```
Turt                 ----MLASFILLTFILNFHSSQ--ACFITNCPPGGKRSHGDVDHM---------RECLRCGPDNRGHCVSPNICCGTEFG  65
Smar                 ---MKSTHFVNIFIYSVFIFIMADGCYITNCPPGGKRSGNEKSGRGV-------RQCTPCGPGGIGRCYGPDICCGANVG  70
Dpul                 MAGLWTFCLIALSMTEMIIPLTAKPCFITNCPPGGKRSSQLVEPSSYL-------ECAPCGPAGKGTCLGANLCCGSHFG  73
Hduj                 -MSLQKFLFSAVVVLAIVLQGAL-ACFVTNCPPGGKRSAFSYAPATAFNR----RQCLACGPAGKGRCFGTSICCGDSFG  74
Vdes                 ----MKLH---VLVLANIVGLSL-TCFITNCPIGGKRSDTGFGLVQFSSDFRKYSQCPPCGPGSTGQCFGPNICCNS-ES  71
Znev                 ----MKMQLGTATLLAVFISLCT-ACLITNCPKGGKRAGTHSQELHTI------RQCARCGPAKLGHCYGPAICCGPQIG  69
Nvit                 ----MSKV---IIVLTTLVALSY-GCLITNCPRGGKRGDPTFLLENIA------RECPACGREEQGRCFGPHICCSPSMG  66
Tcas                 ----MSTIITSIILLVLSESLVS-GCLITNCPRGGKRSKFAISENAV-------KPCVSCGPGQSGQCFGPSICCGP-FG  67
Dmel9566_102-172:.   ----------------------G-----------------------------------------EKCSAPHEHSWGTCYHNALICGVDDE  27
                                    10        20        30        40        50        60        70        80

Consensus            MXXLMXXHFIAIXVLAXFISLSXXGCFITNCPPGGKRSXXXXSXXXVXXXFRKYRQCXXCGPXGKGRCFGPNICCGPSFG

Turt                 CLI---NNHYSSPCRAENLIP-T-PCKIP-GKLCSSG--EGVCTSNGICCNSDGCFNDSTCENDKLSNMQRIFTSD----  133
Smar                 CFV---GTRESAICRLENLYS-L-PCQNE-GRACGT---DGTCSADGFCCSTDQCKADESCRGKVHHTNNLQRVLDGEID  141
Dpul                 CFF---KTEETNVCLLTNLKSTQ-ICNQH-FWKTDLK--SASCSLNGDKI-DGICVADLLCCSLGNLPQDDL-------  137
Hduj                 CFI---NTEETSVCRKENYIR-T-PCFNS-GVACGIND-KGICAADGVCCTEKGCTAEEKCLTLSASMSGYSS-------  140
Vdes                 CLIDAGDSPHLRSCKREALKL-K-PCTNT-GMRCGSEN-KGHCALNRFCCTSEGCMVDEACNGKDHDVIRESLMII----  143
Znev                 CLV---ATPDTARCLSEAASP-V-PCTAPTGAQCGEGKFAGRCTANGVCCTHESCHIDITCQLTTSDAPELIDVSADQTN  144
Nvit                 CLI---GTPETLRCRKESLYS-R-PCVAG-FAMCQGN--SGRCAANGICCSQESCFIDSACKLVDETGNDRKIGAEFGAF  138
Tcas                 CLV---GTPETLRCQREGFFHEREPCIAG-SAPCRKN--TGRCAFDGICCSQDSCHADKSCASDDKSPIDLYTLINYQAE  141
Dmel9566_102-172:.   VVM---NSEGVLDARLRVLFT-N-PTHRE-MLPCSYYL-EGECRFDEAKCR-------------------------  71
                                    90       100       110       120       130       140       150       160

Consensus            CLIDAGXTPETLRCRLENLXSXXEPCTXXTGAXCGSNXFXGRCAANGICCXXXXCXADEXCXXXDHSPXDLXXVXDXQAX

Turt                 ----------------------  133
Smar                 LNDVMGPQR-------------  150
Dpul                 ----------------------  137
Hduj                 ----------------------  140
Vdes                 ----------------------  143
Znev                 PLYSLYSSYQQENPGLGLSE    164
Nvit                 LLENAGTNEHIL----------  150
Tcas                 LAGDK-----------------  146
Dmel9566_102-172:.   ----------------------  71
                                170       180

Consensus            LLXXXGXXXXXXNPGLGLSE
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