

Supplemental Table S1. Prediction of conserved structural domains of FLA proteins in *P. deltoids*.

Name	Precursor protein backbones
PdeFLA1	MSLKSSSLFALCFSSFLFNTVRA SNITQILSQY PDFSTFSSYLTQTQLAGEINS RQTITVLVVENGNMSPLSGKPNGEIKNVLSGHVILDYYDVAKLQKLQNKTA MLTTLFQSSGQAKGQQGFLNVTVLGANSVAFGSAVPGSSLSSNLVKS SVSSQP YNISVLQVSNIIVPAGTGNTNSTT SPVPVGPPKT SPTTAS SPNKPPSTSNPPRP SPTTADGPAAD SPAPSPFAMDGPAA TPAAADGSLAD APSDLKSDASVINTGNN LALLALILLSAFVLA
PdeFLA2	MERLQHLLISLYLLLSINLTTITA Q SPAPAPAPP GPTN LGNTNNGLTILAPSDSA FSALKTGTLRTLTDQEKVELMQFHIVPMFISSSQFDTVSSPLKTHAGSGARFQ LNV TASGNSLNISTGLTNTTISDTVYTDTHLAIYQVDK VLLPLDIF TP KPPPPA PAPAP KLKEESE SPDDAVSKKDISSAVSFVMHHD TVFFIVGT VVAISFSL
PdeFLA3	MQLTVLLSLLFLLSTATTITYG HNITSILQHPSLSTFNHYLTLTHLAGEINRRT TITVCVVDNAAMSEILSKKPSISTIKNILSLHVLLDYFGTKKLHQIRDGTALAA TMFQATGS AP GSTGFVNITDVKGGKVAFGPKDNGGNLDVFYVKSVEEIPYNI SVIQISKLLPSDVAA APTPEPSAMNITDIMS AHGCKVFADTLIANPDA SKTYQ DTIDGGLTVFCPLDDPFKAFLPKFKNLTASGKESLLQFFGVPVYQSLAMLKS NNGIMNTLATNGDKKFDFTVQNDGEDVTLKTRGTTAKIVGTLIDEQPLAIYS IDK VLLP KELFKAAL TPAPAPAPEEAAAD AP KSSKHKKPSADD AP SD SPAD SPD GDAADQTADDNASVRLDGGRLVAMVLSLCLGLLML
PdeFLA4	MAKYLFSSLLLLLTTTATS TFNPICTF SPTPSP TSAT TPAPTP ITNTNTNIAL SP TF APSPIITIP TPAPSSAPTP INNTTTTTL TPTT TPST APTP IPTNKITL TPTF APSL A PTPTII TPILGP SPAPTP ISSSTFTT TPTFDP SPAPTP TNSSIFTATFSSLPP TPTSTFI PQQDDLKFVFQEIQIYNIIDAILGTGDFK N WANALSMADSTTFPISATFFIPSDN SLSPITTSADPDIFPYHIVPQRLSFADLQQFKTFSRLPTLLFDKSILITNNSASHF TLDGSRLTHPDIYTNAAITVHGIDNLL DHSVYGTESGKNSSKPD AVGPPP TPA SPPRPT TPRTFVPSTADDEEFTVHQHGESDAACLCTEVWTVFLVLCVALASKF QRMILVH
PdeFLA5	MMGLCSICSKAA SPPAPTPTP SS SPAPAPAPTTP YKPSLSNLTQDQVKQLILFH ALPHYALADFKNLSQVSPVSTFAGAGGYALNFTDVSGTVHLDSGWSKTKV SSSVHSTDPVAVYQVDKVL FLRRYLVL IYP SPAPAPAP ETSLAAD SP SSDSTGD GSAPGTSLQILLIGSLV
PdeFLA6	MEFSMIIMFSSTLVFLCTPVAYA QTAA TPAPAPTTP SS SPAPAPAPTTP YVSLTDL LSVAGPFHTFLSYLESTKVVDTFQNQANNTDEGITIFKPSLSNLTQDQVKQLI LFHALPHYALADFKNLSQVSPVSTFAGAGGYALNFTDVSGTVHLDSGWSK TKVSSSVHSTDPVAVYQVDK VLLP EAIFGADIPP APAPAPAP ETSLAAD SP SSD STGDGS APGT SPPNSSYRIFGVDVWSQLVLALIGVLVFL
PdeFLA7	MISILAQERLLGAALGAAGFIVYEQRKRIYQSI SEHPQSQLREPIFGKQFR SEFELSWNKAVDQTFGPLVASLNSRQ SPAA APVMPPPT TPVK APPT APSQAPS AQVAT SPGPVDVIKILQKAGH FTVFVRLMQATTEDTELNKELNKTNNGITIFA PSDSAFSSLKAGFLNALSDCKTELVKFHVLPALISSSQFQTVSNPVRTQAGT

	GPRVTLNVTTTGNFVNITTGLTNTSISGTVYTDSQLAIYQIDKVLFPDLDFTPK PPAPAPAPELGKPRKAAPGVESTAPKDN SGALTPLILHDNALLAVSCMVAA IFS
PdeFLA8	MESSPKLSILLILSLSIISSTSIDGVETTTFSNLSPQSPQPQISTSDHFHDHSFSS HTNLLAPILSHLGFTQLAMAVPSLPADSTTTAWSGPSTLFAPSDSSLRTCFS IPDLLHEHIVPGLFSIDYLRKLAFGTKIETLSPGR CITVTSTSLKND SATPSTVK VFIGGVEITHPDLFNNGVLIHGIIRGYIAPLSPFSCDFERLSSLSPFQEGVTPH VTSTTHQQGIGTLVQPAIMRLMLRDAMLRLRSNGFTILSLAMRVKYPELTNL VNMTVFALDDVSIFSGSHGYISSVRFHIVPNHYLSTADLERLPVGATLPTLER GQALVVT SAGGLTG FNTAVPMRINYVRVKVPDVMRNLKIVVHAVYLPFPRIH PTSAAAFDEMMGIGGEGQNIVAAEDAACSAVFEEDGSCGMVPPMPAQVKPS VVVRSDEDDHGL
PdeFLA9	MRKQLLSPFVPFLMFFLYSSTTVAQTPSPAPSGPTNITAILEKAGQFTTLIRLM KSTQEADQINTQLNNSNQGLTVFAPPDNAFTNLKAGTLNSLSDQKQVQLVQ FHIIPNFFSMSSFQTVSNPLRTQAGNSADGEFPLNVTTSGNQVNITTGVNTAT VANTIFTDGQLVVYQVDQVLLPLDLFGTAAAPAPAPSKPKDKVPAKAPAGSK ADASVDSES KGVDEEM
PdeFLA10	MARINPAISQITPTTLTYFLLLLTTTTITPILAITNL TALLSSFPDFSSFTSLL ASTPSITSDLSNRSALTLLVIPNSYLSSSDLTRRLSPSSLTDLLRYHILLQYLSS SDLHQLPPAGALITTLFQTTGRASSNFGSVNITRNPVTNAITISSPSPFSSSNAT VLSLIKTL PYNVSIISVNSLLVPYGF DLMASETRPSLGLNITKALLDGRSFFVA ASLLSASGVVQEFEADEGGAGITLFVPTDSAFSDLSETDVSLQSLPADKKAD VLKFHVLHSYYPLGSLESIVNPVQPTLATEDMGAGSFTLNISRANGSVAIDSG IVLASVTQTVFDQNPVAIFGVSKVLLPKEIFGRNPVLT SKPGNSDMGNALPPA VALSPESSPKMLSSAPGVREENSGVGG LQRFSTLPLLCALVVWYCI
PdeFLA11	MDSHICGVSKTFLFLTLCLSVSSISALPHQNK TGNSTGTGQMINSNSVLVA LLDSHYTELAELVEKALLLQTLEEAVGKHNITIFAPRNEALERQLDPEFKRFL LEPGNLKSLQTLVLFHIIPQRVGSNDWPGHKSNSPRHTTLCNDHLHLITKNSG KKVVGSAELTRPDDVTRPDGVIHGIEQLLVPQSVQEDFNRRRNLR SISAVLPE GAPFVDPRTHRLKKPEPPVRAGSPFVLPIYDAMAPGPSLAPAPAPGPGGPHH HFDGESQVKDFIQTL LLYGGYNEMADILVNLTSLATEMGR LVSEGYVLTVLA PNDEAMAKLT TDQLSEPGAPEQIIYYHIPEYQTEESMYNAVRRFGKIGYDTL RLPHKVAAQEADGSVKFGSGDGSAYLFDPIYTDGRISVQGIDGVLPPEVEK ESTSVKKSVS AVKVATTKPRRGKLMEVACIMLGT LGQDSRFTTCQ
PdeFLA12	MIHQYCHCYCWLKTL SNYRKLSTLLFIPYITRPHILICRLRNSFSTMNSPSTYF WSTSLHAYKGLCIISFEFKHKGSDNNNKEGFGFIFLAKMDSKASSLLFIAFLC LISTSTAFNITKILAQYPEFANFNDLLSQSGLAQEMNSRQTITVLVLDNGSIDG LSGRPLDI AKRILSAHVILDYYDQIKLSKLQKASTIVTTLYQASGVADNRQGF LNISRTAEGIKFGS AMKGAPLVASLVKSIYSQPYNISVLQVSEPIETPGIENMAP PPPPGTAAVPKKAPAPAPSTKTPPAAPPTAKTPAKSPAKSPSKAPAPSKEGPSTP TEAPAEGPVAADGPVAAGGPVADV PADSPADTEVAEEAPAVAPAKAASSRM HVAGATVVIGLFACIMGF
PdeFLA13	MAPSPPCIHIF FASILL SNFHLGFS SSSSSSTLQENHSNGSYSGQINSNSVLVA LLDSHYTELAELVEKALLLQTLEDAVGKHNITIFAPRNEALERDL DPEFKRIN

	<p>LSHNSSLHHHSTLCRDRIKLSQSSEKGLIDSAKIIQVNAVERPDGVIHGIERLL IPRSVQQDFNNRRSLQSIASVKPEGAPAEVDPRTHRLKKPAPPAPKPGSAPVLP DIYDAMAPGPSLAPAPAPGPGGPHHHFNGERQVKDFIETLLLYGGYNEMADILV NLTSLATEMGRVLVSEGYVLTVLAPNDEAMAKLTDDQLSEPGAPEQIIYYHVIP EYQTEESMYNAVRRFGKISYDTLRLPHKVLAQEADGSVKFGHAENSAYLFD PDIYTDGRISVQGIDGVLPLEEKEKSDTKTEMKSVKVAAPQRRGKLLEVA CRMLGTFGQDSHFTTCQ</p>
PdeFLA14	<p>MYFFYSVQHRPHLCPTMQPFILLFWLLFLHTCSQTFCQSPAQSPAATQTKAP VSPPPAGPTDTIQILLKAGRFLSFVRLMKATHVDTQLFSQLNSSTDGITMFAP NDNAFTSLVAGAVGSLNDREKLEFVQFHILPRFLSISDFQTLNPNVKTLAGSD RKFPILTITSDNSVTVSSGLTKTSLNNTIYTDKQVAIYEINKVLVPRDLFPAPP APAPAKPLAEPDPVAPRDASSALVIAWQHRVNVVLFAGGLYIAALVMDP</p>
PdeFLA15	<p>MRQRSFVLVLSLVFFFLHCTKTLCQSPAAPAMTPPKTPVKAPPADSSQAPSA QVATSPGPVDVNKILQKAGHFTVFARLMQATTEDTELNKELENTTNGITILA PTDNAFSSLKAGFLNSLSDDEKTELVKFHVLPAFISTSQFQTVSNPVRTQAGT GPRVTLNVTGTFNFISSGLTNTSISGTVYTDSQLAIYQLDKVLPDIFTPK PPAPAPEPALGPKKAAPDAEAPSAPKDISGAPALLFLLNNALVLAVSCAFGA MIYS</p>
PdeFLA16	<p>MAIALSSFNIFTFLVSTFHLGFSFALQENHSNGTYSQGINSNSVLVALLDS HYTELSELVEKALLQTLEDVAGKHNTIFAPKNEALERDLDPFEKFRLLPEPG NLKSLQTLLLYHIVPNRINPSHNSSLQHHSTLCRDRVKLSSQESGEKGLIDSAKI IQVNAVERPDGVIHGIERLLIPRSVQQDFNNRRSLQSIASVKPEGAEVDPRTH RLKKPAPPAPKPGSAPVLPDIYDAMAGPSLAPAPAPGPGGPHHHFNGEKQVKD FIETLLLYGGYNEMADILVNLTSLATEMGRVLVSEGYVLTVLAPNDEAMAKLT TDQLSEPGAPEQIIYYHVIPYQTEESMYNAVRRFGKISYDTLRLPHKVLAEE ADGSVKFGHPENSAYLFDPIYTDGRISVQGIDGVLPLEEKEKSGPKRKL ALRLLLSHKGEGGCLKWLAGCLGHLDKIHIAPHASK</p>
PdeFLA17	<p>MQRILTILLSLLFLLSTSTTFTRGHNITHILGKHPSTFTNHYLTLTHLAGEINSR TTITVCAVDNAAMSELLSKHPSIATIKNILSLHVLLDYFGTKKLHQIREGTAL AATMFQATGSAPGSTGFVNITDVKGKVAFGPEDNEGNLDVFYVKSLEPIY NISVIQISKVLPDVAAPAPTEPSAMNITDIMSAGCKVFAGTLIANPEASKTY QDNIDGGLTVFCPLDDPFKAFFPKFKNLTASGKVSFLEFFGVPIYQSLAMLKS NNGIMNTLATDGEKKFDFTVQNDGEDVTLKTRISITAKIVGTLIDEQPLAIYTI DKVLLPKELFKAAPTPAPAPAPEKEVADAPKSSKHKKPSSDVVPSDSPADSPD GDLADQTADDNASVTLYGGRLVAMVLSLCSGLLLL</p>
PdeFLA18	<p>MKHHFSVFLFPAIFLLHCTQTLSQTPATAAPAKAPAAASAPPAATSSAQASPP VMVPVQVSKGPVNVIKILQKAGGFVAFIRLIKSTQEDIQVFSQLNDSRDGVTI FAPTDGAFAIAIKSGSGSRFALNVITTENMVNVTSGLTNTSVSAIVYTDSQLAI YQVDKVLLPLDIFAPKALAPAPAPPKPKKDDGAEAPLVPEDTSSSVSCIPLNSL IIFGAGMVAAVFTL</p>
PdeFLA19	<p>MVPQFLLSFLSLLHCPPTLAQSPAAPGPPGPTNVTKILEKGGQFSVFIR LLKATQEDVTLNGQLNNTNNAITIFAPSDNAFSSLKSGTLNSLNDQEKAELV QFHIIQYLSSSQFQTVSNPLTTQAGSGGRLELNVTTTGNSVNITTGLTNTSVS GTIYTDNQLAVYQVDKVLLPLVDIFTPKPPTPAPAPEKPKKRSKAAEAPDAPED</p>

	NSGAVSLTVLNDVVFFGVGIVAAIFSL
PdeFLA20	MKQQYYSLSFSFLLFLHCTTTFAQTSPAA TF AQ AP AVVAAQPHGITNVTKILEKAGHFTIFIRLLRSTQEENHLFSALNDSSSGVTIFAPTDSAFSELKSGTLNLTSDGDKSELVKFHVVPFTLSTSQFQTVSNPLGTWAGTGNRLPLNVTSTYPNSVNI TTGLTNTLSGTVYTDNQLAIYKIEKVLLPKDIFASK APAPAP V APAP EKSTKAVPAATAE SP V AP VDTSALMFTQNHVVGSVIFAAMFAL
PdeFLA21	MATTPLSFFLLSLLLSLSLSLNAQAQTPTAPAPTPSGPVNFTAVLVKGGQFATLIRLLNSTQTLNQIENQLNSSSEGMTIFAPTDNAFNNLKAGALNGLNQEQVQLLQYHTLPKFYTMSNLLVSNPVPTQASGQDGVWGLNFTGQSNQVNVSTGLVEVQINNLRQDSPLAVYPVDKVLLEALFGVKPPTA SPPAP SSKSNSTVAAAEPTSKNSAGGRNVALGLVVGLGLVCMGILS
PdeFLA22	MKQQHSLSSFSFLLLLHCANTFAQTSPAA TF AQ AP AAVVAQPPAA TF TQAAQPHGITNVTKILEKAGHFTIFIRLLRSTQEENHLFSALNDSSSGVTIFAPTDSAFSELKSGTLNTSDGDKSELVKFHVVPFTLSTSQFQTVSNPLGTWAGTGSRLPLNVTSTYPNSVNITTGLTNTLSGTVYTDNQLAIYKIEKVLLPKDIFASK APAPAP V APAP EKPTKAVPSANVE SP V AP VDISSAVTFMHNNVVGLSLVIVAAAMFACNVEGF
PdeFLA23	MASCSHWWH AP VYFIASAVLAFIAISTAMN SP SNNATRPTRPTSNYLSLNASRTLRESGFNIMATLLLI SP EMFFL SP NTTIFAIKDSSLVNTSLPPWFLKNLLQYHTSPLKLSMEDVFKKPQGSCFPTLVDRKKLAVTKIDAKERLAEINHVLVSHPD MVLERRITIHGVL AP FSSLRSKDVFYFGWESIQ AP ICDANSSLVSDANGPRIILEWTRIIHLLSSHRFVSFAIGLNSVLDRILADHKNLSSVTIFAPPELEFVASSSPMLEKIVRLHILPQRATYIELAALPDKQRLRLLPDEDLKITKGVGVGTQGLAINGV EIAAPEIFSSKEFIVHGITQAFKMAKFPNASR
PdeFLA24	MATLQYSLLLSFTLSALVSTILAHNITDILSGFPEYSEFNKYLTQTKLADEINTRQTITVLALNNGAMTALAAKHPLSVIKNALSLLVLDYYDPTKLHQISKGTT LSTTLYQTTGN AP GNLGFVNITDLQGGKVGFSA AP GSKLDSSYTKSVKQVPYNISILEISQPII AP GILT APAPTP SSVNITALLEKAGCKTFASLLQTSGVIKTYQ SAADKGLTIFAPNDEAFKAAGVPDLSKLTNAEIVSLLQYHATATYSPFGSLKTSKDPISTLASNGAGKFDLTVTSAGDSVTLHTGIGPSRVAETVLDSTPLVIFTVD NVLLPVELFGK APSPAP AGEPVS APSPSPSP VAS SPAP ASVE APSP LAA SPPAPP VE TF GG APAD AP FGSENSTADGSAAVHVSVPVQVTVFATVICILMS
PdeFLA25	MKFSMIIVLSSTLLFSCTPLAYAQKVA SPPAPTPTSPAPAPSP YVNLTDLLSVAGPFHNFLNYLESTKVIDTFQNQANNTDEGITIFVPKDDAFKNLKKASLSNLTQDQLKQLILFHALPHYYSLSDFKNLSHVSPVSTFAGAGGYALNFTDTSGTV HLDSGWSKTKVSSSVHSTDPVAIYQVDKVLLEAIFGTDIPP TPAPAPAP DT SP TAD SP TSDDSAGAGS AP GK SPP NSSYRINGVGIWSQLVLAAGVLVFL
PdeFLA26	MPRSPLLALAIISLVLIASTTTVNAHNITRILAKHPQFSTFNHYLTVTHLAAEINRRQTITVLALDNAAMSSLSKQLSVYTLRNVLSLHVLVDYFGTRKLHQITNGTELTATMFQATGS AP GASGYVNITDLNGGKVAFGAEDNDGKLDAVYVKSLEEIPYNISILQISQPLNSAEAE APTAAP TLNVTAILSNQGCKAFSDLLIASGAHT TFEENVDGGLTVFCPTDPVINGFMPKYKNLTAPQKVSLLLYHGIPIYQSLQMLKTSNGIMNTLATNGANKYDFTVQNDGEVVTLETKEPLVVYKINKVCCPGSCLRRLRRKKHRRLRGEGCADGPNAD AP SDESDDQTADNDNGVNKMGGGRL

	AVVARVSFLGW
PdeFLA27	MVPQFLFSASFILFFLLHCPPTLAQSPAAAPAPPGPTNVTKVLEKGGQFSVFIR LLKATQEDVTLNGQLNNTNNAITIFAPSDNAFSSLKSGTLNSLSDQEKAELVQ FHIIPQLSSSQFQTVSNPLTTQAGSGGRLELNVTTTGNSVNITTGLTNTSVSG TIYTDNQLAVYQVDKVLPLDIFTPKPPTPAPAPEKSKKRSKAAAEPESPADT SGAVSFTVLNNVFFGVCMVAAIYSL
PdeFLA28	MDSHYDVSEKTLFLFTLLCFSVASISALPHQNRTGNSTVAGQMINSNSVLVA LLDSHYTELAELVEKALLLQTL EEAVGKHNITIFAPKNEALERQLDPEFKRFIL EPGNLKS LQTLLLFHIIPQRVGSNDWPGHKS NPTRHATLCNDHLHLITKNSG KKFVGAAVLTRPDDVTRPDGVIHGIERLLVPQSVQEDFNRRRNLRISAVLPE GAPEVDPRTHRLKKPEPPVRAGSPFVLPVYDAMSPGPSLAPASAPGPGPHN HFDGESQVKDFIQTL LQYGGYNEMADILVNLTSLATEMGRLVSEGYVLTVLA PNDEAMAKLT TDQLSEPGAPEQIIY YHIIPEYQTEESMYNAVRRFGKIGYDTL RLPHKVVAQEADGSVKFGSGDGSAYLFDPIYTDGRISVQGIDGVLFPEVEK ESTSVKKS VSSVKVATTTPRRGKLMEVACRMLGSLGQDSHFTTCQ
PdeFLA29	MRKQLLSPFVPFLMFFLYSSTTFAQTPSPAPSGPTNITAILAKAGQFTTLIRLLK STQEADQINTQLNNSNQGLTVFAPADNSFANLKAGTLNSLSDQQKVQLVQF HILPNFLSMSNFQTVSNPLRTQAGNSADGEFPLNVTTSGNQVNITTGVNTATV ANTIYTDGQLVVYQVDQVLLPLDLFGTAPAPAPAPSKPEKDVPAKAPAGSKE DASVDSSGASIATVSFGIVLIAAISLKL
PdeFLA30	MSTM LLLFLLILLISSVLAASFNAMEILSTSGYLSMALTLEITSKRLHLES SAATIFAPLDIALARLGQLSVLDLQYHISFVRLSGYLDLSPFGTRIPTLLPNH SLIVTTSLSYFDGKLSINGISIEESALVDFGSLIIFGTSEFFNSSLEISPNLTPAPAP SPSEAWMSTFFGQASHLLMPRGYSIMGTFLDAQLFGIKNQTRLTIFAPVDQA MDAYAKNVSDYSSIFRKHVVPGLFPRQDLEGFNDGTSLPTFSGGFMINLTKS GDVLVLNSVPVIFPEMYQSDWLIHGLNQLLMPPLKEEELVGESFSELDGAE DKPDVLD FDDYVYGAP
PdeFLA31	MAPINPAISHITPTTTLTYFLLLLATT TTTTPILAITNL TALLSSFPDFSSFTSLIT SIPSLTSDLSDRSALTLLVIPNSYLSSSLDLTRRLSPSALADLLRYHILLQYLSSS DLHQVPPSGALITTLFQTTGRASSNSGSVNITRNPVTNAITISSPSPFSSSNATV LSLIMTLPYNVSIISVNSLLVPYGFDLMASETRPTLGLNITKALLDGHSFLVAA SLLSASGVVQFEADEGGAGITLFVPTDSAFSDLSATAISLQSLPADKKADV L KFHVLHSYYPLGSLESIVNPVQPTLATEDMGAGSFTLNISRVNGSVAIDSGIV QASVTQTVFDQNPVVIFGVSKVLLPKEIFGRNPMLTSKPGNTDMGNAQPPVS ALSPENSPKMLSSAPGVREEIKSGVGGLQWLSTLHLLCVFVCNCI
PdeFLA32	MGPQNL MINKSTAKILLHLLLSLLHQITTA TLTDQELDFALSSRLSYGYTLFP NAISTSDLRLQLLNQSSNATSTSTFTLFCPPDSLLFSVDLASTAPHYTKSLFLH VSPSRLSTSDLRNLTAASGGTYIDSLVPNHRLLIANS LAQLNGTVDG SILVNR VRVSVPDFLFGSDIAVHGLDGILVAGFEDKVEDTSFEATWSPANAIGSAERN SPLAGRFPARRRKGRNHRQNGRNGGIRRNRHRGRRINGGRRHRGGRNVSGG TRGDGVTHGAFAMYNHRL
PdeFLA33	MEAF T TLLVLLMIKVLCVSTSP TDIPSR SQDLFVATDEMARAN YFSFVMLINM APLDQKFQGNVTFLMPKDRILSKIRMHPNAVSDFLLRHSIPSLLFDHLLHIP P GSLIPSSNP DYMLNISNKGRKSFFLN NVKISSPDLCTAGSSIRCHGIDGVLLVA

	TDRHPLPACSNSTSPAVVA TPPSP SLPLPDIPSPFPSS APP PGAA APT DQEHNPKH SGSSQLESLSLGGLLKFMATSILLLNARVLYTVGLN
PdeFLA34	MATSPLSLVLLSVFLSLSLHAQAQ APAAPAPAP SGPVNFTAVLVKGG QFVTFIS LLNKTQTFNQIENQINSSSEGMTIFAPTDNAFSLKSGALNGLSQQQQVQLL QYHMLPKFYSLSNLLLVSNPVPTQASGQEGVWGLNFTGQSNQVNVSTGLVE VQVNNALRQDFPLAVYPVDKVL LP PEELFGAKPPSA SPPAP ATKGSSSGKSNSS DTAAEP SP GKNSAGGRNVALGLIFGLGFVSVGILS
PdeFLA35	MKQQSISFFIFLLFLQCTYTFAQ SP AA AP AQ AP AVVA SPP AA APT QAA APH GIT NVTKILEKAG HFTIFIRLLRSTQEENHLFSALNDSSTGLTIFAPTDSAFSELKSG TLNTLSGDGKSELVKFHVVPTFLSTSQFQTVSNPLGTWAGTGNRLPLNVTSY PNSVNITTGLTNTSLSGTVYTDNQLAIYKIEKVLLP KDIFASN APAPAP V APAP EKPAKAVPAANVE SP V AP VDISSAVWFMHNNVVGSGVIVASAVFAL
PdeFLA36	MKQQLISSFSIFLLFLHCANTFAQ IPAA AP AQ AP AVVV APP AA APT QAA APH G ITNVTKILEKAG HFTIFIRLLRSTQEESHLSALNDSSTGLTIFAPTDSAFSELKS GTLNTRLRDGKSELVKFHVVPTFLSTSQFQTVSNPLGTWAGTGSRLPLNVTS YPNSVNITTGLTNTSLSGTVYTDNQLAIYKIEK GMKKVRVSFFKAKGPKA
PdeFLA37	MASHNVTKILEKAG HFTIFIRLLRSTQEENHLFSALNDSSTGLTIFAPTDSAFS ELKSGTLNTRLSDGKSELVKFHVVPTFLSTSQFQTVSNPLGTWAGTGNRLPL NVTSYPNSVNITTGLTNTSLSGTVYTDNQLAIYKIEKVLLP KDIFASN APAPAP V APAP EKPAKAVPAANVE SP V AP VDISSAVWFMHNNVVGSGVIVAAAVFAL
PdeFLA38	MKQQSISFFIFLFFLQCTYTFAQ SP AA AP AQ AP AVVVAQPPAA TP AQAA APH GITNVTKILEKAG HFTIFIRLLRSTQEENHLFSALNDSSTGLTIFAPTDSAFSEL KSGTLNTRLSDGKSELVKFHVVPTFLSTSQFQTVSNPLGTWAGTGSRLPLNV TSYPNSVNITTGLTNTSLSGTVYTDNQLAIYKIEKVLLP KDIFASN APAPAP V A PAP EKPAKAVPAANVE SP V AP VDISSAVWFMHNNVVGSGVIVASAVFAL
PdeFLA39	MPRSLPLLALAI SLVLIAS TTT VNA HN ITRILAKHPQFSTFNHYLTVTHLAAEI NRRQTITVLALDNAAMSSLSISKLSVYTLRNVLSLHVLVDYFGTRKLHQITN GTELTAT MFQATGS AP GASGYVNITDLNGGKVAFGAEDNDGKLDVYVKS EEIPYNISILQISQPLNSAEAE APT A AP TLNVTAILSNQG CKAFSDLLIASGAHT TFEENVDDGLTVFCPTDPVINGFMPKYKNLTAPQKVSLLLYHGIPIYQSLQML KTSNGIMNTLATNGANKYDFTVQNDGEVVTLET KVTTATITGTVKDEEPLV VYKINKVLLPRELFKA AP EKK APAP KGEKDVADGPNAD AP SDESDDQTADN DNGVNKMGGGRLAVVAPSFFFGVVMFFLED
PdeFLA40	MRQQYVFTTLTLLILFSLSCSTTLA Q APAL APAP SGPTNVTKILEKAG QFTLFI RLLKSTQVANQLLQQLNNSNNGMTVFAPTDNAFSSLKSGTLNSLTDEQKVE LVQFHIVPTYLTSSQFQTISNPLRTQAGDSGDGKFPLNITTSGNSVNITTGLTN TSVSGTIYTDGQLAVYQIDQVLQPLQIF AP RPP APAPAP AKSKNKKATTVAD SP DV TP ADNSKAATLQNVGLFGVAALVIALSL

Green: Signal peptide; Red: AGP-like glycosylated regions;
Yellow: Fasciclin domain; Gray: GPI-anchor protein;