```
Lmig        AAALVAAAAL---------ALLAAAAAQDGDKGISKLKKTSSLFPHPRIGRSDYMNLGAGEVG---------EKRGLFQ  61
Turt        ---MVYFISTVSLLLLVTGFSQQASTYNRASDDEVNSYEGDQQLGYTSLGTHGGIQLLAVPRNYLNPFIAKDLFKR--VA  75
Znev        MKQILFSCAMIHVLLLVSSCDEESDSVSTNTDAER---GSSGLIPMPRVGRSDLAWTLQRQGDTVPSSLILKDKRGGLIP  77
Tcas        MKTFLIYSAC-----VVLFCIANCQGEPKEPKRNK-LASVYALTPSLRVGRRSEG---------------TDVKRRKMVS  59
Dmel        MKSMLVHIVL------VIFIIAEFSTAETDHDKNR-RGANMGLYAFPRVGRSDPSLANSLRDGLEAGVLDADFQKKGLVA  73
Apis        IAAALLLTLTFFFTHALRHDSEYSDEYKRDNSRDRRESAVAGLIPFPRVGRSGINSALQMDNLYETQRELRSHKREGLIP  80
Phum        ARNPNVFICLMKMNPSVAFCLCVVAVYSADEKNNKTKRDVSGLFPFPRVGRMDSSWNSRYLGP-------REMKRQGLIP  73
Aaeg        FKTLAYVSLVFVVLSAVKFCRADASDLDSVSEGRHKRGPTVGLFAFPRVGRSDPDLLEWSDAAAVAAALPREAKRQGLVP  80
Dpul16615_28-98 ----------------------------------------KSQSLIPFPRVGRSRSSFIANAVGS----------  25
                                  10        20        30        40        50        60        70        80

Consensus   MKXXLXFIALFXVLLXVXFCXAEASTYSXDSXXNRKXGXVSGLXPFPRVGRSDXSXLLXXDGGYXAXXLXRDXKRRGLVP
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Lmig        FPRVGRA-----------LVHGPLPFPLGVFSPLQLAPHQPADS---AADLGNVSEQQQQQ-----  108
Turt        LPRIGRSDGGWLDDDDYYNRIIKSS-------FTPRVGRSVDAVN-------GDKSMKSSKP-----  123
Znev        MPRVGRSDVWPLTDAGLEKNINGDAGKSTGMWFGPRLGKRRE-GNIDIPADVRDYTPYLTREDEELP  143
Tcas        FPRIGRSESWVPDDNSYGAQRPGANSG--GMWFGPRLGRVQKRSENFTAPIIVHYSPRLGREDSNLD  124
Dmel        FPRVGRGDAHLLALQQVLDKRTGPSAS-SGLWFGPRLGKRSVDAKSFA---------DISKGQKELN  130
Apis        FPRIGRR-----------------SESKNTALWFGPRLGRSVVIPESYDTSYLDSDTPTIIKTDEDDS  131
Phum        FPRVGRN----NDVISQQKRDAMENGG--AMWFGPRLGRFNESKRLRI----------EIGKT------  120
Aaeg        FPRVGRSGMWPKTMMPQQQKRAGNSGANSGMWFGPRLGKRANAASTEITPRLNSERPQIGESRSKLE  147
Dpul16615_28-98 -ARSGGAGN------PMMMGSGGNANGSPNNW----MMNNADIKRHLI---------PRVGKR-----  68
                                  90        100       110       120       130       140

Consensus   FPRVGRSDXWPLDDXXXQKXRAGXSGGXXGMWFGPRLGRRXXAXXSFIXXDLGXYSPXIGKXDXELX
```