```
Turt          NCFNNRYNFISIMKVCLIYISFGCFFVSSLPLNGHSS-DPGQSLGDYTFTGLADDSQQDPSSPSLTPSSGGSPSAGSVAAK  79
Hduj          MNCSPTFFALFLVLFTLVMDTFALPLID----------QRMDETFSDNSPLLRKDKTTPDRSPFKAFE-SRLIDGMALAA  69
Smar          ---MASRVLVVIGALVFIHCVFGSQLVE----------RQLRELFSRR-EQLNNLRRLVNEWDQQLSHISLNIPGSRDDR  66
Dpul          ERWMGSDASGTTLLLVYKNKANFQLEYTKVRSYVERSAEDMNDNMYADIELIEDYPMKPVTMFDILKRVLAQKPAPPEPT  80
Vdes          MVARRAPLGWAVFLLALAAVSLLLADA----------QPAQESPSARMRYLITLKRQGKQVEHLIRELNALTEELKAKE  69
Isca          --MAVQCKTVALLAFVLVACAFV----------GVNADMTEDSIRQIVNRRKGLEVIRDIV----------D  50
Lmig          -----MQKMMEVLVLLGLLAVGLANPA----------EQLQAAAARESTELQRAKRCANVWDDSCV--NGAVSGASDDG  62
Tcas1         -----MRPVLVLVMIFSVSYARYLEPYNYGYP-------RPLVDFLNRL-SLSDKIKRCGNTFDESCA--NLPIIGASSDE  66
Znev          MEWKKEMTLVLYLLVVMATAAWASSK----------EIAQELMDSD-KAAERAKRCVNTGDDSCA--NGYIPGAGADD  65
Znev2         MEWKKEMTLVLYLLVVMATAAWASSK----------EIAQELMDSHIKSLQENRRTVRLLKSLL----------ED  56
Bmor          ------------------------------------------------------------MWDDGCA--NGQLPGAGNDD  18
Tcas2         ---MKTAFLLLFVLMPAVLCYYVHPNLHYFPARVNYRSAPAKSWGALFHRLQLASKRCANTFDESCI--NDVINGAGSDE  75
Dpul1069_5-244 ERWMGSDASGTTLLLVYKNKANFQLEYTKVRSYVERSAEDMNDNMYADIELIEDYPMKPVTMFDILKRVLAQKPAPPEPT  80
                        10        20        30        40        50        60        70        80

Consensus     MXWMKSXXLVLLLLLVLXAXAFASPXXTKVPSYVERSAEPAQELMXXDIXLLEDXKRCXNTWDDSCAXVNXQIPGAGADD

Turt          EWIQLRNLLSELGQQKVLTPSTYRTWKRSCTIDAGMTYNCDFRQLLSAVNARKYLESSLTPGRRKRP----------146
Hduj          ARHGHHANLYAK----------RACKYNLGISNDCEYRDAAQAALRRRFAKSKLSPGKRGSD----------121
Smar          EYLKNLNSPGKR----------NVCALGLGFMDGCDAQSAMEALKAREFFNSLQSPGKRQAESDNNSEA-------125
Dpul          ELIKTPLIRKRT----------CYFNAGMSHSCDYKELLQSADDANHWSSEHTPGKRRKRSSRGRAPAAASTS---143
Vdes          ADIRAQLPPEFI---DPMAPLEKRARSPECYIAAGLSRSCDYKDLIAAVEERDFWNSVNSPGKRRRRGADGEAADGNSSL146
Isca          DLHRQLTTLHKR----------SCHIDAGLNRGCDYKDILDAVEENKFWKSRDSPGRRRRRSVDNTKTK-------108
Lmig          LYFESGSSPGKREVRRLLQQMGRQAAAKRCA-NVW-DDSCVNGGVSGASDDGLYFGSGSSPGKRSLAEQLRRLQLLRAGP140
Tcas1         SWL-AHSSPGKR----------CA-NVW-GESCINGGIIGGGSDQSWLQGDDNPGRR----------110
Znev          DYFSGGNTPGKRATLDTLNPQELRTAWQKCLLNTG-DDSCANGYIPGAGADDDYFSGGNTPGKRSVSSFDVKRRH-------138
Znev2         LDVNMETVQKRT----------SCLINAGLSHSCDNRDFIGAVEENKYWRSLDSPGKRRRRGIFNVQ-------113
Bmor          YYLGGGFNPGKR----------CV-NMW-DEGCINDQINGAGNDDYYLNNGFNPGKRSVIELFKKLH-------73
Tcas2         AFLNGGDNPGKR----------CV-NTF-DESCSNGDINGAGSDDDWLHGDDTPGRR----------120
Dpul1069_5-244 ELIKTPLIRKRT----------CYFNAGMSHSCDYKELLQSADDANHWSSEHTPGKRRKRSSRGRAPAAASTS---143
                        90       100       110       120       130       140       150       160

Consensus     EYXKGGXXPGKRXXXDXLXPXEXRXAXRSCXINAGXSXSCDNXDILGAXXDRXYWXSGDSPGKRRRRSXXGXAXAAASTS

Turt          ----------FSTIYNQPFN  156
Hduj          ----------TPIF  125
Smar          ----------SPRN  129
Dpul          VPEKAAAGVVREILRYHIWCRSQSVTMLEALTRQSTALALYIEPCC  189
Vdes          NRGRVS--------LTSHLDEVRSTDAKLNRLNNKLNSAGVALQPQY  185
Isca          ----------SAPSSGRATTANMARVGQSTAN  130
Lmig          GSKRCA----------NVWDDSCANAGVSGASDDGLFFDSDQSPGK  176
Tcas1         ----------  110
Znev          ----------CLLFPMSPVCRNL  151
Znev2         ----------  113
Bmor          ----------KTKPKL  79
Tcas2         ----------  120
Dpul1069_5-244 VPEKAAAGVVREILRYHIWCRSQSVTMLEALTRQSTALALYIEPCC  189
                        170       180       190       200

Consensus     VPEXAAAGVVREILRYHIWCRSQSVAMLXXLTRQXXFXAXYXSPCN
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