```
Turt          ----MLASFILLTFILNFHSSQ--ACFITNCPPGGKRSHGDVDHM---------RECLRCGPDNRGHCVSPNICCGTEFG  65
Smar          ---MKSTHFVNIFIYSVFIFIMADGCYITNCPPGGKRSGNEKSGRGV-------RQCTPCGPGGIGRCYGPDICCGANVG  70
Dpul          MAGLWTFCLIALSMTEMIIPLTAKPCFITNCPPGGKRSSQLVEPSSYL------EECAPCGPAGKGTCLGANLCCGSHFG  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
Tmol12134_1-128:. ----MSKLVVSIVLLAFIESLVS-GCLITNCPRGGKRSKFGLAETSV-------KPCVSCGPGQSGQCFGPSICCGP-FG  67
                  10        20        30        40        50        60        70        80
Consensus
MXXLMSXXFXXIXXLAXXISLXXXGCXITNCPPGGKRSXFGXXEXSVXXXFRKYRQCXPCGPGGXGXCFGPXICCGPSFG

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
Tmol12134_1-128:. CLL---GTPETLRCQREGFFHEREPCIAG-SAPCRKN--TGRCAFDGICCSQDSCHADKTCTSDEKS----------  128
                  90        100       110       120       130       140       150       160
Consensus
CLIDAGGTPETLRCRRENLXSEREPCXAGTGAXCGXNXFXGRCAANGICCSQDSCHADETCXSDDXSPXDLXXVXDXQAX

Turt          ----------------------  133
Smar          LNDVMGPQR-------------  150
Dpul          ----------------------  137
Hduj          ----------------------  140
Vdes          ----------------------  143
Znev          PLYSLYSSYQQENPGLGLSE    164
Nvit          LLENAGTNEHIL----------  150
Tcas          LAGDK-----------------  146
Tmol12134_1-128:. ----------------------  128
                  170       180
Consensus
LLXXXGXXXXXXNPGLGLSE
```