```
Dmel            ------------MGSSQLLVLICCIPWLCD--------------SNSMGKD-AWLRPGCHKVGNTRKITIPDCVEFTITTN  54
Turt            ------------MATQVQSQLIFLILWIGL-------------MVAIKGADAYAWTRPGCHRLGHTRRVTINGCVEFEMTTN  57
Dpul            ------------MVSTLYFWLVLAVLLTASNGEPRNQPKGSISVSTRSSTS-RGELSGCHQVGHTRRVTIPDCVSFMITTN  68
Aaeg            ----------------MEWLRFATLVLLA---------------TMACARE-TWQKPGCHKVGHTRKISIPDCVEFSITTN  49
Tcas            ----------------MLACWLLFTLLSLSD-----------AFMVKAVTARD-AWQKPGCHKVGHTRKISIPECVEFHMTTN  55
Apis            MSNFGDMDKFRWWKSAAMILIFILAVLPS---------------PLATGSN-TWQKPGCHKVGHTRKISIPNCVEFPITTN  65
Phum            ------------MGKKLNYFPIFFIFFILT-------------MLESSYCQG-IWRRPGCHKVGHTRKVSIPDCVEFHITTN  56
Rpro            ----------------MSMVKILCMFLILT-------------CLDNVFCKD-AWGKPGCHKVGHTRKVSIPDCVEFHVNTN  52
Znev            -------MFPVSWRLQCCYLLFIFVTILS-------------VVSRTRARD-AWERPGCHKVGHTRKISIPDCVEFHITTN  60
Lmig            ------------------------------------------------------MDGGRD-AWEKPGCHRVGHTRKISIPDCIEFPITTN  35
Tcas15086_2-122:. ----------------LACWLLFTLLSLSD-----------AFMVKAVTARD-AWQKPGCHKVGHTRKISIPECVEFHMTTN  54
                                  10        20        30        40        50        60        70        80

Consensus
MSNFGDMXXXXMXXSLACWLIFXXLXLLXNGEPRNQPKGAFMVSXVTARDYAWQKPGCHKVGHTRKISIPDCVEFHITTN

Dmel            ACRGFCESFSVPSIPMMGSSLSV-LFKPPKPVVSVGQCCNMMKSEEIQRRVLCIEGIRNVTFNSALSCSCYHCKKD-  129
Turt            ACRGYCTSFAIPSTED-----SL-LFNRHQVITSIGECCNIMETEDVVARVMCRDGPRTIVFKSAKSCGCFHCKKDL  128
Dpul            ACRGFCESWSVPSSWE-----AL-LKNPEKVITSVGQCCNIMASEDVTVRVMCLGGPRDFTFKSAKTCSCFTCKKD-  138
Aaeg            ACRGFCESFAVPSDPF-----AVGQHKPSQPVTSVGQCCNIMETEDVKVRVLCVNGIRNLTFKSATNCSCYHCKKD-  120
Tcas            ACRGFCESWAVPSGP-------KATPTQPVTSVGQCCNIMETEPVEARVLCVDGVRTLTFKSAVSCSCYHCKKD-  122
Apis            ACRGYCESWAVPSPAD-----TV-MINPHQRITSVGQCCNIMETENVEVNVRCLEGVRKLVFKSALSCSCYHCKKE-  135
Phum            ACRGFCESWSIPSGME-----TL-RVNPFQVITSVGQCCNIMETEDVDVKVMCLEGIRELTFKSAKTCSCYHCKKD-  126
Rpro            ACRGYCESWSVPSPLE-----TV-LHNPRQAVTSIGQCCNIMDTEDVEVSVLCLDGTKDLVFKSAKSCSCYHCKKD-  122
Znev            ACRGYCESWAVPSAID-----TL-RVNPHQAITSVGQCCNIMDTEDVEVQVMCLDGTRDLVFKSAKSCSCYHCKKD-  130
Lmig            ACRGFCESWSVPSALN-----TL-RVNPHQAITSIGQCCNIMETEDVEVRVMCLDGPRDLVFKSAKSCQCYHCKKD-  105
Tcas15086_2-122:. ACRGFCESWAVPSGP-------KATPTQPVTSVGQCCNIMETEPVEARVLCVDGVRTLTFKSAVSCSCYHCKKD-  121
                                  90       100       110       120       130       140       150

Consensus
ACRGFCESWAVPSGPXMGSSLTLGLVNPHQPITSVGQCCNIMETEDVEVRVXCLDGXRDLTFKSAKSCSCYHCKKDL
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