Multiple sequence alignment (positions 1–80, 83–160, 165–233).

Block 1 (residues 1–80)

Name	Sequence	End
Lsal	MELPNSYARRCGLLLPDVDRLYDVLGFDLKLAAASSFSVRIVTRINMLFEYVHRRPCDPKSSNHIPSYIMLLLVLAITFI	80
Rpro	------------------------------MASALSS--------------------SEHKAQQIDECQVTPVIHVL	27
Turt	------------MDLIQVYNFLISIIVVSILIP------------------VLDGSKGCHLRPVIHVL	38
Isca	------------MLICVRSPCSLLASWLILAVL----------AASMGPEESCQLRPVIHVL	40
Smar	---------------MVTLVFMVAAMMCIFSS-----------RLATADECHITPVIHVL	34
Bmor	------------MSVLNTFLVIVALILCYVND--------FPVTGHEVQLPPGTKFFCQECQMTAVIHVL	50
Dpul	-----------------MFLFVGLVSVIRA---------------DECQLTPVIHVL	25
Aaeg	--------------MKSSCVLLKVLACILLP--------GGLNAQKESNDDIQHYTADDCQVTPVIHVL	48
Dmel	----------MLRHLLRHENNKVFVLILLYCVLVSILKLCTAQPDSSVAATDNDITHLGDDCQVTPVIHVL	61
Nvit	--------------MANKKSALLHKTGWFILFIN----------GLSAIVHIDECEVTPVIHVL	40
Apis	------------MSTINQEFFRYLTVLAMCSMAF-------ADNGNGVVVTARSSDDCQVTPVIHVL	48
Phum	------------MIIKRTNIETVILLTIWFPLIFV--------IGHHGIQSSLATDDCQVTPVIHVL	47
Amel	----------MLLYHIDSITYYVVGASVLICLLNE---------TAKAIIGVDECQATPVIHFL	45
Tcas	------------MKPLLSLVTLWKLTIFLSSMCLDPR-------LNSKIQVSGASTTDECQVTPVIHVL	50
Znev	--------MACQQPSIQQIAVSAVLLLSLGYVVLVD-------------AKDECQVTPVIHVL	42
Lmig	---ARGPADECQLTPVIHVL	17
Aric10604_19-121:.	--------------------------VALTSS-------------TVQQCQVEIYNETL	20

Consensus: MELPNSYAXXCMLXLXXXXXVSXVLLLALLXCLLSSXXXXXXXXXXNALNXXXXXSAAXTADECQVTPVIHVLLVLAITFI

Block 2 (residues 83–160)

Name	Sequence	End
Lsal	LHSNIQDAFPNQYP--HLHALGNVPLMFK---------YLVLNSGSR-----KDPACVVRRVERKA--VVDLFCPNSSLG	142
Rpro	---QYPGCVPKPIP-SFACTGRCSSYIQPFKFGIYSCILKLLLSVRLEDLADGEIVHVLSGEWRARGQCCLVLSESQAW	102
Turt	-SHPGCLSKPIP-SFACHGSCSSYVQ-----------VSGSKFWQVERSCMCCQEMGEREA-TVGIFCPKKTP-	97
Isca	-KQPGCQPKPIP-SFACQGSCSSYVQ-----------VSGSRYWQVERSCMCCQEMGEREA-TKAVFCPKG-PG	99
Smar	-KYPGCNQKPIP-SFACQGRCTSYVQ-----------VSGSKMWQMERSCMCCQEMGVREA-NVTLHCPHARPG	94
Bmor	-KHRGCKPKAIP-SFACIGKCTSYVQ-----------VSGSKIWQMERTCNCCQESGEREA-TVVLFCPDAQNE	110
Dpul	-QYPGCIPKPIP-SFACTGKCTSYVQ-----------VSGSKLWQTERSCMCCQESGEREA-TVSLLCPKAAPG	85
Aaeg	-QYPGCVPKPIP-SFACIGRCASYIQ-----------VSGSKIWQMERSCMCCQESGEREA-SVSLFCPKAKNG	108
Dmel	-QYPGCVPKPIP-SFACVGRCASYIQ-----------VSGSKIWQMERSCMCCQESGEREA-AVSLFCPKVKPG	121
Nvit	-QYTGCVPKPIP-SFACKGRCSSYLQ-----------VSGSKIWQMERSCMCCQESGEREA-SVSLFCPKTKAG	100
Apis	-QYPGCVPKPIP-SFACTGRCSSYLQ-----------VSGSKIWQMERSCMCCQESGEREA-SVSLFCPKAKQG	108
Phum	-QYPGCVPKPIP-SFACTGRCSSYLQ-----------VSGSKIWQMERSCMCCQESGEREA-SVNLFCPKAKPG	107
Amel	-QYPGCVPKPIP-SYACRGRCSSYLQ-----------VSGSKIWQMERSCMCCQESGEREA-SVSLFCPRAKPG	105
Tcas	-QYPGCVPKPIP-SFACIGRCASYIQ-----------VSGSKIWQMERSCMCCQESGEREA-SVSLFCPKAKPG	110
Znev	-QYPGCVPKPIP-SFACTGRCSSYLQ-----------VSGSKIWQMERSCMCCQESGEREA-NVSLFCPKAKAG	102
Lmig	-QYPGCVPKPIP-SFACTGRCSSYLQ-----------VSGSKIWQMERSCMCCQESGEREA-SVSLFCPKAKAG	77
Aric10604_19-121:.	---HFRHCLDHSISIQTTRCRGQCYSEEE--------LVYDWEQTSTYRRYKRNFHCCVPKMTEAH-ETLVRCQN----	83

Consensus: LHSQYPGCVPKPIPIQSFACTGRCSSYLQPFKFGIYSXXLXLVSGSKIWQMERSCMCCQESGEREARGSVSLFCPKAKPG

Block 3 (residues 165–233)

Name	Sequence	End
Lsal	QPKVRK----------------VTTKAPSDCMCRPCTAIEQGTVLASDIAGYIDSVGPM-MNSLVSYQ-----	193
Rpro	RKVQKGMKVNLCIKRNVCACLQVTTKAPLECMCRPCTSVEESAIIPQEIAAY-ADEGPL--NNHFLKPQ-----	169
Turt	--KFRK----------------IATKAPVDCMCRPCTGIDDLTIKPQELINL---------TEELRKTDQDGSS	144
Isca	-PKFRK----------------LITRAPVECMCRPCTAPDEASILPQEFVGL---------	134
Smar	EPKFRK----------------VTTRAPVDCMCRPCTSVEKHLVQPQESAPW-LSDPNF-NDAILSV-	143
Bmor	EKRFRK----------------VSTKAPLQCMCRPCGSIEESSIIPQEVAGY-SEEGPL-YNHFRKSL-	160
Dpul	EPKLRR----------------VVTRAPVDCMCRPCTALEESAVMPQEIARF-LDDGSF--PFKL-	131
Aaeg	EKKFKK----------------VSTKAPLECMCRPCTGIEDANVIPQELAAF-ADDGSL-AGYFQKSQFKAAE	163
Dmel	EKKFKK----------------VLTKAPLECMCRPCTSIEESGIIPQEIAGY-SDEGPL-NNHFRRIALQ-----	173
Nvit	DRKFRK----------------VITKAPLDCMCRPCTSIEERIVIPQEIAXL-SNNGPLSNSAHFNNTFKLT	155
Apis	EKKFRK----------------VTTKAPLECMCRPCTGIEESAVIPQEMSNYAADEPPI-NGHFSKSI-	159
Phum	ERKFRK----------------VTTKAPLECMCRPCTGIEPSAIVPQEIAGY-ADEGPL-NNHFRKFE-	157
Amel	EKKFRK----------------VITKAPLECMCRPCTSVEEYAIIPQEIAGF-ADEGPFTTSAHFRRSSDLQ	160
Tcas	ERKFIK----------------VTTKAPLECMCRPCTGVEESAVIPQEIAGY-ADEGPL-SNHFLKSHSQ	162
Znev	ERKFRK----------------VSTKAPLECMCRPCSTVEESAVIPQEIAGY-ADEGPL-SNHFRKSL-	152
Lmig	ERKFRK----------------VSTKAPLECMCRPCTGVEESAVIPQEIAGY-PDNGPL-TAHFRKSQ-	127
Aric10604_19-121:.	-KQFQT----------------VRYRLVTQCECKPCG---------	103

Consensus: EXKFRKGMKVNLCIKRNVCACLQVTTKAPLECMCRPCTXIEESAVIPQEIAGYXADEGPLXXNNHFRKSQXXXXX