

AVR1b 1 MRLSEVLSVVAIGYVTCNATREYSDETNLAMESDLDVRRSLRNGDIAGGRFLRAHEDDDAGERTFSVTDLWVKVAAKK
PsAvh_5 1 MRLQFLVAVAT--LATSATRVPPDANLQSNAP--VQTVTRSR----RFLRTADTDIVYEPKVNHPGKKQVFIEDK

AVR1b 81 LAKAMADPSKEQKAEKNAKKGYSIDKKNWLAIAAPK--QKGYDRITYNGYTFHLYQS-----
PsAvh_5 72 LOKA--LTDPKKNKLYARWYNSGFTVQKQEGGLDQNNRELELTYKNLALGYAKYQARRSQEAK

PsAvh_5 1 MRLQFFLVMA--VA---LATSATRVPPDANLQSNAP--VQTVTRSRFLR-TADTDIVYEPKVNHPCKKQVFIEDKL
PsAvh_24 1 MRLPSILVAASALALLASDASAAVAGASEGTKVSTMAFPDLDVAVSHSAKRSLHDIQVDEDEDERWAGAKLSAAKL

PsAvh_5 73 QKALTDPPKKNKLYARWYNSGFTVQKQEGGLDQ--N-ENRELELTYKNLALGYAKY-----QARRSQEAK----
PsAvh_24 81 EKAVNDSKYAETLMRWKRHGFDIEDTKLSLEASKLSKDPRLNTVYRNYAAWLDKHFHSRVGLKPTTCSTRRSKTRWETA

PsAvh_24 1 MRLPSILLAASALALLASDASALAAVAGASEGTKVSTMAFPDLDVAVSHSAKRSLHDIQVDEDEDERWAGAKLFS
PsAvh_29 1 MRLPSILVAASALAVLASDASALAAVAGASEDAKVMSTMAFPDLDVAVSHSATRFLRGLHESVGEVDEDERLAGDKLFH

PsAvh_24 77 AAKLEKAMNDSKYAETLMRWKRHGFDIEDTKLSLEASKLSKDPRLNTVYRNYAAWLDKHFHSRV-GLKPT-----
PsAvh_29 81 AAKLEKAMNDSKYAETLMRWKRHGFDIEDTKLSLEASKLSKDPRLNTVYRNYAAWLDKHFHSRVGLKPTSGGDDLFNKAK

PsAvh_24 146 -TCSTR---RRS---KTR--WE--LATTRRRCSSGSRPTITN-----RLVYRS---
PsAvh_29 161 LEVAIKDGNVYKRTLFKWKNTNHYESEAVFKQLNALGRKDFDNTLDRLYVDYVIWLVNHVPHPDTLKLANEPLLFKESMLL

PsAvh_29 1 MRLPSILVAASALAVLASDASALAAVAGASEDAKVMSTMAFPDLDVAVSHSATRFLRGLHESVGEVDEDERLAGDKLFH
PsAvh_32 1 MRLFMNMLVAVLAVLASGTAVSADQASVNLVVDVHSS--R---VLSGEDKRFRLRSHQITCDEGK-----

PsAvh_29 81 AAKLEKAMNDSKYAETLMRWKRHGFDIEDTKLSLEASKLSKDPRLNTVYRNYAAWLDKHFHSRVGLKPTSGGDDLFNKAK
PsAvh_32 62 -----ITKHDEE-----RVS-----GENLFGALK

PsAvh_29 161 LEVAIKDGNVYKRTLFKWKNTNHYESEAVFKQLNALGRKDFDNTLDRLYVDYVIWLVNHVPHPDTLKLANEPLLFKESMLL
PsAvh_32 82 VLKMGDWNVYRDKVFORWKNYGHGHTKKSYLEKG-----

PsAvh_29 241 KARTDVDYAQSLFWANKNFSLEKVTENLKLTFANADNKVLRGYTNWLIINNFH
PsAvh_32 114 -----VPDSLVGAYKSYLKLKNTG-----KVFGDHRPHHIEPR

PsAvh_32 1 MRLFMNMLVAVLAVLASGTAVSADQASVNLVVDVHSSRVLSFEDKRFRLRSHQITCDEGKIKTHDDEERVSGENLFGALK
PsAvh_275 1 MRLTNTLVVAVAAILLASENFAATDA----DQATVSKLAAEFDTLVDLVTESKRSRATVDD----GEERKQF

PsAvh_32 81 KVLKMGDWNVYRDKVFORWKNYGHGHTKKSYLEKGVDPDSLVGAYKSYLKLKNTGKVFGDHPRHIEPR
PsAvh_275 71 KLEALKKGG--WTDLFNKWKGNELSPAEOVKLNKKNKLSDDLK-----DALFRNYKDW-----

PsAvh_275 1 MRLTNTLVVAVAAILLASENFAATDAQATVSKLAAEFDTLVDLVTES-----KRSRATVDD--DGEER
PsAvh_189 1 MRLLLVLLVTLVTFISSASATATVTDKIDTVSQTLDSEIDELSRLLTAETDDDNKPFRLGDAKDLTTAGDKTDEE

PsAvh_275 66 RYKQFKLEALKKG--KWD-----IFNKWKGNELSPAEOVKLNK-----KKSDDLKDAFRNYKDW-----
PsAvh_189 81 RGLFSLISSIKNGAKWKSNALEKAFQHMKGHGETPTLAKFLRIGGATEPRYERLYEKLVQDPEPHRYLSSGCDY

PsAvh_189 1 MRLLLVLLVTLVTFISSASATATVTDKIDTVSQTLDSEIDELSRLLTAETDDDNKPFRLGDAKDLTTAG--DKTDE
PsAvh_186 1 MRLLLVLLVTLVTFISSADVASKATPATINS-----DLPVRELTAEATN-TNGKRHLRGDEMSAMDFEDDDYDD

PsAvh_189 79 EERGLFSLISSIKN---GWA--KWKNSA-----LEKAFQHMKGHGETP--T---TLAKRLEIGGATEPRY
PsAvh_186 72 EERGISDVMNRMKASLTGVSATRMKVTLGKMHSTANKMKQKFMERLFRWVYKRGETPLSVRTKTMQKQNYWSARTBRGT

PsAvh_186 1 MR-LLLVLLVTLVTFISSADVASKATPATINSDLPVRELTAEATN-TNGKRHLRGDEMSAMDFEDDDYDDEERGISDV
IPI01 1 MRSLLLTVLLNLVLLAATGAVSSNLNTAVNYASTKLRFLSTBYNADEKRSRGRG--DYNNEVTKPEPNTSDEERAFSSKSKS

PsAvh_186 80 VNRMKASLTGVSATRMKVTLGKMHSTANKMKQKFMERLFRWVYKRGETPLSVRTKTMQKQNYWSARTEGRTREWQCLG
IPI01 80 AEYVKMVLG-----FKLGFSPRTQSKTVLRY-EDKLFALYKSGETPRSLRTELD-----K-----

PsAvh_186 160 STSNADSTAACAEEAKMKHKEVSR-
IPI01 132 -----ASASVFNFRFKWYDKNVGFS