```
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
Tcas8222_1-136:.  ----MSTIITSIILLVLSESLVS-GCLITNCPRGGKRSKFAISENAV-------KPCVSCGPGQSGQCFGPSICCGP-FG  67
                          10        20        30        40        50        60        70        80

Consensus
MXXLMSTXFXXIIXLAXFISLXXXGCXITNCPPGGKRSXFAXSENAVXXXFRKYRQCXPCGPGGXGXCFGPXICCGPSFG
```

```
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
Tcas8222_1-136:.  CLV---GTPETLRCQREGFFHEREPCIAG-SAPCRKN--TGRCAFDGICCSQDSCHADKSCASDDKSPIDLYTLI-----  136
                          90       100       110       120       130       140       150       160

Consensus
CLXDAGGTPETLRCRRENLXSEREPCXAGTGAXCGXNXFXGRCAANGICCSQDSCHADESCASDDXSPIDLXTXIDXQAX
```

```
Turt            ----------------------  133
Smar            LNDVMGPQR-------------  150
Dpul            ----------------------  137
Hduj            ----------------------  140
Vdes            ----------------------  143
Znev            PLYSLYSSYQQENPGLGLSE    164
Nvit            LLENAGTNEHIL----------  150
Tcas            LAGDK-----------------  146
Tcas8222_1-136:.  ----------------------  136
                       170       180

Consensus
LLXXXGXXXXXXNPGLGLSE
```