```
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
Dmel4230_1-107 MTKTTMHWLAHFQIILLCIWLMCPPSSQAIKCDTCGKECASACGTKHFRTCCFNYLRKRSDPDALRQSSN---RRLIDFI  77
                         10        20        30        40        50        60        70        80

Consensus
MTXTTMHXLXXXXIIGLXLWAXCPXSSQALSCDSCGXECXSACGTRHFRTCCFNYLRKRSXPDALXQSXXXXXRLRLELI

Bmor        TRPRYPFFVVQNLPEQWLANLPSDYKPYDDLDT--RQSYDA  111
Znev        VVP-------DPAARDWDLAEEPDTKPPAEPDTRMRLFYNA  110
Dmel        LLQ----------GRALFTQELREERRHNGTLMDLGLNTYYP  108
Lmig        LLP----------------------PDGSAAR---------  66
Aaeg        LSKASHTNRLVGRFRHHRLDDERDSDQQRSVSGRLQLLYEN  120
Tcas        LAK-SRNPYFQRNFLDSFLELPEGVNQDHDMTQ---------  97
Phum        MV-----------------------------II N-------  68
Dmel4230_1-107 LLQ----------GRALFTQELREERRHNGTLMDLGLNTYY-  107
                    90       100       110       120

Consensus
LLPXSXXXXXQXXXRXXFLQEXRDRXPXGXLXXXGXXTYYA
```