Protein multiple sequence alignment (block 1, positions 1–80):

Name	Sequence	End
Turt4	MTKAILIVLCFSILLTAVELQT-VNNLVIETNDDNLVQIAQIEDILVGLDRYIAINHRIRFGRSIKSSNDLSSSLKSISK	79
Turt3	MFINKIKIVVFIVIFGVALSKRRFSEISILNNNKTVVPSENIIGVLSELEKYLAIVGRPRFGRSLNQKSSSKLDTFDCNR	80
Turt2	MSSFSSLLVALNSLVISMVIVINVSKSKEPRILEASDALQHFLKELDRYVAIAGRPRFGRSAYKMPKTIADYFTRKS	80
Bmor	MRLTLSAILLFAAILSCSAQAQY----PRPRRPERFDTAEQISNYLKELQEYYSVHGRGRYGKRQMHIADAESPFFEHSL	76
Znev2	MQNPVNLLLVAGLCVVISMAMPCWSDPSRPTRPKVFTSPDQLRDYLQELGNYYAIEGRPRFGKRLDTRPSNVTAGLSSAA	80
Lmig2	MCAVRALVLAAVALAAVAALSAPDVGQARPERPPMFTSPEELRNYLTQLSDFYASLGRPR----------------	60
Hduj	LSQKRARPAVADLEMLISDPSSYHNSESSARNYDNLVTLASTLKRLQELDKYYSHQARPRYGRSVAE----VVDNTPYRI	76
Aaeg	SSFSRRALVALLVCTLLIDLSSFTD--ARP--QDDPTSVAEAIRLLQELETKHAQHARPRFGKRSYLNPAGERNYYRMIG	76
Dmel	MCQTMRCILVACVALALLAAGCRVEASSRPPRKNDVNTMADAYKFLQDLDTYYGDRARVRFGKRGSLMDILNINLGKNAN	80
Znev1	MQSSLAWFLVVGCALVLMPHVAPTAW-AKPTDPEQLAAMADTLKYLQELDRYYSQVARPRFGKRADLRPVN-EQDLAPDD	78
Lmig1	MSQSRPLALLVVAALVAAAVLVAAAE-AQQADGNKLEGLADALKYLQELDRYYSQVARPRFGKRAELRPDVVDDVIPEEM	79
Smar	LSISTRSTLALICVIVLYVFCAPAQ-ATSG-PDQAVSMTEALKYLQALDKYYSQVARPRFGRSLPMRYPS--KDMSVEA	76
Turt1	KKNVRTCVYAFILVVTIVNLSQQAS-ARPN-IDEMANMAEALRYLEKLDKYYSQIARPRFGRSISD--------TRPG	69
Bpli13883_19-92	AAFILFLIVVSMCENVGAMDNQYSDLPPPPAKPERFTSKQQLKEYLVKLHEYYAIIGRPRFGRSQNL------FNENIQ	73
Bpli13495_14-71	----ILCQLIAETVSFGIRD----TSDEMPERPAVFKSKKELIDYIKRVNEYYGKVGRPRFGKRNY---------	58
Bpli10470_80-117	----------------------------NLIAKLMNMYAISSRSRFGKRSVT----EYKHQH	30
Bpli4070_8-74	IISCIGLAVIAALIGQIEAT----EYPTPPPVPSQFLTPNDVQKYLNQLHNYYMVVGRPRFGKRSRV----RAAD--	67

Consensus:
MSXSRXLILVAILXLVIXAXSSYVASPARPTRPDQFXSMAEXLKYLQELDXYYAIVGRPRFGKRXYLRPDXVSDXFSXXX

Protein multiple sequence alignment (block 2, positions to 90):

Name	Sequence	End
Turt4	RLKSILKRCKL	90
Turt3	ICDKLFR----	87
Turt2	VNEFRFPGFYQ	91
Bmor	NEDGLLKKFGY	87
Znev2	SRGNYFRYPTQ	91
Lmig2	-----------	60
Hduj	RPPYLA-----	82
Aaeg	RIQRLQDEQNS	87
Dmel	NGGEFARGFNE	91
Znev1	SSDRLWRRIAS	89
Lmig1	SADKFWRRFAR	90
Smar	EANRLLEQRRR	87
Turt1	KRDPLLTLVN-	79
Bpli13883_19-92	S----------	74
Bpli13495_14-71	-----------	58
Bpli10470_80-117	NNKKFKNR---	38
Bpli4070_8-74	-----------	67

Consensus:
SXDXLLRRFNX