

Supplementary Table S3 Protein backbones of XYLPs in pepper, tomato and potato

Name	Gene Locus	Protein backbones
CanXYLP1	Capana08g002006	MSIKMTPFALFFLITICTLSSTTVES ASRSAPAPAVDC NN LVLNLAD CL LSFV TNG STETKPQGT CC SGLK MV LKT DAE CL CEGFKNSAQLGVVL NVT KAMSLPAA CH VSA PSVSN C GLSTDTGAAPALSPVAGSPTMSAVAPTTAEGV NGGAPV SP SDSTTLALS VGQLVLT VVVAVFCWF
CanXYLP2	Capana06g000685	MAKSTKITTTIHTFLLLSLFSPLIPSTKS QDSPPAPV APA PSPGVD C FRVLY NMSD CLTFVERKS NLS IPGKG CCP EIAGLLDSNP ICYC QMLGRAHSGAKIGFNIDVDKAV KLPSA C NLEFPSS TCS DLGIPVGAPLASEQSPAPSPGG FATSPTS SDSKDN AASIIVFSKMQ LLGVAIM FFTSLF
CanXYLP3	Capana06g000094	MKMLTSAVFVLAIAIQVSG QSDD C QQVIVGLAP CL DYIQG NAT KPSSG CC TQLATIVKNQP QCLC QVVNG GSASSMGIN VNQT QAMALPKA CNV QTPSVNI CKAT T PSGSPGSPSTPSGGSGK EP SG NSGYR VKLPYSLL F TLVV AASFATVFTI
CanXYLP4	Capana06g000095	MASKMNVMALVMVLNVAIFFNGALG QSS C MTTLVG LSP CL NYVSG NS STPSS CC TSLASVVQSNP QCLC M L VNGGGSNLGIA INQ TLALGLPSA C NLQTPPLSR C NA ANGPTASVPASSPTG STTP SDSSNEIPAT PS GTGTTGSKT VPSTPGSSAAAGSNTKVSM TTTL VGLFLLFVASSALTT RGF
CanXYLP5	Capana06g000084	MASKINVMALVMVLSVAIFFNGALG QSS C MTTLVGLS P CL NYVSG NS STPSS CC TSLAGVVQSNP QCLC M L V NGGGSNLGIA INQ TLALGLPSA C NLQTPPLSR C NAA NGPTASVPASSPTG STTP SDSSNEIPAT PS GTGTTGSKTV PSTPGSSAAAGSNTKVSM TTTL VGLFLLFV TSS FAL TR GF
CanXYLP6	Capana01g001516	MNSKKLVDVFQLSFFSSSFLILLGFSRA NVDKDREE CT NQLVGLAT CL PYVSGEARAP TPD CC TGLKEVLDKS K ICLC ILVKDRNDPSLGLK INAT LALSPL SLCH APP N MS NVTM C TDLLHLAP NS PEAKVFQDFAKSAK GS PAAP STPVSGNTSGKPANASANEKNDGGNRRRWMGFMEMT MSFLVILVLSYLT
CanXYLP7	Capana01g003235	MASSSMKYQFRLVLFMFCVFGNS DTEKDKQE CT QSL IGLAT CL PYVGGNAPAP TPD CC TGLKQVLKSS KKCL CL LIKDRNDPDLGLQL NVT LAL T LP SVCK APAN ISEC PALLHLPAN SP DAQVFYQ IAN GSSSIAG S PLAN SP IPSVG YSPTGGPAGVASAP K SAGCHIGRRWFGLDAIIGVVLIW SLTSDEFFI

CanXYLP8	Capana01g003236	<p>MKYQFRLVLFMFCVFASSATDKDKQECTQSLIGLAT CLPYVGGDAPEPTPDCCTGLKQVLKSNKKCLCLLI KNRNDPDLGLQINVTLALTLPSVCQTPANISECPALL HLPANSPD AQIFYNGSSSIAGSPVANSPIPSVGSSPTGGP AGVASAPKSAGCHIGKRWFGLDANVGVLLVWSLTSNF FI</p>
CanXYLP9	Capana01g000497	<p>MLTSRFTWLITVALTAALLSAATTSAQTPPSCASKLVP CAPFLNSTKPPATCDPLREAVTKDLDCLCKLYENP TLLPSLGINVTQAIGLPKYCDIPGDVSACKAAAPGSS SPSEKAPPVTTPASKDKNGVSKVAWTGMSSLVLIASE VLA</p>
CanXYLP10	Capana03g000752	<p>MAYSSKSFYAVIFSWVFMGLSHGIDLDKNLINALLASGV GDGDGGSGASAMSCMQKLMPCQPALSSHSKNPPPT CCMPLKEMMTNDAKCLCTVFGNADLMKGLNVTQ DEALDFAKSCGAKPDLSLCKNAASPGSAAAPTAPTT PDTNSSASSNKTASPPAESTASVTSKLGGFVAIASFLSL MMLLTV</p>
SlyXYLP1	Solyc01g105010.2.1	<p>MSTSKMNSFALFCLISILFFSCTSVESASRSAPAPAVDCN NLVLNLADCLSFVTNGSTEKKPEGTCCSGLKMVLK TDAECLCEGFKNSAQLGVVLNVTKAMALPAACHVS APSVSNCGLSTDTGAAPALSPIAGSPTISAVAPATTAGVN AVTPVPAPGTSDSTLAALSIGQLGLTLVVAVFCWF</p>
SlyXYLP2	Solyc06g073660.2.1	<p>MAASTISIFTTVLILSLFSSLIPSTKAQDSPPAPEAPAPSPG VDCFRVLNMSDCLAFVERGSNTTPPGKCCPEIAG LLDSNPICLCHMLGRAHSGAKIGFNIDVDKALKLPS ACSLEFPPSTTCSDLGIPVGAPLPSEESPAPSPGFATSP TSDNINAASIIVFYKMQFLIGMAIMFFTSFF</p>
SlyXYLP3	Solyc11g072030.1.1	<p>MASTTSLLLLLSLFSTIVPPFTEAQSMPPMATAESPSMS MSPGSEGPATSGGMDCMTVLLNMSSCLTYVEQDSKL SKPDEQCCPSLAGLLESNPICLCQLLGNPDKIGIQID VNKALKLPNICKLETPPVSTCAAIGIPIAAPTSAEVPV GSPGITNGEVSALSPGGLASSPTTSEDKNNAASIMTFFK MQLVLSLGIFFVTIY</p>
SlyXYLP4	Solyc09g082270.2.1	<p>MANQGSKMSFAIMFAMICSGVVAQSSNDCTNVLISM SPCLNYITGNSSVPTSGCCTQLATVVNNNPSCLCQVL NGGASNLGLNINQTQALALPTACNVQTPPLSQCNAD SPIGSPTGTPTSDGSGRGSNRVSPQDGSNEATSTKMAA PLFFFLLFVASTFTSA</p>
SlyXYLP5	Solyc03g005200.2.1	<p>MANHQRINSRGLVLVLAMIWSGVAAQLSSDCTNVLV SMSPCLNYITGNSSSSPSSGCCTQLGTVVKNNPECLC QVLNGGGSNMGLNINQTQALALPNACKVQTPSISK CNAGSPTSPAGTPSPNTGGSGSGSIPSSRDASNDASLT KMIDLPFFLILFISSYASAFMA</p>

SlyXYLP6	Solyc09g065410.2.1	MQILTSSTIGSALAILLSLFLHVSSQSEDCQEIVIVGLAP CLQYIQGNATTPSSGCCCTQLATIVKTRPRCVCHVFS GVNVNQTLAMALPKACNVHITPSLTLQATSAAAGSP LSSSTPTGERSRTSQSEDDSSRGYSLKLPYYSLFLFTLVIPTF SLFNFI
SlyXYLP7	Solyc09g065420.2.1	MASKRIEMGLTTLVLVFMQWHGVRAQSGCTTALVSL SPCLNYVTGNTTTPSTSCTLQLSRVVASQPRCLCSVL NAGGSSFGVSNQQTQAVALPSACNVQTPPVSRCNAG ANGPAASPADSPADSSKGSTDIPSGTGSKASRGGTSNG SIVELTATWIFIVAFTAFASNFF
SlyXYLP8	Solyc09g065430.2.1	MASKVMNILSLIIVIIALFWSKGEAQSNQCMTTLVGLAP CMNYVTGNSSTPSSTCTTALSSVVQSNPQCLCSLVN GGGSGLGIAINQTLALALPAAENVQTPPLSRCNAAN GPSASVPASSPSGSPAPTGSDETPEIPATPSGSGSTGSKT DTSRNGSSNAGSSSNIKISFTLMGFVLFIVSSVLA
SlyXYLP9	Solyc09g082280.2.1	MASKGIAIICMAFVPIIIAMISVQVAMAQSDCTSTLITM ASCLSFVTGSAKTPSASCCSALSGVLQSKPRCLCVIV NGGSSSLGVQINQQTQALALPSACNLQTPPVSKCYAG NGPVMSPEGAPTEGAPDSSTGIAVSGSKASGSSIMS DGS SLKVPVRAAAGIVLFMASYVFMI
SlyXYLP10	Solyc01g005990.2.1	MSSKLVTFELSFFFLILLGFSSANLKDREECANQLV GLATCLPYVSGEAKSPTPDCTTGLKEVLDKSKICLCI LVKDRNDPSLGLKINATLALSPLTLCHAPPNMSNVS MCPPELLHLAPNSPDAKVFQDFAKSAKGSSAAPSAVPSG NSSGKPANSSTNDKNDDGGHKRRWMGFVEMTMGFLVIL MLSYLT
SlyXYLP11	Solyc01g073680.2.1	MVSCCTMRVQLRLVLLLILCVIGNSDTEKDKEECTQSLI GLATCLPYVGGNAPAPTPDCTTGLKQVLKDSKCKL CLLIKDRNDPDLGLQLNVTALALTPSVCKAPANISEC PALLHLPANSPDAQVFYQIANNSSSIAGSPLAHSPIPSVG SSPTGAPAGAPKSSAGCHIGKRYFGLEAIVGVLLWSLTS NFFIG
SlyXYLP12	Solyc08g079250.2.1	MLSSKLSWLITAAITAALLSPTTIEAQTPSCASQLVPCA AFLNSTKPPASCCDPLREAVTKDLQCLCKLYENPAL LISLGINVTQAIELPKYCINIPGDVSACKAAAPSSSSPS GKTTPPVVTPASKDKNGVSTVAWTGMSSLLMLFASFVLA
SlyXYLP13	Solyc08g007460.2.1	MFSSKMFVLISMALTAAMIFASDAQTTPPSCASKLVPC APYLNSSSPPAECCDPLREAITNDLDCLCKLYENPTL LPSLGINITQALALPRACNIPGDLSACTSGGAPGPSSE GLPPPVTGGNGNNGVNVKFTWSGMSILLLLCASLMIA
SlyXYLP14	Solyc03g118580.2.1	MAYLKSCIVLSILLCFLMGFSHG IHLDKSTILALLASGV GSGSVSAMPVQVKLMPVQPAFAAHMKTTPATCCPTPL KEMISNDAQCLCTVFANSVDMKSMNVVTQDEALSFA KACGAKPDLSLCKKAHGEASAPSPNTSQTNDSSSTNN

		TASPPPA NTASVTSKFGGFVAVASLMSLVI
SlyXYLP15	Solyc05g015490.2.1	MASAYKLVVLLIVSIGIVIAN GDDDKSLGDK C GTEFQK VAAC L TYATGKAPSPSKE CC DAAEDIKDHPV CLCYI IEQIHKGSSPQLKSMGIQEEKLLQLPSA C KLT N ATIS N C PKLLNIPPTSPDYAIFT N ATSKSPVST TP SASS SP DTN KDV SDGYKNGPQLSVTGTIVAVAIFLARTDLLVF
SlyXYLP16	Solyc09g082310.1.1	MADVILILFSVLLLAAGTLF EPPELPPTSPESLSTTIS C AD ELVAFSP C LPYISDPPN N ISDSPPFQ CC D N FSAAFVDN TAI CLC YLVSNPQLLGFPISSMKLLSLNSV C PVEDKE GAENLSLES L C SGSTTLPPFRSIITDHRGSSPRPVR R PT <u>PSSPRPSSPD</u> PGDHDNP <u>SPQAPPVSVSLPPPSSNVGDDP</u> <u>SPGAQATTEC</u> SSAIELMCNYRLWVISAMSILLYLCKKHQ LS
SlyXYLP17	Solyc08g078910.1.1	MAKSSLALFLVFNVLFFTMVSA CYTC PG PIKPNPK TP S <u>PSPNSQTK</u> C PRDALKLG V CANVLNGLL N VTLGT PP V K CC SLLGNLVDLEAAV CLC TALKANILGINLDIPISL SLLLN V C T KEAPKGF CS
SlyXYLP18	Solyc09g082290.2.1	MSYKHLAFPNLVLSWMLLNALSHTING QTIT TP C TGP MITSFT C MNFLT N SSSNVGG L PIED CC NVLKNMMT NAMN CF CLIVTGGIPFQMPMNP N MVMSLPSA C NMA GV PLK C KAPSPPEVVAPGPRSDAGAPS AS PTTAPI IP RS <u>PKDSTVPPPLPSN</u> SSPHADEN N PTL TP SP PT ESLIPAT NT G RL TP AT PS A AP FLGHGIS PL LILVAF GAIC
SlyXYLP19	Solyc09g065440.2.1	MIKQOMENLKVSKSVHDIILLTLVLSFSTFKVVNC QINTA C TSSII ST FT PC LN YL TGSS NG SS PT ED CC NSLKSSM SDSID CI CLIVTGNVPVSIPFIRTLALS LP QA C NSGV PV QC SASGVPLSPGPALF APPP APVPVP PP HHVPA HP PH HQRVA AF PPSL AP HGSRVGKASA EP TP EV DPPSIEDDEP TIEK PT TA AS PPKPSLLPK T TLQ K PQ NT SASSYISSFSSPF MLMLVALVTLFVDKSLILF
SlyXYLP20	Solyc06g054030.2.1	MEGIILSSILTLVLMIFSTQSVSG QIST V C SAAMLRS FS P C INFISNGGS N SS PT SD CC RS L KYVM N GT D CLCLV VTGN V PF RP IN R TLAIS LP KA C KMDG V VP V C KASP <u>SPIPS</u> SPKAANN V Q P Y TP PL RP VAD TR PS PT DIFGD PD TN L GF K PN L IP SPA QGS QR FS V F V LLA AC G V MA L Q FN
SlyXYLP21	Solyc09g082300.2.1	MEGYKFFKDFRRFVPLYAIVLMIFGIQVSG QITTA C SSA MLSS FS P C INFMS N NGSG S PTS ACC QSLKELTAS G KD CLC LIVTGN V PF K IPNR N VAIS LP KA C N K DS V PIE C K GS ST PL PA Q G PAAL SP SG SP FR N PR PP QA SP DGDD V P EP F DP PS GP GS DT TP GL TP PS PT GG L GN P Y NG FS PP SLT DDGS G NTDT G SG FR PN L TP SS AP D SP RF SP F V V L V AC GA IVLKL
SlyXYLP22	Solyc03g119620.1.1	MAFTTVLIFSLLFVFPVPTLS QTFGN L PAG PT ASS C GPL LL R L A P C GP F V Q GG S PS P TER CC S N L R Q L Y I Q Q PD C

		LC LLLNQ TGISTLPIN TTL LALQLPLL CS MHV DNNT CS GSEGLA PR SSTPQVSFGTNN SS VAA SP MVTVPPQTSST FGFGFN SS AA NIN AKESLMIITVLT SWG AFFWL
StuXYLP1	PGSC0003DMP400022 245	MSSKMNSFALFCLISICFFCCRSVESASRSAPAPAVD CN NLVNLAD CLS FVTNGSTEKKPEGT CC SGLK MVLK TDAE CL CEGFKNSAQLGVV LV N VT KAMALPAA CH V S APSVSN C GLSTDTGA AP AL SPI AG PPT ISAV APT TAEGV NVVAPV PAP GTS DST TLAGLSIGQLGLTLV VAV FCWF
StuXYLP2	PGSC0003DMP400047 651	MAS TTTT SL LLLL SLFSTIVPPFTEAQTMPMATAES SP MS IS PA AS GP PATSGGMD CMT VLL NM SS CL TYVEQDSKLT KPDKE CC PSFAGLLESNPI CL CQLLGNPKIGIQIDV NKALKLPNI C KLETPPVSA C AAMGPIAA PT SAEVPAG SP GIANGEVSAL SP GGFASS PT TSEDK NNA ALIMTFFKM QMVLSLGVIFFTIY
StuXYLP3	PGSC0003DMP400056 409	MASAYNLV VLL IVCSGIVLANGDDKSLGDK C GAEFQK VAA CL TYATGKAPSPSKE CC DAAEDIKDHPV CL CYI IEQIHKGSSPQLKSMGIQEDKLLQLPSA C KLT N ASIS N C PKLLNIPPTSPDYAIFSN AT SK SP VST TP SGSSSSSSSS SSPDTNKDVSNGFKNG P QLSVTGTVVAAALVAIFLAVIP RELLVF
StuXYLP4	PGSC0003DMP400008 413	MAKSLALFLVFNVLFFTMVSA CY TC GP IKPNPKPTTP SP SPNSQTK C PKDALKLGI CAN VNLGLL NV TLGT PP V K CC SLIGNLV DLE AAV CL C T TALKANILGINLNI PIS L SLLLNV C SKEAPKGF IC P
StuXYLP5	PGSC0003DMP400050 496	MVSCTMKYQLR LV LVFFILCVFGNSDTEKDKEE C TQSLI GLAT CL PVYVGGNAPAPTPD CC TGLKQVLKASKK CL CL LKDRNDPDLGLQL NV TLALTLPSV C KAPANISE C PALLHLPANS P EAVFYQIAN NS SSSIAG S SAH S PIPSVG SSPTGAPAGAPK SAG CHIGKRWFGLAIVGVLLWSLT SNFFI
StuXYLP6	PGSC0003DMP400055 381	MSSK KL VTFEL SFF LILLGFLSASLDKDREE CAN QLV GLAT CL PFVSS EAK APTPD CC TGLKEVLDKSKI CL CI LVKDRNDPSLGLKIN AT LALS LPT L CH APPNIANVSM C TDLLHLAPNSPDAKVFQDFAKGSSAAPSAPVSGNSSG KPANSSTNDKN DGG HRRRCMGFIEMTMGFLVILVLSYL I
StuXYLP7	PGSC0003DMP400009 912	MAS TT VLI F SL L FV F VPTTLSQTFGNLSAG PT VSS C GPL LLRLAP C GPV V Q GAS PS PTE Q CC SNLRQLYIQ Q PD C LC LL LNQ TG ISTLPIN TT LALQLPLL CS MHV DN DT CS GSEGLA PR SSTPQVSFETNN SS VAA SP MVTVPPKTSST LGFGFN SS AV N FNAKESLMIITVLT SWG ALFWF
StuXYLP8	PGSC0003DMP400055 448	MASKGIA IC MA L VPIIMT MIS VQVAMAQSD C TSTLITM AS CL SFVTGSAKTPSAS CC SALSGVLQSKPR CL C V VIV NGGSSSLGVQIN Q TQALALPSA C NLQTPPVSK C YAG

		NGPVMSP <u>EGAP</u> SEG <u>APDS</u> SSTGIAISGSKASGSSSTS DGSS LKVP IRA <u>AVGIVL</u> F MASYVSMI
StuXYLP9	PGSC0003DMP400028 502	MGLNVKICMTLV AILAIGNNYMISRGAMAQSN C MNAF LSMYS C LSYVTG STPKTP SSS CC SALSGVLQ SQPRC LC TIANGGGSSLG VQINQ TLALALPAA C NL KTP PVS RC YAGNGPAM SPIS R GSPV G SP EGSS DE TADPPMPGKS
StuXYLP10	PGSC0003DMP400033 570	MASKRIEIGITLTLV LMFVQWDG VRA QSG C TTALVSL S P CLNYVTG N TTTP STS CC LQLSRV VASQPR CLC SVLN GGSSFGV SIN QTQ AVAL PSA C NVQTP PVSR C NGGA NGPAAS PAD SP ADSS KG SPD IPS AGTGSKASGGG TS DG SIVELTATWIFTVA FTAF STFF
StuXYLP11	PGSC0003DMP400034 938	MASKINVMALVMVLIVAINW NGALAQSS C MTTLVGL SP CLNYVSG NS ST PS SS CC TSLS SVVQ SN PQ CLC VLV NGG SNL GI AIN QTLALGL PSA C NL QTP PASR C NAA NGPTGSAEVPASS PAG ST TP SDSS NEIP AT PG ATGSK TVP ST PGS SS SPGS NSK F SIS TLV GFL L FVAL T TRV F
StuXYLP12	PGSC0003DMP400033 569	MASKVMNIALIIVIIALFW NEGEAQSN C MTTLVGL AP C MNYVTG NS ST PS ST CC TSLS SVVQ SN PQ CLC SLV NG GG SL GI AIN QTLALALPAA C NVQTP PLS Q C NA ANG PS ASVPASS PSG SP APT GSS DE T PEIP AT PSG SG ST GSK TD TSR NG SS NAG SS NIK IS FSL M GFI L FIV SS VLA
StuXYLP13	PGSC0003DMP400055 449	MANQQIRMSFFAIVFAMIC SGVVAQSSND C TNVLISLT P CLNYITG NS SVPT SG CC TQLATV VNN NP S CLC QVL NGDAS NL GL NIN QTQALAL P TAC C NVQTP PLS Q C NAD SP NG SPT G APT DG SGR GT NGIP SP RD GS ND AT STK MAA PLFF FLL FV AST FTAA
StuXYLP14	PGSC0003DMP400023 778	MANQRNSRGLVLAAMI WSGVAAQLSSD C TNVLV S M SP CLNYITG NS SS PS SG CC TQLG TVV K NN PE CL CQ VL NG GG SN MGL NIN QTQALAL P NA C K VQ TP SIS K C N AG SPT SS PAG TP RP NP TE ASGSG ST PS SR GG ND AS L PK MIHL PF FLL FISS Y AS A FIA
StuXYLP15	PGSC0003DMP400034 936	MKMFA CAIFVAMAIF SIQ VSGQSDN C QQVIVGL AP CL DY I Q G NAT K PS SG CC TQLATIL K NE PQ CLC Q M INGG ASS SL GIN V NTQ Q AMAL PKA C NV QTP SV SL C KAT TP S G SP GSS SG GSK GEP SG NT GY TI K LP F LL FTL V VA AS FTT I
StuXYLP16	PGSC0003DMP400028 420	MEGI LSSIL V LMV F ST Q LVY G Q I STA C SA A ML R S F S P C I N F IS NG GS N SS P TS D CC Q S L K Y V M S NG T D CL CL I VT G N V PF R VP I NT L AIS L PKA C K M D G VP V Q C K A SP S P V PA GP AS L R P TR S L P SP S PKAA K N V P Q PY T PL R PA N K R P N L T PP PID I FG D PD T N L G F K P N L IP S AA Q SS Q R F SV F V L LA A C G V M A L Q F N

StuXYLP17	PGSC0003DMP400055 466	MTYKHLAFLTLVLSWMLLIALLSLQIDG QMVTP C TGP MITSFTP C MNFLT N SSSNVGGLP TDDCC NVLKTMM TNAMN C F CLIVTGGIPFQMPMNPNMV MPLPSA C NM PGVPLK C K <u>APSPEVV</u> <u>APGPRSDAG</u> <u>APSASPTAAPTIPP</u> RSTKDSTVHPPLPSN <u>SSPPADDIPTLT</u> <u>PPSPPTDPSTPANN</u> SDRLTPATP SAAPFLGHGISPLLIMLAAFGAIV
StuXYLP18	PGSC0003DMP400008 483	MLSSKLSWLITVAIMAALLSATTTEA QTPS C ASKLV P C ASFL N STKPPAS CC DPLREAVTKDL Q CL CNLYENPAL LISLGIN V TQAIGLPKY C NIPGDVT A C KAA <u>APSSSSPS</u> EKTPPVTT <u>PASKDKN</u> GVSTVAWTGMSSFLVLFASFVLA
StuXYLP19	PGSC0003DMP400010 019	MAAYPKSCVVVILTCFLMGFSHG IHLDKNTIVAFLASG VGSGSVSAMP C VQKLMP C QPALAAHMKNPPAT CC M PLKEMISNDAQ CL C TVFGNSDVMKSM N V T QDEALN FAK C G AKPDL S C KKAHGEAS <u>APSPATSSDTN</u> SSSS NNTA <u>SPPAA</u> NTASVTSKFGGFVAVASLMSLVI

Note:

Sequences in the **light green** indicate the N-terminal signal peptide.

Sequences colored in **light yellow** indicate the 8-Cys motif.

Sequences in black **bold font** and **red bold** font indicate the nsLTP domain and the N-glycosylation sites, respectively.

Sequences with black underline and red double underline indicate the putative AG site and arabinCanylation site, respectively.

Sequences in **black** indicate the C-terminal GPI-anchor.