```
Lmig              AAALVAAAAL---------ALLAAAAAQDGDKGISKLKKTSSLFPHPRIGRSDYMNLGAGEVG---------EKRAAGL  61
Turt              ---MVYFISTVSLLLLVTGFSQQASTYNRASDDEVNSYEGDQQLGYTSLGTHGGIQLLAVPRNYLNPFIAKDLFKR----  73
Znev              MKQILFSCAMIHVLLLVSSCDEESDSVSTNTDAER---GSSGLIPMPRVGRSDLAWTLQRQGDTVPSSLILKDKRGSSGL  77
Tcas              MKTFLIYSAC-----VVLFCIANCQGEPKEPKRNK-LASVYALTPSLRVGRRSEG----------------TDVKRRIGKM  59
Dmel              MKSMLVHIVL------VIFIIAEFSTAETDHDKNR-RGANMGLYAFPRVGRSDPSLANSLRDGLEAGVLDADFQKKASGL  73
Apis              IAAALLLTLTFFFTHALRHDSEYSDEYKRDNSRDRRESAVAGLIPFPRVGRSGINSALQMDNLYETQRELRSHKRE--GL  78
Phum              ARNPNVFICLMKMNPSVAFCLCVVAVYSADEKNNKTKRDVSGLFPFPRVGRMDSSWNSRYLGP-------REMKRQ--GL  71
Aaeg              FKTLAYVSLVFVVLSAVKFCRADASDLDSVSEGRHKRGPTVGLFAFPRVGRSDPDLLEWSDAAAVAAALPREAKRQ--GL  78
Pcau12217_123-189 ----------------------------DKRKKKKEKEKRKSLLRGLGSMFRVGRHKKDEEEAGNHAPNDVLADEAERQRQENL  56
Pcau12216_152-218 ----------------------------DKRKKKKEKEKRKSLLRGLGSMFRVGRHKKDEEEAGNHAPNDVLADEAERQRQENL  56
                            10        20        30        40        50        60        70        80

Consensus
MKXXLXFIALFXVLLXVXFCXAEADXYKKDXXKEKRKSXVSGLFPFPRVGRSDXDXLXAGXXAXXXVLLDRDEKRRXXGL

Lmig              FQFPRVGRA-------------LVHGPLPFLGVFSPLQLAPHQPADS---AADLGNVSEQQQQQ-----  109
Turt              VALPRIGRSDGGWLDDDDYYNRIIKSS------FTPRVGRSVDAVN-------GDKSMKSSKP-----  123
Znev              IPMPRVGRSDVWPLTDAGLEKNINGDAGKTGMWFGPRLGKRRE-GNIDIPADVRDYTPYLTREDEELP  144
Tcas              VSFPRIGRSESWVPDDNSYGAQRPGANSG-GMWFGPRLGRVQKRSENFTAPIIVHYSPRLGREDSNLD  126
Dmel              VAFPRVGRGDAHLLALQQVLDKRTGPSASSGLWFGPRLGKRSVDAKSFA---------DISKGQKELN  132
Apis              IPFPRIGRR-----------------SESKTALWFGPRLGRSVVIPESYDTSYLDSDTPTIIKTDEDDS  130
Phum              IPFPRVGRN----NDVISQQKRDAMENGG-AMWFGPRLGRFNESKRLRI----------EIGKT-----  120
Aaeg              VPFPRVGRSGMWPKTMMPQQQKRAGNSGASGMWFGPRLGKRANAASTEITPRLNSERPQIGESRSKLE  146
Pcau12217_123-189 RCVPHPGRSDI-------------------------------------------------------  67
Pcau12216_152-218 RCVPHPGRSDI-------------------------------------------------------  67
                            90       100       110       120       130       140

Consensus
VPFPRVGRSDIWPLDDXSXQKXRAGXSGXXGMWFGPRLGRRXXAAXSFIXXDLGXYSPQIGKXDXELX
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