Multiple sequence alignment (positions 1–80):

Name	Sequence	Pos
Turt3	---MRRLTLILLVIGF---IDLTSIAAAKYRNRNQEKVYLCLHNCALCVRFWENLYNGEKCARKCLKNKKRIDPDCKILRF	75
Turt1	--MSLRWFSLFIFYSY-LVFVHSDSSVISNSAENNKLYLCLHNCALCVRVWERLYNGEKCARKCLKFKENIDPDCESLKL	77
Turt2	--MNCLLIGISIVFAY-LVAVGCDPELINSPSPNDKLHLCLHNCALCVRVWEHLYNGEKCALKCLKFKENIDPDCESLKL	77
Hduj	MKTYHRSFFVSVTALITVSFVTAAAPIASKGMVGNISICIANCAQCHDIVGEVFDHRKCSRDCVQRRGTFIPDCTSPVA	80
Isca	-MARILDFPIFLVVSAVAFAVLLSLSSATHTYPSDPVLCINNCGQCKMIYGEYFNGRQCAEECLSTAGFIQPDCDEADS	79
Bmor	-MANKLTAVIVVALAVFMVNLDYANCSPAIASSYDAMEICIENCAQCKKMFGPWFEGSLCAESCIKARGKDIPECESFAS	79
Dmel1	--------------------------MTVDVAQPADTLYLCMKNCEQCKSMYGAYFEGDLCAKSCFRLKGAFIPDCIDVAS	55
Dmel2	CKPLILCTFVAVAMCLLPAISHYTHKRFDSMGGIDFVQVCLNNCVQCKTMLGDYFQGQTCALSCLKFKGKAIPDCEDIAS	80
Smar	RQSESQRAAVSTVVIL--LLLHLDRASSR------SINLCIQNCAQCKKMFGPYFEGQLCAETCIELRAKMTPDCADANS	72
Aaeg	-MASVRIVALFIAIALVLVSEASANPQIDILGGYDMIGVCINNCAQCKKMFGEFFEGHLCAEACIQFKGKMVPDCEDINS	79
Amel	MNTSIRSILLVLFLVYSMVFVLVAGSVPFER----AIGVCIRNCAQCKKMFGPYFLGQKCADSCFKNKGKLIPDCEDEDS	76
Apis	ADLRGSTTSARIAFTIAAVALVLIGIVGYTTADMADVAMCIRNCAQCKKMLGDYFEGPLCADTCVKFKGKMIPDCENIDS	80
Rpro	SKLLCRYTMKKLLLVI-----LLTSFLAEISGR--QIGVCIRNCAQCKKMFGVYFEGQMCADTCLKYKGKLIPDCEDIAS	73
Phum	MSAVCFLNNLLFVVVVLLTTFLCLANSSILPTESNQFGICIRNCAQCKKMFGTYFEGQLCADACVKFKGKVIPDCEDLDS	80
Lmig1	-MALCRRTLLLVALLV---VAVAVCVVPHVAAS--AVGVCIRNCAQCKKMFGPYFEGQLCGDACLKFKGKMVPDCEDAAS	74
Lmig2	-MSGRLVTALLVVLVL---------AATLAPPAAGNAVSVCIRNCAQCKKMYGPYFEGQLCADACLKFGGKMMPDCEDAAS	71
Tcas	MDSGSRNFLVLLLLFA--------SSLLVVDANPIGVCIRNCAQCKKMFGPYFEGQLCADACVKFKGKIIPDCEDITS	70
Znev	MEQRKISEAVVLAMSV-----AFLAATVVVPSGATSYSIGVCIRNCAQCKKMFGPYFEGQLCADACVKFKGKIIPDCEDLAS	77
Tcas1951_10-71	-------------------------AVDTFFSNAS-IPVCITNCVQCKQMFGPYFQGRACGDACVSTNGRLVPDCNNAGT	54
Tcas8660_16-79	-------------------------ASSLLVVDANPIGVCIRNCAQCKKMFGPYFEGQLCADACVKFKGKIIPDCEDITS	55

Consensus: MMAXCRXTXLLLXLVXXLVAVLLAAAXXXSXAXADAIGVCIRNCAQCKKMFGPYFEGQLCADACLKFKGKIIPDCEDIAS

Continued alignment:

Name	Sequence	Pos
Turt3	FKSSSLKLA	84
Turt1	FNQKAFRIK	86
Turt2	FNQKAFRIK	86
Hduj	IREYLNKMI	89
Isca	IVKYLRRKP	88
Bmor	ISPFLNKL-	87
Dmel1	IGQFLNKNE	64
Dmel2	IAPFLNALE	89
Smar	ISPFLNKFE	81
Aaeg	IAPFLNKLN	88
Amel	IQPFLQALD	85
Apis	IAPFLNKLE	89
Rpro	IGPFLNKLI	82
Phum	ISPFLNKVD	89
Lmig1	IAPFLSKLE	83
Lmig2	IAPFLNKLE	80
Tcas	IAPFLNKFE	79
Znev	IAPFLNKFE	86
Tcas1951_10-71	LGNFLKRL-	62
Tcas8660_16-79	IAPFLNKFE	64

Consensus: IAPFLNKLE