

Protein alignment of Ir1

conserved hypothetical protein [Ixodes scapularis]

Sequence ID: [EEC00213.1](#) Length: 260 Number of Matches: 1

Range 1: 82 to 147 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
132 bits(332)	3e-40	Compositional matrix adjust.	65/66(98%)	66/66(100%)	0/66(0%)	+3
Query	3	AQGAVPVYLLDRENQSRKVLNSMIKQKRKEKAGKWDVPVPKVRGVGDSEAFRVLKTGKR				182
		AQGAVPVYLLDRENQSRKVLNSMIKQKRKEKAGKWDVPVPKVRGVGD+EA				
Sbjct	82	AQGAVPVYLLDRENQSRKVLNSMIKQKRKEKAGKWDVPVPKVRGVGDSEAFRVLKTGKR				141
Query	183	KKKAWK	200			
		KKKAWK				
Sbjct	142	KKKAWK	147			

intronic protein 259, isoform B [Drosophila melanogaster]

Sequence ID: [NP_001260347.1](#) Length: 259 Number of Matches: 1

[See 4 more title\(s\)](#) [▼ See all Identical Proteins\(IPG\)](#)

Range 1: 83 to 146 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
102 bits(253)	3e-28	Compositional matrix adjust.	50/64(78%)	55/64(85%)	0/64(0%)	+3
Query	9	GAVPVYLLDRENQSRKVLNSMIKQKRKEKAGKWDVPVPKVRGVGDSEAFRVLKTGKRKK				188
		GA+P YLLDR QS AKVLSNMIKQKRKEKAGKWDVP+PKVR D+E F+VLKTGK K+				
Sbjct	83	GALPHYLLDRGIQSSAKVLSNMIKQKRKEKAGKWDVPPIPKVRAQSDAEVFKVLKTGKTKR				142
Query	189	KAWK	200			
		KAWK				
Sbjct	143	KAWK	146			

ribosome biogenesis protein NSA2 homolog [Aedes aegypti]

Sequence ID: [XP_021700401.1](#) Length: 259 Number of Matches: 1

[See 3 more title\(s\)](#) [▼ See all Identical Proteins\(IPG\)](#)

Range 1: 83 to 146 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
102 bits(253)	2e-28	Compositional matrix adjust.	48/64(75%)	55/64(85%)	0/64(0%)	+3
Query	9	GAVPVYLLDRENQSRKVLNSMIKQKRKEKAGKWDVPVPKVRGVGDSEAFRVLKTGKRKK				188
		GA+P YLLDR QS AKVLSNMIKQKRKEKAGKWDVP+PKVR DSE F+V+++GK K+				
Sbjct	83	GAIPAYLLDRGVQSSAKVLSNMIKQKRKEKAGKWDVPPIPKVRAQADSEVFKVIRSGKTKR				142
Query	189	KAWK	200			
		KAWK				
Sbjct	143	KAWK	146			

ribosome biogenesis protein NSA2 homolog isoform 3 [Homo sapiens]

Sequence ID: [NP_001351435.1](#) Length: 193 Number of Matches: 1

Range 1: 83 to 147 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
110 bits(274)	2e-31	Compositional matrix adjust.	52/65(80%)	59/65(90%)	0/65(0%)	+3
Query	6	QGAVPVYLLDRENQSRKVLNSMIKQKRKEKAGKWDVPVPKVRGVGDSEAFRVLKTGKRK				185
		QGAVP YLLDRE QSRKVLNSMIKQKRKEKAGK+VP+PKVR G++E +V++TGKRK				
Sbjct	83	QGAVPAYLLDREGQSRKVLNSMIKQKRKEKAGKWEVPLPKVRAQGETEVLKVIRTGKRK				142
Query	186	KKAWK	200			
		KKAWK				
Sbjct	143	KKAWK	147			

Protein alignment of Ir2

lamin Dm0-like, partial [Ixodes scapularis]

Sequence ID: [XP_029839273.1](#) Length: 561 Number of Matches: 1

Range 1: 279 to 548 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
502 bits(1292)	4e-177	Compositional matrix adjust.	245/271(90%)	257/271(94%)	1/271(0%)	+1
Query	133	REQYESQMQLNREEMQDIYENKMRDLQSLLEQQRSTDSSTKMEEMRAYKSRLLEGLSKISE				312
		RE YESQMQL+RE+ Q+IYENKMRDLQ LLEQ S+DSS+RMEEMRAYKSRLLEGLSKISE				
Sbjct	279	RELYESQMQLDREKTQNIYENKMRDLQRLLEQSSSDSSSKMEEMRAYKSRIEGLNSKISE				338
Query	313	LESQNLSLTARVRDLERLLDQEREWHGRLMAKEEEISRLRTEIEDQLREYQDLLDIKVA				492
		LESQNLSLTARVRDLERLLDQEREWHGRLMAKEEE+SRLR EIEDQLREYQ+LLDIKVA				
Sbjct	339	LESQNLSLTARVRDLERLLDQEREWHGRLMAKEEEVSRRAEIEDQLREYQNLDDIKVA				398
Query	493	LDLEIAAYRKLLLEGEEESRLHITPSASTSGAEMYTSPLLRGTKRKRTFLSHREEQLNSDVQ				672
		LDLE AAYRKLLLEGEEESRLH TPSASTSGAEMYTSPLLRG KR+ TF SHREEQ N DVQ				
Sbjct	399	LDLETAAYRKLLLEGEEESRLHFTPSASTSGAEMYTSPLLRGAKRRLTF-SHREEQSNFDVQ				457
Query	673	VSASAKGDLEISDHCPDGKYVIVKNKGTKKEVPLAGWRIDRKSGDDEFTFRFHRTHVIQPG				852
		VSASAKGDLEISDHCPDGKYVIVKNKGTKE+PLAGWRIDR+SG+DEFTFRFHRTHVIQPG				
Sbjct	458	VSASAKGDLEISDHCPDGKYVIVKNKGTKEIFLAGWRIDRRSGNDEFTFRFHRTHVIQPG				517
Query	853	TTITVWSSDAGATHSPFSDLVMRNQWPHGE 945				
		TTITVWSSDAGA HSPFSDLVMRNQWPH E				
Sbjct	518	TTITVWSSDAGAAHSPFSDLVMRNQWPHVE 548				

lamin, isoform B [Drosophila melanogaster]

Sequence ID: [NP_001245892.1](#) Length: 622 Number of Matches: 1

[See 9 more title\(s\)](#) [▼](#) [See all Identical Proteins\(IPG\)](#)

Range 1: 270 to 553 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
256 bits(654)	2e-80	Compositional matrix adjust.	131/284(46%)	191/284(67%)	15/284(5%)	+1
Query	127	QLREQYESQMQLNREEMQDIYENKMRDLQSLLEQQRSTDSSTKMEEMRAYKSRLLEGLSKI				306
		+LR QYE QMQ+NR+E+Q +YE+K++ LQ + S + +EE+R+ + R++ LN+ I				
Sbjct	270	ELRAQYEEQMQINRDEIQSLYEDKIQRLQEAAARTSNSTHKSIEELRSTRVRIDALNANI				329
Query	307	SELESQNLSLTARVRDLERLLDQEREWHGRLMAKEEEISRLRTEIEDQLREYQDLLDIK				486
		+ELE N L AR+RDLER LD +RE HG+ + E+E+ RLR E+ QL+EYQDL+DIK				
Sbjct	330	NELEQANADLNARIRDLERQLDNDNRERHGGIEDLLEKELIRLREEMTQQLKEYQDLMDIK				389
Query	487	VALDLEIAAYRKLLLEGEEESRLHITPSASTSGAEMYTSPLLRGT-----KRRR				627
		V+LDLEIAAY KLL GEE+RL+ITP+ +T+ + ++ L T KRRR				
Sbjct	390	VSLDLEIAAYDKLLVGEEARLNITPATNTATVQSFSQSLRNSTRATFSRRTPSAAVKRRR				449
Query	628	TFLSHREEQLNSDVQVSASAKGDLEISDHCPDGKYVIVKNKGTKKEVPLAGWRIDRKSGDD				807
		+ E+ +D VSASAKG++EI + P+GK+V + NKG++EV + GW++ R +				
Sbjct	450	AVVDESESDHSVADYVVSASAKGNVEIKEIDPEGKFVRLFNKGSEEAIGGWQLQRLINEK				509
Query	808	--EFTFRFHRTHVIQPGTTITVWSSDAGATHSPFSDLVMRNQW 933				
		T++FHR+ I+P ITVWS+D A+H PPS LVM++Q+W				
Sbjct	510	GPSTTYKFHRSVRIEPNGVITVWSADTKASHEPSSSLVMKSGKW 553				

LOW QUALITY PROTEIN: lamin Dm0 [Aedes aegypti]

Sequence ID: [XP_021710074.1](#) Length: 579 Number of Matches: 1

Range 1: 249 to 520 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
206 bits(523)	1e-61	Compositional matrix adjust.	118/286(41%)	170/286(59%)	28/286(9%)	+1
Query	130	LREQYESQMQLNREEMQDIYENKMRDLQSLLEQQRSTDSSTKMEEMRAYKSRLLEGLSKIS				309
		L EQYE+++Q ++++D Y+ +MR + D +++ E+ + S + +				
Sbjct	249	LSEQYEAQLQQTQLQDLRDQYDGMRA-----NRDEISELYEVSVPFSSIHTIL----				296
Query	310	ELESQNLSLTARVRDLERLLDQEREWHGRLMAKEEEISRLRTEIEDQLREYQDLLDIKV				489
		L S +R+RDLE L+ ER+ H ++EI RLR +I QL+EYQDL+DIK+				
Sbjct	297	-LTLLXPSFQSRRLDLELQLNAERQRHAEKSKLQDEIERLRNQISQQQLQEQYQDLMDIKI				355
Query	490	ALDLEIAAYRKLLLEGEEESRLHITPSAST-----SGAEMYTSPLLRGTKRKR				627
		+LD+EIAAY KLL EE RL+ITP+ T SGA M +P KRRR				
Sbjct	356	SLDMEIAAYDKLLSSEEVRLNITFGSQTTIFQTSSSSSSTARSGA-MRRTPQRAAAKRRR				414
Query	628	TFLSHREEQLNSDVQVSASAKGDLEISDHCPDGKYVIVKNKGTKKEVPLAGWRIDRKSGDD				807
		T L +E+ SD V++SAKGD+EI + P+GK+V + NK KEV + GW + RK G +				
Sbjct	415	TVLEESDERSVSDFSVTSSAKGDIEIFEVDPEGKFVKLHNKSAKEVQIGGWTLVKRVGTN				474
Query	808	EFTFRFHRTHVIQPGTTITVWSSDAGATHSPFSDLVMRNQWPHGE 945				
		E F+FHRT + G+ +TVWSSD G TH PPS +VM+ Q+W G+				
Sbjct	475	ETVFKFHRTLKVDGGSFVTWSSDLGQTHEPPSTIVMKGQKWFAGD 520				

lamin-B1 isoform 2 [Homo sapiens]

Sequence ID: [NP_001185486.1](#) Length: 376 Number of Matches: 1

Range 1: 38 to 315 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
177 bits(448)	2e-51	Compositional matrix adjust.	100/279(36%)	178/279(63%)	7/279(2%)	+1
Query	127	QLREQYESQMQLNREEMQDIYENKMRDLQSLLEQQRSTDSSTKMEEMRAYKSRLLEGLSKI				306
		++REQ+++Q++L +EE++ Y K+ + + E ++ ++ EE+ + R+E L+S++				
Sbjct	38	EMREQHDAQVRLYKEELEQTYHAKLENARLSSEMNTSTVNSAREELMESRMRIESLSSQL				97
Query	307	SELESQNLSLTARVRDLERLLDQEREWHGRLMAKEEEISRLRTEIEDQLREYQDLLDIR				486
		S L+ ++ + R+++LE LL +E++ R L KE E++ +R +++ QL +Y+ LLD+K				
Sbjct	98	SNLQKESRACLERIQELEDLLAKEKDNSRRMLTDKEREMAEIRDQMQQQLNDYEQLLDVK				157
Query	487	VALDLEIAAYRKLLLEGEEESRLHITPSAST-----SGAEMYTSPLLRGTKRKRTFLSHREE				651
		+ALD+EI+AYRKLLGEE RL ++PS S+ + + RG KRRR + E				
Sbjct	158	IALDMEISAYRKLLLEGEEERLKLSPSPSSRVTVSRASSRSRVTRG-KKRRVDVEESA				216
Query	652	QLNSDVQVSASAKGDLEISDHCPDGKYVIVKNKGTKKEVPLAGWRIDRKSGDDEFTFRFHR				831
		++S + SASA G++ I + DGK++ +KN ++ P+ GW + RK GD +++				
Sbjct	217	SSSVSISHSASATGNVCIEEIDVDGKFIRLKNTSEQDPMGGWEMIRKIGDTSVSYKYTS				276
Query	832	THVIQPGTTITVWSSDAGATHSPFSDLVMRNQW-WPHGE 945				
		+V++ G T+T+H+++AG T SPP+DL+ +NQ W GE				
Sbjct	277	RYVLKAGQVTIWAANAGVTASPTDILWKNQNSWGTE 315				

Protein alignment of Ir3

transcription factor jun-D [Ixodes scapularis]

Sequence ID: [XP_002404571.2](#) Length: 291 Number of Matches: 1
[See 1 more title\(s\)](#) [See all Identical Proteins\(IPG\)](#)

Range 1: 1 to 235 [GenPept](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
353 bits(905)	4e-122	Compositional matrix adjust.	223/238(94%)	224/238(94%)	5/238(2%)	+2
Query	278	MDTTFYEDIRGG--TRLAAGSghaqpttqpqqhqqqqhhpqqqqpqLVRRDDLSSRRKRM				451
Sbjct	1	MDTTFYEDIRGG +RLAAGSQHAQPTTQ QQ Q Q Q LVRRDDLSSRRKRM				57
Query	452	TLDLNSAGRPERKAARFSSLLTSPDLNMLQLASPELERLIIAHNGLVtttptpttQYLFT				631
Sbjct	58	TLDLNSAGRPERKAARFSSLLTSPDLNMLQLASPELERLIIAHNGLVTTTTPTPTTQYLFT				117
Query	632	KTATEEQEQYARGFVDALAQHLQTAGGPSETalsaaaaasdgastssdsFILPSSSEHSL				811
Sbjct	118	KTATEEQEQYARGFVDALAQHLQTAGGPSETALSAAEASDSGASTSSDSFILPSSSEHSL				177
Query	812	GGGDGHVKDEPQTVPNLGATPPLSPIDMRDQERIKLERKRLRNRIAAASKCRKKLERI				985
Sbjct	178	GGGDGHVKDEPQTVPNLGATPPLSPIDMRDQERIKLERKRLRNRIAAASKCRKKLERI				235

Djun gene product [Drosophila melanogaster]

Sequence ID: [AAA28650.1](#) Length: 289 Number of Matches: 1
[See 1 more title\(s\)](#) [See all Identical Proteins\(IPG\)](#)

Range 1: 56 to 237 [GenPept](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
87.0 bits(214)	3e-19	Compositional matrix adjust.	70/195(36%)	103/195(52%)	25/195(12%)	+2
Query	437	RRRSMTLDLNSAGRPERKAARFSSSL-LTSPDLNMLQLASPELERLIIAHNGLVtttptpt				613
Sbjct	56	KR +LDLNS ++ F+ L + SPDL+ + +P+LE+++++N + NKRPGSLDLNSKSAKNKRI--FAPLVINSFDLSSKTVNTPDLEKILLSNNLM---QTPQP				110
Query	614	tQYLFTEKT--ATEEQEQYARGFVDALAQHLQTAGG-----PSETalsaaaaasds				760
Sbjct	111	+ TK T EQ + RGF +AL LH + + +AA + GKVFPFKAGFVTVEQLDFGRGFEEALHNLHTNSQAFPSANSAANSANNTTAAAMTAVNN				170
Query	761	stssdsFILPSSSEHSLGGGDGHVKDEPQTVPNLGATPPLSPIDMRDQERIKLERKRLRN				940
Sbjct	171	S +F + +E G +KDEP N ++P ++PIDM QE+IKLERKR RN GISGGTFFYTNMTE----GFSVIKDEPV---NQASSPTVNPIDMEAQEKIKLERKQRN				222
Query	941	RIAASKCRKKLERI 985				
Sbjct	223	R+AASKCRKKLERI RVAASKCRKKLERI 237				

transcription factor AP-1 isoform X2 [Aedes aegypti]

Sequence ID: [XP_001663792.2](#) Length: 278 Number of Matches: 1

Range 1: 35 to 227 [GenPept](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
119 bits(299)	2e-31	Compositional matrix adjust.	82/202(41%)	119/202(58%)	26/202(12%)	+2
Query	431	SSRKRSMTLDLNSAGRPERKAARFSS-----LLTSPDLNMLQLASPELERLIIAHNGLV				592
Sbjct	35	+S KR TL+LN++ + + ARF++ ++TSPDL +L+L SPELE++II L NSIKRPATIELNLAS---KSRKARFNASVTAPPVITSPDLQVLKLVSPELEKIIINSAAAL-				90
Query	593	tttptpttQYLFTKTATEEQEQYARGFVDALAQHLQ-----TAGGPSETalsaaaaasdg				757
Sbjct	91	+ L+ AT EQEQ+A+GF +AL + + + S + + --PTPTPSSILYPTKATTEQEQFAKFDEALLSMREKDNINKMNNNNNNKSNINNASTT				148
Query	758	astssdsFILPSSSEHSLGGGD-----GHVKDEPQTVPNLGATPPLSPIDMRDQERIKL				919
Sbjct	149	+ S +++ +++ GGD G +K+EPQ VP + P+SPIDM +QERIKL IAAISAISTATTTTHTNTMSGGDITYTDLGVIKEEPQIVPQ---SSPMSPIDMENQERIKL				205
Query	920	ERKRLRNRIAAASKCRKKLERI 985				
Sbjct	206	ERKRLRNR+AASKCRKKLERI ERKRLRNRVAASKCRKKLERI 227				

JUN protein, partial [Homo sapiens]

Sequence ID: [AAH09874.2](#) Length: 231 Number of Matches: 2

Range 1: 125 to 177 [GenPept](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
90.1 bits(222)	6e-20	Compositional matrix adjust.	43/53(81%)	47/53(88%)	1/53(1%)	+2
Query	830	VKDEPQTVPNL-GATPPLSPIDMRDQERIKLERKRLRNRIAAASKCRKKLERI				985
Sbjct	125	+K+EPQTVP + G TPPLSPIDM QERIK ERKR+RNRIAAASKCRKKLERI LKEEPQTVPEMPGETPPLSPIDMESQERIKAEKRMRNRRIAAASKCRKKLERI				177

Range 2: 1 to 31 [GenPept](#) [Graphics](#) [Next Match](#) [Previous Match](#) [First Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
34.3 bits(77)	1.0	Compositional matrix adjust.	17/31(55%)	20/31(64%)	0/31(0%)	+2
Query	632	KTATEEQEQYARGFVDALAQHLQTAGGPSET	724			
Sbjct	1	R T+EQE +A GFV ALA+LH PS T KNVTDEQEGFAEGFVRALAEHLHSQNTLPSVT	31			

Protein alignment of Ir4

TNF receptor-associated factor 4 isoform X2 [Ixodes scapularis]

Sequence ID: [XP_029836788.1](#) Length: 386 Number of Matches: 1

Range 1: 16 to 315 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
54.3 bits(129)	5e-08	Compositional matrix adjust.	70/310(23%)	112/310(36%)	92/310(29%)	+3
Query 213	KVEQMEWLS	EDYYIYGTSIPEKIRCHGCR	CVSNTIYPLENKC	RGHGLCKDCKK	--LDFTC	386
Sbjct 16	KV+ L D+ + +P++ +C C C+	IY L C HGLC DCK+ + F C				73
Query 387	YDHGGDVTADALR	NAVGQTNYAAKRLWILCLFCGSNEAFLNLKDH	-----MYKKHSE-			542
Sbjct 74	+ T + L N RL +LC C L++H + KK S+					133
Query 543	---ELAYMLKSSQ	KTDYEQ-----EKPASTE	EKHRTSALT			638
Sbjct 134	L L+S Q+ + ++	EKP ++				190
Query 639	WRQDNFFQNADDT	VEFVDDEAPACKHCKE	EWDA	RDLGEHEKTC	PKDVQCRYCDEWIK--	812
Sbjct 191	R+D ++ + V C++C+ + EH K C K + C YC ++K					245
Query 813	-----QEELS	DHKNVH-----TILDLQ				866
Sbjct 246	DEKKAHLKICEE	ASIECAFKDFGCKE	KFP	PRKEMQEHEKDPHNALLNQVILKAMDTISELQ		305
Query 867	QRIKEMERCT	896				
Sbjct 306	QRIK+MERC					
	QRIKD	MERCN 315				

TNF receptor-associated factor 4 [Aedes aegypti]

Sequence ID: [XP_001652160.1](#) Length: 481 Number of Matches: 1

[See 1 more title\(s\)](#) [▼ See all Identical Proteins\(IPG\)](#)

Range 1: 213 to 244 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
32.3 bits(72)	0.63	Compositional matrix adjust.	14/32(44%)	17/32(53%)	1/32(3%)	+3
Query 708	CKHCKEEWD	ARDLGEHEKTC	PKKDVQC	-RYCD	800	
Sbjct 213	C HC E+ A L H TCP+ V C + CD					244

TNF receptor-associated factor 6 [Homo sapiens]

Sequence ID: [AAH31052.1](#) Length: 522 Number of Matches: 1

Range 1: 188 to 233 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
32.3 bits(72)	0.001	Compositional matrix adjust.	12/46(26%)	25/46(54%)	0/46(0%)	+3
Query 705	ACKHCKEEWD	ARDLGEHEKTC	PKKDVQCRYCDEWIKQEELS	DHKNV	842	
Sbjct 188	+C +C D H++ CP +V C YC+ + +E++ +H ++					233

Protein alignment of Ir5

dynein light chain 1, cytoplasmic [Ixodes scapularis]

Sequence ID: [XP_002408929.1](#) Length: 89 Number of Matches: 1

[See 1 more title\(s\)](#) [See all Identical Proteins\(IPG\)](#)

Range 1: 1 to 83 [GenPept](#) [Graphics](#)

[▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
175 bits(444)	5e-57	Compositional matrix adjust.	83/83(100%)	83/83(100%)	0/83(0%)	+3
Query	165	MSDKKAVIKNADMSEEMQQDAVDVATQALEKYNIEKDIAAYIKKEFDKKYNPTWHCIVGR				344
		MSDKKAVIKNADMSEEMQQDAVDVATQALEKYNIEKDIAAYIKKEFDKKYNPTWHCIVGR				
Sbjct	1	MSDKKAVIKNADMSEEMQQDAVDVATQALEKYNIEKDIAAYIKKEFDKKYNPTWHCIVGR				60
Query	345	NFGSYVTHETKHFIFYFLGQVAI	413			
		NFGSYVTHETKHFIFYFLGQVAI				
Sbjct	61	NFGSYVTHETKHFIFYFLGQVAI	83			

cut up, isoform F [Drosophila melanogaster]

Sequence ID: [NP_001356933.1](#) Length: 267 Number of Matches: 1

[See 1 more title\(s\)](#) [See all Identical Proteins\(IPG\)](#)

Range 1: 1 to 83 [GenPept](#) [Graphics](#)

[▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
179 bits(455)	4e-56	Compositional matrix adjust.	80/83(96%)	82/83(98%)	0/83(0%)	+3
Query	165	MSDKKAVIKNADMSEEMQQDAVDVATQALEKYNIEKDIAAYIKKEFDKKYNPTWHCIVGR				344
		MSD+KAVIKNADMSEEMQQDAVD ATQALEKYNIEKDIAAYIKKEFDKKYNPTWHCIVGR				
Sbjct	1	MSDRKAVIKNADMSEEMQQDAVDCATQALEKYNIEKDIAAYIKKEFDKKYNPTWHCIVGR				60
Query	345	NFGSYVTHETKHFIFYFLGQVAI	413			
		NFGSYVTHET+HFIYFYFLGQVAI				
Sbjct	61	NFGSYVTHETRHFIFYFLGQVAI	83			

dynein light chain 1, cytoplasmic isoform X1 [Aedes aegypti]

Sequence ID: [XP_021709064.1](#) Length: 128 Number of Matches: 1

[See 3 more title\(s\)](#) [See all Identical Proteins\(IPG\)](#)

Range 1: 37 to 122 [GenPept](#) [Graphics](#)

[▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
172 bits(436)	4e-55	Compositional matrix adjust.	79/86(92%)	83/86(96%)	0/86(0%)	+3
Query	156	SLRMSDRKAVIKNADMSEEMQQDAVDVATQALEKYNIEKDIAAYIKKEFDKKYNPTWHCI				335
		S +MSD+KAVIKNADM EEMQQDAVD ATQALEKYNIEKDIAAYIKKEFDK+YNPTWHCI				
Sbjct	37	SSRMSDRKAVIKNADMGEEMQQDAVDCATQALEKYNIEKDIAAYIKKEFDKRYNPTWHCI				96
Query	336	VGRNFGSYVTHETKHFIFYFLGQVAI	413			
		VGRNFGSYVTHET+HFIYFYFLGQVAI				
Sbjct	97	VGRNFGSYVTHETRHFIFYFLGQVAI	122			

dynein light chain 2, cytoplasmic [Homo sapiens]

Sequence ID: [NP_542408.1](#) Length: 89 Number of Matches: 1

[See 5 more title\(s\)](#) [See all Identical Proteins\(IPG\)](#)

Range 1: 1 to 83 [GenPept](#) [Graphics](#)

[▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
170 bits(431)	3e-54	Compositional matrix adjust.	79/83(95%)	82/83(98%)	0/83(0%)	+3
Query	165	MSDKKAVIKNADMSEEMQQDAVDVATQALEKYNIEKDIAAYIKKEFDKKYNPTWHCIVGR				344
		MSD+KAVIKNADMSE+MQQDAVD ATQA+EKYNIEKDIAAYIKKEFDKKYNPTWHCIVGR				
Sbjct	1	MSDRKAVIKNADMSEDMMQQDAVDCATQAMEKYNIEKDIAAYIKKEFDKKYNPTWHCIVGR				60
Query	345	NFGSYVTHETKHFIFYFLGQVAI	413			
		NFGSYVTHETKHFIFYFLGQVAI				
Sbjct	61	NFGSYVTHETKHFIFYFLGQVAI	83			

Protein alignment of Ir6

LOW QUALITY PROTEIN: uncharacterized protein LOC8050906 [Ixodes scapularis]

Sequence ID: [XP_002434995.2](#) Length: 331 Number of Matches: 1

Range 1: 78 to 323 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
337 bits(864)	3e-115	Compositional matrix adjust.	201/252(80%)	217/252(86%)	11/252(4%)	+1
Query	103	TSLYKKVGRPTYQNREALLTHARRHKHSLPFELKRGDVCRRKQASSQAAQHIIIVPVGAAQ				282
		TS + + G TYQNREALLTHARRHKHSLPFELKRGDVCRRKQASSQAAQHIIIVPVGAAQ				
Sbjct	78	TSWHCQCGA--TYQNREALLTHARRHKHSLPFELKRGDVCRRKQASSQAAQHIIIVPVGAAQ				135
Query	283	VIIVIQDQKTSSGQKSQDIPLHGANRTTGQWRNIVPKAssipmvmpvpsvpplpsavaga				462
		VIIVIQDQKTSSGQK QDIP+HGANRTTGQWRNIVPKASS+P+VMPVPSVPPLPSA+AGA				
Sbjct	136	VIIVIQDQKTSSGQKGQDIPVHGANRTTGQWRNIVPKASSVPIVMPVPSVPPLPSAMAGA				195
Query	463	TLPSTGSGTICEGKVHQASQTNVSCSKRRTKDSSIQASTTTSCMRDASELVDLPPKACRRHR				642
		+L SG+TICEGKVHQASQTNVSCSKRRTKDSSIQASTTTSCMRDASELVDLPPK + +				
Sbjct	196	SLSSGNTICEGKVHQASQTNVSCSKRRTKDSSIQASTTTSCMRDASELVDLPPKXVSKTQ				255
Query	643	AMKTAVQTQTSGFDV---QCKGNQPNL--SRNGSCHKKASHGCSIETQTVESAVCKAKKT				807
		+ + + +S D+ C NL GSCHKKASHGCSIETQT+ESAVCKAKKT				
Sbjct	256	SHEDS----SSDADIWXSTCSARGTNLICPEXGSCHKKASHGCSIETQTIESAVCKAKKT				311
Query	808	RARRTSSKQPPK 843				
		RARRT SKQPPK				
Sbjct	312	RARRTPSKQPPK 323				

Protein alignment of Ir7

ubiquilin-1 [Ixodes scapularis]

Sequence ID: [XP_029826161.1](#) Length: 570 Number of Matches: 1

Range 1: 236 to 451 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
221 bits(563)	7e-68	Compositional matrix adjust.	216/216(100%)	216/216(100%)	0/216(0%)	+2
Query	128	RRMYTELQEPMMNAAQEQFGGNPFASLLNaggagagpgappqpqqeaggqspaNQGTENRN				307
Sbjct	236	RRMYTELQEPMMNAAQEQFGGNPFASLLNAGGAGSPGAPPQEQEAGGQSPSNQGTENRN				295
Query	308	FLpnpwapgsgggspagngtggqappaggvlgglgglggpgtggagmfgtpgMQSVMRQLT				487
Sbjct	296	FLPNFWAPGSGGSPAGNLTGGQAPPAGGVLGGLGGLGGPGTGGAGMFGTSGMQSVMRQLT				355
Query	488	EDPSLMQNMMNAPYVQNMLQALAAFPEDMANQVMASNPFLLAGNPQLQEQMRRIMPQFLQQL				667
Sbjct	356	EDPSLMQNMMNAPYVQNMLQALAAFPEDMANQVMASNPFLLAGNPQLQEQMRRIMPQFLQQL				415
Query	668	QNPEVQGLITNPqamqammqigggmeqLHRVAPSVF	775			
Sbjct	416	QNPEVQGLITNPQAMQAMMQIQQGMEQLHRVAPSVF	451			

ubiquilin, isoform B [Drosophila melanogaster]

Sequence ID: [NP_001285457.1](#) Length: 547 Number of Matches: 2

[See 4 more title\(s\)](#) [▼](#) [See all Identical Proteins\(IPG\)](#)

Range 1: 312 to 416 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
94.0 bits(232)	4e-21	Compositional matrix adjust.	52/105(50%)	89/105(84%)	0/105(0%)	+2
Query	461	MQSVMRQLTEDPSLMQNMMNAPYVQNMLQALAAFPEDMANQVMASNPFLLAGNPQLQEQMRR				640
Sbjct	312	MRSLLQQMADNPFAMNQNLNAPYTRSMMSMSQDPDMAARLLSSSPLMSNNPALQEQVRQ				371
Query	641	LMPQFLQQLQNPEVQGLITNPqamqammqigggmeqLHRVAPSVF	775			
Sbjct	372	MMPQFMAQMNPEVMMNLTNPDAMNAILQIQQGMEQLRSAAPGLV	416			

Range 2: 226 to 274 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#) [▲ First Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
47.8 bits(112)	9e-06	Compositional matrix adjust.	31/62(50%)	39/62(62%)	13/62(20%)	+2
Query	128	RRMYTELQEPMMNAAQEQFGGNPFASLLNaggagagpgappqpqqeaggqspaNQGTENRN				307
Sbjct	226	+R+Y ++QEPMMNAA E FG NPFA L++ GG+G+ P QGTENRN				272
Query	308	FL 313				
Sbjct	273	FL 274				

ubiquilin-1 [Aedes aegypti]

Sequence ID: [XP_001652587.1](#) Length: 505 Number of Matches: 1

[See 1 more title\(s\)](#) [▼](#) [See all Identical Proteins\(IPG\)](#)

Range 1: 296 to 400 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
110 bits(274)	7e-27	Compositional matrix adjust.	67/105(64%)	90/105(85%)	0/105(0%)	+2
Query	461	MQSVMRQLTEDPSLMQNMMNAPYVQNMLQALAAFPEDMANQVMASNPFLLAGNPQLQEQMRR				640
Sbjct	296	MQS+++Q+ ++PSLM NMM+APY +NML+AL+A+P MA +M+ NPLLA NP LQEQMR				355
Query	641	LMPQFLQQLQNPEVQGLITNPqamqammqigggmeqLHRVAPSVF	775			
Sbjct	356	+MPQFLQQLQNFE+Q +++NPQA++A++QIQQGMEQL VAP +	400			

ubiquilin-1 isoform 1 [Homo sapiens]

Sequence ID: [NP_038466.2](#) Length: 589 Number of Matches: 2

[See 5 more title\(s\)](#) [▼](#) [See all Identical Proteins\(IPG\)](#)

Range 1: 377 to 457 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
101 bits(252)	4e-26	Compositional matrix adjust.	47/81(58%)	70/81(86%)	0/81(0%)	+2
Query	461	MQSVMRQLTEDPSLMQNMMNAPYVQNMLQALAAFPEDMANQVMASNPFLLAGNPQLQEQMRR				640
Sbjct	377	MQS+++Q+TE+P LMQN++APY+++M+Q+L+ NP++A Q+M +NPL AGNPQLQEQMR+				436
Query	641	LMPQFLQQLQNPEVQGLITNP 703				
Sbjct	437	+P FLQQ+QNP+ ++NP QLPTFLQQMQNPDTLSAMSNP	457			

Range 2: 273 to 301 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#) [▲ First Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
55.8 bits(133)	8e-11	Compositional matrix adjust.	23/29(79%)	29/29(100%)	0/29(0%)	+2
Query	128	RRMYTELQEPMMNAAQEQFGGNPFASLLN	214			
Sbjct	273	RRMYT++QEPM++AAQEQFGGNPFASL++	301			

Protein alignment of Ir8

small glutamine-rich tetratricopeptide repeat-containing protein beta-like [Ixodes scapularis]

Sequence ID: [XP_029827243.1](#) Length: 324 Number of Matches: 2

[See 2 more title\(s\)](#) ▼ [See all Identical Proteins\(IPG\)](#)

Range 1: 5 to 238 [GenPept](#) [Graphics](#) ▼ [Next Match](#) ▲ [Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
417 bits(1071)	5e-147	Compositional matrix adjust.	232/234(99%)	234/234(100%)	0/234(0%)	+2
Query	200	RRLVLSIVQFLRQQLQTADLSSDAKESVEVAVQCLETAYGVSIDDLSDNDSLLVSRITLLDI				379
		+RRLVLSIVQFLRQQLQTADLSSDAKESVEVAVQCLETAYGVSIDDLSDNDSLLVSRITLLDI				
Sbjct	5	KRLVLSIVQFLRQQLQTADLSSDAKESVEVAVQCLETAYGVSIDDLSDNDSLLVSRITLLDI				64
Query	380	FRFVVVQEHAGVHETLPEPTAQRAEAEKQKQEGNNMMKLEMYTAALECYTKAISLDGNN				559
		FRFVVVQEHAGVHETLPEPTAQRAEAEKQKQEGNNMMKLEMYTAALECYTKAISLDGNN				
Sbjct	65	FRFVVVQEHAGVHETLPEPTAQRAEAEKQKQEGNNMMKLEMYTAALECYTKAISLDGNN				124
Query	560	AVYYCNRAAAHSKLNHNHANAIEDCORALDIDPKYGRAYGRIGLAYASINEHQRAKECYQK				739
		AVYYCNRAAAHSKLNHNHANAIEDCORALDIDPKYGRAYGRIGLAYASINEHQRAKECYQK				
Sbjct	125	AVYYCNRAAAHSKLNHNHANAIEDCORALDIDPKYGRAYGRIGLAYASINEHQRAKECYQK				184
Query	740	AVELDPENQSYINNLRVAEERLGRMPSPGngdarraggvgggaPMDFGSLNNP				901
		AVELDPENQSYINNLRVAEERLGRMPSPGNGDARRAGVGGGAPMDFGSLNNP				
Sbjct	185	AVELDPENQSYINNLRVAEERLGRMPSPGNGDARRAGVGGGAPMDFGSLNNP				238

Range 2: 238 to 251 [GenPept](#) [Graphics](#) ▼ [Next Match](#) ▲ [Previous Match](#) ▲ [First Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
33.5 bits(75)	0.26	Compositional matrix adjust.	14/14(100%)	14/14(100%)	0/14(0%)	+1
Query	898	FTLMNMAATLMQDP 939				
		FTLMNMAATLMQDP				
Sbjct	238	FTLMNMAATLMQDP 251				

small glutamine-rich tetratricopeptide containing protein, isoform B [Drosophila melanogaster]

Sequence ID: [NP_001246058.1](#) Length: 331 Number of Matches: 1

[See 4 more title\(s\)](#) ▼ [See all Identical Proteins\(IPG\)](#)

Range 1: 7 to 227 [GenPept](#) [Graphics](#) ▼ [Next Match](#) ▲ [Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
113 bits(282)	1e-28	Compositional matrix adjust.	73/232(31%)	116/232(50%)	45/232(19%)	+2
Query	200	RRLVLSIVQFLRQQLQTADLSSDAKESVEVAVQCLETAYGVSIDDL-----				340
		+ Y V S ++L+Q +S D ES+EVA+QCL+ A+ + DD+				
Sbjct	7	QSFVRSFSDYDLKKQGDV--MSPDQTESIEVAIQCLQAADFGLG-DDVEAAPAAAGEEQATT				63
Query	341	-----NDSLIVSRITL-----LDIFRfVVVQEHAGVHETLPEPTAQRAE				457
		+D++ +D+F + E+L A				
Sbjct	64	QSSSTASAPDDDAVSGSAGIGAAAAVFNNDIMFELFQSLYTERNFESL-----AL				115
Query	458	AEKQKQEGNNMMKLEMYTAALECYTKAISLDGNNAVYYCNRAAAHSKLNHNHANAIEDCOR				637
		AE K EGN +MK Y AL Y +AI+ D N ++YCNRAAAH +L + A+ DC+				
Sbjct	116	AESKNEGNRLMKENKYNALQLYNRAIAFDPRNPIFYCNRAAAHIRLGENERAVTDCKS				175
Query	638	ALDIDPKYGRAYGRIGLAYASINEHQRAKECYQKAVELDPENQSYINNLRVA				793
		AL + Y KAY R+G+AY+++ ++A++ Y KA+EL+P+N+ Y +NL A				
Sbjct	176	ALVYNNNSKAYCRLGVAYSNMGNFEKAEQAYAKAIELEPDNEVYKSNLEAA				227

small glutamine-rich tetratricopeptide repeat-containing protein beta [Aedes aegypti]

Sequence ID: [XP_001657084.1](#) Length: 327 Number of Matches: 1

[See 2 more title\(s\)](#) ▼ [See all Identical Proteins\(IPG\)](#)

Range 1: 4 to 205 [GenPept](#) [Graphics](#) ▼ [Next Match](#) ▲ [Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
172 bits(436)	4e-51	Compositional matrix adjust.	88/213(41%)	133/213(62%)	14/213(6%)	+2
Query	191	VGGRRLLVLSIVQFLRQQLQTADLSSDAKESVEVAVQCLETAYGVSID---DLSNDSLLVS				361
		+ + V S ++FL QL+ + SSD++ES+EVA+QCLE Y + + D S ++ L				
Sbjct	4	IEAKFFVRSFIRFLNGQLEQPNFSSDSRESLEVAIQCLENVYIEIGQEAEGDNSQENPLNH				63
Query	362	RITLLDIFRfVVVQEHAGVHETLPEPTAQRAEAEKQKQEGNNMMKLEMYTAALECYTKAI				541
		L +++R T T ++ EAE K EGN +MK E Y AL Y +KAI				
Sbjct	64	IDLFVYRS-----TFTNVTPERKQAEENLKNEGNRLMKEEKYQEAINTYSKAI				112
Query	542	SLDGNNAVYYCNRAAAHSKLNHNHANAIEDCORALDIDPKYGRAYGRIGLAYASINEHQRA				721
		SLD N V+YCNRAAA+S+L ++ A +DC+ +L DP Y KAYGR+GLAY+ +N+H++A				
Sbjct	113	SLDATNPVFYCNRAAAYSRLGDYQAAADDCRMSRLYDPNYSKAYGRGLGLAYSRMKNKEQA				172
Query	722	KECYQKAVELDPENQSYINNLRVAEERLGRMPSP 820				
		+ YQ A+ ++P+NQ Y NN+ V +++L + S				
Sbjct	173	LDAYQNALRIEFDNQDYKNNMGVTTQORLEELRS 205				

small glutamine-rich tetratricopeptide repeat-containing protein alpha [Homo sapiens]

Sequence ID: [NP_003012.1](#) Length: 313 Number of Matches: 1

[See 5 more title\(s\)](#) ▼ [See all Identical Proteins\(IPG\)](#)

Range 1: 5 to 228 [GenPept](#) [Graphics](#) ▼ [Next Match](#) ▲ [Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
216 bits(551)	1e-67	Compositional matrix adjust.	116/237(49%)	155/237(65%)	16/237(6%)	+2
Query	200	RRLVLSIVQFLRQQLQTADLSSDAKESVEVAVQCLETAYGVSIDDLSDNDSLLVSRITLLDI				379
		+RL +I+QFL QL+ LSSDA+ES+EVA+QCLETA+GV+++D L + +TL +I				
Sbjct	5	KRLAYAI IQFLHDQLRHGGLSSDAQESLEVAIQCLETAFGVTVED---SDLALPQTLPEI				61
Query	380	FRFVVVQEHAGVHETLPEPTAQRAEAEKQKQEGNNMMKLEMYTAALECYTKAISLD				550
		F + P P+E AEAE+ K EGN MK+E + AA+ Y KAI L+				
Sbjct	62	FEAAATGKEMPQDLRSPARTPSPSEDSAEAEERLKTGNEQMKVENFEAAVHFYGAIELN				121
Query	551	GNNAVYYCNRAAAHSKLNHNHANAIEDCORALDIDPKYGRAYGRIGLAYASINEHQRAKEC				730
		NAVY+CNRAAA+SKL N+A A++DC+RA+ IDP Y KAYGR+GLA +SLN+H A				
Sbjct	122	PANAVYFCNRAAAYSKLGNYAGAVQDCERACIDPAYSKAYGRMGLALSSLNKHVEAVAY				181
Query	731	YQKAVELDPENQSYINNLRVAEERLGRMPSPGngdarraggvgggaPMDFGSLNNP				901
		Y+KA+ELDP+N++Y +NL++AE KLR PSP G D LLNNP				
Sbjct	182	YKKALELDPDNETYKSNLKIARELKLREAPSTGGVGS-----FDIAGLLNNP				228

Protein alignment of Ir9

TNF receptor-associated factor 6-like [Ixodes scapularis]

Sequence ID: [XP_029846366.1](#) Length: 449 Number of Matches: 1

Range 1: 1 to 205 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
385 bits(990)	9e-134	Compositional matrix adjust.	182/205(89%)	191/205(93%)	0/205(0%)	+2
Query	194	MRSIFISGFSDTLDWRPLYFQESSVAQSACSLCGLVSRKIVRLPCDHALCAECHEESQRR				373
		MRS FISGFSDTLDWRPLYFQESSVA SACSLCGL R +VRLPCDH LC+ECH+ESQRR				
Sbjct	1	MRSTFISGFSDTLDWRPLYFQESSVAHSACSLCGLCWRNVRLPCDHILCSECHQESQRR				60
Query	374	GSTCPLDKESFAKENIVHLDISEGYILKRTVACGNAPNGCDFIGQASRLVDHYKQCSFHV				553
		GSTCPLDKESF +NIVHLDISEGYILKRTVACGNAPNGCDFIGQASRLVDHYKQCSFHV				
Sbjct	61	GSTCPLDKESFGDDNIVHLDISEGYILKRTVACGNAPNGCDFIGQASRLVDHYKQCSFHV				120
Query	554	VPCPRCKSSVLRLTELVGHCCKDGCSSSESTTPVPIPNYINVNYDNLEITSSSELKREMLKISE				733
		VPCPRC+SSVLRLTELVGHCCKDGCSS STTPVPIP YINVNYD+LEITSSSELKREM KISE				
Sbjct	121	VPCPRCQSSVLRLTELVGHCCKDGCSSASTTPVPIPYIYNVNDHLEITSSSELKREMFKISE				180
Query	734	DLSSLQTSLNQWFEEVRTLEKSTSK 808				
		+LS LQT LNQWFEEVRT EK+T+K				
Sbjct	181	NLSCLQTGLNQWFEEVRTFEKNTNK 205				

early girl, isoform B [Drosophila melanogaster]

Sequence ID: [NP_001261904.1](#) Length: 315 Number of Matches: 1

[See 4 more title\(s\)](#) [▼ See all Identical Proteins\(IPG\)](#)

Range 1: 8 to 183 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
52.4 bits(124)	2e-07	Compositional matrix adjust.	43/179(24%)	77/179(43%)	13/179(7%)	+2
Query	251	FQESSVAQSACSLC-GLVSRKIVRLPCDHALCAECHEESQRRG				427
		FQ + C +C G++ + + C+HA C C E R TCP+D+ S N+				
Sbjct	8	FQGEVDDELTCPICSGVLEDPQAVMCEHAFRCGCINEWLTRQPTCPVDRNSLTANLRA				67
Query	428	L-DISEGYILKRTVACGNAPNGCDFIGQASRLVDHYKQCSFH---V				592
		+ I + + + + C NAP GC + + H +C + PC + C + +				
Sbjct	68	VPRIILRNLLSRLSITCDNAPYGC TAVLKLDAYNSHLCIHNPKRPF				127
Query	593	ELVGHCCKDGCSSSESTTPV----PIPNYINVNYDNLEITSSSELKREMLKISEDLSSLQTS				757
		EL H C E T + + + + +ELKRE+ + + +++ S				
Sbjct	128	ELKDH---NCVRELRLTLIVKQTERMGELKSELTDQQLTINELKRELQLFKDFMRAMRVS				183

E3 ubiquitin-protein ligase NRDP1 [Aedes aegypti]

Sequence ID: [XP_001658984.1](#) Length: 315 Number of Matches: 1

[See 5 more title\(s\)](#) [▼ See all Identical Proteins\(IPG\)](#)

Range 1: 8 to 183 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
49.7 bits(117)	1e-06	Compositional matrix adjust.	43/183(23%)	79/183(43%)	21/183(11%)	+2
Query	251	FQESSVAQSACSLC-GLVSRKIVRLPCDHALCAECHEESQRRG				427
		FQ + C +C G++ + + C+HA C C E R TCP+D+ N+				
Sbjct	8	FQGDVDDEELICPICSGVLEEPLQAVACEHAFRCACITEWLSRQPTCPVDRNPITNSNLRA				67
Query	428	L-DISEGYILKRTVACGNAPNGCDFIGQASRLVDHYKQCSFH---V				592
		+ I + + + +C NA GC + + L H + +C + +PC + C + +				
Sbjct	68	VPRIILRNLLSRLNISCEANAYGCTLVCLKDLTLATHIECEHNPKRPLPCEKGC				127
Query	593	ELVGHCCKDGCSSSESTTPV-----PIPNYINVNYDNLEITSSSELKREMLKISEDLSSL				748
		E H C E + V + N IN + + +ELKRE+ + + + +				
Sbjct	128	EYKDH---NCFRELRLSLVHNQQQKMSSELKNEIN----DQNLVINELKRELNLVKDFMRAM				180
Query	749	QTS 757				
		+ S				
Sbjct	181	RVS 183				

RING finger protein 151 isoform X1 [Homo sapiens]

Sequence ID: [XP_005255186.1](#) Length: 254 Number of Matches: 1

Range 1: 29 to 153 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
59.7 bits(143)	2e-09	Compositional matrix adjust.	38/126(30%)	54/126(42%)	3/126(2%)	+2
Query	281	CSLCGLVSRKIVRLPCDHALCAECHEESQRRG				460
		CS+C V ++ RLPC H C +C R TCP ++ ++ +VH++ I +				
Sbjct	29	CSVCHGVLRKPARLPCSHIFCKKCILRWLARQKTCPCCKRKEVKRKKVVHNMNKLRTIGRL				88
Query	461	TVACGNAPNGCDFIGQASRLVDHYKQCSFHVVP				634
		V C NA GC + H C F + CP C S V R L H + C S				
Sbjct	89	EVKCKNADAGCIIVTCPLAHRKGHDSCPFELTACFNEGCTSQVPRGT				147
Query	635	TPVPI 652				
		P+				
Sbjct	148	QQRCP 153				

Protein alignment of Ir10

serine/threonine-protein kinase 26 isoform X1 [Ixodes scapularis]

Sequence ID: [XP_029827734.1](#) Length: 582 Number of Matches: 1

Range 1: 13 to 234 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
400 bits(1027)	9e-137	Compositional matrix adjust.	217/222(98%)	219/222(98%)	0/222(0%)	+3
Query 270	ALRKMKVDPELIFTKQERIGKGSFGEVFKGMDNRTQQV	aiikiidleeaedeiedi	qgeim	449		
A +	KVDPELIFTKQERIGKGSFGEVFKGMDNRTQQV	AIKIIDLEEAEDEIEDIQQEIM				
Sbjct 13	ASQFKVDPELIFTKQERIGKGSFGEVFKGMDNRTQQV	AIKIIDLEEAEDEIEDIQQEIM				72
Query 450	VLSQCDSFPWVTKYYSYLKGTKLWII MEYLGGSALDLMKAGRFEELHIAVILREV	LKGL	629			
Sbjct 73	VLSQCDSFPWVTKYYSYLKGTKLWII MEYLGGSALDLMKAGRFEELHIAVILREV	LKGL	132			
Query 630	DYLHCEERKLHRDIKAAANVLLSEMGDVKLADFGVAGQLTNTTSKRNTFVGT	PFWMAPEVIK	809			
Sbjct 133	DYLHCEERKLHRDIKAAANVLLSEMGDVKLADFGVAGQLTNTTSKRNTFVGT	PFWMAPEVIK	192			
Query 810	QSAYDSKADIWSLGITAIELAKGEPNNSDLHPMRVFLIPRT		935			
Sbjct 193	QSAYDSKADIWSLGITAIELAKGEPNNSDLHPMRVFLIPKN		234			

germinal centre kinase III [Drosophila melanogaster]

Sequence ID: [NP_650596.1](#) Length: 642 Number of Matches: 1

[See 2 more title\(s\)](#) [▼ See all Identical Proteins\(IPG\)](#)

Range 1: 6 to 223 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
382 bits(980)	8e-129	Compositional matrix adjust.	203/218(93%)	212/218(97%)	0/218(0%)	+3
Query 282	KVDPELIFTKQERIGKGSFGEVFKGMDNRTQQV	aiikiidleeaedeiedi	qgeim	461		
Sbjct 6	KVDPELIFTKQERIGKGSFGEVFKGMDNRTQQV	AIKIIDLEEAEDEIEDIQQEIM	VLSQ	65		
Query 462	CDSFPWVTKYYSYLKGTKLWII MEYLGGSALDLMKAGRFEELHIAVILREV	LKGLDYLH	641			
Sbjct 66	CDSFPWVTKYYSYLKGTKLWII MEYLGGSALDLMKAG FEE+HI	+ILREV	LKGLDYLH	125		
Query 642	CERKLHRDIKAAANVLLSEMGDVKLADFGVAGQLTNTTSKRNTFVGT	PFWMAPEVIK	QSA	821		
Sbjct 126	ERKLHRDIKAAANVLLSE GDVKLADFGVAGQLTNTTSKRNTFVGT	PFWMAPEVIK	QSY	185		
Query 822	DSKADIWSLGITAIELAKGEPNNSDLHPMRVFLIPRT		935			
Sbjct 186	DAKADIWSLGITAIELAKGEPNNSDLHPMRVFLIPKN		223			

germinal center kinase 1 isoform X4 [Aedes aegypti]

Sequence ID: [XP_021700925.1](#) Length: 691 Number of Matches: 1

Range 1: 43 to 292 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
391 bits(1005)	5e-132	Compositional matrix adjust.	212/250(85%)	228/250(91%)	0/250(0%)	+3
Query 186	DSFPWQLMRRDMDMSVGDHDDLAVYTIAWALKMKVDPELIFTKQERIGKGSFGEVFKGMDN		365			
Sbjct 43	DSSVVVVASRRQRDINSNNNDGPPQMSSSGSEM	KVDPELIFTKQERIGKGSFGEVFKGVDN	102			
Query 366	RTQQVVAIKIIDLEEAEDEIEDIQQEIMVLSQCDSFPWVTKYYSYLKGTKLWII MEYLG		545			
Sbjct 103	RTQQVVAIKIIDLEEAEDEIEDIQQEIMVLSQCDSFPVTRYF	GSYLKGTKLWII MEYLG	162			
Query 546	GSALDLMKAGRFEELHIAVILREV	LKGLDYLHCEERKLHRDIKAAANVLLSEMGDVKLADFG	725			
Sbjct 163	GSALDLMKAG FEE+HIA+ILREV	LKGLDYLH ERKLHRDIKAAANVLLSE+GDVKLADFG	222			
Query 726	VAGQLTNTTSKRNTFVGT	PFWMAPEVIKQSA	YDSKADIWSLGITAIELAKGEPNNSDLHP	905		
Sbjct 223	VAGQLTNTTSKRNTFVGT	PFWMAPEVIKQSMYDSKADIWSLGITAIELAKGEPNSELHP	282			
Query 906	MRVFLFLIPRT		935			
Sbjct 283	MRVFLFLIPKN		292			

serine/threonine-protein kinase 26 isoform 1 [Homo sapiens]

Sequence ID: [NP_057626.2](#) Length: 416 Number of Matches: 1

[See 5 more title\(s\)](#) [▼ See all Identical Proteins\(IPG\)](#)

Range 1: 18 to 234 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
347 bits(889)	7e-119	Compositional matrix adjust.	187/217(86%)	203/217(93%)	0/217(0%)	+3
Query 285	VDPPELIFTKQERIGKGSFGEVFKGMDNRTQQV	aiikiidleeaedeiedi	qgeim	464		
Sbjct 18	ADPEELFTKLERIGKGSFGEVFKGIDNRTQQV	AIKIIDLEEAEDEIEDIQQEITVLSQ	77			
Query 465	DSFPWVTKYYSYLKGTKLWII MEYLGGSALDLMKAGRFEELHIAVILREV	LKGLDYLH	644			
Sbjct 78	DSYVTRYYSYLKGSKLWII MEYLGGSALDLLRAGPFDEFQIATM	LKGLDYLHS	137			
Query 645	ERKLHRDIKAAANVLLSEMGDVKLADFGVAGQLTNTTSKRNTFVGT	PFWMAPEVIK	QSA	824		
Sbjct 138	EKKLHRDIKAAANVLLSE GDVKLADFGVAGQLTDTQIKRNTFVGT	PFWMAPEVI	QSA	197		
Query 825	SKADIWSLGITAIELAKGEPNNSDLHPMRVFLIPRT		935			
Sbjct 198	SKADIWSLGITAIELAKGEPNNSDLHPMRVFLIPKN		234			

Protein alignment of Ir11

TNF receptor-associated factor 5-like [Ixodes scapularis]

Sequence ID: [XP_029845770.1](#) Length: 163 Number of Matches: 1

Range 1: 1 to 163 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
251 bits(642)	8e-85	Compositional matrix adjust.	124/163(76%)	135/163(82%)	0/163(0%)	+3
Query	237	MERKVNMIKGFYPFLDKRQLEFLTSVDEIMSC	ELCNTITKSY	YVAKCRHFF	CPDCYSLIQ	416
Sbjct	1	MERKV MIK FYP L+ RQLEFLTSVD IMSC	ELCNTITK YY+A	C+HFFC	CYSLI+	60
Query	417	KETSPKCPLDNIDWELKTSCCLAECSLNYSR	VRCNPNTGYG	CEYVDYLDR	MNDHVG	YCAFY
Sbjct	61	KE PKCPLD+ D +LKTSCCL E SL+ SRV	RCNPNTGYGC+ L	MNDHVG	YC FY	120
Query	597	PLPCIKCGITVGYNNLVSHLLRSCKFRGNET	ADPKPAVLDAVE	725		
Sbjct	121	P+PCIKCG TVG+ NLVSH+ SCK R	NETADPKPAVLDAVE	163		

TRAF6 [Drosophila melanogaster]

Sequence ID: [AAD47895.1](#) Length: 475 Number of Matches: 1

Range 1: 98 to 227 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
32.7 bits(73)	0.62	Compositional matrix adjust.	35/138(25%)	50/138(36%)	31/138(22%)	+3
Query	312	VDEIMSC	ELCNTITKSY	YVAKCRHFF	CPDCYSLIQ	491
Sbjct	98	LDSRYECAICIDWLNEPVLTS	CGHRFCRSCLTAWMQNNQCCPMDNKRLS	-----AEH		150
Query	492	SL---NYSRVR-----CPNTGYG	CEYVDYLDRMNDHVG	YCAFY-----PLPCI		611
Sbjct	151	DIFPDNYTRREIEQLKRD	CPNSSLGCSVVASPIELHRLP	SCPYPYRQQEPQEEKCPFAKI		210
Query	612	KCGITVGY---NNLVSHL	656			
Sbjct	211	KCDF-VGRPETNQLEEHL	227			

E3 ubiquitin-protein ligase Bre1 isoform X2 [Aedes aegypti]

Sequence ID: [XP_001650655.1](#) Length: 982 Number of Matches: 1

[See 1 more title\(s\)](#) [▼ See all Identical Proteins\(IPG\)](#)

Range 1: 911 to 964 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
38.5 bits(88)	0.007	Composition-based stats.	17/54(31%)	25/54(46%)	0/54(0%)	+3
Query	279	LDKRQLEFLTSVDEIMSC	ELCNTITKSY	YVAKCRHFF	CPDCYSLIQ	440
Sbjct	911	IDEVMLEEIREYKETLTCP	SKVKRKDAVLSKCFHVFCYDCLRTRYETRQRKCP			964

TNF receptor-associated factor 5 isoform b [Homo sapiens]

Sequence ID: [NP_001029082.1](#) Length: 557 Number of Matches: 1

[See 7 more title\(s\)](#) [▼ See all Identical Proteins\(IPG\)](#)

Range 1: 34 to 164 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
57.4 bits(137)	2e-11	Compositional matrix adjust.	44/134(33%)	60/134(44%)	10/134(7%)	+3
Query	297	EFLTSVDEIMSC	ELCNTITKSY	YVAKCRHFF	CPDCYSLIQ	461
Sbjct	34	QFVERLEERYC	ACFCHSVLHNPHQTGCGHRFCQHCILSLRELNTVPICPVDKEVIKSQEV			93
Query	462	LKTSCCLAECSLNYSR	VRCNPNTGYG	CEYVDYLDR	MNDHVG	YCAFYPLPCI--KCGITVG
Sbjct	94	FKDNCKREVLNLY--VYCS	NAP-GCNAKVILGRYQDHLQQCLFQFPVQCSNEKCREPVL			150
Query	636	NNLVSHLLRSCKFR	677			
Sbjct	151	+L HL SC+FR	164			

Protein alignment of Ir12

transcription initiation factor TFIID subunit 1 isoform X2 [Ixodes scapularis]

Sequence ID: [XP_029839716.1](#) Length: 1872 Number of Matches: 1

Range 1: 799 to 1058 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
543 bits(1398)	8e-180	Compositional matrix adjust.	260/260(100%)	260/260(100%)	0/260(0%)	+3
Query	135	QELPLFEVPGPNSKRANNFVRDPLQVFIYRLFWKSTDSPRRIKMEDIKKAPFSSHSESSIR				314
Sbjct	799	QELPLFEVPGPNSKRANNFVRDPLQVFIYRLFWKSTDSPRRIKMEDIKKAPFSSHSESSIR				858
Query	315	KRLKLCADFKRRTGMDSNWWVLKPEFRLPTEDEIRTMVSPEQCCAYYSMISAEQRLKDAGY				494
Sbjct	859	KRLKLCADFKRRTGMDSNWWVLKPEFRLPTEDEIRTMVSPEQCCAYYSMISAEQRLKDAGY				918
Query	495	GEKSLFAPEDENDEEMQVKMDDEVKAAPWNTTRAFISSVKGKCLLQLTGVADPTSCGEGF				674
Sbjct	919	GEKSLFAPEDENDEEMQVKMDDEVKAAPWNTTRAFISSVKGKCLLQLTGVADPTSCGEGF				978
Query	675	SYVRVPNKPQQSKEDGGSQQPVKKTVTGTADLRLRLSLSNAKQLLRKFGVPEDEIKKLSR				854
Sbjct	979	SYVRVPNKPQQSKEDGGSQQPVKKTVTGTADLRLRLSLSNAKQLLRKFGVPEDEIKKLSR				1038
Query	855	WEVIDVVRTLSTEQAKAGEE 914				
Sbjct	1039	WEVIDVVRTLSTEQAKAGEE 1058				

TBP-associated factor 1, isoform F [Drosophila melanogaster]

Sequence ID: [NP_001287201.1](#) Length: 2097 Number of Matches: 1

[See 1 more title\(s\)](#) [▼](#) [See all Identical Proteins\(IPG\)](#) [Ixodes X2 \[Ixodes scapularis\]](#)

Range 1: 829 to 1086 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
449 bits(1156)	1e-144	Compositional matrix adjust.	209/260(80%)	239/260(91%)	2/260(0%)	+3
Query	135	QELPLFEVPGPNSKRANNFVRDPLQVFIYRLFWKSTDSPRRIKMEDIKKAPFSSHSESSIR				314
Sbjct	829	QE PL+EVPGPNSKRANNF RDPLQVFIYRLFWS D+PRRI+M+DIK+AFP+HSESSIR				888
Query	315	KRLKLCADFKRRTGMDSNWWVLKPEFRLPTEDEIRTMVSPEQCCAYYSMISAEQRLKDAGY				494
Sbjct	889	KRLK CADFKRRTGMDSNWWV+KPEFRLP+E+EIR MVSPEQCCAY+SMI+AEQRLKDAGY				948
Query	495	GEKSLFAPEDENDEEMQVKMDDEVKAAPWNTTRAFISSVKGKCLLQLTGVADPTSCGEGF				674
Sbjct	949	GEK LFAP++++DEE Q+K+DDEVK APWNTTRA+I +++GKCLQL+G ADPT CGEGF				1008
Query	675	SYVRVPNKPQQSKEDGGSQQPVKKTVTGTADLRLRLSLSNAKQLLRKFGVPEDEIKKLSR				854
Sbjct	1009	SYVRVPNKP Q+KE+ SQ K++VTGTADLRLRL L AK+LLR+F VPE+EIKKLSR				1066
Query	855	WEVIDVVRTLSTEQAKAGEE 914				
Sbjct	1067	WEVIDVVRTLSTEQAKAGEE 1086				

transcription initiation factor TFIID subunit 1 isoform X2 [Aedes aegypti]

Sequence ID: [XP_021710567.1](#) Length: 1962 Number of Matches: 1

Range 1: 815 to 1073 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
449 bits(1155)	7e-145	Compositional matrix adjust.	209/260(80%)	239/260(91%)	1/260(0%)	+3
Query	135	QELPLFEVPGPNSKRANNFVRDPLQVFIYRLFWKSTDSPRRIKMEDIKKAPFSSHSESSIR				314
Sbjct	815	QE PL+EVPGPNSKRANNFVRDPLQVFIYRLFWS D+PR+I+M+DIKAPF+HSESSIR				874
Query	315	KRLKLCADFKRRTGMDSNWWVLKPEFRLPTEDEIRTMVSPEQCCAYYSMISAEQRLKDAGY				494
Sbjct	875	KRLKQCADFKRRTGMDSNFVVIKPEFRLPSEEEIRAMVSPEQCCAYFSMIAAEQRLKDAGY				934
Query	495	GEKSLFAPEDENDEEMQVKMDDEVKAAPWNTTRAFISSVKGKCLLQLTGVADPTSCGEGF				674
Sbjct	935	GEK +FA +++DEEMQ+KMDDEVK APWNTTRA+I +++GKCL+QLL G ADPT CGEGF				994
Query	675	SYVRVPNKPQQSKEDGGSQQPVKKTVTGTADLRLRLSLSNAKQLLRKFGVPEDEIKKLSR				854
Sbjct	995	SYVR+FNKP Q ++ QP K+TVTGTADLRLRLSL+NAK LLRKF VPE+EIKKLSR				1053
Query	855	WEVIDVVRTLSTEQAKAGEE 914				
Sbjct	1054	WEVIDVVRTLSTEQAKAGEE 1073				

transcription initiation factor TFIID subunit 1 isoform X4 [Homo sapiens]

Sequence ID: [XP_024308197.1](#) Length: 1800 Number of Matches: 1

Range 1: 678 to 935 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
466 bits(1199)	8e-151	Compositional matrix adjust.	217/259(84%)	241/259(93%)	1/259(0%)	+3
Query	135	QELPLFEVPGPNSKRANNFVRDPLQVFIYRLFWKSTDSPRRIKMEDIKKAPFSSHSESSIR				314
Sbjct	678	Q PLFEVPGPNSKRAN +RDFLQVFIYRLFWS D PRRI+MEDIKKAPFSSHSESSIR				737
Query	315	KRLKLCADFKRRTGMDSNWWVLKPEFRLPTEDEIRTMVSPEQCCAYYSMISAEQRLKDAGY				494
Sbjct	738	KRLKLCADFKRRTGMDSNWWVLKSDFRLPTEEEIRAMVSPEQCCAYYSMIAAEQRLKDAGY				797
Query	495	GEKSLFAPEDENDEEMQVKMDDEVKAAPWNTTRAFISSVKGKCLLQLTGVADPTSCGEGF				674
Sbjct	798	GEKS FAP+EN+E+ Q+K+DDEV+ APWNTTRAFI+++KGKCLL+TGVADPT CGEGF				857
Query	675	SYVRVPNKPQQSKEDGGSQQPVKKTVTGTADLRLRLSLSNAKQLLRKFGVPEDEIKKLSR				854
Sbjct	858	SYV++PNKP Q K+D QPVKKTVTGTADLRLRLSL NAKQLLRKFGVPE+EIKKLSR				916
Query	855	WEVIDVVRTLSTEQAKAGE 911				
Sbjct	917	WEVIDVVRT+STEQA++GE 935				

Protein alignment of Ir13

RUN domain-containing protein 1 isoform X1 [Ixodes scapularis]

Sequence ID: [XP_029837219.1](#) Length: 564 Number of Matches: 1
[See 2 more title\(s\)](#) [See all Identical Proteins\(IPG\)](#)

Range 1: 1 to 268 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
349 bits(895)	9e-117	Compositional matrix adjust.	266/268(99%)	266/268(99%)	0/268(0%)	+1
Query	196	MEVSSPEDIERESFDEADPLERWAPVGSSEIDDAWDDHDACslseferlrrhleeegqqln				375
		MEVSS EDIERESFDEADPLERWAPVGSSEIDDAWDDHDACSLSEFERLRHLEEEQEQLN				
Sbjct	1	MEVSSLEDIERESFDEADPLERWAPVGSSEIDDAWDDHDACSLSEFERLRHLEEEQEQLN				60
Query	376	SSLVALTTHFAQVQFRLKQIVNASQeekevllkeleeFAFRGIPDLRSYQTGVGillset				555
		SSLVALTTHFAQVQFRLKQIVNASQEEKEVLLKELEEFAPFRGIPDLRSYQTGVGILLSET				
Sbjct	61	SSLVALTTHFAQVQFRLKQIVNASQEEKEVLLKELEEFAPFRGIPDLRSYQTGVGILLSET				120
Query	556	egeqeeekleqqrqkqkelieqlkeqledlekYAFETGEAGMPSSMVLERQTVIIIEHLkek				735
		EQEKEEKLQQRQKQKELIPQLKEQLEDLEKYAFETGEAGMPSSMVLERQTVIIIEHLKEK				
Sbjct	121	EQEKEEKLQQRQKQKELIPQLKEQLEDLEKYAFETGEAGMPSSMVLERQTVIIIEHLKEK				180
Query	736	lplnldeidlldpddlrkqidQAVREMVNPFVKMKEQLVSQLKTQISDLERFIQFIQEGGS				915
		LPLNLDELDDLDPDDLRRKQIDQAVREMVNPFVKMKEQLVSQLKTQISDLERFIQFIQEGGS				
Sbjct	181	LPLNLDELDDLDPDDLRRKQIDQAVREMVNPFVKMKEQLVSQLKTQISDLERFIQFIQEGGS				240
Query	916	DGKPRCTCNCFPVHGKVDVSHSETSSSECY 999				
		DGKPRCTCNCFPVHGKVDV HSETSSSECY				
Sbjct	241	DGKPRCTCNCFPVHGKVDVLHSETSSSECY 268				

uncharacterized protein Dmel_CG3703 [Drosophila melanogaster]

Sequence ID: [NP_569874.1](#) Length: 711 Number of Matches: 1
[See 2 more title\(s\)](#) [See all Identical Proteins\(IPG\)](#)

Range 1: 112 to 281 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
81.6 bits(200)	1e-16	Compositional matrix adjust.	79/177(45%)	116/177(65%)	10/177(5%)	+1
Query	400	HFAQVQFRLKQIVNASQeekevllkeleeFAFRGIPDLRSYQTGVGillsetegeqeeekl				579
		HFA VQ R++QIV A EE++ LL++LE+FAF+GIPD + Q+ +				
Sbjct	112	HFAHVQVRVQIIVEAPEERDQLLRDLEDFAFQGIPT--AVQS-----KESHPDKPASDG				164
Query	580	eqqrqkqkelieqlkeqledlekYAFETGEAG-MPSSMVLERQTVIIIEHLkekplnlde				756
		E+ ++LI+QLK QL +LE+ A+E GE G +P ++LE+Q I++ L+ KL L +++				
Sbjct	165	EKDGHGPDSQLIQQLKSQLTELEQIAYEAGEPGILPQHVLLEKQKFILDELRAKLNLQVEQ				224
Query	757	ld--lldpddlrkqidQAVREMVNPFVKMKEQLVSQLKTQISDLERFIQFIQEGGSDG				921
		+ L + LR Q+D A+ E V P+KMKEQLV+QLKTI+DLERFI F+Q + +G				
Sbjct	225	HELPAIQLRQVQVNAIGEFVGPLMKKEQLVQLKTIQITDLERFIAFLQCDATIEG				281

RUN domain-containing protein 1 [Aedes aegypti]

Sequence ID: [XP_001657703.1](#) Length: 700 Number of Matches: 1
[See 1 more title\(s\)](#) [See all Identical Proteins\(IPG\)](#)

Range 1: 102 to 281 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
101 bits(252)	2e-23	Compositional matrix adjust.	100/180(56%)	132/180(73%)	4/180(2%)	+1
Query	376	SSLVALTTHFAQVQFRLKQIVNASQeekevllkeleeFAFRGIPDLRSYQTGVGillset				555
		S+L+ALT+HFAQVQ RL+QIV A EE++ LLK LEEFAF GIP+L+ I				
Sbjct	102	SNLIALTSHFAQVQLRLRQIIVEAPEERDNLKNLEEFAPFLGIPQLQDSDNKNKIPEIVA				161
Query	556	egeqe-ekleqqrqkqkelieqlkeqledlekYAFETGEAGMPSSMVLERQTVIIIEHLke				732
		+ ++ E +E R+KQ LI+QLK QL DLE+YA+E+G +P +++LE+Q VII+ +K				
Sbjct	162	DLDRSPESVEHLREKQHALIDQLKNQLIDLERYAYESGAGILPHTILLEKQKVIIDEIKN				221
Query	733	kplnldeidldpddlrkqidQAVRE-MVNPFVKMKEQLVSQLKTQISDLERFIQFIQ				903
		K+ LNL+ELD L +DLR Q+D A+ E +VNP+KMKEQLVSQLKTI DLERFI F+Q				
Sbjct	222	KINLNLNELDLPLQTTEDLRNQVDTALDEQLVNPLKMKEQLVSQLKTIQDLERFISFLQ				281

RecName: Full=RUN domain-containing protein 1 [Homo sapiens]

Sequence ID: [Q96C34.3](#) Length: 613 Number of Matches: 1
[See 1 more title\(s\)](#) [See all Identical Proteins\(IPG\)](#)

Range 1: 91 to 316 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
95.1 bits(235)	3e-25	Compositional matrix adjust.	105/228(46%)	146/228(64%)	24/228(10%)	+1
Query	373	NSSLVALTTHFAQVQFRLKQIVNASQeekevllkeleeFAFRGIPDLRSYQ-----T				528
		+S+L+AL++HFAQVQFRL+Q+V + E++ LL+ELE+FAFRG P + Y+				
Sbjct	91	DSALLALSSHFAQVQFRLRQVVRGAPAEQQRLLRELEDFAFRGCPHVLGYEGGPDASDE				150
Query	529	GVGI-----llsetegeqeeekleqqrqkqkelieqlkeqledlekYAFETGEA-GMP				681
		G G+ ++EQE++E+LE QR+KQKELI QLK QL+DLE +A++ G +P				
Sbjct	151	GDGLPGDRPFWLRGEDQSEQEKQERLETQREKQKELILQLKTQLDDLETFAYQEGSYDSL				210
Query	682	SSMVLERQTVII-EHLkekplnldeidlldpddlrkqidQAVREMVNPFVKMKEQLVSQL				858
		S+VLERQ VII E +K+ +++ L ++LR+++D AV ++VNP ++KEQLV QL				
Sbjct	211	QSVVLEQRVVIDELIKKLDNMNEDISSLSTEELRQRVDAAVAQIVNPARVREQLVEQL				270
Query	859	KTQISDLERFIQFIQEGGSDGKPRCT---CNCFPVHGKVDVSHSETSS 990				
		KTQI DLE FI FIQ E G P T C C GK S T S				
Sbjct	271	KTQIRDLQEMFINFIQDE--VGSPLQTGGGHCECKAGGKTGNCSRTGS 316				

Protein alignment of Ir14

methionine--tRNA ligase, cytoplasmic [Ixodes scapularis]

Sequence ID: [XP_029846836.1](#) Length: 962 Number of Matches: 1

Range 1: 251 to 492 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
429 bits(1103)	1e-143	Compositional matrix adjust.	240/242(99%)	240/242(99%)	0/242(0%)	+2
Query 215	LTSPMKVKAKVEANGEaspeikleeeekelsaaevGKAfSAWNDPKNLakelkkkpcpilp					394
Sbjct 251	LTSPMKVKAKVEANGEASPEIKLEEEKELSAAEVGKAF AWNDPKNLAKELKKKPCPILP					310
Query 395	kkGERNVLITSALPYVNNVPHLGNIVGSVLSADVFARYCRLRNWNTLYVCGTDEYGTATE					574
Sbjct 311	KKGERNVLITSALPYVNNVPHLGNIVGSVLSADVFARYCRLRNWNTLYVCGTDEYGTATE					370
Query 575	TKALEMGITPREICDRFNKLHADIYKWFNISFDHFGRTTTEQQTKIAQDIFLKLHKNQYM					754
Sbjct 371	TKALEMGITPREICDRFNKLHADIYKWFNISFDHFGRTTTEQQTKIAQDIFLKLHKNQYM					430
Query 755	LEEVEQLFCNRCERFLADRFVEGTCPFCAVEDARGDQCDCSLINPTELKQARCKLCK					934
Sbjct 431	REEVEQLFCNRCERFLADRFVEGTCPFCAVEDARGDQCDCSLINPTELKQARCKLCK					490
Query 935	EP	940				
Sbjct 491	EP	492				

Methionyl-tRNA synthetase [Drosophila melanogaster]

Sequence ID: [NP_611382.1](#) Length: 1022 Number of Matches: 1

[See 1 more title\(s\)](#) [▼](#) [See all Identical Proteins\(IPG\)](#)

Range 1: 252 to 430 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
266 bits(680)	2e-81	Compositional matrix adjust.	121/179(68%)	143/179(79%)	2/179(1%)	+2
Query 401	GERNVLITSALPYVNNVPHLGNIVGSVLSADVFARYCRLRNWNTLYVCGTDEYGTATETK					580
Sbjct 252	GERNVLITSALPYVNNVPHLGNi+G VLSAD++ARY R +NTL +CGTDEYGTATE K					311
Query 581	ALEMGITPREICDRFNKLHADIYKWFNISFDHFGRTTTEQQTKIAQDIFLKLHKNQYMLE					760
Sbjct 312	AL +TPREICD++ +LH IY+WF I FD+FGRTT++QT I Q+ F + K Y++					371
Query 761	EVVEQLFCNRCERFLADRFVEGTCPF--CAYEDARGDQCDCSLINPTELKQARCKLC					931
Sbjct 372	E VEQL C +C+RFLADRFVEGTCP C YEDARGDQCD C KL+N TEL + RCK+C					430

methionine--tRNA ligase, cytoplasmic [Aedes aegypti]

Sequence ID: [XP_001649418.2](#) Length: 966 Number of Matches: 1

Range 1: 254 to 432 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
262 bits(670)	3e-80	Compositional matrix adjust.	117/179(65%)	144/179(80%)	2/179(1%)	+2
Query 401	GERNVLITSALPYVNNVPHLGNIVGSVLSADVFARYCRLRNWNTLYVCGTDEYGTATETK					580
Sbjct 254	G++N LITSALPYVNNVPHLGNi+G VLSADVFARY RL +NTLY+CGTDEYGTATETK					313
Query 581	ALEMGITPREICDRFNKLHADIYKWFNISFDHFGRTTTEQQTKIAQDIFLKLHKNQYMLE					760
Sbjct 314	AL +TP++ICD++ ++H IY+WF I FD+FGRTT +QT+I QD+F L+ ++					373
Query 761	EVVEQLFCNRCERFLADRFVEGTCPF--CAYEDARGDQCDCSLINPTELKQARCKLC					931
Sbjct 374	V+QL C +C+R+LADRFVEGTCP+ C YEDARGDQCD C KLIN EL+ RCK+C					432

methionine--tRNA ligase, cytoplasmic isoform X1 [Homo sapiens]

Sequence ID: [XP_006719461.1](#) Length: 666 Number of Matches: 1

Range 1: 28 to 205 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
297 bits(760)	8e-95	Compositional matrix adjust.	135/178(76%)	154/178(86%)	0/178(0%)	+2
Query 401	GERNVLITSALPYVNNVPHLGNIVGSVLSADVFARYCRLRNWNTLYVCGTDEYGTATETK					580
Sbjct 28	GERNVLITSALPYVNNVPHLGNi+G VLSADVFARY RLR WNTLY+CGTDEYGTATETK					87
Query 581	ALEMGITPREICDRFNKLHADIYKWFNISFDHFGRTTTEQQTKIAQDIFLKLHKNQYMLE					760
Sbjct 88	ALE G+TP+EICD+++ +HADIY+WFNISFD FGRTTT QQTKI QDIF +L K ++L+					147
Query 761	EVVEQLFCNRCERFLADRFVEGTCPFCAVEDARGDQCDCSLINPTELKQARCKLCK					934
Sbjct 148	+ VEQL C C RFLADRFVEG CPFC YE+ARGDQCD C KLIN ELK+ +CK+C+					205

Protein alignment of Ir15

unconventional myosin-Va [Ixodes scapularis]

Sequence ID: [XP_029843866.1](#) Length: 1825 Number of Matches: 2

Range 1: 1203 to 1441 [GenPept](#) [Graphics](#)

▼ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps	Frame
447 bits(1150)	3e-144	Compositional matrix adjust.	239/239(100%)	239/239(100%)	0/239(0%)	+3
Query	177	KEIMRLHELEMENSKLKEDVKKMVKTLATEDKTSREKDLNMNHYESIQDeleerrreeclql				356
Sbjct	1203	KEIMRLHELEMENSKLKEDVKKMVKTLATEDKTSREKDLNMNHYESIQDELEERRREECLOL				1262
Query	357	rAVLANQSEDLKSVVALDSYRGNMDRIANEDGELLMAFETQKKLIROLEAELOQTEKVRMQS				536
Sbjct	1263	RAVLANQSEDLKSVVALDSYRGNMDRLNEDGELLMAFETQKKLIROLEAELOQTEKVRMQS				1322
Query	537	MEHEFRDEIKKLQEDNDRQOKLISQNLKKTPOAQSDAILQHEINRLTGENVDLREKIDGL				716
Sbjct	1323	MEHEFRDEIKKLQEDNDRQOKLISQNLKKTPOAQSDAILQHEINRLTGENVDLREKIDGL				1382
Query	717	AEQLKKYKRQLKIYAKKMKDGGILDQAEVKVEVGEDHGRKNMFEIKHKDAQNLGMFEYRK				893
Sbjct	1383	AEQLKKYKRQLKIYAKKMKDGGILDQAEVKVEVGEDHGRKNMFEIKHKDAQNLGMFEYRK				1441

Range 2: 1454 to 1474 [GenPept](#) [Graphics](#)

▼ Next Match ▲ Previous Match ▲ First Match

Score	Expect	Method	Identities	Positives	Gaps	Frame
38.5 bits(88)	0.012	Compositional matrix adjust.	18/21(86%)	19/21(90%)	0/21(0%)	+2
Query	929	GLEAKLAVTLLPGLPAYILFM	991			
Sbjct	1454	DLKPKLAVTLLPGLPAYILFM	1474			

myosin V [Drosophila melanogaster]

Sequence ID: [AAC99496.1](#) Length: 1792 Number of Matches: 2

Range 1: 1185 to 1412 [GenPept](#) [Graphics](#)

▼ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.2 bits(108)	1e-08	Compositional matrix adjust.	75/249(30%)	127/249(51%)	38/249(15%)	+3
Query	186	MRLHELEMENSKLKEDVKKMVKTLATEDKTSREKDLMN-HYESIQDeleerrreeclqlrA				362
Sbjct	1185	R+ ELE+EN KL+ + + L T K E + +N ++Q+E+ RRREEC+QL+A				1240
Query	363	VLANQSEDLKSVVALDSYRGNMDRLNEDGELLMAFETQKKLIROLEAELOQTEKVRMQSME				542
Sbjct	1241	VL QS+ ++S L+ M R N+ EL+ AF +QR + RQLE+EL+ S				1296
Query	543	HEFRDEIKKLQEDNDRQOKLISQNLKKTPOA-----QSDAILQHEINRLTGENVDLREK				704
Sbjct	1297	E EI++L + D QR++ +++ + + Q+D L+ E + + + + ++E+				1356
Query	705	VMTOQEIERLNNEKDELQKVMFESIDEFEDSNVDTLRQNDRYLRRELQKAVAQFLLVQEE				
Query	705	IDGLAEQLKKYKRQLKIYAKKMKDGGILDQAEVKVE-----VGEDHGRKNMFEIKH				854
Sbjct	1357	+ +LK Y+ +DGG Q E K+E D G N+ + K				1403
Query	855	KLANAKLKAYR-----QDGG---QLEHKIEEEMIRNKSNGTSADVGVANVTQRKS				
Query	855	KDAQNLGMF 881				
Sbjct	1404	++ Q L F QNPQGLMKF 1412				

unconventional myosin-Vb isoform X2 [Aedes aegypti]

Sequence ID: [XP_021696415.1](#) Length: 1888 Number of Matches: 2

Range 1: 1284 to 1488 [GenPept](#) [Graphics](#)

▼ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps	Frame
56.6 bits(135)	2e-08	Compositional matrix adjust.	62/209(30%)	117/209(55%)	13/209(6%)	+3
Query	186	MRLHELEMENSKLKEDVKKMVKTLATEDKTSREKDLNMNHYESIQDeleerrreeclqlrAV				365
Sbjct	1284	+R ELE+E KL++D + ++ + +++L + ++Q+EL+RRR+EC+ L+AV				1340
Query	366	IRASELEVEIEIKLRQDYNLLRNSI---KRGVEDRELEAQNALQELKRRRDECISLKAV				
Query	366	LANQSEDLKSVVALDSYRGNMD---RLNEDGELLMAFETQKKLIROLEAELOQTEKVRMQS				536
Sbjct	1341	LA QS L+++ N D R++++SEL+ AF+ QR + RQLE+EL+				1399
Query	537	LAQQSHSLRTL-GQSQVNPNGDSSLRIHDEGELMEAFQAQKLVNRQLESELRAMMDASNE				
Query	537	MEHEFRDEIKKLQEDNDRQOKLISQNLKKTPO-----AQSDAILQHEINRLTGENVDLR				698
Sbjct	1400	E I+ L+++ Q ++ L + + QSD L+HE+ + T VDL+				1459
Query	699	TLVENNKVIEALRKREVQELQMILQGRDLSNEDNLEALRQSDOYLRLHELKKSTAAYVDLQ				
Query	699	ERIDGLAEQLKKYKRQLKIYAKKMKDGGI 785				
Sbjct	1460	E+++L ++ + ++ T + ++D GI EQVNELLAKINELTKKNILSNRLRDNGI 1488				

Range 2: 1527 to 1552 [GenPept](#) [Graphics](#)

▼ Next Match ▲ Previous Match ▲ First Match

Score	Expect	Method	Identities	Positives	Gaps	Frame
37.0 bits(84)	0.030	Composition-based stats.	14/26(54%)	22/26(84%)	0/26(0%)	+2
Query	914	KQPYSGLEAKLAVTLLPGLPAYILFM	991			
Sbjct	1527	Q+ + L+ ++AVTL+PGLPAY++FM	1552			
Query	914	QRLVTDLKRPRVAVTLIFGLPAYVFM				

unconventional myosin-Va isoform 5 [Homo sapiens]

Sequence ID: [NP_001369278.1](#) Length: 1879 Number of Matches: 2

Range 1: 1353 to 1505 [GenPept](#) [Graphics](#)

▼ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps	Frame
90.1 bits(222)	4e-21	Compositional matrix adjust.	68/164(41%)	103/164(62%)	22/164(13%)	+3
Query	435	LNEDGELLMAFETQKKLIROLEAELOQTEKVRMQSMEHEFRDEIKKLQEDNDRQOKLISQN				614
Sbjct	1353	LNEDGEL + +E K+ R LE++LQ+K ++ R EI+ L+E+N+RQO+L++QN				1412
Query	615	LNEDGELWLVEGLQKANRLLESQLQSKRSHENEAELARGEIQSLKEENNRQQQLLAQN				
Query	615	LKKTPOAQSDAILQHEINRLTGENVDLREKIDGLAEQLKKYKRQLKIYAKKMKD-----				776
Sbjct	1413	L+ P+A+ +A LQHEI RL T EN+DL E+++ + ++K K+OLK++AKK+ +				1472
Query	777	LQLPPERARIEASLQHEITRLTNENLDLMEQLEQDKRTVRRLKKQLKVFAKKIGELEVGM				
Query	777	-----GSLDQAEVKVEVGEDHGRKNMFEIKHKDAQNLGMFEYRK 893				
Sbjct	1473	G I+D+ V N+P R KD Q GM EYRK				1505
Query	1473	ENISPGQIIDEPIRPV-----NIPR-KEKDFQ--GMLEYKK				

Range 2: 1505 to 1539 [GenPept](#) [Graphics](#)

▼ Next Match ▲ Previous Match ▲ First Match

Score	Expect	Method	Identities	Positives	Gaps	Frame
33.1 bits(74)	4e-21	Composition-based stats.	19/35(54%)	21/35(60%)	5/35(14%)	+2
Query	902	KFDHQKPYSGLEAKL-----AVTLLPGLPAYILFM	991			
Sbjct	1505	K D QR L ++L A^V L+PGLPAYILFM	1539			
Query	902	KEDEQLKVRNLIILELKPRGVAVNLIFGLPAYILFM				

Protein alignment of Ir16

adenosine kinase 2 [Ixodes scapularis]

Sequence ID: [XP_002405419.1](#) Length: 348 Number of Matches: 1

[See 1 more title\(s\)](#) [See all Identical Proteins\(IPG\)](#)

Range 1: 153 to 348 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
397 bits(1020)	2e-139	Compositional matrix adjust.	191/196(97%)	194/196(98%)	0/196(0%)	+3
Query	120	QPDNKALMEEASHYYISGFFLSVSLDSILTVAKHACSKGKTFMNL SAPFLCRIFKEQMM				299
		+PDNKALMEEAS+YYISGFFLSVSLDSILTVAKHACSKGKTFMNL SAPFLC IFKEQMM				
Sbjct	153	KPDNKALMEEASYYISGFFLSVSLDSILTVAKHACSKGKTFMNL SAPFLCSI FKEQMM				212
Query	300	QAFFYIDILFGNETEAREFADVHNLGTTDTVEIAKLISKFPKESGHFERMVVITQGAEDV				479
		QAFFYIDILFGNETEAREFA+VHNLGTTDTVEIAKLISKFPKESGHFERMVVITQGAEDV				
Sbjct	213	QAFFYIDILFGNETEAREFANVHNLGTTDTVEIAKLISKFPKESGHFERMVVITQGAEDV				272
Query	480	IVAQGNDTQTFPVPKLKTEDIVDTNGAGDAFVGGFLAMYLLGKPIETCVRCGITVSVEVI				659
		IVAQGNDTQTF VPKLKTEDIVDTNGAGDAFVGGFLAMYLLGKPIETCVRCGITVSVEVI				
Sbjct	273	IVAQGNDTQTFFSVPKLKTEDIVDTNGAGDAFVGGFLAMYLLGKPIETCVRCGITVSVEVI				332
Query	660	KKSGCTLPDRESVHV 707				
		KKSGCTLPDRESVHV				
Sbjct	333	KKSGCTLPDRESVHV 348				

adenosine kinase, isoform C [Drosophila melanogaster]

Sequence ID: [NP_001287054.1](#) Length: 345 Number of Matches: 1

[See 4 more title\(s\)](#) [See all Identical Proteins\(IPG\)](#)

Range 1: 151 to 336 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
170 bits(430)	3e-50	Compositional matrix adjust.	86/186(46%)	124/186(66%)	0/186(0%)	+3
Query	120	QPDNKALMEEASHYYISGFFLSVSLDSILTVAKHACSKGKTFMNL SAPFLCRIFKEQMM				299
		+P NKAL++ A +YYISGFFL+V+ SI+ VA A +K + F MNLSAPF+ + + ++				
Sbjct	151	EPSNKALVDNAQYYYISGFFLTVNPPSIMQVAATAHAKQRPFLMNL SAPFISQFYMAPLL				210
Query	300	QAFFYIDILFGNETEAREFADVHNLGTTDTVEIAKLISKFPKESGHFERMVVITQGAEDV				479
		A PY+DI+FGNE EA+ FA+ + D EI K + K++ R+ ++TQG + V				
Sbjct	211	AALPYVDIIIFGNEAEAAQAFAEAAQOWPFGDLREIGKRLVAMEKKNPTRPRIAILTQGCDFV				270
Query	480	IVAQGNDTQTFPVPKLKTEDIVDTNGAGDAFVGGFLAMYLLGKPIETCVRCGITVSVEVI				659
		++ Q + Q FVP KL +IVDTNGAGDAFVGGFL+ ++ GK ++ C+RCG + +I				
Sbjct	271	LLIQDQSVQEFPPVTKLAVHEIVDTNGAGDAFVGGFLSQFVQGS�DVCIRCGNYAAGHII				330
Query	660	KKSGCT 677				
		K GCT				
Sbjct	331	KNPGCT 336				

adenosine kinase [Aedes aegypti]

Sequence ID: [XP_001652432.2](#) Length: 344 Number of Matches: 1

Range 1: 149 to 344 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
204 bits(518)	2e-63	Compositional matrix adjust.	99/196(51%)	136/196(69%)	3/196(1%)	+3
Query	117	ROPDNKALMEEASHYYISGFFLSVSLDSILTVAKHACSKGKTFMNL SAPFLCRIFKEQM				296
		+ +N+ ++ A ++YISGFFL+VSL+SILTVAKHA SK + F MNLSAPF+ + PK+ +				
Sbjct	149	KSAENEKYLQNAEYFYISGFFLTVSLESILTVAKHALSKDRLFMMNL SAPFIPQFFKDNL				208
Query	297	MQAFFYIDILFGNETEAREFADVHNLGTTDTVEIAKLISKFPKESGHFERMVVITQGAED				476
		Q PYIDILFGNETEA FA+ GT D EI IS PK++ +R+ +ITQG++				
Sbjct	209	DQVMPYIDILFGNETEALAFAEAAQKFGTEDLKEIGLKISALPKQNESRKRVAIITQGSDF				268
Query	477	VIVAQGNDTQTFPVPKLKTEDIVDTNGAGDAFVGGFLAMYLLGKPIETCVRCGITVSVEV				656
		V++ + FVP KL + IVDTNAGDAFVGGFLA + + +TC+ CGI + ++				
Sbjct	269	VLLIRDGTITEFFVEKLAADQIVDTNGAGDAFVGGFLAQLVQKRNFDTCIECGIWAARKI				328
Query	657	IKKSGCT---LPDRES 695				
		I++SGCT +PD E+				
Sbjct	329	IQRSGCTFEGVPDFEA 344				

adenosine kinase [Homo sapiens]

Sequence ID: [AAB01689.1](#) Length: 334 Number of Matches: 1

Range 1: 144 to 334 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
181 bits(458)	9e-54	Compositional matrix adjust.	86/191(45%)	121/191(63%)	0/191(0%)	+3
Query	129	NKALMEEASHYYISGFFLSVSLDSILTVAKHACSKGKTFMNL SAPFLCRIFKEQMMQAF				308
		N L+E+A YI+GFFL+VS +S+L VA HA + F +NLSAPF+ + +KE +M+				
Sbjct	144	NWMLVEKARVCYIAGFFLTVSPESVLKVAHHASENNRIFTNL SAPFISQFYKESLMKVM				203
Query	309	PYIDILFGNETEAREFADVHNLGTTDTVEIAKLISKFPKESGHFERMVVITQGAEDVIVA				488
		PY+DILFGNETEA FA T D EIAK PK + +R+V+ TQG +D I+A				
Sbjct	204	PYDILFGNETEAAATFAREQGFETKDIKEIAKKTQALPKMNSKRQRIVIFTQGRDDTIMA				263
Query	489	QGNDTQTFPVPKLKTEDIVDTNGAGDAFVGGFLAMYLLGKPIETCVRCGITVSVEVIKKS				668
		++ F V +I+DTNAGDAFVGGFL+ + KP+ C+R G + +I+++				
Sbjct	264	TESEVTAFAVLDQDQREIIDTNAGDAFVGGFLSQLVSDKPLTECIRAGHYAASIIIRRT				323
Query	669	GCTLPDRESVH 701				
		GCT P++ H				
Sbjct	324	GCTFPEKPDFH 334				

Protein alignment of Ir17

serine/threonine-protein kinase 26 isoform X2 [Ixodes scapularis]

Sequence ID: [XP_029827735.1](#) Length: 574 Number of Matches: 1

Range 1: 125 to 226 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
218 bits(554)	1e-69	Compositional matrix adjust.	102/102(100%)	102/102(100%)	0/102(0%)	+3
Query	3	DYLCERKLRDRIKAANVLLSEMGDVKLADFGVAGQLTNTTSKRNTFVGTPFWMAPEVIK				182
		DYLCERKLRDRIKAANVLLSEMGDVKLADFGVAGQLTNTTSKRNTFVGTPFWMAPEVIK				
Sbjct	125	DYLCERKLRDRIKAANVLLSEMGDVKLADFGVAGQLTNTTSKRNTFVGTPFWMAPEVIK				184
Query	183	QSAYDSKADIWSLGITAIELAKGEPPNSDLHPMRVLFLIPKN		308		
		QSAYDSKADIWSLGITAIELAKGEPPNSDLHPMRVLFLIPKN				
Sbjct	185	QSAYDSKADIWSLGITAIELAKGEPPNSDLHPMRVLFLIPKN		226		

germinal centre kinase III [Drosophila melanogaster]

Sequence ID: [NP_650596.1](#) Length: 642 Number of Matches: 1

[See 2 more title\(s\)](#) [▼ See all Identical Proteins\(IPG\)](#)

Range 1: 122 to 223 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
207 bits(528)	4e-65	Compositional matrix adjust.	97/102(95%)	99/102(97%)	0/102(0%)	+3
Query	3	DYLCERKLRDRIKAANVLLSEMGDVKLADFGVAGQLTNTTSKRNTFVGTPFWMAPEVIK				182
		DYLH ERKLRDRIKAANVLLSE GDVKLADFGVAGQLTNTTSKRNTFVGTPFWMAPEVIK				
Sbjct	122	DYLHSEKLRDRIKAANVLLSEQGDVKLADFGVAGQLTNTTSKRNTFVGTPFWMAPEVIK				181
Query	183	QSAYDSKADIWSLGITAIELAKGEPPNSDLHPMRVLFLIPKN		308		
		QS YD+KADIWSLGITAIELAKGEPPNS+LHPMRVLFLIPKN				
Sbjct	182	QSQYDAKADIWSLGITAIELAKGEPPNSELHPMRVLFLIPKN		223		

serine/threonine-protein kinase 26 isoform X5 [Aedes aegypti]

Sequence ID: [XP_021700926.1](#) Length: 622 Number of Matches: 1

Range 1: 122 to 223 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
211 bits(538)	7e-67	Compositional matrix adjust.	98/102(96%)	100/102(98%)	0/102(0%)	+3
Query	3	DYLCERKLRDRIKAANVLLSEMGDVKLADFGVAGQLTNTTSKRNTFVGTPFWMAPEVIK				182
		DYLH ERKLRDRIKAANVLLSE+GDVKLADFGVAGQLTNTTSKRNTFVGTPFWMAPEVIK				
Sbjct	122	DYLHSEKLRDRIKAANVLLSELGDVKLADFGVAGQLTNTTSKRNTFVGTPFWMAPEVIK				181
Query	183	QSAYDSKADIWSLGITAIELAKGEPPNSDLHPMRVLFLIPKN		308		
		QS YDSKADIWSLGITAIELAKGEPPNS+LHPMRVLFLIPKN				
Sbjct	182	QSMYDSKADIWSLGITAIELAKGEPPNSELHPMRVLFLIPKN		223		

serine/threonine-protein kinase 25 isoform 3 [Homo sapiens]

Sequence ID: [NP_001269234.1](#) Length: 332 Number of Matches: 1

[See 2 more title\(s\)](#) [▼ See all Identical Proteins\(IPG\)](#)

Range 1: 35 to 136 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
200 bits(508)	2e-64	Compositional matrix adjust.	95/102(93%)	97/102(95%)	0/102(0%)	+3
Query	3	DYLCERKLRDRIKAANVLLSEMGDVKLADFGVAGQLTNTTSKRNTFVGTPFWMAPEVIK				182
		DYLH ERK+HRDIKAANVLLSE GDVKLADFGVAGQLT+T KRNTFVGTPFWMAPEVIK				
Sbjct	35	DYLHSEKRIHRDIKAANVLLSEQGDVKLADFGVAGQLTDTQIKRNTFVGTPFWMAPEVIK				94
Query	183	QSAYDSKADIWSLGITAIELAKGEPPNSDLHPMRVLFLIPKN		308		
		QSAYD RADIWSLGITAIELAKGEPPNSDLHPMRVLFLIPKN				
Sbjct	95	QSAYDFKADIWSLGITAIELAKGEPPNSDLHPMRVLFLIPKN		136		

Protein alignment of Ir18

fibrillin-2 isoform X2 [Ixodes scapularis]

Sequence ID: [XP_029839014.1](#) Length: 2880 Number of Matches: 28

Range 1: 2490 to 2756 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
491 bits(1265)	7e-159	Compositional matrix adjust.	256/267(96%)	260/267(97%)	0/267(0%)	+1
Query	148	KFPVSPCKSKCLNTEGSGYICSCDDGYVLAEDKVSCKDVECATDRHNCEHSCINTQGSYR				327
Sbjct	2490	ELPVSFCKSKCLNTEGSGYICSCDDGYVLAEDKVSCKDVECATDRHNCEHSCINTQGSYR				2549
Query	328	CSCKDGYNVLESQCLDVNECREQPHLCAPSGTCTNVPGSYRCNCPRGYITDVSGQSKDD				507
Sbjct	2550	CSCKDGYNVLESQCLDVNECREQPHLCAPSGTCTN+PGSYRCNCPRGYITD SGQSKDD				2609
Query	508	NECLSQPCGTANCVNTVGSYSCSPNGFSFDEIMTSCVGGSGCSNSPCLFECMPTGSGGF				687
Sbjct	2610	NECLSQPCGTANCVNTVGSYSC+CPNGFSFDEIMTSCVGGSGCSNSPCLFECMPTGSGGF				2669
Query	688	LCSCPEGYQRIQGQGHCLSTHPESSTLgpgkgvpggvgIPTYDIDNAGPQDPDKVISTEGC				867
Sbjct	2670	LCSCPEGYQRIQGQGHCLSTHPESSTLGP GKGVPG VGIP YD+ NAGPQDPDKVISTEGC				2729
Query	868	YSCKLNGGSVQRRARRGLTNGTLSRRLT	948			
Sbjct	2730	YSCKLNGGSVQRRARRGL NGT SRRLT				
		YSCKLNGGSVQRRARRGLNNGTSSRRLT	2756			

dumpy, isoform X [Drosophila melanogaster]

Sequence ID: [NP_001260039.1](#) Length: 14825 Number of Matches: 19

[See 1 more title\(s\)](#) [▼ See all Identical Proteins\(IPG\)](#)

Range 1: 185 to 369 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
119 bits(299)	2e-29	Compositional matrix adjust.	84/190(44%)	108/190(56%)	15/190(7%)	+1
Query	172	SKCLNTEGSGYICSCDDGYVLAEDKVSCKDVECATDRHNC--EHSCINTQGSYRCCKDG				345
Sbjct	185	AECCNLPAHFLCKCKDGY-EGDGEVLCTDVDECR-NPENCGPNALCTNTPGNYTCSCPDG				242
Query	346	Y---NVLESQCLDVNECREQPHLCAPSGTCTNVPGSYRCNCPRGYITDVSGQS-CKDDNE				513
Sbjct	243	YVGNPFYREGCQDVDEC-SYPNVCGPGAICTNLEGSYRCDCPPGYDGDGRSESGCVDQDE				301
Query	514	CLSQPCG-TANCVNTVGSYSCSPNGFSFDEIMTSCVGGSGCS-NSPCLF--ECMPTGSG				681
Sbjct	302	C PCG A+C+NT GS+ C CP+G+S D M C C+ N+PC EC+ G G				359
Query	682	GFLCSCPEGY	711			
Sbjct	360	F C CP G+ SFQCRCPSGF	369			

fibrillin-1 [Aedes aegypti]

Sequence ID: [XP_021695535.1](#) Length: 1425 Number of Matches: 11

Range 1: 587 to 792 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
119 bits(299)	1e-29	Compositional matrix adjust.	72/207(35%)	106/207(51%)	8/207(3%)	+1
Query	166	CKSKCLNTEGSIYSCDDGYVLAEDKVSCKDVDECATDRHNCEHSCINTQGSYRCSCKDG				345
Sbjct	587	C + C+N G Y C+C+ G+ L +D+ +C+DVDEC+T H+C H C+N G++ C C G CSNICINLLGDYKCACEAGFELEDDQQTCDVDECSTKIHDCSHICVNVPGTFECECPSG				646
Query	346	YNVLESQ--CLDVNECREQPHLCAPSGTCTNVPGSYRCNCPRGYITDVSGQSCKDDNECL				519
Sbjct	647	+ + + C D+NEC P+ C N+PGS+RC C G+ ++ ++C D +EC FILGRDKFTCEDINECETLPNKADCEHHICINLPGSHRCGEDGHRLELDNRTCSIDIECS				706
Query	520	SQPCG-TANCVNTVGSYSCSPNGFSFDEIMTSCVGGSGCS---NSPCLFECMPTGSGG				684
Sbjct	707	+ + +C NT GS+ CSCP+G D +C+ C N C C G DELKRCSHDCFNKGSFECSCPSGLRLDVKVTCLDIDECKINNFGGCSHIC-ENQHGS				765
Query	685	FLCSCPEGYQRIGQGHCLSTHPESSTL	765			
Sbjct	766	F C CPEG H E S L FKCLCPEGMNLGDDQATCEDHDECSIL	792			

Range 2: 546 to 732 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#) [▲ First Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
116 bits(290)	2e-28	Compositional matrix adjust.	71/190(37%)	102/190(53%)	10/190(5%)	+1
Query	166	CKSKCLNTEGSIYSCDDGYVLAEDKVSCKDVDECATDRHNCEHSCINTQGSYRCSCKDG				345
Sbjct	546	C C N GSY CSC G+ L ++ +C+D+DEC + NC + CIN G Y+C+C+ G CSDTCTNLPGSYHCSCPVGFEELGRNRHTCEDIDECIENNGNCSNICINLLGDYKCACEAG				605
Query	346	YNVLESQ--CLDVNECREQPHLCAPSGTCTNVPGSYRCNCPRGYITDVSGQSCKDDNECL				519
Sbjct	606	+ + + Q C DV+EC + H C S C NVPG++ C CP G+I +C+D NEC FELEDDQQTCDVDECSTKIHDC--SHICVNVPGTFECECPSGFILGRDKFTCEDINECE				663
Query	520	SQPCGT---ANCVNTVGSYSCSPNGFSFDEIMTSCVGGSGCSNS--PCLFECMPTGSGG				684
Sbjct	664	+ P +C+N GS+ C C +G + +C CS+ C +C T G TLPNKADCEHHICINLPGSHRCGEDGHRLELDNRTCSIDIECSDELKRCSHDCFNKGS				722
Query	685	FLCSCPEGYQ	714			
		F CSCP G +				

Range 3: 625 to 818 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#) [▲ First Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
107 bits(267)	2e-25	Compositional matrix adjust.	69/198(35%)	106/198(53%)	14/198(7%)	+1
Query	157	VSPCKSKCLNTEGSIYSCDDGYVLAEDKVSCKDVDECAT--DRHNCEHSCINTQGSYRC				330
Sbjct	625	+ C C+N G++ C C G++L DK +C+D++EC T ++ +CEH CIN GS+RC IHDCSHICVNVPGTFECECPSGFILGRDKFTCEDINECETLPNKADCEHHICINLPGSHRC				684
Query	331	SCKDGYNV-LESQ-CLDVNECREQPHLCAPSGTCTNVPGSYRCNCPRGYITDVSGQSCKD				504
Sbjct	685	C+DG+ + L+++ C D++EC ++ C S C N GS+ C+CP G DV +C D GCEGDGHRLELDNRTCSIDIECSDELKRC--SHDCFNKGSFECSCPSGLRLDVKVTCLD				742
Query	505	DNEC----LSQPCGTANCVNTVGSYSCSPNGFSFDEIMTSCVGGSGCS--NSPCLFECM				666
Sbjct	743	+EC + C C N GS+ C CP G + + +C CS N C C+ IDECKINNFGGCSHI-CENQHGSFKCLCPEGMNLGDDQATCEDHDECSILNGGCSQRCV				801
Query	667	PTGSGGFLCSCPEGYQRI	720			
Sbjct	802	GG+ C C G+ + -NFLGGYRCESGPFALM	818			

Range 4: 422 to 647 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#) [▲ First Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
106 bits(265)	4e-25	Compositional matrix adjust.	74/229(32%)	104/229(45%)	50/229(21%)	+1
Query	166	CKSKCLNTEGSIYSCDDGYVLAEDKVSCKDVDECATDRHNCEHSCINTQGSYRCSCKDG				345
Sbjct	422	C C N+EGS+ CSC GY L+E+ SC D++EC +C H CIN GS++CSC G CDHACHNSEGSFHCSCSHGYRLSENGHSCLDINECEKSNHGCHSHICINLLGSHQCSCPKG				481
Query	346	YNVLE-----SQCLDVNECRE				393
Sbjct	482	++E C+DVNEC LYLMDEGKTCDFVDECELNNGGCSHGCHYEYHGVVSCTCPKGFELERNNFKTCIDVNECEH				541
Query	394	QPHLCAPSGTCTNVPGSYRCNCPRGYITDVSGQSCKDDNECLSQPCGTAN-CVNTVGSYS				570
Sbjct	542	+ C S TCTN+PGSY C+CP G+ + +C+D +EC+ +N C+N +G Y RNGGC--SDTCTNLPGSYHCSCPVGFEELGRNRHTCEDIDECIENNGNCSNICINLLGDYK				599
Query	571	CSCPNGFSFDEIMTSCVGGSGCSNS--PCLFECMPTGSGGFLCSCPEGY	711			
Sbjct	600	C+C GF ++ +C CS C C+ G F C CP G+ CACEAGFELEDDQQTCDVDECSTKIHDCSHICVNV-PGTFECECPSGF	647			

Range 5: 345 to 524 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#) [▲ First Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
92.4 bits(228)	2e-20	Compositional matrix adjust.	62/188(33%)	95/188(50%)	19/188(10%)	+1
Query	184	NTEGSSYICSCDDGYVLAEDKVSCKDVDECATDRHNCEHSCINTQGSYRCSCCKDGYNVL--				357
		N + +CSC G+ L D+ +C D++EC D CE +C+N +G ++CSC +G+				
Sbjct	345	NPDSETLCSCPKGFKLDSQRTCHDINECHEDNNGGCEQNCLNFEGGHKCSCYEGFEPSPD				404
Query	358	-ESQCLDVNECREQPHLCAPSGTCTNVPGSYRCNCPRGYITDVSGQSCKDDNECLSQPCG				534
		C+D++EC C C N GS+ C+C GY +G SC D NEC				
Sbjct	405	DNRSCVDIDECSMSQGGC--DHACHNSEGSFHCSCSHGYRLSENGHSCLDINECEKSNHG				462
Query	535	TAN-CVNTVGSYSCSCPNGFSFDEIMTSC-----VGGSGCSNSPCLFECMPTGSGGFL				690
		++ C+N +GS+ CSCP G E +C + GCS+ C +E G				
Sbjct	463	CSHICINLLGSHQCSCPGLYLMEDGKTCDFVDECELNNGGCSHG-CHYE-----HGVVS				516
Query	691	CSCPEGYQ 714				
		C+CP+G++				
Sbjct	517	CTCPKGFE 524				

Range 6: 796 to 951 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#) [▲ First Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
83.2 bits(204)	3e-17	Compositional matrix adjust.	55/158(35%)	78/158(49%)	8/158(5%)	+1
Query	166	CKSKCLNTEGSSYICSCDDGYVLAEDKVSCKDVDECATDRHNCEHSCINTQGSYRCSCCKDG				345
		C +C+N G Y C C+ G+ L D +C+ + CA C+H C G CSC++G				
Sbjct	796	CSQRCVNFLGGYRCECESGFALMNDNKTCSEVSNPCALRNGGCQHFCNLHNGVPSCSCREG				855
Query	346	YNVLESQ---CLDVNECREQPHLCAPSGTCTNVPGSYRCNCPRGYITDVSGQSCKDDNEC				516
		+ V +S C+D++EC + P+ C N GSY C C G+ + GQ C D NEC				
Sbjct	856	FMVSKSNSASCVDIDEC-QTPNDNNCQQKCVNTEGSYTCECFAGFEKNDLGQ-CIDVNEC				913
Query	517	LSQPCG---TANCVNTVGSYSCSCPNGFSFDEIMTSCV 621				
		L G A C+N GS+ C CP G + +C				
Sbjct	914	LENNGGCGNKAKCINLAGSHRCVCPTGHRMGKDRKTCF 951				

Range 7: 185 to 359 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#) [▲ First Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
77.8 bits(190)	2e-15	Compositional matrix adjust.	65/181(36%)	85/181(46%)	13/181(7%)	+1
Query	193	GSYICSCDDGYVLAEDKVSCKDVDECATDRHNCEHSCINTQGSYRCSCCKDGYNVL--ESQ				366
		G Y C C GY + SC D+DEC RH C H+C NT G Y+CSC G +				
Sbjct	185	GDYRCECPGYY--QQHDHSCDHIDECCLGRHLCSHNCHNTAGDYQCSCPGLKLSTDSKT				242
Query	367	CLDVNECREQPH--LCAPSGTCTNVPGSYRCNCPRGYITDVSGQSCKDDNECLSQPCGTA				540
		C D++EC EQ + LC C N GSYRC CP G D G C+ + C + G +				
Sbjct	243	CDDIDECDEQDNEDLCG-DLNCLNTYGSYRCVCPEGKELDEYG-ICRQMDLCTTNNGGCS				300
Query	541	N-CVNTVGSYSCSCPNGFSFDEIMTSCVGGSGC--SNSPCLFECMPTGSGGFLCSCPEGY				711
		+ C C CP+ E +C + C +N C C P LCSCP+G+				
Sbjct	301	HICTFFNRETFCDCPDDMELAEKGKTCTTINDCNLNNGGCSHICNPDSET--LCSCPKEG				358
Query	712	Q 714				
		+				
Sbjct	359	K 359				

Range 8: 215 to 400 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#) [▲ First Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
72.8 bits(177)	1e-13	Compositional matrix adjust.	64/191(34%)	85/191(44%)	13/191(6%)	+1
Query	166	CKSKCLNTEGSSYICSCDDGYVLAEDKVSCKDVDECATDRHNCEH-----SCINTQGSYRC				330
		C C NT G Y CSC G L+ D +C D+DEC D + E +C+NT GSYRC				
Sbjct	215	CSHNCHNTAGDYQCSCPGLKLSTDSKTDDIDEC--DEQDNEDLCGDLNCLNTYGSYRC				272
Query	331	SCKDGYNVLE-SQCLDVNECREQPHLCAPSGTCTNVPGSYRCNCPRGYITDVSGQSCKDD				507
		C +G + E C ++ C C S CT C+CP G++C				
Sbjct	273	VCPEGKELDEYIGICRQMDLCTTNNGGC--SHICTFFNRETFCDCPDDMELAEKGKTCTTI				330
Query	508	NECLSQPCGTANCVNTVGSYSCSCPNGFSFDEIMTSCVGGSGCS--NSPCLFECMPTGSG				681
		N+C G ++ N CSCP GF D +C + C N C C+ G				
Sbjct	331	NDCNLNNGGCSHICNPDSETLCSCPKEGFKLDSQRTCHDINECHEDNNGGCEQNCL-NFEG				389
Query	682	GFLCSCPEGYQ 714				
		G CSC EG++				
Sbjct	390	GHKCSCYEGFE 400				

Score	Expect	Method	Identities	Positives	Gaps	Frame
67.8 bits(164)	4e-12	Compositional matrix adjust.	72/257(28%)	92/257(35%)	75/257(29%)	+1
Query 178	CLNTEGSGYICSCDDGYVLAEDKVSCKDVECATDRHN-----CEHSCINT	312				
	C N G Y C+C GY LA+D SC+D++EC C H C+N					
Sbjct 34	CRNAYGGYECTCPAGYELADDDRSCQDINECEAYGQEEDDYDEAGHGVGICSHCVNA	93				
Query 313	QGSYRCSCKDGYNV-----LESQCLDVNE-----	384				
	GS+ C C D +++ + C D+ E					
Sbjct 94	VGSFECRCPDNFHNLHDDRRTCVDRFCADLYENPNKTRCSHECKDGTGTFVCSCEFYILD	153				
Query 385	-----CR-----EQPHLCAPSGTCTNVPGSYRCNCPRGYITDVSGQSCKDDNEC-L	519				
	CR E C P G C + G YRC CP GY SC D +EC L					
Sbjct 154	EYDQKTRCRNVYSCGEEYKKRCNP-GVCRMIAGGDYRCECPLGY--QQHDSCHDIDEC	210				
Query 520	SQPCGTANCNTVSGSYSCSCPNFGFSFDEIMTSCVGGSGCSNSPCL-----FECMPTGSGG	684				
	+ + NC NT G Y CSCP G +C C C+ T G					
Sbjct 211	GRHLCSHNCNTAGDYQCSGKGLKSTDSKTCDDIDECDEQDNEDLCGDLNCLNT-YGS	269				
Query 685	FLCSCPEGYQRIGQGHC 735					
	+ C CPEG + G C					
Sbjct 270	YRCVCEGKELDEYGIC 286					

Score	Expect	Method	Identities	Positives	Gaps	Frame
56.2 bits(134)	2e-08	Compositional matrix adjust.	52/184(28%)	75/184(40%)	30/184(16%)	+1
Query	247	SCKDVDECATDRHNCEHSCINTQGSYRCSCKDGYNVLESQ--CLDVNECR-----				390
		C+D+DEC H C++ C N G Y C+C GY + + C D+NEC				
Sbjct	17	ECEDIDECVETEHGCDY-CRNAYGGYECTCPAGYELADDDRSCQDINECEAYGQEEDDY				75
Query	391	--EQPH-LCAPSGTCTNVPGSYRCNCPRGYITDVSGQSCKDD--NECLSQPCGT---ANC				546
		E H + S C N GS+ C CP + + ++C D + P T C				
Sbjct	76	EDEAGHGVGICSHCVNAVGSFECRCPDNFHLNHDRRTCVRDFCADLYENPNKTRCSHEC				135
Query	547	VNTVGSYSCSCPNFGFSFDEI-MTSCVGGSGCSN-----SPCLFECMPTGSGGFLCSCPE				705
		+ + CSCP + DE +C C +P + C G + C CP				
Sbjct	136	KDGTEGFVCSCEPFYILDEYDQKTCRNVS CGEEYKKRCNPGV--CRMIAGGDYRCECPL				193
Query	706	GYQR 717				
		GYQ+				
Sbjct	194	GYQQ 197				

Score	Expect	Method	Identities	Positives	Gaps	Frame
33.9 bits(76)	0.26	Compositional matrix adjust.	27/104(26%)	40/104(38%)	19/104(18%)	+1
Query	454	NCPRGYITDVSGQSCKDDNECLSQPCGTANCVNTVSGSYSCSCPNFGFSFDEIMTSCVGGSG				633
		+C G + G+ C+D +EC+ G C N G Y C+CP G+ + SC +				
Sbjct	5	HCREGLRLNSHGE-CEDIDECVETEHGCDYCRNAYGGYECTCPAGYELADDDRSCQDINE				63
Query	634	CSN-----SPCLFECMPTGSGGFLCSCPEGYQ		714		
		C EC+ G F C CP+ +				
Sbjct	64	CEAYGQEEEDDYDEAGHGVGICSHCEV-NAVGSFECRCPDNFH		106		

fibrillin, partial [Homo sapiens]

Sequence ID: [CAA45118.1](#) Length: 3002 Number of Matches: 27

Score	Expect	Method	Identities	Positives	Gaps	Frame
177 bits(449)	1e-48	Compositional matrix adjust.	116/312(37%)	148/312(47%)	72/312(23%)	+1
Query 142	CTKFPVSPCKSKCLNTEGSGYICSCDDGYVLAEDKVSCKDVECATDRHNCEHSCINTQGS	321				
	C + P PC C NTEGSY CSC GY+L ED SCKD+DECAT +HNC+ C+NT G					
Sbjct 2579	CNQAP-KPCNFICKNTEGSGYQCSCKPGYILQEDGRSCKDLDECATKQHNCQFLCVNTIGG	2637				
Query 322	YRCSCKDGYNVLESQCLDVNECREQPHLCAPSGTCTNVPGS-----	444				
	+ C C G+ + C+D NEC +LC G C N PGS					
Sbjct 2638	FTCKCPGPGFTQHHTSCIDNNECTSDINLCGSKGICQNTPGSFTCECQRGFSLDQTGSSCE	2697				
Query 445	-----YRCNCPRGYITDVSGQSCKDDNECLS-QPCGTANCNVNT	558				
	YRC+CP+GY+ C D+NECLS CG A+C NT+					
Sbjct 2698	DVDECEGNHRQHCGCQNIIGGYRCSCPQGYLQHYQWNQCVDENECLSAHICGGASCHNTL	2757				
Query 559	GSYSCSCPNFGFSFDEIMTSC--VGGSGCSNSPCLFECMPTGSGGFLCSCPEGYQRIGQGH	732				
	GSY C CP GF +++ C + G + +PC + C T GG+LC CP GY RIGQGH					
Sbjct 2758	GSYKCMCPAGFOYEQFSGGCQDINECGSAQAPCSYGCSENT-EGGYLCGCPPGYFRIGQGH	2816				
Query 733	CLSTHPESSTLgpgkgvpvgvgIPTYDIDNAGPQDP-----DKVISTEGCYSCKLNGGS	894				
	C+S + P+ P D +S E CY CK+NG					
Sbjct 2817	CVS-----GMGMGRGNPEPPVSGEMDDNLSPEACYECKINGYP	2855				
Query 895	VQRARRGLTNGT 930					
	+ +R TN T					
Sbjct 2856	KRGRKRSTNET 2867					

Protein alignment of Ir19

TNF receptor-associated factor 4 isoform X2 [Ixodes scapularis]

Sequence ID: [XP_029836788.1](#) Length: 386 Number of Matches: 2

Range 1: 9 to 249 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
166 bits(419)	1e-47	Compositional matrix adjust.	107/294(36%)	144/294(48%)	53/294(18%)	+1
Query 133	QFNIPYHEVKGFTGLGVDFLRFPCKVPDSARCKHCSCIPKRICHLLCPQHGLCLDCKNDY					312
	+FNIPY +VKG F GLGVDFLRFP C+VPD A+CK C CIP+RI LLCP HGLC DCK +					
Sbjct 9	KFNIPIYCKYKGFIGLVDFLRFP CQVPDRACKICDCIPERIYTLLCPHHGLCSDCKEFF					68
Query 313	QGYVCNVCHINTTPEQLGALRSDYNLDGLRLVLCNVCDDe111ggleehlyKHTNQGHK					492
	G+YC C I+TTPEQLGALRSDYNLDGLRL+VLC +CD++LLL					
Sbjct 69	IGFYCRECDIHTTPEQLGALRSDYNLDGLRLKVLCPMCDKKLLL-----					112
Query 493	EASKVQETTNQHGVDVAEKPLRVSYAVSARCHFCNENVKNSDYVEHVMHVQQRNSQGDSI					672
	G++ E + +C C V N + H + ++R S					
Sbjct 113	-----GELEEHNRSCEPKIVKKCSDCGVKVLNENLQSHQEVECCQKRVVLCGSC					160
Query 673	VQETANEDTAMEVQETESDETRPHTDNKEHHLNREHHKNCDDAVTCSRCLFVQRNYMS					852
	+ + + H + C + V C C V R S					
Sbjct 161	KSAMSRDKLGV-----HDQVCPEKPVVCDCKGEVLRKDES					196
Query 853	QHTLLTTCPKRTIYCKLCYSSFPCLTEETHKYQCPKMERECSDCGVNVLENLKN					1014
	+H CP R + C+ C S+ +E+ H+ QC + C C + + ++ K					
Sbjct 197	KHA-SECPMRVVCCECEGSGYAYSSEKEHRKQCEIKKLACEYCKLYLKGDDDEK					249

Range 2: 116 to 147 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#) [▲ First Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
43.5 bits(101)	2e-04	Compositional matrix adjust.	19/32(59%)	27/32(84%)	0/32(0%)	+1
Query 928	EETHKYQCPKMERECSDCGVNVLENLKNHLE					1023
	EE ++ +CPK+ ++CSDCGV VLNENL++H E					
Sbjct 116	EEHNRSCEPKIVKKCSDCGVKVLNENLQSHQE					147

transcription factor grauzone [Aedes aegypti]

Sequence ID: [XP_001659339.1](#) Length: 640 Number of Matches: 1

[See 1 more title\(s\)](#) [▼ See all Identical Proteins\(IPG\)](#)

Range 1: 424 to 521 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
31.6 bits(70)	1.5	Compositional matrix adjust.	23/98(23%)	41/98(41%)	12/98(12%)	+1
Query 763	HLNREHHKNCDDAVTCSRCLFVQ-RNYMSQHTLLTTCPKR-TIYCKLCYSSFPCLT---					927
	H++ ++H+ + C+ C F + + QH L K C +C F L+					
Sbjct 424	HVHEKYHRKMSEKNFQCAHCDKFYAFESMLKQHERLVHTKECHFVCHICARGFQALSSYS					483
Query 928	-----EETHKYQCPKMERECSDCGVNVLENLKNHL					1020
	EE K + P+ +CS C + V +N + H+					
Sbjct 484	SHLASHDEEAKDKPPEERLQCSVCSIWVYKQNYRKHV					521

TNF receptor-associated factor 4 isoform X3 [Homo sapiens]

Sequence ID: [XP_011523808.1](#) Length: 454 Number of Matches: 2

Range 1: 140 to 224 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
57.0 bits(136)	7e-08	Compositional matrix adjust.	32/85(38%)	47/85(55%)	3/85(3%)	+1
Query 778	HHKNCDDAVTC-SRCGLFVQRNYMSQHTLLTTCPKRTIYCKLCYSSFPCLTEETHKYQCP					954
	H C + + +C +R + +QH CPKRT C C F T ++H+YQCP					
Sbjct 140	HEGMCPQESVYCENKCGARMRRLLAQHATSECPKRTQPCTYCTKEFVFDTIQSHQYQCP					199
Query 955	KMERECSD-CGVN-VLNENLKNHLE					1023
	++ C + CGV V E+L HL+					
Sbjct 200	RLPVACPNQCGVGTVAREDLPGHLK					224

Range 2: 86 to 167 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#) [▲ First Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
38.9 bits(89)	0.045	Compositional matrix adjust.	23/82(28%)	37/82(45%)	2/82(2%)	+1
Query 778	HHKNCDDAVTC-SRCGLFVQRNYMSQHTLLTTCPKRTIYCKLCYSSFPCLTEETHKYQCP					954
	H C + + +C +R + + H CPKR + C+ C F E+H+ CP					
Sbjct 86	HLNTCSFNVIPCPNRCPMKLSRRDLPAHLQHDCKPRRLKCEFCGDFSGEAYESHEGMCP					145
Query 955	KMERECSD-CGVNVLENLKNH					1017
	+ C + CG ++ L H					
Sbjct 146	QESVYCENKCGARMRRLAQH					167

Protein alignment of Ir20

protein SGT1 homolog [Ixodes scapularis]

Sequence ID: [XP_029842401.1](#) Length: 337 Number of Matches: 1

Range 1: 1 to 197 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
384 bits(986)	7e-135	Compositional matrix adjust.	185/197(94%)	187/197(94%)	7/197(3%)	+2
Query 203	MAGSLETILSKANSAFVDENYTEALNLYNKALEESPSDAEIYVKRSHAHFRLGNWQASFD					382
	MA SLETILSKANSAFVDENYTEALNLYNKALEESPSDAEIYVKRSHAHFRLGNWQA+FD					
Sbjct 1	MADSLLETILSKANSAFVDENYTEALNLYNKALEESPSDAEIYVKRSHAHFRLGNWQATFD					60
Query 383	DLKAALMHGHQSAKAFLRMGISAFHLGKFQDAKDALEKGRALDSTETQFNEWLDKCGAQL					562
	DLKAALMHGHQSAKAFLRMG+SAFHLGKFQDAKDALEKGRALDSTETQF EWLDKCGAQL					
Sbjct 61	DLKAALMHGHQSAKAFLRMGVSAFHLGKFQDAKDALEKGRALDSTETQFCEWLDKCGAQL					120
Query 563	KTS EDTKQRPAPVPPPSAQSRIRHEWYQTESHVTITILLKNQKAENIE-----IRFKA					721
	KTS EDTKQKQ APVPPPSAQSRIRHEWYQTESHVTITILLKNQKAENIE IRFKA					
Sbjct 121	KTS EDTKQRSAPVPPPSAQSRIRHEWYQTESHVTITILLKNQKAENIETSFTRDTIRFKA					180
Query 722	RLPSGDDYELFLEVAHP 772					
	RLPSGDDYELFLEVAHP					
Sbjct 181	RLPSGDDYELFLEVAHP 197					

small glutamine-rich tetratricopeptide containing protein, isoform B [Drosophila melanogaster]

Sequence ID: [NP_001246058.1](#) Length: 331 Number of Matches: 1

[See 4 more title\(s\)](#) [▼](#) [See all Identical Proteins\(IPG\)](#)

Range 1: 117 to 214 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
66.2 bits(160)	3e-12	Compositional matrix adjust.	32/98(33%)	56/98(57%)	0/98(0%)	+2
Query 218	ETILSKANSAFVDENYTEALNLYNKALEESPSDAEIYVKRSHAHFRLGNWQASFDLCAA					397
	E+I ++ N + Y EAL YN+A+ P + Y R+ AH RLG + + D K+A					
Sbjct 117	ESIKNEGNRLMKENKYNEALLQYNRAIAFDPKNPIFYCNRAAAHIRLGENERAVTDCRSA					176
Query 398	LMHGHQSAKAFLRMGISAFHLGKFQDAKDALEKGRALD 511					
	L++ + +KA+ R+G++ ++G F+ A+ A K L+					
Sbjct 177	LVYNNYSKAYCRLGVAYSNMGNFEKAEQAYAKAIELE 214					

small glutamine-rich tetratricopeptide repeat-containing protein beta [Aedes aegypti]

Sequence ID: [XP_001657084.1](#) Length: 327 Number of Matches: 1

[See 2 more title\(s\)](#) [▼](#) [See all Identical Proteins\(IPG\)](#)

Range 1: 86 to 177 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
59.7 bits(143)	4e-10	Compositional matrix adjust.	30/92(33%)	54/92(58%)	0/92(0%)	+2
Query 218	ETILSKANSAFVDENYTEALNLYNKALEESPSDAEIYVKRSHAHFRLGNWQASFDLCAA					397
	E + ++ N +E Y EALN Y+KA+ ++ Y R+ A+ RLG++QA+ DD + +					
Sbjct 86	ENLKNEGNRLMKEEKYQEALNTYSKAISLDATNPVFCYNRAAAYSRLGDYQAAADDCRMS					145
Query 398	LMHGHQSAKAFLRMGISAFHLGKFQDAKDALE 493					
	L + +KA+ R+G++ + K + A DA +					
Sbjct 146	LRYDPNYSKAYGRLGLAYSKMNKHEQALDAYQ 177					

protein SGT1 homolog isoform A [Homo sapiens]

Sequence ID: [NP_006695.1](#) Length: 333 Number of Matches: 1

[See 3 more title\(s\)](#) [▼](#) [See all Identical Proteins\(IPG\)](#)

Range 1: 21 to 195 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
121 bits(303)	2e-31	Compositional matrix adjust.	63/183(34%)	99/183(54%)	15/183(8%)	+2
Query 245	AFVDENYTEALNLYNKALEESPSDAEIYVKRSHAHFRLGNWQASFDLKAALMHGHQSAK					424
	A +DE+ AL KALE+ P DA+ Y +R++ H LGN+ + D K +L ++					
Sbjct 21	ALIDEDPQAALEELTKALEQKPDDAQYYCQRAYCHILLGNYCVAADAKKSL ELNPNNST					80
Query 425	AFLRMGISAFHLGKFQDAKDALEKGRALDSTETQFNEWLDKCGAQLKTS EDTKQRPAPVP					604
	A LR GI +H + A + +G+ LDS + F+ W+ +C SE					
Sbjct 81	AMLRKGIC EYHEKNYAAALETFTTEGQKLDSADANFSVWIKRCQEAQNGSESEVW-----					134
Query 605	PPSAQSRIRHEWYQTESHVTITILLKNQKAENIEIRFK-----ARLPSGDDYELFLEV					763
	+ QS+I+++WYQTES V IT+++KN + ++ + F +LPSG+DY L LE+					
Sbjct 135	--THQSKI KYD WYQTESQVVITLMIKNVQKNDVNVEFSEKELSALVKLP SGEDYNLKL EL					192
Query 764	AHP 772					
	HP					
Sbjct 193	LHP 195					

Protein alignment of Ir21

E3 ubiquitin-protein ligase TRIM68-like [Ixodes scapularis]

Sequence ID: [XP_029828056.1](#) Length: 508 Number of Matches: 5

Range 1: 203 to 417 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
213 bits(542)	2e-65	Compositional matrix adjust.	119/215(55%)	146/215(67%)	0/215(0%)	+3
Query	132	DRDSWKLKAEDTNHTLESVRNDLGKKTADRDSWKF LA EHATRTLESVRNALRR TK ADRDS				311
Sbjct	203	+RD WKLKAED + TLES+ NDLGK ADRDSWK AE A+R LESVRN L +T ADRDS ERD G WKLKAEDASRTLES LC NDLGKTMADRDSWKLKAEDASRMLESVRNDLGKTMADRDS				262
Query	312	WKLKAEDASRTLRVVRKDLGKKTADRDSWKLKAEDTNHTLESVRNDLGKTTADRDSWKLK				491
Sbjct	263	WKLKAEDA R LK VR DL K TADR D W+LKA+D ++ ++ R+DL + TADR D +WK WKLKAEDAIRMLKSVRNDLAKTTADR DC WELKAKDASNIVKIAR DDL AQMTADR DN WKFT				322
Query	492	AEDTNHTLESVRNDLGKTTADRDSWKF LA EHATRTLESVRNDLGKTTADRDSWKRKAEDA				671
Sbjct	323	A + N LE +R+ L K ADRDSWKF A +R LES+R L + TADRDSWK KA D+ AGNANLNLEGLRDVLAKAAADRDSWKF K AGDTSRKLES SL RESLTQMTADRDSWKYKAGDS				382
Query	672	SNTVKSARNDLAQMKQDKDI*KVTAGVTNFNLDV L 776				
Sbjct	383	++S L + D K+ A N L++L GRMLES L HQSLTEKTAYGDSWKLKADDANR K LEIL 417				

Range 2: 160 to 393 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#) [▲ First Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
206 bits(524)	9e-63	Compositional matrix adjust.	118/234(50%)	153/234(65%)	0/234(0%)	+3
Query	87	NQTSLYKKVGGRP T ADRDSWKLKAEDTNHTLESVRNDLGKKTADRDSWKF LA EHATRTLE				266
Sbjct	160	N + + + K TA + W+ +A + + ++ + N L + +RD WK AE A+RTLE NHSCMLKLRLQET T ASLEK W QQEASERSELVK CL DNTLAEIKLERD G WKLKAEDASRTLE				219
Query	267	SVRNALRR TK ADRDSWKLKAEDASRTLRVVRKDLGKKTADRDSWKLKAEDTNHTLESVRN				446
Sbjct	220	S+ N L +T ADRDSWKLKAEDASR L+ VR DLGK ADRDSWKLKAED L+SVRN SLCNDLGKTMADRDSWKLKAEDASRMLESVRNDLGKTMADRDSWKLKAEDAIRMLKSVRN				279
Query	447	DLGKTTADRDSWKLKAEDTNHTLESVRNDLGKTTADRDSWKF LA EHATRTLESVRNDLGK				626
Sbjct	280	DL KTTADR D W+LKA+D ++ ++ R+DL + TADR D +WKF A +A LE +R+ L K DLAKTTADR DC WELKAKDASNIVKIAR DDL AQMTADR DN WKFTAGNANLNLEGLRDVLAK				339
Query	627	TTADRDSWKRKAEDASNTVKSARNDLAQMKQDKDI*KVTAGVTNFNLDVLLGAL 788				
Sbjct	340	ADRDSWK KA D S ++S R L QM D+D K AG + L+ L +L AAADRDSWKF K AGDTSRKLES SL RESLTQMTADRDSWKYKAGDSGRMLES L HQSL 393				

Range 3: 226 to 429 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#) [▲ First Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
206 bits(523)	1e-62	Compositional matrix adjust.	113/204(55%)	141/204(69%)	0/204(0%)	+3
Query	117	GRPTADRDSWKLKAEDTNHTLESVRNDLGKKTADRDSWKF LA EHATRTLESVRNALRR TK				296
Sbjct	226	G+ ADRDSWKLKAED + LESVRNDLGK ADRDSWK AE A R L+SVRN L +T GKTMADRDSWKLKAEDASRMLESVRNDLGKTMADRDSWKLKAEDAIRMLKSVRNDLAKTT				285
Query	297	ADRDSWKLKAEDASRTLRVVRKDLGKKTADRDSWKLKAEDTNHTLESVRNDLGKTTADR D				476
Sbjct	286	ADR D W+LKA+DAS +K R DL + TADR D +WK A + N LE +R+ L K ADR D ADR DC WELKAKDASNIVKIAR DDL AQMTADR DN WKFTAGNANLNLEGLRDVLAKAAADR D				345
Query	477	SWKLKAEDTNHTLESVRNDLGKTTADRDSWKF LA EHATRTLESVRNDLGKTTADRDSWKR				656
Sbjct	346	SWK KA DT+ LES+R L + TADRDSWK+ A + R LES+ L + TA DSWK SWKF K AGDTSRKLES SL RESLTQMTADRDSWKYKAGDSGRMLES L HQSLTEKTAYGDSWKL				405
Query	657	KAEDASNTVKSARNDLAQMKQDKD 728				
Sbjct	406	KA+DA+ ++ R LA+ ++++ KADDANR K LEILRESLAETTENRE 429				

Range 4: 254 to 495 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#) [▲ First Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
176 bits(446)	3e-51	Compositional matrix adjust.	109/242(45%)	142/242(58%)	21/242(8%)	+3
Query	117	GRPTADRDSWKLKAEDTNHTLESVRNDLGKKTADRDSWKF LA EHATRTLESVRNALRR TK				296
Sbjct	254	G+ ADRDSWKLKAED L+SVRNDL K TADR D W+ A+ A+ ++ R+ L + GKTMADRDSWKLKAEDAIRMLKSVRNDLAKTTADR DC WELKAKDASNIVKIAR DDL AQMT				313
Query	297	ADRDSWKLKAEDASRTLRVVRKDLGKKTADRDSWKLKAEDTNHTLESVRNDLGKTTADR D				476
Sbjct	314	ADR D +WK A +A+ L+ +R L K ADRDSWK KA DT+ LES+R L + TADR D ADR DN WKFTAGNANLNLEGLRDVLAKAAADRDSWKF K AGDTSRKLES SL RESLTQMTADR D				373
Query	477	SWKLKAEDTNHTLESVRNDLGKTTADRDSWKF LA EHATRTLESVRNDLGKT-----				629
Sbjct	374	SWK KA D+ LES+ L + TA DSWK A+ A R LE +R L +T SWKYKAGDSGRMLES L HQSLTEKTAYGDSWKLKADDANR K LEILRESLAETTENRENWKR				433
Query	630	-----TADRDSWKRKAEDASNTVKSARNDLAQMKQDKDI*KVTAGVTNFNLDV				773
Sbjct	434	TADRDSWKRKAEDA +T++S + L + D + K + + N + RALMAIRSQREMTADRDSWKRKAEDAKSTLES LP DSLPRTTADGESWKC S VILENCIAVI				493
Query	774	LL 779				
Sbjct	494	L+ 495				
		LV				

Range 5: 400 to 420 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#) [▲ First Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
42.4 bits(98)	4e-04	Compositional matrix adjust.	20/21(95%)	20/21(95%)	0/21(0%)	+1
Query	808	GDSWKLKAIDANR K LEILRES 870				
Sbjct	400	GDSWKLKA DANR K LEILRES GDSWKLKADDANR K LEILRES 420				

collagen alpha-2(IV) chain-like [Homo sapiens]

Sequence ID: [XP_003959982.2](#) Length: 396 Number of Matches: 3

[See 1 more title\(s\)](#) [See all Identical Proteins\(IPG\)](#)

Range 1: 145 to 316 [GenPept](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
44.7 bits(104)	2e-07	Compositional matrix adjust.	46/172(27%)	62/172(36%)	0/172(0%)	+2
Query	137	RQLEAQGGGHQPHAGKRTQRPWKEDGGQRQLEILSGACHPHAGKRTQRP*KDEGGQRQLE				316
		R L+ +G P PW+E G R LE + P P ++ G R LE				
Sbjct	145	RPLDRRGSVASPGEKGECPVWREGGVWRPLERRASVASPGQKGECPVWREGGVWRPLE				204
Query	317	AQGGGRQPHAEKSTQRPWKEDGGQRQLEAQGGGHQPHAGKRTQRPWKDDGGQRQLEAQGG				496
		+G P + PW+E R LE + P PW++ R LE +G				
Sbjct	205	RRGSVASPGEKGECPVWREGGVWRPLERRASVASPGQKGECPVWREGGVWRPLERRGS				264
Query	497	GHQPHAGKRTQRPWKDDGGQRQLEILSGACHPHAGKRTQRPWKDDGGQRQLE				652
		P PW + G R LE + P PW + G R LE				
Sbjct	265	VASPGEKGECPVWTEGGVWRPLERRASVASPGEKGECPVWTEGGVWRPLE				316

Range 2: 170 to 347 [GenPept](#) [Graphics](#) [Next Match](#) [Previous Match](#) [First Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
41.2 bits(95)	3e-06	Compositional matrix adjust.	46/178(26%)	62/178(34%)	0/178(0%)	+2
Query	128	GGQRQLEAQGGGHQPHAGKRTQRPWKEDGGQRQLEILSGACHPHAGKRTQRP*KDEGGQR				307
		G R LE + P PW+E G R LE P P ++ R				
Sbjct	170	GVWRPLERRASVASPGQKGECPVWREGGVWRPLERRGSVASPGEKGECPVWREGRVWR				229
Query	308	QLEAQGGGRQPHAEKSTQRPWKEDGGQRQLEAQGGGHQPHAGKRTQRPWKDDGGQRQLEA				487
		LE + P + PW+E R LE +G P PW + G R LE				
Sbjct	230	PLERRASVASPGQKGECPVWREGGVWRPLERRGSVASPGEKGECPVWTEGGVWRPLER				289
Query	488	QGGGHQPHAGKRTQRPWKDDGGQRQLEILSGACHPHAGKRTQRPWKDDGGQRQLEAQ				661
		+ P PW + G R LE + P PW++ G R L+ +G				
Sbjct	290	RASVASPGEKGECPVWTEGGVWRPLERRASVASPGEKGECPVWREGGVWRPLDRRG				347

Range 3: 95 to 263 [GenPept](#) [Graphics](#) [Next Match](#) [Previous Match](#) [First Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
38.5 bits(88)	2e-05	Compositional matrix adjust.	44/169(26%)	64/169(37%)	2/169(1%)	+2
Query	161	GHQPHAGKRTQ--RPWKEDGGQRQLEILSGACHPHAGKRTQRP*KDEGGQRQLEAQGGGR				334
		GH AG++ + PW E R LE + P P ++ R L+ +G				
Sbjct	95	GHSEAAAGEKGECPVWTEGGVWRPLERRASVASPGEKGECPVWREGRVWRPLDRRGSA				154
Query	335	QPHAEKSTQRPWKEDGGQRQLEAQGGGHQPHAGKRTQRPWKDDGGQRQLEAQGGGHQPHA				514
		P + PW+E G R LE + P PW++ G R LE +G P				
Sbjct	155	SPGEKGECPVWREGGVWRPLERRASVASPGQKGECPVWREGGVWRPLERRGSVASPGE				214
Query	515	GKRTQRPWKDDGGQRQLEILSGACHPHAGKRTQRPWKDDGGQRQLEAQ				661
		PW++ R LE + P PW++ R LE +G				
Sbjct	215	KGECPVWREGRVWRPLERRASVASPGQKGECPVWREGGVWRPLERRG				263

Protein alignment of Ir22

glutathione S-transferase, putative, partial [Ixodes scapularis]

Sequence ID: [EEC11349.1](#) Length: 197 Number of Matches: 1

Range 1: 60 to 197 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
275 bits(702)	7e-95	Compositional matrix adjust.	134/138(97%)	136/138(98%)	0/138(0%)	+2
Query	107	EEQQRVRDMVEMQAFDIIMYCVRVCYDPEYTD	DKRRQFLTEV	APDKLKQFVT	FLAKAGPF	286
Sbjct	60	EEQQRVRDMVEMQAFD+IMYCVRVCYDPEYT+DKRRQFLTEV	APDKLKQFVT	FLAKAGPF		119
Query	287	VAGDKVTYADFILYEALQVVRAMGPSSFKNYPELEKYCARVAALPGLREYLASPRFKAWP				466
Sbjct	120	VAGDKVTYADFILYEALQVVRAMGPSSFKNYPELEKYCARVAALPGLREYLASPRFKAWP				179
Query	467	FWSPFAKALAVQHQPFTD	520			
Sbjct	180	FWSPFAKALAVHQPFTD	197			

glutathione S-transferase 1-1 [Aedes aegypti]

Sequence ID: [XP_001654674.2](#) Length: 222 Number of Matches: 1

Range 1: 137 to 190 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
35.8 bits(81)	0.016	Compositional matrix adjust.	15/54(28%)	29/54(53%)	0/54(0%)	+2
Query	251	QFVTFLAKAGPFFVAGDKVTYADFILYEALQVVRAMGPSSFKNYPELEKYCARVA				412
Sbjct	137	EFLEVYLGKTTYVAGDKLTVADFCILATITTMKVAAEIDFSKYP	SIERWYAQLS			190

glutathione S-transferase Mu 1 isoform X1 [Homo sapiens]

Sequence ID: [XP_005270839.1](#) Length: 184 Number of Matches: 1

Range 1: 57 to 179 [GenPept](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
80.9 bits(198)	3e-22	Compositional matrix adjust.	44/126(35%)	70/126(55%)	3/126(2%)	+2
Query	107	EEQQRVRDMVEMQAFDIIMYCVRVCYDPEYTD	DKRRQFLTEVAPDKLKQFVTFLAKAGPF			286
Sbjct	57	EE++ RVD++E Q D M +CY+PE+ +K + E P+KLK + FL K P+	EEKIRVDILENTQMDNMHQLGMICYNPEF--EKLKPKYIEELPEKLKLYSEFLGRR-PW			113
Query	287	VAGDKVTYADFILYEALQVVRAMGPSSFKNYPELEKYCARVAALPGLREYLASPRFKAWP				466
Sbjct	114	AG+K+T+ DF++Y+ L + R P +P L+ + +R L + Y+ S RF P	FAGNKITFVDFLVYDVLDLHRIFEKPKCLDAFPNLKDFISRFEGLEKISAYMKSSRFLPRP			173
Query	467	FWSPFA 484				
		+S A				
Sbjct	174	VFSKMA 179				