

**Supplemental Table S2.** Prediction of conserved structural domains of FLA proteins in *Salix suchowensis*.

Name	Precursor protein backbones
SsuFLA1	<p>MDSHYGVSKQTLFLFTLLCFSVASISALPHQNKGTGNSTVTGQMINSNSVLVALLDSEHYTELAELVEKALLLQTL EEAVGKHNITIFAPRNEALERQLNPEFKRFLLEPGNLKSLQTL LLFHIIPQRVDP AHHS LQRPPGVNHKNSGKKLVGSAALTRPNDVTRPDGVIHGIERLLVPQSVQEEFNRRRNLRSSISAVLPEGAP EVDPRTHRLKKSEPPVRAGSQPVLPIYDAMSPGPSLAPAPAPGPGGPHHHFDGESQVKDFIQTL LHYGGYNEMADILVNLTSLATEMGR LVSEGYVLT V LAPNDEAMAKLTTDQLSEPGAPEQIIYYHIIPEYQTEESMYNAVRRFGKIGYDTRLRLPHKVVAQEA DGSVKFGSGDGSAYLFD PDIYTDGRISVQ GIDGVLP E VEKESTSVKKS VSSV KIATTTPRRGKLMEVACRVLGTFGQDSHFTTCQ</p>
SsuFLA2	<p>MRKQLLSPFVPFLMFFFLYSSTSLAQTPSPAPSGPTNITAILEKAGQFTTLIRLLMKSTQEADQINTQLNNSNQGLTVFAPT DNSFSSLKAGTLNSLSDQQKVQLVQFHILPSFLSMSNFQTVSNPLRTQAGNSADGEFPLNVTTSGNQVNITTGVNSATVANTIYTDGQLVVYQVDQVLLPLDLFGAAPAPAPAPSKPEKDVPAKAPAGSKEDASVDASGASIAAVSFGAVLIAAISLKI</p>
SsuFLA3	<p>MSEMLSKNPSITTIKNILSLHVLLDYFGAKKLHQIRDGSALSATMFQATGSAPGSTGFVNITDVKGKVAFGPKDNGGNLDVFYVKSVEEIPYNISVIQSKLFPSDVAAAPTPAPSAMNLTDIMSAHGCKVFADTLIANPDASKTYQDNIDGGLTVFCPLDDPFKAFLPKFKNL TASGKESFLEFYGVPIYQSLAMLKSNNGIMNTLATNGDKKFDFTVQNDAEDVTLKTRSTTAKIVGTLIDEQPLAIYSIDKVLLPKELFKAAPTPAPAPAPEEAADAPKSSKHKKPAADAAPSDSPADSP EGD AADQTADNNASVRLDGGRLVAIVLSLCLGLLLL</p>
SsuFLA4	<p>MDKYLLSFLLLLTTTTTTATSRSSSTFNIISTFGPTPSPPTSAA TPAPNPITNSNTRI AFSPTYAPSPITTVPTTPAPSSAPTPINNTTNTSATLAPTTTPTLTAPAPTPATETTLTPTSAPSPAPTPTTETTLTPTSAPITAPTPSITSILETSPAPTPIS TPVTTVTFSLSPTPRSP LTPQQDELKFVIEQEIYNVIDAILGAGDFKNWANALTMADSTTFPISSTFFIPSDNSLSPATTTADPDIVPYHIVPQRLSFADLQQFKAFSRLPTLLFDKSLITNNSASNFTLDASRLTHPNIYTNA AIAVHGIDNLLDHSVYGTESGKKSSKPNAAAGPPP TPDSPPPRAFVPSTADHEELTVHHHGESDAACLCTGVWTVFLVLC AALASKFHIMTLVH</p>
SsuFLA5	<p>MQQFILLLSLLFLHNCSTRLCQSSVQSPPTTKAPVPPPSLAVPTDTIKILLKAGRFLSFVRLMKATQVDTQLFSQLNSSTDGITIFAPNDNAFSSRVAGAVGSLNDR EKLEFVQFHILPRFLSISDFQTVSNPVKTLAGSDNKLPLTITTS DNSVKISSGLTKTSISNTIYTDKQVAIYEV D KVLVPKDLFPPAPPAPAPSKPVEESPVVPRDASAGAIIVLHHHLVFFGVGVYIAALVFTL</p>
SsuFLA6	<p>MRQRSVSLVFLSLILFFLQYCTR TSGQSPAAAPAMPPTTPVKAPPNAPSQAPSAQVATSPGPVDVGKILQKAGHFTVFVRLMQATTEDAELNKELNTTNNGITIFAPSDNAFSSLSKSGFLNALSD EDKTELVKFHVLPALISSSQFQTVSNPVRTQAGTGPRVALNVTTTGNFVNISTGLTNTSISGT VYTDSQLAIYQIDKVLFPVDIFT PKPPAPAPAPPELGKPGKAAPGAE SPTAPKEISGALTPLILVHNNALTLAVSCMV</p>

	AAIFS
SsuFLA7	MTMRKQLLSPLVPFLIFFLCISTTVAQTPSPAPSGPANITAVLEKAGQFATFIRL MKSTQEANQINTQLNNSNQGLTVFAPTDNAFTNLKAGTLNSLSDQQKVQLV QFHILPNFLSMSSFQTVSNPLRTQAGNSAAGEFPLNVTTSGNQVNISTGVDTA TVANTIFTNGQLVVYQVDQVLLPLDLFGTAAAPAPAPSKPDKDVPKAPAGS KEDASVDTSGATIAAVSVSAVLIAAISLKL
SsuFLA8	MRRQSFIASFLLFFLLCTKTLGQSPAAAPVKAPTAAAAQTEAAQVAAAPGPV DIIKILQKAGHFTVFVRLMQATTEDIELNKELNNTNNGITIFAPSDNAFSSLKA GFLNSLSDDEKTELVKFHVLPAFIASSQFQTVSNPVRTQAGTGPRVTLNVTTA GNFVNISTGLTNTSLSTVYTDSQLAIYQVDKVLFPDIFTPKPPAPAPAPAELE RPKKAAPDVEAPTAAKDISGAFTAVVHNNAVLLAISVVAAIFFP
SsuFLA9	MGMAQINPAISHITPTTTLCTCYFLLLLLSTTPILAITNITALLSSFPDFSSFTSLLA STPSITSDLSNRSALTLLVIPNSYLSSSLDLTRRLSPSSRTDLLRYHILLQYLS DLHHLPPAGALITTLFQTTGRASANFGSVNITRNPVTNAITISSPSPFSSSNATV LSLIKTLPYNVSIISVNSLLVPYGFDLMASETRPPLGLNITKALLDGHNFVAA SLLSASGVVQEFAYEGGAGITLFVPTDSAFADLSENDPTLATEDMGAGSFT LNISRANGSVAIDSGIVLASVTQTVFDQNPVAFGVSKVLLPKEIFGSPVLT KPGNSDMGNAQPPAVALSPESAPKMLSSAPGAREEIKSGVGGSQWLSNLPFL CVVAVWYCI
SsuFLA10	MDSHIYGVSKKTLFLFTLLCLSVSSISALPHQNKAGNSTGSGQMINSNSVLVA LLDSHYTELAELVEKALLLQTL EEAVGKHNITIFAPRNEALERQLDPEFKRFL LEPGHKSNSPSRHTTLCNDHQHLITQNSGKKLVGSAEVRPDDVIRPDGVIHGI ERLLIPQSVQEDFNRRRNLRSSISAVLPEGAP EVDPRTHRLKKPEPPVRAGSPP VLPIYDAMSPGPSLAPAPAPGPGGPHHHFDGESQVKDFIQTL LLYGGYNEMA DILVNLTSLATEMGRVLVSEGYVLTVLAPNDEAMAKLTDDQLSEPGAPEQIIYY HIIPEYQTEESMYNAVRRFGKIGYDTLRLPHKVVAQEADGSVKFGSGDGSAY LFDPDYTDGRISVQGIDGVLFPEVEKESTSVKKSFSVSVKATTNPRRGKLM VACRMLGTLGQDSRSLHVNEYTVKSRRKRKKRVKMAGTMKTIDKW
SsuFLA11	MDSHIYGVSKKTLFLFTLLCLSVSSISALPHQNKAGNSTGSGQMINSNSVLVA LLDSHYTELAELVEKALLLQTL EEAVGKHNITIFAPRNEALERQLDPEFKRFL LEPGNLKSLQTL LLFHII PQRVGSNDWPGHKSNSPSRHTTLCNDHQHLITQNSG KKLVGSAEVRPDDVIRPDGVIHGI ERLLIPQSVQEDFNRRRNLRSSISAVLPEG AP EVDPRTHRLKKPEPPVRAGSPPVLPIYDAMSPGPSLAPAPAPGPGGPHHHF DGESQVKDFIQTL LLYGGYNEMADILVNLTSLATEMGRVLVSEGYVLTVLAPN DEAMAKLTDDQLSEPGAPEQIIYYHIIPEYQTEESMYNAVRRFGKIGYDTLRL PHKVVAQEADGSVKFGSGDGSAYLFDPDYTDGRISVQGIDGFCFPRSRRKV LLLRNPSVLLRLPLPIQEEGN
SsuFLA12	MDSHIYGVSKKTLFLFTLLCLSVSSISALPHQNKAGNSTGSGQMINSNSVLVA LLDSHYTELAELVEKALLLQTL EEAVGKHNITIFAPRNEALERQLDPEFKRFL LEPGNLKSLQTL LLFHII PQRVGSNDWPGHKSNSPSRHTTLCNDHQHLITQNSG KKLVGSAEVRPDDVIRPDGVIHGI ERLLIPQSVQEDFNRRRNLRSSISAVLPEG AP EVDPRTHRLKKPEPPVRAGSPPVLPIYDAMSPGPSLAPSSRTRWAHHHFD GESQVKDFIQTL LLYGGYNEMADILVNLTSLATEMGRVLVSEGYVLTVLAPND EAMAKLTDDQLSEPGAPEQIIYYHIIPEYQTEESMYNAVRRFGKIGYDTLRLP

	HKVVAQEADGSVKFGSGDGSAYLFDPDYTDGRISVQGIDGVLFPEVEKEST SVKKSFSVSVKVATTNPRRGKLMVACRMLGTLGQDSRFTTCQ
SsuFLA13	MDSKASSLLFIAFLCLISTSTAFNITRILAQYPEFASFNDLLSQSGLAQEMNGR QTITVLALDNGSIDGLSGRPLDIAKRILSAHVILDYDQIKLSKLQKASTIVTT LYQASGVAEDRQGFLNISRTAEGIKFGSAMKGAPLSASLVKSIYSQPYNISVL QVSEPIETPGIENMAPPPPGTAAVPPKTPAPAPSTKTPPAAPTAKTPAKSPAK SPSKAPAPSKEGPSTPTEAPAGGPVADGPVADVPSNSPGPDKAASSRMHVAG ATVVIGLFIACIMGF
SsuFLA14	MESSLKFLILLIFSFSIITISIAFDGVETTTNLSPSPPPQQQRITSPPPQVSNSDNL HDHSFFSHTTLLAPILSHLGFTQLAMVAPSLSADPTTTAWSGPFTLFAPSDSSL STCFSCSIPDLLREHIVPGLFTIDYLRKLAFGTKIETLSPGRCMTVTSNSLNND TVSHSSVKVFIGGVEITHPDLFNNGVLIHGIQGYIAPLSPLSCDVERLSSLSFP NHERVTPHVTSTTHQQGVGTLMQPAIMRLMLRDAMLRLRNNGFTILSLAMR VKYPELVTLANMTVFALDDVSIFSGSHGYINSVRFHIVPNHYLSITDLERLPV GASLPTLERGQALVVTSAGGFNMAVPMRINYVRVKVPDLMKNLKIHAVHSVY LPFPRIHPTSAAPYDEITGGGGGGYNVVAEEAEDGACSMVYEEDGSNCW MVPPMPAQVKPSVAVQIDEDHHGL
SsuFLA15	MESSLKFLILLIFSFSIITISIAFDGVETTTNLSPSPPPQQQRITSPPPQVSNSDNL HDHSFFSHTTLLAPILSHLGFTQLAMVAPSLSADPTTTAWSGPFTLFAPSDSSL STCFSCSIPDLLREHIVPGLFTIDYLRKLAFGTKIETLSPGRCMTVTSNSLNND TVSHSSVKVFIGGVEITHPDLFNNGVLIHGIQGYIAPLSPLSCDVERLSSLSFP NHERVTPHVTSTTHQQGVGTLMQPAIMRLMLRDAMLRLRNNGFTILSLAMR VKYPELVTLANMTVFALDDVSIFSGSHGYINSVRFHIVPNHYLSITDLERLPV GASLPTLERGQALVVTSAGGFNMAVPMRINYVRVKVPDLMKNLKIHAVHSVY LPFPRIHPTSAAPYDEIIGGGGGGYNVVAAEEAEDGACSMVYEEDGSNCW MVPPMPAQVKPSVAVQIDEDHHGL
SsuFLA16	MAMAPSTSCSNIFFAFLLLSFFYPGFSSTLQENHGNGSYSGQISSNSVLV ALLDSHYTELAELVEKALLQTLEDVGEHNITIFAPKNEALERDLDFEFKRF LLEPGNLKSLQTLLLYHIVPNRINLSRNTSAHHRSTLCRDRIKLSSQESGEKFI DSAKIIQVNAVERPDGVIHGIERSLQSIKAVKPEGAPAEVDPRTHRLKKPAPPSK PAPAPGPGGPHHHFNGEKQVKDFIETLLLYGGYNEMADILVNLTSLATEMGR LVSEGYVLTVLAPNDEAMAKLTQDSEPGEQIIYYHVIPEYQTEESMYN AVRRFGKISYDTRLRLPHKVLAQEADGSVKFGHAENSAYLFDPDYTDGRISV QGIDGVLFPLEEEKLDTKTEIKSVKVAAPQRRGKLLEVACRMLGTGFKDSH FTTCQ
SsuFLA17	MAATKILLSLLSLFSLPSSFSIPTETLREAAVTLNSNGYLSMSLTPLVSNLL PHITPSLTIFSPCDTAFTQAGQPPLSILRLHFSPLSFPLNSLESLSLGAKIPTLFPN HSLTITSTGYDISLNGVKIRDSPVYDDGSLVILGVDRFFDPGFGASGQNLGCS VKVSSDCYSYNEASRVLKSKEYSVMASFLDLQLMAGFKDKTALTIFAPVDE VIKAFLGDLSEYSSMFRKHVVPCKIMWGDVNFDDGVVLETYLKGFIAVS TSGDNLMLNDQASVNFPMYHNDWLVIHGLRSILMEPESEYSFLDDGDEF
SsuFLA18	MRPQSFIISVLSLILFFLHCTKTLCQSPAAAPAMAPPTTPVKAPFADSSQAPSAQ VATSPGPVDINKILQKAGHFTVFARLMQATTEDTELNKNLNTNNGITILAPT DSAFSSLKAGFLNSLSDKTELVKFHVLPAFISTSQFQTVSNPVRTQAGTGP

	RVTNLNVTTTGNFVNISGLTNTSISGTVYTDSQLAIYQLDKVLYPLDIFTPKPP APAP <sup>EP</sup> ALGKPGKA <sup>AP</sup> GVE <sup>SPT</sup> AP <sup>KD</sup> ISAAPTQLFLHDNALLAVSCAFAVIIS
SsuFLA19	MAMAMAQSSSNIFFTFLLFSTFHLGFSSA <sup>LQ</sup> ENHSNETYSGQINSNSILVALL DSHYTELAELVEKALLLQTLEDAVGKHNITIFAPKNEALERDLDPFKRFLLE PGNLKSLQTLLLYHIVPDRVNLSHTSSVHHHSTLCSDRVKLSGQKSGDNLIDS AKIIQVNAVERSDGVIHGIEKLLIP <sup>RS</sup> VQQDFNNRRSLRSISAVKPEG <sup>AP</sup> EVDP RTHRLKIP <sup>AP</sup> PEKPGSPVLPIDYDAM <sup>AP</sup> GPSL <sup>AP</sup> AS <sup>TP</sup> AP <sup>GG</sup> PHNHFNGEKQV KDFIETLLSYGGYNEMADILVNLT <sup>SL</sup> ATEMGRVLVSEGYVLTVLAPNDEAMA KLPTDQLSEPGAPEQIIYYHVIPEYQTEESMYNAVRRFGKISYDTLSLPHKVL SQEADGSVKFGDAENSAYLFDPIYTDGRISVQGIDGVL <sup>FP</sup> IEEKEKSQTKME IKSVKVAVKPQRRGRLLLEVACRMLGTFGQDSHFTTCQ
SsuFLA20	MQRLTLLLSLIFFLSTATTFTRG <sup>HN</sup> ITHILGKHP <sup>SF</sup> STFNHYLT <sup>TL</sup> HLAGEINRR TTITICAVDNAAMSELLSKHPSIATIKNILSLHVLLDYFGTKKLHQI <sup>RD</sup> GTALA ATMFQATGS <sup>AP</sup> GSSGFVNITDVKGKVGFGPEDNEGNLDVFYVKSLEEIPYN ISVIQISKVLPDVA <sup>APT</sup> PEPSAMNLTDIMSAHG <sup>CK</sup> VFADALLANPEASKTY QDNMDGGLTVFCPLDDPFKAFSPRFKNLTASGKVSFLEFFGVPVYQSLAMLR SNGIMNTLATDGEKKFDFTVQNDGEEVTLKTRSVTAKIAGTLIDEQPLAIY TIDKVLLP <sup>KEL</sup> FKA <sup>APAPAP</sup> EKEVA
SsuFLA21	MKNHFSVFLFSAILLSLHCNQTL <sup>QS</sup> PAA <sup>AP</sup> AK <sup>AP</sup> AAAS <sup>APP</sup> PAATSTAQAS <sup>SP</sup> PVMVPVQVSKGPVNVIKILQKAGGFAVFIRLIKSTQEDIQVFSQLNDSRDGVT IFAPTDGAFS <sup>AI</sup> KSGVLNSLSVLNSLS <sup>SD</sup> HQKIELVQFHIIPKILTTANFQT <sup>VS</sup> NP ITTLAGSGSRFALDVITTENMVNVTSGLTNTSVSAIVYTDSQLAIYQVDKVLL PLDIF <sup>AP</sup> KS <sup>LAPAPSPP</sup> KPKKDDGEE <sup>TP</sup> VVPEDISGAVSCAMLNSLVIFGAGM AAAVFPL
SsuFLA22	MLLKLAQ <sup>SP</sup> AA <sup>AP</sup> GPPGPANVTKILEKGG <sup>QF</sup> SVFTRLLKATREDVT <sup>LN</sup> GQLN NTNNAITIFAPSDSAFSSLKPGTLNSLNDQEKAELVQFHIIPQYLSSSQFQTLN VTTAGNSVNITTGLTNTSVSGTIYTDNQLAVYQVDKVLLP <sup>VD</sup> IF <sup>TP</sup> KPPPP <sup>AP</sup> AP <sup>EK</sup> TRRGSKSAE <sup>SP</sup> DTSVDNSGAVTLNVLDNAVFFGVGIVAVIFSL
SsuFLA23	MKQQCSLSFFSFLLLRCTSTFA <sup>QS</sup> PAAA <sup>AP</sup> AAQ <sup>AP</sup> AAVVAQPPAA <sup>TP</sup> AAQAQ PHGAITNVTKILEKAG <sup>HFT</sup> IFIRLLRSTQEDSHLFSALNDSSSGVTIFAPTDGAF SELKSGTLN <sup>TL</sup> SDGDKSELVKFHVVP <sup>TF</sup> LSTSQFQTVTNPLGTWAGTGNRLP LNVTSYPNSVNITTGLTNTSLSGTVYTDSQLAIYKIEKVLLP <sup>KD</sup> IFASK <sup>APAPA</sup> PV <sup>APAP</sup> EKPTKAVPAATVE <sup>SPVAP</sup> VDIPVHFCSLKIMWWDPLA
SsuFLA24	MATTPLSLFLLSLLLSLSLYAQAQ <sup>TPA</sup> APAP <sup>TP</sup> SGPVNFTAVLEKGGQFVTLIR LLNKTQTLN <sup>QID</sup> NQLN <sup>SS</sup> SEGMTVFAPTDNAFN <sup>NL</sup> KAGALNDLSQ <sup>QE</sup> QASG PDGVWGLNFTGQSNQVNVSTGLVLVQINN <sup>AL</sup> RQDFPLAVYPVDKVLLPEAL FGVKPPSA <sup>SPPAP</sup> SSKSNATEAAAGPTTDN <sup>NA</sup> AGGRNVALGLVVGLGLVCIGI LS
SsuFLA25	MTLHLRTA <sup>AP</sup> AAQ <sup>APP</sup> AVVAQPPAA <sup>TP</sup> TQAA <sup>AP</sup> HGITNVTKILEKAG <sup>HFT</sup> IFIRL LRSTQEENHLFSALNDSSSGLTIFAPTD <sup>SA</sup> FSELKSGTLN <sup>TL</sup> SDGDKSELVKFH VVPTFLSTSQFQTVSNPLGTWAGTGSRLPLNVTSYPNSVNITTGLTNTSLSGT VYTDSQLAIYKIEKVLLP <sup>KD</sup> IFASN <sup>APAP</sup> EPVQ <sup>AP</sup> VREKPTKAVPAANVE <sup>SPV</sup> AP <sup>VD</sup> ISSSVTFMQNSVIGSVGIVLAAAMFAL

SsuFLA26	MKKQYSSISFSVFILFLHCSNTFAQSPAAAPAAQAPPAVVAQPPAATPTQAAAAPN GITNVTRILEKAGHFTIFIRLLRSTQEENHLFSALNDSSSGLTIFAPTDsafSEL KSGTLNtLSDGDKSELVKFHVVPTFLSTSQFQTVSNPLGTWAGTGSRLPLNV TSYPNSVNITTGLTNTSLSGTVYTDNQLAIYKIEKVLLPKDVFVGSKAPAPAPA APVREKPTKAVPEATVESPVSPVDISSALMFTHNNVVGsvGMVAAAMFAL
SsuFLA27	MKKQYSSISFSVFILFLHCSNTFAQSPAAAPAAQAPPAVVAQPPASTPTQAAAAPN GITNVTRILEKAGHFTIFIRLLRSTQEENHLFSALNDSSSGLTIFAPTDsafSEL KSGTLNtLSDGDKSELVKFHVVPTFLSTSHRLPLNVTSYPNSVNITTGLTNTS LSGTVYTDNQLAIYKIEKVLLPKDVFVGSKAPAPAPAAPAREKPTKAATVESPV SPVDISGALMFTHNNVVGsvGIVAAAMFAL
SsuFLA28	MRKQYSLSSFSFFILFLHCTNTFAQSPAAAPAAQAPAAVVAQPPAATPTQAAAAP HGITNVTKILEKAGHFTIFIRLLRSTQEENHLFSALNDSSSGLTIFAPTDsafSE LKSGTLNtLSDGDKSELVKFHVVPTFLSTSQFQTVSNPLGTWAGTGSRLPLN VTSYPNSVNITTGLTNTSLSGTVYTDSQLAIYKIEKVLLPKDIFASNAPAPAPV QAPVREKPTKAVPAANVESPVAPVDISSSVTFMQNSVIGsvGIVAAAMFAL
SsuFLA29	MKKQYSSISFSVFILFLHCSNTFAQSPAAAPAAQAPPAVVAQPPAATPTQAAAAPN GITNVTRILEKAGHFTIFIRLLRSTQEENHLFSALNDSSSGLTIFAPTDsafSEL KSGTLNtLSDGDKSELVKFHVVPTFLSTSQFQTVSNPLGTWAGTGSRLPLNV TSYPNSVNITTGLTNTSLSGTVYTDNQLAIYKIEKVLLPKDVFVGSKAPAPAPA APVREKPTKAVPEATVESPVSPVDISSALIHTSLAHCIVIFFIEH
SsuFLA30	MASCSHWWHAPVYFIASAVLAFIAISTALNSPPSKATRPTRPISNHISLNASRT LRESGFNIMATLLLIAPEMFFSSENTTIFAIDSSSLVNTSIPPWFLKNLLKYHTS PMKLSMEDVFKKPQGSCFPTLVDRKKLAVTKIDAKQRLAEINHVLVSHPD VLERQIAIHGVLAPFSSLRSKDVYLGWESIQAPICDDNSSLVSDATDPGIVLE WTRIIHLLSSHRFVSFAIGLNSVLDRILADHKNLSSVTIFAPPEFDFVASSSPML ERIVRLHILPQRATYKDLAALPDKHRLRLLPDVDLEITNDVNVYTQGLAING VEIAAPEILSSKEFIVHGITQAFKMAKFPNASR
SsuFLA31	MAALRYSLLSFTLSALVSTVLAHNITDILSGFPEYSEFNKYLTQTKLADEINT RQTITVLALNNGAMSALAAKHPLSVIKNALSLLVLDYFDPTKLHQISKGST LSTTLYQTTGNAPGNLGFVNITDLQGGKVGFSAAPGSKLESSYTKSVKQVP YNISILEISQPIIAPGILTAPAPTPSAGCKTFASLLQTSGVIKMYQSAADKGLTIF APNDEAFKAAGVPDLSKLTNAEVVSLQYHATASYSPPFGLKTSKDPISTLAS NGAGKFDLTVTSAGDSVTLHTGIGPSRVAETVLDSTPLVIFTVDNVLLPVELF GKAPSPAPAEPPVSAPSPSPIASTPAPAAIVEAPSPLAAAPPAPEVETPGGAPADA PFGSENSTADGNAAVHVIVPVQVTVFAAVICSILMS
SsuFLA32	MEFSVLIVLSSALLFACAPLAYAQKVASPPAPTPTPSPAPAPSPFYVNLTL LLSV AGPFQNFNLNyleSTKVIDTFQNQANNTDEGITIFVPKDDAFKNLKNPSLSNLT QDQLKQLILFHALPHFYSLSDFKNLSQVSPISTFAGAGGYALNFTDSSSGTVHL DSGWSKTKVSSSVHATDPVAIYQVDKVLLPEAIFGTDIPPAPAPAPETSPITA DSPITSDDTTGSSPANSLPNSSFRINGVGIWSQLVLGIAGVVVFL
SsuFLA33	MPRPLPLTLAVSLALLASTATVNAHNITRILAKHPQFSTFNHYLTVTHLAAEI NRRQTITVLALDNAAMSSLLSKQLSVYTLRNVLSLHVLVDYFGTRKLHQITN GTEVTATMFQATGSAPGSSGYVNITDLNGGKVAFGAEDSNGKIDAVYVKSLV EIPYNISVLQISQPLNSAEAEAPTAAPTLNVTAILSKQGCKAFSDLLIASGAHT

	TFEENV DGG LTVFCPTDAVINGFMPKYKNLTAPQKVSLLLYHGIPYQSLQML KTSNGLMNTLATNGANKYDFTVQNAGEVVTLETKVTTATITGTVKDEEPLV VYKINKVLLPRELFKAVQKAPAPKGAKVVADGPAADAPSDDESVDQTADNNG VNKIDGGRLAVVALSLFYGVVMFS
SsuFLA34	MKRQISFSFSLVLLFLHCSQTLSPPTAPAKAPAAATAPPLAATSAQASPPV MVPVQVSKGPVNVIKILQKAGHFAILTRLIKSTQEDIQLFSQLNDSRDGVTIFA PTDGAFSAIIKSGVLNSLTDHQKIELVQFHIPRVLSTANFQTVSNPITTLAGSG SRFTLDVITTESMVNVTTGLTNTSVSAIVYTDSQLAIYQVDKVLLPLDIFAPK PLAPAPAPQPKKDDGEESPMIPEDTSGSVTCMVHNTLFMFGVGIVAAAIPL
SsuFLA35	MVPQFLFSASFILFLLYCPTILAQSPAAAPAPAGPTNVTKVLEKGGQFSVFIR LLKATQEDVTLNGQLNNTNNAITIFAPSDSAFSSLKSGTLNSLNDQEKAELVQ FHIIPQFLSSSQFQTVSNPLTTQAGSGGRLELNVTTTGNSVNITTGLTNTSVSG TIYTDNQLAVYQVDKVLLPLDIFTPKPPTPAPAPEKTKKRSKAAAPESEADA SGAVSFAVLNNVFFGVCMVAIYSL
SsuFLA36	MSLRFSPVFALCFSLLFFNTARAFNITQILSQYSDFKTFSSYLTETQLAGEINS RQTITVLVVEDGNMSPLSGKPKDEIKNVLSGHVILDYYDVAKLQKLQNKTA MLTTLFQSSGQAVGQQGFLNVTVLSTNSVAFGSAAPGSSLSSNLVKS SVSSQP YNISVLQVSNIIVPAGTGKTNSTTSPVTIGSPKTSPSPASPEKPPSSSNPPPSK APAPSTAKPPPTNAPAPSMVKPPAANAPSATPEAMSTSPVEGPSPATADGPSA DSPITLSPAMDGPVAAAPAADGPLADAPSDPKSDASVINPGNNLASFAPILL AFALA
SsuFLA37	MATVLLFFLILLISSSVLAASFNSNALEILSASGYLSMALTLQITSKRLNLES SAATIFAPLDIAFARVGQLSALDLQYHISPLRLSGDYLSLSPFGAKIPTLLPNHS LTVTSLGYFDGKLSINGISIEESALVDFGSLIIFGMGEFFSSSLEISPNITPAPSP SPVTSLGDTSQNEPSGMDADYLGQASHLLITIFAPLDQAMEEYAKNASDYS SIFRHHVVPGLFPRQDLEGFNDGTSPLTFFRGFMINLTRSGDVLVLNGVPLIFP DMYQSGWLVIHGLNQLLMPPMKEIVGESFSELDGGEDKPDVLD FDEYVYGSP
SsuFLA38	MDSKVSSLLFIAILFLLSSTSTAFNITKILAQYPEFASFNDLLAQSGLAQEINGR ETITVLALDNGSIDGLSGRPVDIAKRILSAHVILDYYDQIKLSKLQKASTIVTT LFQASGIADDRQGFLNVSKTAEGIKFGSAMKGAPLVASLVKSVYAQPYNISV LQVSEPIEAPGIENMAPPPAAVPKKAPAPAAKTPSKAPAPSKVEPSTPAESP TEGPVAADVPAASPLADAPLADEVPAKAASSQM HVGGAVVVVGLLACMVG F
SsuFLA39	MAPINPAISHITPTTTLTYFILLLLTTTTTTTPILAITNLTALLSSFPDFSSFTSLIA STPSLTSDLSDRSALTLLVIPNSYLSSSLDLTRRLSPSALADLLRYHILLQYLSF SDLHQVPPSGTLITTLFQTTGRASSNSGSVNTLPYNVSIISVNSLLVPYGF DLM ASET RPTLGLNITKELLDGHNFFVAASLLSASGVVQEFEADEGGAGITLFVPT DSAFSDL SATAISLQSLPADKKADV LKFHVLHSYYPLGSLESIVNPVQPTLAT EDMGAGSFTLNISRVNGSVAIDSGIVQASVTQTVFDQNPVVIFGVSKVLLPKE IFGRNPVLTSPKPSDMGNAQPPVSVLSPETSPKMLSSAPGVREEIKSGVGGL QWLSTLPLL FVVFVCNCI
SsuFLA40	MSPQDL MINKSTSKILLHLLLSLLHQITTAALTDQQLEFALLSLRSHGYTLFP NAISTDLRFHLLNQTN NATSTFTLFSPPDSLLFSVDLSSTASHYTKSLFLHVS



	<p>PSRLSMSDFRNLTAAASGGTYIDSLVPNHRLLINNSQARLNGTVDGSVLVNRV  RVSVPDFLFGSDIAVHGLDGILVAGFDDKVEDTSFEAATS<span>SP</span>ANEIWSAELN<span>SP</span>  PAVRFPARKRNGKNRRRNGKNRRRNGRNGGITRSNHRGRRIHDGFGRRGGGR  NIGGGTRGDGTHGAFSKYNNRL</p>
SsuFLA41	<p>METFTLLVLLMKVLVCAT<span>SP</span>TGIPSKSQDLVVATNEMARAN<span>YFSFVLLINMS</span>  PLDQRLQENVTFMLPKDRMLSKIRMHQNAVSGFLLRHSIPSPLLFDHLQHIPP  GSLIPSSDPDYMLNISNKGRKNFSLNNVRITSPNLC TAGSSIRCHGIDGVL FVA  TDRPHLPACSNSS<span>SP</span>AV<span>AP</span>PLPSDIPSPF<span>SP</span>APAGAA<span>AP</span>TDQEH<span>SP</span>KHSGSSH  LESPSPGGLLK FVATSILVLNVWVL</p>
SsuFLA42	<p>MATSPLSLILSLFLSLHAQAQ<span>AP</span>A<span>AP</span>ASSGPVNFTAVLEKGG<span>QFVTFM</span>  RLLNKTQTFNQIENQLNSSSEGMTIFAPTDNAFN NLKAGALNGLSQQQVQ  LLQYHMLSKFYSLSNLLVSNPVSTQASGHEGVWGLNFTGQSNQVNVSTGL  VEVQINNPLRQDFPLAVYPIDKVLLPEELFGVNRTIA<span>SP</span>PPATSSGKSNSSETA  AAEP<span>SP</span>GKNSAGGRNVALGSIVGLGLVCMGIIS</p>
SsuFLA43	<p>MKPQYFLSSFSIFLLFLHCTNTFAQ<span>SP</span>AA<span>AP</span>AQPPAVVA<span>SP</span>AA<span>TP</span>TQAA<span>AP</span>HG  ITNVTKILEKAGHFTIFIRLLRSTQEENHLFSALNDSSTGLTIFAPTDSAFSELK  SGTLNLTSDGDKSELVKFHVVPFTLSTSQFQTVSNPLGTWAGTGNRLPLNVT  SYPNSVNITTGLTNTSLSGAVYTDNQ LAIYKIEKVLLPKDIF<span>AP</span>N<span>AP</span>APAPVKP  <span>AP</span>EKPAKEVPEVTAE<span>SP</span>AASVDISSARIFTRNLVVG SAGLLASAMFSL</p>
SsuFLA44	<p>MKQQLISSFSMIFLFLHCANTFAQIPAA<span>AP</span>AQ<span>AP</span>AVVVA<span>SP</span>AA<span>TP</span>TQAA<span>AP</span>H  GITNVTKILEKAGHFTIFIRLLRSTQEENHLFSALNDSSTGLTIFAPTDSAFSEL  KSGTLNLTSDGDKSELVKFHVVPFTLSTSQFQTVSNPLGTWAGTGNRLPLNV  TSYPNSVNITTGLTNTSLSGAVYTDNQ LAIYKIEKVLLPKDIFASN<span>AP</span>APAPVA  <span>PA</span>EKPAKAVPAATVE<span>SP</span>AASVDISSALIFTHNLVVG SAGLLASAIFSL</p>
SsuFLA45	<p>MKPQYFLSSFSIFLLFLHCTNTFAQ<span>SP</span>AA<span>AP</span>AQPPAVVA<span>SP</span>AA<span>TP</span>TQAA<span>AP</span>HG  ITNVTKILEKAGHFTIFIRLLRSTQEENHLFSALNDSSTGLTIFAPTDSAFSELK  SGTLNLTSDGDKSELVKFHVVPFTLSTSQFQTVSNPLGTWAGTGNRLPLNVT  SYPNSVNITTGLTNTSLSGAVYTDNQ LAIYKIEKVLLPKDIF<span>AP</span>N<span>AP</span>APAPVKP  <span>AP</span>EKPAKEVPEVTAE<span>SP</span>AASVDISSARIFTRNLVVG SAGLLASAMFSL</p>
SsuFLA46	<p>MDRLQHLLISLYLLILFINLTKTTAQ<span>SP</span>APAPAPP GPTNVIKILKKAGHFKNFIR  LLKSTQLDSNLNSQLGNTNNGLTIFAPSDTAFSVLKTGTLP SLTDQEKLELMQ  FHIVPMFISSSQFETVSSPLKTHAGSGARTHQH HYFDTVYMDTNLAIYQVDK  VLLPLDIF<span>TP</span>K<span>PA</span>PAPAPELKAESE<span>SP</span>DDAVSKKDISSGVSFAMLRD TVLFIAA  TVAAISFSL</p>

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