
FADDETLNRMGKEHALVVCNHRSDIDWLVGWILAQRSGCLGSALAVMKSSKFLPVIGWSMWFSEYLFLE
RNWAKDESTLQSGQLQRLNDFPRPFWLALFAEGTRFTEAKLKAAQEYAASSELVPRNVLIIPRTKGFVSAV
SNMRSFVPAIYDMTVAIPKTSPPPTMLRLFLKGQPSVVHVHIKCHSMKDLPEPEDEIAQWCRDQFVAKDAL
LDKHIAADTFPGQKEQNIGRPIKSLAVVSVWACLLTLGAMKFLHWSNLFSSWKGIASAFGLGIITLCMQ
ILIRSSQSERSTPAKVAPAKPKDNHQSGPSSQTEVEEKQK
>BnLPAAT2-4 NP_001302955.1 1-acyl-sn-glycerol-3-phosphate
acyltransferase 2 [*Brassica napus*]
MAMAAAVIVPLGILFFISGLVNVNLLQAVCYVLIRPLSKNTYRKINRVVAETLWLELVWIVDWWAGVKIQ
VFADDETFNRMGKEHALVVCNHRSDIDWLVGWILAQRSGCLGSALAVMKSSKFLPVIGWSMWFSEYLFLE
ERNWAKDESTLQSGQLQRLNDFPRPFWLALFVEGTRFTEAKLKAAQEYAASSQLPVPRNVLIIPRTKGFVSA
VSNMRSFVPAIYDMTVAIPKTSPPPTMLRLFLKGQPSVVHVHIKCHSMKDLPESDDAIAQWCRDQFVAKDA
LLDKHIAADTFPGQKEHNIGRPIKSLAVVSVWACLLTLGAMKFLHWSNLFSSWKGIASAFGLGIITLCM
QILIRSSQSERSTPAKVAPAKPKDKHQSGSSSQTEVEEKQK
>BnLPAAT4-2 Lysophosphatidyl acyltransferase 4-2 [*Brassica napus*]
AHV90569.1
MEVCGDSDNLKNRHLTPLRTLRLGLIILLIFLSTAFMFLIYFAPPFALALRLLSVHQSRKSISFIFGHWLA
LWPYLFKEVNGTTVIFSGDTLPVEKRVLLIANHRTEVDWMYLWNIALRKGLGYIKYVLKSSLMRLPIFG
WGFHVLEFIPVERKREVDEPVMLQMLSTFKDPREPLWLALFPEGTDFTTECKRSQKFAAEAGLPTLSNV
LLPKTRGFSVCLEALHNSLDAVYDLTIAYKPRCPSFMDNVFGTDPSEVHIHVRRLAKEIPASEAGSSAW
LMDSFKSKDKLLSDFNAQGGQFPNQRPEEELSILKCIATFGVIVSLTVLFLYLTLYSHSCFKVYVGLSFTY
LSFATYYKFRSPSPVSGCKGGSCSKESKTH
>BnLPAAT4-1 Lysophosphatidyl acyltransferase 4-1 [*Brassica napus*]
AHV90568.1
MEVTGSDSDNLKNRPLTPLRTLRLGLIILLIFLSTAFMFLIYFAPPFALALRLLSVHQSRKSISFIFGHWLA
LWPYLFETINGTTVIFSGDTLPVEKRVLLIANHRTEVDWMYLWNIALRKGLGYIKYVLKSSLMRLPIFG
WGFHVLEFIPVERKREVDEPVMLQMLSSFKDPREPLWLALFPEGTDFTTECKRSQKFAAEAGLPTLSNV
LLPKTRGFSVCLDALHNSLDAVYDLTIAYKPRCPSFMDNVFGTDPSEVHIHVKRVLTKEIPASEAESSAW
LMDSFKSKDRLLSDFNAQGGQFPNQRPEEELSILKCIATFGVIVSLTVLFLYLTLYSHSCFKVYVGLSFTY
LSFATYYKFRSPSPVSGCKGGSSCKEAKTH
>BnLPAAT5 Probable 1-acyl-sn-glycerol-3-phosphate acyltransferase 5
[*Brassica napus*] XP_013749364.1
MEKKLKNSNNLSLIRMLRGIIICMLVLVSTAFMMLIFWGFLSAVVMRLFSLHYSRKCVYFFFGSWLALWPF
LFEKINRTKVIFSGDKVPCESRVLLIANHRTEVDWMYFWDLALRKQIGNMKYVLKSSLMKLPLFGWAFH
LFEFIPVERKWKVDEANLRQMVSFDPDRLGLWGLFPEGTDYTEAKCERSKKFAAENGLPELNNVLLPK
TKGFVSCLEELDSSLDVYDVTIGYKTRCPSFLDNVYGTEPSEVHIHIRRISQNPQIPNEEKEINAWLMNT
FQIKDQLLSEFYSRGHFPNEGTEKEFSTIKQLINCLAVIVFTIICTHLTFFSSMIWFKIYVSLVCAYLTY
ATHFNLRPAPLVETAKKSFYSKKNLF

>RcLPAATB B-class lysophosphatidate acyltransferase [*Ricinus communis*]
AFR42414.1
MESTGGGSFMRNRRLESFLNTDSSTNVNETSRKLVRKEVEQRPNNVDVYVDDDGWISGLISWVRIVVCFVS
MMITTFI WASLMLLLLPWPYERIRQGNIIYGHVTGRILMWILGNPLKIEGVEFSNEKAIYISNHSSPIDIF
LIMWLTPTGTGVGAKKEIIWYPLFGQLYVLANHLRIDRSNPAAAIQSMKEVACAVIKNNLSLIIFPEGTR
SKSGRLLPFKKGFVHLALQTRLPIVPIVLTGTHRAWRKDSLHVRPAPINVKYLRPIKTDNWTDDKVDDYV
KLLHDMYVENLPESQRPLS

>AhLPAATB Lysophosphatidyl acyltransferase 6 [*Arachis hypogaea*]
AGT57763.1
MENS GG GALLRNRRLSFLDTSSGLRVEEAPKILVKEKPELWLKKDVYMDNGWVSSII SWIRIVTCFVS
MMVTTFIWALIMVVLIPWPYERIRQGNIIYGHVTGRMLMWILGNPIKIEGA EYNNERAIYISNHASPIDIF
LIMWLTPTGTGVGIAKKEIVWYPLFGQLYVLANHLRIDRSNPTS AIESMNEVARAVVRNNLSLIIFPEGTR
SKNGRLLPFKKGFVHLALQTRLPIVPMVLTGTHQAWRKGSLHVRPTPLAVKYLPPISTENWKA EKIDYV
KMVHDLYAAQLPETQRPLA

>GmLPAAT3 1-acyl-sn-glycerol-3-phosphate acyltransferase 3 [*Glycine max*]
XP_025981491.1
MGAKHFLEKIIIGYVGGEIAD EDGVFQGGIGPALADAEGGP IEPGLVGGVVGLENPFRCGVD ELDEAVA
LGLARELVADDFDGDHLAGGGEAVAQAVFFVLLRPLSKNCYSRINKLLTESLWLELIWLIDWWAGIKIEL
YTDSETLQLMGKKILGKENALVICNHRSDIDWLGWVLAQRSGCLGSTVAIMKKEVKFLPVLGWSMWFAE
YIFLERDWAKDETSLSKSGFRHLEHMPFPFWLALFVEGTRFTQT KLLQAQEF AASKGLPIPRNVLIPTKGFV
FVTAVQSLRPFVPAIYDCTYAVPKSEASPTLVRI FKGISCPVKVQIKRHKMEELPETDDGIGQWCKDAFV
AKDALLEKYSTTEIFSEQDLQ QIRRHKTSILVVVCWLCLLGFLVYEFFQWTSLLSSWEGILFTVLFLLLV
TVIMEIFIHSSQSERSKPPMVLP TQDPMKQKLLQT

>BrLPAAT3 1-acyl-sn-glycerol-3-phosphate acyltransferase 3 [*Brassica rapa*]
XP_009144912.1
MAIPAALVFVPVGVFLVSLIVNLIQLVFFIIVRPFSKSLYRRINKNVVELLWLQLIWLIDWWACIKVN
IYADAETLQLLGKEHALVLSNHRSDIDWLGWVMAQRAGCLGSSLAIMKKEAKYLP IIGWSMWFS DYIFL
ERSWDKDEKTLTAGFKRFEDFPMTFWLALFVEGTRFTQEKLEAAQEYASIRSLPSPRNVLIPTKGFVSA
VSHIRSFVPAVYDCTLTVRNNQPKPTLLRMFSGQSSELNLQLRRHKMSDLPETDDGIAQWCQDLFITKDA
QLETYFTKDFVSDLDVHQINRPIKPLIVIVVWVCLLMYGGFKLLQWLSMVASWEIICLFV VILVIATITM
QVLIQSSESHSTPAKRPLQEQLISA

>AhLPAAT1 1-acyl-sn-glycerol-3-phosphate acyltransferase 1, [*Arachis hypogaea*]
XP_025672028.1
MSSVHALLSTSLSQSPLSSMFFNSSPSMEMFQLCTYKRPTYDHRVLR TSLSYAQRRLTGIPRKH RNDLWV
SFCPNEELCRPRYSCNLRYQNKHARDTFARCELAAAGDSHSLSADLKMESKVRGACFYAVTALS AVFLFV
LMLVGHPFVLLFDRQRRKFHHYVAKVWASLTVA PFYRIKFEGLENLPPDTPAVYVSNHQSF LDIYTLT
LGRSFKFISKTGIFLFP IIGWAMFLLGTIPLKRMDSR SQMDCLKRCMDLIRKGASVVFVPEGTRSKDGKL
GAFKKGAFSIAAKTNAPVVPITLIGTGQIMPAGREGIVNIGWVKVVIHKPLRGKDAEMLCKEARTTIAGV
L

>AhLPAAT2 1-acyl-sn-glycerol-3-phosphate acyltransferase 2 [*Arachis hypogaea*]
XP_025604428.1
MGIAAAVVVPFGLLFFTSGLAVNLIQAVSYVLRPLSKNLHRRINRVVAELLWLELVWLIDWWAGVKVE
VFTDHETFQLMGKEHALVICNHRSDIDWLVGWVLAQRSGCLGSTLAVMKKSSKFLPVIGWSMWFS EYLFL
ERSWAKDESTLKSIGIQLSDFLPFWLALFVEGTRFTQAKLLAAQEYAASAGLP IPRNVLIPTKGFVSA
VSHMRSFVPAIYDVTVAIPKCSPTPTMLRLLKGQPSVVQVHIKRHLMNELPETDEAVAQWCRDVFVAKDA
LLDKHIAEDTFSDKELQDTGRPKKSLLV TISWGLIVTGAVKFLRWTSLLSSWKGIAISTASLAVVTGLM
QILIMFSQSERSTPAKVLPAPKPKSTGEQVEDKNVKQQ

>AhLPAAT3 1-acyl-sn-glycerol-3-phosphate acyltransferase 3 [*Arachis hypogaea*]
XP_025613857.1
MAFPAAVFILPAGTLFILSGLIVNAIQIVVFILFRPISRNLFR RINNMLTQSLWLELIFLIDWWGA IKIE
LHMDSESRLMGKENALLCNHRSDIDWLGIFAL AQRSGCLGSSLAIMKKELKYLPVIGWSMWFC DYIFL
EREWAKDERTLSSGLKQLENSPLPFWLALFVEGTRFTPDKLLAAQAF AASRGLPIPKNVLIPTK GIVCV
VENIRSFTPAIYDCTYSVKKGDTPTMLRLFKGQSSSVKLQIQRLKMEDLPHTPNEIAEWCKDLFISKDA
MLERYNTTDVFSDAELQDLGRSKKSIFVVL CWTCLLGFLLYEFFKSTKLLSTWEGILCTVLFV VVTLVM
ELLIHATQSERSTRMNLPTQDPLRQKLLQ

>RcLPAAT1 1-acyl-sn-glycerol-3-phosphate acyltransferase 1, [*Ricinus communis*]
XP_015580987.1

MELAFHPTHSNPLRLCYKRSSVHALSSSSLLSSVHKGLHVGSSPVKRAIMRSTNNSAFSGSLCIPRKLVA
 VPWAEELNWPFDKSLHKNKLPRKTVVRSELVGNANPESAHPLSDIKLGAKVRGICFYAVTAIAAIFLF
 VLMLVQHPFVLLLLDRYRRKTQFFIAKIWAMITVAPFFKIEFEGLENLPSDAPAVYVSNHQSFLLDIYTLL
 TLGRSFKFISKGTGIFLFPPIIGWAMFMLGVIPKRMDSRSQLECLKRCIELVKKGTSVFFFPEGTRSKDGK
 LGIFKKGAFSVAAKTKVPVPITLMGTGKIMPAGMESILNLGSVKVVIHKPVEGSNPEVLCNEVRNTIAS
 VLNQQS

>RcLPAAT2 A-class lysophosphatidate acyltransferase-2 [*Ricinus communis*]
 AFR42413.1
 MAVAAVAVILPLGVLFLLSGLVNVNLFQAICFVLIRPISKSSYRMINRALAELLWLELVLDWWAKIKIQ
 VYTDRETLCLMGKEHALILANHRSDIDWLVGWMLAQAGCLGSALAVMKKSSKFLPVIGWSMWFSEYLF
 ERSWAKDESTLKSIGIQLKDFPRPFWLGLFVEGTRFTKAKLLAAQQYAASQGLPIPRNVLIPTKGFVSA
 VSNMRSFVPAIYDVTVAIPKNSPQPTMLRFLFKGQSSVVHVHIKRHLMKDLPETDDAVAQWCKDLFVAKDA
 LLDKHIAEDTFSEQLQDIGRPKSLVVVTLWSCLLIFGTLLKFLQWSSLLSSWKGIALLSMSALAIVTVLM
 HILIRFSQSEHSTPAQVAPANHAQVAPENPQNGGEPSEKAENKQD

>RcLPAAT3 Lysophosphatidic acid acyltransferase 3 [*Ricinus communis*]
 AJP36329.1
 MAIPAALAIVPIGILFFVSGFVVNLIQAVLFILVRPVSKSLHRRINKIVAELLWLELIWLDWWAHLKIE
 VYADDETFFELMGKEHALLICNHRSDIDWLVGWMLAQAGCLGSALAVMKKQAKVLPPIIGWSMWFSDYLF
 ERSWAKDETTLKSGFKRLEDFPMPFWLALFVEGTRFTEAKLQAAQYAVTRGLPIPRNVLLPTKGFVSA
 VVHMRSFVPAIYDCTVDVDSQAPPTMLRIFRRQSSVINLQIKRHSMEVPEADGISQWCKDVFVTKDA
 MLEKYHTKGTFSQKHQHIHGRPKSLFVVFWSNLLIFGIVMSFQFLSFLNSWQVLSFSVTLLVLVTIVM
 QILIHSSSEHSTPPPKLTFSDQAKERLLQK

>RcLPAAT4 Lysophosphatidic acid acyltransferase 4 [*Ricinus communis*]
 AJP36330.1
 MEVCKPPNHTYRQKNRPLTLFRLRLGLICLMVFVSTAFMFLVYFAPLAFLTRFASVHFRRRASSFIFSIW
 LSMWPFLFEKINGTKVVFSGDDIPAEERVLIANHRTEVDWMLWDLALRKGLGSIKYILKSSLMKLPV
 FGWGFHILEFISVDRKWEVDEPVMRIMLSTFKGPQDPLWLALFPEGTDFTTEKKCLGSQKFAAEVGLPVLK
 NVLLPKTRGFCVCLEVLRLGSLDAVYDVSIAYKHQCPFLDNVFGLDPAEVHIHRIIPVNDIPVSDSEAA
 TWLMNTFQIKDELKSGFKTRGHFPNEGTEGELSTLRCLVNITIVISLTAIFTYTLTFSSVWFKIYVSLAC
 VFLSLVITYFNFLPLPVVDSFNSMFSYKKI

>RcLPAAT5 Lysophosphatidic acid acyltransferase [*Ricinus communis*]
 EEF43306.1
 MEVRGAVFSPDGTGGRALTPLRMIRGIMCLLMLLVSAFMMLVYFGFASSVIMRLFSIRYSRKATSFFFGA
 WLALWPSLFEKINKTKVVFSGETVPAKECVLLIANHRTEVDWMLWDLAWRKGLGFIKYVLKSSLMKLP
 IFGWGFHILEFIPVERKWEVDGSMNRVLSSFKDPKDPLWLALFPEGTDFTDQKCERSKKYAAENGLPIL
 NNVLLPKTKGFYACLECLRGSMDAVYDVTIGYKPRCPSLLDNVFGVNPSEVHIHVRRIALDGIKSEEEV
 AAWLMNTFQLKDQLLSNFYSQGHFPHQGTGGGLSTLKCFCVNFLALILLISILCCYLASATHFDVRPMLL
 SFLSCQ

>GmLPAAT2 1-acyl-sn-glycerol-3-phosphate acyltransferase 2 [*Glycine max*]
 XP_003535857.1
 MTAVVVVPLGLLFFASGLIVNLIQAICYVVVRPVSKNLYRRMNRVVAELLWLELVWIIDWWAGVKVQVFT
 DPETFRSMGKEHALVISNHRSDIDWLVGWVLAQRSGCLGSTLAVMKKSSKFLPVIGWSMWFSEYFLERS
 WAKDERTLKSGLQQLRDFPLPFWLALFVEGTRFTQAKLLAAQYEAASAGLPVPRNVLIPTKGFVSAVNH
 MRSFVPAIYDVTVAIPKSSPAPTMLRFLRGKSSVVHVHIKRHAMKDLPEEDEAVAQWCRDMFVAKDTLLD
 KHIAEDTFSDQELQDTGRPIKSLVVVISWACVVVMGVVKFLQWSSLLSSWKGVAFSAFGLGVVTLMLHIL
 IMFSQSERSTPTKVAPAKSKNSEQLEARDNKQD

>CsLPAAT3 PREDICTED: 1-acyl-sn-glycerol-3-phosphate acyltransferase 3
 [*Camelina sativa*] XP_010479592.1
 MTIPVALVFIPVGVLFLLISGLIVNIIQLVFFITVRPFSRSLYRRINKTVAELLWLQLIWLFDDWWACIKIN
 LYADAETLELIGKEHALVLSNHRSDIDWLIGWVMAQRAGCLGSSLAIMKKEAKYLPPIIGWSMWFSDYIFL
 ERSWAKDENNLKAGFKRLEDFPMTFWLALFVEGTRFTQEKLEAAQYASIRSIPSPRVLIPTKGFVSA
 VSHIRSFVPAIYDCTVTVQNIQPTPTLLRMFSGQSSEVNLMRRHKMSDLPETDDGIAQWCQDLFITKDA
 QLEKYFTKDFSDLDVHQINRPIKPLIVVIIWLCLLIYGGFKLFQWLSVVASWKIIFLLVFFLVIIATITM
 QVLIQSSSQSRSTPAKRPLQEQLITA

>HnLPAAT3 1-acyl-sn-glycerol-3-phosphate acyltransferase 3 [*Helianthus annuus*]
 XP_021973179.1
 MALAAVVVLPVGLLFLSGLVINFLQALFFVIVRPCSKNVYRKMNHAQLLWLEVWVLFDDWWAHIKVDL

YIDSETLELMGKEHALLICNHKSDIDWLGWVLAQRAGCLGSTLSLIKSLKLLPVIGWSMWFTEYIFLE
RSWAKDEHTLKAGFENLTDFFMPFWLAVFVEGTRFTQAKLIAAQEYAIAMKLPIPRNLLIPRTKGFVA
NHLRSFVPAIYNCTVAIPKDEPLPTILRMFRGRSSTVHIHIKRLICELPETDSGIKQWCRDRFVEKDAS
LELHKSNSFDSSECHSIGRPKSLFVVIFWSWLLLYGAIKFFEWCSFSWGTIAFCALLLLFVILMQIL
ILFSQSEKSDSLRSQTINYKEDTLNQKLIP

>HnLPAAT4 probable 1-acyl-sn-glycerol-3-phosphate acyltransferase 4
[*Helianthus annuus*] XP_021983651.1

MDDCQALNSDTNSELKHYALTPLRLLRGLACLVVYLSTAFMFLVYFSPVAAVFLRLFSVHYSRKACSFLE
GLWLALWPFLEKINKTKVVSGETVPEKERVLLIANHRTEVDWMYLWDLALRKGCLGCIKYVLKSSLMK
LPIFGWGFHIFEFISVERKWEVDEPIMRKMLSTFTNPLDPLWLAVFPEGTDFTQKCIKSQKYAAENGLP
ILKNVLLPKTRGFHACVEILRGSLDAVYDVTIAYKNRCPTFMDNVFGVEPSEVHVHVRISLEEIPVSED
ECNTWLLNTFHQDKQLLSDFIAQGYFPNEGTEGDLSTFKCLVNCTIVLVITSVFAYLAVFSSVWFKVYVA
LSCAYLACATAYNFWPSPILDYVKGLLSGKKSS

>AtLPAAT1 Phospholipid/glycerol acyltransferase family protein
[*Arabidopsis thaliana*] NP_194787.2

MDVASARSISSHPYSGKPICSSQSSLIRISRDKVCCFGRISNGMTSFTTSLHAVPSEKFMGETRRTGIG
WSNRSLRHDPPYRFLDKKSPRSSQLARDITVRADLSGAATPDSSFPPEIKLSSRLRGIFFCVVAGISATF
LIVLMIIGHPPFVLLFDPYRRKFHHFIAKLWASISYIPFYKINIEGLENLPSSDTPAVYVSNHQSFLDIYT
LLSLGKSFKFISKTGIFVIPIIGWAMSMGMVPLKRMDDPSQVDCLKRCMELLKKGASVFFFPEGTRSKD
GRLGSFKKGAFTVAAKTGVAVVPITLMGTGKIMPTGSEGILNHGNVRVIIHKPIHGSKADVLCNEARSKI
AESMDL

>AtLPAAT2 Lysophosphatidyl acyltransferase 2 [Arabidopsis thaliana]
ABG48392.1

MVIAAAVIVPLGLLFFISGLAVNLFQAVCYVLIRPLSKNTYRKINRVVAETLWLELVWIVDWWAGVKIQV
FADNETFNRMGKEHALVVCNHRSDIDWLVGWILAQRSGCLGSALAVMKKSSKFLPVIGWSMWFSEYLFLE
RNWAKDESTLKSGLQRLSDFPRPFWLALFVEGTRFTEAKLKAAQEYAASELPIPRNVLIPTKGFVSAV
SNMRSFVPAIYDMTIVTIPKTSPPPTMLRLFKGQPSVVHVHIKCHSMKDLPESDDAIAQWCRDQFVAKDAL
LDKHIAADTFPGQEQNIGRPIKSLAVVLSWACVLTLAGAIKFLHWAQLFSSWKGITISALGLGIITLCMQ
ILIRSSQSERSTPAKVVPAPKPDNHHPESSSQTETEKEK

>AtLPAAT3 Lysophosphatidyl acyltransferase 3 [Arabidopsis thaliana]
AT1G51260

MKIPAAALVFIPVGVFLISGLIVNIIQLVFFIIVRPFSSLYRRINKNVAELLWLQLIWLFDDWACIKIN
LYVDAETLELIGKEHALVLSNHRSDIDWLGWVMAQRVGCLGSSLAIMKKEAKYLPPIGWSMWFSDYIFL
ERSWAKDENTLKAGFKRLEDFPMTFWLALFVEGTRFTQEKLEAAQEYASIRSLPSRNVLIPTKGFVSA
VSEIRSFVPAIYDCTLTVHNNQPTPTLLRMFSGQSSEINLQMRHKMSELPEPDDGIAQWCQDLFITKDA
QLEKYFTKDFVSDLEVHQINRPIKPLIVVIIWLGLFVFGGFKLLQWLSIVASWKIILLFVFFLVIATITM
QILIQSSSQSRSTPAKRPLQEQLISA

>AtLPAAT4 Lysophosphatidyl acyltransferase 2 [Arabidopsis thaliana]
AT1G75020

MEVCGDLKSDNLKNRPLTPLRILRGLMILLVFLSTAFMFLLYFAPIAALGLRLLSVQQSRKVVSILIFGLW
LALWPYLFETVNGTTVVFGSDIIPVEKRVLLIANHRTEVDWMYLWNIALRKGCLGYIKYVLKSSLMKLPI
FGWGFHVLEFIPVERKREVDEPVLLQMLSSFQDPQEPLWLALFPEGTDFTTEKCKRSQKFAAEVGLPALS
NVLLPKTRGFVGCLEVLHNSLDAVYDLTIAYKPRCPSFMDNVFGTDPSEVHIHVRVLLKEIPANEAESS
AWLMDSFKLKDQLLSDFNAQGKFPNQRPEEELSVLKCIATFAGVISLTVVFIYLTLYSHSCFKVYACLSG
TYLTFATYYKFQSPGCFREDSCVKNH

>AtLPAAT5 Lysophosphatidyl acyltransferase 5 [Arabidopsis thaliana]
[Arabidopsis thaliana] At3g18850

MEKKSVPNSDKLSLIRVLRGIICLMVLVSTAFMMLIFWGFLSAVVLRLFSIRYSRKCVSFFFGSWLALWP
FLFEKINKTKVIFSGDKVPCEDRVLLIANHRTEVDWMYFWDLALRKGQIGNIKYVLKSSLMKLPLFGWAF
HLFEFIPVERRWEVDEANLRQIVSSFQDPRDALWLALFPEGTDYTEAKCQSKKFAAENGLPILNNVLLP
RTKGFVSCQLQELSCSLDAVYDVTIGYKTRCPSFLDNVYGIPESEVHIHRRINLTQIPNQEKDINAWLMN
TFQLKDQLLNDFYSNGHFPNEGTEKEFNTKKYLINCLAVIAFTTICTHLTFFSSMIWFRIYVSLACVYLT
SATHFNLSRVPLVETAKNSLKLNVK

>BnPAH1-1 Phosphatidate phosphatase 1 [*Brassica napus*] XP_013750374.1
MSLVGRFGSLISQGVYSVATPFHPPFGGAIDAIVVQQEDGSFRSTPWYVRFQGVLGKAEKFKISVNG
TEADFHMYLDNSGEAYFIREVDPAAANDDTENNNGNENGLRLEHSLSDAGAEREGFNSLSRLDRTESDC
NRRYYDFQDDDDDDPPSPTSEYGEGQGSSEVVLVSVDGRILTAPVSAAEQEAENLRLNTPQFHLAPGDG
TEFCEGNTFASSETSWDTEFISKVESSEKVDSSRDITVKDSHYTELSQPGENVKSEEPANLKEGELL
STAVTENARGEEEVAVETVNTLIDGSESSTTQLTTEEVRITEESVDANTESECEDEQTNTSAETAILIES
EASERVSIDSTREEDEQLTPSKPNKDSNRNTIDSVAATSSVDIELKYELSLCKDELRLQGMGLTAAAEVF
NTHIISIEEYKNSAASILESENLVVRIRETYPWPKKAARIILGKVAFDLDDIQLPEDVISVEENESSKPK
DDDEAAATTPSSSGRRWRLWPIPFRRVKTIETHTSSNSSSEEDLFVDSEPLQNSPEVLSAAESRHESPRR
QLVRTNVPTNEQIASLNLKDGQNMITFSFSTRVLGTQQVDAHIYRWRWDTKIVISDVGDTITKSDVLGQF
MPLVGKDWTQSGVAKLFSIAIKENGYQLLFLSARAIQAYLTRSFLNNLKQDGKALPNGPVVISPDGLFPA
LYREVIRRAPHFEFKIACLEDIKLFPKDYNPFYAGFGNRDTELSYRKLGIPIKGKIFIINPKGEVATGHR
IDVKKSYTSLHTLVNDMFPTSLVEQEDYNPWNFWKLPEVEVD

>BnPAH2 Phosphatidate phosphatase 2 [*Brassica napus*] XP_013644973.1
MNAVGRIGSYIYRGVGTSGPFHPPFGGAIDIIVVEQPDGTFKSSPWYVRFQGVLGKRRNLKIEVNG
VDSGFTMYLAHTGQAYFLRQVEDVLGEVYTLSSGDEAETSRRKSSSSSDGVDDKKIKIPLKSKSCNYDGV
VGGKPGILGFVFGGRSVKVDGVTSMERAEIAADLLDVKWSNIDTRKCVKGKASKSFDISILETPLVASP
TLQYLDEKEQDCFRENNVVEDDDDDYSLLLVENGSSSTVFSVTTSQSGSNVEPPPLAQDSVNLDSKQQVL
GVPEYQADKTSLQEGSSTGSLVQDDFEKTQPTNGATVQQPEVEEEQFSFSDIGCKSAETSSQESSFLHT
VKVEIYDENEISPENGVEVLSEPIEIERKKDISGEEMERLAESLPIMRLHNNNDIDAGPCRQPMQSFD
SSNTLKPSSRGSPSLKAFEHVITNPEVVELSLCKHLLREGMGAEAAASQAFNSEKLDMEKFASLGPSVLEN
DMLIVKIGGCYFPWDAAPIILGAVSFGTSQVFEPKGMIVVDRNEKPDDAVLAPSGGSWNLWPFSQRRSR
NDSEASSKDAAEREKKQEKSSPRPVKKTVRALTPTSEQLASLNLKEGMNTVNFTFSTNIVGTQQVDARI
YLWKWDARIVVSDVDGTITRSDVLGQFMPLVGIDWSQTGVTHLFSAVKENGYQLMFLSARAIQSASVTRQ
FLVNLKQDGKALPDGPVVISPDGLFPFLFREVIRRAPHFEFKISCLEEIRALFPPEHNPYAGFGNRDTE
ISYLVKGIPIRGKIFTINPKGEVAVNRRVDTRSNTLHALVNGMFPATTTSSPEDFNTWNFWKLPPPLM

>BnPAH1-2 Phosphatidate phosphatase 1 [*Brassica napus*] CDY41298.1
MSLVGRVGSLSISQGVYSVATPFHPPFGGAIDVIVVQQEDGSFRSTPWYVRFQGVLGKAEKFKISVNG
DEADFHMYLDNSGEAYFIREVDPETTNDLISSEDSNGSERVLTLEHSSSDVGAGELREGLSSLNRLDRT
ESDSNGRYYDFQDDPPSPTSEYGSARFDNLNVESYGDSPPGLDSEVVLVSVDGHILTAPVSAAEQEAENL
RLNTPQFHLAPGDGTEFCGSTEFASSSETSWDTEFISKVESSNAVNIKSKKVDIGCEVCNDENAKSEEA
ASTLEVQNLKEGELVPTTIKESVRGEDEVAIVGSCLEKSEPAIFEIQNLKEGELVPIETVTTLVDGSES
STTQLTIEEVRTSEESNTDPSAETAILIENKEGEIIESEERSVDSTREEDEQLTPSKEPEEDNNTT
ESVAETSNIARSETELKYELSLCKDELRLQGMGLTAAAEVFNTHLISTEEYKNSATSILESENLVVRIRET
YMPWPKKAARIVLGKVVFDLLEIQLPEDVISVEETKPKDDETAAVTTTPSSSGRRWRLWPIPFRRVKTV
TTSSNSSSEEDLFVDSEPLQNSPEVLSTNESPRRQLVRTNVPTNEQIASLNLKDGQNMITFSFSTRVLG
TQQVDAHIYRWRWDTKIVISDVGDTITKSDVLGQFMPLVGRDWTQSGVAKLFSIAIKENGYQLLFLSARAI
VQAYLTRSFLNNLKQDGKALPNGPVVISPDGLFPALYREVIRRAPHFEFKIACLEDIKKLFPEHYNPYAG
FGNRDTELSYSKLGIPIKGKIFIINPKGEVATGHRVDVKKSYTSLHTLVNDMFPTSLVEQEDYNPWNFW
KLPIEEVD

>AhPAH1-1 Phosphatidate phosphatase 1 [*Arachis hypogaea*] XP_025605008.1
MNVVGKVGSLITQGVYSVATPFHPPFGGAVDVIVVQQQDGTFRSTPWYVRFQGVLGKAEKFKIRINVG
VEANFHMYLDNSGEAYFIKEVDDDKDVESVADEDAGQSDFTHVHRLDHSISDSGVLRLKANRDPQIQRV
ESDLDRYYELQDDEPGVDGSFELSEYGSNRYDNPNGENGLDSHGSHPEVVLVSVDGHMMTAPICRSEQN
DEENVQLKNPQFHLGPAEGTEFCGNEFTSDENAWAADYIRKLDSTDDVPSCSYNRNGGDTTSEIVAKV
HQREEVHVRYAEATLVIKDQENYVQSDTEEVASGLRRETVFKSCLALDQFGQDENADSEDEGSPAKVQK
SADEYNANCSVGNENAEQENIKSPCSIDELSPSRPTSYSDENGSTKVELGGVQEVDDKASVHVDTDSGSHS
VTNDNETEGNDELIENSVLTDGVDDSKQIPALDDANNLSEEIIEPQPTTSNDEDQSYGLGFEISLCGHEL
KVGMSVAAAETFDAHRISAEFRASAPLIKENLNVKFRERYLLWEKAAPLILGMAVFLDSPVNPDD
TIPVEQGDALSRDGDAGSASSGRRWRLWPIPFRRVKTLHSTSNASSDEIFVDTESELQSSLLDPSPKSY
NPGSPHKQFVRTNVPGNEQIASLNLKEGQNLVTFSTRVLGTQQVDAHIYLVKWDKIVISDVGDTITK
SDVLGQFMPLVGKDWSQSGVARLFSIAIKENGYQLLFLSARAIQAYLTRNLLNLKQDGNTLPNGPVIS
PDGLFPFLYREVIRRAPHFEFKIACLEDIKRFPADYNPFYAGFGNRDTELSYRKIGIPKGKIFIINPKG
EVAISQRIDSKSYTSLHTLVNDMFPTSLVEHEDFNSWNYWRVPIPDVNDN

>AhPAH2-1 Phosphatidate phosphatase 2 [*Arachis hypogaea*] QHN88458.1
MQAVERLGSFITRGVSTVSMFPPIYGGAVDIVVQQQKDGFSKSSPWVRFGLHRVLKADEKKVISVNG
SEAGFHMHMNHKEGAFFLRDTHCEQQGDEDSGSSSESSSGEDADVLPWGRKRNFKSKCKFDPDGSFVA

DMNALNNDKIVDRNTNSRGSRLFRLVLGQRSFNGEVDEDAEDLLERAEIAANLLDLKWSTNLKFDQLPRRE
RKNTRGGTLENGLHSSKVDDLHAQQRDCHSVLDMFVDADFELPKFKQSRTISVYRPHRKANKVRADTP
TSEQLASLNLQEGRNLTFRYSTAMLGTQKIDARIYLWKWNTRIVISDVGDTITRSDVLGQVMPLVGIDW
SQTGVAHLFSAIQDNGYQLLFLSARAIQACHTRRFLFNLKQDGKVLDPGPPVVISPDGLFPALYREVIRR
APHEFKIACLEEIRALFPPDCNPFYAGFGNRDTDELSYLVKVGIPKGKIFIIINPRGEIAVNCFDAQSYPSL
HAVVDGIFPPTDSSEQVYL

>AhPAH2-2 Phosphatidate phosphatase 2 [*Arachis hypogaea*] QH029627.1
MRRIGSYITQGVYTVSGPFHPFGGAVDIVVVEQPDGTFKSSPWYVRFKGKFGVLKAREKIVDINVNGVDA
DFHMLDHLKGEAYFFREVDAEYGDVVIYSSGDEYDDNRSRNLNDMQIERLRSKSCNYDSSENSGNAGA
RSRGSLLGFVFGKRSIEEGEECGDKYGEQMAPAEIAADLLELKWSTNIKSDRRPPRFVDRKRIAKSSSD
GDVLQEAALPPELVKEEEAASFNSNSNEHGHDKTMKIDVAHEVECDSENGKQGGLAHECADFPVELVEVEA
EGGFERKLSEGELAPVSFAFASPTGVASVDDNISADEVAQSVVFFETSEKATVDCANESSATSHDVSSTFS
PPKELLGVQATTKSPAAGLVVEENFLFSDLDESKINDQLDRPVSPESVDKEEEEEEEHSCDDGDVKDDN
LVSEKGDHLHSSSPMAIPRTEAAGEDIGHTGSLPNITTRSVSLGQPEASYPLSQSLDTRSKSLPWLFPENE
DSSEANGNQLSNAKSGVSPSPSGWRLWPFSSVSQTYVPPMPSDTKDTTFEQSSSENTISTDPNKNELKTD
PKKKHVRVKVPTSEQIASLHLKEGGNTVMFTFTSTMLGRQQVDCRIYLWKWNTRIVISDVGDTITKSDVL
GQFMPLVGIDWSQTGVAHLFSAIKENGYQLLFLSARSISQAYLTRQFLFNLKQDGKALPDGPPVVISPDGL
FPSLYREGQNLFFLLFLITSL

>GmPAH1 Phosphatidate phosphatase 1 [*Glycine max*] XP_003541397.1
MNVVGKVGSLITQGVYSVATPFHPFGGAVDIVVQQQDGTFRSTPWYVRFKGKFGVLKGAEKFVRINVNG
VEANFHMVYLDNSGEAYFLKEVDDDKGVDSIEAVQDSIDKKNGYLINVHRLDHSISDSGVLRLKDESDSL
VSQQLQRAESDIDRRFYEFPPDRSSLEDSVELSEYESNSYESLEGDNFGESQGSHPMVLVSVGDHILTAP
ISESEQAEENVQLKTPQFHLGPGEETDLCEGNGEFSTGENAWAAGYINQLGAQTNTVQPRLCDTNGDDNT
SKLLLKLKQGEAAHICEAQDTLEIKNQDHIKTDKGAASGIKRENVFKSYLELQDFGQQAGNADLQDIGS
SLEIQNSAEESNASCPVVDENEQESIAISKNGDELSPHSGSTSSNGHRSKSELEIQEVEKNASGKIETA
SGSHSVTTDTEQNDHEVDKSVSNDELDESQQTALPKDVTRATSEVVEPQTETSNKGDQSHLGLGFEMSLCG
HELVGMGSIAAAEEVFEAHRISVVDFTSSAPSIKKNQNLVIKFKERYMTWEKAAPLVLMGMAVYGLDLPE
SKDTIPVEQDHALKSRDDDLGSSSSGRRWRLWPIPFKRVKTFEHTNSNSNEEVFLDSESGSLIEPTPTS
STQGSSHKQFLRTNVPTTEQIASLNLKEGQNLVTFSTFSTRVLGTQQVDAHIYLWKWNARIVISDVGDTIT
KSDVLGQFMPLVGKDWTSQSGVARLFCAIKENGYQLLFLSARAIQAYLTRNLLNLKQDGKTLPLNGPVVI
SPDGLFPSLYREVIRRAPHEFKIACLEDIKRLFPSDYNPFYAGFGNRDTDELSYRKIGVPGKIFIIINPK
GEVAISHRIGAKSYTSLHTLVNDMFPTSLVEQEDYNSWNYWKTPLPDID

>GmPAH2 Phosphatidate phosphatase 2 [*Glycine max*] XP_006578018.1
MQAVGRIISQGVYTFSGPFHPFGGAVDIVVVEQDGTFRSTPWYVRFKGKFGVLKAREKVVVICVNGVQA
GFQMHLDHLKGEAFFLREIDAQEEEAAILMFSSSGDDADDQTRSHSLRSESLNYDAAAEVVGRTTSSRRSR
ILGLVFGRRSLKREDGAGVGDDGVDGIGNRVGSLEAEIAANLLDINWSTNPSAEQGDVIANPSGDG
EVVVENGELNEEACFGGECDLNWKIEVYDIAESDVQVACVEVEVEACVEKELNGEEVSIAPGENSNESS
SETSKLVDCSSEQAHEVMYLAGPECEEVHVHVHDEVHVGATVLLAEDTEAAEVIENADLESHSRIQQT
SSDSDDIRYNEVVVEEQPTSPKSQTVKMGLGHYSNEKVEPNCCIIPSSYSILADQALDDNNMKDKDVSST
LSSPLDSVDDSLPRKASRRSSPSEDENFLFSGHDKSVINDRFERSFSPEHVDKEDHVSYGNDSEKLT
ISNPIDIPMKAAGEEVVQFSGSLPNISSGSDIMVEHNVRYPCLQSLDSKSTSLPWAFFPGKDDLECLKSD
EDKGNQLSHEGQGAQDYNDSEGLKGPSTRNPSAGGSWRIWPFSLRREGSRKSMPLPSPSDSKNTTFVNS
PENTISTDMNKNELKPNLMKKVKEMTPTSEQLASLNLKDGMMNTVTFTFSTAVLGKQQVDCRIYLWKWNA
RIVISDVGDTITRSDVLGQFMPLVGIDWSQTGVAHLFSAIKENGYQLLFLSARSISQAYITRQFLNLKQ
DGKVLDPGPPVVISPDGLFPSLYREVIRRVPHFKIACLEDIKALFPSDSSPFYAGFGNRDTDEISYLVK
IPLGKIFIIINPRGEVVRNRRVDAKSYTSLHALVNGMFPTSSSEQEDFNSWNFWKLPPPAIDI

>AtPAH1 Phosphatidic acid phosphohydrolase 1 [*Arabidopsis thaliana*]
AT3G09560

MSLVGRVGSLSIQGVYSVATPFHPFGGAIDVIVVQQQDGSFRSTPWYVRFKGKFGVLKGAEKFVRISVNG
TEADFHMYLDNSGEAYFIREVDPAANDTNNLISGSENNNGNQNGVTYRLEHSLSDSGTGELREGFDPLS
RLRTESDCNRRFYDFQDDPPSPSTSEYGSARFDNLNVESYGDSQGSSEVVLVSDIGHILTAPVSAEQE
AENLRLNTPQFHLAPGDGTEFCGNTFASSETPWDTEYIDKVEESDTANIASDKVDAINDERNDLDSH
SRDNAEKDSDHAERDLLGSCLEQSELTKTSENVKSEEPGPTFEDRNLKEGEFPLRTITENDRSEDEV
TIESIDTLVDSFESSTTQITIEEVKTTEGSRISVDSNADSECKDEQTSAAETAILINNQESSISVDSNP
DSECKDEQPRISAETAILINNQEGGIIIESEDQDSERVSIDSTREEVEQLTPSKPTDKDNEDRKT
VVSVGVTSSVD EGEPTDQRYELSLCKDELQGMGLSAAAEVFDAMHISKEEYINSATSILESEN
LVVRIRETYMPWTKAARIVLGKAVFDLDDIQQPDDVISVEENESPKPKDDETTITPSSSGTRWKLWPI
PFRRVKTVETHTGSNSSE

EDLFVDSEPLQNSPETQSTTESRHESPRRQLVVRTNVPTNEQIASLNLKDGQNMITFSFSTRVLGTQQVD
AHIYRWRWDTKIVISDVGITITKSDVLGQFMPIGKDWTSQSGVAKLFS AIKENG YQLLFLSARAIVQAYL
TRNFLNNLKQDGKALPTGPVVISPDGLFPALYREVIRRAPHEFKIACLEDIRKLFPTDYNPFYAGFGNRD
TDELSYRKLGI PKGKIFI INPKGEVATGHRIDVKKSYTSLHTLVNDMFPTSLVEQEDYNPWNFWKLP
EVE
>AtPAH2 Phosphatidic acid phosphohydrolase 2 [*Arabidopsis thaliana*]
AT5G42870
MNAVGRIGSYIYRGVGTVSGPFHFGGAIDIIIVVEQPDGTFKSSPWYVRFGKFQGV LKNGRN LIRIDVNG
VDSGFNMYLAHTGQAYFLREVEDVVGESSEGEVYTLSSGDEAETTSRDDVVDKVKIPLKSRSCNYDSPSP
RTGNGKIVGKPGILGYVFGGRSVRESQDCGVERAEIAADLLEV KWTNIDTRKRKGKMSSESLDGKDYGE
STSTSGKSCVEGSSSEMIVSDSILETPLVASPTLRFLDEKEQDFRESTNVEDYCEEDGSSGVVVENGLCE
ASNMFVSVTSEGSGNVEIFVEPRTEALAEADAVSGSDLDSKQELLRAPESVEIATLGSADQADMGSIGTSQ
EGSSTGSPVQDENKITIKDMHISAGDFEKSQSASGESILQPEIEEEQFSFSDLDECKPGGNSSVGSSSD
TVKVDGKESYDETKTSPENGVDNTMALSEPINIERKKDIFTDEMERLVGSLPIMRLQNIDMDASPSQPL
SQSFDPCFNTSKLDLREDESSGGLDAESVAESSPKLKAFKHVIANPEVVELSLCKHLLSEGMGAEAAASQ
AFNSEKLDMEKFASLGPSILENDKLVVKIGGCYFPWDAAPIILGVVSFGTAQVFEPKGMIAVDRNEKPG
DVLAQGSWSKLWPFSLRRSTKEAEASPSGDTAPEEKQEKSSPRPMKKTVRALTPTSEQLASLDLKDGM
NSVTFTFSTNIVGTQQVDARIYLWKWNSRIVVSDVGTITRSDVLGQFMPLVGIDWSQTGVTHLFSVAVKE
NGYQLIFLSARAISQASVTRQFLVNLKQDGKALPDGPVVISPDGLFPSLFREVIRRAPHEFKIACLEEIR
GLFPPEHNPFYAGFGNRDTEISYLVKGI PRGKIFI INPKGEVAVNRRIDTRSYTNLHTLVNRMFPATSS
SEPEDFNTWNFWKLPPPSLM

>AhDGAT1C Diacylglycerol O-acyltransferase 1C [*Arachis hypogaea*]
XP_025688510.1
MAISDVHETSVAGDGANHSSLRQRHSRVASSGGNMFDEAEASAEAVMIASSGSDDSLNEKIGAAREEKVK
ERQKQKEEDRKPPDHASRNEVDGERAAAGDNFTYRASVPVHRRIKDSPLSSRNIFKQSHAGLFNLCVVV
LIAVNSRLIIENIMKYGWLINSGFWFSSKSLDWPLLMCCISLNLFP LAAFMVEKLAQKKRISEPVIFLL
HTIIMTGEILFPVLVILSCDSTFLSGLTLMMVACIIWLKLVSYAHTSHDLRSLSLSEIEKGETLPNNLNME
HPYRVSFERSMAYFMVAPTLCYQPSYPRTPSVRKGWVFRQLIKLVIFTGLMGFIIIEQYMHPIVQNSQHPFK
GNLLYG FERTLKL SVPNVYVWL CMFYCFFHLWLNILAEVLQFGDREFYKDWWNAKTVD EYW RWNWMPVHK
WMVRHIYFPCIRHGMSKLCIAVPCHKFKLWAFIGIMFQVPLSIVTNFLHEKCKSSMVGNMVFWFTFCILG
QPMCVLLYYHDWMNRHREHN

>AhDGAT1-3 Diacylglycerol acyltransferase 1 [*Arachis hypogaea*] ATG83402.1
MAIQSVGATATVQGDGANSSTVRRRRSGGATSATPLEKVELDAFDGESSEELAKDSSSDNNNGNV
DDASKGNRQQNAADFS AVNF DYRPSFPAHRRIRDSPLSSGNIFKQSHAGLFNLCIVVLVAVNSRLIIENL
MKYGWLIKTDWFSSSTLSLWPLFMCCLTLLLPVASFIVEKLAQH KYIPEPVVILHIIITSTSLLYPI
FVILRSDSAFLSGVTLM LFACIVWLKLVS YGHTNYDLRALAISNEKVEGLPSTLSMDYPYDVSIRRLAYF
MLAPTLCYQPSYPRTPSIRKGWVFRQLVTLIIFTGLMGFIIIEQYINPIVQNSQHPLKGNLLYAIERVLKL
SVPNLYVWL CMFYCFFHLWLNILAE LLRF GDREFYKDWWNAKTVD EYW RLWNMPVHKWMIRHLYFPCIRH
GVPKGVALLIAFLVSALFHEL CIAVPCHIFKLWAFIGIMQVPLVLITNYLQNKFRSSMVGNMIFWFIFC
ILGQPMCVLLYYHDLMSRKVKTE

>GmDGAT1A Diacylglycerol O-acyltransferase 1A [*Glycine max*]
NP_001237289.1
MAISDEPETVATALNHSSLRRRPTAAGLFNSPETTTDSSGDDLAKDSGSDDISSDAANSQPQKQD TDF
SVLKFA YRPSVPAHRKV KESPLSSDTIFRQSHAGLFNLCIVVLVAVNSRLIIENLMKYGWLKSGFWFSS
KSLRDWPLFMCCLSLVFPFAAFIVEKLAQKCIPEPVVVVLHIIITSASLFYPVLVILRCDS AFLSGVT
LMLFACVWLKLVS YAHTNYDMRALT KSVEKGEALPDTL NMDYPYNVSFKSLAYFLVAPTLCYQPSYPR
PYIRKGWLF RQLVKLIIFTGVMGFIIIEQYINPIVQNSQHPLKGNLLYAIERVLKLSVPNLYVWL CMFYC
FHLWLNILAE LLRF GDREFYQDWWNAKTVEDYWRMWNMPVHKWMIRHLYFPCLRHGIPKAVALLIAFLVS
ALFHEL CIAVPCHIFKLWAFGGIMFQVPLVFITNYLQNKFRNSMVGNMIFWFIFSILGQPMCVLLYYHDL
MNRKGKLD

>OeDGAT1 Acyl-CoA:diacylglycerol acyltransferase 1 [*Olea europaea*]
AAS01606.1
MTIPELPESLETTTLNSHHSRAASTVRRRSIDVAVLES DSN SLEAVNDS DSDVNNTNEMGNLRGGV VESA
LEEPS ELGT EGRNGKEENEHVRTGESNQEMEVLASAKFAHRPSAPVHRRIKESPLSSDAIFKQSHAGLF

NLCIVVLVAVNSRLIIENLMKYGWLINSGFWFSSTSLKDWPLLMCCLSLPIFPLAAFFVEKLVLLKYISE
CVAVFLHILITTAAILYPVLVILRCDASVLSGVTLMLFACIVWLKLVSYAHASHDMRALAKSLDKGETLS
GYWNSDDSYGASFQSLAYFMVAPTLCYQPSYPTSCIRKGWVVRQLIKLIIFTGFMGFIVEQYINPIVRN
SQHPLKGNLLYAIERVLKLSVPNLYVWLCMFYCFFHLWLNILAELLCFGDREFYKDWNAKTVEEYWRMW
NMPVHKWVMVRHIYFPCLRNGMPRGGAILIAFLISAIFHEL CIAVPCHIFKFWAFIGIMFQVPLVILTNYL
QDKFQNSMVGNMIFWCFFSILGQPMCLLLYYHDLNMRKASAK

>BnDGAT1 Diacylglycerol acyltransferase [*Brassica napus*] AAD45536.1
MAILDSGGVAVPPTENGVAIDLRLHRRKSSSDSSNGLLSDTSPSDDVGAAAAERDRVDSAAAAEAQGTAN
LAGGDAETRESAGGDVRFYRPSVPAHRRRTRESPLSSDAIFKQSHAGLFNLCVVVLVAVNSRLIIENLMK
YGWLIRTDWFWSSTSLRDWPLFMCCLSLSVFPLAAFTVEKMLVQKFISEPVAIILHVIITMTEVLYPVYV
TLRCDASFLSGVTLMLLTLCIVWLKLVSYAHTSYDIRTLANSADKVDPEISYYVSLKSLAYFMVAPTLCYQ
PSYRSPCIRKGWVARQLAKLVIFTGLMGFIIIEQYINPIVRNSKHPLKGDLLYAIERVLKLSVPNLYVWL
CMFYCFFHLWLNILAELLCFGDREFYKDWNAKSVGDYWRMWNMPVHKWVMVRHVYFPCLRKIPKVPAAII
IAFLVSAVFHEL CIAVPCRLFNWAFMGIMFQVPLVFITNLFQERFGSMVGNMIFGSASCIFGQPMCGLL
YYHDLNMRKGSMS

>CsDGAT1B Diacylglycerol O-acyltransferase 1B [*Camelina sativa*]
AQU71886.1
MAILDSGGGGVSTATATENGGGGFVDLRRRKSRSDSNGVLCGSDNPPSDDVGAPADVRDRIDSVVNDDAQ
GTTANLAGDNEIRETGGGGRGGGGEGGRGNAETTYRPSVPAHRRARESPLSSDAIFKQSHAGLFNLCV
VVLIAVNSRLIIENLMKYGWLIRTDWFSSRSLRDWPLFMCCLSLSFFPLAAFTVEKLVLLQKCISEPVVI
FLHIIITMTEVLYPVYVTLSCDSAFLSGVTLMLLTLCIVWLKLVSYAHTNYDIRTLANSADKANPEVSYYV
SLKSLAYFMVAPTLCYQPSYRSPCIRKGWVARQFAKLVIIFTGFMGFIIIEQYINPIVRNSKHPLKGDLLY
AIERVLKLSVPNLYVWLCMFYCFFHLWLNILAELLCFGDREFYRDWNAKSVGDYWRMWNMPVHKWVMVRH
IYFPCLRSKIPKTLAIIIAFLVSAVFHEL CIAVPCRLFKLWAFIGIMFQVPLVFITNYLQERFGSTVGNM
IFWFIFCIFGQPMCVLLYYHDLNMRKGSMS

>AhDGAT2 Diacylglycerol acyltransferase type 2 [*Arachis hypogaea*]
AEO11788.1
MEDRGNTVAAPPAEEKVFRSTEVFAAESSSKSGKFKTTLALALWLGAIHFNGALMLFALLFLPLSKALLV
FALLFVFMVIPIDEKSKFGRKLSRYICKNACSYFPITLHVEDIKAFNSNRAYVFGFEPHSVLPIGVVALA
DNTGFMPLPKIKVLASSAVFYTPFLRHIWTWLGTPATKKNFLSLLDNGYSCILIPGGVQETFLMEHGTE
TAYLKARKGFIRIAMQKGQPLVPVFCFGQSDIYKWWKPGGKLILNFARAIKFTPIYFWGIFGSPPIPKHP
MYVVVGRPIELDKNPEPTTEEVATVHSQFVASLQDLFERYKARAGYPNLELRIV

>AhDGAT2D Diacylglycerol acyltransferase type 2D [*Arachis hypogaea*]
XP_025682671.1
MEVRGNTVAPPAEEKVFRSTEVFAPESSSKSGKFKTTLALALWLGAIHFNGALMLFALLFLPLSKALLV
FALLFVFMVIPIDEKSKFGRKLSRYICKNACSYFPITLHVEDIKAFNSNRAYVFGFEPHSVLPIGVVALA
DNTGFMPLPKIKVLASSAVFYTPFLRHIWTWLGTPATKKNFLSLLDNGYSCILIPGGVQETFLMEHGTE
TAYLKARKGFIRIAMQKGQPLVPVFCFGQSDIYKWWKPGGKLILNFARAIKFTPIYFWGIFGSPPIPKHP
MYVVVGRPIELDKNPEPTTEEVATVHSQFVASLQDLFERYKARAGYPNLELRIV

>AhDGAT2-1 Diacylglycerol acyltransferase type 2 [*Arachis hypogaea*]
AEO11791.1
MEDRGNTVAAPPAEEKVFRSTEVFAPESSSKSGKFKTTLALALWLGAIHFNGALMLFALLFLPLSKALLV
FALLFVFMVIPIDEKSKFGRKLSRYICKNACSYFPITLHVEDIKAFNSNRAYVFGFEPHSVLPIGVVALA
DNTGFMPLPKIKVLASSAVFYTPFLRHIWTWLGTPATKKNFLSLLDNGYSCILIPGGVQETFLMEHGTE
TAYLKARKGFIRIAMQKGQPLVPVFCFGQSDIYKWWKPGGKLILNFARAIKFTPIYFWGIFGSPPIPKHP
MYVVVGRPIELDKNPEPTTEEVATVHSQFVASLQDLFERYKARAGYPNLELRIV

>OeDGAT2 Diacylglycerol acyltransferase type 2 [*Olea europaea*] ADG22608.1
MTSENGDMRRRQLLVSESAQQPTPAEFKGTQGSIFHTILALVLWLGSVHFNIIVVLASFVFLSFTKALM
VIGLLVILMVAPIDDRNKWGRKLARYICKHAGVYFPVNLYVEDIKAFDPNESYVFGYEPHSVWPIGVSL
ADLTGFMPLQKIKVLASTAVFYTPFLRHIWSWLGLTPATRKNFTSLLASGYSCIIIPGGVKEALYMEHGS
EIAYLKTRRGFVRIAMEMGKPLVPVFCFGQTNVYKWWKPSGKLYLEFSRAIKFAPIFFWGLGSPLPLRH
PMHVVVGRPIVPKRNPPQPTVEEVAEVHGQFVEALQELFERHKARVGYTDMQLKIL

>GmDGAT2D Diacylglycerol O-acyltransferase 2D [*Glycine max*] BCB92186.1
MAAEPVSDGGAAAEKLISGREEFGDSSNLLSAILAMVLWLGAIHFNIALILLAVFFLPLSKSLLVFGFLF
GFMVLPINEKSRFGRRLSRFICKHACNYFPITLHVEDMKAFDPNRAYVFGYEPHSVLPIGIVALADHTGF
MPLPKVKVLASSTVFYTPFLRHLWTWLGTPATKKNFISLLASGHSCILIPGGVQEAFFMQHGTEIAFLK
ARRGFVRVAMVKGKPLVPVFCFGQSNVYKWWKPGGKLFLKFARAIKFTPICFWGIFGSPLPFRHPMHVVV

GRPIEVDKNREPTTEEVAKIHGLFVEALQDLFERHKARAGYPNLELRIV
>EgDGAT2D Diacylglycerol O-acyltransferase 2D [*Elaeis guineensis*]
XP_010932136.1
MPRVTHLGDIIYPAAHRNTRRILSLSLTRSHEASWRMDHNGDRQAAVLDDSAGAGEAAVYRGTEYSVVRT
TVALALWLGLIHFNVALVLTALLLLPARLAAAVFALLLVFMAIPLDENSKWGRKLSRWICKYAVGYFPVT
LYVEDIKVFDPNQAYVFAFEPHSVLPIGVVALADLTGFMPLTKVKVLASSAVFYTPFLRHLWTWGLVSA
SRKNFYAYLEAGYSCIVVPGGVQEMLMHDHDESEVAFLLKARKGFVRIAMETGRPIVPVFCFGQSYVYKWWK
PSGKLFVWIARAIFKFTPIVFWGRFGSPIFRHPMHVVVGKPIGLKRNPKPTIEEINEVHAQFVAAFQELF
EKHKTRAGYPDLRLRLV
>AhDGAT3-1 Diacylglycerol acyltransferase [*Arachis hypogaea*] ABW34442.1
MEVSGAVLRNVTCPSFSVHVSSRRRGDSCVTPVVRMRKKAVVRCCCGFSDSGHVQYYGDEKKKENGTM
LSTKKKLKMLKKRVLFDDLQGNLTWDAAMVLMKQLEQVRAEEKELKKKRKQEKKEAKLKASKMNTNPDCE
SSSSSSSESESESECDNEVDMKKNIKVGVAVAVADSPRKAETMILYTSLVARDVSANHHHHNAVE
LFSRNDISVGSINGGLKNENTAVITTEAIPQKRIEVCMGNKCKKSGSIALQEFERVVGAEGGAAA
VVGCKCMGKCSAPNVRIQNSTADKIAEGFNDSVKVPANPLCIGVAWRMLKPLWLRFLGENQESTNE
>GmDGAT3 Diacylglycerol O-acyltransferase 3 [*Glycine max*] XP_003542403.1
MEISGSVLRQLSYVSGYGTPTSRGVASRVGLRMGTGSGFCDEGHLQYYQDTKKILTTPKKLKLLKGFSKL
GLASDPEKLMFHDLLQGNLTSDAGEVLLRELEAARAKEKEMKKKRKQEKIKAKLKASKMNCESSSSSSSES
SDSDGDCDQVDMNCFRAGAGVVVPAPVEESPLPKTPIVEDTNAKAHRDAMALCSKNDISVSSVRDCIKS
ESAVVTAAPQKRIEVCMTCKRSGAAALMQEFERVVGVEGGAVVSCCKMGKCKTAPNVKVQNSVDHSLA
RGLDDSVNIPANPLCIGVGLGDVDAIVARFLGESHTDIGMIGATAT
>AhDGAT3-2 Diacylglycerol acyltransferase [*Arachis hypogaea*] ABW34442.1
MEVSGAVLRNVTCPSFSVHVSSRRRGDGCFTVPVVRMRKKAVVRCCCGFSDSGHVQYYGDEKKREKGTDM
LSTKKKLKMLKKRVLFDDLQGNLTSDAAAEVLMKQLEQVRAEEKELKKKRKQEKKEAKLKASKMNTNPDCE
ESSLSSESESESECDNEVDMKKNIKVGVATADSPRKAETMIYTPPLLPEDVSANHHHHNAVELFSRN
NDISVGSINGGLKNENAAVITTEAIPQKRIEVCMGNKCKKSGSIALQELERVIGAEGGAAA
VVGCKCMGKCSAPNVRIQNSTADKIAEGFNDSVKVPANPLCIGVALEDVETIVARFLGENQESTNE
>AhDGAT3-3 Soluble diacylglycerol acyltransferase [*Arachis hypogaea*]
AAx62735.1
MEVSGAVLRNVTCPSFSVHVSSRRRGDSCVTPVVRMRKKAVVRCCCGFSDSGHVQYYGDEKKKENGTM
LSTKKKLKMLKKRVLFDDLQGNLTWDAAMVLMKQLEQVRAEEKELKKKRKQEKKEAKLKASKMNTNPDCE
SSSSSSSESESESECDNEVDMKKNIKVGVAVAVADSPRKAETMILYTSLVARDVSANHHHHNAVE
LFSRNDISVGSINGGLKNENTAVITTEAIPQKRIEVCMGNKCKKSGSIALQEFERVVGAEGGAAA
VVGCKCMGKCSAPNVRIQNSTADKIAEGFNDSVKVPANPLCIGVAWRMLKPLWLRFLGENQESTNE
>CsDGAT3-1 Diacylglycerol acyltransferase 3 [*Camelina sativa*]
XP_010479249.2
MEVSGVLRQVPCVSGSVADGRYSGRLRLVSDXGXTRTVSFRARKLRGVVCNNEFADKGHVNYIIEPTRCG
EAEKVKVMEKEKKALKKKAKILKSLSKNLDMFSSIGFGLVPEAGLVGEIQTKTISEATEILVKQLEQLK
AEEKLLKKQRKEEKAKAKALKKMTMDSESSSSSESSSDSDCDKGKVDMSSLRNKAQPILEPLQPEATLV
TTLPRIQEDAQSKDTSEALQIALQTSTVFPSMANPGQTMKKVEAVPVVGLPLKRVEVCMGGKCKKLGA
VLLDEFQKAMTGFQGSVAVACKCMGKCRDGPNVVRVNETDAVMTDSVMTPSKTVCLGVGLQDVETIVTSFF
DEECSRENSVVSF
>CsDGAT3-2 Diacylglycerol acyltransferase 3 [*Camelina sativa*]
XP_010461643.1
MEVSGVLRQVPCVSGSVANGRYSGRLRLVSNFSGNTRTVSFRTRKLRGVVCNNEFAEKGHVNYIIEPTRC
GEAKDKVKVMEKEKKALKKKAKILKSLSKNLDMFSCIGFGLDPEAGLVGEVQTKTISEATEILVKQLEQL
KAEEKLLKKQRKEEKAKAKALKKMTMDSESSSSSESSSDSDCDKGKVDMSSFRNKAQPILEPLQPEATL
VTTLPRIQEDAQSFKDTSEALQIALQRTSTVFPSMANPGQTMKKVEAVPVVGLPLKRVEVCMGGKCKKLGA
AVLLDEFQKAMTGFEGSAVACKCMGKCRDGPNVVRVNETDAVMTDSVMTPSKTVCVGVGLQDVETIVTSF
FDEECSRENSVVSF
>CsDGAT3-3 Diacylglycerol acyltransferase 3 [*Camelina sativa*]
XP_010500353.1
MEVSGVLRQVPCVSGSVADGRYSGRLRLVSDISGNTRTVSFRTRKLRGVVCNNEFAEKGHVNYIIEPTRC
GEAEKEMIKVMEKEKKALKKKAKILKSLSKNLDMFSSIGFGLDPEAGLVGEIQTKTISEATEILVKQLE
QLKAEEKLLKKQRKEEKAKAKALKKMTMDSESSSSSESSSDSDCDKGKVDMSSFRNKAQPILEPLQPEA
TLTTLPKILEDQAQSFKDTSEALQIALQTSTVFPSMANPGQTLKKVDAVSVVGLPLKRVEVCMGGKCKKMG
GAVLLDEFQKAMTGFEGSAVACKCMVKCRDGPNVVRVNETVAVMTDSVMTPSKTVCVGVGLQDVETIVTS

FFDEECSENSVVSF

>AtDGAT1 Diacylglycerol acyltransferase 1 [*Arabidopsis thaliana*]
AAF19262.1

MAILDSAGVTTVTENGGGEFVDLRLRRRKSRSDSSNGLLLSGSDNNSPDDVGAPADVRDRIDSVVND
AQGTANLAGDNNNGGDNNGGGRGGGEGRGADATFTYRPSVPAHRRARESPLSSDAIFKQSHAGLFNLCV
VVLIAVNSRLIIENLMKYGWLIRTDWFSSRSLRDWPLFMCCISLSIFPLAAFTVEKLVQKYISEPVVI
FLHIIITMTEVLYPVYVTLRCDSAFLSGVTLMMLTLCIVWLKLVSYAHTSYDIRSLANAADKANPEVSYYV
SLKSLAYFMVAPTLCTYQPSYPRSAIRKGVVARQFAKLVIFTGFMGFIIIEQYINPIVRNSKHPLKGDLLY
AIERVLKLSVPNLYVWLCLMFYCFHFLWLNILAEELLCFGDREFYKDWNNAKSVGDYWRMWNMPVHKWVMVRH
IYFPCLRSKI PKTLAIIIAFLVSAVFHELCAVPCRLFKLWAFGLGIMFQVPLVFITNYLQERFGSTVGNM
IFWFIFCIFGQPMCVLLYYHDLNMRKGSMS

>AtDGAT2 Diacylglycerol acyltransferase 2 [*Arabidopsis thaliana*]
NP_566952.1

MGGSREFRAEEHSNQFHSIIAMAIWLGAIHFNVALVLCSLIFLPPSLSLMVLGLLSLFIFIPIDHRSKYG
RKLARYICKHACNYFPVSLYVEDYEAQPNRAYVFGYEPHSLVPIGVVALCDLTGFMPIPNIKVLASSAI
FYTPFLRHIWTWGLTAASRKNFTSLDSDGYSCVLVPGGVQETFMQHDENVFLSRRRGFVRIAMEQGS
PLVPVFCFGQARVYKWWKPDCLYLKLSRAIRFTPICFWGVFGSPLPCRQPMHVVGKPIEVTKTLKPTD
EEIAKFHGGYVEALRDLFERHKS RVGYDLELKIL

>AtDGAT3 Diacylglycerol acyltransferase 3 [*Arabidopsis thaliana*]
OAP16619.1

MEVSGVVLRLQIPCVSSGSVAGLRLVSEFSGNTRTVGFRTRFRGIVCNNEFADKGHVNYIEPTRCGEEK
EKVKVMEKEKKALKKKAKVLKSLSKNLDMFSSIGFGLDPEAGLVGEIQTKTISEATEILVKQLEQLKAAE
KILKKQRKEEKAKAKAMKKMTEMDSSESSSSSESSSDCDKGKVVDMSSLRNKAKPVLEPLQPEATVATLP
RIQEDAISCKNTSEALQIALQTSTIFPSMANPGQTLKTVEAVSVVGLPLNRVEVCMGGKCKKSGGALLLD
EFQRAMTGFEGSAVACKCMGKCRDGPVNRVVKETDAVMTDSVRTPSKTL CVGVGLQDVETIVTSFFDEEC
SREGLGSFSY

>TmDGAT1 Putative diacylglycerol acyltransferase [*Tropaeolum majus*]
AAM03340.2

MVAESSQNTTTMSGHGSDLNFRRRKPPSSSVIEPSSSGFTSTNGVPATGHVAENRDQDRVGAMENATG
SVNLIGNGGGVIGNEEKQVGETDIRFTYRPSFPAHRRVRESPLSSDAIFKQSHAGLFNLCIVVLIAVNS
RLIIENLMKYGWLIDTGFWFSSRSLGDWSIFMCCLTLPIFPLAAFIVEKLVQRNHI SELVAVLLHVIVST
AAVLYPVIVILTCDSDVYMSGVVLMLFGCIMWLKLVSYAHTSSDIRTLAKSGYKGDHPNSTIVSCSYDVS
LKSLAYFMVAPTLCTYQPSYPRSSCIRKGVVVRQFVKLVIFGLMGFIIEQYINPIVRNSKHPLKGDFLYA
IERVLKLSVPNLYVWLCLMFYSFFHLWLNILAEELRFGDREFYKDWNNAKTVAEYWKMMWNMPVHRWMVRHL
YFPCLRNGIPKEGAIIIAFLVSGAFHELCAVPCHVFKLWAFIGIMFQVPLVLITNYLQEKFSNSMVGNM
IFWFIFCILGQPMCVLLYYHDLINLKEK

>JrDGAT3 Diacylglycerol O-acyltransferase 3 [*Juglans regia*]
XP_018840223.2

MEASGFSFRRIPLSGAKADTRSSKPSISCVSVGSRKLRVLGFQQSRARVRPRKAYGAMNMIMNSGFCDN
GHKRYYYVSPMCSGKKEKEKEKSVNSCSSLTAKKKLKLFKGLAEDLAKFSDMGFGLDAYDGLAADVQQA
IADAVEVLMSQLQHLRAAEELKKRRKQENAKLKDRQMNIMLDCESSSSSSSESSDSECEDVIDMSFLRSEP
LTQATLPVLDEVQLVSQENVTTTLTLP SRLTQEGSAVLSDGLGDLKSENEVERCTGIGTSSSSNSFGHNDR
CSSVTGSSAKRIEVCMMGGKCKKSGAATLLEEFQKVTGVEGAVVGCKCLGKCRDGPVNRILNSVDGSEAEG
ADVSVRSPNLPLCIGVGLDDVGIVAKFFGDEPKDSGLAAASLQNFL

>PfDGAT1 Diacylglycerol acyltransferase [*Perilla frutescens*] AAG23696.1

MAILDSPEILDTTSSADNGAAHHTTLRRRQSARSVPPLDSDSNSLEAESAINDSENVNRNDANLIENLR
GGAVESENEKQESYKKEEGAKVKENGETSNGNGTDVMAVKFTFRPAAPAHRRKNKESPLSSDAIFKQSHAG
LFNLCIVVLVAVNSRLIIENLMKYGWLKSGFWFSSTSLRDWPLLMCCLSLPVFALASFLVEKLVKLNII
PEWVAVFLHVTITTVEILFPVVILRCDSAVLSGVTLMMLFACTVWLKLVSYAHTNYDLRVLAKSLDKWEA
MSRYWNLDYAYDVSFKSLAYFMVAPTLCTYQPSYPRACIRKGVVVRQLIKLVIFTGLMGFIIEQYINPIV
QNSQHPLKGNLLYAIERVLKLSVPNLYVWLCLMFYCFHFLWLNILAEELLCFGDREFYKDWNNARTVEEYWR
MWNMPVHKWVMVRHIYCPCLQNGIPKIVAVLIAFLVSAIFHELCAVPCQIFKFWAFSGIMLQVPLVIVTN
YLQEKFKNSMVGNMMFWCFFCIFGQPMCVLLYYHDLNMRKASAR

>SaDGAT1 O-acyltransferase [*Striga asiatica*] GER56917.1

MAILESPESLDTTSSAENGHRDHATTTLRRRPSARSVEPLLESDSSSLDGETAVNDGERYQSDANSAK
LCGGAIESNEEREAAATGSEGFTCGKGEAEKVKEGDGKGVDA LAVKFAYRPSAPAHRRIKESPLSSDAIFK
QSHAGLFNLCIVVLVAVNGRLIIENLMKYGWLKAGFWFSSKSLRDWPLFIVSLPVFPLAAFLVEKLVKQ

KYIHEWVAVFLHVVITTTTEILYPVVVILRCDSAVLSGVTLMFLACIVWLKLVSYAHTNYDLRVLAKSLDK
WEALSSYWNMDYSYDISFKSLVYFIVAPTLCYQPSYPTSCIRKGWVVRQLIKLVIFTGFMGFIVEQYIN
PIVQNSQHPLKGNLLYAVERVLKLSVPNLYVWLCMLNILAELLRFGDREFYKDWNNARTVEEPVHKWMMVR
HIYFPCLRNGIPKVVAVLIAFLVSAIFHEL CIAVPCHMFKLWAFIGQLVATVKRELF CGVKLVGNMMFW
CFFCIVGQPMCVELLYYHDLNMRKASAR

>ShDGAT2 Diacylglycerol acyltransferase 2 [*Salvia hispanica*] AXN76729.1
MSSESNGDVRRRRSPSSEAESDAPPTAAEFKGTGRGSLMNSIIAIVLWLGSVHLIVSIVLASFFFLPFPKS
LGGIVLLFVFMVIPINERSRWGRNLARYICKHAVGYFPVALHVENIKAFDPNEAYVFGYEPHSVWPIGVI
AIADLTGFMPLPKIKVLASSAVFYTPFMRHLWTWLGLSAATRKNFTALLSSGYSCIIIPGGVQEACYPEH
GSEVAFQLSRKGFVRIAIETGKPLVPVFCFGQTDVYKWWRPGGKLFREFSRAIKFTPIVFWGVLGSPLPF
RQPLHVVGEPILVKKNSQPTKEEVMEVHARFVEALQDLFQRHKARVGH PDLQLRIL

>HiDGAT2 Acyl-CoA:diacylglycerol acyltransferase [*Handroanthus
impetiginosus*] PIN08318.1

MAAEANGDVKQRKSPSEAAEPPTPAEFKGTQGPLLHTILALVLWLGSVHLNFLVVLFAFVFLPFPKALG
VIGLLLI F MVIPIDERSKWGRRLSRYICKHAVGYFPVTLYVEDIKAFDPNEAYVFGYEPHSVWPIGVVAL
ADLTGFMPLPRIKVLASTAVFYTPFLRHVWSWLGLSPATRENFSSLLTSGYSCIIIPGGVQEALYMEKGS
EVAFIQKRRGFVRIAMETGKPLVPVFSFGQSDVYRWWKPRGKLYREFSRAIKFAPIIFWGVLGSPLPLRH
PMHVVVGRPIMLKKNPQPTAEVVAEVHAQFIEALKDLFERHKERVGYGDLHLRIL