```
Apis            ---------MKYFVTIFMV----------FHISLILLQKTSTASPLDNYLDK----DSIEENGVELLTDIEEYMDKDADDNG  59
Vdes            -MVAQLLAGKSGIEESALREFDEEAYDVCRRYIALHDTERRTGVHLPLQGGNFRESVGGGSLNTARDGIVGDEEDGEATS  79
Rpro            MNSISELVSQVAFLTDKT----------SVLFIVTLSVALVLITASPPLAM----HLDY--------EPIVEQEEIGVESP  59
Aaeg            ---------MNKYLMGRLL----------ICLLVMFV--ASAQSASSYFYDS----EEPYGGNMLDGADSTEEADKSFADDS  57
Tcas            ---------MKY--TWLVL----------AACMVLVLAELLPGAAAGPYLDD----------------DEGLPSDDDYTENA  45
Dpul            ---------MT--------------------------NEQQSAGLNYFTD----NA----------------------------  17
Amel            ---------MKFGLFW--L----------FCLLTVAI--FTDRTFGSPYIDD----EE----------DSLQIADSDYTDNA  45
Nvit            ---------MKIGLIG--L----------VC-IGVFV--LAESVSAGPYFDD----EE----------EALA-SDADYSDNA  43
Dmel6171_5-84:. ------LALSLAVLVVLI----------LHSSQVSSTSTTTSTSASATTTT----------------AATTTTDSSTTTTT  49
                        10        20        30        40        50        60        70        80

Consensus
MXXXXXLAMKYGLXXXLLREFDEEAYDXCLXVVXLXXTXTXXAASPYLDDGNFREEXYGGXXXXXXDXXXEXDXDYTDNA
```

```
Apis            F--ALDFPDVQKRKLSSHRIFR----------------------RYCVPRGENCDHRPKYCCNSSSCRCNLWGVNCKCQR  115
Vdes            TGIALSREIRRPPSRARVYAYRGQGEEGDYGVSTEYTKVVSSKKRSCIRRGGSCDARPGDCCYHSSCRCNLWGTNCRCMR  159
Rpro            S-DRIMYGGQ--------YQVK----------------------RACVARGGNCDHRASDCCYSTACRCNLWGANCRCQR  108
Aaeg            LMDNIFRQGADKRAGSLIHVYR----------------------RSCIRRGGTCEHRTNDCCYNSSCRCNLWGSNCRCQR  115
Tcas            I-DRLLQSAQKRS--SLIYLFR----------------------RACVRRGGNCDHRPNDCCYNSSCRCNLWGSNCRCQR  100
Dpul            --EPLMENAQK----------------------------------RSCIRRGGSCDHRRNDCCFSSSCRCNLWGSNCRCHR  62
Amel            L-ENLMRAAQQKRT-SLIYLFR----------------------RACIPRSGNCDHRPKDCCYSSSCRCNLWGSNCRCQR  101
Nvit            L-ENLMHAVQQKRA-SWISMYR----------------------RACVRRNGNCDHRPNDCCFSSSCRCNLWGSNCRCQR  99
Dmel6171_5-84:. ESSTTTTASTKKKHRRRRVIIR----------------------RVIIRRGRE----------------------------  80
                        90       100       110       120       130       140       150       160

Consensus
LXXNLMRAAQXKRARSLIYXXRGQGEEGDYGVSTEYTKVVSSKKRACIRRGGNCDHRPNDCCYSSSCRCNLWGSNCRCQR
```

```
Apis            MGFFQRW--GK--  124
Vdes            MGLLQRWINGRRR  172
Rpro            KGLFTKL--G---  116
Aaeg            MGLFQKW--G---  123
Tcas            MGLFQKW--G---  108
Dpul            AGLFQKW--G---  70
Amel            MGLFQKW--G---  109
Nvit            VGLFQKW--G---  107
Dmel6171_5-84:. -------------  80
                       170

Consensus
MGLFQKWINGXRR
```