```
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
Tcas2233_1-136 MKTFLIYSAC-----VVLFCIANCQGEPKEPKRNK-LASVYALTPSLRVGRRSEG----------TDVKRRIGKM  59
                        10        20        30        40        50        60        70        80

Consensus   MKTXLXXXALFXVLLXVLFCIAXASXYXXDXKRNXKLXXVSGLFPFPRVGRSDXXXLLXXDGGYXAXXLXRDVKRRXXGL

Lmig        FQFPRVGRA----------LVHGPLPFLGVFSPLQLAPHQPADS---AADLGNVSEQQQQQ-----  109
Turt        VALPRIGRSDGSGWLDDDDYYNRIIKSS------FTPRVGRSVDAVN-------GDKSMKSSKP-----  124
Znev        IPMPRVGRSDV-WPLTDAGLEKNINGDAGKTGMWFGPRLGKRRE-GNIDIPADVRDYTPYLTREDEELP  144
Tcas        VSFPRIGRSESNWVPDDNSYGAQRPGANSG-GMWFGPRLGRVQKRSENFTAPIIVHYSPRLGREDSNLD  127
Dmel        VAFPRVGRGDAEHLLALQQVLDKRTGPSASSGLWFGPRLGKRSVDAKSFA----------DISKGQKELN  133
Apis        IPFPRIGRR----------SESKTALWFGPRLGRSVVIPESYDTSYLDSDTPTIIKTDEDDS  130
Phum        IPFPRVGRN-----NDVISQQKRDAMENGG-AMWFGPRLGRFNESKRLRI----------EIGKT-----  120
Aaeg        VPFPRVGRSGMNWPKTMMPQQQKRAGNSGASGMWFGPRLGKRANAASTEITPRLNSERPQIGESRSKLE  147
Tcas2233_1-136 VSFPRIGRSESNWVPDDNSYGAQRPGANSG-GMWFGPRLGRVQKRSENFTAPIIVHYSPRLGRE-----  122
                        90       100       110       120       130       140

Consensus   VPFPRVGRSDSNWXLDDNSYXXXRXGXXXGXGMWFGPRLGRRQXAXEXFIAPXLXXYSPXIGKEDXELX
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