```
Hduj        ----------MNQLSVFLTFALFMVISTVAATAISDAPAKPDDKPSSTAGQTVRIAEHRYAGFKRPDPFA---------- 60
Dpul        EAQQQQQQQHRMKLTMLATVLAAVLVLGVGRATAAPADSSSTATGRRLLHSPNPTSHSKSIDSKNGVPSNSFQLARSPVE 80
Bmor        ------MRIAAVMLLAVSVAVTFCVCCCDGANLRRIQPDDDED-------------------FRPHPL---------- 43
Lmig        ------------------------------------------LADDLLEASKRQLA------------------------ 14
Smar        ----------MNCTVIFLVHYLVLVCTFVSSSNGSPSVARSSKHDSRLANIMAPYLYLKLHDQAARRPVDSESESVKDEV 70
Znev        -----------MVATLILTLGVYLVLQYQHHAAVDAAPSSSDVVAAGGSNLEGPGQRGRSRSFLQTPPRSPQYMRARLVP 69
Tcas        ------MGMKSFFTGVFLISSVYLLFIHQFQNVSAAPGNANNVDSHRL-----------------RARPFARLTPRTQYSR 58
Dmel        MGPRSCTHFATLFMPLWALAFCFLVVLPIPAQTTSLQNAKDDRRLQELESKIG-GEIDQPIANLVGPSFSLFGDRRNQKT 79
Amel        ---MDRAFFRRFPILHHTDMNLTFVLTCVMAIIWLFFAKCETEIVSNL-------------RQRFRNRPLLREYNVENL-- 63
Aaeg        -----MARLTLSILISLTIYFTYQAVASEALSTSGVRSSSNSQSTRSSEAMESLLGRDDGLNKLQSVWFKNVYSRRSAGP 75
Phum        ----------MFSVIEKPSLRTYLIILPENTFGDDLTNKSKLKYFEK-------------RQQIERLPFISLVLERKQ-- 55
Tcas4071_1-112 ------MGMKSFFTGVFLISSVYLLFIHQFQNVSAAPGNANNVDSHR----------------LRARPFARLTPRTQYSR 58
                      10        20        30        40        50        60        70        80

Consensus
XXXXXXMXXXMFFLXVFLXXXXYLVVLXVXANTSXXAPXSXDVXSXRLANXEGPGXRDXSRXXLRXRPFAXLYXRRXXXX

Hduj        ----------DYGHFRFGKRAPQPSFADYGHLRFGKRAPSPSYADYGHLRFGRSASP 107
Dpul        LGSSNPKLQAKLPPAIVQSNDDDETTGFGD----EDFADEGHMRYGKR----DFDDYGHMRFGRR--- 137
Bmor        ----------YRDYGLIRSRVIRGDDTFDDYGHLRFGRSDD- 74
Lmig        ----------SDDYGHMRFGK----RQPPA-APAAPASVPVAPRFDDYGHFRFGKRRPQ 58
Smar        ES----------EFDDFFESFDKTK--RNFDDYGHMRFGKR----EFDDYGHPRYGRSA-- 113
Znev        VEPAADILNDF---------IIDDESMDFNK----RQSDDYGHMRFGKR---EQFDDYGHMRFGRSLD- 121
Tcas        IKAEPFNEFI----------VDDDDLFELSKR---QTSDDYGHLRFGKRGE-EPFDDYGHMRFGRSGSD 113
Dmel        MSFGRRVPLISRPIIPI--ELDLLMDNDDERTKAKRFDDYGHMRFGKRGGDDQFDDYGHMRFGR---- 141
Amel        ----------LEEDDFTNLNKR---QQFDDYGHLRFGKR---EQFEDYGHMRFGRNHHK 106
Aaeg        VGPGHIGTYTVLQRSPAGGVADINFIDDEDIE--KRFDDYGHMRFGKRGGGEQFDDYGHMRFGRR--- 138
Phum        ----------DNMADKRQ----DQFDDYGHMRFGKRG--EDLDDYGHMRFGKRY-- 93
Tcas4071_1-112 IKAEPFNEFI----------VDDDDLFELSKR---QTSDDYGHLRFGKRGE-EPFDDYGHMRFGRSGS- 112
                      90       100       110       120       130       140

Consensus
XXXXPFNXFIXLPXXPXXXVDDDDFFDFGKRXXXXQFDDYGHMRFGKRGGDEQFDDYGHMRFGRSXSX
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