Supplemental Figure S1. Sequence Comparisons Between AtGPAT9 and Other Plant and Mammalian Proteins.

The amino acid sequence of AtGPAT9 was aligned and compared individually to that of mouse GPAT3 (A), AtLPEAT1 (B), and AtLPEAT2 (C), and AtGPAT7 (D) using the ClustalX algorithm (Thompson et al., 1997). Identical amino acid residues are marked with asterisks, highly similar residues with two dots, and similar residues with one dot.

(A) mouse GPAT3

CLUSTAL X (1.81) multiple sequence alignment

AtGPAT9 mGPAT3	MSSTAGRLVTSKSELDLDHPNIEDYLPSG MEGADLAVKLLSTWLTLVGGLILLPSAFGLSLGISEIYMKILVKTLEWATLRIQKGAPKE :. : : . *: . *: . *.
AtGPAT9 mGPAT3	SSINEPRGKLSLRDLLDISPTLTEAAGAIVDDSFTRCFKSNP SALKNSASVGIIQRDESPMEKGLSGLRGRDFELSDVFYFSKKGLEAIVEDEVTQRFSSEE *:::: :* .** :* *: .:. ***:**: *.*:
AtGPAT9 mGPAT3	PEPWNWNIYLFPLYCFGVVVRYCILFPLRCFTLAFGWIIFLSLFIPVNA LVSWNLLTRTNVNFQYISPRLTMVWVLGVLVRYCFLLPLR-VTLAFIGISLLIIGTTLVG .** *: * :: :**:****:*:*** .**** * :* : .: .
AtGPAT9 mGPAT3	LLKGQDRLRKKIERVLVEMICSFFVASWTGVVKYHGPRPSIRPKQVYVANHTSMIDFIVL QLP-DSSLKNWLSELVHLTCCRICVRSLSGTIHYHNKQYRPQKGGICVANHTSPIDVLIL * :. *:: ::: * : * : * : : : : : ****** **.::*
AtGPAT9 mGPAT3	EQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRSEAKDREIVAKKLRDHVQGADSNPL ATDGCYAMVGQVHGGLMGIIQRAMVKACPHVWFERSEIKDRHLVTKRLKEHIADKKKLPI .:*:: * * * :*::* ::::: :*:*:**********
AtGPAT9 mGPAT3	LIFPEGTCVNNNYTVMFKKGAFELDCTVCPIAIKYNKIFVDAFWNSRKQSFTMHLLQLMT LIFPEGTCINNTSVMMFKKGSFEIGGTIYPVAIKYNPQFGDAFWNSSKYNLVSYLLRIMT ************************************
AtGPAT9 mGPAT3	SWAVVCEVWYLEPQTIRPGETGIEFAERVRDMISLRAGLKKVPWDGYLKYSRPSPKHSER SWAIVCDVWYMPPMTREEGEDAVQFANRVKSAIAVQGGLTELPWDGGLKRAKVKDTFKEE ***:**:**: * * . ** .::**:**: *:::***** ** ::*.
AtGPAT9 mGPAT3	KQQSFAESILARLEEK QQKNYSKMIVGNGSPNLARD :*:.::: *:

136 residues identical (based on 376 aa in AtGPAT9: 36% identical)
90 residues highly similar (60% identical + highly similar)
44 residues similar (72% identical + similar)

(B) AtLPEAT1

CLUSTAL X (1.81) multiple sequence alignment

AtGPAT9 AtLPEAT1	MSSTAGRLVTSKSELDLDHPNIEDYLPSGSSINEPRGKLSLRDLLDISPTLTEAAGAI MESELKDLNSNSNPPSSKEDRPLLKSESDLAAAIEELDKKFAPYARTDLYGTMGLGPFPM *.* *: *:*:*:* *:: *: *: *: *: *:
AtGPAT9 AtLPEAT1	VDDS-FTRCFKSNPPEPWNWNIYLFPLYCFGVVVRYCILFPLRCFTLAFGWIIFLSLF TENIKLAVALVTLVPLRFLLSMSILLLYYLICRVFTLFSAPYRGPEEEEDEGGVVFQEDY .:: :: .: * : .: **: * : * : * * : * * : *
AtGPAT9 AtLPEAT1	IPVNALLK-GQDRLRKKIERVLVEMICSFFVASWTGVVKYHGPRP AHMEGWKRTVIVRSGRFLSRVLLFVFGFYWIHESCPDRDSDMDSNPKTTSTEINQKGEAA ::. : * : :.**: :: ::: .
AtGPAT9 AtLPEAT1	SIRPKQVYVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRSE TEEPERPGAIVSNHVSYLDILYHMSASFPSFVAKRSVGKLPLVG-LISKCLGCVYVQREA : .*:: . *:**.* :*:: . : ::: * : *: * : ::*:
AtGPAT9 AtLPEAT1	-AKDREIVAKKLRDHVQGADSNPLLIFPEGTCVNNNYTVMFKKGAFELDCTVCPIA KSPDFKGVSGTVNERVREAHSNKSAPTIMLFPEGTTTNGDYLLTFKTGAFLAGTPVLPVI : * : *: .:.::*: *.** .:::***** .*.:* : **.**** *:
AtGPAT9 AtLPEAT1	IKYNKIFVDAFWNSRKQSFTMHLLQLMTSWAVVCEVWYLEPQTIRPGETGIEFAERVR LKYPYERFSVAWDTISGARHILFLLCQVVNHLEVIRLPVYYPSQEEKDDPKLYASNVR :** *:: . : : : * *:: *: * .* : :***
AtGPAT9 AtLPEAT1	DMISLRAGLKKVPWDGYLKYSRPSPKHSERKQQSFAESILARLEEK KLMATEGNLILSELGLSDKRIYHATLNGNLSQTRDFHQKEE- .:::* . * *: : : : : **
71 residues i 93 residues h 51 residues s	dentical (19% identical) ighly similar (44% identical + highly similar) imilar (57% identical + similar)

(C) AtLPEAT2

CLUSTAL X (1.81) multiple sequence alignment

Atgpat9	MSSTAGRLVTSKSELDLDHPNIEDYLPSGSSINEPRGKLSLRDLLDI
AtlpEAT2	MADPDLSSPLIHHQSSDQPEVVISIADDDDDESGLN-LLPAVVDPRVSRGFEFDHLNP ** .:* * :: * *:: **:** * *:
AtgPAT9	SPTLTEAAGAIVDDSFTRCFKSNPPEPWNWNIYLFPLYCFGVVVRYCILFPLRCFTLAFG
AtlPEAT2	YGFLSESEPPVLGPTTVDPFRNNTPGVSGLYEAIKLVICLPIALIRLVLFAASLAVG *:*: .::. : . *:.*.* . : : *: :.: :**. :**.*
AtGPAT9	WIIFLSLFIPVNALLKGQDRLRKKIERVLVEMICSFFVASWTGVVKYHGPRPSIRPKQVY
AtlPEAT2	YLATKLALAGWKDKENPMPLWRCRIMWITRICTRCILFSFGYQWIRRKGKPARREIAPIV :: : : : * :* : .:.: :: :* : ::
AtgPAT9	VANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRSEAKDREIVAKK
AtlPEAT2	VSNHVSYIEPIFYFYELSPTIVASESHDSLPFVG-TIIRAMQVIYVNRFSQTSRKNAVHE *:**.* *: *. : ::: : : : **:.:: *:.***:::
AtGPAT9	LRDHVQGADSNPLLIFPEGTCVNNNYTVMFKKGAFELDCTVCPIAIKYNKIFVDAFWN
AtlPEAT2	IKRKASCDRFPRLLLFPEGTTTNGKVLISFQLGAFIPGYPIQPVVVRYPHVHFDQSWGNI :: : **:***** .*.: : *: ***: *:.::* ::* *.
AtGPAT9	SRKQSFTMHLLQLMTSWAVVCEVWYLEP
AtlPEAT2	SLLTLMFRMFTQFHNFMEVEYLPVIYPSEKQKQNAVRLSQKTSHAIATSLNVVQTSHSFA *.**. *. ** *:: ::.
AtGPAT9	QTIRPGETG
Atlpeat2	DLMLLNKATELKLENPSNYMVEMARVESLFHVSSLEATRFLDTFVSMIPDSSGRVRLHDF :: *:*
Atgpat9	IEFAERVRDMISLRAGLKKVPWDG
AtlPEAT2	LRGLKLKPCPLSKRIFEFIDVEKVGSITFKQFLFASGHVLTQPLFKQTCELAFSHCDADG :::*: ::*: ::*:: ::*:
AtGPAT9	QQSFAESILARLEEK
AtlPEAT2	DGYITIQELGEALKNTIPNLNKDEIRGMYHLLDDDQDQRISQNDLLSCLRRNPLLIAIFA
Atgpat9	
AtlPEAT2	PDLAPT

74 residues identical (20% identical)
89 residues highly similar (43% identical + highly similar)
58 residues similar (59% identical + similar)

(D) AtGPAT7

CLUSTAL X (1.81) multiple sequence alignment

AtGPAT9 AtGPAT7	MSSTAGRLVTSKSELDLDHPNIEDYLPSGSSINEPRGKLSLRDLLDISPTLTE MESSTTTSYSVVSELEGTLLKNPKPFAYFMLVAFEASGLIRFATLLFLWPIIALLDVLGY *.*:: : ***: *.:*: *:*.: * * :: : .*
AtGPAT9 AtGPAT7	AAGAIVDDSFTRCFKSNPPEPWNWNIYLFPLYCFGVVVRYCILRNGSLKLMIFVATAGLHESEIESVARAVLPKFFMDDISMDAWRAFGSCDKRVVVTRMPRV*.: :::: :: *: : :* :***
AtGPAT9 AtGPAT7	FPLRCFTLAFGWIIFLSLFIPVNALLKGQDRLRKK-IERVLVEMICSFFVASWTGV MVERFAKDHLSADEVIGTEIVVNRFGYATGLIQETNVDQSVFNSVANLFVDRRPQLGLGR : * . :. :. * ** : . :::: ::: :.: :.:** . :
AtGPAT9 AtGPAT7	HTSMIDFIVLEQ HIISDSPTFLSLCEEQVHAPVPSNYNGHNQRLHVQPLPVIFHDGRLVKLPTPATALIILL : *.* ** ::: * .: ::: :::
AtGPAT9 AtGPAT7	MTAFAVIMQKHPGWVG-LLQSTILESVGCIWFNRSEAKORE WIPFGIILAMIRIFVGFLLPLWAIPYVSRIFNTRFIVKGKPPAQATTGNPGVLFVCTHRT .*.:*: :** ** : *. *: .* .*
AtGPAT9 AtGPAT7	IVAKKLRDHVQGADSNPLLIF LMDPVVLSYVLGRSIPAVTYSISRLSEILSPIPTFRLTRIRDVDAEMIKKELSNGDLVVY :: ::**
AtGPAT9 AtGPAT7	PEGTCVNNNYTVMFKKGAFELDCTVCPIAIKYNKIFVDAFWNSRKQSFTMHLLQLMTS PEGTTCREPFLLRFSALFAELTDNIVPVAMNYRVGFFHATTARGWKGLDPIFFFMNPRPV **** .: : : *. ** .: *:*::*. ** : . :.::: .
AtGPAT9 AtGPAT7	WAVVCEVWYLEPQTIRPGETGIEFAERVRDMISLRAGLKKVPWDGYLKYSRPSPKHSERK YEVTFLNQLEVEATCSSGKSPYDVANYVQRILAATLGFECTNFTRKDKYRVLAGNDGTVS : *. * .*: :.*: *: ::: *:: .: *** : :
AtGPAT9 AtGPAT7	QQSFAESILARLEEK YLSFLDQVKKVVTTFKPFLH ** :.: :
68 residues 85 residues 54 residues	identical (18% identical) highly similar (41% identical + highly similar) similar (55% identical + similar)

Supplemental Figure S2. Sequence Comparison of Selected GPAT9 Enzymes from Plants.

Amino acid sequences from Aquilegia coerulea, Arabidopsis thaliana, Brachypodium distachyon, Cucumis sativus, Gossypium raimondii, Physcomitrella patens, Salix purpurea, Selaginella moellendorffii, and Solanum tuberosum were aligned using the ClustalX algorithm as described in Figure S1 above. Amino acids identical in all ten proteins are shaded in black, similar residues are shaded in grey. Name abbreviations indicate the first letter of the genus, and the first two letters of the species.

GraGPAT9B	GraGPAT9A	1	
SyuGPAT9 MDTPG-NIKKTSISELDDRPN E. TPSGTSIGEPDKK SIRAL StuGPAT9 MDTPG-NIKKTSISELDDRPN E. TPSGTSIGEPDKK SIRAL AthGPAT9 MSTAG-RLVKSSSELDPRN E. TPSGSSIREPDKK RIRDI AthGPAT9 MSGAA-LLKSSSSELDDRPN E. TPSGSSIREPDKK RIRDI AcoGPAT9 MSGAA-LLKSSASELDIDRPN E. TPDSLEQEPTAK RIRDI AcoGPAT9 MSGAA-LLKSSASELDIDRPN E. TPDSLEQEPTAK RIRDI SmoGPAT9 MGIQRTGVKDSNQLRDSSLFRF9QSEVDLYQHD E. TLDSAAEPAAPHQNK LIC DI SmoGPAT9 MGIQRTGVKDSNQLRDSSLFRF9QSEVDLYQHD E. TLDSAAEPAAPHQNK LIC DI SpuGPAT9 MGGQFKGSADGINAGEAGRGICNEV A. TUNTVEEDSSEAYLDNK CHRDI SpuGPAT9 4 DISPTL EA GAT DDSFTRCFKSNPPEPNNNN YL PL CC GVVIRVLLI E PUVLVL StuGPAT9 4 DISPTL EA GAT DDSFTRCFKSNPPEPNNNN YL PL CC GVVIRVLLI E PUVLVL StuGPAT9 4 DISPTL EA GAT DDSFTRCFKSNPPEPNNNN YL PL CC GVVIRVLLI E PUVLVL AthGPAT9 4 DISPTL EA GAT DDSFTRCFKSNPPEPNNNN YL PL CC GVVIRVLL PLAVLUL AcoGPAT9 4 DISPTL EA GAT DDSFTRCFKSNPPEPNNNN YL PL CC GVVIRVLL PLAVLUL AcoGPAT9 3 DISPTL FA GAT DDSFTRCFKSNPPEPNNNN YL PL CC GVVIRVLL PLAVLUL BdGRAT9 3 DISPTL FA GAT DDSFTRCFKSNPPEPNNNN YL PL CC GVVIRVLL PLAVLUL BdGRAT9 3 <td>GraGPAT9B</td> <td>1</td> <td></td>	GraGPAT9B	1	
Studeration International and the student of the s	SpuGPAT9	1	
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ALIGHTY Image: Construction of the state of the st	A+hCPAT9	1	
Gradphip International Display in the set of solid of the set of	CeaCPAT9	1	
ACCGATS 1 ACCGATS 1 SmoGPAT9 1 MGIQRTGVKDSNQLRDSSLFRPSQSEVDLYQHD EDILDSAAEPAAPHQNK GraGPAT9 1 GraGPAT9 1 GraGPAT9 1 GraGPAT9 4 LDISPTLEAA GAIVDDSFTRCFKSNFPEEPWNWN YUFPL.CCGVVTRYLLUERMRALVL SpuGPAT9 4 LDISPTLEAA GAIVDDSFTRCFKSNFPEEPWNWN YUFPL.CCGVVTRYLLUERMRALVL SpuGPAT9 4 LDISPTLEAA GAIVDDSFTRCFKSNFPEEPWNWN YUFPL.CCGVVTRYLLUERMRALVL StuGPAT9 4 LDISPTLEAA GAIVDDSFTRCFKSNFPEEPWNWN YUFPL.CCGVVTRYLLEERWRVLVL StuGPAT9 4 LDISPTLEAA GAIVDDSFTRCFKSNFPEEPWNWN YUFPL.CGVVRYCLUERCFTRURVLL StuGPAT9 4 LDISPTLEAA GAIVDDSFTRCFKSNFPEEPWNWN YUFPL.CFGVVRYCLUERCFTRURVLL ActopAT9 3 LDISPTLEAA SugPaT9 3 LDISPTLEAA GAIVDSFTRCFKSNFPEEPWNWN YUFPL.CFGVVRYCLUERCFTRURVLL PARVLIL PaGPAT9 3 LDISPTLEAA GAIVDSFTRCFKSNFPEEPWNWN YUFPL.CFGVVRYCLUERCFTRURVLL PARVLIL PaGPAT9 105 TICWUFFLS		1	
BUISTATS INSTRUMENT TRANSFERENCES DE DE LESAREPARHONC LEOR PpaGPAT9 INSTRUMENT DE LEOR INSTRUMENT DE LEOR GraGPAT98 4 LDISPATIERA GAIN DDSETRECEKSNEPEEMNNN VIEPLICEGVVFRVLI LEPKRALVI GraGPAT98 46 LDISPATIERA GAIN DDSETRECEKSNEPEEMNNN VIEPLICEGVVFRVLI LEPKRALVI SpuGPAT9 44 LDISPATIERA GAIN DDSETRECEKSNEPEEMNNN VIEPLICEGVVFRVLI LEPKRALVI SpuGPAT9 44 LDISPATIERA GAIN DDSETRECEKSNEPEEMNNN VIEPLICEGVVFRVLI LEPKRALVI CsaGPAT9 44 LDISPATIERA GAIN DDSETRECEKSNEPEEMNNN VIEPLICEGVVRYGILLETERVIL AcogPAT9 44 LDISPATIERA GAIN DDSETRECEKSNEPEEMNNN VIEPLICEGVVRYGILLETERVIL AcoGPAT9 44 LDISPATIERA GAIN DDSETRECEKSNEPEEMNNN VIEPLICEGVVRYGILLETERVIL AcoGPAT9 34 LDISPATIERA GAIN DDSETRECEKSNEPEEMNNN VIEPLICEGVVRYGILLETERVILL AcoGPAT9 34 LDISPATIERA GAIN DDSETRECEKSNEPEEMNNN VIEPLICEGVVRYGILLETERVILL BdIGPAT9 34 LDISPATIERA GAIN DDSETRECEKSNEPEEMNNN VIEPLICEGVVRYGILLETERVILL BdIGPAT9 34 LDISPATIERA GAIN DDSETRECEKSNEPEEMNNN VIEPLICEGVVRYGING KYHGPRESKEPK SmGPAT9 34 LDISPATIERA GAIN DDSETRECEKSNEPEEMNNN VIEPLICEGVVRYGING KYHGPRESKEPK SmGPAT9 35 LDISQVISEA SAIN DDSETRECEKSNAPEEPENNNN VIEPLICEGVVRYGING KYHGP	RCOGFAIJ Rdicpama	1	
SINGSPAT9 1 MSIGNIO NODAGINASSITUTIONE DISALTANT - GNA HAUDE PpaGPAT9 1	SmoCPAT9	1	
GraGPAT9 1 GraGPAT9A 45 LDISPAL EA GAI DDSFTRCFKSNPEEPNNWN YLFEL CCGVVFRYLILEFWRVLVI SpuGPAT9 SpuGPAT9 44 LDISPTL EA GAI DDSFTRCFKSNPEEPNNWN YLFEL CCGVVRYGILEFWRVLVI StuGPAT9 SpuGPAT9 44 LDISPTL EA GAI DDSFTRCFKSNPEEPNNWN YLFEL CCGVVRYGILEFWRVLVI StuGPAT9 AthGPAT9 45 LDISPTL EA GAI DDSFTRCFKSNPEEPNNWN YLFEL CGVVRYGILEFLRVI AthGPAT9 AthGPAT9 45 LDISPTL EA GAI DDSFTRCFKSNPEEPNNWN YLFEL CGVVRYGILFERRVI AthGPAT9 SuGGPAT9 44 LDISPTL EA GAI DDSFTRCFKSNPEEPNNWN YLFEL CGVVRYGILFERRVI AcoGPAT9 30 LDISPL EA GAI DDSFTRCFKSNPEPENNWN YLFEL CGVVRYGILFERRVIL SmoGPAT9 1015PL EA GAI DDSFTRCFKSNPEPENNWN YLFEL CGVVRYGILFERRVIL ERVIL SmoGPAT9 54 LDISQVL EA SAI DDSFTRCFKSNPEPENNWN YLFEL CGVVRYGILFERRVIL ERVIL SmoGPAT9 54 LDISQVL EA SAI DDSFTRCFKSNPEPENNWN YLFEL CGVVRYGIN HERVRVL SmoGPAT9 105 SVEVANTELSC TPHELL GNDNLRKK ERAVEN CSFVASWTGV KYHGPRSMPK StuGPAT9 104 105 TISWIFLSC TPHELL GNDNLRKK ERAVEN CSFVASWTGV KYH	DracDADO	1	
GraGPAT9A 45 LDISPALTEA.GAT.DDSFTRCFKSNPEEPWNWN.YLFPL.CCGVVFRYLIL EMRALVL GraGPAT9B 46 LDISPTLTEA.GAT.DDSFTRCFKSNPEEPWNWN.YLFPL.CCGVVFRYLIL EMRALVL SpuGPAT9 44 LDISPTLTEA.GAT.DDSFTRCFKSNPEEPWNWN.YLFPL.CCGVVFRYGIL ENVLVL StuGPAT9 40 LDISPTLTEA.GAT.DDSFTRCFKSNPEEPWNWN.YLFPL.CCGVVFRYGIL ENVLVL AthGPAT9 40 LDISPTLTEA.GAT.DDSFTRCFKSNPEEPWNWN.YLFPL.CCGVVFRYGIL ENVLVL AthGPAT9 45 LDISPTLTEA.GAT.DDSFTRCFKSNPEEPWNWN.YLFPL.CCGVVFRYGIL ENVLVL AcoGPAT9 44 LDISPTLTEA.GAT.DDSFTRCFKSNPEEPWNWN.YLFPL.CCGVVFRYGIL ENVLVL AcoGPAT9 40 LDISPLTEA.GAT.DDSFTRCFKSNPEEPWNWN.YLFPL.CCGVVFRYGIL ENVLVL Bargerand 45 LDISPLTEA.GAT.DDSFTRCFKSNPEEPWNWN.YLFPL.CCGVVFRYGIL ENVLVL AcoGPAT9 30 LDISPLTEA.GAT.DDSFTRCFKSNPEEPWNWN.YLFPL.CGVVFRYGIL ENVLVL Bargerand 30 LDISPLTEA.GAT.DDSFTRCFKSNPEEPWNWN.YLFPL.CGVVFRYGIL ENVLVL Bargerand 30 LDISPLTEA.GAT.DDSFTRCFKSNPEEPWNWN.YLFPL.CGVVFRYGIL ENVLVL Bargerand 30 LDISPLTEA.GAT.DDSFTRCFKSNPEEPWNWN.YLFPL.CGVVFRYGIL ENVLVL SmoGPAT9 30 LDISPLTEA.GAT.DDSFTRCFKSNPEEPWNWN.YLFPL.CGVVFRYGIL ENVLVL SmoGPAT9 104 STGWTFRACKSAT.DFLECOMPARANTYLEPU.CGVVFRYGIL ENVLVL <t< td=""><td>PPAGPATS</td><td>T</td><td>MEGDQFKGSADGINAGEAGKGICNEVVADEBNINVEEDSSEAILDNKMQERDI</td></t<>	PPAGPATS	T	MEGDQFKGSADGINAGEAGKGICNEVVADEBNINVEEDSSEAILDNKMQERDI
GraGPAT9A 45 LDISPALTEALGAT DDSFTRCEKSNPPEPUNNNVILFPL CCGVVFRULLE EMRALVE GraGPAT9B GraGPAT9B 46 LDISPTTTEALGAT VDSFTRCEKSNPPEPUNNNVILFPL CCGVVFRULLE EVRVIVU SpuGPAT9 44 LDISPTTTEALGAT VDSFTRCEKSNPPEPUNNNVILFPL CCGVVFRULLE EVRVIVU AthCPAT9 45 510GPAT9 44 LDISPTTTEALGAT VDSFTRCEKSNPPEPUNNNVILFPL CCGVVFRUELE ELRCFTL CsaGPAT9 44 LDISPTTEALGAT VDSFTRCEKSNPPEPUNNNVILFPL CCGVVFRUELE ELRCFTL CsaGPAT9 44 LDISPTTEALGAT VDSFTRCEKSNPPEPUNNNVILFPL CCGVVFRUELE ELRCFTL CsaGPAT9 45 LDISPTTEALGAT VDSFTRCEKSNPPEPUNNNVILFPL CCGVVFRUELE ELRCFTL CsaGPAT9 46 LDISPTTEALGAT VDSFTRCEKSNPPEPUNNNVILFPL CCGVVFRUELE ELRCFTL SacGPAT9 30 LDISPTTEALGAT VDSFTRCEKSNPPEPUNNNVILFPL CCGVVFRUELE ELRCFTL SacGPAT9 59 LDISGVI EALGAT VDSFTRCEKSNPPEPUNNNVILFPL CCGVVRYGLL ELRVILT SmoGPAT9 59 LDISQVI EALGAT VDSFTRCEKSNPPEPUNNN VILFPL CCGVVRYGLL ELRVILT SmoGPAT9 105 TIGWI ELSC IP HELL GNDNLRKK ERALVEL CSFFVASWTGV KYHGERPSMPK SpuGPAT9 106 TVGWI ELSC IP HELL GNDNLRKK ERALVEL CSFFVASWTGV KYHGERPSMPK SpuGPAT9 106 TIGWI ELSC IP HELL GNDKLRKK ERALVEL CSFFVASWTGV KYHGERPSMPK SpuGPAT9 106 TIGWI ELSC IP HELL GNDKLRKK ERALVEL CSFFVASWTGV KYHGERPSMPK SpuGPAT9 106			
GradPAT9B 46 LDISPTL IPAGAT / DDSFTRCEKSNPPEPNNNNYYIFPL/CCGVVIRYLLE PVRVIVL SpuGPAT9 44 LDISPTL IPAGAT / DDSFTRCEKSNPPEPNNNNYYIFPL/CCGVVIRYGIL PVRVIVL StuGPAT9 44 LDISPTL IPAGAT / DDSFTRCEKSNPPEPNNNNYYIFPL/CCGVVIRYGIL PVRVIVL AthGPAT9 45 LDISPTL IPAGAT / DDSFTRCEKSNPPEPNNNNYYIFPL/CGVVIRYGIL PVRVIVL AthGPAT9 44 LDISPTL IPAGAT / DDSFTRCEKSNPPEPNNNNYYIFPL/CGVVIRYCIL PVRVIVL BdiGPAT9 30 LDISPTL IPAGAT / DDSFTRCEKSNPPEPNNNNYYIFPL/CGVVIRYCIL PVRVIVL BdiGPAT9 30 LDISPL IPAGAT / DDSFTRCEKSNPPEPNNNNYYIFPL/CGVVIRYCIL PVRVIVL BdiGPAT9 31 LDISOVL PAGAT / DDSFTRCEKSNPPEPNNNNYYIFPL/CGVVIRYCIL PVRVIVL SmoGPAT9 59 LDISOVL PAGAT / DDSFTRCEKSNPPEPNNNNYYIFPL/CGVVIRYCIL PVRVIVL SmoGPAT9 59 LDISOVL PAGAT / DDSFTRCEKSNPPEPNNNNYYIFPL/CGVVIRYCIL PVRVIVL SmoGPAT9 54 LDISOVL PAGAT / DDSFTRCEKSNPPEPNNNYYIFPL/CGVVIRYCIL PVRVIVL SmoGPAT9 104 LGNIFLSCTIP/HFLL/GDNDLRKK/ DRALVELICSFVASWTGV/KYHGPRSPMPRK SnucpAtt 105 TIGWIFLSCTIP/HFLL/GDNDLRKK/ DRALVELICSFVASWTGV/KYHGPRSPMPRK StuGPAT9 104 TGWIFLSSTIP/HLL/GDNDLRKK/ DRALVELICSFVASWTGV/KYHGPRSPMPRK StuGPAT9 104 TGWIFLSSTIP/HFL/GDNDK/RK/ DRALVER/VENCSFVASWTGV/	GraGPAT9A	45	LDISPALTEAAGAIVDDSFTRCFKSNPPEPWNWNVYLFPLWCCGVVFRYLILFPMRALVI
SpuGPAT944LDISPTLIEA GAT VDSFTRCFKSNPEPEWNNN YTFPL/CCGVVIRVGIL EVRVLVLStuGPAT940LDISPTLIEA GAT VDSFTRCFKSNPEPEWNNN YTFPL/CCGVVIRVGIL PIRVIVLAthGPAT945LDISPTLIEA GAT VDSFTRCFKSNPEPEWNNN YTFPL/CCGVVIRVGIL PIRVIVLAthGPAT945LDISPTLIEA GAT VDSFTRCFKSNPEPEWNNN YTFPL/CCGVVIRVGIL PIRVIVLAcoGPAT930LDISPLIEA GAT VDSFTRCFKSNPEPEWNNN YTFPL/CCGVVIRVGIL PIRVILLAcoGPAT930LDISPLIEA GAT VDSFTRCFKSNPEPEWNNN YTFPL/CGGVVRYGL PIRVLILSmoGPAT933LDISGVLEA GAT VDSFTRCFKSNPEPEWNNN YTFPL/CGGVVRYGL PIRVLILSmoGPAT954LDISQVLEA SAIT DDSFTRCFKSNPEPEWNNN YTFPL/CGGVVRYGL PIRVLILPpaGPAT954LDISQVLEA SAIT DDSFTRCFKSNPEPEWNNN YTFPL/CGGVVRYGL PIRVLILGraGPAT9A105TIGNIELSC IP HFLL GNDNLRKK BRALVELICSFFVASWTGV KYHGPRSMPKSpuGPAT9104AIGWIELSS IP HLL GHDKLRKK BRALVELICSFFVASWTGV KYHGPRSMPKSpuGPAT9104AIGWIELSS IP HLL GHDKLRKK BRALVELICSFFVASWTGV KYHGPRSFEPKAthGPAT9105TIGNIELSC IP HLL GHDKLRKK BRALVELICSFFVASWTGV KYHGPRSFEPKStuGPAT9104AIGWIELSS IP HLL GHDKLRKK BRALVELICSFFVASWTGV KYHGPRSFEPKStuGPAT9104TIGNIELSS IP HLL GHDKLRKK BRALVELICSFFVASWTGV KYHGPRSFEPKAthGPAT9105TIGNIELSS IP HLL GUDKRRK, BRALVELICSFFVASWTGV KYHGPRSFEPKAthGPAT9104TIGNIELSS IP HLL GUDKRRK, BRALVELICSFFVASWTGV KYHGPRSFEPKAthGPAT9104TIGNIELSS IP HLL GUDKRRK, BRALVELICSFFVASWTGV KYHGPRSFEPKAthGPAT9105TIGNIELSS IP HLL GUDKRRK, BRALVELICSFFVASWTGV KYHGPRSFEPKAthGPAT9105TIGNIELSS IA HFL G	GraGPAT9B	46	LDISPTLTEAAGAIVDDSFTRCFKSNPPEPWNWNVYLFPLWCCGVVIRYLILFPVRVIVI
StuGPAT9 40 LDISPTLTEALGAIT DDSFTRCFKSNPPEPWNWN YLFPL, CLGVVVRYGTLFPLRVIT AthGPAT9 45 LDISPTLTEALGAI VDDSFTRCFKSNPPEPWNWN YLFPL, CLGVVVRYGTLFPLRVIT CsaGPAT9 44 LDISPTLTEALGAI VDDSFTRCFKSNPPEPWNWN YLFPL, CGGVVVRYGTLFPLRVIT AcoGPAT9 30 LDISPTLTEALGAI VDDSFTRCFKSNPPEPWNWN YLFPL, CGGVVVRYGTLFPLRVITL BdiGPAT9 33 LDISPVLTEALGAI VDDSFTRCFKSNPEPWNWN YLFPL, CGVVVRYGTLFPLRVITL SmoGPAT9 59 LDISGVLSEALSAI VDDSFTRCFKSNPEPWNWN YLFPL, CGVVVRYGTLFPLRVITL SmoGPAT9 54 LDISQVLSEALSAI VDDSFTRCFKSNPEPWNWN YLFPL, CGVVVRYGTLFPRVRULL PpaGPAT9 54 LDISQVLSEALSAI VDDSFTRCFKSNPEPWNWN YLFPL, CGVVVRYCTLFPRVRULL SmoGPAT9 59 LDISQVLSEALSAI VDDSFTRCFKSNPEPWNWN YLFPL, CGVVVRYCTLFPRVRULL SmoGPAT9 105 TTGWITELSCTPVHFLLGGNDNLRKKVERALVEL CSFFVASWTGV KYHGPRPSMRPK SpuGPAT9 104 AIGWITELSCTPVHFLLGGNDNLRKKVERALVEL CSFFVASWTGV KYHGPRPSMRPK StuGPAT9 104 AIGWITELSCTPVHFLLGGNDRKRKVERALVEL CSFFVASWTGV KYHGPRPSMRPK StuGPAT9 105 AFGWITELSCTPVHFLLGGNDRKRKVERCLVEL CSFFVASWTGV KYHGPRPSTRPK AthGPAT9 105 AFGWITELSCTPVNLLGGNDRKRKVERCLVEL CSFFVASWTGV KYHGPRPSTRPK StuGPAT9 104 TIGWITELSCTPVNLLGGNDRKKKERCLVEL CSFFVASWTGV KYHGPRPST	SpuGPAT9	44	LDISPTLTEAAGAIVDDSFTRCFKSNPPEPWNWNVYLFPLWCCGVVIRYGILFPVRVLVI
AthGPAT9 45 LDISPTLTEALGAIVDSFTRCFKSNPPEPWNWN YLFPLYCGGVVVRYCILFPLRCFI CsaGPAT9 44 LDISPTLTEALGAIVDSFTRCFKSNPPEPWNWN YLFPLYCGGVVVRYCILFPLRVLIL AcoGPAT9 30 LDISPTLTEALGAIVDDSFTRCFKSNPPEPWNWN YLFPLYCGGVVRYGLIFPLRVLIL BdiGPAT9 31 LDISPVLTEALGAIVDDSFTRCFKSNPPEPWNWN YLFPLYCGGVVRYGLIFPLRVLIL SmoGPAT9 59 LDISQVLSEALSAIVDDSFTRCFKSNPPEPWNWN YLFPLYCGGVVRYGLIFPLRVLIL PpaGPAT9 54 LDISQVLSEALSAIVDDSFTRCFKSNPEPEWNWN YLFPLYCGGVVRYGLIFPLRVLL GraGPAT98 106 TVGWITELSCTIPVHLLLKGHDKLQKN/BEALVELICSFFVASWTGVVKYHGPRPSMRPK SpuGPAT9 104 AIGWITELSCTIPVHLLLKGHDKLQKN/BEALVELICSFFVASWTGVVKYHGPRPSMRPK StuGPAT9 104 AIGWITELSCTIPVHLLLKGHDKRKKIERSLVPVTCMFVASWTGVVKYHGPRPSMRPK StuGPAT9 104 TIGWITELSCTIPVHLLLKGHDKRKKIERSLVPVTCMFVASWTGVVKYHGPRPSMRPK StuGPAT9 104 TIGWITELSCTIPVHLLKGDNKRRQVERVLECLICSFVASWTGVVKYHGPRPSMRPK StuGPAT9 104 TIGWITELSCTIPVHLLKGDNKKRRQVERVLECLICSFVASWTGVVKYHGPRPSMRPK StuGPAT9 104 TIGWITELSCTIPVHLLKGDNKKRRQVERVLECLICSFVASWTGVVKYHGPRPSMRPK StuGPAT9 104 TIGWITELSCTIPVHLLKGDNKKRRQVERVLECLICSFVASWTGVVKYHGPRPSMRPK SaGPAT9 104 TIGWITELSCTIPVNLLKGDNKKRKERLERKLVEN CSFVASWTGVVKYHGP	StuGPAT9	40	LDISPTLTEAAGAIIDDSFTRCFKSNPPEPWNWNIYLFPLWCLGVVVRYGILFPIRVIVI
CSaGPAT9 44 LDIS PTLIEAR GAIVDDSFTRCFKSNPPEPWNWN YLFPL/CCGVVIRYLFI PARVLIL AcoGPAT9 30 LDIS PALTEAR GAIVDDSFTRCFKSNPPEPWNWN YLFPL/CFGVVIRYGILYPWRVLVL BdiGPAT9 33 LDIS PVLTEAR GAIVDDSFTRCFKSNPPEPWNWN YLFPL/CFGVVVRYGLLPURVLVL SmoGPAT9 59 LDIS GVLSEAR SAIVDDSFTRCFKSNSPEPWNWN YLFPL/CFGVVRYGLLPURVLL PpaGPAT9 54 LDIS OVLSEAR SAIVDDSFTRCFKSNAPEPWNWN YLFPL/VMGVAVRYLILPURVLL GraGPAT98 105 TIGWIFLSC IPVHFLLKGNDNLRKKNERALVEL CSFFVASWTGV KYHGPRPSMRPK GraGPAT98 106 TVGWIFLSC IPVHFLLKGNDNLRKKNERALVEL CSFFVASWTGV KYHGPRPSMRPK SpuGPAT9 104 TIGWIFLSC IPVHLLKGNDKLRKKIERALVEL CSFFVASWTGV KYHGPRPSMRPK SpuGPAT9 104 TIGWIFLSC IPVHLLKGNDKKRKIER SFVASWTGV KYHGPRPSMRPK StuGPAT9 104 TIGWIFLSC IPVHLLKGNDKKRENEVUVM CSFFVASWTGV KYHGPRPSIRPK StuGPAT9 104 TIGWIFLSC IPVHLLKGNDKKRENEVUVM CSFFVASWTGV KYHGPRPSIRPK StuGPAT9 104 TIGWIFLSS IPVNLLKGDDKKRENEVUVM CSFFVASWTGV KYHGPRPSIRPK StuGPAT9 104 TIGWIFLSS IPVNLLKGDKKRENEVEN CSFFVASWTGV KYHGPRPSIRPK StuGPAT9 104 TIGWIFLSS IPVNLLKGDKKRENEVEN CSFFVASWTGV KYHGPRPSIRPK StuGPAT9 104 TIGWIFLSS IPVNLLKGDKKRENEVEN CSFFVASWTGV KYHGPRPSRPR PK </td <td>AthGPAT9</td> <td>45</td> <td>LDISPTLTEAAGAIVDDSFTRCFKSNPPEPWNWNIYLFPLYCFGVVVRYCILFPLRCFTI</td>	AthGPAT9	45	LDISPTLTEAAGAIVDDSFTRCFKSNPPEPWNWNIYLFPLYCFGVVVRYCILFPLRCFTI
AcoGPAT9 30 LDIS PALIEAA GAIL DDSFTRCFKSN PEPEWNWN YLFPLACFGVVIRYGLI PURVLVL BdiGPAT9 33 LDIS PVLTEAA GAIV DDSFTRCFKSN SPEPWNWN YLFPLACFGVVVRYGLI PURVLLI SmoGPAT9 59 LDIS GVLSEAA SAIV DDSFTRCFKSN SPEPWNWN YLFPLACFGVVVRYGLI PURVLLI PpaGPAT9 54 LDIS QVLSEAA SAIV DDSFTRCFKSN SPEPWNWN YLFPLACGVVRYGLI PURVLLI GraGPAT9A 105 TIGWIFLSC IPVHFLI KGNDNLRKKMERALVEL GSFFVASWTGV KYHGPRPSMRPK SpuGPAT9 104 AIGWIFLSC IPVHLLI KGNDNLRKKMERALVEL GSFFVASWTGV KYHGPRPSMRPK SpuGPAT9 104 AIGWIFLSC IPVHLLI KGNDKLRKKMERALVEL GSFFVASWTGV KYHGPRPSRPK StuGPAT9 104 AIGWIFLSC IPVHLLI KGNDKLRKK ERALVEL GSFFVASWTGV KYHGPRPSRPK StuGPAT9 104 AIGWIFLSC IPVHLLI KGNDKLRKK ERALVEL GSFFVASWTGV KYHGPRPSRPK StuGPAT9 104 TIGWIFLSC IPVHLLI KGNDKLRKK ERALVEM GSFVASWTGV KYHGPRPSRPK StuGPAT9 104 TIGWIFLSC IPVHLLI KGNDKWRK ERALVEM GSFVASWTGV KYHGPRPSRPK CsaGPAT9 104 TIGWIFLSC IPVHLLI KGNDKWRKQMERYLVEL GSFVASWTGV KYHGPRPSRPK StuGPAT9 104 TIGWIFLSC IPVHLLI KGNDKWRKQMERYLVEL GSFVASWTGV KYHGPRPSRPK StuGPAT9 104 TIGWIFLSC IPVHLLI KGNDKWRKQMERYLVEL GSFVASWTGV KYHGPRPSRPK BdiGPAT9 3 GLGMVFFAAF FPVHFIL KGNDKWRKQMERYLVEL GSFVASWT	CsaGPAT9	44	LDISPTLTEAAGAIVDDSFTRCFKSNPPEPWNWNIYLFPLWCCGVVIRYLFLFPARVLII
BdiGPAT9 33 LDISPULTEAGGAL VDDSFTRCFKSNSPEPWNWN YLFPLWCFGVVRYGLLFPLRVLTL SmoGPAT9 59 LDISGVLSEAASAI VDDSFTRCFKSNIPEPWNWN YLLPLWCLGVIRYCILFPRVLLL PpaGPAT9 54 LDISQVLSEAGSAI DDSFTRCFKSNAPEPWNWN YLFPLWVMGVAVRYLILFPTRVLL GraGPAT9A 105 TIGWI FLSCFIP HFLLKGNDNLRKKMERALVELICSFFVASWTGV KYHGPRPSMRPK GraGPAT9B 106 TVGWI FLSCFIP HFLLKGNDNLRKKMERALVELICSFFVASWTGV KYHGPRPSMRPK SpugPAT9 104 AIGWI FLSCFIP HLLLKGHDKLQKNMERALVELICSFFVASWTGV KYHGPRPSMRPK SpugPAT9 104 AIGWI FLSCFIP HLLLKGHDKLRKK ERSLVEVI CMFFVASWTGV KYHGPRPS RPK StuGPAT9 100 TIGWI FLSCFIP HLLKGHDKLRKK ERSLVEVI CMFFVASWTGV KYHGPRPS IRPK StuGPAT9 100 TIGWI FLSCFIP HLLKGHDKRKK ERSLVEVI CMFFVASWTGV KYHGPRPS IRPK ScaGPAT9 100 TIGWI FLSSFIP HNLLKGHDKRKK ERSLVEVI CSFFVASWTGV KYHGPRPS IRPK AcoGPAT9 104 TIGWI FLSSFTA HFLKGDDKWRRQMERYLVELICSFFVASWTGV KYHGPRPSRPS BdiGPAT9 93 GLGWMVFFAAFFV HFLKGDNKWRRQMERYLVELICSFFVASWTGV KYHGPRPSRPSRPR PpaGPAT9 114 ALGWI FLSSFTA HFLKGDNKWRRQMERYLVELICSFFVASWTGV KYHGPRPSRPSRPR SmoGPAT9 105 TVGWI FLGAFIP HFLKGNDKWRRQUERYLVELICSFFVASWTGV KYHGPRPSRPRR SmoGPAT9 114 ALGWI FLSSFT IP HFLKKDHMRK ERGLVEFICSVFVAS	AcoGPAT9	30	LDISPALTEAAGAIIDDSFTRCFKSNPPEPWNWNVYLFPLWCFGVVIRYGILYPVRVLVI
SmoGPAT9 59 LDISGVLSEAASALVDDSFTRCFKSNIPEPWNWNTYLLPLWCLGVIVRYCILFPVRVLLL PpaGPAT9 54 LDISQVLSEACSALDDSFTRCFKSNAPEPWNWNTYLFPLWVMGVAVRYLLLFPIRVILL GraGPAT9A 105 TIGWITFLSCTIPVHFLKGNDNLRKKMERALVELTCSFFVASWTGVKYHGPRPSMRPK GraGPAT9B 106 TVGWITFLSCTIPVHLLKGHDKLQKNMERALVELTCSFFVASWTGVKYHGPRPSMRPK SpuGPAT9 104 AIGWITFLSCTIPVHLLKGHDKLQKNMERALVELTCSFFVASWTGVKYHGPRPSMRPK SpuGPAT9 104 AIGWITFLSCTIPVHLLKGHDKLRKKTERSLVEVICHFVASWTGVKYHGPRPSMRPK StuGPAT9 100 TIGWITFLSCTIPVHLLKGHDKLRKKTERSLVEVICHFVASWTGVKYHGPRPSIRPK AthGPAT9 100 TIGWITFLSCTIPVHLLKGHDKRKKTERSLVEVICHTCSFFVASWTGVKYHGPRPSIRPK AthGPAT9 100 TIGWITFLSCTIPVHLLKGUDRLKKTERSLVEVICHTCSFFVASWTGVKYHGPRPSIRPK AcoGPAT9 100 TIGWITFLSCTIPVHLLKGUDRLRKKTERSLVEMTCSFFVASWTGVKYHGPRPSIRPK AchGPAT9 104 TIGWITFLSCTIPVHLKGUDRLRKKTERSLVEMTCSFFVASWTGVKYHGPRPSIRPK AchGPAT9 104 TIGWITFLSCTIPVHFLKGUDRLRKKTERSLVEMTCSFFVASWTGVKYHGPRPSIRPK AchGPAT9 104 TIGWITFLSCTIPVHFLKGUDRLRKKTERSLVELTCSFFVASWTGVKYHGPRPSIRPK SaGPAT9 104 TIGWITFLSCTIPVHFLKGUDRLRKKTERSLVELTCSFFVASWTGVKYHGPRPSIRPK BdiGPAT9 13 GLGWAVFAAFAYFNUKTKGUDRLKGURRNERALVELVELTCSFFVASWTGVKYHGPRPSIRPK <td>BdiGPAT9</td> <td>33</td> <td>LDISPVLTEAAGAIVDDSFTRCFKSNSPEPWNWNIYLFPLWCFGVVVRYGLLFPLRVLTI</td>	BdiGPAT9	33	LDISPVLTEAAGAIVDDSFTRCFKSNSPEPWNWNIYLFPLWCFGVVVRYGLLFPLRVLTI
PpaGPAT954LDISOVESACSAT DDSFTRCFKSNAPEPWNWN YEFPL VMGVAVRYLLEFETRVILLGraGPAT9A105TIGWI FESC IP VHFLKGDDNLRKKMERALVELT SFFVASWTGV KYHGPRPSMRPKGraGPAT9B106TVGWI FESC IP VHLLKGDDKLRKK ERSLVPY CMFFVASWTGV KYHGPRPSMRPKSpuGPAT9104AIGWI FESS IP HELKGDDKLRKK ERSLVPY CMFFVASWTGV KYHGPRPSMRPKStuGPAT9100TIGWI FESS IP VHLLKGDDKLRKK ERSLVPY CMFFVASWTGV KYHGPRPSRPKStuGPAT9100TIGWI FESS IP VHLLKGDDKLRKK ERSLVPY CMFFVASWTGV KYHGPRPSIRPKAthGPAT9105AFGWI FESE IP VHLLKGDDKLRKK ERSLVPY CMFFVASWTGV KYHGPRPSIRPKCsaGPAT9104TIGWI FEST IP NLLKGDDKLRKK ERSLVPM CSFFVASWTGV KYHGPRPSIRPKAcoGPAT990TIGWI FEST IP NLLKGDDKLRKK ERSLVEM CSFFVASWTGV KYHGPRPSRRPKBdiGPAT993GLGWNVFFAA FP VHFLKGDNKLRSK ERSLVEM CSVFVASWTGV KYHGPRPSRRPKBdiGPAT9114ALGWI FEGA IP VHFLKNHDQLRRQ ERGLVFF CSVFVASWTGV KYHGPRPSRRPRPpaGPAT9114ALGWI FESE FP HFALKNHDQLRRQ ERGLVFF CSVFVASWTGV KYHGPRPSRRPRSpuGPAT9164QVFVANHTSMIDF I LEQM AFAVIMQKHPGWVGL CSTILES GCIWFNRS AKDREIVSpuGPAT9164QVFVANHTSMIDF I LEQM AFAVIMQKHPGWVGL CSTILES GCIWFNRS AKDREIVStuGPAT9164QVFVANHTSMIDF I LEQM AFAVIMQKHPGWVGL CSTILES GCIWFNRS AKDREIVCsaGPAT9164QVFVANHTSMIDF I LEQM AFAVIMQKHPGWVGL CSTILES GCIWFNRS AKDREIVCsaGPAT9164QVFVANHTSMIDF I LEQM AFAVIMQKHPGWVGL CSTILES GCIWFNRS AKDREIVCsaGPAT9164QVFVANHTSMIDF I LEQM AFAVIMQKHPGWVGL CSTILES GCIWFNRT AKDREIVCsaGPAT9164QVFVANHTSMIDF I LEQM AFAVIMQKHPGWVGL CSTILES GCIWFNRT AKDREIV	SmoGPAT9	59	LDISGVLSEAASAIVDDSFTRCFKSNIPEPWNWNIYLLPLWCLGVIVRYCILFPVRVLLI
GraGPAT9A 105 TIGWI ELSC IPVHFLKGNDNLRKK ERALVELICSFFVASWTGV KYHGPRPSMRPK GraGPAT9B 106 TVGWI ELSC IPVHLLKGHDKLQKN ERALVELICSFFVASWTGV NYHGPRPSMRPK SpuGPAT9 104 AIGWI ELSC IPVHLLKGHDKLQKN ERALVELICSFFVASWTGV KYHGPRPSMRPK StuGPAT9 100 TIGWI ELSC IPVHLLKGHDKLRKK ERSLVEVICMFFVASWTGV KYHGPRPSMRPK AthGPAT9 100 TIGWI ELSC IPVHLLKGHDKLRKK ERSLVEVICMFFVASWTGV KYHGPRPSIRPK AthGPAT9 100 TIGWI ELSC IPVHLLKGHDKLRKK ERSLVEVICM CSFFVASWTGV KYHGPRPSIRPK CsaGPAT9 104 TIGWI ELST IPVNLLKGDKLRKK ERSLVEVICG SFFVASWTGV KYHGPRPSIRPK CsaGPAT9 104 TIGWI ELSS TAVHFLKGDKWRRQ ERYLVELICSFFVASWTGV KYHGPRPSIRPK AcoGPAT9 90 TIGWI ELSS TAVHFLKGDKWRRQ ERYLVELICSFFVASWTGV KYHGPRPSIRPK BdiGPAT9 3 GLGWMVFFAAFFPVHFLKGDNKWRRQ ERYLVELICSFFVASWTGV KYHGPRPSRRPK BdiGPAT9 119 TVGWI ELGAF IPVHFLKGDNKWRRQ ERYLVELICSFFVASWTGV KYHGPRPSRRPK SmoGPAT9 119 TVGWI ELGAF IPVHFLKGDNKWRRQ ERYLVELICSFFVASWTGV KYHGPRPSRRPK SmoGPAT9 119 TVGWI ELGAF IPVHFLKGDNKRK ERKLVEM CSVFVASWTGV KYHGPRPSRRPK SmoGPAT9 114 ALGWI FEAFFP HFAL NHDQLRRQ ERGLVEF CSVFVASWTGV KYHGPRPSRRFK SmoGPAT9 166 QVFVANHTSMI DF I LEQM SEAVEQKHPGWGL CST LESVGCIWENST	PpaGPAT9	54	LDISQVLSEACSAIIDDSFTRCFKSNAPEPWNWNIYLFPLWVMGVAVRYLILFPIRVILI
GraGPAT9A105TIGWI FLSCFIPVHFLLKGNDNLRKK ERALVELICSFFVASWTGV KYHGPRPSMRPKGraGPAT9B106TVGWI FLSCFIPVHLLKGHDKLQKN ERALVELICSFFVASWTGV NYHGPRPSMRPKSpuGPAT9104AIGWI FLSCFIPVHLLKGHDKLRKK ERSLVEVI CMFFVASWTGV KYHGPRPSRPKStuGPAT9100TIGWI FLSCYIPVHLLKGHDKFRKK ERCLVELICSFFVASWTGV KYHGPRPSIRPKAthGPAT9105AFGWI FLSCYIPVHLLKGHDKFRKK ERCLVELICSFFVASWTGV KYHGPRPSIRPKCsaGPAT9104TIGWI FLSCYIPVHLLKGDRKRRK ERFLVELICSFFVASWTGV KYHGPRPSIRPKCsaGPAT9104TIGWI FLSST IPVNLLKGDRKRRQ ERYLVELICSFFVASWTGV KYHGPRPSIRPKAcoGPAT990TIGWI FLSST TAVHFLKGDNKMRRQ ERYLVELICSFFVASWTGV KYHGPRPSRPKBdiGPAT993GLGWMVFFAA FPVHFLKGDNKRRQ ERYLVELICSFFVASWTGV KYHGPRPSRPKBdiGPAT993GLGWMVFFAA FPVHFLKGDNKRRQ ERYLVELICSFFVASWTGV KYHGPRPSRPKPpaGPAT9114ALGWI FLSLFFPLHFALKNHDQLRRQ ERYLVELICSVFVASWTGV KYHGPRPSRRPRPpaGPAT9114ALGWI FLSLFFPLHFALKNHDQLRRQ ERGLVEFMCSVFVASWTGV KYHGPRPSRRFKGraGPAT9A165QVFVANHTSMIDFI LEQM AFAVIMQKHPGWVGLLQST LESVGCIWFNR AKDREIVSpuGPAT9164QVFVANHTSMIDFI VLEQM AFAVIMQKHPGWVGLLQST LESVGCIWFNR AKDREIVSugPAT9160QVFVANHTSMIDFI VLEQM AFAVIMQKHPGWVGLLQST LESVGCIWFNR AKDREIVSaGPAT9164QVFVANHTSMIDFI VLEQM AFAVIMQKHPGWVGLLQST LESVGCIWFNR AKDREIVSaGPAT9164QVFVANHTSMIDFI VLEQM AFAVIMQKHPGWVGLLQST LESVGCIWFNR AKDREIVAcoGPAT9160QVFVANHTSMIDFI VLEQM AFAVIMQKHPGWVGLLQST LESVGCIWFNR AKDREIVSaGPAT9164QVFVANHTSMIDFI VLEQM AFAVIMQKHPGWVGLLQST LESVGCIWFNR AKDREIVCsGPAT9			
GraGPAT9B106TVGWI IFLSCF IPVHLLLKGHDKLQKN ERALVELTCSF FVASWTGVINYHGPRPSMRPKSpuGPAT9104AIGWI IFLSSY IPVHLLKGHDKLRKK ERSLVEV I CMF FVASWTGVVKYHGPRPSRPKStuGPAT9100TIGWI IFLSCY IPVHLLKGHDKFRKK ERCLVELTCSF FVASWTGVVKYHGPRPSIRPKAthGPAT9105AFGWI IFLSL IPVNALKGQDRLRKK ERVLVEM CSF FVASWTGVVKYHGPRPSIRPKCsaGPAT9104TIGWI IFLST IPVNLLKGPKLRAK ERFLVELTCSF FVASWTGVVKYHGPRPSIRPKAcoGPAT990TIGWI IFLST IPVNLLKGPKLRAK ERFLVELTCSF FVASWTGVVKYHGPRPSIRPKAcoGPAT990TIGWI IFLST IPVNLLKGPKLRAK ERFLVELTCSF FVASWTGVVKYHGPRPSIRPKBdiGPAT993GLGWNVFFAAFPP HFLKGQNKLRSK ERKLVEM CSVFVASWTGVVKYHGPRPSSRPYSmoGPAT9119TVGWI IFLGAF IPVHFIL KHDHMRRK ERGLVEF CSVFVASWTGVVKYHGPRPSRPRPpaGPAT9114ALGWI IFLSL FP HFALKNHDQLRRQ ERGLVEF CSVFVASWTGVVKYHGPRPSRRTKGraGPAT9A165QVFVANHTSMIDF I LEQM AFAVIMQKHPGWVGLI QST ILESVGCIWFNRSE AKDRE IVSpuGPAT9164QVFVANHTSMIDF I VEQM AFAVIMQKHPGWVGLI QST ILESVGCIWFNRSE AKDRE IVSpuGPAT9164QVFVANHTSMIDF I VEQM AFAVIMQKHPGWVGLI QST ILESVGCIWFNRSE AKDRE IVStuGPAT9160QVFVANHTSMIDF I VEQM AFAVIMQKHPGWVGLI QST ILESVGCIWFNRSE AKDRE IVStuGPAT9164QVFVANHTSMIDF I VEQM AFAVIMQKHPGWVGLI QST ILESVGCIWFNRSE AKDRE IVAthGPAT9165QVFVANHTSMIDF I VEQM AFAVIMQKHPGWVGLI QST ILESVGCIWFNRSE AKDRE IVAthGPAT9164QVFVANHTSMIDF I VEQM AFAVIMQKHPGWVGLI QST ILESVGCIWFNRTE AKDRE IVAcoGPAT9164QVFVANHTSMIDF I VEQM AFAVIMQKHPGWVGLI QST ILESVGCIWFNRTE AKDRE IVAcoGPAT9164QVFVANHTSMIDF I VEQM AFAVI	GraGPAT9A	105	TIGWIIFLSCFIPVHFLLKGNDNLRKKMERALVELICSFFVASWTGVVKYHGPRPSMRPF
SpuGPAT9104AIGWI IFLSS IP VHLLE KGHDKLRKK ERSLVEVI CMFFVASWTGV KYHGPRPSRRPKStuGPAT9100TIGWI FLSC IP VHLLE KGHDKFRKK ERCLVEL CSFFVASWTGV KYHGPRPSIRPKAthGPAT9105AFGWI FLSL IP VNALK GQDRLRKK ERVLVEM CSFFVASWTGV KYHGPRPSIRPKCsaGPAT9104TIGWI FLST IP VNLL KGPKLRAK ERFLVEL CSFFVASWTGV KYHGPRPSIRPKAcoGPAT990TIGWI FLSS TAVHFLK GDKWRRQ ERYLVEL CSFFVASWTGV KYHGPRPSIRPKAcoGPAT990TIGWI FLSS TAVHFLK GDKWRRQ ERYLVEL CSFFVASWTGV KYHGPRPSIRPKBdiGPAT993GLGWAV FFAA FP VHFLK GDKKRRQ ERYLVEL CSFFVASWTGV KYHGPRPSRPRBdiGPAT993GLGWAV FFAA FP VHFLK GDNKLRSK ERKLVEM CSVFVASWTGV KYHGPRPSRPRPpaGPAT9114ALGWI FLSL FP HFAL KNHDQLRRQ ERGLVEF CSVFVASWTGV KYHGPRPSRPRPpaGPAT9114ALGWI FLSL FP HFAL KNHDQLRRQ ERGLVEF CSVFVASWTGV KYHGPRPSRRPRPpaGPAT9166QV FVANHTSMIDF I LEQM AFAVIMQKHPGWVGL OSTI LESVGCIWFNRS AKDREIVSpuGPAT9164QV FVANHTSMIDF I LEQM AFAVIMQKHPGWVGL OSTI LESVGCIWFNRS AKDREIVSpuGPAT9164QV FVANHTSMIDF I LEQM AFAVIMQKHPGWVGL OSTI LESVGCIWFNRS AKDREIVSpuGPAT9164QV FVANHTSMIDF I LEQM AFAVIMQKHPGWVGL OSTI LESVGCIWFNRS AKDREIVStuGPAT9165QV FVANHTSMIDF I LEQM AFAVIMQKHPGWVGL OSTI LESVGCIWFNRS AKDREIVSaGPAT9164QV FVANHTSMIDF I LEQM AFAVIMQKHPGWVGL OSTI LESVGCIWFNRS AKDREIVCsaGPAT9164QV FVANHTSMIDF I LEQM AFAVIMQKHPGWVGL OSTI LESVGCIWFNRS AKDREIVCsaGPAT9164QV FVANHTSMIDF I LEQM AFAVIMQKHPGWVGL OSTI LESVGCIWFNRT KKDREIVAcoGPAT9164QV FVANHTSMIDF I LEQM AFAVIMQKHPGWVGL OSTI LESVGC	GraGPAT9B	106	TVGWIIFLSCFIPVHLLLKGHDKLOKNMERALVELICSFFVASWTGVINYHGPRPSMRPF
StuGPAT9100TIGWIIFLSCYIPVHLLLKGHDKFRKKIERCLVELICSFFVASWTGVKKYHGPRPSIRPKAthGPAT9105AFGWIIFLSLFIPVNALLKGQDRLRKKIERVLVEMICSFFVASWTGVKYHGPRPSIRPKCsaGPAT9104TIGWIIFLSTFIPVNLLKGPKLRAKIERFLVELICSFFVASWTGVKYHGPRPSIRPKAcoGPAT990TIGWIIFLSTFIPVNLLKGDKWRQMERYLVELICSFFVASWTGVKYHGPRPSIRPKBdiGPAT993GLGWMVFFAAFFPVHFLKGDKKRSKIERKLVEMCSVFVASWTGVKYHGPRPSRPSSmoGPAT9119TVGWIIFLGAFIPVHFILFKHDHMRRKIERGLVEFICSVFVASWTGVKYHGPRPSRRPRPpaGPAT9114ALGWIIFLSLFFPHFALKNHDQLRRQIERGLVEFICSVFVASWTGVKYHGPRPSRRPRSpuGPAT9166QVFVANHTSMIDFITLEQMIAFAVIMQKHPGWVGLIQSTILESVGCIWFNRSPARDRERVSpuGPAT9164QVFVANHTSMIDFITLEQMIAFAVIMQKHPGWVGLIQSTILESVGCIWFNRSPARDRERVStuGPAT9160QVFVANHTSMIDFITLEQMIAFAVIMQKHPGWVGLIQSTILESVGCIWFNRSPARDRERVStuGPAT9164QVFVANHTSMIDFITLEQMIAFAVIMQKHPGWVGLIQSTILESVGCIWFNRSPARDREIVStuGPAT9165QVFVANHTSMIDFITLEQMIAFAVIMQKHPGWVGLIQSTILESVGCIWFNRSPARDREIVStuGPAT9164QVFVANHTSMIDFITLEQMIAFAVIMQKHPGWVGLIQSTILESVGCIWFNRSPARDREIVAthGPAT9165QVFVANHTSMIDFITLEQMIAFAVIMQKHPGWVGLIQSTILESVGCIWFNRSPARDREIVCsaGPAT9164QVFVANHTSMIDFITLEQMIAFAVIMQKHPGWVGLIQSTILESVGCIWFNRSPARDREIVCsaGPAT9164QVFVANHTSMIDFITLEQMIAFAVIMQKHPGWVGLIQSTILESVGCIWFNRSPARDREIVCsaGPAT9164QVFVANHTSMIDFITLEQMIAFAVIMQKHPGWVGLIQSTILESVGCIWFNRSPARDREIVCsaGPAT9164QVFVANHTSMIDFITLEQMIAFAVIMQKHPGWVGLIQSTILESVGCIWFNRSPARDREIVCsaGPAT9165QVFVANHTSMIDFITLEQMIAFAVIMQKHPGWVGLIQSTILESVGCIWFNRSPARDREIVCsaGPAT9 <t< td=""><td>SpuGPAT9</td><td>104</td><td>AIGWIIFLSSYIPVHLLLKGHDKLRKKIERSLVEVICMFFVASWTGVVKYHGPRPSRRPF</td></t<>	SpuGPAT9	104	AIGWIIFLSSYIPVHLLLKGHDKLRKKIERSLVEVICMFFVASWTGVVKYHGPRPSRRPF
AthGPAT9105AFGWI IELSLEIPVNALLKGQDRLRKKTERVLVEMTCSFFVASWTGVVKYHGPRPSIRPKCsaGPAT9104TIGWI IELST IPVNLLKGHPKLRAKLERFLVELTCSFFVASWTGVVKYHGPRPSIRPKAcoGPAT990TIGWI IELSS TAVHFLKGNDKWRQMERYLVELTCSFFVASWTGVVKYHGPRPSMRPKBdiGPAT993GLGWMVFFAAFPVHFLKGQNKLRSKTERKLVEMVCSVFVASWTGVVKYHGPRPSRPRSmoGPAT9119TVGWI IELGAFIPVHFLKGQNKLRSKTERKLVEMVCSVFVASWTGVVKYHGPRPSRPRPpaGPAT9114ALGWI IELSLFPLHFALKNHDQLRRQIERGLVEFVCSVFVASWTGVVKYHGPRPSRPRSmoGPAT9165QVFVANHTSMIDFI ILEQMTAFAVIMQKHPGWVGLI QST ILESVGCIWFNRSFAKDREIVGraGPAT98166QVFVANHTSMIDFI ILEQMSSFAVIMQKHPGWVGLI QST ILESVGCIWFNRSFAKDREIVSpuGPAT9164QVFVANHTSMIDFI VLEQMTAFAVIMQKHPGWVGLI QST ILESVGCIWFNRSFAKDREIVStuGPAT9160QVFVANHTSMIDFI VLEQMTAFAVIMQKHPGWVGLI QST ILESVGCIWFNRSFAKDREIVAthGPAT9165QVFVANHTSMIDFI VLEQMTAFAVIMQKHPGWVGLI QST ILESVGCIWFNRSFAKDREIVCsaGPAT9164QVFVANHTSMIDFI VLEQMTAFAVIMQKHPGWVGLI QST ILESVGCIWFNRSFAKDREIVCsaGPAT9164QVFVANHTSMIDFI VLEQMTAFAVIMQKHPGWVGLI QST ILESVGCIWFNRSFAKDREIVCsaGPAT9164QVFVANHTSMIDFI VLEQMTAFAVIMQKHPGWVGLI QST ILESVGCIWFNRSFAKDREIVCsaGPAT9164QVFVANHTSMIDFI VLEQMTAFAVIMQKHPGWVGLI QST ILESVGCIWFNRTFAKDREIVCsaGPAT9164QVFVANHTSMIDFI VLEQMTAFAVIMQKHPGWVGLI QST ILESVGCIWFNRTFAKDREIVCsaGPAT9164QVFVANHTSMIDFI VLEQMTAFAVIMQKHPGWVGLI QST ILESVGCIWFNRTFAKDREIVCsaGPAT9150QVFVANHTSMIDFI VLEQMTAFAVIMQKHPGWVGLI QST ILESVGCIWFNRTFAKDREIVCsaGPAT9150QVFVANHTSMIDFI VLEQMTAFAVIMQKHPGWVGLI QST ILE	stuGPAT9	100	TIGWITELSCYIPVHLLLKGHDKERKKIERCLVELICSEFVASWTGVVKYHGPRPSIRP
CsaGPAT9104TIGWIIFLSTFIPVNLLKGHPKLRAKIERFLVELICSFFVASWTGVVKYHGPRPSIRPKAcoGPAT990TIGWIIFLSSFTAVHFLLKGNDKWRRQMERYLVELICSFFVASWTGVVKYHGPRPSMRPKBdiGPAT993GLGWMVFFAAFFPVHFLLKGQNKLRSKTERKLVEMCSVFVASWTGVVKYHGPRPSRPSSmoGPAT9119TVGWIIFLGAFIPVHFILKKDHMRRKTERGLVEFICSVFVASWTGVVKYHGPRPSRPRPpaGPAT9114ALGWIIFLSLFFPHFALKNHDQLRRQTERGLVEFMCSVFVASWTGVVKYHGPRPSRPRSmoGPAT9165QVFVANHTSMIDFIILEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRSEAKDREIVGraGPAT98166QVFVANHTSMIDFIILEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRSEAKDREIVSpuGPAT9164QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRSEAKDREIVStuGPAT9164QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRSEAKDREIVStuGPAT9164QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRSEAKDREIVStuGPAT9164QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRSEAKDREIVStuGPAT9164QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRSEAKDREIVStuGPAT9164QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRSEAKDREIVAthGPAT9165QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRSEAKDREIVAthGPAT9164QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRTELKDREIVAcoGPAT9150QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRTEAKDREIVBdiGPAT9153QVFVANHTSMIDFILEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRTEAKDREIVBdiGPAT9153QVFVANHTSMIDFILEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRDLKDREVV	AthGPAT9	105	AFGWLIFLSLFIPVNALLKGODRLRKKIERVLVEMICSFFVASWTGVVKYHGPRPSIRP
AcoGPAT990TIGWI IFLSSFTAVHFLLKGNDKWRRQMERYLVEL I CSFFVASWTGVVKYHGPRPSMRPKBdiGPAT993GLGWMVFFAAFFPVHFLLKGQNKLRSK IERKLVEMMCSVFVASWTGVKYHGPRPSRPYSmoGPAT9119TVGWI IFLGAF IPVHFILRKHDHMRRK IERGLVEF I CSVFVASWTGVKYHGPRPSRPRPpaGPAT9114ALGWI IFLSLFFPLHFALKNHDQLRRQ IERGLVEFMCSVFVASWTGVKYHGPRPSRPRGraGPAT9A165QVFVANHTSMIDF I LEQMTAFAVIMQKHPGWVGLI QSTILES VGCIWFNRSEAKDREIVGraGPAT9B166QVFVANHTSMIDF I LEQMTAFAVIMQKHPGWVGLI QSTILES VGCIWFNRSEAKDREIVSpuGPAT9164QVFVANHTSMIDF I VLEQMTAFAVIMQKHPGWVGLI QSTILES VGCIWFNRSEAKDREIVStuGPAT9160QVFVANHTSMIDF I VLEQMTAFAVIMQKHPGWVGLI QSTILES VGCIWFNRSEAKDREIVStuGPAT9164QVFVANHTSMIDF I VLEQMTAFAVIMQKHPGWVGLI QSTILES VGCIWFNRSEAKDREIVStuGPAT9164QVFVANHTSMIDF I VLEQMTAFAVIMQKHPGWVGLI QSTILES VGCIWFNRSEAKDREIVStuGPAT9165QVFVANHTSMIDF I VLEQMTAFAVIMQKHPGWVGLI QSTILES VGCIWFNRSEAKDREIVStuGPAT9164QVFVANHTSMIDF I VLEQMTAFAVIMQKHPGWVGLI QSTILES VGCIWFNRSEAKDREIVAcoGPAT9164QVFVANHTSMIDF I VLEQMTAFAVIMQKHPGWVGLI QSTILES VGCIWFNRSEAKDREIVBdiGPAT9150QVFVANHTSMIDF I VLEQMTAFAVIMQKHPGWVGLI QSTILES VGCIWFNRTEAKDREIVBdiGPAT9153QVFVANHTSMIDF I VLEQMTAFAVIMQKHPGWVGLI QSTILES VGCIWFNRTEAKDREIVBdiGPAT9153QVFVANHTSMIDF I VLEQMTAFAVIMQKHPGWVGLI QSTILES VGCIWFNRTAKDREIVBdiGPAT9153QVFVANHTSMIDF I VLEQMTAFAVIMQKHPGWVGLI QSTILES VGCIWFNRTAKDREIVBdiGPAT9154QVFVANHTSMIDF I VLEQMTAFAVIMQKHPGWVGLI QSTILES VGCIWFNRTAKDREIV	CsaGPAT9	104	TIGWI IFLSTEIPVNLLLKGHPKLRAKI ERFLYELICSFFVASWTGVVKYHGPRPSIRP
BdiGPAT993GLGWMVFFAAFFPVHFLLKGQNKLRSKIERKLVEMMCSVFVASWTGVIKYHGPRPSSRPYSmoGPAT9119TVGWIIFLGAFIPVHFILRKHDHMRRKIERGLVEFICSVFVASWTGVIKYHGPRPSRRPRPpaGPAT9114ALGWIIFLSIFFPHFALKNHDQLRRQIERGLVEFICSVFVASWTGVIKYHGPRPSRRTKGraGPAT9A165QVFVANHTSMIDFIILEQMTAFAVIMQKHPGWVGLIQSTILESVGCIWFNRSFAKDREIVGraGPAT9B166QVFVANHTSMIDFIILEQMTAFAVIMQKHPGWVGLIQSTILESVGCIWFNRSFAKDREIVSpuGPAT9164QVFVANHTSMIDFIVLEQMTPFAVIMQKHPGWVGLIQSTILESVGCIWFNRSFAKDREIVStuGPAT9160QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLIQSTILESVGCIWFNRSFAKDREIVAthGPAT9165QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLIQSTILESVGCIWFNRSFAKDREIVAthGPAT9164QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLIQSTILESVGCIWFNRSFAKDREIVAcoGPAT9164QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLIQSTILESVGCIWFNRSFAKDREIVBdiGPAT9150QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLIQSTILESVGCIWFNRTFAKDREIVBdiGPAT9150QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLIQSTILESVGCIWFNRTFAKDREIVBdiGPAT9150QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLIQSTILESVGCIWFNRTFAKDREIVBdiGPAT9150QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLIQSTILESVGCIWFNRTFAKDREIVBdiGPAT9150QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLIQSTILESVGCIWFNRTFAKDREIV	ACOGPAT9	90	TIGWITELSSETAVHELLKGNDKWRROMERYLVELICSEEVASWTGVVKYHGPRPSMRP
SmoGPAT9119TVGWIIFLGAFIPVHFILRKHDHMRRKIERGLVEFICSVFVASWTGVVKYHGPRPSRRPRPpaGPAT9114ALGWIIFLSIFFPLHFALKNHDQLRRQIERGLVEFICSVFVASWTGVVKYHGPRPSRRTKGraGPAT9A165QVFVANHTSMIDFIILEQMTAFAVIMQKHPGWVGLIQSTILESVGCIWFNRSEAKDREIVGraGPAT9B166QVFVANHTSMIDFIILEQMTAFAVIMQKHPGWVGLIQSTILESVGCIWFNRSEAKDREIVSpuGPAT9164QVFVANHTSMIDFIVLEQMTPFAVIMQKHPGWVGLIQSTILESVGCIWFNRSEAKDREIVStuGPAT9160QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLIQSTILESVGCIWFNRSEAKDREIVAthGPAT9165QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLIQSTILESVGCIWFNRSEAKDREIVAthGPAT9164QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLIQSTILESVGCIWFNRSEAKDREIVBdiGPAT9150QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLIQSTILESVGCIWFNRTEAKDREIVScaGPAT9164QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLIQSTILESVGCIWFNRTEAKDREIVAcoGPAT9150QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLIQSTILESVGCIWFNRTEAKDREIVBdiGPAT9153QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLIQSTILESVGCIWFNRTEAKDREIVBdiGPAT9153QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLIQSTILESVGCIWFNRTEAKDREIV	BdigPAT9	93	GLGWMVFFAAFFPVHFLLKGONKLRSKTERKLVEMMCSVFVASWTGVLKYHGPRPSSRPY
PpaGPAT9 114 ALGWI IFLSL FFLHFALKNHDQLRRQIERGLVEFMCSVFVASWTGVVKYHGPRPSRTK GraGPAT9A 165 QVFVANHTSMIDFIILEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRSEAKDREIV GraGPAT9B 166 QVFVANHTSMIDFIILEQMSSFAVIMQKHPGWVGLLQSTILESVGCIWFNRSEAKDREIV SpuGPAT9 164 QVFVANHTSMIDFIVLEQMTPFAVIMQKHPGWVGLLQSTILESVGCIWFNRSEAKDREIV StuGPAT9 160 QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRSEAKDREIV AthGPAT9 160 QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRSEAKDREIV StuGPAT9 160 QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRSEAKDREIV StuGPAT9 160 QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRSEAKDREIV StuGPAT9 160 QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRSEAKDREIV StuGPAT9 160 QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRSEAKDREIV AthGPAT9 165 QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRTEAKDREIV BdiGPAT9 164 QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLIQSTILESVGCIWFNRTEAKDREIV BdiGPAT9 150 QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLIQSTILESVGCIWFNRTEAKDREIV BdiGPAT9 153 QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGFIQKTILESVGCIWFNRDLKDREVV	SmoGPAT9	119	TVGWITELGAFTPVHETLERHDHMERKTERGIVEFTCSVEVASWTGVVKYHGPRESERPE
GraGPAT9A 165 QVFVANHTSMIDFIILEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRSFAKDREIV GraGPAT9B 166 QVFVANHTSMIDFIILEQMSSFAVIMQKHPGWVGLLQSTILESVGCIWFNRSFAKDREIV SpuGPAT9 164 QVFVANHTSMIDFIVLEQMTPFAVIMQKHPGWVGLLQSTILESVGCIWFNRSFAKDREIV StuGPAT9 160 QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILEGVGCIWFNRSFAKDREIV AthGPAT9 165 QVYVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRSFAKDREIV CsaGPAT9 164 QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRSFAKDREIV AcoGPAT9 150 QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRTFAKDREIV BdiGPAT9 150 QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRTFAKDREIV	PpaGPAT9	114	ALGWI IFLSLFFPLHFALKNHDQLRRQIERGLVEFMCSVFVASWTGVVKYHGPRPSRRTF
GraGPAT9A165QVFVANHTSMIDFIILEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRSAKDREIVGraGPAT9B166QVFVANHTSMIDFIILEQMSSFAVIMQKHPGWVGLQSTILESVGCIWFNRTAKDREIVSpuGPAT9164QVFVANHTSMIDFIVLEQMTPFAVIMQKHPGWVGLQSTILESVGCIWFNRSAKDREIVStuGPAT9160QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLQSTILESVGCIWFNRSAKDREIVAthGPAT9165QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLQSTILESVGCIWFNRSAKDREIVCsaGPAT9164QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLQSTILESIGCIWFNRTAKDREIVBdiGPAT9150QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLQSTILESVGCIWFNRTAKDREIVBdiGPAT9153QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLQSTILESVGCIWFNRTAKDREIVBdiGPAT9153QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLQSTILESVGCIWFNRTAKDREIVBdiGPAT9153QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLQSTILESVGCIWFNRTAKDREIVBdiGPAT9153QVFVANHTSMIDFITLEQMTAFAVIMQKHPGWVGLQSTILESVGCIWFNRTAKDREIVBdiGPAT9153QVFVANHTSMIDFITLEQMTAFAVIMQKHPGWVGLQSTILESVGCIWFNRTAKDREIVBdiGPAT9153QVFVANHTSMIDFITLEQMTAFAVIMQKHPGWVGFIQKTILESVGCIWFNRDAKDREIV	-		
GraGPAT9B166QVFVANHTSMIDFIILEQMSSFAVIMQKHPGWVGLIQSTILESVGCIWFNRTFAKDRETVSpuGPAT9164QVFVANHTSMIDFIVLEQMTPFAVIMQKHPGWVGLLQSTILESVGCIWFNRSFAKDREIVStuGPAT9160QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILEGVGCIWFNRSFAKDREIVAthGPAT9165QVYVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRSFAKDREIVCsaGPAT9164QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESIGCIWFNRSFAKDREIVAcoGPAT9164QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESIGCIWFNRTFLKDREIVAcoGPAT9150QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRTFLKDREIVBdiGPAT9153QVFVANHTSMIDFIILEQMTAFAVIMQKHPGWVGFIQKTILESVGCIWFNRNDLKDREVV	GraGPAT9A	165	QVFVANHTSMIDFIILEOMTAFAVIMOKHPGWVGLOSTILESVGCIWFNRSDAKDREI
SpuGPAT9164QVFVANHTSMIDFIVLEQMTPFAVIMQKHPGWVGLIQSTILESVGCIWFHRSFAKDREIVStuGPAT9160QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILEGVGCIWFNRSFAKDREIVAthGPAT9165QVYVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRSFAKDREIVCsaGPAT9164QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESIGCIWFNRFFLKDREIVAcoGPAT9150QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRFFLKDREIVBdiGPAT9153QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGFLQSTILESVGCIWFNRTFLKDREIV	GraGPAT9B	166	OVFVANHTSMIDFIILEOMSSFAVIMOKHPGWVGLLOSTILESVGCIWFNRTEAKDRET
StuGPAT9160QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILEGVGCIWFNRSPAKDREIVAthGPAT9165QVYVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRSPAKDREIVCsaGPAT9164QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESIGCIWFNRTPLKDREIVAcoGPAT9150QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRTPLKDREIVBdiGPAT9153QVFVANHTSMIDFIILEQMTAFAVIMQKHPGWVGFIQKTILESVGCIWFNRNDLKDREVV	SpuGPAT9	164	OVFVANHTSMIDFIVLEOMTPFAVIMOKHPGWVGLIOSTILESVGCIWFHRSFAKDREI
AthGPAT9165QVYVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRSFAKDREIVCsaGPAT9164QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESIGCIWFNRTELKDREIVAcoGPAT9150QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRTEAKDREIVBdiGPAT9153QVFVANHTSMIDFIILEQMTAFAVIMQKHPGWVGFIQKTILESVGCIWFNRNDLKDREVVCmacDamo1700VFVANHTSMIDFIILEQMTAFAVIMQKHPGWVGFIQKTILESVGCIWFNRNDLKDREVV	StuGPAT9	160	OVEVANHTSMIDEIVLEOMTAFAVIMOKHPGWVGLIOSTILEGVGCIWENRSEAKDREI
CsaGPAT9 164 QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESIGCIWFNRTELKDREIV AcoGPAT9 150 QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRTEAKDREIV BdiGPAT9 153 QVFVANHTSMIDFIILEQMTAFAVIMQKHPGWVGFIQKTILESVGCIWFNRNDLKDREVV	AthGPAT9	165	OVYVANHTSMIDFIVLEOMTAFAVIMOKHPGWVGLIOSTILESVGCIWENRSEAKDREIN
AcoGPAT9 150 QVFVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLQSTILESVGCIWFNRTEAKDREIV BdiGPAT9 153 QVFVANHTSMIDFIILEQMTAFAVIMQKHPGWVGFIQKTILESVGCIWFNRNDLKDREVV	CsaGPAT9	164	OVEVANHTSMIDEIVI.EOMTAEAVIMOKHPGWVGI.LOSTILESIGCIWENRTELKDREIV
Bdigpar9 153 QVFVANHTSMIDFIILEQMTAFAVIMQKHPGWVGFIQKTILESVGCIWFNRNDLKDREVV	ACOGPAT9	150	OVEVANHTSMIDEIVI.EOMTAEAVIMOKHPGWVGI.OSTILESVGCIWENRTEAKDREIN
	BdigPAT9	153	OVEVANHTSMIDET TLEOMTAFAVIMOKHPGWVGFIOKTILESVGCIWENRNDI.KDREVN
	SmogPat9	179	OVEVANHTSMIDET TI. EOMTAFAVIMOKHPGWVGI LONTVILESI GOIWENRTDSKDRHVI
PpaGPAT9 174 OVEVANHTSMIDEVILEOMIGESALMOKHPGWVGEI OTTVLESI GCIWENRTEANDRHAW	PpaGPAT9	174	OVEVANHTSMIDEVILEOMTGESAIMOKHPGWVGFIOTTVLESI GCIWENRTEANDRHAI

GraGPAT9A GraGPAT9B SpuGPAT9 StuGPAT9 AthGPAT9 CsaGPAT9 AcoGPAT9 BdiGPAT9 SmoGPAT9 PpaGPAT9	225 226 224 220 225 224 210 213 239 234	RKLREHSQGADNNPLLIFPEGTCVNNQYSVMFKKGAFELGCTVCPIAIKYNKIFVD KKLREHSQGVDNNPLLIFPEGTCVNNQYSVMFKKGAFELGCTICPIAIKYNKIFVD KKLRDHVQGADNNPLLIFPEGTCVNNHYTVMFKKGAFELDSTVCPIAIKYNKIFVD KKLRQHVEGADNNPLLIFPEGTCVNNHYTVMFKKGAFELDCTVCPIAIKYNKIFVD KKLRDHVQGADNNPLLIFPEGTCVNNHYSVMFKKGAFELGCSVCPIAIKYNKIFVD KKLRDHVQGADNNPLLIFPEGTCVNNHYSVMFKKGAFELGCSVCPIAIKYNKIFVD KKLRDHVQGADNNPLLIFPEGTCVNNHYTVMFKKGAFELGCTVCPIAIKYNKIFVD KKLRDHVQGADNNPLLIFPEGTCVNNHYTVMFKKGAFELGCTVCPIAIKYNKIFVD KKLRDHVQFDNNPLLIFPEGTCVNNHYTVMFKKGAFELGCTVCPIAIKYNKIFVD KKLRDHVQFDNNPLLIFPEGTCVNNQYTVMFKKGAFELGCAVCPIAIKYNKIFVD SEKLRKHVIDPSNLLIFPEGTCVNNEYIVMFKKGAFELDCTVCPVAIKYNKIFVD	AFW AFW AFW AFW AFW AFW AFW AFW AFW
GraGPAT9A GraGPAT9B SpuGPAT9 StuGPAT9 AthGPAT9 CsaGPAT9 AcoGPAT9 BdiGPAT9 SmoGPAT9 PpaGPAT9	285 286 284 280 285 284 270 273 299 294	ISRKQSFTMHLLQLMTSWAVVCDVWYLEPQNLRPGETPIEFAERIRDIISVRAGLKK ISRKQSFTMHLLQLMTSWAVVCDVWYLEPQNLRPDETPIEFAERVRDIISVRAGLKK ISRKQSFTTHLLQLMTSWAVVCDVWYLEPQNLRPGETPIEFAERVRGIISDRAGLKK ISKKQSFTTHLLQLMTSWAVVCDVWYLEPQNIRPGETPIEFAERVRDIISVRAGLKK ISRKQSFTMHLLQLMTSWAVVCDVWYLEPQVLKPGETGIEFAERVRDIICARAGLKK ISRKQSFTMHLLQLMTSWAVVCDVWYLEPQVLKPGETPIEFAERVRDIICARAGLKK ISRKQSFTMHLLQLMTSWAVVCDVWYLEPQVLKPGETPIEFAERVRDIICARAGLKK ISRKQSFTMHLLRLMTSWAVVCDVWYLEPQVLKPGETSIEFAERVRDIISVRAGLKK ISRKQSFTMHLLRLMTSWAVVCDVWYLEPQVLKPGETSIEFAERVRDIISVRAGLKK ISRKQSFTMHLLRLMTSWAVVCDVWYLEPQTIRPGETSIAFTERVRDMIAARAGLKK ISRKQSFTMHLQRLMTSWAVVCDVWYLEPQTIRPNETPIEFAERVRDMIAARAGLKK ISRKQSFTMHLLRLMTSWAVVCDVWYLEPQTIRPNETPIEFAERVRDIISVRAGIKK	(VPW (VPW (VPW (VPW (VPW (VPW (VPW (VAW (VPW
GraGPAT9A GraGPAT9B SpuGPAT9 StuGPAT9 AthGPAT9 CsaGPAT9 AcoGPAT9 BdiGPAT9 SmoGPAT9 PpaGPAT9	345 346 344 340 345 344 330 333 359 354	GYLKYSRPSPKHRERKOQSFAESVLRGLELEEK GYLKYSRPSPKHREQKOQSFAESVLRRLEEN	

Supplementary Figure S3. Sequence Alignment and Identity/Similarity Shading of Various Plant LPEAT1 Proteins.

Phylogenetic tree depiction of this alignment makes up part of Figure 1 in the main body of the text.

TcLPEAT1	1	-MESELKDLNSKPAKTTQKPDPTHDDGSTKDDRPLLKSDSSSADT-NIQ
VvLPEAT1	1	-MESELKDLDPRSNSQDVSSKDDRPLLKSDSTVVSQDNLQ
GmLPEAT1	1	-MESELKDLNSKPPNGNGNSVRDDRPLLKPEPPVSADSIA
PpLPEAT1	1	-MESELKDLNSKPAKPVADDGSGEPAHDDASGKDDRPLLKPDLAPQVSTEELQ
Cclpeat1	1	-MESELKDLNSKQLKSTASSDDGGSAKDDRPLLKPDAAENIQ
PtLPEAT1	1	-MDTELKSMNPDPPKPE-QPDPASR-DDGSNSKDDRPLLKSDSNRISSTTGESIE
RcLPEAT1	1	-MDTELKDINPEPSKSKPEPEPAPDDGS-SKDDRPLLKSDSNRMSTENIE
StLPEAT1	1	-MESELQKLPQPETTRPSQPESIDEGSTKDDRPLLKPDPTNPQLQVQSQSSSPSIE
AtLPEAT1	1	-MESELKDLNSNSNPPSSKEDRPLLKSESDLAAAIE
OslPEAT1	1	MALPLHDATTSPSDPDDLGGGGEEEEERLASKPLLSSPST-YPSAGTEEGVEEL
Silpeat1	1	-MAPNDAATTAPSEPESVGG-RMSSEDTVATRPLLSSPST-SPSAASTAPVQESIE
ZmLPEAT1	1	-MALDTADADAPRLRLDASAAV PLLSDDGS-TAAGETAE
TcLPEAT1	48	ELEKKFAAYVRNDVYGTMGRGKLPLKEKLLLGIALVTLLPVRIVLGMTILVFYYLICRVC
VvLPEAT1	40	ELEKKFAAYVRSDAYGPMGCGELPLKEKLLLAFALVTLVPIRLVVAFTILVVYYLICRVC
GmLPEAT1	40	DMEKKFAAYVRRDVYGTMCRGELPTKEKLLLGFALVTLLPIRVVLAVTILLFYYLICRVC
PpLPEAT1	53	ELEKKCAAYVRRDAYGTMCRGELTVKEKVLLGLALVTLVPIRVVLAMTILVIYYLICRIC
CcLPEAT1	42	ELEKKFAPYVRNDVYGTMGRGELPLAEKFLIGIAMVTLLPIRVVLAMTVLVIYYLICRVC
PtLPEAT1	53	ELEKKFAAYVRNDVYGPMGRGELPLVEKVLLGIAVVTLVPIRFVLALIILVVYYIICRVC
RcLPEAT1	49	ELEKKFAAYVRNDVYGPMCRAELPLAEKLLLGIALVTLVPIRTLLAITVLLVYYAICRIC
StlPEAT1	56	ELEKKYAPYVRHDVYGIMCRGELPWTEKVLLGIALVTLVPMRVIGATTVLVVYYLICKIC
AtLPEAT1	36	ELDKKFAPYARTDLYGTMCLGPFPMTENIKLAVALVTLVPLRFLLSMSILLLYYLICRVF
OslPEAT1	54	ELDRRYAPYARRDAYGAMGRGPLGAAGAGRLAVGAAVLFPLRLAAGVLVLVAYYLVCRVC
Silpeat1	54	ELDRRYAPYARRDAYGPMCLGPVGAAEAFRLAFAAVVLIPLRVVAGMLVLVVYYLVCRVC
ZmLPEAT1	39	QLDARYAPYARRDAYGTMGRGPLPAAQAVRLALAAAVLLPLRFVAGMLVLLLYYLVCRAC
TclPEAT1	108	LFLAPNREDEOEDYAHMGGWRRAVIVRSCRLFSRVMLFLVGFYWLNETH
VvLPEAT1	100	TLFSAPNREGEDEOEDYAHMGGWRRAVIVOCCRFLSRALLFTLGFYWINVTY
GmLPEAT1	100	TLFSAPTGEEEQEDYAHMSGWRRTIIVSCGRALSRLMLFIFGFYWIPESN
PpLPEAT1	113	TLFSVPNRDEEQEDYAHMGGWRRAVIVQCGRSLSRLMLFVLGFYWINETY
CclPEAT1	102	TLFSAPNR-GEDEQEDYAHMG <mark>GWRR</mark> SVIVVSCRFLSRVMLSVLGFYWITETF
PtLPEAT1	113	TLFSAPNRDEEEEQEDFAHMG <mark>GWRR</mark> AVIVWCCRFLSRMLLFVLGFYWISVSY
RcLPEAT1	109	TLFSAPNRDEEEEQEDFAHMG <mark>GWRR</mark> AVIVWC <mark>G</mark> RFLSRVMLFVFGFYWIKETY
StlpEAT1	116	TAFWAPNREDEQEDYAHTG <mark>GWRR</mark> TVMMQS <mark>C</mark> MFLSRVMLFVFGFYWIHETY
AtLPEAT1	96	TLFSAPYRGPEEEEDEGGVVFQEDYAHME <mark>GWKR</mark> TVIVRS <mark>C</mark> RFLS <mark>R</mark> VLLFVFGFYWIHESC
OslPEAT1	114	TLRVEEEEREGGGGGAAGEVEGDGYARLE <mark>GWRR</mark> EGVVRC <mark>C</mark> RALARAMLFVF <mark>GFYWI</mark> REYD
Silpeat1	114	TLRVEEE-REGGEGDGYARLE <mark>GWRR</mark> EGVVWC <mark>C</mark> RALARAMLFVFGFYWIREYD
ZmLPEAT1	99	TLFVDADGGRPRLA <mark>GWRR</mark> KAVLRS <mark>C</mark> CALS <mark>R</mark> VMLFVF <mark>GFYWI</mark> RETR
TclPEAT1	158	RDSANTQENSKTEGINQSEEQE <mark>R</mark> P GAIVSNHVSYLDILYHM<mark>S</mark>SSFPSFVAK
VvLPEAT1	152	RDPLTTEDEGKDEDEEPERPGAIISNHVSYLDILYHMSSSFPSFVAK
GmLPEAT1	150	SASQEDKSRQPEE-LRRPGVIISNHVSYLDILYHMSSSFPSFVAK
PpLPEAT1	163	RIPSDAQPNPTTDCKDEGEEEGTE <mark>R</mark> P <mark>G</mark> AII <mark>SNHVSYLDILYH</mark> MSSSFPSFVAK
CcLPEAT1	153	RILDVQEKSENEAKNQSKDEDEAKDQDEESG <mark>R</mark> P <mark>G</mark> AII <mark>SNHVSYLDILYH</mark> M <mark>S</mark> SSFPSFVAK
PtLPEAT1	165	RDIELPDQNKSSSQNEGKDQSEEPERL <mark>G</mark> AII <mark>SNH</mark> VSYLDILYH <mark>MS</mark> AS <mark>FPSFVAK</mark>
RcLPEAT1	161	RILEPPQDEGKDQSEDPERPGAII <mark>SNHVSYLDILYH</mark> MSSSFPSFVAK
StlPEAT1	166	QPINLNGNSNNEDGSKLQAEELERPGAIV <mark>SNHISYLDILYH</mark> K <mark>S</mark> SSFPSFVAK
AtLPEAT1	156	PDRD-SDMDSNPKTTSTEINQKGEAATEEPE <mark>R</mark> P <mark>G</mark> AIV <mark>SNH</mark> VSYLDILYH <mark>MS</mark> AS <mark>FPSFVAK</mark>
OslPEAT1	174	CRFPDAEDEHQEQSKELG <mark>R</mark> P <mark>G</mark> AVV <mark>SNH</mark> V SYVDILYHM<mark>S</mark>SS<mark>FPSFVAK</mark>
Silpeat1	165	CRFPDAEVEHVDQSKEME <mark>R</mark> P <mark>G</mark> AIV <mark>SNH</mark> VSYVDILYH <mark>MS</mark> AF <mark>FPSFVAK</mark>
ZmLPEAT1	144	RRSTNAKGLNQDQFEESQ <mark>R</mark> PCAIV <mark>SNH</mark> VSYVDILYH <mark>MS</mark> ASFPSFVAK

TclPEAT1	209	R <mark>SV</mark> AKIPLVGLIS	K <mark>CLGC</mark> VY <mark>VQRE</mark> S	SKSSDF <mark>KGV</mark> AGVVI	ERVCEAHQNESA	P <mark>M</mark> MMLFPEGT
VvLPEAT1	199	RSV <mark>A</mark> KLPLIGLIS	K <mark>CLGC</mark> VY <mark>VQRE</mark> S	SKSSDF <mark>KGV</mark> AGVV1	ERVCEAHQNKFA	P <mark>M</mark> MMLFPEGT
GmLPEAT1	194	RSVAKLPLVGLIS	K <mark>CLGC</mark> VY <mark>VQRE</mark> S	SRSSDF <mark>KGV</mark> SAV <mark>V</mark> I	D <mark>R</mark> IREAHQNESA	PLMMLFPEGT
PpLPEAT1	216	RSVAKLPLVGLIS	K <mark>CLGC</mark> VY <mark>VQRE</mark> S	SKSSDF <mark>KGV</mark> SGVV1	E <mark>R</mark> VKEAHQNNSA	P <mark>PMMLFPEGT</mark>
CclPEAT1	213	RSVAKLPLVGLIS	K <mark>CLGC</mark> VY <mark>VQRE</mark> S	SKSSDF <mark>KGV</mark> SGVV1	E <mark>R</mark> VREAHRDKSA	P <mark>M</mark> MMLFPEGT
PtLPEAT1	219	RSVAKLPLVGLIS	K <mark>CLGC</mark> VYVQRES	SKSSDF <mark>KGV</mark> SGIVI	E <mark>R</mark> VKESHENSSA	P <mark>M</mark> MMLFPEGT
RclpEAT1	208	R <mark>SV</mark> AKLPLVGLIS	K <mark>CLGC</mark> VY <mark>VQRE</mark> S	SKSSDF <mark>KGV</mark> AGVVI	ERVREAHQNKSA	P <mark>IMM</mark> LFPEGT
StlpEAT1	218	R <mark>SV</mark> AKLPLVGLIS	K <mark>CLGC</mark> VY <mark>VQRE</mark> S	SKSPDF <mark>KGV</mark> SG <mark>VV</mark> N	IE <mark>R</mark> IREAHQNKSA	PIML <mark>LFPEGT</mark>
AtLPEAT1	215	R <mark>SV</mark> GKLPLVGLIS	K <mark>CLGC</mark> VY <mark>VQRE</mark> A	KSPDF <mark>KGV</mark> SGT <mark>V</mark> N	IE <mark>R</mark> VREAHSNKSA	PTIMLFPEGT
OslPEAT1	221	R <mark>SV</mark> ARLPMVGLIS	K <mark>CLGC</mark> IFVQRE <mark>S</mark>	KTSDF <mark>KGV</mark> SGA <mark>V</mark> I	E <mark>R</mark> IQRAHQQKNS	P <mark>M</mark> ML LFPEGT
Silpeat1	212	R <mark>SV</mark> ARLPLVGLIS	K <mark>CLGC</mark> IFVQRE <mark>S</mark>	SKTSDF <mark>KGV</mark> SGA <mark>V</mark> I	E <mark>R</mark> IQRAHQQKNA	P <mark>M</mark> ML LFPEGT
ZmLPEAT1	191	E <mark>SV</mark> SRLPLIGLIS	NCLGCIFVQRES	SKSSEA <mark>kgv</mark> sgavi	ERIQDVCQDKNT	P <mark>M</mark> ML LFPEGT
TclPEAT1	269	TTNGDFLLPFKIG	AFLARAPVVPVI	LRYPYQRFSVAWI	DSIS <mark>G</mark> LR H VVFLL	CQFVNRMEVT
VvLPEAT1	259	TTNGGFLLPFKIG	AFLAKAPVLPVI	LRYPYQRFSPAWI)SIS <mark>G</mark> VR H VIFLF	CQFVNHIEVT
GmLPEAT1	254	TTNGEFLLPFKTG	GFLAKAPVLPVI	LQYHYQRFSPAWI	SIS <mark>G</mark> VR H VIFLL	CQFVNYMEVI
PpLPEAT1	276	TTNGDFLLPFKTG	AFLAKAPVLPVI	LRYPYERFSPAWI)SISGVRHVIFLF	CQFVNHIEVT
CclpEAT1	273	TTNGDYLLPFKTG	AFLARAPVLPVI	LRYPYQRFSPAWI	DSIS <mark>G</mark> AR H VFFLL	CQFVNHIEVT
PtLPEAT1	279	TTNGDFLLPFKTG	AFLATAPVRPVI	LRYPYQRFSPAWI)SIS <mark>G</mark> AL H VFYLF	CQFINHMEAV
RcLPEAT1	268	TTNGDFLLPFKTG	AFLAGAPVLPVI	LRYPYQRFSPAWI	SIS <mark>G</mark> VR H VIFLL	CQFVNCIEVT
Stlpeat1	278	TTNGDFLLPFKSG	AFLSGAPVQPVI	LRYPYQRLSPAWI)SI <mark>SG</mark> ARHVILLL	CQFVNYLEAT
AtLPEAT1	275	TTNGDYLLTFKTG	AFL <mark>AGTPV</mark> LPVI	IKYPYERFSVAWI)TISGARHILFLL	CQVVNHLEVI
Oslpeat1	281	TTNGDYLLPFKTG	AFLAKAPVKPVI	LRYPYKRFSPAWI)SM <mark>SG</mark> ARHVFLLL	CQFVNNLEVI
Silpeat1	272	TTNGDYLLPFKTG	A <mark>FL</mark> AKA <mark>PVQ</mark> PVI	LRYPYKRFNPAW	SM <mark>SG</mark> ARHVFLLL	CQFVNYVEVT
ZmLPEAT1	251	TTNGDYLLPFKTG	AFLAGA <mark>PV</mark> QPVI	LKYPYRRFSPAWI)SMD <mark>G</mark> ARHVFLLL	CQFVNHMEVV
_						
TCLPEAT1	329	WLPVYYPSQQEKD	DQKLYANNVRRI	MANEGNLILSDIC	GLAEKRTYHAALN	GLFC
VvLPEAT1	319	RLPVYIPSQQEKD	dpklya <mark>nnvr</mark> ki	MASEGNLIMSDIC	GLAEKRIYHAALN	GLFC
GmLPEAT1	314	RLPVYHPSQQEMD	DPKLYANNVRRI	MATEGNLILSDIC	GLAEKRIYHAALN	GNNSLPSVLH
PpLPEAT1	336	RLPVYYPSQQEKD	DPKLYATNVRRI	MASEGKATQSDIC	ELA EKRVYHAALN	GNNSRPSVLH
CCLPEAT1	333	SLPVYHPSQQEKD	DPKLYAENVRRI	MASERN TVSDIC	LAFKRIYHAALN	GNNSLPSVLH
PtLPEAT1	339	WLPVYYPSQEEKD	DPKLYASNVRRI	MAREGN KMSDIC	LAEKRIYHTALN	GNISLPSVLH
RCLPEAT1	328	RLPVYYPSQEEKD	DPKLYANNVRRI	MAHEGN LMSDIC	LA KRVYHAALN	GLF
StLPEAT1	338	WLPVYYPSQQEKD	DPRLYAENVRRI	MAHEGN LLSDIC	LA KRVYHAALN	GLFC
AtLPEAT1	335	RLPVYYPSQEEKD	DPKLYASNVRKI	MATEGNLILSELO	JLSDKRIYHATLN	GNLSQTRDFH
USLPEAT1	341	HLPVYYPSEQEKE	dpklyannvrki ddylyannvrki	MAVEGNLILSDIC	5LAEKRVYHAALN	GNNSLPRALH
SILPEAT1	332	HLPVYYPSEQEKD	DPKLYANNVRKI	MAVEGNLILSDIC	JAEKRVYHAALN	GN-SLPRALH
ZmlpEAT1	311	KLPVYYPSQLEKE	DPKLYA <mark>NNVR</mark> KI	LAMEGN_VLSNI(ELAEKRVYHAAL T	GS-SLPGARH
	202	00				
	203 272	Q3				
VVLFEATL Cmt DEATL	5/5 27/	OKDE				
	206	QUDF QUDF				
COLDENEI	370	U U U U U U U				
	200	QUUD VUUD				
PELPEATI	399	Ωνηη				
RCLPEATI						

RCLPEATI		
StlpEAT1	392	QQ
Atlpeat1	395	QKEE
4	101	0 T T D D

OSLPEATI 401 QKDD SiLPEATI 391 QKDD ZmLPEATI 370 EKDD

Supplementary Figure S4. Sequence Alignment and Identity/Similarity Shading of Various Plant LPEAT2 Proteins. Phylogenetic tree depiction of this alignment makes up part of Figure 1 in the main body of the text.

Pplpeat2	1	MADNDLASPLISSPPSDHPHLILTVQDDTDTD-HNNHNGNHG
VvLPEAT2	1	MAGTGADLITPLISSQPSDQPELILTVDDRPGFESFSDHCSSNG
PtlPEAT2	1	MANHDLESPLISSQPSDPPHIILNVHDSDSSIQQS
RclPEAT2	1	MTDDSLSSPLLQPQPSDHPPVILSIRDNHNHYYHR
CclPEAT2	1	MADHHRDHDHDLSSPLIQSPRSDHSPVIISIEADGNDTVSDPATQDQL
TclPEAT2	1	MAEHDLTSPLISPRSSDQPQTVLIVSDDEDSEPSDRPPSNQQ
Atlpeat2	1	MADPDLSSPLIHHQSSDQPEVVISIADDDDDESGLNLLPAVV
GmLPEAT2	1	MADDSDLTSPLLSSSSSSSDHVVVTVHPSAAP
StlpEAT2	1	MSDHSIFAPLLPSDHLPHKSNGDDQEHAPEPHVILTVEDDGVQHQLSNG
Silpeat2	1	MASTSPSP-ASLFTPLLSGSVAPARAANGHANNHRHHGDSDG
Zmlpeat2	1	MASTCLAP-ASLSTPLLSDSIARAPAANGHATNHRHHHHDDSDG
Oslpeat2	1	MASRNPSP-ASIST <mark>PL</mark> ISDSISPTPTTNGHAGHHNHHDDDEE
Ρητ.ΡΕΔΤ?	42	SFTVPCSTTADPERMHT
VVLPEAT2	45	
P+LPEAT2	36	
RCLPEAT2	36	HISVPPPSTVDPFRMMTP
CCLPEAT2	49	NISVPGPNTANPELNDTRYHNNPGNPYWFIGSDGISVPGPNTANPELNDTP
TCLPEAT2	43	
Atlpear2	43	DPPPVLGPTTVDPERMNTP
GmLPEAT2	34	
Stlpear2	50	DFDMPGSTTVDPFRNNTP
Silpeat2	42	AAODRGPSPADPERNGTP
Zmlpear2	44	AARDRGPSPADPERNG
Oslpeat2	42	SPWSPRGVSPADPERMGTP
PpLPEAT2	78	EIRG-LYEWLKIGICLPIALARLVLFGASILIGFVATKLALQGWKDKKNPMP
VvLPEAT2	83	KIDG-FYEWFKILVCVPIAAIRLVLFGLCLLVGYLATKFALQGWKDKQNPMP
PtLPEAT2	75	DIEG-LYELIKIVICLPIAIVRLVLFGVCLATGYVATKIALLGWRDKHNPMP
RcLPEAT2	74	KIEG-VYEVLKSLICLPIALARLVLFGACILVGYLATKLALGGWKDKNNPMP
CcLPEAT2	88	HVVG-VYEFVKIVVCFPIVLIRLVLFGFCILVGYLATKLALEGWKDKQNPMP
TclPEAT2	98	FVSG-VYEVIKILLCLPIALARLVLFGVCLAVGYIATRIALEGWKDKQNPMP
AtLPEAT2	83	GVSG-LYEAIKLVICLPIALIRLVLFAASIAVGYLATKLALAGWKDKENPMP
GmLPEAT2	68	AIEG-LYEWAKTVLCLPLAALRLAIFGLCLALGYVATKVALQGWKDKENPMP
Stlpeat2	89	RVEG-VYEWLKIVVCLPITLVRLVLFGLALMIGYVATRTALLGWKDRSSPMP
Silpeat2	82	AWGGGVYAWARTLLLAPVAAVRLVLFGLATAIGYAATWVALRGWADVQDRP-REGAGPMP
ZmLPEAT2	84	AWGCGVYAWSRTLLLPVALVRLALFCLSIAIGYAATWVALRCWADTHGRP-RVGGGPMP
OsLPEAT2	85	GWCG-AYELVRALVCAPVAAARLVLFGLSLAVGYAATWVALRGWVDVRERAAQEGAGPMP
PplPEAT2	129	KWRCRIMWITRVCTRCILFSFGYHWIRRKGKPAPREIAPIVVSNHVSFIEPIFYFYELFP
VvLPEAT2	134	KWRCRVMWVTRICSRCILFSFGYHWIKRRGRPASRETAPIVVSNHVSYVEPIFFFYELFP
PtlPEAT2	126	KWRSRLMWLTRGCTRCILFSFGYHWIKRKGKLAPREIAPIVVSNHVSYIDPIFYFFEFFP
RcLPEAT2	125	KWRSSYHWIKRKCNPAPREIAPIVVSNHVSYIEPIFYFYELFP
CclPEAT2	139	VWRSRLMWVTRVCSRCILFSFGYHWIRRKGKPAPRQIAPIVVSNHISYIEPIFFFYELFP
TclPEAT2	149	KWRSRIMWVTRVCARFILFSFGYQWIRRKGKPAPRDVAPIVVSNHVSYIEPIFYFYELFP
Atlpeat2	134	LWRCRIMWITRICTRCILFSFGYQWIRRKGKPARREIAPIVVSNHVSYIEPIFYFYELSP
GmlPEAT2	119	KWRCRVMWITRLCARCILFSFGYQWIKRKGKPAPREIAPIIVSNHVSYIEPIFYFYELFP
StlPEAT2	140	KWRSRLMWVTRMSARTILFSFGYQWIRRKGKPAPREIAPIVVSNHVSYIDPIFFFYELFP
Silpeat2	141	AWRRRLMWITRISARCILFSFGYHWIRKKGRPAPRELAPIVVSNHVSYIEPIFFFYELFP
Zmlpeat2	143	AWRRRLMWITRISARCILFSFGYHWIRKKGRPARRELAPIVVSNHISYIEPIFFFYELFP
OslPEAT2	144	AWRRRLMWITRISARCILFSFGYHWIRRKGKPAPRELAPIVVSNHVSYIEPIYFFYELFP

PpLPEAT2	189	TIV <mark>ASESHD</mark> SLP <mark>L</mark> VGTIIRAMQVIYV <mark>NRF</mark> SAS <mark>SRK</mark> HAVSEIKRKA <mark>S</mark> CDRFPRVLLFPEGT
VvLPEAT2	194	TIVASESHDSLPFVGTIIRAMQVIYVNRFSQS <mark>SRKQ</mark> AVNEIKKKASCERYPRVLLFPEGT
Ptlpeat2	186	TIVAAESHDSMPFVGTIIRAMQVIYVNRFSPSSRKLAVNEIKRKASCGRFPRVLLFPEGT
Rclpeat2	168	TIVAAESHDSIPFVGTIIRAMOVIYVNRFSOSSRKLAVNEIKRKASCDRFPRVLLFPEGT
CclPEAT2	199	TIVASE SHDSIPFVGTIIRAMOVIYVDRFSOSSRKNAVSEIKRKASCDRFPRVLLFPEGT
TCLPEAT2	209	TTVASESHDSTPFVGTTTRAMOVTYVNRFSOASRKNAVNETKRRASCDTFPRILLFPEGT
A+LPEAT2	194	TIVASESHDSI PEVGTITRAMOVIYVNRESOTSRKNAVHETKRKASCORFPRILLEPEGT
GmLPEAT2	179	TIVAAFSHDSTPFVCTITRAMQVIIVNRFLPSSRKOAVRFIKRRASONRFPRVLLFPFCT
	200	
C-IDEAE2	200	
SILPEAIZ	201	
ZIILPEATZ	203	
OSLPEATZ	204	TIVSSDSHDSIPFVGTIIRAMQVIIVDRESPASKKSAVNEIKKKAAONSEPRVLLEPEGT
Ροιρεάτ2	249	TTNGRET ISEELGAFIPCEPTOPUTVRYPHVHEDOSWGHTSLAKIMERMETOFHNEMEVE
VVLPEAT2	254	TTNGRUT I SEOLGAFT PCYPTOPUVVRYPH THEDOSWGHT SLGRIMERMETOFHNEMEVE
D+LPEAT2	246	TTNGKVLISEOLGAFIPCVAWOPVTVRVPHVHFDOSWGMOBICKIMI HTTGTMKTHEVE
	270	
COLFEAT2	220	
CCLFEAI2	259	
TCLPEATZ	269	
ATLPEATZ	254	TTNGKVLISFQLGAFIPGYPLQPVVVRYPHVHFDQSWGNISLLTLMFRMFTQFHNFMEVE
GmLPEAT2	239	TTINGRN LISFQLGAFIPGYPLQPVLVRYPHVHFDQSWGHVSLGKLMFRMFTQFHNFFEVE
StLPEAT2	260	TTNGRSIISFQLGAFIPGYPIQPVIVRYPHVHFDQSWGNVSLAMLMFRMFTQFHNFMEVE
Silpeat2	261	ITTNGRFLISFQHGAFIPCYPVQPVVVRYPHVHFDQSWGNLSLKLMFKMFTQFHNFMEVE
ZmLPEAT2	263	ITTNGRFLISFQH GAFI PGYPVQPVVVRYPHVHEDQSWGNLSLLKLMFKMFTQEHNFMEVE
OslPEAT2	264	TTNGRFLISFQHGAFIPCYPVQPVIVRYPHVHEDQSWGN SLGKLMFKMETQFHNEMEVE
PDI.PEAT?	309	YL PWYSDI DNKKESAVRESERTCHAMATSI NWOTSHSYCDI MI I MKATOSKSKI ERDAS
	317	
D+IDFAT2	306	
DOIDENT2	200	
COLDENT2	200	
TOT DEAT2	320	
ICLFEAIZ	229	
ALLPEAIZ	200	
GHLPEAIZ	299	
Stlpearz	320	Y DV TPHENRRESAVRESQRIGHAVASALNVVQISHSYGDVELLARALEANQENPSE
SILPEATZ	321	Y DEV VIPPEIKQENALIFAENIN I AMARALNV DETSISIGDSMIMARAVEAGKANCSN
ZHLPEAIZ	323	ILPVVIPPEIKQENALIFAEDISIAMARALNVIPISISIGDSMIMARAILAGAVNGSN
OSLPEATZ	324	YLEVVIPPEIKQENALHFAENISIAMAHALNVIPUSISIGUSMIMARAVEDGKVNCSN
PpLPEAT2	369	YMVEMATVKSLLHISSMEAVDFLDKFLSMNPDPRGHVNYSGFLRVLRLKACTFSEEIFAF
VvLPEAT2	372	YMVEMARVESSFHLSTLEAVDFLDTFLSMNPDPSGCVKIHDFFRVLRLKPCYLSEKIFGF
Ptlpeat2	364	YMVEMAKVESLFHINSLEAVNFLDKFLSMNPDASGRVKFNDFLRAFRLRTCTLSEELFGF
RcLPEAT2	346	YMVEMAKVESLYHISSLEAVDFLDKFLSMNPDPSGRVKFHDFLRAMRLRTCSLLEEIFGF
CclPEAT2	377	YMVEMARVGSIFHISSLEAVNFLEKFLSMNPDPSGCVKLLDFLSVLRLKTCPLSDEIFGF
TclPEAT2	387	YMVEMARIESLYHISSLEAVDFLDKFLSMNPDTSGCVKLHDFLRVLRLKACTLSEEIFGF
AtLPEAT2	372	YMVEMARVESLEHVSSLEATRELDTEVSMIPDSSGRVRLHDELRGLKLKPCPLSKRIFEF
GmLPEAT2	356	FMVEMTKVESLEHTSSMEAVDELDKELAMNPDSSGRVOYHDELRVLRLKACPLSAKTESE
Stlpear2	378	YI VEMAGVEAEFHI SSIEAVDELOVELSMNPDSRGOVETHHELKVI.RUKPSTI.SEKTEGE
Silpear2	379	YNVEMAWVKDMYGVSTAFAMELLEHELAMNPDSDGRWKAODEWAYFGUDCSPLCKKTEHY
Zmlpear2	381	
OSLPEAT2	382	YNVEMAWVKETYGVSTSEAMALLEDEL CMSPDKDGRWNAODEWAHFGUNCTPLCKKTEOY
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	502	
Pplpeat2	429	IDVEKSGSIIFKQFLFGSVHVLKQPLFRRACELVFSEYVSGENDYISEQEFGESVRPAIP
VVLPEAT2	432	1DVDKSGRV1FKQFLFGSAHVMKQPLFRQACELAFAECDSDGDLYISEQELGDSIRPVIP
PtLPEAT2	424	LDVEKNGSITFKQFLYGSAHVMKRPLFHQSCELAFAQCDTRGHNQISEQELGETIRHAIP
RcLPEAT2	406	VDVEKIGSINEKQELYGSAHVMKQBLERQTCELACTRCSGGEDNLISKEQLGDT RLA P

CclPEAT2	437	IDVDKNGSITFKQFLYASAHVMKLPLFWQACELAFAECDPDGNGFISENQLEVTIRPAIP
TclPEAT2	447	LDVEKNGSITFKQFLFGSAHVLKQPLFRQACELAFAECDVEGENYFMEKDLADILRHAIP
Atlpeat2	432	IDVEKVGSITFKQFLFASGHVLTQPLFKQTCELAFSHCDADGDGYITIQELGEALKNTIP
GmLPEAT2	416	IDVEKSGTITFRQFLYGSAHVMSQPGFHQACEEAFAGCGGAVKAYVVEQELRDFIQPVIL
StlPEAT2	438	IDVQKSGKITFKQFLVGSAHILKQPLFHQACESAFTACDGDGKNYIMEKEFGDSLMLSIP
Silpeat2	439	FDFSIKESITFRQFLVGCAHLRKQPLFQGACETAFEKCRDPETSEISRGQLADILRLSML
ZmLPEAT2	441	FDLGIKESITFRQFLVGCAHLRKQPLFQGACETAFEKCRDPETSEISRAQLADVLRLSML
OslPEAT2	442	FDFEAKESITFRQFLIGCAHLRKQPSFQDACETAFERCRNPLTSHIGREQLADVLRSSML
PplPEAT2	489	DLNED-EVHELFNLFDADGDGRISKDEFWTCLKRNPLLTALFSPCLLNKDISQDGNRLEE
VvLPEAT2	492	DLNED-EIQEMFNLFDTDKDGRVSKDDFSNCLRRHPLLIALFSPSLLHNA
Ptlpeat2	484	DFDED-EIHELFSIFDMDGDGSVSKDNFLYCLRQNPLLIALFKPCLVHKDSSQVGQGILE
RclPEAT2	466	DLDDA-EIHELFKLFGGNDDGRASKETFMCCLKKNPLLTALFWPCLVYKDSLECGGRMLE
CclPEAT2	497	DLNKY-EIDSLFRLFDSDGDGRVSRDDFICCLRKNPLLIAIFSPTLLHTDLSEARNRMPG
TclPEAT2	507	ELNED-EIHGLFNLFDTDK <mark>D</mark> GRISRDDFFSC <mark>L</mark> RKN <mark>P</mark> LL <b>I</b> SL <mark>F</mark> SPRLLHRDTSKAGDRMLE
Atlpeat2	492	NLNKD-EIRGMYHLLDDDQDQRISQNDLLSCLRRNPLLIAIFAPDLAPT
GmLPEAT2	476	NWSED-EVHELFMVFDNDNDGRIDKNDFLSCLRKTPLLIAFFTLQLQQKEFEGNGVIE
Stlpeat2	498	GLSNN-EIRGLFTLFDIDRDGKMSKDDFIGCTRRYPLLTALFSPCVLQQICP
Silpeat2	499	LPSDD-GMQKLFKTFDVDGDEKISRDDFITCLGRFPFLLAFFAAPINGEVYIEIV
Zmlpeat2	501	LPSGD-RMLDLFKTFDIDGDEKISKDDFMTCLGRFPFLLAFFAAPINGEVYIEIV
OslPEAT2	502	ELMTDNGMMKLFKTLDVDDDDGISKDDLMASLRKLPFMTALFARRINGEVYIEIV
PpLPEAT2	548	IV-

VvLPEAT2		
PtlPEAT2	543	EIV
RclPEAT2	525	ELV
CclPEAT2	556	DVI
TclPEAT2	566	EIV
Atlpeat2		
GmlPEAT2	533	IV-
Stlpeat2		
Silpeat2		
Zmlpeat2		
OslPEAT2		



**Supplemental Figure S5**. Characterization of *GPAT9* T-DNA Insertions

(A) Representation of *GPAT9* T-DNA insertion locations. For both lines T-DNA left border primers will generate amplicons with gene specific primers flanking either side of the insertion suggesting there are multiple insertions with inverse orientation. The *gpat9-1* insertions are 46 bp upstream of the coding sequence. The *gpat9-2* insertion is at the end of the 4th exon. Pictured is just the first four exons out of 12 in *AtGPAT9.* 

**(B)** RT-PCR of full length *GPAT9* coding sequence from leaves of homozygous *gpat9-1*.

**(C)** qPCR results for *GPAT9* wild-type (Col-0) and *GPAT9/gpat9-2* leaves.

### Methods:

(A) For insertion site sequencing the left border-gene junction was amplified by PCR with GoTaq® Flexi (Promega), gel purified by QIAquick Gel Extraction Kit (QIAGEN) and sequenced from both the left border primer and a flanking gene-specific primer by Eurofins (http://www.eurofinsgenomics.com/).

**(B-C)** Leaf RNA extraction with RNeasy Plant Mini Kit (QIAGEN) and treated with RNase-free DNase (Qiagen) and on-column DNase digestion. RNA was quantified using a Nanophotometer (Implen Inc). cDNA was synthesized using SuperScript III First-Strand Synthesis System for RT-PCR (Life Technologies). RT-PCR utilized standard conditions as per GoTaq® Flexi (Promega) protocol with 30 cycles of amplification. For qPCR transcript levels were analyzed by quantitative PCR (qPCR) using Platinum SYBR Green qPCR SuperMix-UDG (Life Technologies) and the Stratagene Mx3005P Quantitative PCR system (Agilent Technologies Inc). Transcript was normalized to the *TIP41-like* gene (Czechowski et al., 2005). **(A-C)**, the sequences for primers utilized are shown in supplemental table S1.



### **Supplemental Figure S6.** Analysis Of Viability in Wild-Type and *GPAT9-2/gpat9-2* Pollen.

(A-B) Alexander staining (Peterson et al., 2010) for pollen abortion. Purple = non-aborted pollen, green pollen (black arrows) = aborted pollen. Pollen from wild-type (A), and *GPAT9/gpat9-2* (B) plants.

**(C-D)** Nitro blue tetrazolium staining for pollen viability (Regan and Moffatt, 1990). Viable pollen stain black. Anthers from wild-type (C), and *GPAT9/gpat9-2* (D) plants. **Supplemental Figure S7.** Genetic Complementation of *gpat9-2* Mutants with Transgenic Plant *GPAT9*.

Hemizygous *gpat9-2* plants were transformed with different binary vectors, with or without functional full-length plant ORFs driven by the *AtGPAT9* promoter. T4 generation seeds from DsRed-fluorescent and sulfadiazine-resistant representative lines from: negative control B110 (A, D); AtGPAT9prom::AtGPAT9 (pE434, B, E); or AtGPAT9prom::VfGPAT9 (pE437, C, F) were sown on solid agar media containing sulfadiazine. Wide-angle views of the agar plates are shown in the top panels, close views of the same plates are shown in the bottom panels. Note the high proportion of stunted and aborted seedlings on the negative control plate compared to the high number of healthy, complemented seedlings established on both the E434 and E437 plates.





### Supplemental Figure S8. Lipid Characterization of Wild-Type and *GPAT9-*2/gpat9-2 Plants.

(A) The relative fatty acid composition of leaves. Average and standard deviation. n = 5 for wild-type (Col-0), and 13 for *GPAT9-*2/gpat9-2.

(B) Total seed fatty acid content from seeds of plants grown at the same time under 24 hr light ~150-170  $\mu$ mol/m²/sec white light. 30 seeds per FAME analysis from a single plant. n = 19-20 individual plants per line.

**(C)** The average fatty acid composition of seeds from part B. Bars are average and standard deviation.

**Supplemental Figure S9.** Seed Fatty Acid Composition of *GPAT9* amiRNA Knockdown Lines. Fatty acid compositions are from seed samples analyzed for total oil content in Figure 5A of the main text. Average  $\pm$  S.D.



**Supplemental Figure S10**. Expression of *GPAT9* in Developing Seeds of Wild-Type and *GPAT9* amiRNA Knockdown Lines.

*GPAT9* transcript was normalized to *TIP41-like* (Czechowski et al., 2005). Two biological replicates for Col-0, and three biological replicates for each amiRNA knockdown line. Each biological replicate is the average of three technical replicates.



#### Methods:

Frozen developing seeds (9-11 DAF) were separated from silique tissue by silique popping method (Bates et al., 2013). ~50 µL volume of frozen seeds per biological replicates were mechanically pulverized to a fine powder with steel beads (TissueLyser LT, QIAGEN), RNA was extracted and used for cDNA synthesis using SuperScript III First-Strand Synthesis System for RT-PCR (Life Technologies). RT-PCR utilized standard conditions as per Maxima SYBR Green/ROX qPCR Master Mix (Thermo) and BioRad CFX96[™] Real-Time System and C1000[™] Thermal Cycler with 45 cycles of amplification. The sequences for primers utilized are shown in supplemental table S1.

Α TAG MAG PA LPA 2 Col-0 12 Origin В В 100 Percent of Col-0 activity 80 60 40 20 0 tine² tine 12

**Supplemental Figure S11.** Developing Seed Microsome GPAT Assays of Wild-Type and amiRNA Knockdown Lines.

GPAT assays with developing 9-11 DAF seed microsomes utilizing 3.55 nmol [¹⁴C]glycerol 3-phosphate and 25 nmol palmitoyl-CoA, for 15 min at 24°C.

(A) Phosphor image of TLC plate indicating that [¹⁴C]LPA was the major product of developing seed microsome activity with palmitoyl-CoA.

(B) Percent of wild-type (Col-0) GPAT activity in *GPAT9* amiRNA knockdown lines 2 and 12. Mean and S.D. of two replicate assays.

**Supplementary Figure S12.** Testing of Protein:Protein Interactions Between AtLPAAT2, AtDGAT1, and AtLPCAT2.

Cub-LexA bait fusions and Nub prey fusions were produced as described in Figure 8 and in the main text. (A-B) Prototrophic growth assay of yeast strains containing various combinations of Arabidopsis acyltransferase bait plasmids co-expressed with potential NubG-fusion acyltransferase prey plasmids. Serial dilutions of cells expressing different bait-prey combinations were plated on non-selective (A) or selective (B) media. (C) Quantitative measurement of  $\beta$ -galactosidase activity from cell lysates of the strains used in the serial dilution assays. Cultures used for serial dilutions shown in A. and B. contained bait and prey combinations as numbered in C.



Supplementary Figure S13. Sequence Identity Comparisons Between AtGPAT1 and

AtGPAT9 to the Animalia Subset of the NCBI Protein Database.

The top hits to AtGPAT9 and AtGPAT1 are shown first, followed by the best hits from within the individual species that provided the top hits to the alternate AtGPAT sequence. See text for additional details.

#### >AtGPAT9

MSSTAGRLVTSKSELDLDHPNIEDYLPSGSSINEPRGKLSLRDLLDISPTLTEAAGAIVDDSFTRCFKSNPPEPWNW NIYLFPLYCFGVVVRYCILFPLRCFTLAFGWIIFLSLFIPVNALLKGQDRLRKKIERVLVEMICSFFVASWTGVVKY HGPRPSIRPKQVYVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRSEAKDREIVAKKLRDH VQGADSNPLLIFPEGTCVNNNYTVMFKKGAFELDCTVCPIAIKYNKIFVDAFWNSRKQSFTMHLLQLMTSWAVVCEV WYLEPQTIRPGETGIEFAERVRDMISLRAGLKKVPWDGYLKYSRPSPKHSERKQQSFAESILARLEEK

vs Metazoa/Animalia:

PREDICTED: glycerol-3-phosphate acyltransferase 3 [Orcinus orca] Sequence ID: ref|XP 004282203.1|Length: 438Number of Matches: 1 Gene-associated gene details Map Viewer-aligned genomic context Range 1: 75 to 429GenPeptGraphics Next Match Previous Match First Match

Alignment statistics for match #1

Score		Expect	Method		Identit	ies	Positiv	res	Gaps	Frame
259 bits(6	61)	2e- 82()	Composit: matrix ad	ional djust.	139/360	(39%)	211/360	)(58%)	17/360(4%	)
Feature	es:									
Query	24	DYLPS( D P	GSSINEPRGF ++ RG4	K-LSLRDLLD - L D+	ISPTLTEA S EA	AGAIVI IV-	DDSFTRCI +D T+ I	FKSNPP F S	EPWNW WN	N 78 N
Sbjct	75	DESPME	EKGLSGLRGF	RDFELSDVFY	FSKKGLEA	IVI	EDEVTQRI	FSSEEL	VSWNLLTRT	N 131
Query	79	IYI + Y-	LFPLY( + P ++	CFGVVVRYCI	LFPLRCFT I. PLR T	LAFGW: LAF	IIFLSLF: T FL +	IPVNAL +	LKGQDRLRK I. + I.B	K 131 +
Sbjct	132	VNFQY	ISPKLTMVW	VLGVIVRYCV	LLPLRV-T	LAFVG	ISFLVIG	TTLVGQ	LP-ESSLRN	R 189
Query	132	IERVLV + ++	VEMICSFFVA C V	ASWTGVVKYH + +G + YH	GPRPSIRP + +	KQVYVZ + VZ	ANHTSMII ANHTS II	DFIVLE D ++I	QMTAFAVIM +A++	Q 191
Sbjct	190	LSELVE	HLTCCRICVE	RALSGTIHYH	NKQYRPQK	GGICV	ANHTSPI	DVLILT	TDGCYAMVG	Q 249
Query	192	KHPGWV H G -	VGLLQSTILE +G++0 +++	SVGCIWFNR -S +WF R	SEAKDREI SE KDR +	VAKKLI V K+LI	RDHVQGAI R+H+	DSNPLL P+L	IFPEGTCVN IFPEGTC+N	N 251
Sbjct	250	VHGGLN	MGIIQRAMVI	SCPHVWFER	SEMKDRHL	VTKRLI	REHIADKI	KKLPIL	IFPEGTCIN	N 309
Query	252	NYTVMI +MI	FKKGAFELDO FKKG+FE+	CTVCPIAIKY T+ P+AIKY	NKIFVDAF N F DAF	WNSRKO WNS K	QSFTMHL + +L	LQLMTS L++MTS	WAVVCEVWY WA+VC+VWY	L 311 +
Sbjct	310	TSVMMI	FKKGSFEIGO	GTIYPVAIKY	NPQFGDAF	WNSSK	YNMVSYL	LRMMTS	WAIVCDVWY	M 369
Query	312	EPQTIE P T	RPGETGIEFA GE ++FA	AERVRDMISL A RV+ I++	RAGLKKVP + GL ++P	WDGYLI WDG LI	KYSRPSPI K ++	KHSERK E +	QQSFAESIL 0+++++ I+	A 371
Sbjct	370	PPMTRE	EEGEDAVQFA	ANRVKSAIAI	QGGLTELP	WDGGLI	KRAKVKD'	FFKEEQ	QKNYSKMIV	G 429

#### >AtGPAT1

MVLPELLVILAEWVLYRLLAKSCYRAARKLRGYGFQLKNLLSLSKTQSLHNNSQHHLHNHHQQNHPNQTLQDSLDPL FPSLTKYQELLLDKNRACSVSSDHYRDTFFCDIDGVLLRQHSSKHFHTFFPYFMLVAFEGGSIIRAILLLSCSFLW TLQQETKLRVLSFITFSGLRVKDMDNVSRSVLPKFFLENLNIQVYDIWARTEYSKVVFTSLPQVLVERFLREHLNAD DVIGTKLQEIKVMGRKFYTGLASGSGFVLKHKSAEDYFFDSKKKPALGIGSSSSPQDHIFISICKEAYFWNEEESMS KNNALPRERYPKPLIFHDGRLAFLPTPLATLAMFIWLPIGFLLAVFRISVGVFLPYHVANFLASMSGVRITFKTHNL NNGRPEKGNSGVLYVCNHRTLLDPVFLTTSLGKPLTAVTYSLSKFSEFIAPLKTVSLKRDRKKDGEAMQRLLSKGDL VVCPEGTTCREPYLLRFSPLFAELTEDIVPVAVDARVSMFYGTTASGLKCLDPIFFLMNPRPVYCLEILKKLPKEMT CAGGKSSFEVANFIQGELARVLGFECTNLTRRDKYLVLAGNEGIVR

vs Metazoa/Animalia:

PREDICTED: ancient ubiquitous protein 1-like isoform X1 [Xiphophorus maculatus]

Sequence ID: <u>ref|XP_005811174.1|</u>Length: 415Number of Matches: 1 <u>Gene</u>-associated gene details

Map Viewer-aligned genomic context

Range 1: 20 to 262<u>GenPeptGraphics</u> Next Match Previous Match <u>First Match</u> Alignment statistics for match #1

Score		Expect	Method		Identities	Positives	Gaps	Frame
59.3 bits(1	42)	3e- 10()	Composition matrix adju	al st.	69/256(27%)	109/256(429	\$) 31/256(12%)	
Feature	es:							
Query	336	LATLAM +A L +	IFIWLPIGFLLAV · I+ P+G L +	/FRISVG\ + RI +G\	7 7	-FLPYHVANFL F+ V +	ASMSGVRITFKTH +S+ G+ + +	383
Sbjct	20	VALLLI	LIYSPVGVCLMI	LMRIFIGV	/HVFLVSCAIPD	SFVRRFVVRVM	SSVLGMHVRQR	77
Query	384	NLNNGR N R	RPEKGNSGVLYVO N+ L VO	CNHRTLLI CNH T I	)PVFLTTSLG ) + L T	KPLTAVTYSLS P +	KFSEFIAPLKTVS ++ + + S	441
Sbjct	78	NPR	SRDKNTK-LCVC	CNHVTEFI	OHNIINLLTPFN	ITPQLEGSTGFM	CWARGFMEIHSAS	133
Query	442	LKRDRK ++	KDGEAMQRLLSP GE++OR S	KGDI I	LVVCPEGTTCRE LV E TT	LL+FS	ELTEDIVPVAVDA LTE I PVA+	497
Sbjct	134	SQE	AVGESLQRYCS	ADGAPPLI	LVFPEEDTTNGF	RAGLLKFSSWPF	TLTESIQPVALRV	190
Query	498	RVSMFY +	GTTASGLKCLDE +T D	PIFFLMNE ++ +E	PRPVYCLEILKK P VY + L	KLPKEMTCAGGK + ++ G+	SSFEVANFIQGEL S+ E AN +O I	557
Sbjct	191	SRPLLS	LSTVESSWLTDI	LWTFFSI	PCTVYHVSWLPE	VSRQDGE	STQEFANKVQELI	246
Query	558	ARVLGF A LG	ECTNLTRRDK T +T+ DK	573				
Sbjct	247	AIELGI	VSTKITKADK	262				

#### >AtGPAT9

MSSTAGRLVTSKSELDLDHPNIEDYLPSGSSINEPRGKLSLRDLLDISPTLTEAAGAIVDDSFTRCFKSNPPEPWNW NIYLFPLYCFGVVVRYCILFPLRCFTLAFGWIIFLSLFIPVNALLKGQDRLRKKIERVLVEMICSFFVASWTGVVKY HGPRPSIRPKQVYVANHTSMIDFIVLEQMTAFAVIMQKHPGWVGLLQSTILESVGCIWFNRSEAKDREIVAKKLRDH VQGADSNPLLIFPEGTCVNNNYTVMFKKGAFELDCTVCPIAIKYNKIFVDAFWNSRKQSFTMHLLQLMTSWAVVCEV WYLEPQTIRPGETGIEFAERVRDMISLRAGLKKVPWDGYLKYSRPSPKHSERKQQSFAESILARLEEK

PREDICTED: glycerol-3-phosphate acyltransferase 4-like [Xiphophorus maculatus] Sequence ID: ref|XP 005812873.1|Length: 455Number of Matches: 1 IEDYLPSGSSINEPRGKLSLRDLLDISPTLTEAAGAIVDDSFTRCFKSNPPEPWNW---- 77 Query 22 I+D S + EPR +L+ D+ +A I+DD T+ F + E WN Sbjct 93 IODLRHSAGCL-EPRFELA----DVFFFCRKALENIIDDDVTKRFSAOKLENWNLLTRS 146 -----NIYLFPLYCFGVVVRYCILFPLRCFTLAFGWIIFLSLFIPVNALLKGQDRLRK 130 Query 78 ++ + L+ GV++RY +L P R G +F+ L V L +T.R Sbjct 147 NHNFCYISLKVLALWILGVLIRYGVLLPFRVTVAITGIFLFIVLSTVVG--LIPCTKLRT 204 Query 131 KIERVLVEMICSFFVASWTGVVKYHGPRPSIRPKQVYVANHTSMIDFIVLEQMTAFAVIM 190 + + M V S TG++ YH + + + VANHT+ +D I+L ++++ Sbjct 205 YLSDKVHLMGYRLCVRSLTGIITYHNRKNKPKNDGICVANHTTPVDGIILANDHCYSLVG 264 Query 191 OKHPGWVGLLQSTILESVGCIWFNRSEAKDREIVAKKLRDHVQGADSNPLLIFPEGTCVN 250 Q H G +G++Q + +S IWF R E KDR +VAK+L+DHV + +P+LIFPEG CVN Sbjct 265 QLHGGLLGMIQRAMAKSSPHIWFERDEVKDRRLVAKRLKDHVADENKHPVLIFPEGFCVN 324 Query 251 NNYTVMFKKGAFELDCTVCPIAIKYNKIFVDAFWNSRKQSFTMHLLQLMTSWAVVCEVWY 310 N +MF+KG+FE+ CT+ P AIKY+ F DAFWNS K +LL++M+SWA+VC VWY Sbjct 325 NTSVMMFRKGSFEIGCTIYPAAIKYDPRFGDAFWNSSKFGLVGYLLRMMSSWAIVCSVWY 384 Query 311 LEPQTIRPGETGIEFAERVRDMISLRAGLKKVPWDGYLKYSRPSPKHSERKQQSFAESIL 370 L P + GE ++FA RV+ I+ + GL + WD LK ++ E +QQ +++ +LSbjct 385 LPPMNRKEGEDAMQFANRVKAAIAAQGGLVDLIWDAGLKRTKVKDTFKEDQQQLYSKILL 444 Query 371 ARLEE 375 E Sbjct 445 GDHEN 449

AtGPAT9 vs Xiphophorus maculates (top AtGPAT1 hit):

PREDICTED: glycerol-3-phosphate acyltransferase 4-like [Xiphophorus maculatus] Sequence ID: ref|XP_005812873.1|Length: 455Number of Matches: 1 Related Information Gene-associated gene details Map Viewer-aligned genomic context Range 1: 93 to 449GenPeptGraphics Next Match Previous Match First Match

Sco	re	Expect	. 1	lethod	Ident	ities	Positi	ves	Gaps	Frame
235 bits(6	00)	1e- 74()	Composi matrix	tional adjust.	131/36	5(36%)	200/365(	54%) 19/	'365(5%)	
Featur	es:									
Query	22	IEDYLI I+D	PSGSSINE S + E	PRGKLSLRDLI PR +L+	LDISPTLT D+	'EAAGAIV +A I+	DDSFTRC	FKSNPPEF F + E	WNW WN	77
Sbjct	93	IQDLRI	HSAGCL-E	PRFELA	-DVFFFCF	KALENII	DDDVTKR	FSAQKLEN	WNLLTRS	146
Query	78		NIYLFP ++ +	LYCFGVVVRY( L+ GV++RY	CILFPLRC +L P R	FTLAFGW G	IIFLSLF: +F+ L	IPVNALLK V L	GQDRLRK +LR	130
Sbjct	147	NHNFC	YISLKVLA	LWILGVLIRY	GVLLPFRV	TVAITGI	FLFIVLS	TVVGLI	PCTKLRT	204
Query	131	KIERVI +	LVEMICSF + M	FVASWTGVVK V S TG++ V	YHGPRPSI YH +	RPKQVYV + + V	ANHTSMII ANHT+ +1	DFIVLEQM D T+L	ITAFAVIM ++++	190
Sbjct	205	YLSDK	/HLMGYRL	CVRSLTGIITY	YHNRKNKP	KNDGICV	ANHTTPV	DGIILAND	HCYSLVG	264
Query	191	QKHPGV O H G	VGLLQST +G++O	ILESVGCIWFN + +S IWF	NRSEAKDR R E KDR	EIVAKKI +VAK+I	RDHVQGA	DSNPLLIF + +P+LIF	PEGTCVN PEG CVN	250
Sbjct	265	QLHGG]	LLGMIQRA	MAKSSPHIWF	ERDEVKDR	RLVAKRI	KDHVADEI	NKHPVLIF	PEGFCVN	324
Query	251	NNYTVI N +1	4FKKGAFE 4F+KG+FE	LDCTVCPIAIE + CT+ P AIE	KYNKIFVE KY+ F E	AFWNSRK AFWNS K	QSFTMHL +L	LQLMTSWA L++M+SWA	VVCEVWY +VC VWY	310
Sbjct	325	NTSVM	IFRKGSFE	IGCTIYPAAI	KYDPRFGE	AFWNSSK	FGLVGYL	LRMMSSWA	IVCSVWY	384
Query	311	LEPQT: L P	IRPGETGI + GE +	EFAERVRDMIS +FA RV+ I-	SLRAGLKK + + GL	VPWDGYI + WD I	.KYSRPSPI .K ++	KHSERKQÇ E +OC	SFAESIL	370
Sbjct	385	LPPMNI	RKEGEDAM	QFANRVKAAIA	AAQGGLVE	LIWDAGI	KRTKVKD'	IFKEDQQQ	LYSKILL	444
Query	371	ARLEE E	375							
Sbjct	445	GDHEN	449							

AtGPAT1 vs Orcinus orca (top AtGPAT9 species hit):

PREDICTED: neuropilin-2 isoform X6 [Orcinus orca] Sequence ID: ref|XP 004262866.1|Length: 901Number of Matches: 1 Related Information Gene-associated gene details Map Viewer-aligned genomic context Range 1: 827 to 882GenPeptGraphics Next Match Previous Match First Match Alignment statistics for match #1 Expect Method Score Identities Positives Gaps Frame 30.4 0.041() Compositional matrix 14/56(25%) 27/56(48%) 0/56(0%) adjust. bits(67) Features: Query 335 PLATLAMFIWLPIGFLLAVFRISVGVFLPYHVANFLASMSGVRITFKTHNLNNGRP 390

Sbjct 827 PIPAYWYYVMAAGGAVLVLVSVALALVLHYHRFRYAAKKTDHSITYKTSHYTNGAP 882

Supplemental Table S1. Primers utilized for PCR, RT-PCR, & qPCR.

Purpose	Primer Name	Sequence (5' to 3')
Genotyping gpat9-1 (Salk_052947C)		
Gene specific	GPAT9 salk F1	ACTTTCTTTGGAGAGTCGCTGT
Gene specific	GPAT9 salk R1	CATCAACAATGGCACCAGCA
T-DNA left border	LBb1.3	ATTTTGCCGATTTCGGAAC
Genotyping gpat9-2 (GABI_867A06)		
Gene specific	GPAT9 GK F1	GCAGGCGTGATTTGCTAGAC
Gene specific	GPAT9 GK R1	AATGCGGTCATCTGCTCCAA
T-DNA left border	08409	ATATTGACCATCATACTCATTGC
Genotyping qrt1-4 (CS25041)		
Gene specific	Qrt F2	TTTGCCTCTCAGGGTGTTTC
Gene specific	Qrt R1	AATGAGAGCTATGCGGGAGA
T-DNA left border	LBb1.3	ATTTTGCCGATTTCGGAAC
GPAT9 RT-PCR (Fig. S1)		
	GPAT9 ORF start	ATGAGCAGTACGGCAGGGAGGC
	GPAT9 ORF end	TGCAAAAGTGAGTTATGTTTATTGAGA
qPCR of GPAT9 (Fig. S1)		
	GPAT9LP1046	AGAGAGGGTCAGAGACATGA
	G9 qPCR R 1172	CGACTCTGCGAAACTCTGTTG
	qTIP41-like829F	ACATTTCAGTCTCTATCTGCGAAAGG
	qTIP41-like946R	GGATCTTCAGTTTCTGTGTCGTATGC

**Supplemental Table S2**. Gene identifiers for GPAT9, LPEAT1, and LPEAT2 sequences used in Figures1 and S1 in the main text. AGI locus identifiers for the three Arabidopsis genes are described at The Arabidopsis Information Resource (TAIR) homepage (<u>https://www.arabidopsis.org/</u>). The Genbank accession numbers are shown for tung tree GPAT9 (*Vernicia fordii*, Gidda et al., 2009) and *Ricinus communis* GPAT9 [originally annotated as a putative LPAAT, Burgal et al., (2008)]. All other identifiers are as listed for each species in the Phytozome 10.3 database (<u>http://phytozome.igi.doe.gov/pz/portal.html#</u>).

*: not analyzed in this study.

Species	<u>GPAT9</u>	LPEAT1	LPEAT2
Arabidopsis thaliana	At5g60620	At1g80950	At2g45670
Vernicia fordii	FJ479751	*	*
Physcomitrella patens	Phpat.011G104300	*	*
Selaginella	152980	*	*
moellendorffii			
Aquilegia coerulea	Aquca_047_00038.1	*	*
Brachypodium	Bradi1g25790	*	*
distachyon			
Solanum tuberosum	PGSC0003DMT400032021	*	*
Salix purpurea	SapurV1A.0039s0700	*	*
Gossypium raimondii	Gorai.012G158300 and	*	*
	Gorai.005G258500		
Cucumis sativus	Cucsa.099550	*	*
Zea mays	GRMZM2G165681	GRMZM2G096010	GRMZM2G116243
Setaria italica	Si030220m	Si022261m	Si006175m
Oryza sativa	LOC_Os07g34730	LOC_Os05g28960	LOC_Os06g49790
Citrus clementina	Ciclev10028668m	Ciclev10001396m	Ciclev10019536m
Glycine max	Glyma.09G119200	Glyma.04G033600	Glyma.03G019200
Prunus persica	ppa007262m	ppa006689m	ppa003784m
Populus trichocharpa	Potri.004G183300	Potri.014G042200	Potri.014G074300
Ricinus communis	ACB30546	30174.m008937	30170.m014002
Theobroma cacao	Thecc1EG006479t1	Thecc1EG033997t1	Thecc1EG005455t1
Vitis vinifera	GSVIVT01023935001	GSVIVT01009661001	GSVIVT01027580001

# SUPPLEMENTAL REFERENCES

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