```
Bmor        --MFKITAILSLMLIGTTLWAAS------LSCDSCGNECTSACGTRHFRSCCFNYLRRKRGPESVKIWTPSARDNNLDSI  72
Znev        ---MVGSPQITLLMTGMMLWWVC-TWSVALSCDSCGRECQASCGTRNFRTCCFNYLRKRSGGGAAAEEEGDGPRLRLELR  76
Dmel        MTKTTMHWLAHFQIILLCIWLMCPPSSQAIKCDTCGKECASACGTKHFRTCCFNYLRKRSDPDALRQSSN---RRLIDFI  77
Lmig        ----------TQCWFPGALVVALC-----SATCDFCGRECSKACGTNYFRTCCLNYLRKRSGP------P----GLHLELM  56
Aaeg        KMMNRSAACVSIILIYCVLWVAC-SFPMALSCDSCGRECASACGTRHFRTCCFNYLRKRSSAPPISTAPPPPAPISMEQW  79
Tcas        ----MNKNLLVVLIVIGVVWGEA------QSCTSCGSECQSACGTRHFRTCCFNYIKKRSSD-SLAVDP----SLRLELW  65
Phum        ----------MIVVVILWATALSLPYSGSCDSCGKECQSACGTRGFRACCLNYLKKRSST-PLSMGS----EMRLELM  63
Tmol8657_5-99 -------LVVVLIVIAGVVWGEV------QSCTSCGSECQSACGTRHFRTCCFNYLKKRNSD-SLAMDP----SLRLELW  62
                          10        20        30        40        50        60        70        80

Consensus
XXMXXXXALXXLXIIGGVLWAXCXSXXXALSCDSCGRECQSACGTRHFRTCCFNYLRKRSSPXSLAMDPPXXXXLRLELW

Bmor        TRPRYPFFVVQNLPEQWLANLPSDYKPYDDLDT--RQSYDA  111
Znev        VVP-------DPAARDWDLAEEPDTKPPAEPDTRMRLFYNA  110
Dmel        LLQ----------GRALFTQELREERHNGTLMDLGLNTYYP  108
Lmig        LLP----------------------PDGSAAR---------  66
Aaeg        LSKASHTNRLVGRFRHHRLDDERDSDQQRSVSGRLQLLYEN  120
Tcas        LAK-SRNPYFQRNFLDSFLELPEGVNQDHDMTQ---------  97
Phum        MV-----------------------------IIN--------  68
Tmol8657_5-99 LAKRNPYFQQQRNFLDSSLEMPETVNHDHDIT---------  94
                      90        100       110       120

Consensus
LXXRSPXFXXQRNFRDXFLEXPXDVXPDXDXXTRXRLXYXA
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