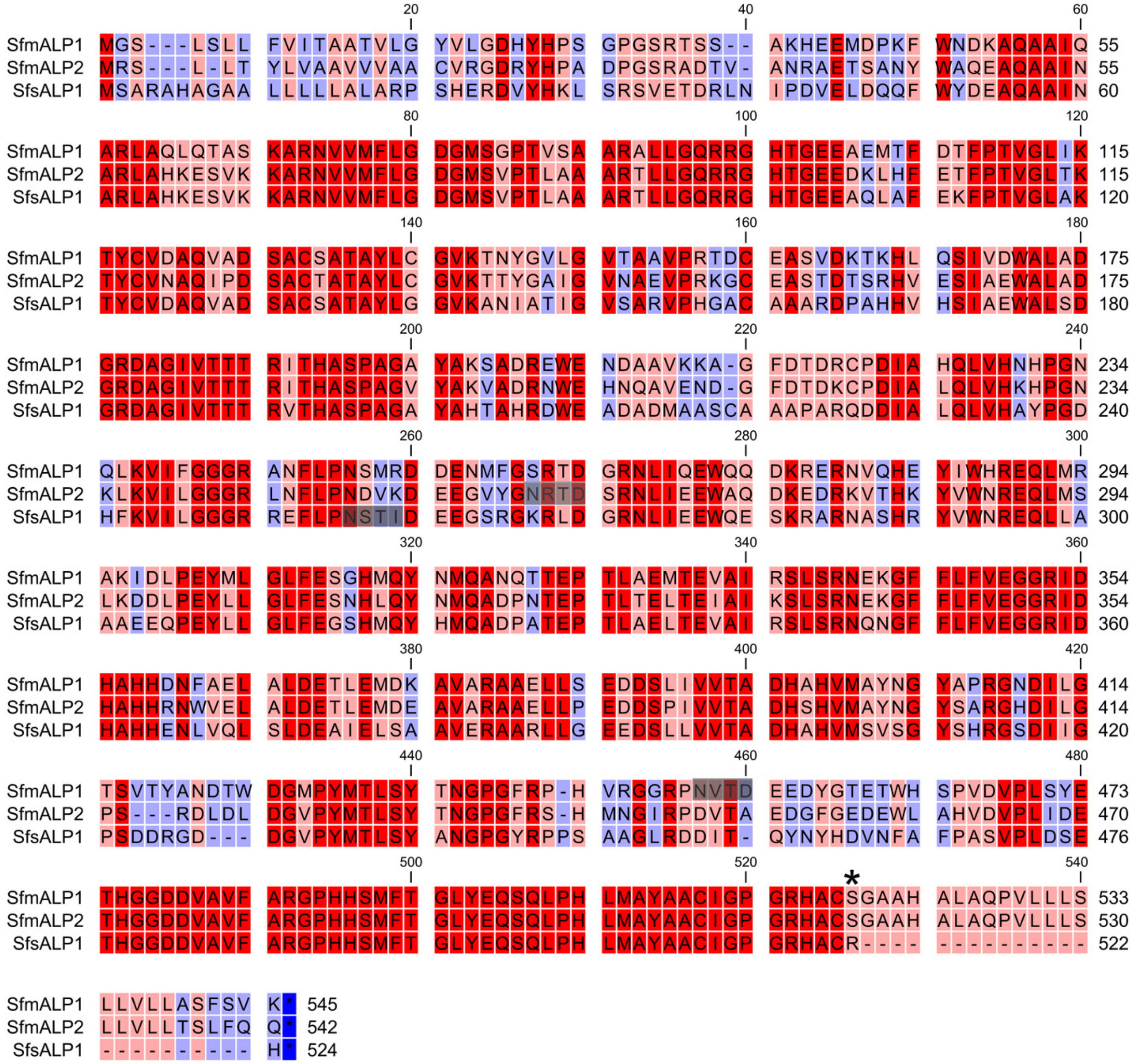
Figure S1.- Alignment of the predicted SfmALP1, SfmALP2 and SfsALP1 protein sequences obtained using the CLC Genomics Workbench v8.0 software. In dark are residues predicted to contain N-glycosylation sites according to the NetNGlyc 1.0 server (http://www.cbs.dtu.dk/services/NetNGlyc/). Residues are colored according to the conservation in all three sequences from blue (low conservation) to red (high conservation). Asterisk denotes residue predicted to function as GPI-anchor site in SfmALP1 and SfmALP2 by PredGPI, fragANCHOR, and GPI-SOM databases.



```
                                  20                     40                     60
                                   |                      |                      |
SfmALP1  MGS---LSLL  FVITAATVLG  YVLGDHYHPS  GPGSRTSS--  AKHEEMDPKF  WNDKAQAAIQ   55
SfmALP2  MRS---L-LT  YLVAAVVVAA  CVRGDRYHPA  DPGSRADTV-  ANRAETSANY  WAQEAQAAIN   55
SfsALP1  MSARAHAGAA  LLLLLALARP  SHERDVYHKL  SRSVETDRLN  IPDVELDQQF  WYDEAQAAIN   60

                                  80                    100                    120
                                   |                      |                      |
SfmALP1  ARLAQLQTAS  KARNVVMFLG  DGMSGPTVSA  ARALLGQRRG  HTGEEAEMTF  DTFPTVGLIK  115
SfmALP2  ARLAHKESVK  KARNVVMFLG  DGMSVPTLAA  ARTLLGQRRG  HTGEEDKLHF  ETFPTVGLTK  115
SfsALP1  ARLAHKESVK  KARNVVMFLG  DGMSVPTLAA  ARTLLGQRRG  HTGEEAQLAF  EKFPTVGLAK  120

                                 140                    160                    180
                                   |                      |                      |
SfmALP1  TYCVDAQVAD  SACSATAYLC  GVKTNYGVLG  VTAAVPRTDC  EASVDKTKHL  QSIVDWALAD  175
SfmALP2  TYCVNAQIPD  SACTATAYLC  GVKTTYGAIG  VNAEVPRKGC  EASTDTSRHV  ESIAEWALAD  175
SfsALP1  TYCVDAQVAD  SACSATAYLG  GVKANIATIG  VSARVPHGAC  AAARDPAHHV  HSIAEWALSD  180

                                 200                    220                    240
                                   |                      |                      |
SfmALP1  GRDAGIVTTT  RITHASPAGA  YAKSADREWE  NDAAVKKA-G  FDTDRCPDIA  HQLVHNHPGN  234
SfmALP2  GRDAGIVTTT  RITHASPAGV  YAKVADRNWE  HNQAVEND-G  FDTDKCPDIA  LQLVHKHPGN  234
SfsALP1  GRDAGIVTTT  RVTHASPAGA  YAHTAHRDWE  ADADMAASCA  AAPARQDDIA  LQLVHAYPGD  240

                                 260                    280                    300
                                   |                      |                      |
SfmALP1  QLKVIFGGGR  ANFLPNSMRD  DENMFGSRTD  GRNLIQEWQQ  DKRERNVQHE  YIWHREQLMR  294
SfmALP2  KLKVILGGGR  LNFLPNDVKD  EEGVYGNRTD  SRNLIEEWAQ  DKEDRKVTHK  YVWNREQLMS  294
SfsALP1  HFKVILGGGR  REFLPNSTID  EEGSRGKRLD  GRNLIEEWQE  SKRARNASHR  YVWNREQLLA  300

                                 320                    340                    360
                                   |                      |                      |
SfmALP1  AKIDLPEYML  GLFESGHMQY  NMQANQTTEP  TLAEMTEVAI  RSLSRNEKGF  FLFVEGGRID  354
SfmALP2  LKDDLPEYLL  GLFESNHLQY  NMQADPNTEP  TLTELTEIAI  KSLSRNEKGF  FLFVEGGRID  354
SfsALP1  AAEEQPEYLL  GLFEGSHMQY  HMQADPATEP  TLAELTEVAI  RSLSRNQNGF  FLFVEGGRID  360

                                 380                    400                    420
                                   |                      |                      |
SfmALP1  HAHHDNFAEL  ALDETLEMDK  AVARAAELLS  EDDSLIVVTA  DHAHVMAYNG  YAPRGNDILG  414
SfmALP2  HAHHRNWVEL  ALDETLEMDE  AVARAAELLP  EDDSPIVVTA  DHSHVMAYNG  YSARGHDILG  414
SfsALP1  HAHHENLVQL  SLDEAIELSA  AVERAARLLG  EEDSLLVVTA  DHAHVMSVSG  YSHRGSDIIG  420

                                 440                    460                    480
                                   |                      |                      |
SfmALP1  TSVTYANDTW  DGMPYMTLSY  TNGPGFRP-H  VRGGRPNVTD  EEDYGTETWH  SPVDVPLSYE  473
SfmALP2  PS---RDLDL  DGVPYMTLSY  TNGPGFRS-H  MNGIRPDVTA  EDGFGEDEWL  AHVDVPLIDE  470
SfsALP1  PSDDRGD---  DGVPYMTLSY  ANGPGYRPPS  AAGLRDDIT-  QYNYHDVNFA  FPASVPLDSE  476

                                 500                    520    *               540
                                   |                      |                      |
SfmALP1  THGGDDVAVF  ARGPHHSMFT  GLYEQSQLPH  LMAYAACIGP  GRHACSGAAH  ALAQPVLLLS  533
SfmALP2  THGGDDVAVF  ARGPHHSMFT  GLYEQSQLPH  LMAYAACIGP  GRHACSGAAH  ALAQPVLLLS  530
SfsALP1  THGGDDVAVF  ARGPHHSMFT  GLYEQSQLPH  LMAYAACIGP  GRHACR----  ----------  522

SfmALP1  LLVLLASFSV  K*  545
SfmALP2  LLVLLTSLFQ  Q*  542
SfsALP1  ----------  H*  524
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Figure S2.- Alignment of the predicted SfmALP2 protein sequences in the Ben and 456 strains of *S. frugiperda*. obtained using the CLC Genomics Workbench v8.0 software. In dark are residues predicted to contain N-glycosylation sites according to the NetNGlyc 1.0 server (http://www.cbs.dtu.dk/services/NetNGlyc/). Residues are colored according to the conservation in all three sequences from blue (not conserved) to red (conserved).

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                                20                    40
Ben SfmALP2  MRSLLTYLVA AVVVAACVRG DRYHPADPGS RADTVANRAE TSANYWAQEA 50
456 SfmALP2  MRSLLTYLVA AVVVAASVRG DRYHPADPGS RADTVVNRAE TSANYWAQEA 50
                     60                    80                  100
Ben SfmALP2  QAAINARLAH KESVKKARNV VMFLGDGMSV PTLAAARTLL GQRRGHTGEE 100
456 SfmALP2  QAAINARLAH KESVKKARNV VMFLGDGMSV PTLAAARTLL GQRRGHTGEE 100
                               120                   140
Ben SfmALP2  DKLHFETFPT VGLTKTYCVN AQIPDSACTA TAYLCGVKTT YGAIGVNAEV 150
456 SfmALP2  DKLHFETFPT VGLTKTYCVN AQIPDSACTA TAYLCGVKTT YGAIGVNAEV 150
                    160                   180                  200
Ben SfmALP2  PRKGCEASTD TSRHVESIAE WALADGRDAG IVTTTRITHA SPAGVYAKVA 200
456 SfmALP2  PRKGCEASTD TSRHVESIAE WALADGRDAG IVTTTRITHA SPAGVYAKVA 200
                               220                   240
Ben SfmALP2  DRNWEHNQAV ENDGFDTDKC PDIALQLVHK HPGNKLKVIL GGGRLNFLPN 250
456 SfmALP2  DRNWEHNQAV ENDGFDTDKC PDIALQLVHK HPGNKLKVIL GGGRLNFLPN 250
                    260                   280                  300
Ben SfmALP2  DVKDEEGVYG NRTDSRNLIE EWAQDKEDRK VTHKYVWNRE QLMSLKDDLP 300
456 SfmALP2  DVKDEEGVYG NRTDTRNLIE EWAQDKEDRK VTHKYVWNRE QLMSLKDDLP 300
                               320                   340
Ben SfmALP2  EYLLGLFESN HLQYNMQADP NTEPTLTELT EIAIKSLSRN EKGFFLFVEG 350
456 SfmALP2  EYLLGLFESN HLQYNMQADP TTEPTLTELT EIAIKSLSRN EKGFFLFVEG 350
                    360                   380                  400
Ben SfmALP2  GRIDHAHHRN WVELALDETL EMDEAVARAA ELLPEDDSPI VVTADHSHVM 400
456 SfmALP2  GRIDHAHHRN WVELALDETL EMDKAVARAA ELLSEDDSLI VVTADHSHVM 400
                               420                   440
Ben SfmALP2  AYNGYSARGH DILGPSRDLD LDGVPYMTLS YTNGPGFRSH MNGIRPDVTA 450
456 SfmALP2  AYNGYSARGH DILGPSRDLD LDGVPYMTLS YTNGPGFRSH MNGIRPDVTA 450
                    460                   480                  500
Ben SfmALP2  EDGFGEDEWL AHVDVPLIDE THGGDDVAVF ARGPHHSMFT GLYEQSQLPH 500
456 SfmALP2  EDDFREDEWL AHVDVPLIDE THGGDDVAVF ARGPHHSMFT GLYEQSQLPH 500
                               520                   540
Ben SfmALP2  LMAYAACIGP GRHACSGAAH ALAQPVLLLS LLVLLTSLFQ Q 541
456 SfmALP2  LMAYAACIGP GRHACSGAAH ALAQPVLLLS LLVLLTSLFQ Q 541
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