

**Supporting Figures.** Alignments of all sequences identified in this study grouped according to their gene superfamily (in alphabetical order). Cys: yellow, Arg and Lys: blue and Glu and Asp: red. Predicted signal sequences are underlined in black. Predicted mature toxin regions are underlined in green. \*Marks sequences that may have derived from housekeeping proteins or serve in endogenous processes in the venom gland rather than in envenomation.

### A2 superfamily

```

1          10          20          30          40          50          60  63
A2_Amz1.10 MRCLAFVL-VALLLFTAMATTGASNRVNAANGKASDLISLAVRNGCCSPPCRQQNPKLCPSS
A2_Amz1.2  MRCLAFVLVVTLLLFTAMATTGASNRVNAANGKASDLISLAVRNGCCKYPPCRWNNPQLCRPS
A2_Ps1.8   MRCLAFVLVVTLLLFTAMATTGASNRVNAANGKASDLISLAVRNGCCKYPPCRWNNPQLCRPS
A2_Ps1.11 MRCLAFVLVVTLLLFTAMATTGASNRVNAANGKASASISLAVRNSCCNPPCRWNNPHTCFPS
A2_Amz1.9  MRCLAFVLVVTLLLFTAMATTGASNRVNAANGKASDLISLAVRNGCCSNPACRNGNPGLCGSG
A2_Amz1.9ii FTAMAATGASNRVNAANGKASDLISLAVRNGCCSNPACGNGNPGLCGSG

```

### B2 superfamily

```

1          10          20          30          40          50          60
B2_Amz1
B2_Amz1ii
B2_Ps1
B2_Ps1ii
B2_Ps2
MLRLIIAAVLVSACLAFPNREDAAQDMANTQPFAPGLQGMQ-----MPAAMPN
MLRLIIAAVLVSACLAFPNREDAAQDMANMQPFAPGLQGMQ-----MPAPMPN
MLRLIIAAVLVSACLAFPNREDAAQDMANMQPFAPGLQGMQEMPAAMPNMQGMLMPAAMPN

70          80          90          100         110         120
B2_Amz1
B2_Amz1ii
B2_Ps1
B2_Ps1ii
B2_Ps2
MPGMPGMPAGQFLPFNPYPGFFKRAADENLEKRKHQSQFNDNQSPFGSSADDGLGMF
MQGMQGMPPGMPAGQFLPFNPYPGFFKRVADENLEKRKHQSQFNDNQSPFGSSADDGLGMF
MQG---MQGMPPGMPAGQFLPFNPYPGFFKRVADENLEKRKHQSQFNDNQSPFGSSADDGLGMF
MQG---MQGMPPGMPAGQFLPFNPYPGFFKRVADENLEKRKHQSQFNDNQSPFGSSADDGLGMF
MQG---MQGMPPGMPAGQFLPFNPYPGFFKRVADENLEKRKHQSQFNDNQSPFGSSADDGLGMF

130         140         150         160         170         174
B2_Amz1
B2_Amz1ii
B2_Ps1
B2_Ps1ii
B2_Ps2
NFENFMKENPDKLPFANMGATADLGNFAPSGNDQQEDQFRFFFDEQQ
NFENFMKENPDKLPFANMGATADLGNFAPSGNDQQEDQFRFFFDEQQ
SFENFMKENPDKLPFANMGATADLGNFAPSGNDQLEDQFRFFFDEQQ
SFENFMKENPDKLPFANMGATADLGNFAPSGNDQLEDQFRFFFDEQQ
NFENFMKENPDKLPFANMGATADLGNFAPSGNDQLEDQFRFFFDEQQ

```

### B4 superfamily

```

1          10          20          30          40          50          60
B4_Amz1
B4_Amz1ii
MQSFTWCLLVPLLLFLYLTQRSDTADHEGAATEVRSADHIPKHVRQALKRRYDGRYGRKKQHVSRRS
MQSFTWCLLVPLLLFLYLTQRSDTADHEGAATEVRSADHIPKHVRQALKRRYDGRYGRKKQHVSRRS

70          80          90          100         103
B4_Amz1
B4_Amz1ii
PSIARVRRHQHREVAEKRNEKAEFTKEELDELGR
PSIARVRRHQHREVAEKRNEKAEKKEELDELGR

```

### Con-ikot-ikot superfamily

```

1          10          20          30          40          50
Con-ikot-ikot_Amz8.1
Con-ikot-ikot_Ps8.1
Con-ikot-ikot_Amz8.1i
Con-ikot-ikot_Ps8.2
Con-ikot-ikot_Ps48.1
Con-ikot-ikot_Ps48.1ii
Con-ikot-ikot_Ps48.2
MTMDMKMTFSGFVLVVLVTTVVGSSVRRGEVSD-----NLIH-CWLPHFRECLLYCWS
MTMDMKMTFSGFVLVVLVTTVVGSSVRRGEVSD-----NLIH-CWLPHFRECLLYCWS
MTMDMKMTFSGFVLVVLVTTVVGSSVRRGEVSD-----NLIH-CWLPHFRECLLYCWS
MTMDMKMTFSGFVLVVLVTTVVGSSVRRGEVSD-----NLIH-CKLLPHFRECLLYCWS
MTMNMSMTLIAFAMVVMASSSVIGSIPRQCKGKDFPCGSKRYHRCCRYAMRDCLKTCPR
MTMNMSMTLIAFAMVVMASSSVIGSIPRQCKGKDLPCGNKRYHRCCRQAMWDCPCMW

60          70          80          90          100         110
Con-ikot-ikot_Amz8.1
Con-ikot-ikot_Ps8.1
Con-ikot-ikot_Amz8.1i
Con-ikot-ikot_Ps8.2
Con-ikot-ikot_Ps48.1
Con-ikot-ikot_Ps48.1ii
Con-ikot-ikot_Ps48.2
IELLPVDCFATCTYVIGDIFGAQTS-SCTIFKTCYVRCMELGLKSEDHCWEGIANTVT
IELLPVDCFATCTYVIGDIFGAQTS-SCAIFKTCYVRCMELGLKSEDHCWEGIANTVT
IELLPVDCFATCTYVIGDIFGAQTS-SCTIFKTCYVRCMDLGTSEDHCWEGTANTVT
IELLPVDCFATCTYVIGDIFGAQTS-SCTIFKTCYFLCMEDGKSEDHCWEVTTNTVT
DDTHNKCWSPCYKTAAEKFGCRPGN-GCCPTFLDRISGCLMEDRPLKVCWRRTKSV--
DDTH-KCWSPCYKTAAEKFGCRPGN-GCCPTFLDRMSGCLMEDRPLKVCWRRTKSV--
FKTHWKCWSHCYGLAARKFGCNPSDHGCCPKFLEKMSECLMKGSPTDECWSKTKSV--

120         126
Con-ikot-ikot_Amz8.1
Con-ikot-ikot_Ps8.1
Con-ikot-ikot_Amz8.1i
Con-ikot-ikot_Ps8.2
Con-ikot-ikot_Ps48.1
Con-ikot-ikot_Ps48.1ii
Con-ikot-ikot_Ps48.2
GAVGLDTC
GAVGLDTC
GAVGLDTC
GAVGLYTC
-----AC
-----PCR
-----PCR

```

## Cono-NPY superfamily\*

1 10 20 30 40 50 60 70 80

Cono-NPY\_Ps1 MHKALLSALLVIVSLVVAASDF-----PKKPAQFNSPQEVKRYVRYVHLAIASRLRYGRSIN--KRSV  
 Cono-NPY\_Ps2 MHKALLSALLVIVSLVVA--L-----PKKPAQFNSPQEVKRYVRYVHLAIAAGRLRYGRSIN--KRSV  
 Cono-NPY\_Ps3 MQKALLSALLVIVSLVVVAVTRQKVVKPVVVKPKKFKSIVLELAYLFLKLNYYRILSKPRFGRSLNISKRSRKHGALRS

## Conoporin\_Amz1\*

1 10 20 30 40 50 60 70

MKTAQPHKMGVFPFALKTMVTVFLLLMGNTSPVHPVVLSSAISLSTVATIASGVISAGTSLAGVTLQGLAAS  
 GYRVTCITIQVENWTRYPLLYPSVRIANSGLVLTAPTALPGKKFAFATRMPAHRAGVYGTVSWEMHGTDRR  
 FVLMWSAPFNHFYSNWLGLGMTKGVAGLARNTWFQMYGGNSHDLTFREFFKKRTDPVIVRNDKFEV  
 VGIMTNIHRAQIKVIVRPTRNWKLADPIRLSLQQQKRALQRDN

## Conopressin superfamily\*

1 10 20 30 40 50

Conopressin\_Amz1 MTRSAMLMGR-LTLVVC---LLLTTQACFIRNCPKGGKRDVDRHPPKLCMSCSFGQC  
 Conopressin\_Amz1ii MTRSAMLMGR-LTLVVC---VLLTTQACFIRNCPKGGKRDVDRHPPKLCMSCSFGQC  
 Conopressin\_Ps1 MTRSAMLMGR-LTLVVC---LLLTTQACFIRNCPKGGKRDVDRHPPKLCMSCSFGQC  
 Conopressin\_Ps2 MTRSAMQMGRRLLTLVVCVLLLLLTTQACFIRNCPKGGKRDVFAIKPTKPCMSCSFGQC  
 Conopressin\_Ps2ii MTRSAMQMGRRLLTLVVCVLLLLLTTQACFIRNCPKGGKRDVFAIKPTKPCMSCSFGQC

60 70 80 90 100 110

Conopressin\_Amz1 VGPNI CCGDTGCEMGTP EANTCAREDEDPTPCLVIGSPCTLNNPGNTHGNCV SFGICCV  
 Conopressin\_Amz1ii VGPNI CCGDTGCEMGTP EANTCAREDEDPTPCLVIGSPCTLNNPGNTHGNCV SFGICCV  
 Conopressin\_Ps1 VGPNI CCGDTGCEMGTP EANTCAREDEDPTPCLVIGSPCTLNNPGNTHGNCV SFGICCV  
 Conopressin\_Ps2 VGPYI CCGDTGCEMGTP EAIKCAKEDEDPTPCLVIGSPCTLNNPGNTHGNCV SFGMCCV  
 Conopressin\_Ps2ii VGPYI CCGDTGCEMGTP EAIKCAKEDEDPTPCLVIGSPCTLNNPGNTHGNCV SFGMCCV

120 129

Conopressin\_Amz1 DDTCFFDLGCCL  
 Conopressin\_Amz1ii DDTCFFDLGCCL  
 Conopressin\_Ps1 DDTCVFDLGCCL  
 Conopressin\_Ps2 DDTCSIESGCP  
 Conopressin\_Ps2ii DDTCSIESGCP

## D superfamily

1 10 20 30 40 50 60

D\_Ps49.1 MPKLEMMMLVLLILPLSYF DAGGQAVQGY DAGMDR YLLP RKLPRILYCAKKVDQNSGWVRCCTTL  
 D\_Ps49.1ii MPKLEMMMLVLLILPLSYF DAGGQAVQGY DAGMDR YLLP RKLPRILYCAKKVDQNSGWVRCCTTL

70 80 91

D\_Ps49.1 KCGKNCCPKGWGCIRGADPNDAQCSQ  
 D\_Ps49.1ii KCGKNCCPKGWGCIRGADPNDAQCSQ

## DivMKFPLLISL superfamily

1 10 20 30 40 50

DivMKFPLLISL\_Ps6.27 MKSTLFLMVLTA AVFLTFFTETDTMSVFKARERKRVHPCGTGTFSDCRNQPDGTVCCIKGS  
 DivMKFPLLISL\_Ps6.27ii MKSTLFLMVLTA AVFLTFFTETDTISVFKAGERKRAHPCGTGTFSDCRNQPDGTVCCRNGS  
 DivMKFPLLISL\_Ps6.27iii MKSTLFLMVLMA AVFLTFFTETDTISVFKAGERKRAHPCGTGTFSDCRNQPDGTVCCRNGS

60 67

DivMKFPLLISL\_Ps6.27 CHGSAICY  
 DivMKFPLLISL\_Ps6.27ii CHGFACY  
 DivMKFPLLISL\_Ps6.27iii CHGFACY

## H superfamily

1 10 20 30 40 50 60

H\_Amz7.7 MNTAGRLLLLCLALGLVFE S L GKAVPDDVNAERDTPDFHKDAR-QL E I L T E P E L D C G G V T C K  
 H\_Ps1 MNTAGRLLLLCLTLGLVFE S L GKTVPDDVNAERDTPDFHKDAR-QL E I L S R S - - D C G G R S C K  
 H\_Ps7.7 MNTAGRLLLLGLALGLVFE Y L GKAVA D D V D T H R D T D P D D K D L R D S L K I V K R T E S D C G G V P C K  
 H\_Ps7.7ii MNTAGRLLLL-CLALGLVFE S L GKTVAD D V D T H R D T D P D D K D L R D S L K I V K R T E S D C G G V P C K

70 80 89

H\_Amz7.7 ASCCVKI DEEEICTVFE C I E P D P Q S L Q  
 H\_Ps1 YGCCVNINGKKRC-I I C N R P D L Q S L Q  
 H\_Ps7.7 F G C C K T E D G K K K C R E L G C - K P  
 H\_Ps7.7ii F G C C K T G G K K R C R E L G C - K P











## Putative MGGRF superfamily

putativeMGGRF\_Amz1 MGG**R**FVLTALIAMTLLSLVLTSTVHGHLPWL-L**K**-----QWIG**R**F**K**SSSLGML**R**MG  
 putativeMGGRF\_Amz1i MGG**R**FVLTALIAMTLLSLVLTSTVHGHLPWL-L**K**-----QWIG**R**F**K**SSSLGML**R**MG  
 putativeMGGRF\_Amz2 MGG**R**FVVTALIAMTLLSLVLTSTV**D**RRIFWV**D**SN**R**PNLQ**R**IGQ-----  
 putativeMGGRF\_Amz3 MGG**R**FVLTALIAMTLLSLVLTSTVH**D**RRIVWV**D**SN**R**PNLQ**R**IGQ-----  
 putativeMGGRF\_Amz3i MGG**R**FVVTALIGMTLLSLVLTSTV**D**RRIVWV**D**SN**R**PNLQ**R**IGQ-----

putativeMGGRF\_Amz1 **R**S**Y**T**F**G**D**S**D**V**R**R**A**V**S**T**G**H**K**GTGGNGWQ  
 putativeMGGRF\_Amz1i **R**S**Y**T**F**G**D**S**N**V**R**R**A**V**S**T**G**H**K**GTGGNGWQ  
 putativeMGGRF\_Amz2 **R**S**Y**T**F**G**D**W**N**I**R**R**A**V**S**T**G**H**K**R**T**D**G**NG**R**Q  
 putativeMGGRF\_Amz3 **R**S**Y**T**F**G**D**W**N**I**R**R**A**V**S**T**G**H**K**R**T**D**G**NG**R**Q  
 putativeMGGRF\_Amz3i **R**S**Y**T**F**G**D**W**N**I**R**R**A**V**S**T**G**H**K**R**T**D**G**NG**R**Q

## Putative MKAVA superfamily

putativeMKAVA\_Amz22.1 M**K**AVAVFLVVALAVAYGQFF**C**P**K**S**K**D**E**P**L**N**C**F**E**SMPNSAT**C**MQST**D**GSLSYAC**G**  
 putativeMKAVA\_Amz22.1i M**K**AVAVFLVVALAVAYGQFF**C**P**K**S**K**D**E**P**L**N**C**F**E**SMPNSAT**C**MQST**D**GSLSYAC**G**

putativeMKAVA\_Amz22.1 **Y****C**G**K**K**R****E**T**C**S**G**N**K**V**P**V**R**N**Y****D****C**Q**R**N**K**V**P**N**P****C**G**P**G**G**A**A**L  
 putativeMKAVA\_Amz22.1i **Y****C**G**K**K**R****E**T**C**S**G**N**K**V**A**V**R**N**Y****D****C**Q**R**N**K**V**P**N**P****C**G**P**G**G**A**A**L

## Putative MSGLR superfamily

putativeMSGLR\_Ps7.1 MSGL**R**VVLFALLLLVYLVTS**K**R**D**G**D**GLT**K**V**V****K**N**K**R**A**VTAIG**R**K**M**M**R**S**V**H**R**SGG**C**P  
 putativeMSGLR\_Amz7.1 MSGL**R**VVLFALLLLVYLVTS**K**R**D**G**D**GLT**K**V**V****K**N**K**R**A**VTAIG**R**K**M**M**R**S**V**H**R**SGG**C**P  
 putativeMSGLR\_Amz7.1i MSGL**R**VVLFALLLLVYLVTS**K**R**D**G**D**GLT**K**V**V****K**N**K**R**A**VTAIG**R**K**M**M**R**S**V**H**R**SGG**C**P  
 putativeMSGLR\_Amz7.2 MSGL**R**VVLFALLLLVYLVTS**K**R**D**G**D**GLT**K**A**V****K**N**K**R**A**VIAIG**W**K**M**M**K**S**V**H**R**SGG**C**P

putativeMSGLR\_Ps7.1 **T****K****C**P**D****K****D****E****C****C**S**G**S**K****C**I**N**I**Y**G**R****N**V**C**V**K**I**P**T**S****R**  
 putativeMSGLR\_Amz7.1 **T****K****C**P**D****K****D****E****C****C**S**G**S**K****C**I**N**I**Y**G**R****N**V**C**V**K**I**P**T**S****R**  
 putativeMSGLR\_Amz7.1i **T****R****C**P**D****K****D****E****C****C**S**G**S**K****C**F**N**L**F**G**R****N**V**C**V**K**I**P**T**S****Q**  
 putativeMSGLR\_Amz7.2 **T****T****C**P**D****K****D****E****C****C**S**D****S**T**C**V**D**V**Y**G**S**N**L****C**L**R**T**S**T**P**P

## Putative MWSGK superfamily

putativeMWSGK\_Ps9.1 MWNG**K**D**D**QAAFLALVLMVAWALGTTA**E**S**C**S**P**D**R**I**Y**Y**S**D**F**E**A**ASGVWYLIL**S**R**E**S**D**  
 putativeMWSGK\_Ps9.1ii MWNG**K**D**D**QAAFLALVLMVAWALGTTA**E**S**C**S**P**D**R**I**Y**Y**S**D**F**E**A**ASGVWYLIL**S**R**E**S**D**  
 putativeMWSGK\_Amz9.1 MWS**G****K**D**D**QATFLALVLMVWALGTTA**E**S**C**S**P**D**R**I**N**Y**S**D**F**E**A**ASGVWYLIL**S**R**E**S**D**  
 putativeMWSGK\_Amz9.1i MWS**G****K**D**D**EAAFLALVLMVLWALGTTA**E**S**C**S**P**D**R**I**Y**Y**S**D**F**E**A**ASGVWYLIL**S**R**E**S**D**

putativeMWSGK\_Ps9.1 **E****R****Y****R**V**S**GL**D**LN**A**Y**R**Y**G**G**K**LLV**D**V**S**WIFL**K**R**T**T**R**G**C****E****K**V**T**T**R****C**E**V**S**G**N**T****C**V**D**T**T**G  
 putativeMWSGK\_Ps9.1ii **E****R****Y****K**V**S**GL**D**LN**A**Y**R**Y**S**G**K**LLV**D**V**S**WIFL**K**R**T**T**R**G**C****E****K**V**T**T**R****C**E**V**S**G**N**T****C**V**D**T**T**G  
 putativeMWSGK\_Amz9.1 **E****R****Y****R**V**S**GL**D**LN**A**Y**R**Y**G**G**K**LLV**D**V**S**RIFL**K**R**T**T**R**G**C****E****K**F**T**T**R****C**E**V**S**G**N**T****C**V**D**T**T**G  
 putativeMWSGK\_Amz9.1i **E****R****Y****R**V**S**GL**D**LN**A**Y**R**Y**G**G**K**LLV**D**V**S**WIFL**K**R**T**T**R**G**C****E****K**F**T**T**R****C**E**V**S**G**N**T****C**V**D**T**T**G

putativeMWSGK\_Ps9.1 YH**Q**V**V****K**Y**I**VAL**D**AN**Y**L**V**V**H**R**T**L**Q**GN**P**Y**T**L**D**I**Y**S**R**T**G**V**G**R**R**L**K**H**L**P**Q**Y**I**R**D**A**I**E  
 putativeMWSGK\_Ps9.1ii YH**Q**V**V****K**Y**I**VAL**D**AN**Y**L**V**V**H**R**T**L**Q**GN**P**Y**T**L**D**I**Y**S**R**T**G**V**G**R**R**L**K**H**L**P**Q**Y**I**R**D**A**I**E  
 putativeMWSGK\_Amz9.1 YH**Q**V**V****K**Y**I**VAL**D**AN**Y**L**V**V**H**R**T**L**Q**GN**P**Y**T**L**D**I**Y**S**R**T**G**V**G**R**R**L**K**H**L**P**Q**Y**I**R**D**A**I**E  
 putativeMWSGK\_Amz9.1i YH**Q**V**V****K**Y**I**VAL**D**AN**Y**L**V**V**H**R**T**L**Q**GN**P**Y**T**L**D**I**Y**S**R**T**G**V**G**R**R**L**K**H**L**P**Q**Y**I**R**D**A**I**E

putativeMWSGK\_Ps9.1 **M**T**C**G**K****D**I**A**T**I****D**S**F**W**L**G**K**Y**S**P**G****D**F**I**S**Y****C**F  
 putativeMWSGK\_Ps9.1ii **M**T**C**G**K****D**I**A**T**I****D**S**F**W**L**G**K**Y**S**P**G****D**F**I**S**Y****C**F  
 putativeMWSGK\_Amz9.1 **M**T**C**G**K****D**I**A**T**I****D**S**F**W**P**G**K**Y**S**P**G****D**F**I**S**N****C**F  
 putativeMWSGK\_Amz9.1i **M**T**C**G**K****D**I**A**T**I****D**S**F**W**P**G**K**Y**S**P**G****D**F**I**S**N****C**F



## S superfamily

1 10 20 30 40 50 60

S\_Ps8.3 VMWKMGMAMFVLLLLFTPTSSQQGDDVQARKIRSKNVFLRTVAKTNKRCDDGTGYGSKFSGCN  
S\_Ps8.1 MMWKMGMAMFVLLLLFTLPLFGQQGDDVQARKMRSKNVFHRMTAKTTKRCDDGTGFGSQTNCN  
S\_Amz8.1 MWKMGMAMFVLLLLFTLTSQQGDDVQARKMRSKNVFHRMTAKTTKRCDDGTGYGSEFTNCN  
S\_Ps8.2 MMWKMGMAMFVLLLLFTLPLFGQQGDDVQARKIRPNVFLRTVAKSTRGCSGSGYTS SP-KCN  
S\_Amz8.3 LLLFTLTSQQGDDVQARKTRSKNVFLRTVAKSTS GCSGSGYTS SP-KCN

70 80 87

S\_Ps8.3 GTCFCPPSSPCYCSYSTYCIKCC  
S\_Ps8.1 GSCFCS SGGFCYCGYYRGS CMCTCTG  
S\_Amz8.1 GSCFCS SGGFCYCGYYRGS CICTCAG  
S\_Ps8.2 GACNCFRSG-CWCRPF SNGCYCYC  
S\_Amz8.3 GACNCFRSG-CWCRPF SSGCYCYC

## SF-01 superfamily

1 10 20 30 40 50 60

Sf-01\_Ps2 MKSAVFMAL SMTISIVFTM-ESA IAPGTRCSKPEKGRCPFISGTCGQYNRLDDFIYCDH  
Sf-01\_Amz1 MKSAVFMAL SMSISIVFTKAEFSVVKVDCS DP-KGTC PFTGTGAYYRSGNANYCFR  
Sf-01\_Amz1i MKSAVFMAL SMSISIVFTKAEFSVVKVDCS DP-KGTC PFTGTGAYYRSGNANYCFR  
Sf-01\_Amz2 MKSAVFMAL SMSISIVFTK-ESA IPPGTRCS DP-KGTC PFTGTGAYYRSGNANYCFR

70 80 90 100 110 120

Sf-01\_Ps2 DCTCFGTNICPTDKDHAL--KVF T SILFTCHPI SKIRKCDNGHVS L V F F P P G S I G L V R  
Sf-01\_Amz1 VCKCKGTNDCLIDEDHALVRGNKTFPSTVFTCKPIREFRECKDGETALVYPQPGLIRQIR  
Sf-01\_Amz1i VCKCKGTNDCLIDEDHALVRGNKTFPSTVFTCKPIREFRECKDGETALVYPQPGLIRQIR  
Sf-01\_Amz2 VCKCKGTNDCLIDEDHALVRGNKTFPSTVFTCKPIREFRECKDGETALVYPQPGLIRQIR

130 140 146

Sf-01\_Ps2 CICS GGRKNVQVEQD GKFHFV C--S  
Sf-01\_Amz1 CLCSRGW--RYEYAGNGKVKCLR LT  
Sf-01\_Amz1i CLCSRGW--RYEYAGNGKVKCLR LT  
Sf-01\_Amz2 CLCSRGW--RYEYAGNGKVKCLR LT

## SF-06 superfamily

1 10 20 30 40 50 60

SF-06\_Ps1 MLLMFAWTLMTAMMVMNAS S KDCPLLDDSNPLKRRCLWNNAI CGKSVSGKCTSLCNCRNGQ  
SF-06\_Ps1ii MLLMFAWTLMTAMMVMNAS S KDCPLLDDSNPLKRRCLWNNAI CGKSVSGKCTSLCNCRNGQ

70 80 90 100 110 120

SF-06\_Ps1 KCSMNSTHTITVVPYYINGVPPVKKRYYTCDVAHLGQCSSTQFALYSLIYFETELKNAKVY  
SF-06\_Ps1ii KCSMNSTHTITVVPYYINGVPPVKKRYYTCDVAHLGQCSSTQFALYSLIYFETELKNAKVY

130 140 150

SF-06\_Ps1 CECRSPKVVYLR LFTPKRYICRRAPRTG  
SF-06\_Ps1ii CECRSPKVVYLR LFTPKRYICRRAPRTG

## SF-mi1 superfamily

1 10 20 30 40 50

SF-mi1\_P29.2 MSKTGLVLLVLYLLSSTVNLQQT EDDQAFIKIR SPTLTRI-LERSGSCVPQSGGGCTG  
SF-mi1\_Ps9.2ii MSKTGLVLLVLYLLSSTVNLQQT EDDQAFIKIR SPTLTRI-LERSGSCVPQSGGGCTG  
SF-mi1\_Ps9.1 MSKTGLVLLVLYLLSSTVNLQQN EDDKAFMKIM IPTLTRV-LERSGSCVPQSGGGCTG  
SF-mi1\_Ps9.1ii MSKTGLVLLVLYLLSSTVNLQQN EDDKAFMKIM IPTLTRV-LERSGSCVPQSGGGCTG  
SF-mi1\_Amz9.1 MSKTGLVLLVLYLLSSTVNLQQT EDDKAFMKIM IPTLTRV-LERSGSCVPQSGGGCTG  
SF-mi1\_Amz9.1i MSKTGLVLLVLYLLSSTVNLQQT EDDKAFMKIM IPTLTRV-LERSGSCVPKSGGGCTG  
SF-mi1\_Amz9.1ii MSKTGLVLLVLYLLSSTVNLQQT EDDKAFMKIM IPTLTRV-LERSGSCVPKSGGGCTG  
SF-mi1\_Ps9.3 MSKTGLVLLVLYLLSSTVNLQQS DDDQAF--ISPTLRRVLLERGRSGCVPKPGGCTG

60 70 80

SF-mi1\_P29.2 TC--PG-TCVGSVKGCTCNVSG  
SF-mi1\_Ps9.2ii TC--PG-TCVGSVKGCTCNVSG  
SF-mi1\_Ps9.1 TC--PG-ICGSRYGCA CKTTG  
SF-mi1\_Ps9.1ii TC--PG-TCGSRYGCA CKTTG  
SF-mi1\_Amz9.1 TC--PG-TCGSIKGCACCKTTG  
SF-mi1\_Amz9.1i TC--PG-TCGSIKGCACCKTTG  
SF-mi1\_Amz9.1ii TC--PG-TCGSIKGCACCKTTG  
SF-mi1\_Ps9.3 TCSQPGYICAVGL-QCRCKRA

## SF-mi2\_Ps1

1 10 20 30 40 50 60 62

MRFYLLLTVTL LLASFTAA DVGLRQAMRRDASGHCTAHCECGNHNMCCCHK EKC VNGRC TK

# T superfamily

	1	20	40	60	80	97					
T_Ps5.8	MRCLPVFF	ILLLLIPSAPSVH	-----	ARPKTKD	VSLASFHGNAKR	IP--QRLLR	I---CCLYG-NPQC-CT				
T_Ps1.12	MRCLPVFI	ILLLLIPSAPSVH	-----	AQPKTKD	VPLASFYINR	STL--RRLWNA	R---SCCPM---CLCR				
T_Ps1.13	MRCLPVFI	ILLLLIPSAPSVH	-----	ARQKTKD	VPLASFHNTK	STL--BSLWNA	R---SCLM---CGSG				
T_Ps5.4	MRCLPVFV	ILLLLIPSAPNVH	-----	ARPKTKD	VPLASIHNA	RFTL--LRQWNR	--TCCQFY--PSC-CPTRK				
T_Amz5.10ii	MRCLPVFI	ILLLLIPSAPNVH	-----	ARPKTKD	VPLASFHNA	RFTL--LRQWNR	--TCCQFY--PSC-CPTRK				
T_Amz5.10	MRCLPVFI	ILLLLIPSAPNVH	-----	ARPKTKD	VPLASFHNA	RFTL--LRQWNR	--TCCQFY--PSC-CPTRK				
T_Amz5.11	MRCLPVFV	ILLLLIPSAPSVH	-----	VRPKTKD	VSLASFHNA	KRTL--QRLLWNR	--CCSR--GSC-CLGW				
T_Amz5.1	MRCLPVFI	ILLLLIPSAPSVH	-----	ARAKTKH	VPLASFHNV	RRTL--QTLWNR	--QCCFTQ--SGC-CPWGK				
T_Ps5.1	MRCLPVFI	ILLLLIPSAHSIL	-----	ARPKTEV	VPLASL	NAKRTL--QTLWNA	R---CCDKR--PWC-CLG				
T_Ps5.1ii	MRCLPVFI	ILLLLIPSAHSIL	-----	ARPKTEV	VPLASL	NAKRTL--QTLWNA	R---CCDKR--PWC-CLG				
T_Amz5.12	MRCLPVFI	ILLLLIPSAHSIL	-----	ARPKTEV	VPLASL	NAKRTL--QTLWNA	R---CCDKR--PWC-CLG				
T_Ps1.14	MRCLPVFI	ILLLLIPSAHSVH	-----	AQPKTKD	VPLPSFHN	NAKRTL--QRWR	PT---LCLRM--VNCVPLWQ				
T_Ps1.14ii	MRCLPVFI	ILLLLIPSAHSVH	-----	AQPKTKD	VPLPSFHN	NAKRTL--QRWR	PT---LCLRM--VNCVPLWQ				
T_Ps1.15	MRCLPVVI	ILLLLIPSAHSVH	-----	AQPKTKD	AVPLPSFHN	NAKRTL--QRWR	PN---LCLRM--VNCVPL				
T_Ps1.15ii	MRCLPVFI	ILLLLIPSAHSVH	-----	AQPKTKD	VPLPSFHN	NAKRTL--QRWR	PN---LCLRM--VNCVPL				
T_Ps5.5	MRCLPVFI	ILLLLIPSAHSVH	-----	AQPKTKD	VPLPSFHN	NAKRTL--QR	HRKS---WCCQNM--LRC-CGQSN				
T_Ps5.6	MRCLPVFI	ILLLLIPSAHSVH	-----	AQPKTKD	VPLPSFHN	NAKRTL--QR	HRKS---WCCQNM--LRC-CGQSN				
T_Ps5.7	MRCLPVFI	ILLLLIPSAHSVH	-----	AQPKTKD	VPLPSFHN	NAKRTL--QR	HRKS---WCCQNM--LNC-CVSS				
T_Ps5.22	MRCLPVFI	ILLLLIPCAHSIP	-----	ARLTKD	VLASL	NAKRI	L--QRQK--QCCSN--PTC-CTG				
T_Ps5.21	MRSLPAFI	ILLLLIPSPHSIL	-----	AQPKTKD	VPLASFL	NAKRTQ--QR	FWN---HCCQNM--PAC-CRYGRKMA				
T_Amz5.18	MRSLPAFI	ILLLLIPSPHSIL	-----	AQPKTKD	VPLASFL	NAKRTQ--QR	FWN---HCCQNM--PAC-CRYGRKMA				
T_Ps5.13	MRSLPAFI	ILLLLIPSPHSIL	AR	PMTKD	VPLASFAQPKTKD	VPLASFL	NAKRTQ--QR	FWN---HCCQNM--PAC-CRYGRKMA			
T_Amz5.18ii	MRSLPAFI	ILLLLIPSPHSIL	AR	PMTKD	VPLASFAQPKTKD	VPLASFL	NAKRTQ--QR	FWN---HCCQNM--PAC-CRYGRKMA			
T_Ps1.16	MRCLPVFI	ILLLLIPFAPS	VAR	PTTKD	VPLASFHAR	LTKD	VPLASFL	NAMRP	---QR	---C	CRPG-QRWC-C
T_Amz5.17	MRCLPVFI	ILLLLIPFAPS	VAR	PTTKD	VPLASFHAR	LTKD	VPLASFL	NAMRP	---QR	---C	CRPG-QRWC-C
T_Amz5.17ii	MRCLPVFI	ILLLLIPFAPS	VAR	PTTKD	VPLASFHAR	LTKD	VPLASFL	NAMRP	---QR	---C	CRPG-QRWC-C
T_Ps5.14	MRCLPVFI	ILLLLIPFAPS	VAR	PTTKD	VPLASFHAR	LTKD	VPLASFL	NAMRP	---QR	---C	CRPG-QRWC-C
T_Ps5.14ii	MRCLPVFI	ILLLLIPFAPS	VAR	PTTKD	VPLASFHAR	LTKD	VPLASFL	NAMRP	---QR	---C	CRPG-QRWC-C
T_Ps5.3	MRCLPVFI	ILLLLIPFAPS	VAR	PTTKD	VPLASFHAR	LTKD	VPLASFL	NAMRP	---QR	---C	CRPG-QRWC-C
T_Ps5.25	MRCLPVFI	ILLLLIPFAPS	VAR	PTTKD	VPLASFHAR	LTKD	VPLASFL	NAMRP	---QR	---C	CRPG-QRWC-C
T_Amz5.16	MRCLPVFI	ILLLLIPFAPS	VAR	PTTKD	VPLASFHAR	LTKD	VPLASFL	NAMRP	---QR	---C	CRPG-QRWC-C
T_Amz5.16ii	MRCLPVFI	ILLLLIPFAPS	VAR	PTTKD	VPLASFHAR	LTKD	VPLASFL	NAMRP	---QR	---C	CRPG-QRWC-C
T_Amz5.6	MRCLPVFI	ILLLLIPFAPS	VAR	PTTKD	VPLASFHAR	LTKD	VPLASFL	NAMRP	---QR	---C	CRPG-QRWC-C
T_Ps5.10	MRCLPVFI	ILLLLIPSAHSVI	-----	AGPKTKD	VSLASFL	NAMRP	---RKL	---C	ISG-SMYC-CS	FKALTLFRPS	
T_Ps5.11	MRCLPVFI	ILLLLIPSAHSVI	-----	ARPKTKD	APLASSHYNAMGTT	---KR	---WCCAF-HANC-C				
T_Ps5.2	MRCLPVFI	ILLLLIPSAHSV	-----	ARPKTKD	APLASSHYNAMGTT	---KR	---LCCVL-HTC-C				
T_Amz5.14	MRCLPVFI	ILLLLIPSAHSVI	-----	ARPKTKD	YVPLASFHGNT	KRTL--QILRK	I---CCPM---HC-CW				
T_Ps5.2ii	MRCLPVFI	ILLLLIPSAHSVI	-----	ARPKTKD	YVPLASFHGNT	KRTL--QILRK	I---CCPM---HC-CW				
T_Ps5.3	MRCLPVFI	ILLLLIPSAHSVI	-----	ARPKTKD	YVPLASFHGNT	KRTL--QILRK	I---CCPM---HC-CW				
T_Amz5.13	MSCFPVFI	ILLLLVPSAPSI	-----	APQTKD	GVSLASFHGN	AKRTL--QR	---KCCPVW--FLC-CLAGI	IRYQG			
T_Amz5.13ii	MSCFPVFI	ILLLLVPSAPSI	-----	APQTKD	GVSLASFHGN	AKRTL--QR	---KCCPVW--FLC-CLAGI	IRYQG			
T_Amz5.13iii	MSCFPVFI	ILLLLVPSAPSI	-----	APQTKD	GVSLASFHGN	AKRTL--QR	---KCCPVW--FLC-CLAGI	IRYQG			
T_Ps5.12	MRCLPVFI	ILLLLIPSAHSV	-----	ARPKTKD	VPLASFL	NAQQT	---QR	LGK---VCCTP	PIYWHC-CHNK		
T_Ps5.9	MRCLPVFI	ILLLLIPSAHSV	-----	GRPKTKD	VPLASFL	NAQQT	---QR	LGK---VCCNT	PG-CPHG		
T_Amz5.19	MRCLPVFI	ILLLLIPSAHSV	-----	ARLTKD	APLASSQ	NPMRTR--QH	---WCCTPL--RTWC-CP	IVGK			
T_Amz5.19ii	MRCLPVFI	ILLLLIPSAHSV	-----	ARLTKD	APLASSQ	NPMRTR--QH	---WCCTPL--RTWC-CP	IVGK			
T_Ps5.15	MRCLPVFI	ILLLLVPS--GII	-----	ARPKTKD	VALVPH	AMRTR--QP	GR---WCCAG-HGF-CG				
T_Ps5.24	MRCLPVFI	ILLLLVPS--GII	-----	ARPKTKD	VALVPH	AMRTR--QP	GR---WCCAG-HGF-CG				
T_Amz5.15	MRCLPVFI	ILLLLIPSAHSV	-----	ARPKTKD	VPLASFL	NAQQT	---QR	LGK---VCCTP	PIYWHC-CHNK		
T_Amz5.15ii	MRCLPVFI	ILLLLIPSAHSV	-----	ARPKTKD	VPLASFL	NAQQT	---QR	LGK---VCCTP	PIYWHC-CHNK		
T_Amz5.15iii	MRCLPVFI	ILLLLIPSAHSV	-----	ARPKTKD	VPLASFL	NAQQT	---QR	LGK---VCCTP	PIYWHC-CHNK		
T_Amz5.20	MRCLPVFI	ILLLLIPSAHSV	-----	ARPKTKD	VPLASFL	NAQQT	---QR	LGK---VCCTP	PIYWHC-CHNK		
T_Amz5.21	MRCLPVFI	ILLLLIPSAHSV	-----	ARPKTKD	VPLASFL	NAQQT	---QR	LGK---VCCTP	PIYWHC-CHNK		
T_Ps5.16	MLCLPVFI	ILLLLVSPAAILP	-----	VSLQR	LTVSPK	FAMRTA--QHVP	FMR	LRCCPY	---IC-CG		
T_Amz5.8	MLCLPVFI	ILLLLVSPAAILP	-----	VSLQR	LTVSPK	FAMRTA--QHVP	FMR	LRCCPY	---IC-CG		
T_Amz5.8ii	MLCLPVFI	ILLLLVSPAAILP	-----	VSLQR	LTVSPK	FAMRTA--QHVP	FMR	LRCCPY	---IC-CG		
T_Ps5.16ii	MLCLPVFI	ILLLLVSPAAILP	-----	VSLQR	LTVSPK	FAMRTA--QHVP	FMR	LRCCPY	---IC-CG		
T_Ps5.16iii	MLCLPVFI	ILLLLVSPAAILP	-----	VSLQR	LTVSPK	FAMRTA--QHVP	FMR	LRCCPY	---IC-CG		
T_Ps5.17	MLGLPVFI	ILLLLVSPAAILR	-----	VSLQR	LTVSPK	FAMRTA--QHVP	FMR	LRCCPY	---IC-CG		
T_Amz5.5	MLGLPVFI	ILLLLVSPAAILR	-----	VSLQR	LTVSPK	FAMRTA--QHVP	FMR	LRCCPY	---IC-CG		
T_Amz5.5ii	MLGLPVFI	ILLLLVSPAAILR	-----	VSLQR	LTVSPK	FAMRTA--QHVP	FMR	LRCCPY	---IC-CG		
T_Amz5.4	MLCLPVFI	ILLLLVSPAAILP	-----	VSLQR	LTVSPK	FAMRTA--QHVP	FMR	LRCCPY	---IC-CG		
T_Ps5.18	MLCLPVFI	ILLLLVSPAAILP	-----	VSLQR	LTVSPK	FAMRTA--QHVP	FMR	LRCCPY	---IC-CG		
T_Amz5.2	MLCLPVFI	ILLLLVSPAAILP	-----	VSLQR	LTVSPK	FAMRTA--QHVP	FMR	LRCCPY	---IC-CG		
T_Amz5.9	MLCLPVFI	ILLLLVSPAAILP	-----	VSLQR	LTVSPK	FAMRTA--QHVP	FMR	LRCCPY	---IC-CG		
T_Amz5.7	MFGLPVFI	ILLLLVSPAAILP	-----	VSLQR	LTVSPK	FAMRTA--QHVP	FMR	LRCCPY	---IC-CG		
T_Ps2	MNCLPVFI	IVLLLIHSSQV	-----	HSLKR	TKML--HQTAR	GF--V	R---I	ACVLQ--LSCG			
T_Ps5.19	MNCLPVFI	IVLLLIHSSQV	-----	HSLKR	TKML--HQTAR	GF--V	R---I	ACVLQ--LSCG			
T_Ps5.23	MNCLPVFI	IVLLLIHSSQV	-----	HSLKR	TKML--HQTAR	GF--V	R---I	ACVLQ--LSCG			
T_Amz5.24	MNCLPVFI	IVLLLIHSSQV	-----	HSLKR	TKML--HQTAR	GF--V	R---I	ACVLQ--LSCG			
T_Amz5.24i	MNCLPVFI	IVLLLIHSSQV	-----	HSLKR	TKML--HQTAR	GF--V	R---I	ACVLQ--LSCG			
T_Amz5.24ii	MNCLPVFI	IVLLLIHSSQV	-----	HSLKR	TKML--HQTAR	GF--V	R---I	ACVLQ--LSCG			
T_Ps5.20	MNCLPVFI	IVLLLIHSSQV	-----	HSLKR	TKML--HQTAR	GF--V	R---I	ACVLQ--LSCG			
T_Amz5.23	MNCLPVFI	IVLLLIHSSQV	-----	HSLKR	TKML--HQTAR	GF--V	R---I	ACVLQ--LSCG			
T_Amz5.26	MNCLPVFI	IVLLLIHSSQV	-----	HSLKR	TKML--HQTAR	GF--V	R---I	ACVLQ--LSCG			
T_Amz5.22	MNCLPVFI	IVLLLIHSSQV	-----	HSLKR	TKML--HQTAR	GF--V	R---I	ACVLQ--LSCG			
T_Amz5.22i	MNCLPVFI	IVLLLIHSSQV	-----	HSLKR	TKML--HQTAR	GF--V	R---I	ACVLQ--LSCG			
T_Amz5.25	MNCLPVFI	IVLLLIHSSQV	-----	HSLKR	TKML--HQTAR	GF--V	R---I	ACVLQ--LSCG			
T_Ps1	MRCLPVFI	ILLLLIPSAHSV	-----	ARPKTKD	VSLASFHNA	RIP--QRLLR	I---GCCIFG-TTA				

## U superfamily

1 10 20 30 40 50 60 70 80  
U\_Ps8.1 MNRMGFFLTLT IAML L TSL I RTHGAKLKI KRDCPSNVCVTGKGGPKCGCCNARCI N L CQIVGRRRGSNRNVYYNNN  
U\_Ps8.1ii MNRMGFFLTLT IAML L TSL I RTHGAKLKI KRDCPSNVCVTGKGGPKCGCCNARCI N L CQIVGRRRGSNRNVYYNNN

## V superfamily

1 10 20 30 40 50 60 70 79  
V\_Ps15.1 MSTPRMMPLVLLLLL SLATHCGDQA IQGRRLSARLLRGYKERGLS I KTCGTNGARCCGLCPSPGKNCSCLPFGK  
V\_Ps15.1ii MSTPRMMPLVLLLLL SLATHCGDQA IQGRRLSARLLRGYKERGLS I KTCGTNGARCCGLCPSPGKNCSCLPFGK  
V\_Ps15.1iii MSTPRMMPLVLLLLL SLATHCGDQA IQGRRLSARLLRGYKERGLS I KTCGTNGARCCGLCPSPGKNCSCLPFGK  
V\_Amz15.2 MSTPRMMPLVLLLLL SLATHCGDQA IQGRRLSARLLRGYKERGLS I KTCGTNGARCCGLCPSPGKNCSCLPFGK  
V\_Amz15.1 MSTPRMMPLVLLLLL SLATHCGDQA IQGRRLSARLLRGYKERGLS I KTCGTNGARCCGLCPSPGKNCSCLPFGK  
V\_Amz15.1ii MSTPRMMPLVLLLLL SLATHCGDQA IQGRRLSARLLRGYKERGLS I KTCGTNGARCCGLCPSPGKNCSCLPFGK

**Supporting Table 1.** Information on transcriptome sequencing and assembly

<i>Conus</i> species	Samples sequenced per lane	Before quality/adaptor trimming			After quality/adaptor trimming		
		Number of reads	Read length (nt)	Medium quality	Number of reads	Read length(nt)	Medium quality
<i>Andremenezi 1</i>	5	63,598,020	101	32	58,834,536	69-101	37
<i>Andremenezi 2</i>	5	57,226,346	92	30	54,177,324	65-92	35
<i>Praecellens 1</i>	4	76,907,910	101	32	70,826,570	69-101	37
<i>Praecellens 2</i>	9	34,635,096	125	32	32,695,570	85-125	37
<i>Geographus</i>	2	158,004,874	101	30	146,630,264	67-101	35

**Assembly stats**

	N50 (bp)	Total size (bp)	Number of contigs	Contigs with homology with UniProtKB/conoserver	Alignment rate of reads to all contigs
<i>Andremenezi 1</i>	621	125,728,996	345,144	35,181	97.84%
<i>Andremenezi 2</i>	256	50,778,327	219,674	13,837	95.70%
<i>Praecellens 1</i>	505	72,259,543	207,619	21,605	98.65%
<i>Praecellens 2</i>	547	2,884,375	5,726	983	95.48%
<i>Geographus</i>	725	164,302,283	420,919	35,097	98.73%

**Supporting Table 2.** Venom composition of the two species of *Splinoconus* (*C. lenavati* and *C. tribblei*) and *C. geographus* (subgenus *Gastridium*). Relative expression levels are provided for each superfamily, from highest to lowest expression. Number of individual sequences per superfamily is shown in parentheses.

<i>C. lenavati</i>		<i>C. tribblei</i>		<i>C. geographus</i>	
<i>Superfamily</i>	Expression Level	<i>Superfamily</i>	Expression Level	<i>Superfamily</i>	Expression Level
B2	28.3 % (2)	Con-ikot-ikot	35.7 % (12)	B	32.0 % (3)
Con-ikot-ikot	23.3 % (10)	B2	35.0 % (1)	O1	26.9 % (15)
T	15.5 % (5)	O2	12.6 % (4)	A	13.8 % (6)
U	12.1 % (2)	P	5.6 % (4)	B2	5.4 % (1)
O2	11.1 % (11)	O1	3.1 % (6)	Con-ikot-ikot	4.2 % (5)
P	2.8 % (4)	G-like	0.9 % (1)	M	4.0 % (3)
O1	1.7 % (14)	Conkunitzin	0.9 % (3)	C	3.3 % (1)
M	0.96 % (11)	M	0.86 % (12)	T	2.4 % (10)
G-like	0.88 % (1)	H	0.84 % (2)	S	2.3 % (5)
Conodipine	0.67 % (3)	O3	0.58 % (4)	Insulin	1.1 % (2)
O3	0.65 % (3)	I2	0.55 % (3)	O2	1.5 % (4)
Y	0.64 % (1)	L	0.52 % (2)	Conoporin	1.06 % (3)
Conopressin	0.38 % (2)	Conopressin	0.49 % (3)	I3	0.53 % (2)
I1	0.19 % (3)	D	0.43 % (1)	O3	0.41 % (2)
I2	0.17 % (5)	Dip	0.28 % (3)	Conkunitzin	0.30 % (4)
L	0.15 % (5)	N	0.23 % (3)	J	0.23 % (1)
W	0.09 % (1)	W	0.21 % (1)	PH4	0.18 % (1)
SF-02	0.09 % (1)	B1	0.19 % (1)	Conodipine	0.17 % (3)
B1	0.08 % (2)	Y	0.14 % (1)	Conopressin	0.14 % (2)
A	0.05 % (5)	I1	0.13 % (2)	Conohyal	0.14 % (1)
H	0.05 % (1)	SF-04	0.12 % (3)	Mr30	0.01 % (1)
Conkunitzin	0.04 % (4)	Y2	0.10 % (1)		
Kun	0.04 % (1)	Div.MKFPLLFI	0.10 % (3)		
F	0.03 % (1)	NL	0.08 % (1)		
C	0.02 % (1)	SF-02	0.08 % (1)		
Div.MKFPLLFI	0.01 % (3)	F	0.05 % (1)		
Div.M---L-LTVA	0.01 % (2)	S	0.05 % (2)		
A-like	0.005 % (2)	Div.MSTLGMTLL	0.05 % (1)		
SF-04	0.004 % (3)	SF-01	0.03 % (1)		
SF-06	0.003 % (1)	U	0.03 % (1)		
Y2-like	0.002 % (3)	Div.M---L-LTVA	0.01 % (2)		
SF-01	0.002 % (1)	Div.MSKLVILAVL	0.01 % (1)		
S	0.002 % (5)	Y2-like	0.01 % (2)		
R	0.002 % (1)	K	0.01 % (1)		
E	0.001 % (1)	A-like	0.003 % (2)		
I3	0.001 % (1)	J	0.003 % (1)		
SF-03	0.001 % (1)	R	0.002 % (1)		
SF-05	0.0005 % (1)	SF-03	0.001 % (1)		
SF-mi2	0.0002 % (1)	I3	0.0002 % (1)		
SF-mi4	0.0002 % (1)				

**Supporting Table 3.** Pairwise dN/dS ratios of rbh pairs between *C. andremenezi* (Amz) and *C. praecellens* (Ps)

Sequence pair	Sequence alignment, Amz (top), Ps (bottom)	Dn/Ds
I4_Amz12.1 I4_Ps12.2ii	<pre> ATGTTTGGTC ATACGTCAGT CAATTTTCTT CTGCTCTCCA TCATGGTTTT ATGTTTGGTT ATACATCAGT CAATTTTCTT CTGCTCTCCA TCACGATTTT CGGCATGGTG GCAACGGTTA TTTGCTCGTG TGGAAAGAGT ATCTCGAGTG CAGCATGGTG GCAACGGTTG TTTGCTCGTG TGGAAAGAGT ATCTCGAGTG AAAACGTGTG ACAGCCAGGG GAAGAGATCT GCTCGTGCTC CAATCATGTG AAAACGTGTG ACAGCCGGGG GAAGAGATCT GCTCGTGCTC CAATCATGTG TGCTGTCCCT TGAATCCACC CCACAGTGAT CAGTGCATGA CGTTGACTGC TGCTGTCCCT TGAATCCACC CCACAGTGAT CAGTGCATGA CGTTGACTGC GTGCAGCATA ATGCTCAGTG GATTGGTTCG CCGCAGAACA ATTCAGATGC GTGCAACATA ATGCTCAGTG GATTGGTTCG CCGCAGAGCA ATTCAGACGC AAGAAAGATT CCTTCGTATG ACGCGCGGTC TTGCCGACTA G AAGAAAGATT CCTTCGTATG ACGCGTGGTC TTGCCGACTA G </pre>	1.43
putativeMSGLR_Amz7.1 putativeMSGLR_Ps7.1	<pre> ATGTCGGGAT TGAGAGTGGT GTTGTTCGCC CTCTACTTTC TGGTGTATCT ATGTCGGGAT TGAGAGTGGT GTTGTTCGCC CTCTACTTTC TGGTGTATCT GGTAACCTCT AAACGGGATG GAGATGGACT GACAAAAGTG GTCAAGAACA GGTAACCTCT AAACGGGATG GAGATGGACT GACAAAAGTG GTCAAGAACA AACGAGCGGT AACAGCTATC GGGAGGAAAA TGATGAGAAG TGTGCACCGA AACGAGCGGT AACAGCTATC GGGAGGAAAA TGATGAGAAG TGTGCACCGA TCAGGCGGCT GCCCTACAAA GTGCCCGGAT AAAGACGAAT GCTGCTCCGG TCAGGCGGCT GCCCTACAAA GTGCCCGGAT AAAGACGAAT GCTGCTCCGG AAGTAAATGT ATCAATATCT ATGGTTCGTAA CGTATGTGTA AAGATACCCA AAGTAAATGT ATCAATATCT ATGGTTCGTAA CGTATGTGTA AAGATACCCA CATCACGATG A CATCACGATG A </pre>	2.24
O2_Amz7.1ii O2_Ps7.1	<pre> ATGCAGAAAC TGACAATCCT GCTTCTTGT TCTGCTGTAC TGGTGTGAC ATGGAGAAAC TGACAATCCT GCTTCTTGT TCTGCTGTAC TGGTGTGAC CCAGGCCCTC ATTCAAGGTG GTGGAGAAAA ACGCCAAAAG GCAAAGATCA CCAGGCCCTG ATTCAAGGTG GTGGAGAAAA ACGCCAAAAG GCAAAGATCA ACTTTTTTTC AAAAAGAAAG CCATCTTCTA AGCGTTGGTG GGGGCATGAC ACTTTTTTTC AAAAAGAAAG CCATCTTCTA AGCGTTGGTG GGGGCATGAC GAATGCCGTT ATTGGTTGGG GCCTTGTGAG CTGGACTCGG ATTGTTGTTC GAATGCCGTT ATTGGTTGGG GCCTTGTGAG CTGGACTCGG ATTGTTGTTC TGATAGTTGT GAGGAAAAGT TCTGCGGGTT GTGGTGA TGATAGTTGT GAGGAAAAGT TCTGCGGGTT GTGGTGA </pre>	0.196
V_Amz15.2 V_Ps15.1	<pre> ATGTCAACAC CAAGAATGAT GCCACTCGTC CTCCTGCTTC TGTTGTCCCT ATGTCAACAC CAAGAATGAT GCCACTGCTC CTCCTGCTTC TGTTGTCCCT GGCAACCCAT TGTGGTGACG GACAGGCGAT CCAAGGGGAC AGACGCCTAA GGCAACCCGT TGTGGTGACG GACAGGCTAT CCAAGGGGAC AGACGCCTAA GTGCGAGACT TCTAAGAGGA TACAAGGAAC GTGGTCTATC AATCAAGACG GTGCGAGACT TCTAAGAGGA TACAAGGAAC GTGGTCTATC AATCAAGACG TGCGGAACCT GCAATGGCGC GCGATGCTGT GGAATCTGTC CATGCTCTCC TGCGGAACCT GCAATGGCGC GCGATGCTGT GGAATCTGTC CATGCTCTCC GGGCGAGAAA AACTGTTCTT GTTTGCCGTT TGGGAAATAA GGGCGAGAAA AACTGTTCTT GTTTGCCGTT TGGGAAATAA </pre>	0.226
M_Amz3.3ii M_Ps3.11	<pre> ATGCTGAAAA TGGGAGTGTT GCTATTTCATC TTTCTGGTCC TGTTTCCCCT ATGCTAAAAA TGGGAGTGTT GCTATTTCATA TTTCTGTTCC TGTTTCCCCT GGCAACGCTC CAGCTGGATG CAGATCAACC TGTAGAACGA TATGCGGAGA GGCAACGCTC CAGCTGGATG CAGATCAACC TGTAGAACGA TATGCGGAGA CCAAACAGGA CCTCAACCCA GATGAAAGGA GGGCAAACAT AATGCTTACT CCAAACAGGA CCTCAACCCA GATGAAAGGA GGGCAAACAT AATGCGTATT CTGCGTCGGA GCGGACGTC ATGCTGCAAA CCGCCGAATT GTGAAGTTG CTGCTTCAGA GGCAGACGTC ATGCTGCAAA CCGCCGTGGT GTGAAATGTG TAATGCTGTC TTCTAG </pre>	1.83
O1_Amz6.21 O1_Ps6.15	<pre> ATGAAACTGA CGTGCCTGTT GATCGTCGCC GTGCTGTTCC TGACGGCCTG -----TTCC TGACGGCCTG TCAACTCCTT ACAGCTGATG ACTCCAGAGA TAAGCCGGGG TATCCTGCTT TCAACTCCTT ACAGCTGATG ACTCCAGAGA TAAGCCGGGG TATCCTGCTT TGAGGTCGAT TATCAAGACG TGGAGTTCCA GGCAATCCAG GTCGGTGAGG TGAGGTCGAT TATCAAGACG TGGAGTTCCA GGCAATCCAG GTCGGTGAGG ACGTGCACCT ATCCATACTA TGACTGTGAC AGTAGTGAAG AGTGTGCTC ACGTGCACCT ATCCATACTA TGACTGTGAC AGTAGTGAAG AGTGTGCTC TAAAGGCTGT ATGTTTCGAGA TGACGGCGGG GCAGTATTGC GTGTAA TAAAGGCTGT ATGTTTCGAGA TGACGACGGG GCAGTATTGC GTGTAA </pre>	0.416
putativeMWSGK_Amz9.1ii putativeMWSGK_Ps9.1	<pre> ATGTGGAGCG GAAAGGATGA GGCTGCATTC CTTGCTTTGG TGCTGATGGT ATGTGGAACG GAAAGGATCA GGCTGCGTTC CTTGCTTTGG TGCTGATGGT GCTCTGGGCT CTCGGTACCA CAGCGGAATC CTGTTCCCCA GACCCATCT GGCCTGGGCT CTCGGTACCA CAGCGGAATC CTGTTCCCCA GACCCATCT ACTACAGCGA TTTTGAGGCA GCCTCGGGCG TCTGGTACTT GATTCTTTCA ACTACAGCGA TTTTGAGGCA GCCTCGGGCG TCTGGTACTT GATTCTTTCA AGGGAAAGCG ATGAGAGATA CAGAGTGTCT GGACTCGATC TAAATGCTTA AGGGAAAGCG ATGAGAGATA CAGAGTGTCT GGACTCGATC TAAATGCTTA </pre>	1.24

	TCGTTACGGC GGCAAATTGT TGGTAGACGT GTCTTGGATT TTCTTGAAAA TCGTTACGGC GGCAAATTGT TGGTAGACGT GTCTTGGATT TTCTTGAAAA GAACTACTCG TGGCTGTGAA AAGTTTACCA CGAGGTGCGA AGTGTCTGGC GAACTACTCG TGGCTGTGAA AAGTTTACCA CGAGGTGCGA AGTGTCTGGC AATACCTGCG TCGACACAAC AGGATATCAC CAAGTCGTAA AATATTATAT AATACCTGCG TCGACACAAC AGGATATCAC CAAGTCGTAA AATATTATAT CGTTGCCCTC GACGCCAACT ACCTCGTTGT CCACAGAACC TTACAAGGAA CGTTGCCCTC GACGCCAACT ACCTCGTTGT CCACAGAACC TTACAAGGAA ACCCGTACAC GCTTGATATC TACAGCCGAA CTGGTGTGGG ACGTCGTCTT ACCCGTACAC GCTTGATATC TACAGCCGAA CTGGTGTGGG ACGTCGTCTT AAACACCTTC CTC AATACAT CCGTGATGCT ATTGAGATGA CATGCGGGAA AAACACCTTC CTC AATACAT CCGTGATGCT ATTGAGATGA CATGCGGGAA AGATATTGCT ACTATCGACA GTTTCTGGCC TGGAAAGTAT TCCCTGGAG AGATATTGCT ACTATCGACA GTTTCTGGCC TGGAAAGTAT TCCCTGGAG ACTTCATCAG TAACTGCTTT TAA ACTTCATCAG TAACTGCTTT TAA				
O1_Amz6.4 O1_Ps6.4ii	ATGAAACTGA CGTGCATGAT GATTGTTGCT GTGCTGTTCT TGACCACCTG ATGAAACTGA CGTGCATGAT AATCGTTGCT GTACTGTTCT TGACCACCTG GGTATTCATC ACGGCTGATG ACTCCAGAAA TGGATTGGAG AATCTTCCTC GGTATTCATC ACGGCTGA--CTCCAGAAA TGGATTGGAG AATCTTCCTC GGATGGCAGC TCACGAAATA AAGAACCCCG AAGCCTCTAA GTTGAACAAC GGATGGCAGC TCACGAAATA AAGAACCCCG AAGCCTCTAA GTTGAACAAC AGAGACGACG ACTGCGTTGC TGGTGGTCAA GGTGTGGGCT TTCCGAAAAT AGAGACGACG ACTGCGTTGC TGGTGGTCAA GGTGTGGGCT TTCCGAAAAT TGGAGGGCCA TGCTGCAGTG GCTGGTGCTT TATCGTCTGC ACTTAA TGGAGGGCCA TGCTGCAGTG GCTGGTGCTT TTTCTGCTGC TTCTAA			0.505	
SF-01_Amz1ii SF-01_Ps1	ATGAAGTCGG CAGTCTTCAT GATGGCGCTG TCTATGTCCA TTTCCATTGT ATGAAGTCGG CAGTCTTCAT GATGGCGCTG TCTATGTCCA TTTCCATTGT CTTTACAAAG GCAGAGGAAT CAGTAGTAAA AGACGTGGAT TGCAGCGATC CTTTACAAAG GCAGAGGAAT CAGTAGTAAA AGACGTGGAT TGCAGCGATC CGAAAGGAAC GTGTCTTTT ACTGACGGAA CGTGTGGAGC ATATTACCGC CGAAAGGAAC GTGTCTTTT ACTGACGGAA CGTGTGGAGC ATATTACCGC TCGGGTAATG CCAATTACTG CTTCCTGTGC TGCAAATGCA AAGGCACAAA TCGGGTAATG CCAATTACTG CTTCCTGTGC TGCAAATGCA AAGGCACAAA TGACTGCCTT ATTGATGAAG ATCATGCATT AGTACGTGGA AACAAGACTT TGACTGCCTT ATTGATGAAG ATCATGCATT AGTACGTGGA AACAAGACTT TTCCAGCAC TGTTTTCAC TGAAGCCGA TCAGGGAATT TAGAGAATGT TTCCAGCAC TGTTTTCAC TGAAGCCGA TCAGGGAATT TAGAGAATGT AAAGACGGTG AAAGTGCCTT GGTGTATCCT CAACCTGGAC TCATCAGGCA GCCGACGGTG AAATGCTTT GGTGTATCCT CAACCTGGAC TCATCAGGCA GATTGCATGC CTATGTTCCC GTGGCTGGAG GTACGAATAT GCTGGCAATG GATTCTATGC CTATGTTCCC GTGGCCGGAG GTACGACAAA GCTGGCAATG GAAAGGTCAA GTGTTTACGA CTGACATAA GAAAATACAA GTGTTT-TGA CTGA-----			1.26	
PH4_Amz1ii PH4_Ps1	ATGAATCCTA CGACCAACCC CGCCCATCCT ATGAACCCTA TGAACCCTA -----A TGAACCCTA CAGTCCTATG AATCCTACGA CCAACCCCGC CCAACCTATG AACCTTATGA CAGTCCTATG AATCCTGTCA ACAGCTTGTA CAATCCCATA AAATTAACAT ACACCTACAG TCCTATGAAT CCTGTCAACA GCTTGTTACAA TCCCATGAAC ACCCCTTCCG CCTCCTA--TGCAAGTG GCTTCC----- TTAATATAACC CCTTCCGCC TCCTCTGGGC GCCTCCTACC TCCTTCCCTC -----TATT TCCTCACTTC TCCTCTGGGC GCCTCCTACC TCCTTCCCTC TACGAAGACT GCCTCAAAC TTCTCCAGGG TTCTCAGGTG GCTGCGTCAC TACGAAGACT GCCTCAAAC TTCTCCAGGG TTCTCAGGTG GCTGCGTCAC CGCTCAATCT TCAAACGAAC TTCCCGTACT CCTACCAGTC TGGTATGTAT CGCTCTATCT TCAAACGAAC TTCCCGTACT CCTACCAGTC CGGTATGTTT TCTCCTTTCT TCTTGCCCC GTATCAGCCG TCGGGCGCGC GCCAAGCCCT TCTCCTTTCT TCTTGCCCC GTATCAGCCA TCGGGCGCGC TCCAAGCCCT GTCTCCGCC TATGGCTTCG CTGCTGGTGT TCCTGGTGCC TTGGCATGGA GTATCCGCC TATGGCTTCG CTGCTGGTGT TCCTGGTGCC TTGGCATGGA ATCAGTTCGG GGGAGCTGCC TGGAAATCCCT ATTCCGCCAT GGGTTACGGA ATCAGTTCGG GGGAGCTGCC TGGAAATCCCT ATTCCGCCAT GGGTTACGGA GCTTATCCTC AGTGGCCGTT TCAGTTTGGC CACATGTGGC CGCTCAACCC GCTTATCCTC AGTGGCCGTT TCAGTTTGGC CACATGTGGC CTTTCAACCC TTACTACCAG ACCGTGTTGC CCGCCCAAGA GGGCATCTGC TCTTTTGACC TTACTACCAG ACCGTGTTGC CCGCCCAAGA GGGCATCTGC TCTTTTGACC GACCCTTCAA GTGTTGGGGC AGCCCCACTT GTATCCCAT TGAAGCCATT GACCCTTCAA GTGTTGGGGC AGCCCCACTT GTATCCCAT TGAAGCCATT TGTGACAAGA TTTTGTACTG CAGCAACCAC GCCGACGAAG ACCCGCGACT TGTGACAAGA TTTTGTACTG CAGCAACCAC GCCGACGAAG ACCCGCGACT TTGCATTGTG GGGCGGCGTC CTGGCTATGA CATCCTCGTG TCCTACCTGG TTGCATTGTG GGGCGGCGTC CTGGCTATGA CGTCCCTCGT TCCTACCTGG CACTGCCGGA TCAGCAGTGG ATGCTGCAGA AACTCTTCAA CAACGTGGAC CACTGCCGGA TCAGCAGTGG ATGCTGCAGA AACTCTTCAA CAACGTGGAC GTTTACACGA CCGCATATGC ACTGAGATTG ACGACCAGCC TAGGCGATCT GTTTACACGA CCGCATATGC ACTGAGATTG ACGACCAGCC TAGGCGATCT CCGTGGTCT TTTGCTCTCA CCGACGAGAA CATCAACAAC ACCAAGACGG			0.915	

	CCGCTGGTCT TTGGCTCTCA CCGACGAGAA CATCAACAAC ACCAAGACGG TGATGGAGGC GGGAAGAAG GACAACGAGG ATCCCTTGGT AGCCTTGGGC TGATGGAGGC GGGAAGAAG GACAACGAGG ATCCCTTGGT AGCCTTGGGC ATGAAAGACT CATCTTGGGA GTCCATCAAG TTCCTCTTCA ACCGCTTGTT ATGAAAGACT CATCTTGGGA GTCCATCAAG TTCCTCTTCA ACCGCTTGTT GGACACGGGC TTCATTTTGA ACTGA GGACACGGGC TTCATTTTGA ACTGA		
T_Amz5.3 T_Ps5.14	ATGCGCTGTC TCCCAGTCTT CATCACTCTG CTGCTGCTGA TTCCATCTGC ----- ACATAGCGTT ATTGCCCGAC CAAAGACCAA AGATGATGTG CCCCCTGGCAT ACATAGCGTT ATTGCCCGAC CAAAGACCAA AGATGATGTG CCCCCTGGCAT CTTTCCACGA TAATCCAATG GGAACCGAAC AAAGAGATTG GTGCTGCAAA CTTTCCACGA TAATCCAATG GGAACCGAAC AAAGAGATTG GTGCTGCAAA CCAGGCAAGA GATGGTGTCTG TTGA CCAGGCAAGA GATGGTGTCTG TTGA	0.335	
P_Amz9.1ii P_Ps9.7	ATGCATCTGT CACTGGCAGG CTCAGCTGTT TTGATGTTGC TTCTGCTGTT ATGCATCTGT CACTGGCAGG CACAGCTGTT TTGATGTTGC TTCTGCTGTT TGCCTTGGGC AACTTTCGTTG GGGTCCAGCC CGGACAGATA ACAAGAGATG TGCCTTGGGC AACTTTCGTTG GGGTCCAGCC AGGACAGACA ACAAGAGATG TGGACAATGG ACAGCTCAGC GACAACCGCC CTAACCTGCG ATCGCGGTGG CGGACAATGG ACAGCTCAGC GACAACCGCC CTAACCTGCG ATCGCGGTGG CAGCCAATGA GTCTCTTCAA GACACTTGAT AAACGAGGGT GGTGTGCCCTC CAGCCAATGA GTCTCTTCAA GACACTTGAT AAACGAGGGT GGTGTGCCCTC GTCTTGCACC ACGAATGGGG ACTGCGGTTT ACCGTGTTAT TGTACGACTG GTCTTGCACC ACGAATGGGG ACTGCGGTTT ACCGTGTTAT TGTACGACTG GAGGTCATTG CCAACACTAC CCGGGAACCTC CGTAG ATGGTTCGTTG CAAGCCCTCT CCGTGA-----	2.35	
H_Amz7.7 H_Ps7.7	ATGAACACTG CTGGCCGACT CCTGCTTCTG TGCCTCGCTC TGGGCCTGGT ATGAACACTG CTGGCCGACT CCTGCTTCTG GGCCTCGCTC TGGGCCTGGT GTTTCAATCT CTGGGAAAAG CCGTGCCTGA TGACGTAAAC GCTGAGAGAG GTTTCAATCT CTGGGAAAAG CCGTGCCTGA TGACGTAGAC ACTCACAGAG ACACAGATCC TTTCCACAAA GATGCACGGC A---GTTAGA GATCTTGACG ACACAGATCC TGATGACAAA GATCTACGGG ATTCATTAATA GATCGTGAAG GAACCCGAGT TGGACTGCGG CCGTGTAAAC TGTAAGCAAC GCTGCTGTGT AGGACTGAGT CCGACTGCGG CCGTGTAAAC TGTAAGCAAC GCTGCTGTGT AAAAATCGAC GAGGAAGAGA TATGCACAGT CTTTGTACTGT ATCGAACCTG AACAGAGGAC GGAAGAAGA AATGCAGAGA ACTGGGCTGT A--AACCTA ACCCACAGAG CCTGCAGTAA G-----	3.31	
O1_Amz6.18 O1_Ps6.13ii	ATGAAACTGA CCTACGCTTT GATCGTCGCC ATGCTGTTCC TGACGCCTG ATGAAACTGA CCTACGCTTT GATCGTCGCC ATGCTGTTCC TGACGCCTG TCAGCTCATT ACAACTCATG ACTCCAGAGG TAGGCAGGAG TATCGTGTG TCAGCTCATT ACAACTGATA ACTCCAGAGG TAGGCAGGAG TATCGTGTG CGAATGCGAG AACCAAAATG CAGAATTACA AGATCTTCAG GTTGACCAAG CGAGGGCGAG AACCAAGATG CAGAATTACA AGATCTTCAA GTTGACCAAG GGGTGTGTTG CACCCGGCGG CCGTGTACT CTTCGGCATA TAAATGTCTG AGGTGTGATC CACCCGGCGC CCGTGTACT CTTCGGCATA TAAATGTCTG CAGTAAA-GT ATGTAA--GT TAAAGAAGAA CCGGAATCCA GTTTGCGTGA CCATGCATGT TCGTACCCGC CACCCGGACA AGGAAAAGGA AAATGCACGA AAAAATAG ACGCTTAG	2.82	
P_Amz9.7 P_Ps9.12	ATGCATCTGT CACTGGCAGG CTCAGCTGTT TTGATGTTGC TTCTGCTGTT ATGCATCTGT CACTGGCAGG CTCAGCTGTT TTGATGTTGC TTCTGCTGTT TGCCTTGGGC AGCTTCATTG GGGTCCAGGC AGGACAGATA ACAAGAGATG TGCCTTGGGC AACTTCATTG GGGTCCAGGC AGGACAGATA ACAAGAGATG TGGACAACGG ACAGCTCAGC GACAAGCTCC GCAACCTGCA ATCACTGTGG TGGACAACGG ACAGCTCACA GACAAGCTCC GCAACCTGCA ATCACTGTGG GAGTCAAGGA GTCTCTTCAA GTTAGTTGCT AAACAACAGA GGTGTGGCGG GAGTCAAGGA GTCTCTTCAA GTTAGTTGCT AAACAACAGA GGTGTGGCGA GACTTGCACG TCTAGGCCCTG TGTGCGGCTA CCTTTGTTTT TGCCATTGGG GACTTGTCTG TCTAGTCTG AGTGCAGGCTA CCTTTGTTTT TGCCATTGGG GACGCTGCTG GCCAGTGGAA TGA GAAGCTGCCA ATTCTAG---	1.79	
M_Amz3.5 M_Ps3.14	ATGTCGAAAA TGGGAGTGGT GCTAATCATC TTTCTGGTCC TGTTTTCTCT ATGTCGAAAA TGGGAGTGGT GCTAATCATC TTTCTGGTCC TGTTTTCCAT GGCAGCGCTC CAGCTGGATG CAGATCGACC TGTAGAACGA CATGCGAAGA GGAAACGCTC CAGCTGGATG CAGATCGACC TGTGGAACGA TATGCGAAGA ACAAAACAGAA CCTCAACCCA GATAAAAAGGG GAATCGCCAT AATTATGCT ACAAAACAGAA CCTCAACCCA GATAAAAAGGG GAATAGCCAT AATTATGCT GTGTGTGTCGG AATGCTGTAG TCCGGCAGAT TGCAGACGCA GGGCATCGTG GCGTGTGTCGG AATGCTGTAG TCCGGCAGAT TGCAGACGCA GGGCATCGTG TATTTGCTGC AATTAG TATTTGCTGC AATTAG	0.6451	
I1_Amz11.1	ATGAAGCTGT CCGTGACGTT TCTTCTTATT CTGATGATTC TGCCATCGAT	2.59	



I1_Ps11.1	ATGAAGCTGT CTGTGACGTT TCTTCTTATT CTGATGATTC TGCCATCGAT GACTGGGGAG AAGTCTAGCA AGCGAACACT GAGGGGTGCT AGTC TGAGAG GACTGGGGAG AAGTCTAGCA AGCGTATACT GAGGGGTGCT AGTC TGAGAG GCATCGTGAG GGGATACTGC TTTGTGCAAG AAC---CATG CGAAGAAAAAT GCTTCTTGTTG GGATGAATGC TCAAGCATAG GACTACCATG CGGAATTCAT TTCCAGTGTCT GTTCGAGGTG TTTGTATGATC CAGAGGTGTG TTTGGACTTT TTCCACTGCT GTTCGAGGTG TTTGTATGAAC TACAACCTGTG TTTGGAATCG CACGGGACCT TGTCCCATAC TCGGCCGTTA G CTCG---CCT TGTCCCATAC TCGGCCGTTA G	
P_Amz9.4 P_Ps9.5	ATGCATCTGT CACTGGCAGG CTCAGCTGTT TTGATGTTGC TTCTGCTGTT ATGCATCTGT CACTGGCAGG CTCAGCTGTT TTGATGTTGC TTCTGCTGTT TGCCTTGGGC AACTTTGTGTT GGGTCCAGCC AGGACAGATA ACAAGAGATG TGCCTTGGGC AACTTTCGTTG GGGTCCAGCC AGGACAGATA ACAAGAGATG TGGACAATGG ACAGCTCAGG GACAACCGCC TTAACCTGCA ATCGCAGTGG TGGACAATGG ACAGCTCAGG GACAACCGCC TTAACCTGCA ATCGCAGTGG AAGCCAGTGA GTCTCTTCAA GTCACCTTAT AAACGAAGGC CGTGTACGG AAGCCAGTGA GTCTCTTCAA GTCACCTTAT AAACGAAGGC CGTGTACGG GTCTTGCAGG AACAATTTCC ACTGCAATCG CTTCTGTTAC TGTGGGAACA GTCTTGCAGG AATAATTTCC ACTGCAATCG CTTCTGTTAC TGTGGGAACA AAAAATGCAA ATGA AAAAATGCAA ATGA	0.293
O1_Amz6.26 O1_Ps6.11	ATGAAACTGA CGTGCATGAT GATCGTTGCT GTGCTGTTCT TGACCGCCTT ATGAAAGTGA CGTACATGAT GATTGTTGCT GTGCTGTTCT TGACCGCCTT CATATCTATC ACGGCTGATG ACTCCAGAAA TGGATTGGAG AATCTTGTTT CATATCTATC ACGGCTGATG ACTCCAGAAA TGGATTGGAG AATCGGGTTC GGAAGGCACG TCACGAAATG AAGAACCCCA AAGCCTCTGT ATTGAAACAAG GGATGGCAGG TTACGAAATG AAGAACCTCA AAGCCTCTGT ATCAAAGAAG A---GAGAAG ACTGCGAAGC AGGTGGTTCA GGTGTATGT ATGGGAGTGA ACCGGCGGAC CGTGCAAAGC CCCTAAATGG GGTGTATGT ATGGTACACGA GTGCTGCAGT GGCCTGTGCT TTCTCGTCTG CTTCTAA--- --- GTGCTGCGGT GGCCTGTGTA TTTTGTGCTG CTTTAAATA TGA	0.685
T_Amz5.24ii T_Ps5.19	ATGAAGTGTCT TTCCGGTCTT CTTTATCGTT CTTACTGCTGA TTGCTCATTC ATGAAGTGTCT TTCTGGTCTT C---ATCGTT CTTACTGCTGA TTGCTCATTC ATCTCAAGTT GCTGAGCATT CGAAGTTGGG GCGGATCAAA ATGTTGAGAC ATCTCAAGTT GTTGAACATT CGAAGTTGGA GCGGATCAAA ATGTTGAGCT GGTTAACTGC GGCAATAATA CTGGAGGATG AAGGATTTCC GGAGCTTTGC GGTCAATTCG GGAACGATA TTTGGAGACAG GAGGATGGCC GGAGGTTTGC TGCCCTTCTG ACAAAGATG CTGTGAAGCC TTGTGCAAT AA TGCCCTTTTA AAAGCCGTTG CTGTGAGTAG ----- -----CTGA CGTGCATGAT GATCGTGCCT GTGCTGTTCC TGACGGCCTG ATGAAACTGA CGTGCATGAT GATCGTGCCT GTGCTGTTCC TGACGGCCTG TCAATTCATT ACAGCTGATG ATTCCAGAGA TAAGCAGGAA TATCCTGCTG TCAATTCATT ACAGCTGATG ATTCCAGAGA TAAGCAGGAG TATCCTGCTG AGAGGTGCGAG AATCAAGAGG CAAAATTCGA AGCGCTCCAT GTCGACCAAG AGAGGTGCGAG AATCAAGAGG CAAAATTCGA AGCGCTCCAT GTCGACCAAG TCGTGCAAGG GGCCCAATTT AGCTTGTGCG CGTAACTATC ACTGCTGCAG TCGTGCAAGG GGCCCAATTT AGCTTGTGCG CGTAACTATC ACTGCTGCAG CAAATCCTGT AAAGCGAAGT CGCGCTACAA TGGCTCTTGC CAGTGA CAAATCCTGT AAAGCGAAGT CGCGCTACAA TGGCTCTTGC CAGTGA	2.3
O1_Amz6.22 O1_Ps6.16	-----CTGA CGTGCATGAT GATCGTGCCT GTGCTGTTCC TGACGGCCTG ATGAAACTGA CGTGCATGAT GATCGTGCCT GTGCTGTTCC TGACGGCCTG TCAATTCATT ACAGCTGATG ATTCCAGAGA TAAGCAGGAA TATCCTGCTG TCAATTCATT ACAGCTGATG ATTCCAGAGA TAAGCAGGAG TATCCTGCTG AGAGGTGCGAG AATCAAGAGG CAAAATTCGA AGCGCTCCAT GTCGACCAAG AGAGGTGCGAG AATCAAGAGG CAAAATTCGA AGCGCTCCAT GTCGACCAAG TCGTGCAAGG GGCCCAATTT AGCTTGTGCG CGTAACTATC ACTGCTGCAG TCGTGCAAGG GGCCCAATTT AGCTTGTGCG CGTAACTATC ACTGCTGCAG CAAATCCTGT AAAGCGAAGT CGCGCTACAA TGGCTCTTGC CAGTGA CAAATCCTGT AAAGCGAAGT CGCGCTACAA TGGCTCTTGC CAGTGA	0.11
I2_Amz11.7 I2_Ps6.28	ATGATGTTTC GATTGACGAC AGTCAGCTGT TTCCTGCTGG TCATTGTTCT ATGATGTTTC GATTGACGAC AGTCAGCTGT TTCCTGCTGG TCATTGTTCT TCTGAACCTG GTTGTGCTTA CCGATGCCTG TTTACTACGAT GTAGGAGACC TCTGAACCTG GTTGTGCTTA CTGATGCCTG TAAGACTGAC G---AATTTT CATGCTCAAG TAATAAAGAA TGCTGTATCT CAGAATGCTG CGACGGGATA CATGCTCAAG TGATGACGAG TGTGTGTTG CGCAATGCTA TGACTGGAAA TGCTTACCAT GGTGTACCTG GCCAGTATAC AAGAGGGGGC GACGCCACGT TGTAACCCAC ATTATCCCTG GCCACCTAC AAGAGGGGGC GACGCCAAGT TTTATTCAAA GTATTTGGCC AACGTTGA GCCATTCAAA GTATTTGGCC AACGTTGA	0.767
T_Amz5.4ii T_Ps5.18	ATGCTCTGTC TTCCGGTCTT TATCATCCTT CTGCTGTTGG TTTACCCCGC ATGCTCTGTC TTCCGGTCTT TATCATCCTT CTGCTGTTGG TTTACCCCGC AGCTACTCTG CCTGTGGAAT CAGAGCTGCA AAGAGATTTG ACTCAGGTAT AGCTACTCTG CCTGTGGAAT CAGACCTGCA AAGAGATTTG ACTCAGGTAT CTGCTGAAGA TTTTGGGATG AGAACTGAAT ACGAAC---- --GTCGTAAG CGTCAAAGA TTTTGGGATG AGAACTGAAT TCAAACCTGAA ACCTGTTTGG CAATGGGGCG ACTGCTGTAA TAATGGCGAT TGCTGTAACCT GA----- CAAAGGCCCA CCTGCTGTGG AAGAGGCATT TGCTGCAAAAT GGCCCAATC ----- CTCCACAGTA TGA	3.59
M_Amz3.7 M_Ps3.2	ATGATGTCTA AACTGGGAGT CTTGTTGACC ATCTGTCTGC TTCTGTTTCC ATGATGTCTA AACTGGGAGT CTTGTTGCCC ATCTGTCTGC TTCTGTTTCC CCTTACTGTT CTTCGGCTGG ATGGAGTCCA AGGCAGACAC CATCTCACAG CCTTACTGCT CTTCAGCTGG ATGGAGTCCA AGGCAGACAC CATCTCACAG TTCAGCCTCT CCGTAGACTG ACGGCTCGGA GCTCCCAACC ACAGCATCGC TTCACCCTCT CCGTAGACTG ACGGCTCGGA GCTCCCAACC ACAGCATCGC GCCTGGGATG AAGAGAAAAA GTGTTGTACG GGTCAATGCC ATATCTGCTG	1.51

	CCGTGGGATG AAGAGAAAA GTGTTGTACG GGTCAATGCC ATCTCTGCTG GCCTTGTGTG GGATGA GCCTTGTGTG GGATGA	
SF-mil_Amz SF-mil_Ps9	ATGTCGAAAA CAGGACTTGT GCTGGTTGTC CTTTACCTTC TTTCTTCTAC ATGTCGAAAA CAGGACTTGT GCTGGTTGTC CTTTACCTTC TTTCTTCTCC CGTAAACCTT CAGCAGACTG AAGATGACAA GGCTTTCATG AAGATCATGA TGTA AACCTT CAGCAGAAATG AAGATGACAA GGCTTTCATG AAGATCATGA TCCCTACACT GACGCGTGT CTGGAAGAT CCGGAAGCTG CAGTCCCCAA TCCCTACACT GACGCGTGT CTGGAAGAT CCGGAAGCTG CAGTCCCCAA AGTGGAGGAG GCTGCACGGG GACTTGCCCG GGGACTGCG AGGGATCCAT AGTGGAGGAG GCTGCACGGG GACTTGCCCG GGGATTGCG AGGGAAGCCG CAAAGGATGT GCATGTAAAA CTACCGGATA A CTACGGATGT GCATGTAAAA CTACCGGATA A	2.89
O1_Amz6.17 O1_Ps6.21	ATGAAACTGA CGTGCATGTT GATCGTCGCC GTGCTGTTCC TGACGGCCTG ATGAAACTGA CGTGCATGTT GATCGTCGCC GTGCTGTTCC TGACAGCCTG TCAACTCGTT ACAGCTGATG ACTCCAGAGA TAAGCAGGAG TACCATGCAC TCAACTCGTT ACAGCTGATG ACTCCAGAGA TAAGCAGGAG TACCATGCAC TGGGGTCGAT ACTCGGTATG CAGAATTCTA AAGATTCCAG GCCATGCTCG TGGGGTCGAT ACTCGGTATG CAGAATTCCA ATGATTCCAG GCCATGCACG GAACCTGGTA AATACTGTCA ATTTCCCTGT TGCCCTGGTC TGAAGTGTG GGACTTGGTA AATACTGTCA ATTTCCCTGT TGCCCTGGTC TGAAGTGTG CCGCATCCAT GATGAAAGCT GGTGCTTGAG GAAATAG CCGCATCAAT GATGAAAGCT GGTGCTTGAG GAAATAG	1.32
B2_Amz1ii B2_Ps1ii	----- ATGTTGCGAC TGATAATCGC GCCTGCTGCTC GTCTCCGCTT GCCTCGCTTT ----- CCCTGAAAC AGGGAGGACG CCGCCCAAGA CATGGCCAAC ATGCAGCCCT -----A TGCCCAAC-- -ATGCAGGGA TTGCACCGGG ATTGCAGGGA ATGCAGGAAA TGCCCGCCCC CATGCCAAC ATGCAGGGAA TGCCGGGAAT GCCGGGAATG CCCGCTGGTC AGTTCTTGCC ATGCAGGGAA TGCCGGGAAT GCCGGGAATG CCCGCTGGTC AGTTCTTGCC TTTCAACCTT TATCCTGGCT TTGGATTCAA GAGGGTTGCC GATGAGAACC TTTCAACCTT TATCCTGGCT TTGGATTCAA GAGGGTTGCC GATGAGAACC TAGAGAAGAG GAAACATCAG TCTCAATFCA ACGACAACCA ATCTCCCTTT TAGAGAAGAG GAAACATCAG TCTCAATFCA ACGACAACCA GTCTCCCTTT GGCTCGTCA CCGATGGCCT AGGAATGTTT AACTTCGAGA ACTTCATGAA GGCTCGTCA CCGATGGCCT AGGAATGTTT AACTTCGAGA ACTTCATGAA AGAAAACGCC GACAAACTTC CGTTCGCGAA CATGGAGGGT GCCGACACTG AGAAAACCCC GACAAACTTC CGTTCGCGAA CATGGAGGGT GCCGACACTG CCGACCTTGG CAACTTCGCG CCCAGCGGAA ACGACCAACA GGAGGACCAG CCGACCTTGG CAACTTCGCG CCCAGCGGAA ACGACCAACT GGAGGACCAG TTCCGCTTCT TCGACGAGCA ACAATAA TTTCGCTTCT TCGACGAGCA ACAATAA	0.794
T_Amz5.12 T_Ps5.1	-----CTT CTGCTGCTGA TTCCATCTGC ATGCGCTGTC TCCAGTCTT CATCATCCTT CTGCTGCTGA TTCCATCGGC ACCTAGCATT CTGGCCCGAC CGAAGACCGA AGTTGATGTG CCCCTGGATT ACATAGCATT CTGGCCCGAC CGAAGACCGA AGTTGATGTG CCCCTGGATT CTTTGGATGA TAATGCAAAG CGAACCTTAC AAACACTTTG GAACGCACGC CTTTGGATGA TAATGCAAAG CGAACCTTAC AAACACTTTG GAACGCACGC AATGAATGCT GTGATGATCG CCCTTGGTGC TGTGTTGGGT GA GATGAATGCT GTGATAAACG CCCTTGGTGC TGTGTTGGGT GA	1.52
O2_Amz1.9 O2_Ps1.16	ATGGAGAAC TGACAATACT GGTTCCTGCT GCTGCTATAC TGTTGTCGAC ATGGAGAAC TGACAATACT GGTTCCTGTT GCTGCTATAC TGTTGTCGAC CCAGGTCATG GTTCAAGGTG ACAGAGATCA ACCTGCAGAT CGTAATGCAC CCAGGTCATG GTTCAAGGTG ACAGAGATCA ACCTGCAGAT CGTAATGCAC TGCCAAGAGA CGATTACTCA CGTCGAGCGA ACCGAAAGTT CATGCGTGT TGCCAAGAGA CGATTACTCA CGTCGAGCGA ACAGAAAGTT CATGCGTGT CTATACGATA ACTGTTGCGG CAGCAGCAA TGTCGTTGCC CAGGCATTGC CTATACGATA ACTGTTGCGG CAGCAGCAA TGTCGTTGCC CAGGCATTGC AGCAGTGATG TCCTATCATC CGGCAGTGGT ACAACTTCTG ACACTCGCTT AGCAGTGATG TCCTATCATC CGGCAGTGGT ACAACTTCTG ACACTCGCTT AG AG	0.374
Conopressin_Amz1ii Conopressin_Ps1	ATGACGCGTT CAGCCATGCT GATGGGACGA CTGACGTTGG TGGTGTGTGT ATGACGCGTT CAGCCATGCT GATGGGACGA CTGACGTTGG TGGTGTGTTT GCTGCTCACT ACCCAGGCTT GCTTTATCAG AAACCTGCCA AAAGGTGGTA GCTGCTCACT ACCCAGGCTT GCTTTATCAG AAACCTGCCA AAAGGTGGTA AGAGAGATGT GGACGATAGA CATCCTCCA AGCTGTGCAT GTCCGTGAGC AGAGAGATGT GGACGATAGA CATCCTCCA AGCTGTGCAT GTCCGTGAGC TTTGGCCAGT GTGTGGGGCC CCATATCTGC TGTGGAGATA CAGGATGCCA TTTGGCCAGT GTGTGGGGCC CCATATCTGC TGTGGAGATA CAGGATGCCA AATGGGAACG CCAGAAGCGA ACACGTGCGC CAGAGAGGAC GAGGATCCTA AATGGGAACG CCAGAAGCGA ACACGTGCGC CAGAGAGGAC GAGGATCCTA	0.557

	CACCTTGCCT TGTCATTGGT AGTCCCTGCA CTCTGAACAA CCCAGGCAAC CACCTTGCCT TGTCATTGGT AGCCCCTGCA CTCTGAACAA CCCAGGCAAC ACCCACGGCA ACTGTGTGAG TTTCGGCATC TGCTGTGTGG ATGACACTTG ACCCACGGCA ACTGTGTGAG TTTCGGCATC TGCTGTGTGG ATGACACTTG TTTCTTCGAC TTGGGATGCC TGTAG TGCTTTCGAC TTGGGATGCC TGTAG	
O1_Amz6.24 O1_Ps6.23	ATGAAGTTGA CGTGCCTGTT GATCGTTGCC GTGCTGTTCC TAACGGCCTG ATGAAGTTGA CGTGCCTGTT GATCGTTGCC GTGCTGTTCC TGACGGCCTG TCAACTCATT ACAGCTGATG ACTCCAGCGA TTTACAGGAG TTTCTTCGTC TCAACTCATT ACAGCTGATG ACTCCAGCGA TTTACAGGAG TTTCTTCGTC GGAAGATGAT CGACAGATTG CTGGACACGA AAGCAGCGCA GGAGCGCTGC GGAAGATGAT CGACAGATTG CTGAACACGA AAGCAGCGCA GGAGCGCTGC CTTGGTGGAT CAAGTCCGTG TACCGCATTC TCGGGCAACT GCTGCAATTA CTTGGTGGAT CAAGTCCGTG TACCGCATTC TCGGGCAACT GCTGCAATTA TTGCGCTTTT TTTTGGTGCA CATAA TTGCGCTTTT TTTTGGTGCA CATAA	0.532
I3_Amz11.3 I3_Ps11.2	ATGAAGCTGT CTTTGGCGAT CGTTCTGATT CTGATTCTTC TAACCTTAAG ATGAAGCTGT CTTTGGCGAT CGTTCTGATT CTGATTCTTC TAACCTTAAG CACCGGAGCG GAGACGTCTG ACAACCGAGC AAGCAGGACT ATCAC----- CACCGGAGCT GAAACGTCTG ACAACAGTGC AAGCAGGACT GTCACTGCAG ----- ---GCTGCTA TCAACATGCA AAGGCAAGGA TGAGACGTGC TAAAAGACAC TCCGCTGCTA TCAACATGCA AAAGCAAGGA TGAGACGTGC AGCTATGACG ACGATTGTTG TGGATCACTC TGTTGTTTCC GGGTCTATGG AGCGATGACG ACGATTGTTG TGGATCACTC TGTTGTTTCC GGGTCTATGG ATGCCAACTG GCATACGTGC CGTGCCCTGCC GTAA ATGCCAACTG GCATACGTGC CGTGCCCTGCC GTAA	0.465
T_Amz5.23 T_Ps5.20	ATGAATTGTC TTCCAGTCTT CTTCATCGTT CTTACTGCTGA TTGCTCATT ATGAAGTGTG TTCCAGTCTT CTTCATCGTT CTTACTGCTGA TTGCTCATT ATCTCAAGTT GTTGAGCATT CGAAGTTGAA GCGGACCAA ATGTTGCGCC ATCTCAAGTT GTTGAGCATT CGAAGTTGAA GCGGACCAA ATGTTGCGCC GGTCAACTAC GAGAGAGAAG ATTGAGGTTG CTCTAGAGGT GTGCTGCCTG GGTCAACTAC GATAGAGAAG ATTGAGGTTG CTCTAGAGGT GTGCTGCCTG GCTAGCTCAA CTTTTTGCTG TGCTGCCAAG TCGTAG GCTAGCTCAA CTTTTTGCTG TGCTGCCAAG TCGTAG	0.861
T_Amz5.10ii T_Ps5.4	ATGCGCTGTC TCCAGTCTT CGTCATTCTT CTGCTGCTGA TTCCATCTGC ATGCGCTGTC TCCAGTCTT CGTCATTCTT CTGCTGCTGA TTCCATCTGC TCCTAACGTT CATGCCCGAC CGAAGACCAA AGATGATGTG CCCCTGGCAT ACCTAACGTT CATGCCCGAC CGAAGACCAA AGATGATGTG CCCCTGGCAT CTTTCCACGA TAATGCAGAG CGAACCCTAC TAAGACAATG GAACAAACGC CTATCCATGA TAATGCAGAG CGAACCCTAC TAAGACAATG GAACAAACGC ACGTGCTGCC AATTTTTATCC GTCTTGCTGT CCTACCAGAA AATGA ACGTGCTGCC AGTTTTATCC GTCTTGCTGT CCTACCAGAA AATGA	0.287
M_Amz3.2 M_Ps3.9	ATGTGCAAAA TGGGAGTGGT GCTATTACCC TTTCTGGTCC TGTTTTCCCCT ATGTGCAAAA TGGGAGTGGT GCTATTACCC TTTCTGGTCC TGTTTTCCCCT GGCAACGCTC CAGCTGAATG CAGATCGACC TGTGGAACGA TATGCGAAGA GGCAACGCTC CATCTTGATG CAGATCGACC TGTAGAACGA TATGCGGAGA ACAAAACAGGA CCTCAACCCA TATAAAAGGA CAA---TCAT ATTATCTGCT ACGAACAGGA CCTCAACCCA GATGAAAGGA GAAAAATCAT AATACCTGCT CTGAGTGGGA GGGGTTGCTG TCGTACGGGG AGTTGCCATA TTGGGCGATC CTGAGTGGGA GGGGTTGCTG TCGTACGGGG ACTTGCCATA TTGGGCGATC GTCCTACGCG GTACGCCAAA AGTGTCAATG CTGCGGTTAG GTATTACGTG GAAAGTGATT GGTGTCATTG CTGCGGTTAG	2.79
M_Amz2 M_Ps2iii	ATGTCTAAAC TGGGAGTCTG GCTGTTTCATC TTTCTGGTTC TGTTTTCCCAT ATGTCTAAAC TGGGAGTCTG GCTGTTTCATC TTTCTGGTTC TGTTTTCCCAT GACAACTGTT CAGCTGGATG GAGATCAGCC CGCTAATCGT CATGCAGACG GACAACTGTT CAGCTGGATG GAGATCAGCC CGCTAATCGT CATGCAGACG AAAGGGGCCA GGGCCTAACA GACCAGTATC GAAACTTGAG GCATGTTCTG AAAGGGGCCA GGGCCTAACA GACCAGTATC GAAACTTGAG GCATGTTCTG AAAAGGGGTT TGAGATGCGC TGGTGCTTCA TATGATCCCA ATTCCTGGTG AAAAGGGGTT TGAGATGCGC TGGTGCTTCA TACGATCCCA ATTCCTGGTG GACGCTTGTT TGA GACGCTTGTT TGA	0.001