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T.t Factor C used for database
query was derived from NCBI nucleotide
sequence Accession: D90271

BLAST® » **tblastn-SRA** » results for RID-J1VCKEWG016

Important update
The **ClusteredNR** database is now the **default** Protein BLAST database. [Learn more about ClusteredNR](#)

Job Title [Protein Sequence...](#)
RID [J1VCKEWG016](#) Search expires on 11-23 05:54 am
Program TBLASTN
Database SRA
Query ID Id|Query_4248615
Description [unnamed_protein_product...](#)
Molecule type amino acid
Query Length 1020

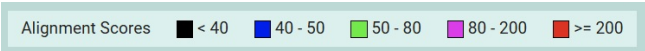
Descriptions

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
▼	▼	▼	▼	▼	▼	▼	
SRX202160	280	280	14%	8e-88	88.36%	450	SRA:SRR610305.479185.2
SRX202160	270	270	14%	5e-84	88.89%	465	SRA:SRR610305.232327.2
SRX202160	264	264	14%	8e-82	88.81%	478	SRA:SRR610305.180089.2
SRX202160	258	258	15%	2e-79	84.71%	515	SRA:SRR610305.301708.2
SRX202160	253	310	18%	3e-78	88.06%	433	SRA:SRR610305.137101.2
SRX202160	241	241	13%	1e-73	83.82%	465	SRA:SRR610305.122589.2
SRX202160	238	238	12%	8e-73	92.56%	382	SRA:SRR610305.60037.2
SRX202160	236	347	21%	4e-72	85.27%	467	SRA:SRR610305.120947.2
SRX202160	236	236	12%	9e-72	93.70%	499	SRA:SRR610305.155304.2
SRX202160	233	283	14%	1e-70	92.62%	472	SRA:SRR610305.132002.2
SRX202160	226	283	19%	2e-68	86.18%	388	SRA:SRR610305.92503.2
SRX202160	225	225	14%	8e-68	79.72%	464	SRA:SRR610305.169430.2
SRX202160	214	214	11%	5e-64	90.18%	367	SRA:SRR610305.189719.2
SRX202160	215	215	14%	5e-64	79.29%	469	SRA:SRR610305.210950.2
SRX202160	211	211	11%	2e-62	91.45%	522	SRA:SRR610305.194753.2
SRX202160	162	276	13%	6e-62	91.46%	460	SRA:SRR610305.133258.2
SRX202160	207	244	18%	2e-61	79.85%	404	SRA:SRR610305.183291.2
SRX202160	203	203	11%	8e-60	86.11%	450	SRA:SRR610305.279849.2
SRX202160	195	195	11%	2e-57	90.00%	395	SRA:SRR610305.195808.2
SRX202160	181	240	16%	3e-57	68.91%	496	SRA:SRR610305.192653.2
SRX202160	194	194	14%	8e-57	62.94%	457	SRA:SRR610305.282736.2
SRX202160	193	193	10%	2e-56	91.09%	469	SRA:SRR610305.159223.2
SRX202160	193	193	14%	3e-56	60.96%	462	SRA:SRR610305.244020.2

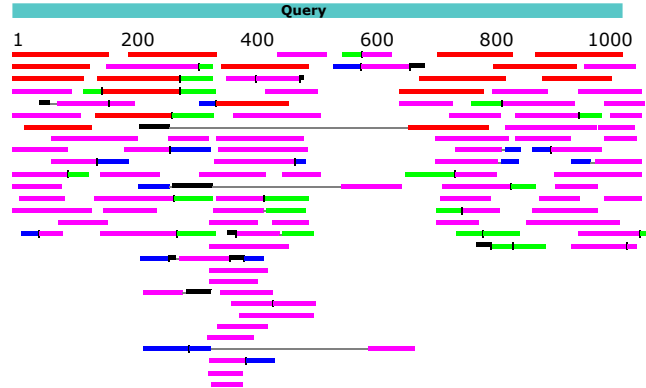
Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
SRX202160	178	233	13%	5e-55	82.18%	415	SRA:SRR610305.152419.2
SRX202160	188	188	14%	1e-54	60.99%	430	SRA:SRR610305.124202.2
SRX202160	186	186	11%	4e-54	70.09%	400	SRA:SRR610305.150040.2
SRX202160	184	240	17%	6e-53	55.41%	492	SRA:SRR610305.381659.2
SRX202160	123	246	12%	1e-52	81.94%	363	SRA:SRR610305.271769.2
SRX202160	174	243	15%	2e-49	60.51%	448	SRA:SRR610305.232653.2
SRX202160	169	169	8%	6e-49	94.05%	255	SRA:SRR610305.330331.2
SRX202160	171	171	9%	7e-49	91.67%	370	SRA:SRR610305.71990.2
SRX202160	169	212	14%	9e-49	58.78%	451	SRA:SRR610305.716947.2
SRX202160	169	169	11%	9e-48	68.81%	476	SRA:SRR610305.213439.2
SRX202160	122	248	14%	2e-47	78.38%	346	SRA:SRR610305.307671.2
SRX202160	164	164	8%	4e-47	91.25%	241	SRA:SRR610305.117350.2
SRX202160	163	246	21%	1e-46	78.79%	315	SRA:SRR610305.263645.2
SRX202160	125	202	14%	5e-46	73.33%	456	SRA:SRR610305.296844.2
SRX202160	130	202	14%	8e-46	70.37%	456	SRA:SRR610305.133991.2
SRX202160	162	162	8%	2e-45	90.80%	449	SRA:SRR610305.147146.2
SRX202160	154	201	9%	2e-45	95.95%	353	SRA:SRR610305.302701.2
SRX202160	161	161	9%	5e-45	92.22%	483	SRA:SRR610305.161135.2
SRX202160	157	157	7%	1e-44	97.37%	228	SRA:SRR610305.116683.2
SRX202160	149	238	12%	6e-44	92.96%	374	SRA:SRR610305.255423.2
SRX202160	145	193	12%	4e-43	62.75%	491	SRA:SRR610305.82426.2
SRX202160	154	211	18%	4e-43	59.02%	369	SRA:SRR610305.176373.2
SRX202160	154	154	14%	1e-42	52.41%	447	SRA:SRR610305.499919.2
SRX202160	151	151	9%	2e-42	79.78%	269	SRA:SRR610305.87460.2
SRX202160	154	228	12%	2e-42	90.91%	450	SRA:SRR610305.209724.2
SRX202160	139	191	14%	2e-42	95.71%	433	SRA:SRR610305.587240.2
SRX202160	154	225	15%	2e-42	64.55%	460	SRA:SRR610305.193065.2
SRX202160	151	151	13%	6e-42	54.55%	406	SRA:SRR610305.271268.2
SRX202160	152	268	19%	1e-41	56.25%	484	SRA:SRR610305.209629.2
SRX202160	117	266	18%	6e-40	60.00%	441	SRA:SRR610305.244830.2
SRX202160	136	178	10%	1e-38	77.78%	360	SRA:SRR610305.736053.2
SRX202160	139	139	8%	3e-38	80.49%	298	SRA:SRR610305.350008.2
SRX202160	135	135	9%	8e-37	65.26%	306	SRA:SRR610305.393793.2
SRX202160	101	191	13%	2e-36	66.20%	433	SRA:SRR610305.189814.2
SRX202160	122	170	10%	4e-36	78.38%	410	SRA:SRR610305.232597.2
SRX202160	135	258	14%	5e-36	87.50%	468	SRA:SRR610305.204499.2
SRX202160	134	134	8%	1e-35	68.27%	449	SRA:SRR610305.213632.2
SRX202160	132	132	7%	1e-35	84.51%	344	SRA:SRR610305.767547.2
SRX202160	130	130	6%	7e-35	95.31%	280	SRA:SRR610305.83961.2
SRX202160	129	129	8%	7e-35	72.73%	258	SRA:SRR610305.716410.2
SRX202160	128	128	8%	2e-34	70.59%	261	SRA:SRR610305.326762.2
SRX202160	127	166	10%	2e-34	95.08%	199	SRA:SRR610305.63226.2
SRX202160	82.4	162	13%	6e-34	48.68%	412	SRA:SRR610305.585142.2
SRX202160	128	128	12%	9e-34	50.41%	398	SRA:SRR610305.144057.2
SRX202160	126	126	8%	2e-33	71.25%	316	SRA:SRR610305.637738.2
SRX202160	127	127	13%	6e-33	45.77%	465	SRA:SRR610305.244045.2
SRX202160	124	124	6%	8e-33	87.30%	327	SRA:SRR610305.272757.2

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
SRX202160	126	126	6%	1e-32	95.16%	485	SRA:SRR610305.133655.2
SRX202160	125	125	6%	2e-32	92.18%	453	SRA:SRR610305.231346.2
SRX202160	123	123	8%	2e-32	70.37%	320	SRA:SRR610305.691564.2
SRX202160	122	122	7%	3e-32	72.60%	274	SRA:SRR610305.406882.2
SRX202160	102	153	10%	3e-31	69.23%	344	SRA:SRR610305.677355.2
SRX202160	120	209	17%	7e-31	79.17%	442	SRA:SRR610305.49279.2
SRX202160	119	119	10%	1e-30	57.73%	400	SRA:SRR610305.180913.2
SRX202160	116	193	14%	2e-30	53.12%	434	SRA:SRR610305.219525.2
SRX202160	117	117	8%	2e-30	70.59%	271	SRA:SRR610305.33690.2
SRX202160	115	167	7%	6e-30	86.44%	245	SRA:SRR610305.624115.2
SRX202160	117	117	6%	9e-30	90.00%	414	SRA:SRR610305.246371.2
SRX202160	113	113	6%	2e-29	94.83%	175	SRA:SRR610305.15666.2
SRX202160	113	113	7%	6e-29	77.94%	312	SRA:SRR610305.496280.2
SRX202160	112	112	9%	7e-29	57.30%	276	SRA:SRR610305.417286.2
SRX202160	113	113	9%	2e-28	57.30%	401	SRA:SRR610305.76737.2
SRX202160	98.6	142	10%	5e-28	73.68%	308	SRA:SRR610305.482048.2
SRX202160	106	106	10%	2e-26	56.07%	335	SRA:SRR610305.304253.2
SRX202160	106	106	5%	4e-26	94.23%	373	SRA:SRR610305.279398.2
SRX202160	104	104	8%	8e-26	62.03%	323	SRA:SRR610305.650681.2
SRX202160	102	102	7%	3e-25	64.29%	256	SRA:SRR610305.627443.2
SRX202160	101	101	6%	9e-25	81.67%	317	SRA:SRR610305.193684.2
SRX202160	79.3	130	10%	3e-24	94.74%	515	SRA:SRR610305.303934.2
SRX202160	98.2	98.2	5%	4e-24	93.75%	190	SRA:SRR610305.379792.2
SRX202160	66.2	166	10%	5e-24	59.57%	321	SRA:SRR610305.308767.2
SRX202160	88.6	129	6%	5e-24	92.68%	316	SRA:SRR610305.637237.2
SRX202160	97.1	97.1	5%	1e-23	77.36%	163	SRA:SRR610305.518233.2
SRX202160	98.2	98.2	15%	6e-23	33.55%	442	SRA:SRR610305.744412.2
SRX202160	96.3	164	10%	7e-23	50.00%	336	SRA:SRR610305.602632.2
SRX202160	90.9	90.9	5%	1e-21	81.25%	173	SRA:SRR610305.507110.2
SRX202160	92.8	175	10%	1e-21	55.21%	344	SRA:SRR610305.243725.2

Graphic Summary



Distribution of the top 156 Blast Hits on 100 subject sequences



Alignments

Alignment view

Pairwise

☐ CDS feature

Restore defaults

SRX202160
Sequence ID: **SRA:SRR610305.479185.2** Length: 450 Number of Matches: 1
Range 1: 13 to 450

Score	Expect	Method	Identities	Positives	Gaps	Frame
280 bits(715) 8e-88() Compositional matrix adjust. 129/146(88%) 141/146(96%) 0/146(0%) +1						
Query 190	SFP	PKCIRECAKVS	PEHGKVNAPSGNMIEGATLRFSCDSPYYLIGQETLTCQNGQW	SG	249	
Sbjct 13	AH	PKCIRECSMVSS	LEHGKVN	SPSADLIEGATLRFSCDSPYYLIGQETLTCQNGQW	SG	192
Query 250	QIP	QCKKLVFC	PDLPVNHAHQVKIGVEQKYGFPPQGT	TEVYTCSGNYFLMGFNTL	KCN	309
Sbjct 193	QIP	QCKKLVFC	PDLPVSHAHQVKIGLEQKYGFPPQGT	TEVYTCTGNYFLMGLDTL	KCN	372
Query 310	PD	GSWSGSPSCVKV	ADREVD	CDSKA	335	
Sbjct 373	PD	GSWSGTQPS	CVKVADREVN	CDSKA	450	

SRX202160
Sequence ID: **SRA:SRR610305.232327.2** Length: 465 Number of Matches: 1
Range 1: 31 to 462

Score	Expect	Method	Identities	Positives	Gaps	Frame
270 bits(689) 5e-84() Compositional matrix adjust. 128/144(89%) 138/144(95%) 0/144(0%) -1						
Query	849	LEIHVNPNPYDPGNLNF	DIALIQLKTPVLTTRVQ	PICLPDITTREHLKEGT	LAVVTGWG	908
Sbjct	462	LEIHVNPNPYDPGNLNF	DIALIQLKT V LTRVQ	PIC PTD+TTRE+LKEG	LAVVTGWG	
		LEIHVNPNPYDPGNLNF	DIALIQLKTSVAL TTRVQ	PICPPTDLTTRENLK	EGALAVVTGWG	283
Query	909	LNENNTYSEMIQ	QAVLPVVAASTCEE	GYKEADLPLTVTENM	FCAGYKKGRYD	ACSGD
Sbjct	282	LNENNTYSEMIQ	QAVLPVVAASTCEE	GY+++LPLTVTENM	FCAGYKGRYD	ACSGD
		LNENNTYSEMIQ	QAVLPVVAASTCEE	GYDGLPLTVTENM	FCAGYKGRYD	ACSGD
Query	969	PLVFADDSRT+RRW	LEGIVS	WG		
Sbjct	102	PLVFADDSRT+RRW	LEGIVS	WG		
		PLVFADDSRTDRRW	LEGIVS	*GT		

SRX202160
Sequence ID: **SRA:SRR610305.180089.2** Length: 478 Number of Matches: 1
Range 1: 1 to 426

Score	Expect	Method		Identities	Positives	Gaps	Frame
264 bits(674) 8e-82() Compositional matrix adjust. 127/143(89%) 133/143(93%) 1/143(0%) +1							
Query	337	DFLDDVGE	PVRIHCPAGCSLTAGTVMGTAIYHELSSVCRAAIHAGKLPNSGGAVHVVNG				396
Sbjct	1	DFLDDVGE	VRIHCPAGCSLTAGTVMGTAIYHELSSVCRAAIHAGKLPNSGGAVHVVNG				180
Query	397	PYSDFL	GSDLNGIKSEELKSLARSFRFDYVSSSTAGRSGCPD	GWFEVEENCYVVT	SKQRA		456
Sbjct	181	PYSDFL	GSDLNGIKSEELKSLARSFRFDYVSSSTAGRSGCPD	GWFEVEENCYVVT	SKQRA		357
Query	457	WE	RAQGVCTNMAARLAVL	DKDLI			
Sbjct	358	WE	RAQGVCTNMAARLAVL	DKDVI			

SRX202160
Sequence ID: **SRA:SRR610305.301708.2** Length: 515 Number of Matches: 1
Range 1: 58 to 513

Score	Expect	Method	Identities	Positives	Gaps	Frame
258 bits(658) 2e-79() Compositional matrix adjust. 133/157(85%) 142/157(90%) 5/157(3%) -3						

Query 2 VLASFLVSLVLGLLAQQMRPVQSRGVDLGLCDETRFECKCGDPGYVFNVPKQCTYFYR 61
Sbjct 513 VLASFLVSLVLGLLAQQMRPVQSRGVDLGLCDDTRFECKCGDPGYXFNVPAKQCTYFYR 334

Query 62 WRPYCKPCDDLEAKDICPKYKRCQECKAGLDSCVTCPPNKYGTWCSGECQCKNGGICDQR 121
Sbjct 333 WRPYCKPCD LEAKD+CPKYKRCQEC+AGLDSCV+CPPNKYGTWCSGECQCKNGGICDQR 154

Query 122 TGACTCRDRYEGAHCEILKGCPLLPDSQVQEVNRNP 158
Sbjct 153 TGACTCRDRYEGHCEILQR--FVPTYLQ---IRNTP 58

SRX202160
Sequence ID: **SRA:SRR610305.137101.2** Length: 433 Number of Matches: 2
Range 1: 30 to 431

Score	Expect	Method	Identities	Positives	Gaps	Frame
253 bits(647) 3e-78() Compositional matrix adjust. 118/134(88%) 129/134(96%) 0/134(0%) +3						
Query	138	ILKGCPLLPDSQVQEVNRNPPNDPQTIDYSCSPGFKLKGVARISCLPNGQWSSFPKICIR	197			
Sbjct	30	IL+GCPLL SD QVQEV+NPP++PQTIDYSCSPGFKLKGVARITCLPNGQWSSFPKICIR	209			
Query	198	ECAKVSSPEHGKVNAPSGNMIEGATLRFSCDSPYYLIGQETLTCQNGQWSGQIPQCKKL	257			
Sbjct	210	EC+ VSS EHGKVN+PS ++IEGATLRFSCDSPYYLIGQETLTCQNGQWSGQIPQC+KL	389			
Query	258	ECSMVSSLEHGKVNPSADLIEGATLRFSCDSPYYLIGQETLTCQNGQWSGQIPQCKKL				
Sbjct	390	VFCPDLDPVNHAEH 271 VFCPDLDPV+HAEH 431 VFCPDLDPVSHAHH 431				

Range 2: 57 to 392

Score	Expect	Method	Identities	Positives	Gaps	Frame
57.0 bits(136) 1e-08() Compositional matrix adjust. 36/123(29%) 56/123(45%) 11/123(8%) +3						
Query	203	SSPEHGKVNAPSGNMIEGATLRFSCDSPYYLIGQETLTCQNGQWSGQIPQCKKL	VFCPD	262		
Sbjct	57	SDPQVQEVKNPPN---DPQTIDYSCSPGFKLKGVARITCLPNGQWSSFPKICIRE--CSM		221		
Query	263	LDPVNHAEHQVKIGVEQKYGFPGTEVTYTCSGNYFLMGFNTLKCNDPGSWSGSQPSCV		322		
Sbjct	222	+ + H + V +G + ++C Y+L+G TL C +G WSG P C		383		
Query	323	VSSLEHGK-----VNSPSADLIEGATLRFSCDSPYYLIGQETLTCQNGQWSGQIPQCK				
Sbjct	384	KVA 325 K+ 392 KLV 392				

SRX202160
Sequence ID: **SRA:SRR610305.122589.2** Length: 465 Number of Matches: 1
Range 1: 39 to 446

Score	Expect	Method	Identities	Positives	Gaps	Frame
241 bits(616) 1e-73() Compositional matrix adjust. 124/136(91%) 132/136(97%) 0/136(0%) +3						
Query	777	QAGISRWLADHNMWFLQCGGSLLEKWIIVTAACHVTYSATAEIIDPSQFKIYLGKyyrdd				836
Sbjct	39	++GISRWLADHNMWFLQCGG+LLNEKWI+TAACHVTYSATAEIIDPSQFK YLGKYRDD				218
Query	837	RSGISRWLADHNMWFLQCGGALLNEKWIITAACHVTYSATAEIIDPSQFKFYLGKYRDD				
Sbjct	219	srdddyVQVREAEIHHVNPNDPGNLFNFDIALIQLKTPVTLTTRVOPICLPTDITTREHL				896
		S+DDDYVQVREA+EIHHVNPNDPGNLFNFDIALIQLKT V LTTTRVOPICLPTD+TTRE+L				
Query	897	SKDDDYVQVREAEIHHVNPNDPGNLFNFDIALIQLKTSVALTTRVOPICLPTDLTTREN				398
Sbjct	399	KEGT LAVVTGWGLNEN 912				
		KEG LAVVTGWGLNEN				
		KEGALAVVTGWGLNEN 446				

SRX202160
Sequence ID: **SRA:SRR610305.60037.2** Length: 382 Number of Matches: 1
Range 1: 19 to 381

Score	Expect	Method	Identities	Positives	Gaps	Frame
238 bits(607) 8e-73() Compositional matrix adjust. 112/121(93%) 117/121(96%) 0/121(0%) +1						
Query	691	SSQPSTVDLASKVKLPEGHYRVGSRAIYTCESRYELLGSGQRRCDNSNGNWSGRPASCIP				750
Sbjct	19	S+ PSTVDL+SKVKLPEG YRVGS+AIYTCESRYELLGSGQRRCDNSNG WSGRPASCIP				198
Query	751	VCGRSDSPRSPFIWNGNSTEIGQWPWQAGISRWLADHNMWFLQCGGSLLEKWIIVTAAHC				810
Sbjct	199	VCGRSDSPRSPFI NGNSTEIGQWPWQAGISRWLADHNMWFLQCGG+LLNEKWI+TAAHC				378
Query	811	V 811				
Sbjct	379	V 381				

SRX202160
Sequence ID: **SRA:SRR610305.120947.2** Length: 467 Number of Matches: 3
Range 1: 3 to 389

Score	Expect	Method	Identities	Positives	Gaps	Frame
236 bits(603) 4e-72(2) Compositional matrix adjust. 110/129(85%) 123/129(95%) 0/129(0%) -1						
Query	139	LKGCPLLPSDSQVQEVNRNPPDNPTIDYSCSPGFKLKGVARISCLPNGQWSSFPPKCIRE				198
Sbjct	389	L+GC LL SD QVQEV+NPP+++PTIDYSCSPGFKLKG+ARI+CLPNGQWSSFPPKCIRE				210
Query	199	CAKVSPEHGKVNAPSGNMIEGATLRFSCDSPYYLIGQETLTCQNGQWSGQIPQCKKLV				258
Sbjct	209	C+ VSS EHGK+N+PS ++IEGATLRFSCDSPYYLIGQETLTCQNGQWSGQIPQC+KLV				30
Query	259	FCPDLDPVN 267				
Sbjct	29	FCPDLDPV+ 3				

Range 2: 383 to 457

Score	Expect	Method	Identities	Positives	Gaps	Frame
53.5 bits(127) 4e-72(2) Composition-based stats. 22/25(88%) 22/25(88%) 0/25(0%) -2						
Query	116	GICDQRTGACTCRDRYEGAHCEILK 140				
Sbjct	457	GICD RTGACTCRDRYEG HCEI K 383				

Range 3: 30 to 365

Score	Expect	Method	Identities	Positives	Gaps	Frame
57.4 bits(137) 9e-09() Compositional matrix adjust. 36/123(29%) 56/123(45%) 11/123(8%) -1						
Query	203	SSPEHGKVNAPSGNMIEGATLRFSCDSPYYLIGQETLTCQNGQWSGQIPQCKLVFCPD				262
Sbjct	365	S P+ +V P + T+ +SC + L G +TC NGQWS P+C + +				210
Query	263	SDPQVQEVKNPPN---DPQIDYSCSPGFKLKGMARITCLPNGQWSSFPPKCIR-----E				
Query	263	LDPVNHAEHQVIGVEQKYGFQGTETVYTCSGNYFLMGFNTLKCNDGSGWSGQSPSCV				322
Sbjct	209	V+ EH +G + +C Y+L+G TL C +G WSG P C				39
Query	323	CSMVSSLEHG---KINSPSADLIEGATLRFSCDSPYYLIGQETLTCQNGQWSGQIPQCQ				
Sbjct	38	KVA 325				
		K+ 30				

SRX202160
Sequence ID: **SRA:SRR610305.155304.2** Length: 499 Number of Matches: 1
Range 1: 1 to 381

Score	Expect	Method	Identities	Positives	Gaps	Frame
236 bits(603) 9e-72() Compositional matrix adjust. 119/127(94%) 124/127(97%) 0/127(0%) -2						
Query	1	MVLASFVLSGLVLGILAQQMRPVQSRGVLDGLCD+TRFECKCGDPGYVFNVPKQCTYFY				60
		MVLASFVLSGLVLG+LAQQM PVQSRGVLDGLCD+TRFECKCGDPGYVFNVP KQCTYFY				

Sbjct 381 MVLASFVSLVGLLGLLAQQMHPVQSRGVDLGLCDDTRFECKCGDPGYVFNPAKQCTYFY 202
Query 61 RWRPYCKPCDDLEAKDICPKYKRCQECKAGLDSCVTCPPNKYGTWCSGECQCKNGGICDQ 120
Sbjct 201 RWRPYCKPCD LEAKD+CPKYKRCQEC+AGLDSCV+CPPNKYGTWCSGECQCKNGGICDQ 22
Query 121 RTGACTC 127
Sbjct 21 RTGACTC 1

SRX202160
Sequence ID: **SRA:SRR610305.132002.2** Length: 472 Number of Matches: 2
Range 1: 107 to 472

Score	Expect	Method	Identities	Positives	Gaps	Frame
233 bits(595)	1e-70()	Compositional matrix adjust.	113/122(93%)	120/122(98%)	1/122(0%)	+2
Query 322	VKVADREVDCSKAVDFLDDVGEPVRIHCPAGCSL	TAGTVWGTAIYHELSSVCRAAIHAG	381			
Sbjct 107	LKVADREVNCDSKAVDFLDDVGEPVKIHCPAGCSL	TAGTVWGTAIYHELSSVCRAAIHAG	286			
Query 382	KLPNSGGAVHVVNNGPYSDFLGSDLNGIKSEELKSLARSFRFDYVSSSTA	-GRSGCPDGM	440			
Sbjct 287	KVPNSGGAVHVVNNGPYSDFLASDLNGIKSDELKSLAQSFYVSSSTAGGKSGCPDGM		466			
Query 441	FE	442				
Sbjct 467	FE	472				

Range 2: 40 to 111

Score	Expect	Method	Identities	Positives	Gaps	Frame
49.7 bits(117)	5e-06()	Compositional matrix adjust.	21/24(88%)	23/24(95%)	0/24(0%)	+1
Query 300	LMGFNTLKCNDGWSGSPSCVK	323				
Sbjct 40	LMGLDTLKCNDGWSGTQPSVK	111				

SRX202160
Sequence ID: **SRA:SRR610305.92503.2** Length: 388 Number of Matches: 2
Range 1: 2 to 370

Score	Expect	Method	Identities	Positives	Gaps	Frame
226 bits(575)	2e-68()	Compositional matrix adjust.	106/123(86%)	117/123(95%)	0/123(0%)	-1
Query 136	CEILKGCPLLPSDSQVQEVNPPDPQTIDYSCSPGFKLKGVARISCLPNGQWSSFPPKC	195				
Sbjct 370	CEIL+GCPLL SD QVQEV+NPP++PQTIDYSCSPGFKLKG+ARI+CLPNGQWSSFPPKC	191				
Query 196	IRECAKVSSPEHGKVNAPSGNMIEGATLRFSCDSPYYLIGQETLTCQNGQWSGQIPQCK	255				
Sbjct 190	IREC+ VSS EHGKVN+PS ++IEGA LRFSCDSPYYLIGQETLTCQNGQWSGQIPQC+	11				
Query 256	KLV	258				
Sbjct 10	KLV	2				

Range 2: 2 to 337

Score	Expect	Method	Identities	Positives	Gaps	Frame
57.4 bits(137)	6e-09()	Compositional matrix adjust.	37/123(30%)	56/123(45%)	11/123(8%)	-1
Query 203	SSPEHGKVNAPSGNMIEGATLRFSCDSPYYLIGQETLTCQNGQWSGQIPQCKLVFCPD	262				
Sbjct 337	SDPVQVQEVKNPPN---DPQTIDYSCSPGFKLKGMARITCLPNGQWSSFPPKCIR-----E	182				
Query 263	LDPVNHAHQVIGVEQKYGFQGTETVYTCSGNYFLMGFNTLKCNDGWSGSPSCV	322				
Sbjct 181	CSMVSSLEHG---KVNSPSADLIEGAILRFSCDSPYYLIGQETLTCQNGQWSGQIPQCQ	11				
Query 323	KVA	325				

Sbjct 10 KLV 2

SRX202160
Sequence ID: **SRA:SRR610305.169430.2** Length: 464 Number of Matches: 1
Range 1: 1 to 429

Score	Expect	Method	Identities	Positives	Gaps	Frame
225 bits(574)	8e-68()	Compositional matrix adjust.	134/143(94%)	138/143(96%)	0/143(0%)	+1
Query 655	PPSRTNSISRVGSPFLr1pr1plplaraakpppkprSSQPSTVDLASKVKLPEGHYRVGS					714
Sbjct 1	PPSRTNSISRVGSPFLRLPLPLPLARAA PPPKPRS+ PSTVDL+SKVKLPEGHYRVG					180
Query 715	RAIYTCESRYEYELLSQGRRCDSNGNWSGRPASCIPVCGRSDSPRSPFIWNGNSTEIGQW					774
Sbjct 181	+AIYTCESRYEYELLSQGRRCDSNG WSGRPASCIPVCGRSDSPRSPFI NGNSTEIGQW					360
Query 775	PWQAGISRWLADHNMMWFLQCGGS 797					
Sbjct 361	PWQAGISRWLADHNMMWFLQCGGA 429					

SRX202160
Sequence ID: **SRA:SRR610305.189719.2** Length: 367 Number of Matches: 1
Range 1: 32 to 367

Score	Expect	Method	Identities	Positives	Gaps	Frame
214 bits(544)	5e-64()	Compositional matrix adjust.	101/112(90%)	108/112(96%)	0/112(0%)	+2
Query 857	YDPGNLNFIDIALIQKTPVTLTTRVQPTICLPTDITTREHLKEGT LAVVTGWGLNENNTYS					916
Sbjct 32	YDPGNLNFIDIALIQKT V LTTRVQPTICLPTD+TTRE+LKEG LAVVTGWGLNENNTYS					211
Query 917	EMIQQAVLPVVAASTCEEYKADLPLTVTENMFCAGYKKGRYDACSGDSGG 968					
Sbjct 212	EMIQQAVLPVVAASTCE+GY+++ LPLTVTENMFCAGYK+GRYDACSGDSGG					367

SRX202160
Sequence ID: **SRA:SRR610305.210950.2** Length: 469 Number of Matches: 1
Range 1: 10 to 429

Score	Expect	Method	Identities	Positives	Gaps	Frame
215 bits(547)	5e-64()	Compositional matrix adjust.	131/140(94%)	135/140(96%)	0/140(0%)	+1
Query 627	WSAPKPRCIKVITCONPPVPSYGSVEIKPPSRTNSISRVGSPFLr1pr1plplaraakpp					686
Sbjct 10	WSAPKPRCIKVITCQ PPVPSYGSV+IKPPSRTNSISRVGSPFLRLPLPLARAA PP					189
Query 687	pkprSSQPSTVDLASKVKLPEGHYRVGSRAIYTCESRYEYELLSQGRRCDSNGNWSGRPA					746
Sbjct 190	PKPRS+ PSTVDL+SKVKLPEGHYRVGS+AIYTCESRYEYELLSQGRRCDSNG WSGRPA					369
Query 747	SCIPVCGRSDSPRSPFIWNG 766					
Sbjct 370	SCIPVCGRSDSPRSPFI NG 429					

SRX202160
Sequence ID: **SRA:SRR610305.194753.2** Length: 522 Number of Matches: 1
Range 1: 29 to 379

Score	Expect	Method	Identities	Positives	Gaps	Frame
211 bits(537)	2e-62()	Compositional matrix adjust.	107/117(91%)	113/117(96%)	0/117(0%)	-3
Query 1	MVLASFLVSGVLGLAQQMHPVQSRGVDLGLCD+TRFECKCGDPGYVFNPMKQCTYFY					60
Sbjct 379	MVLASFLVSGVLGL+LAQQM PVQSRGVDLGLCD+TRFECKCGDPGYVFNVP KQCTYF					200
Query 61	RWRPYCKPCDDLKADICPKYKRCQECKAGLDSCVTCPPNKYGTWCSGECQCKNGGI					117

Sbjct 199 RWRPYCKPCD LEAKD+CP+YKRCQEC+AGLDSCV+CPPNKYGTWCSGECQCKNGGI
RWRPYCKPCDKLEAKDVCPEYKRCQECRAGLDSCVSCPPNKYGTWCSGECQCKNGGI 29

SRX202160
Sequence ID: **SRA:SRR610305.133258.2** Length: 460 Number of Matches: 3
Range 1: 92 to 337

Score	Expect	Method	Identities	Positives	Gaps	Frame
162 bits(411)	6e-62(3)	Compositional matrix adjust.	75/82(91%)	79/82(96%)	0/82(0%)	+2
Query 72	LEAKDICPKYKRCQECKAGLDSCVTCPPNKYGTWCSGECQCKNGGICDQRTGACTCRDRY					131
Sbjct 92	LEAKD+CPKYKRCQEC+AGLDSCV+CPPNKYGTWCSGECQCKNGGICDQRTGACTCRDRY					271
Query 132	EGAHCEILKGCPLLPDSQVQE		153			
Sbjct 272	EG HCEIL+GCPLL SD QVQE		337			

Range 2: 337 to 459

Score	Expect	Method	Identities	Positives	Gaps	Frame
80.5 bits(197)	6e-62(3)	Compositional matrix adjust.	35/41(85%)	40/41(97%)	0/41(0%)	+1
Query 154	VRNPPDNPQTIDYSCSPGFKLKGVARISCLPNGQWSSFPFK		194			
Sbjct 337	V+NPP++PQTIDYSCSPGFKLKG+ARI+CLPNGQWSS PPK		459			

Range 3: 1 to 42

Score	Expect	Method	Identities	Positives	Gaps	Frame
33.5 bits(75)	6e-62(3)	Composition-based stats.	13/14(93%)	13/14(92%)	0/14(0%)	+1
Query 46	GYVFNVPKQCTYF		59			
Sbjct 1	GYVFNVP KQCTYF		42			

SRX202160
Sequence ID: **SRA:SRR610305.183291.2** Length: 404 Number of Matches: 2
Range 1: 1 to 402

Score	Expect	Method	Identities	Positives	Gaps	Frame
207 bits(526)	2e-61()	Compositional matrix adjust.	127/134(95%)	130/134(97%)	0/134(0%)	+1
Query 653	IKPPSRNTSISRVGSPFLrlrlplplaraakppkprSSQPSTVDLASKVKLPEGHYRV		712			
Sbjct 1	IKPPSRNTSISRVGSPFLRLPLRLPLARAA PPKPRS+ PSTVDL+SKVKLPEGHYRV		180			
Query 713	GSRAIYTCESRYELLGSQGRRCDSNGNWSGRPASCIPVCGRSDSPRSPFIWNGNSTEIG		772			
Sbjct 181	GS+AIYTCESRYELLGSQGRRCDSNG WSGRPASCIPVCGRSDSPRSPFI NGNSTEIG		360			
Query 773	QWPWQAGISRWLAD		786			
Sbjct 361	QWPWQAGISRWLAD		402			

Range 2: 148 to 288

Score	Expect	Method	Identities	Positives	Gaps	Frame
37.7 bits(86)	0.046()	Compositional matrix adjust.	18/47(38%)	27/47(57%)	1/47(2%)	+1
Query 209	KVNAPSGNMIEGATLRFSCDSPYY-LIGQETLTCQNGQWSGQIPQC		254			
Sbjct 148	KV P G+ G+ ++C+S YY L+G + C NG+WSG+ C		288			

SRX202160

Sequence ID: **SRA:SRR610305.279849.2** Length: 450 Number of Matches: 1
Range 1: 127 to 450

Score	Expect	Method	Identities	Positives	Gaps	Frame
203 bits(516) 8e-60() Compositional matrix adjust. 93/108(86%) 100/108(92%) 0/108(0%) +1						
Query 22	PVQSRGVDLGLCDETRFECKCGDPGYVFNVP	PMKQCTYFYRWRPYCKPCDDLEAKDICPKY	81			
Sbjct 127	PVQSRGVD+GLCD+TRFECKCGDPGYVFNVP+KQCTYFYRWRPYCKPCD	LEAKD+CPKY				
Query 82	KRCQECKAGLDSCVTCPPNKYGTWCSGECQCKNGGICDQRTGACTCRD	129				
Sbjct 307	KRCQEC+AGLDSCV CPPN+YGTWCSGECQCKNG + GACTCRD					
	KRCQECRAGLDSCVICPPNRYGTWCSGECQCKNGVFVTRGQGACTCRD	450				

SRX202160

Sequence ID: **SRA:SRR610305.195808.2** Length: 395 Number of Matches: 1
Range 1: 66 to 395

Score	Expect	Method	Identities	Positives	Gaps	Frame
195 bits(496) 2e-57() Compositional matrix adjust. 99/110(90%) 106/110(96%) 0/110(0%) +3						
Query 1	MVLASFVLSGLVLGILAQQMRPVQSRGVDLGLCDETRFECKCGDPGYVFNVP	PMKQCTYFY	60			
Sbjct 66	MVL SFLVLSGLVLG+LAQQMRPVQSRGVD+GLCD+TRFECK GDPGYVFNVP+KQCTYFY					
	MVLTSFLVLSGLVLGLAQQMRPVQSRGVDVGLCDDTRFECKRGDPGYVFNVPKQCTYFY	245				
Query 61	RWRPYCKPCDDLEAKDICPKYKRCQECKAGLDSCVTCPPNKYGTWCSGEC	110				
Sbjct 246	RWRPYCKPCD LEAKD+CPKYKRCQEC+AGLDSCV CPPN+YGTWCSGEC					
	RWRPYCKPCDKLEAKDVCPKYKRCQECRAGLDSCVICPPNRYGTWCSGEC	395				

SRX202160

Sequence ID: **SRA:SRR610305.192653.2** Length: 496 Number of Matches: 2
Range 1: 1 to 357

Score	Expect	Method	Identities	Positives	Gaps	Frame
181 bits(459) 3e-57(2) Composition-based stats. 89/119(75%) 106/119(89%) 0/119(0%) -2						
Query 789	MWFLQCGGSLLNKWIWTAAHCVTYSATAEIIDPSQFKIYLGKyynddsrdddyVQVREA	848				
Sbjct 357	+WF+ CGGSLLNKWK++TAAHCVTYS+TA +I+PSQFKIYLGKYR+D +DD+YVQ++E					
	VWFILCGGSLLNKWIWTAAHCVTYSSTAFLIEPSQFKIYLGKYRNDKDEYVQIKEV	178				
Query 849	LEIHVNPNDPGLNFDIALIQLKTPVLTITRVQPICLPTDITTREHLKEGTLAVVTGW	907				
Sbjct 177	ETHVNP YDP N DIALI+LK PV LTTRV+P+CLPTD+TTRE+LKEGT AVVTGW					
	REIHVNPFDYPATFNSDIALIRLKNPVILTTRVKPVCLPTDLTTRENLKEGTKAIVTGW	1				

Range 2: 354 to 491

Score	Expect	Method	Identities	Positives	Gaps	Frame
59.3 bits(142) 3e-57(2) Compositional matrix adjust. 28/47(60%) 32/47(68%) 1/47(2%) -3						
Query 743	GRPASCIPVCGRSDSPRSPFIWNGNSTEIGQWPHQAGISRWLADHNM	789				
Sbjct 491	GRPASCIPVC +P PFI NG T+IGQWPH AGI+RW +					
	GRPASCIPVC-DDQTPSLPFIINGVVTDIGQWPHAGIARWYPEQKF	354				

SRX202160

Sequence ID: **SRA:SRR610305.282736.2** Length: 457 Number of Matches: 1
Range 1: 23 to 451

Score	Expect	Method	Identities	Positives	Gaps	Frame
194 bits(494) 8e-57() Compositional matrix adjust. 90/143(63%) 111/143(77%) 1/143(0%) +2						
Query 334	KAVDFLDDVGEVPRIHCPAGCSLTAGTVWGTAIYHELSSVCRAAIHAGKLPNSGGAVHVV	393				
Sbjct 23	KA++ LDDVGE+RIHCPAGCSLT G+VWGT IY ELSSVCRAAIH+G + NSGG+V V+					
	KAIELDDVGEPIRIHCPAGCSLTLSVWGTVIYRELSSVCRAAIHSGISNSGGSVQVI	202				
Query 394	NNGPYSDFLGSDLNGIKSEELKSLARSFRFDVSSSTAG-RSGCPDGWFEVEENCVVTS	452				

Sbjct 203 NNGPYSDf+ S+ GI S+ L+S A SFR + G+ CP GW+++E C Y+TS
NNGPYSDfVASNAyGISSKVLRSQAVSfRLVSTETQHNGNQKECPPGWYQIENKCFYITS 382

Query 453 KQRAWERAQGVCTNMAARLAVLD 475
K R+W RAQGVC+NMA+ LAVLD

Sbjct 383 KHR5WNRAQGVCSNMASSLAVLD 451

SRX202160
Sequence ID: **SRA:SRR610305.159223.2** Length: 469 Number of Matches: 1
Range 1: 3 to 305

Score	Expect	Method	Identities	Positives	Gaps	Frame
193 bits(491)	2e-56()	Compositional matrix adjust.	92/101(91%)	98/101(97%)	0/101(0%)	+3
Query 920	QQAVLPVVAASTCEEgyKEADLPLTVTENMFCAGYKGRYDACSgDSGGPLVFADDSRTE					979
Sbjct 3	QQAVLPVVAASTCE+GY+++ PLTVTENMFCAGYK+GRYDACSgDSGGPLVFADDSRT+					182
Query 980	RRWVLEGIVSWGSPSGCGKANQYGGFTKVNVLfSWIRQfI*			1020		
Sbjct 183	RRWVLEGIVSWGSPSGCGK NQYGGFTKVNVLfSWIRQfI*			305		

SRX202160
Sequence ID: **SRA:SRR610305.244020.2** Length: 462 Number of Matches: 1
Range 1: 22 to 459

Score	Expect	Method	Identities	Positives	Gaps	Frame
193 bits(490)	3e-56()	Compositional matrix adjust.	89/146(61%)	111/146(76%)	1/146(0%)	+1
Query 334	KAVDFLDDVGEPVRIHCPAGCSLTAGTVWGTAIYHELSSVCRAAIHAGKLPNSGGAVHV					393
Sbjct 22	KA++ LDDVGEP+RIHCPAGCSLT G+VWGT IY ELSSVCRAAIH+G + NSGG+V V+					201
Query 394	NNGPYSDfLGSDLNgiKSEELKSLARSFRfDYVSSSTAGR-SGCPDGWfEVEENCVVTS					452
Sbjct 202	NNGPYSDf+ S+ GI S+ L+S A SFR + G+ CP GW+++E C Y+TS					381
Query 453	KQRAWERAQGVCTNMAARLAVLDKDL 478					
Sbjct 382	K R+W R QGVC+NMA+ LAVLD +					459

SRX202160
Sequence ID: **SRA:SRR610305.152419.2** Length: 415 Number of Matches: 2
Range 1: 3 to 305

Score	Expect	Method	Identities	Positives	Gaps	Frame
178 bits(451)	5e-55(2)	Composition-based stats.	93/101(92%)	98/101(97%)	0/101(0%)	+3
Query 822	PSQfKIYLGKyyrddsrdddyVQVREALEIHVNPNYDPGNLNFdIALIQLKTPVTLTTRV					881
Sbjct 3	PSQfK YLGKYYRDDS+DDdyVQVREALEIHVNPNYDPGNLNFdIALIQLKT + LTTRV					182
Query 882	QPICLPTDITTREHLKEGT LAVVTGwGLNENNTYSEMIQQA			922		
Sbjct 183	QPICLPTD+TTRE+LKEGT LAVVTGwGLNENNTYSEMIQQ+			305		

Range 2: 301 to 414

Score	Expect	Method	Identities	Positives	Gaps	Frame
54.7 bits(130)	5e-55(2)	Compositional matrix adjust.	26/38(68%)	33/38(86%)	1/38(2%)	+1
Query 921	QAVLPVVAASTCEEgyKEADLPLTVTE-NMFCAGYKKG			957		
Sbjct 301	+AVLPVVAASTCE+GY+++ PLTVTE N +CAGY +G			414		

SRX202160

Sequence ID: **SRA:SRR610305.124202.2** Length: 430 Number of Matches: 1
Range 1: 3 to 425

Score	Expect	Method	Identities	Positives	Gaps	Frame
188 bits(477)	1e-54()	Compositional matrix adjust.	86/141(61%)	110/141(78%)	0/141(0%)	-3
Query 66	CKPCDDLEAKDICPKYKRCQECKAGLDSCVTCPPNKYGTWCSGECQCKNGGICDQRTGAC					125
Sbjct 425	C+PC+D+ +D+CPKYK+C ECK LD CV+CPPN+YG WC+G C CKNGG C+Q TG C					246
Query 126	TCRDREYGAHCEILKGCPLLPDSQVQEVNPPDNPTIDYSCSPGFKLKGVARISCLPN					185
Sbjct 245	CR +EG+ACEI KGC L S+ V E R P NPQTI YSC PGFKL+G +RI CLP+					66
Query 186	GQWSSFPKPCIRECAKVSSPE 206					
Sbjct 65	GQWTLNPPSCIQQCARLSAPE 3					

SRX202160

Sequence ID: **SRA:SRR610305.150040.2** Length: 400 Number of Matches: 1
Range 1: 44 to 394

Score	Expect	Method	Identities	Positives	Gaps	Frame
186 bits(472)	4e-54()	Compositional matrix adjust.	82/117(70%)	100/117(85%)	0/117(0%)	-1
Query 697	VDLASKVKLPPEGHYRVGSRAITYTCESRYELLGSGRRCDSENGWSGRPASCIPVCGRSD					756
Sbjct 394	V+ ++ LP+GHY VG++A YTCES+YY+LLGS+GRRCS+G W GRPASCIPVCGRSD					215
Query 757	SPRSPFIWNGNSTEIGQWPWQAGISRWLADHNWFLQCGGSLLEKWIWTAACHVTY					813
Sbjct 214	SPRSPFI NG T+IGQWPW AGI+RW + +WF+ CGGSLLEKWW+TAAHCVTY					44

SRX202160

Sequence ID: **SRA:SRR610305.381659.2** Length: 492 Number of Matches: 2
Range 1: 3 to 446

Score	Expect	Method	Identities	Positives	Gaps	Frame
184 bits(467)	6e-53()	Compositional matrix adjust.	82/148(55%)	110/148(74%)	0/148(0%)	+3
Query 155	RNPPDNPTIDYSCSPGFKLKGVARISCLPNGQWSSFPKPCIRECAKVSSPEHGKVNAPS					214
Sbjct 3	R P NPQTI YSC PGFKL+G +RI CLP+GQW++ PP CI++CA++S+PEHG+V					182
Query 215	GNMIEGATLRFSCDSPYYLIGQETLTCQNGQWSGQIPQCKKLVFCPDLPVNHAHQVK					274
Sbjct 183	+++EGAT FSCD YYLIG+ETL+C GQW G IP C+KL+FCPDL + +V					362
Query 275	IGVEQKYQGFPQGTETVYTCSGNYFLMG 302					
Sbjct 363	+ EQ+YGO+PQG+ VT+ CS N++ +G					446

Range 2: 27 to 311

Score	Expect	Method	Identities	Positives	Gaps	Frame
56.2 bits(134)	3e-08()	Compositional matrix adjust.	33/103(32%)	48/103(46%)	8/103(7%)	+3
Query 222	TLRFSCDSPYYLIGQETLTCQNGQWSGQIPQCKKLVFCPDLPVNHAHQVKIGVEQKY					281
Sbjct 27	T+ +SC + L G + C +GQW+ P C + C L H E V +					182
Query 282	GQFPQGTETVYTCSGNYFLMGFNTLKCPDGSWSGSPSCVKV 324					
Sbjct 183	+G T++C Y+L+G TL C+P G W G PSC K+					311

SRX202160

Sequence ID: **SRA:SRR610305.271769.2** Length: 363 Number of Matches: 3
Range 1: 15 to 230

Score	Expect	Method	Identities	Positives	Gaps	Frame
123 bits(309)	1e-52(3)	Compositional matrix adjust.	59/72(82%)	65/72(90%)	1/72(1%)	-2
Query 398	VHVVNNGPYSDFLGSDLNGIKSEELKSLARSFRFDYVSSSTAGR-SGCPDGFVEEENCV					448
Sbjct 230	VHVVNNGPYSDFLASDLNGXKSDCLKSLAQSFYFDYVSSSTAGRSGCPDGFVEEENCV					51
Query 449	YVTSKQRAWERA	460				
Sbjct 50	YVTSK + ++					
	YVTSKETSLGKS	15				

Range 2: 232 to 363

Score	Expect	Method	Identities	Positives	Gaps	Frame
90.9 bits(224)	1e-52(3)	Compositional matrix adjust.	43/44(98%)	44/44(100%)	0/44(0%)	-1
Query 346	VRIHCPAGCSLTAGTVMGTAIYHELSSVCRAAIHAGKLPNSGGA					389
Sbjct 363	VRIHCPAGCSLTAGTVMGTAIYHELSSVCRAAIHAGK+PNSGGA					232

Range 3: 2 to 37

Score	Expect	Method	Identities	Positives	Gaps	Frame
31.6 bits(70)	1e-52(3)	Composition-based stats.	12/12(100%)	12/12(100%)	0/12(0%)	-3
Query 453	KQRAWERAQGVC	464				
Sbjct 37	KQRAWERAQGVC	2				

SRX202160

Sequence ID: **SRA:SRR610305.232653.2** Length: 448 Number of Matches: 2

Range 1: 2 to 448

Score	Expect	Method	Identities	Positives	Gaps	Frame
174 bits(440)	2e-49()	Compositional matrix adjust.	105/157(67%)	119/157(75%)	16/157(10%)	+2
Query 812	TYSATAEIIDPSQFKIYLGKyyrddsrdddyVQVREAEIHVNPYDPGNLNFIDIALIQL					871
Sbjct 2	TYSATAEIIDPSQFK YLGKYYRDDS+DDDYVQVREA+EIHVNPYDPGNLNFIDIALIQL					181
Query 872	KTPVTLTTRVQICLPTDITTREHLKE-----GTLAVVTGWGLNENNTYSEMIQOAV					923
Sbjct 182	KT V LTTTRVQICLPTD+TTRE+LKE G T + + ++QQA					358
Query 924	LPVVAASTCEEYKEADLPLTVTENMFCAGYKKGGRYD	960				
Sbjct 359	E+GY+++ LPLTVTEN+ CAGYK+GRYD					
	-----PREQGYQDSGLPLTVTENIVCAGYKQGRYD	448				

Range 2: 256 to 360

Score	Expect	Method	Identities	Positives	Gaps	Frame
69.7 bits(169)	5e-13()	Composition-based stats.	32/35(91%)	33/35(94%)	0/35(0%)	+1
Query 897	KEGTLAVVTGWGLNENNTYSEMIQOAVLPVVAAST					931
Sbjct 256	+ G LAVVTGWGLNENNTYSEMIQOAVLPVVAAST					360

SRX202160

Sequence ID: **SRA:SRR610305.330331.2** Length: 255 Number of Matches: 1

Range 1: 1 to 252

Score	Expect	Method	Identities	Positives	Gaps	Frame
169 bits(429)	6e-49()	Compositional matrix adjust.	79/84(94%)	82/84(97%)	0/84(0%)	+1

Query 715 RAIYTCESRYIELLSQGRRCDSNGNWSGRPASCIPVCGRSDSPRSPFIWNGNSTEIGQW 774
+AIYTCESRYIELLSQGRRC+SNG WSGRPASCIPVCGRSDSPRSPFI NGNSTEIGQW
Sbjct 1 QAIYTCESRYIELLSQGRRCNSNGKWSGRPASCIPVCGRSDSPRSPFIWNGNSTEIGQW 180

Query 775 PWQAGISRWLADHNMMFLQCGGSL 798
PWQAGISRWLADHNMMFLQCGG+L
Sbjct 181 PWQAGISRWLADHNMMFLQCGGAL 252

SRX202160
Sequence ID: **SRA:SRR610305.71990.2** Length: 370 Number of Matches: 1
Range 1: 82 to 369

Score	Expect	Method	Identities	Positives	Gaps	Frame
171 bits(433)	7e-49()	Compositional matrix adjust.	88/96(92%)	93/96(96%)	0/96(0%)	+1
Query 1	MVLASFLVSLVGLGILAQQMRPVQSRGVDLGLCDETRFECKGDPGYVFNVP	60				
Sbjct 82	MVLASFLVSLVGLG+LAQQM PVQSRGVDLGLCD+TRFECKGDPGYVFNVP KQCTYFY	261				
Query 61	RWRPYCKPCDDLLEAKDTCPKYKRCQECKAGLDSCVT	96				
Sbjct 262	RWRPYCKPCD LEAKD+CPKYKRCQEC+AGLDSCV+ RWRPYCKPCDKLEAKDVC	369				

SRX202160
Sequence ID: **SRA:SRR610305.716947.2** Length: 451 Number of Matches: 2
Range 1: 3 to 395

Score	Expect	Method	Identities	Positives	Gaps	Frame
169 bits(428)	9e-49(2)	Compositional matrix adjust.	77/131(59%)	99/131(75%)	1/131(0%)	+3
Query 329	VDCDSKAVDFLDDVGEPVRIHCPAGCSLTAGTVMGTAIYHELSSVCRAAIHAGKLPNSGG	388				
Sbjct 3	++CD+KA++ LDDVGEP+RIHCPAGCSLT G+VMGT IY ELSSVCRAAIH+G + NSGG	182				
Query 389	AVHVVNNGPYSDFLGSDLNGIKSEELKSLARSFRFDYVSSSTAG-RSGCPDGFVEVEENC	447				
Sbjct 183	+V V+NNGPYSDF+ S+ GI S+ L+S A SFR + G + CP GW+++E C	362				
Query 448	VYVTSKQRAWE 458					
Sbjct 363	Y+TSK + E FYITSKTQKLE 395					

Range 2: 379 to 447

Score	Expect	Method	Identities	Positives	Gaps	Frame
43.1 bits(100)	9e-49(2)	Composition-based stats.	17/23(74%)	20/23(86%)	0/23(0%)	+1
Query 453	KORAWERAQGVCTNMAARLAVLD 475					
Sbjct 379	K R+W RAQGV+NMA+ LAVLD KHRSWNRAQGVCSNMASSLAVLD 447					

SRX202160
Sequence ID: **SRA:SRR610305.213439.2** Length: 476 Number of Matches: 1
Range 1: 146 to 472

Score	Expect	Method	Identities	Positives	Gaps	Frame
169 bits(428)	9e-48()	Compositional matrix adjust.	75/109(69%)	93/109(85%)	0/109(0%)	+2
Query 301	MGFNTLKCNPDGWSGSPSCVKVADREVDGSKAVDFLDDVGEPVRIHCPAGCSLTAGT	360				
Sbjct 146	+G +++ C PDGWSG OPSCVKVA++ ++CD+KA++ LDDVGEP+RIHCPAGCSLT G+	325				
Query 361	VWGTAIYHELSSVCRAAIHAGKLPNSGGAVHVVNNGPYSDFLGSDLNGI 409					
Sbjct 326	VWGT IY ELSSVCRAAIH+G + NSGG+V V+NNGPYSDF+ S+ GI VWGTVIYRELSSVCRAAIHSGIISNSGGSVQVINNGPYSDFVASNAYGI 472					

SRX202160
Sequence ID: **SRA:SRR610305.307671.2** Length: 346 Number of Matches: 3
Range 1: 2 to 223

Score	Expect	Method	Identities	Positives	Gaps	Frame
122 bits(307)	2e-47(2)	Compositional matrix adjust.	58/74(78%)	65/74(87%)	1/74(1%)	+2
Query 184	PNGQWSSFPK CIR-ECAKVSSPEHGKVNAPSGNMIEGATLRFSCDSPYYLIGQETLTCQ					242
	PNGQWSSF + + EC+ VSS EHGKVN+PS ++IEGATLRFSCDSPYYLIGQETLTCQ					
Sbjct 2	PNGQWSSFSTQMLFVECSMVSSLEHGKVNPSADLIEGATLRFSCDSPYYLIGQETLTCQ					181
Query 243	GNGQWSGQIPQCKK 256					
	GNGQWSGQIPQC+ 223					
Sbjct 182	GNGQWSGQIPQCQN 223					

Range 2: 220 to 345

Score	Expect	Method	Identities	Positives	Gaps	Frame
84.7 bits(208)	2e-47(2)	Compositional matrix adjust.	37/42(88%)	41/42(97%)	0/42(0%)	+1
Query 256	KLVFCPDLDPVNHAHQVKIGVEQKYGFQPGTEVTTYTCSGN 297					
	+LVFCPDLDPV+HAEHQVKIG+EQKYGQ POGTEVTTYTC+GN					
Sbjct 220	ELVFCPDLDPVSHAEHQVKIGLEQKYGQSPQTEVTTYTCGN 345					

Range 3: 5 to 217

Score	Expect	Method	Identities	Positives	Gaps	Frame
40.4 bits(93)	0.003()	Compositional matrix adjust.	24/78(31%)	34/78(43%)	7/78(8%)	+2
Query 244	NGQWSGQIPQCKKLVFCPDLDPVNHAHQVKIGVEQKYGFQPGTEVTTYTCSGNYFLMGF 303					
	NGQWS Q V C + + H + V +G + ++C Y+L+G					
Sbjct 5	NGQWSSFSTQ-MLFVECSMVSSLEHGK-----VNSPSADLIEGATLRFSCDSPYYLIGQ 163					
Query 304	NTLKCNPDGWSGSGQSPSC 321					
	TL C +G WSG P C					
Sbjct 164	ETLTCQNGQWSGQIPQC 217					

SRX202160
Sequence ID: **SRA:SRR610305.117350.2** Length: 241 Number of Matches: 1
Range 1: 2 to 241

Score	Expect	Method	Identities	Positives	Gaps	Frame
164 bits(415)	4e-47()	Composition-based stats.	73/80(91%)	77/80(96%)	0/80(0%)	+2
Query 436	CPDGWFEIENCVVVTSKQRAWERAQGVCTNMAARLAVLDKDLIPSSLTETLRGKGLTTT 495					
	CPDGWFEIENCVVVTSKQRAWERAQGVCTNMAARLAVLDKD+IPSSLTETLRGKGL TT					
Sbjct 2	CPDGWFEIENCVVVTSKQRAWERAQGVCTNMAARLAVLDKDVIPSSLTETLRGKGLATT 181					
Query 496	WIGLHRLDAEKPFWELMDR 515					
	WIGLHRLDA+ F+WELMDR					
Sbjct 182	WIGLHRLDADNHFIWELMDR 241					

SRX202160
Sequence ID: **SRA:SRR610305.263645.2** Length: 315 Number of Matches: 3
Range 1: 9 to 305

Score	Expect	Method	Identities	Positives	Gaps	Frame
163 bits(413)	1e-46()	Compositional matrix adjust.	87/99(88%)	94/99(94%)	1/99(1%)	+3
Query 539	VYLDI-RDQLQPWVKTKSCFQPSFACMMDLSDRNKAKCDDPGPLENGHATLHGQSIDGF 597					
	VY+ I + QLPWVKTKSCFQPSF CMMDLSD+NKAKC+DPGPLENGHA LHGQSIDGF					
Sbjct 9	VYIWSKIQLQPWVKTKSCFQPSFVCMMDLSDKNKAKCNDPGPLENGHAKLHGQSIDGF 188					
Query 598	YAGSSIRYSCEVLHYLSGtetvtcttngtWSAPKPRCIK 636					
	YAGSS+RYSCEVLHYLSGTETV+CT+NGTWSAPKPRCIK					
Sbjct 189	YAGSSVRYSCEVLHYLSGTETVSCTSNGTWSAPKPRCIK 305					

Range 2: 153 to 305

Score	Expect	Method	Identities	Positives	Gaps	Frame
43.9 bits(102)	2e-04()	Compositional matrix adjust.	20/51(39%)	32/51(62%)	1/51(1%)	+3
Query 207	HGKVNAPSGN-MIEGATLRFSCDSPYYLIGQETLTCQNGNQWSGQIPQCKK			256		
	H K++ S + G+++R+SC+ +YL G ET++C NG WS P+C K					
Sbjct 153	HAKLHGQSIDGFYAGSSVRYSCVHLHYLSGTETVTSCTSNGTWSAPKPRCIK			305		

Range 3: 123 to 305

Score	Expect	Method	Identities	Positives	Gaps	Frame
38.9 bits(89)	0.010()	Compositional matrix adjust.	19/64(30%)	32/64(50%)	3/64(4%)	+3
Query 260	CPDLDPVNHAHQVIGVEQKYGFQPGTEVTYTCSGNYFLMGFNTLKCNDGSGWSGSP			319		
	C D P+ + ++ Q F G+ V Y+C ++L G T+ C +G+WS +P					
Sbjct 123	CNDPGPLENGHAKLH---GQSIDGFYAGSSVRYSCVHLHYLSGTETVTSCTSNGTWSAPKP			293		
Query 320	SCVK 323					
	C+K					
Sbjct 294	RCIK 305					

SRX202160

Sequence ID: **SRA:SRR610305.296844.2** Length: 456 Number of Matches: 2

Range 1: 6 to 230

Score	Expect	Method	Identities	Positives	Gaps	Frame
125 bits(314)	5e-46(2)	Compositional matrix adjust.	55/75(73%)	66/75(88%)	0/75(0%)	+3
Query 329	VDCDSKAVDFLDDVGEPVRIHCPAGCSLTAGTVWGTAIYHELSSVCRAAIHAGKLPNSGG			388		
	++CD+KA++ LDDVGEP+RIHCPAGCSLT G+VWGT IY ELSSVCRAAIH+G + NSGG					
Sbjct 6	INCDTKAIELLDDVGEPRIHCPAGCSLTGGSVWGTVIYRELSSVCRAAIHSGIISNSGG			185		
Query 389	AVHVVNNGPYSDFLG 403					
	+V V+NNGPYS F G					
Sbjct 186	SVQVINNGPYSRFCG 230					

Range 2: 220 to 450

Score	Expect	Method	Identities	Positives	Gaps	Frame
77.4 bits(189)	5e-46(2)	Compositional matrix adjust.	37/77(48%)	50/77(64%)	1/77(1%)	+1
Query 400	DFLGSDLNGIKSEELKSLARSFRFDYVSSSTAG-RSGCPDGWFEVEENCVVYTSKORAWE			458		
	DF+ S+ GI S+ L+S A SFR + G + CP GW+++E C Y+TSK R+W					
Sbjct 220	DFVASNAYGISKVLRSQAVSFRVLVSTETQHNGNQKECPPGWYQIENKCFYITSKHSWN			399		
Query 459	RAQGVCTNMAARLAVLD 475					
	RA GVC+N A+ LAVLD					
Sbjct 400	RALGVCSNXASSLAVLD 450					

SRX202160

Sequence ID: **SRA:SRR610305.133991.2** Length: 456 Number of Matches: 2

Range 1: 6 to 248

Score	Expect	Method	Identities	Positives	Gaps	Frame
130 bits(327)	8e-46(2)	Compositional matrix adjust.	57/81(70%)	71/81(87%)	0/81(0%)	+3
Query 329	VDCDSKAVDFLDDVGEPVRIHCPAGCSLTAGTVWGTAIYHELSSVCRAAIHAGKLPNSGG			388		
	++CD+KA++ L+DVGEP+RIHCPAGCSLT G+VWGT IY ELSSVCRAAIH+G + NSGG					
Sbjct 6	INCDTKAIELLNDVGEPRIHCPAGCSLTGGSVWGTVIYRELSSVCRAAIHSGIISNSGG			185		
Query 389	AVHVVNNGPYSDFLGSDLNGI 409					
	+V V+NNGPYSDF+ S+ GI					
Sbjct 186	SVQVINNGPYSDFVASNAYGI 248					

Range 2: 262 to 450

Score	Expect	Method	Identities	Positives	Gaps	Frame
71.6 bits(174)	8e-46(2)	Compositional matrix adjust.	33/63(52%)	43/63(68%)	1/63(1%)	+1
Query 414	LKSLARSFRFDYVSSSTAG-RSGCPD	GWFEVEENCVVYTSKQRAWERAQGVCTNMAARLA	472			
	L+S A SFR + G + CP GW+++E C Y+TSK R+W	RAQGVC+NMA+ LA				
Sbjct 262	LRSQAVSFRLVSTETQHNGNQKECP	PGWYQIENKCFYITSKHRSWNRAQGVCSNMASSLA	441			
Query 473	VLD	475				
	VLD					
Sbjct 442	VLD	450				

SRX202160

Sequence ID: **SRA:SRR610305.147146.2** Length: 449 Number of Matches: 1
Range 1: 3 to 263

Score	Expect	Method	Identities	Positives	Gaps	Frame
162 bits(410)	2e-45()	Compositional matrix adjust.	79/87(91%)	85/87(97%)	1/87(1%)	+3
Query 406	LNGIKSEELKSLARSFRFDYVSSSTAGR-SGCPD	GWFEVEENCVVYTSKQRAWERAQGVCTNMAARLA	472			
	LNGIKS+ELKSLA+SFRFDYVSSSTAGR SGCPD	GWFE+EENCVVYT+KQRAWERAQGVCTNMAARLA				
Sbjct 3	LNGIKSDELKSLAQSFYVSSSTAGRSGCPD	GWFEIEENCVVYTTKQRAWERAQGVCTNMAARLA	182			
Query 465	TNMAARLAVLDKDLIPSSLTETLRGKG	491				
	TNMAARLAVLDK +IPSSLT+TLRGKG					
Sbjct 183	TNMAARLAVLDKXVIPSSLTETLRGKG	263				

SRX202160

Sequence ID: **SRA:SRR610305.302701.2** Length: 353 Number of Matches: 2
Range 1: 39 to 260

Score	Expect	Method	Identities	Positives	Gaps	Frame
154 bits(388)	2e-45(2)	Compositional matrix adjust.	71/74(96%)	72/74(97%)	0/74(0%)	+3
Query 725	YELLGSQGRRCDSNGNWSGRPASCIPVCGRSDSPRSPFI	WNGNSTEIGQWPWQAGISRWL	784			
	YELLGSQGRRCDSNG WSGRPASCIPVCGRSDSPRSPFI	NGNSTEIGQWPWQAGISRWL				
Sbjct 39	YELLGSQGRRCDSNGKWSGRPASCIPVCGRSDSPRSPFI	WNGNSTEIGQWPWQAGISRWL	218			
Query 785	ADHNMMWFLQCGGSL	798				
	ADHNMMWFLQCGG+L					
Sbjct 219	ADHNMMWFLQCGGAL	260				

Range 2: 281 to 346

Score	Expect	Method	Identities	Positives	Gaps	Frame
47.4 bits(111)	2e-45(2)	Composition-based stats.	21/22(95%)	22/22(100%)	0/22(0%)	+2
Query 805	VTAACHVTYSATAEIIDPSQFK	826				
	+TAAACHVTYSATAEIIDPSQFK					
Sbjct 281	LTAACHVTYSATAEIIDPSQFK	346				

SRX202160

Sequence ID: **SRA:SRR610305.161135.2** Length: 483 Number of Matches: 1
Range 1: 144 to 413

Score	Expect	Method	Identities	Positives	Gaps	Frame
161 bits(408)	5e-45()	Compositional matrix adjust.	83/90(92%)	87/90(96%)	0/90(0%)	+3
Query 1	MVLASFLVSGVLGLAQOMRPVQSRGVDLGLCDETRFECKGDPGYVFNVP	KQCTYFY	60			
	MVLASFLVSGVLGL+LAQOM PVQSRGVDLGLCD+TRFECKGDPGYVFNVP	KQCTYFY				
Sbjct 144	MVLASFLVSGVLGLLAQOMHPVQSRGVDLGLCDDTRFECKGDPGYVFNVP	AKQCTYFY	323			
Query 61	RWRPYCKPCDDLEAKDICPKYKRCQCEKAG	90				
	RWRPYCKPCD LEAKD+CPKYKRCQCEC+AG					
Sbjct 324	RWRPYCKPCDKLEAKDVC PKYKRCQCECAG	413				

SRX202160
Sequence ID: **SRA:SRR610305.116683.2** Length: 228 Number of Matches: 1
Range 1: 1 to 228

Score	Expect	Method	Identities	Positives	Gaps	Frame
157 bits(396)	1e-44()	Compositional matrix adjust.	74/76(97%)	76/76(100%)	0/76(0%)	+1
Query 326	DREVDKCDKAVDFLDDVGEPVRIHCPAGCSLTAGTVWGTAIYHELSSVCRAATHAGKLPN					385
Sbjct 1	DREV+CDKAVDFLDDVGEPVRIHCPAGCSLTAGTVWGTAIYHELSSVCRAATHAGK+PN					180
Query 386	SGGAVHVVNNGPYSD 401					
Sbjct 181	SGGAVHVVNNGPYSD 228					

SRX202160
Sequence ID: **SRA:SRR610305.255423.2** Length: 374 Number of Matches: 3
Range 1: 160 to 372

Score	Expect	Method	Identities	Positives	Gaps	Frame
149 bits(377)	6e-44(2)	Compositional matrix adjust.	66/71(93%)	69/71(97%)	0/71(0%)	-3
Query 67	KPCDDLEAKDICPKYKRCQECKAGLDSCVTCPPNKYGTWCSGECQCKNGGICDQRTGACT					126
Sbjct 372	KPCD LEAKD+CPKYKRCQEC+AGLDSCV+CPPNKYGTWCSGECQCKNGGICDQRTGACT					193
Query 127	CRDRYEGAHCE 137					
Sbjct 192	CRDRYEG HCE 160					

Range 2: 3 to 161

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.2 bits(108)	6e-44(2)	Composition-based stats.	25/53(47%)	30/53(56%)	1/53(1%)	-1
Query 137	EILKGCPLLPSDSQVQEVNRNPPDNPTIDYSCSPGFK - LKGVARISCLPNGQW					188
Sbjct 161	+IL+GCPLL SD QVQEV+ + LK RI+CLPNGQW					3

Range 3: 47 to 106

Score	Expect	Method	Identities	Positives	Gaps	Frame
42.0 bits(97)	0.001()	Compositional matrix adjust.	17/20(85%)	20/20(100%)	0/20(0%)	-2
Query 155	RNPPDNPTIDYSCSPGFKL 174					
Sbjct 106	+NPP++PTIDYSCSPGFKL 47					

SRX202160
Sequence ID: **SRA:SRR610305.82426.2** Length: 491 Number of Matches: 2
Range 1: 94 to 399

Score	Expect	Method	Identities	Positives	Gaps	Frame
145 bits(365)	4e-43(2)	Compositional matrix adjust.	64/102(63%)	83/102(81%)	2/102(1%)	+1
Query 693	QPSTVDL--ASKVKLPFGHYRVSRAIYTCESRYELLGSGRRCDNSNGNWSGRPASCIP					750
Sbjct 94	+PS++++ ++ LP+GHY VG++A YTCES+YY+LLGS+GRRRC+S+G W GRPASCIP					273
Query 751	VCGRSDSPRSPFIWNGNSTEIGQWPQAGISRWLADHNWML 792					
Sbjct 274	VCGRSDSPRSPFI NG T+IGQWPW AGI+RW + +W 399					

Range 2: 413 to 490

Score	Expect	Method	Identities	Positives	Gaps	Frame
48.1 bits(113)	4e-43(2)	Composition-based stats.	19/26(73%)	24/26(92%)	0/26(0%)	+2
Query 798	LLNEKWIIVTAAHCVTYSATAEIIDPS	823				
	LLNEKW+TAAHCVTYS+T +I+PS					
Sbjct 413	LLNEKWITAAHCVTYSSTVFLIEPS	490				

SRX202160
Sequence ID: **SRA:SRR610305.176373.2** Length: 369 Number of Matches: 2
Range 1: 2 to 367

Score	Expect	Method	Identities	Positives	Gaps	Frame
154 bits(390)	4e-43()	Compositional matrix adjust.	72/122(59%)	91/122(74%)	0/122(0%)	-3
Query 140	KGCPLLPDSQVQEVNPPDNPTIDYSCSPGFKLKGVARISCLPNGWSSFPKCIREC	199				
	KGC L S+ V E R P NPOTI YSC PGFKL+G +RI CLP+GOW++ PP CI+C					
Sbjct 367	KGCLLPQSNPGVIEERKPKVNPQTISYSCLPGFKLQGPSRIICLPSCGQWTLNPPSCIQQC	188				
Query 200	AKVSSPEHGKVNAPSGNMIEGATLRFSCDSPYYLIGQETLTCQNGQWSGOIPQCKKLVF	259				
	A++S+PEHG+V +++EGAT FSCD YYLIG+ETL+C GOW G IP C+KL+P					
Sbjct 187	ARLSAPEHGEVTFRGKDLLEGATATFSCDRYYLIGKETLSCHPGGQWYGDIPSCQKLIF	8				
Query 260	CP 261					
	CP					
Sbjct 7	CP 2					

Range 2: 14 to 310

Score	Expect	Method	Identities	Positives	Gaps	Frame
56.6 bits(135)	1e-08()	Compositional matrix adjust.	33/107(31%)	49/107(45%)	8/107(7%)	-3
Query 218	IEGATLRFSCDSPYYLIGQETLTCQNGQWSGOIPQCKKLVFCDLPVNHAEHQVKIGV	277				
	+ T+ +SC + L G + C +GOW+ P C + C L H E V					
Sbjct 310	VNPQTISYSCLPGFKLQGPSRIICLPSCGQWTLNPPSC--IQQCARLSAPEHGE-----V	155				
Query 278	EQKYGFPGQTEVTYTCSGNYFLMGFNTLKCNDGWSGSGQPSCKVK	324				
	+ +G T++C Y+L+G TL C+P G W G PSC K+					
Sbjct 154	TFRGKDLLEGATATFSCDRYYLIGKETLSCHPGGQWYGDIPSCQKL	14				

SRX202160
Sequence ID: **SRA:SRR610305.499919.2** Length: 447 Number of Matches: 1
Range 1: 2 to 436

Score	Expect	Method	Identities	Positives	Gaps	Frame
154 bits(390)	1e-42()	Compositional matrix adjust.	76/145(52%)	97/145(66%)	1/145(0%)	-3
Query 357	TAGTVWGTATYHELSSVCRAAIHAGKLPNSGGAVHVNNGPYSDFLGSDNLNGIKSEELKS	416				
	T G+V G LSSVCRAAIH+G + NSGG+V V+NNGPYSDF+ S+ GI S+ L+S					
Sbjct 436	TLGSVLGNRYLS*LSSVCRAAIHSGIISNSGGSVQVINNGPYSDFVASNAYGISSKVLRS	257				
Query 417	LARSFRFDYVSSSTAG-RSGCPDGFVEVEENCVVYTSKQRAWERAQGVCTNMAARLAVLD	475				
	A SFR + G + CP GW+++E C Y+TSK R+W RAQGV+C+NMA+ LAVLD					
Sbjct 256	QAVSFRVLSTETQHNGNQKECPPGWYQIENKCFYITSKHSRWNRAQGVCSNMASLAVLD	77				
Query 476	KDLPSSLTETLRGKGLTTTWIGLH	500				
	+ SL++ L KGL WIGL					
Sbjct 76	SAVAQQSLSDIILNKKGLVKIWIQLQ	2				

SRX202160
Sequence ID: **SRA:SRR610305.87460.2** Length: 269 Number of Matches: 1
Range 1: 2 to 268

Score	Expect	Method	Identities	Positives	Gaps	Frame
151 bits(382)	2e-42()	Composition-based stats.	81/89(91%)	85/89(95%)	0/89(0%)	+2
Query 826	KIYLGKyyrddsrdddyVQVREALEIHVNPNDPGLNFDIALIQLKTPVTLTTRVQPIC	885				
	K YLGKYYRDDS+DDDYVQVREA+EIHVNPNDPGLNFDIALIQLKT V LTTTRVQPIC					

Sbjct 2 KFYLGKYYRDDS KDDDYVQVREAIEIHVNP NYDPGNLNF DIALIQLKTS VALTTTRVQPIC 181
Query 886 LPTDITTREHLKEGT LAVVTGWGLNENNT 914
LPTD+TTRE+LKEG LAVVTGWGLNENNT
Sbjct 182 LPTDLTTREN LKEGALAVVTGWGLNENNT 268

SRX202160
Sequence ID: **SRA:SRR610305.209724.2** Length: 450 Number of Matches: 2
Range 1: 103 to 366

Score	Expect	Method	Identities	Positives	Gaps	Frame
154 bits(388)	2e-42()	Compositional matrix adjust.	80/88(91%)	84/88(95%)	0/88(0%)	-1
Query 1	MVLASFLVSGLVGLIAQQMRPVQSRGVDLGLCDETRFECKCGDPGYVFNVP	60				
	MVLASFLVSGLVGL+LAQQM PVQSRGVD GLCD+TRFECKCGDPGYVFNVP					
Sbjct 366	MVLASFLVSGLVGLLAQQMHPVQSRGVDPLGLCDDTRFECKCGDPGYVFNVP	187				
Query 61	RWRPYCKPCDDLAKDTCPKYKRCQECK 88					
	RWRPYCKPCD LEAKD+CPKYKRCQEC+					
Sbjct 186	RWRPYCKPCDKLEAKDVCPKYKRCQECR 103					

Range 2: 3 to 131

Score	Expect	Method	Identities	Positives	Gaps	Frame
74.7 bits(182)	9e-15()	Compositional matrix adjust.	33/43(77%)	35/43(81%)	0/43(0%)	-2
Query 79	PKYKRCQECKAGLDSCVTCPPNKYGTWCSGECQCKNGGICDQR 121					
	P + AGLDSCV+CPPNKYGTWCSGECQCKNGGICDQR					
Sbjct 131	PSTNDVKS VGAGLDSCVSCPPNKYGTWCSGECQCKNGGICDQR 3					

SRX202160
Sequence ID: **SRA:SRR610305.587240.2** Length: 433 Number of Matches: 2
Range 1: 1 to 210

Score	Expect	Method	Identities	Positives	Gaps	Frame
139 bits(351)	2e-42(2)	Compositional matrix adjust.	67/70(96%)	68/70(97%)	0/70(0%)	-2
Query 712	VGSRAIYTCESRYYELLGSGRRCD SNGNWSGRPASCIPVCGRSDSPRSPFIWNGNSTEI 771					
	VGS+AIYTCESRYYELLGSGRRCD SNG WSGRPASCIPVCGRSDSPRSPFI NGNSTEI					
Sbjct 210	VGSQAIYTCESRYYELLGSGRRCD SNGKWSGRPASCIPVCGRSDSPRSPFIWNGNSTEI 31					
Query 772	GQNPWQAGIS 781					
	GQNPWQAGIS					
Sbjct 30	GQNPWQAGIS 1					

Range 2: 198 to 431

Score	Expect	Method	Identities	Positives	Gaps	Frame
51.2 bits(121)	2e-42(2)	Compositional matrix adjust.	49/80(61%)	57/80(71%)	3/80(3%)	-3
Query 637	VITCQNPPVPSYGSVEIKPP-SRTNSISRVGSPFlrplrpplaraakpppkprSSQPS 695					
	VITCQ PPVPSYGSV+ P + N V L + + LPLARAA PPPKPRS+ PS					
Sbjct 431	VITCQTPPVPSYGSVDXNPQVDKLNQSCWVA--ILEVATVTLPLARAAGPPPKPRSAPPS 258					
Query 696	TVDLASKVKLPEGHYRVGSR 715					
	T+DL+SKVKLPEGHYR G +					
Sbjct 257	TMDLSSKVKLPEGHYRWGLK 198					

SRX202160
Sequence ID: **SRA:SRR610305.193065.2** Length: 460 Number of Matches: 2
Range 1: 125 to 445

Score	Expect	Method	Identities	Positives	Gaps	Frame
154 bits(388)	2e-42()	Compositional matrix adjust.	71/110(65%)	85/110(77%)	3/110(2%)	-1

Query 703 VKLPEGHYRVGSRAIYTCESRYVELLGSQGRRCDSNGNWSGRPASCI PVCGRSDSPRSPF 762
+ LP+GHY VG++A YTCES+YY+LLGS+GRRCS+G W GRPASCI PVCGRSDSPRSPF
Sbjct 445 IVLKPGHYHVGTAQSYTCESQYYKLLGSKGRRCESSGTWGRPASCI PVCGRSDSPRSPF 266

Query 763 IWNNGNSTEIGQWPWQAGISRWLADHNMWFLQCGGSL LNEKWIVTAACHVT 812
I NG T+IGQWPW AGI+RW + +WF+ CGGS K HC T
Sbjct 265 IINGVVTDIGQWPWHAGIARWYPEQEVNFI LCGGSFTE*K---VGYHCCT 125

Range 2: 1 to 159

Score	Expect	Method	Identities	Positives	Gaps	Frame
71.6 bits(174)	1e-13()	Composition-based stats.	39/53(74%)	49/53(92%)	0/53(0%)	-2
Query 798	LLNEKWIVTAACHCVTYSATAEIIDPSOFKTYLGKyynddsrdddyVOVREALE				850	
Sbjct 159	LLNEKW++TAAHCVTVYS+TA +I+PSOFKTYLGKYYR+D +DD+YVQ++E E				1	

SRX202160

Sequence ID: **SRA:SRR610305.271268.2** Length: 406 Number of Matches: 1
Range 1: 10 to 405

Score	Expect	Method	Identities	Positives	Gaps	Frame
151 bits(382)	6e-42()	Compositional matrix adjust.	72/132(55%)	92/132(69%)	2/132(1%)	+1
Query 330	DCDSKAVDFLDDVGEPVRIHCPAGCSL TAGTVMGTAIYHELSSVCRAAIHAGKLPNSGGA				389	
Sbjct 10	+CD+KA++ LDDVGEP+RIHCPAGCS T G+VMGT IY ELSSVCRAAIH+G + NSGG+				189	
Query 390	VHVVNNGPYSDFLGSDLNGIKSEELKSLARSFRFDYVSSSTAGRSGCPDGWF--EVEENC				447	
Sbjct 190	V V+NNGPY DF+ S+ GI S+ L+S A SFR + T + ++ C				369	
Query 448	VYVTSKQRAWER 459					
Sbjct 370	Y+TSK R+W R FYITSKHRSWNR 405					

SRX202160

Sequence ID: **SRA:SRR610305.209629.2** Length: 484 Number of Matches: 4
Range 1: 3 to 386

Score	Expect	Method	Identities	Positives	Gaps	Frame
152 bits(383)	1e-41()	Compositional matrix adjust.	72/128(56%)	92/128(71%)	0/128(0%)	+3
Query 134	AHCEILKGCPLLPDSQVQEVNRNPPDNPTIDYSCSPGFKLKGVARISCLPNGQWSSFP				193	
Sbjct 3	++CEI KGC L S+ V E R P NPOTI YSC PGFKL+G +RI CLP+GQW++ PP				182	
Query 194	KCIRECAKVSSPEHGKVNAPSGNMIEGATLRFSCDSPYYLIGQETLTCOGNGQWSGOIPQ				253	
Sbjct 183	CI++CA++S+PEHG+V ++EGAT FSCD YYLIG+ETL+C GQW G IP				362	
Query 254	CKKLVFCEP 261					
Sbjct 363	C+K P CQKADLLP 386					

Range 2: 90 to 374

Score	Expect	Method	Identities	Positives	Gaps	Frame
56.2 bits(134)	3e-08()	Compositional matrix adjust.	33/103(32%)	47/103(45%)	8/103(7%)	+3
Query 222	TLRFSCDSPYYLIGQETLTCOGNGQWSGOIPQCKKLVFCPDLPVNHAHQVIGVEQKY				281	
Sbjct 90	T+ +SC + L G + C +GQW+ P C + C L H E V +				245	
Query 282	GQFPQGETVYTCSGNYFLMGFNTLKNPDGWSGSGSPSCVKV 324					
Sbjct 246	+G T++C Y+L+G TL C+P G W G PSC K				374	

Range 3: 419 to 481

Score	Expect	Method	Identities	Positives	Gaps	Frame
31.6 bits(70)	0.001(2)	Composition-based stats.	10/21(48%)	17/21(80%)	0/21(0%)	+2
Query 272	QVKIGVEQKYGFPGGTEVTY 292					
	++ + EQ+YGG+PQG+ VT+					
Sbjct 419	RLDVSEQQYGYPPQGSNVTF 481					

Range 4: 358 to 426

Score	Expect	Method	Identities	Positives	Gaps	Frame
28.1 bits(61)	0.001(2)	Composition-based stats.	11/23(48%)	15/23(65%)	0/23(0%)	+1
Query 252	PQCKKLVFCPDLDPVNHAEHQVK 274					
	P KKL+FCPDL V + +V+					
Sbjct 358	PHVKKLIFCPDLKGVYNGNIKVR 426					

SRX202160

Sequence ID: **SRA:SRR610305.244830.2** Length: 441 Number of Matches: 5

Range 1: 55 to 294

Score	Expect	Method	Identities	Positives	Gaps	Frame
117 bits(294)	6e-40(4)	Compositional matrix adjust.	48/80(60%)	67/80(83%)	0/80(0%)	+1
Query 272	QVKIGVEQKYGFPGGTEVTYTCSGNYFLMGFNTLKCNPDGSHSGSQPSCVKVADREVDC 331					
	+V + EQ+YGG+PQG+ VT+ CS N++L+G +++ C PDGSHSG QPSCVKVA+ ++C					
Sbjct 55	KVDVSEQQYGYPPQGSNVTFKCSLNHYLIGKSSITCKPDGSHSGRQPSCVKVAENVINC 234					
Query 332	DSKAVDFLDDVGEPVRIHCP 351					
	D+KA++ LDDVGEP+RIHCP					
Sbjct 235	DTKAIELDDVGEPRIHCP 294					

Range 2: 354 to 440

Score	Expect	Method	Identities	Positives	Gaps	Frame
48.9 bits(115)	6e-40(4)	Compositional matrix adjust.	21/29(72%)	26/29(89%)	0/29(0%)	+3
Query 371	SSVCRAAIHAGKLPNSGGAVHVVNNGPYS 399					
	+SVCRAAIH+G + NSGG+V V+NNGPYS					
Sbjct 354	TSVCRAAIHSGIISNSGGSVQVINNGPYS 440					

Range 3: 296 to 352

Score	Expect	Method	Identities	Positives	Gaps	Frame
33.5 bits(75)	6e-40(4)	Compositional matrix adjust.	14/19(74%)	15/19(78%)	0/19(0%)	+2
Query 352	AGCSLTAGTVWGTAIYHEL 370					
	GCSLT G+VWGT IY EL					
Sbjct 296	TGCSLTLSVWGTVIYREL 352					

Range 4: 2 to 37

Score	Expect	Method	Identities	Positives	Gaps	Frame
23.5 bits(49)	6e-40(4)	Composition-based stats.	8/12(67%)	10/12(83%)	0/12(0%)	+2
Query 255	KKLVFCPDLDPV 266					
	+KL+FCPDL V					
Sbjct 2	QKLIFCPDLKGV 37					

Range 5: 85 to 213

Score	Expect	Method	Identities	Positives	Gaps	Frame
43.1 bits(100)	7e-04()	Compositional matrix adjust.	17/43(40%)	28/43(65%)	0/43(0%)	+1

Query 215 GNMIEGATLRFSCDSPYYLIGQETLTCQGNQWSGQIPOCKKL 257
G +G+ + F C +YLIG+ ++TC+ +G WSG+ P C K+
Sbjct 85 GQYPQGSNVTFKCSLNHYLIGKSSITCKPDGWSWGRQPSCKVKV 213

SRX202160
Sequence ID: **SRA:SRR610305.736053.2** Length: 360 Number of Matches: 2
Range 1: 3 to 245

Score	Expect	Method	Identities	Positives	Gaps	Frame
136 bits(342)	1e-38(2)	Compositional matrix adjust.	63/81(78%)	75/81(92%)	0/81(0%)	-2
Query 872	KTPVTLTTRVQICLPTDITTREHLKEGT LAVVTGWLNNNTYSEMIQQAVLPVVAAST	931	+ PV LTRV+P+CLPTD+TTRE+LKEGT AVVTGWLNNEN++YSE++QQAVLPVV+AST			
Sbjct 245	ENPVILTTRVKPVCLPTDLTTRENLKEGT KAVVTGWLNNENDSYSEVLQQAVLPVVSAST	66				
Query 932	CEEGYKADLPLVTENMFCA	952	C++GYK A LPLVTENM CA			
Sbjct 65	CQQGYKNASLPLVTENMICA	3				

Range 2: 242 to 322

Score	Expect	Method	Identities	Positives	Gaps	Frame
42.4 bits(98)	1e-38(2)	Composition-based stats.	18/27(67%)	19/27(70%)	0/27(0%)	-3
Query 846	REALETHVNPVDPGNLNFDIQLK	872	+E EIHVP YDP N DI LIQLK			
Sbjct 322	KEVREIHNPFYDPATFNSDITLIQLK	242				

SRX202160
Sequence ID: **SRA:SRR610305.350008.2** Length: 298 Number of Matches: 1
Range 1: 2 to 247

Score	Expect	Method	Identities	Positives	Gaps	Frame
139 bits(351)	3e-38()	Compositional matrix adjust.	66/82(80%)	72/82(87%)	0/82(0%)	-1
Query 925	PVVAASTCEEYKADLPLVTENMFCAGYKKGRYDACS GGGPLVFADDSRTERRVWL	984	PVV+ASTC++GYK A LPLVTENM CAGYK+G+ DAC GDSGGPLVFAD S+ ER VWL			
Sbjct 247	PVVSASTCQQGYKNASLPLVTENMICAGYKEGKTDACGGDSGGPLVFADYSQRRERVWL	68				
Query 985	EGIVSWGSPSGCGKANQYGGFT	1006	EGIVSWGSPSGCG NQYGGFT			
Sbjct 67	EGIVSWGSPSGCGHPNQYGGFT	2				

SRX202160
Sequence ID: **SRA:SRR610305.393793.2** Length: 306 Number of Matches: 1
Range 1: 3 to 287

Score	Expect	Method	Identities	Positives	Gaps	Frame
135 bits(341)	8e-37()	Compositional matrix adjust.	62/95(65%)	77/95(81%)	0/95(0%)	+3
Query 329	VDCDSKAVDFLDDVGEPVRIHCPAGCSL TAGTVMGTAIYHELSSVCRAAIHAGKLPNSGG	388	++CD+KA++ LDDVGEP+RIHCPAGCSLT G+VMGT IY ELSSVCRAAIH+G + NSGG			
Sbjct 3	INCDTKAIELLDDVGEPRIHCPAGCSLTLGSVMGTVIYRELSSVCRAAIHSGIISNSGG	182				
Query 389	AVHVVNNGPYSDFLGSDLNGIKSEELKSLARSFRF	423	+V V+NNGPYSDF+ S+ GI S+ K + FR			
Sbjct 183	SVQVINNGPYSDFVASNAYGISSKVTKVSSS*FRL	287				

SRX202160
Sequence ID: **SRA:SRR610305.189814.2** Length: 433 Number of Matches: 3
Range 1: 31 to 243

Score	Expect	Method	Identities	Positives	Gaps	Frame
101 bits(251)	2e-36(3)	Compositional matrix adjust.	47/71(66%)	56/71(78%)	0/71(0%)	+1

Query 353 GCSLTAGTVWGTAIYHELSSVCRAAIHAGKLPNSGGAVHVNNNGPYSDFLGSDLNGIKSE 412
CSLT G+VMGT IY ELSSVCRAAIH+G + NSGG+V V+NNGPYSDF+ S+ GI S+
Sbjct 31 ACSLTLGSVWGTVIYRELSSVCRAAIHSGIISNSGGSVQVINNGPYSDFVASNAYGISSK 210

Query 413 ELKSLARSFRF 423
L+S A SFR
Sbjct 211 VLRSQAVSFRL 243

Range 2: 260 to 403

Score	Expect	Method	Identities	Positives	Gaps	Frame
64.3 bits(155)	2e-36(3)	Compositional matrix adjust.	25/48(52%)	35/48(72%)	0/48(0%)	+2
Query 428	SSTAGRSGCPDGFVEEENCYVVTISKORAWERAQGVCTNMAARLAVLD	475	++ + CP GW+++E C Y+TSK R+W RA GVC+NMA+ LAVLD			
Sbjct 260	NTNGNQKECPPGWYQIENKCFYITSKHSWNRALGVCNMASSLAVLD	403				

Range 3: 3 to 32

Score	Expect	Method	Identities	Positives	Gaps	Frame
25.8 bits(55)	2e-36(3)	Composition-based stats.	9/10(90%)	10/10(100%)	0/10(0%)	+3
Query 344	EPVRIHCPAG	353				
Sbjct 3	EPIRIHCPAG	32				

SRX202160

Sequence ID: **SRA:SRR610305.232597.2** Length: 410 Number of Matches: 2
Range 1: 118 to 339

Score	Expect	Method	Identities	Positives	Gaps	Frame
122 bits(306)	4e-36(2)	Compositional matrix adjust.	58/74(78%)	64/74(86%)	0/74(0%)	+1
Query 947	ENMFCAGYKGRYDACSGDSGGPLVFADDSRTERRWVLEGIVSWGSPSGCGKANQYGGFT	1006	+NM CAGYK+G+ DAC GDSGGPLVFAD S+ ER WVLEGIVSWGSPSGCG NQYGGFT			
Sbjct 118	KNMICAGYKEGKTACGGDSGGPLVFADYSQREVRWVLEGIVSWGSPSGCGHPNQYGGFT	297				
Query 1007	KVNVFLSWIROFI*	1020	+V+ FLSWI OFI*			
Sbjct 298	RVHSFLSWINQFI*	339				

Range 2: 8 to 91

Score	Expect	Method	Identities	Positives	Gaps	Frame
47.8 bits(112)	4e-36(2)	Composition-based stats.	19/28(68%)	28/28(100%)	0/28(0%)	+2
Query 911	ENNTYSEMIQQAVLPVVAASTCEEYKE	938	+N++YSE++QQAVLPVV+ASTC++GYK+			
Sbjct 8	KNDSYSEVLQQAVLPVVSASTCQQGYKK	91				

SRX202160

Sequence ID: **SRA:SRR610305.204499.2** Length: 468 Number of Matches: 2
Range 1: 123 to 338

Score	Expect	Method	Identities	Positives	Gaps	Frame
135 bits(340)	5e-36()	Compositional matrix adjust.	63/72(88%)	70/72(97%)	0/72(0%)	-2
Query 922	AVLPVVAASTCEEYKEADLPLTVTENMFCAGYKGRYDACSGDSGGPLVFADDSRTERR	981	+VLPVVAASTCE+GY+++ LPLTVTE MFCAGYK+GRYDACSGDSGGPLVFADDSRT+RR			
Sbjct 338	SVLPVVAASTCEQGYQDSGLPLTVTEYMFACAGYKGRYDACSGDSGGPLVFADDSRTDRR	159				
Query 982	WVLEGIVSWGSP	993				
Sbjct 158	WVLEGIVSWGSP	123				

Range 2: 41 to 466

Score	Expect	Method	Identities	Positives	Gaps	Frame
123 bits(308)	1e-31()	Composition-based stats.	74/152(49%)	92/152(60%)	20/152(13%)	-3
Query 879	TRVQPICLPDITTREHLKEGT	LAVVTGWLNNNTYSEMIQQA	VPVAASTCEEGYK-	937		
Sbjct 466	TRVQPICLPDITTREHLKEGT	LAVVTGWLNNNTYSEMIQQA	++ + + +	287		
Query 938	-----EADLPLTVTENMFCAGYKKGRYDACS	G--DSGGPLVFADDSRTERRWLEGIV	988			
Sbjct 286	RACH*Q*QSTCSVQVTS-----RGAMMPAVGTV	EDH*CLLMIPAPIGGGSW--KGSS	137			
Query 989	SWGSPSGCGKANQYGGFTKVN	VFLSWIRQFI*	1020			
Sbjct 136	+ +P+GCGK+NQYGGFTKVN	VFLSWIRQFI*	41			

SRX202160
Sequence ID: **SRA:SRR610305.213632.2** Length: 449 Number of Matches: 1
Range 1: 3 to 314

Score	Expect	Method	Identities	Positives	Gaps	Frame
134 bits(337)	1e-35()	Compositional matrix adjust.	71/104(68%)	74/104(71%)	25/104(24%)	-1
Query 1	MVLASFLVSGLVL-----	GILAQMRPVQSRGVDLGLCDE	35			
Sbjct 314	MVLASFLVS L L	G+LAQOM PVQSRGVDLGLCD+	135			
Query 36	TRFECKCGDPGYVFNVP	MPKQCTYFYRWRPYCKPCDDLEAKDICP	79			
Sbjct 134	TRFECKCGDPGYVFNVP	KQCTYFYRWRPYCKPCD LEAKD+CP	3			

SRX202160
Sequence ID: **SRA:SRR610305.767547.2** Length: 344 Number of Matches: 1
Range 1: 111 to 323

Score	Expect	Method	Identities	Positives	Gaps	Frame
132 bits(333)	1e-35()	Compositional matrix adjust.	60/71(85%)	63/71(88%)	0/71(0%)	+3
Query 14	GILAQMRPVQSRGVDLGLCDE	TRFECKCGDPGYVFNVPMPKQCTYFYRWRPYCKPCDDLE	73			
Sbjct 111	AISPKNKCTPVQSRGVDLGLCDD	TRFECKCGDPGYVFNVPKQCTYFYRWRPYCKPCDKLE	290			
Query 74	AKDICPKYKRC	84				
Sbjct 291	AKD+CPKYKRC	323				

SRX202160
Sequence ID: **SRA:SRR610305.83961.2** Length: 280 Number of Matches: 1
Range 1: 1 to 192

Score	Expect	Method	Identities	Positives	Gaps	Frame
130 bits(326)	7e-35()	Compositional matrix adjust.	61/64(95%)	64/64(100%)	0/64(0%)	+1
Query 957	GRYDACS	GGPLVFADDSRTERRWLEGIVSWGSPSGCGKANQYGGFTKVN	VFLSWIR	1016		
Sbjct 1	GRYDACS	GGPLVFADDSRTDRRWLEGIVSWGSPNGCGKSNQYGGFTKVN	VFLSWIR	180		
Query 1017	QFI*	1020				
Sbjct 181	QFI*	192				

SRX202160
Sequence ID: **SRA:SRR610305.716410.2** Length: 258 Number of Matches: 1
Range 1: 3 to 233

Score	Expect	Method	Identities	Positives	Gaps	Frame
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129 bits(325)		7e-35()	Compositional matrix adjust.		56/77(73%)	69/77(89%)	0/77(0%)	+3
Query	329	VDCDSKAVDFLDDVGEPVRIHCPAGCSLTAGTVWGTAIYHELSSVCRAAIHAGKLPNSGG	388					
Sbjct	3	++CD+KA++ LDDVGEP+RIHCPAGCSLT G+VWGT IY ELSSVCRAAIH+G + NSGG INCDTKAIELLDDVGEPRIHCPAGCSLTGSGVWGTVIYRELSSVCRAAIHSGIISNSGG	182					
Query	389	AVHVVNNGPYSDFLGSD	405					
Sbjct	183	+V V+NNGPYSDF+ S+ SVQVINNGPYSDFVASN	233					

SRX202160
Sequence ID: **SRA:SRR610305.326762.2** Length: 261 Number of Matches: 1
Range 1: 1 to 255

Score	Expect	Method	Identities	Positives	Gaps	Frame
128 bits(322)	2e-34()	Compositional matrix adjust.	60/85(71%)	70/85(82%)	0/85(0%)	+1
Query	339	LDDVGEPVRIHCPAGCSLTAGTVWGTAIYHELSSVCRAAIHAGKLPNSGGAVHVVNNGPY	398			
Sbjct	1	LDDVGEP+RIHCPAG SLT G+VWGT IY ELSSVCRAAIH+G + NSGG+V V+NNGPY LDDVGEPRIHCPAGRSLTLGSGVWGTVIYRELSSVCRAAIHSGIISNSGGSVQVINNGPY	180			
Query	399	SDFLGSDLNGIKSEELKSLARSFRF	423			
Sbjct	181	SDF+ S+ GI S+ L+S A SFR SDFVASNAYGISSKVLRSQAVSFRL	255			

SRX202160
Sequence ID: **SRA:SRR610305.63226.2** Length: 199 Number of Matches: 2
Range 1: 3 to 185

Score	Expect	Method	Identities	Positives	Gaps	Frame
127 bits(319)	2e-34()	Compositional matrix adjust.	58/61(95%)	61/61(100%)	0/61(0%)	+3
Query	220	GATLRFSCDSPYYLIGQETLTCQGNQWSGQIPQCKLVFCPLDPVNHAEHQVKIGVEQ	279			
Sbjct	3	GATLRFSCDSPYYLIGQETLTCQGNQWSGQIPQC+KLVFCPLDPV+HAEHQVKIG+EQ GATLRFSCDSPYYLIGQETLTCQGNQWSGQIPQCQKLVFCPLDPVSHAEHQVKIGLEQ	182			
Query	280	K 280				
Sbjct	183	K 185				

Range 2: 3 to 119

Score	Expect	Method	Identities	Positives	Gaps	Frame
39.3 bits(90)	0.003()	Compositional matrix adjust.	15/39(38%)	22/39(56%)	0/39(0%)	+3
Query	287	GTEVTYTCSGNYFLMGFNTLKCNDPGSWSGSQPSCVKVA	325			
Sbjct	3	G + ++C Y+L+G TL C +G WSG P C K+ GATLRFSCDSPYYLIGQETLTCQGNQWSGQIPQCQKLV	119			

SRX202160
Sequence ID: **SRA:SRR610305.585142.2** Length: 412 Number of Matches: 2
Range 1: 1 to 228

Score	Expect	Method	Identities	Positives	Gaps	Frame
82.4 bits(202)	6e-34(2)	Compositional matrix adjust.	37/76(49%)	50/76(65%)	0/76(0%)	-2
Query	425	YVSSSTAGRSGCPDGMFEVEENCYVYTSKORAWERAQGVCTNMAARLAVLDKDLIPSSLT	484			
Sbjct	228	Y +S+ + CP G +++E C Y+TSK R+W RAQGV+C+NMA+ LAVLD + SL+ Y*NSTQWNQKECPGXYQIENKCFYITSKHSWNRAQGVCSNMASLAVLDGAVAQQSL5	49			
Query	485	ETLRGKGLTTTWIGLH	500			
Sbjct	48	+ L KGL WIGL DILNKKGLVKIWIQLQ	1			

Range 2: 219 to 407

Score	Expect	Method	Identities	Positives	Gaps	Frame
80.5 bits(197)	6e-34(2)	Composition-based stats.	40/65(62%)	49/65(75%)	2/65(3%)	-3
Query 366	IYHELSSVCRAAIHAGKLPNSGGAVHVVNNGPYSDFLGSDLNGIKSEELKSLARSFRFDY					425
	IY ELSSVCRAAIH+G + NSGG+V V+NNGPYSDF+ S+ GI S+ +S A SFR					
Sbjct 407	IYRELSSVCRAAIHSGIISNSGGSVQVINNGPYSDFVASNAYGISSKVPVSQAVSFRL --					234
Query 426	VSSST					430
	VS+ T					
Sbjct 233	VSTET					219

SRX202160

Sequence ID: **SRA:SRR610305.144057.2** Length: 398 Number of Matches: 1
Range 1: 34 to 396

Score	Expect	Method	Identities	Positives	Gaps	Frame
128 bits(321)	9e-34()	Compositional matrix adjust.	61/121(50%)	80/121(66%)	1/121(0%)	+1
Query 381	GKLPNSGGAVHVVNNGPYSDFLGSDLNGIKSEELKSLARSFRFDYVSSSTAG-RSGCPDG					439
	G + NSGG+V V+NNGPYSDF+ S+ GI S+ L+S A SFR + G + CP G					
Sbjct 34	GIISNSGGSVQVINNGPYSDFVASNAYGISSKVLRSQAVSFRLVSTETQHNGNQKECPPG					213
Query 440	WFEVEENCYVVTSKQRAWERAQGVCTNMAARLAVLDKDLIPSSLTETLRGKGLTTTWIGL					499
	W++++ C Y+TSK R+W RA GVC+NMA+ LAVLD + SL++ L KGL WIGL					
Sbjct 214	WYQIENKCFYITSKHRSWNRALGVCSNMASSLAVLDSAVAQQLSDIILNKKGLVKIWIIGL					393
Query 500	H					500
Sbjct 394	Q					396

SRX202160

Sequence ID: **SRA:SRR610305.637738.2** Length: 316 Number of Matches: 1
Range 1: 43 to 282

Score	Expect	Method	Identities	Positives	Gaps	Frame
126 bits(317)	2e-33()	Compositional matrix adjust.	57/80(71%)	68/80(85%)	0/80(0%)	+1
Query 697	VDLASKVKLPEGHYRVGSRAIYTCESRYELLGSGRRCDNNGWNGRPPASCIPVCGRSD					756
	V+ ++ LP+GHY VG++A YTCES+YY+LLGS+GRRCS+S+G W GRPASCIPVCGRSD					
Sbjct 43	VNPVDQIILPKGHYHVGTSQASYTCESQYKLLGSKGRRCESSGTWGRPPASCIPVCGRSD					222
Query 757	SPRSPFIWNGNSTEIGQWNP 776					
	SPRSPFI NG T IGQWNP					
Sbjct 223	SPRSPFIINGVVTGIGQWNP 282					

SRX202160

Sequence ID: **SRA:SRR610305.244045.2** Length: 465 Number of Matches: 1
Range 1: 3 to 425

Score	Expect	Method	Identities	Positives	Gaps	Frame
127 bits(318)	6e-33()	Compositional matrix adjust.	65/142(46%)	86/142(60%)	14/142(9%)	-2
Query 1	MVLASFLVSLVLGILAQQMRPVQSR-----GVDLGLCDETRFECKGDPGVVFN					50
	++L+S + + I P+S GVD LCD+ F C CG PGY F+					
Sbjct 425	IMLSSLFIIWFISIAG*SGMPRRSTSGFGKLLGNIGVD-KLCDKIFICACGKPGVTFH					249
Query 51	VPMKQCT---YFYRWRYCKPCDDLEAKDICPKYKRCQECKAGLDSCVTCPPNKGVTWCS					107
	+P+KQC F W C+PC+D+ +D+CPKYK+C ECK LD CV+CPPN+YG WC+					
Sbjct 248	IPIKQCISIDKFKFWETSCEPCNDISPEDVCPKYKQCLECKHNLDRCVSCPPNRYGDWCN					69
Query 108	GEQCCKNGGICDQRTGACTCRD 129					
	G C CKNGG C+Q TG C CR+					
Sbjct 68	GVCDCKNGGTGNQETGECFCRE 3					

SRX202160

Sequence ID: **SRA:SRR610305.272757.2** Length: 327 Number of Matches: 1

Range 1: 3 to 191

Score	Expect	Method	Identities	Positives	Gaps	Frame
124 bits(312)	8e-33()	Compositional matrix adjust.	55/63(87%)	60/63(95%)	0/63(0%)	+3
Query 258	VFCPLDPVNHAHQVIGVEQKYGFPGTEVTTYTCSGNYFLMGFNTLKCNPDGWSWGS					317
Sbjct 3	VFCPLDPV+HAEHQVIG+EQKYGFPGTEVTTYT +GNYFLMG +TLKCNPDGWSG+					182
Query 318	QPS 320					
Sbjct 183	QPK 191					

SRX202160

Sequence ID: **SRA:SRR610305.133655.2** Length: 485 Number of Matches: 1
Range 1: 2 to 187

Score	Expect	Method	Identities	Positives	Gaps	Frame
126 bits(316)	1e-32()	Compositional matrix adjust.	59/62(95%)	62/62(100%)	0/62(0%)	+2
Query 959	YDACSGDSGGPLVFADDSRTERRRWLEGIVSWGSPSGCGKANQYGGFTKVNVLFSWIRQF					1018
Sbjct 2	YDACSGDSGGPLVFADDSRT+RRWLEGIVSWGSP+GCGK+NQYGGFTKVNVLFSWIRQF					181
Query 1019	I* 1020					
Sbjct 182	I* 187					

SRX202160

Sequence ID: **SRA:SRR610305.231346.2** Length: 453 Number of Matches: 1
Range 1: 68 to 259

Score	Expect	Method	Identities	Positives	Gaps	Frame
125 bits(314)	2e-32()	Composition-based stats.	59/64(92%)	60/64(93%)	0/64(0%)	+2
Query 858	DPGNLNFIDIALIQLKTPVTLTTRVQPICLPDITTREHLKEGT LAVVTGWLNNNTYSE					917
Sbjct 68	DPGNLNFIDIALIQLKT V LTTRVQPICLPD TTRE+LKEG LAVVTGWLNNNTYSE					247
Query 918	MIQQ 921					
Sbjct 248	MIQQ 259					

SRX202160

Sequence ID: **SRA:SRR610305.691564.2** Length: 320 Number of Matches: 1
Range 1: 69 to 311

Score	Expect	Method	Identities	Positives	Gaps	Frame
123 bits(309)	2e-32()	Compositional matrix adjust.	57/81(70%)	67/81(82%)	0/81(0%)	+3
Query 343	GEPVRIHCPAGCSLTAGTVWGTAIYHELSSVCRAAIHAGKLPNSGGAVHVNNNGPYSDFL					402
Sbjct 69	GEP+RIHCPAGCSLT G+VWGT IY ELSSVCRAAIH+G + NSGG+V V+NNNGPYSDF+					248
Query 403	GSDLNGIKSEELKSLARSFRF 423					
Sbjct 249	S+ GI S+ L+S A SFR ASNAVGISSKVLRSQAVSFRL 311					

SRX202160

Sequence ID: **SRA:SRR610305.406882.2** Length: 274 Number of Matches: 1
Range 1: 55 to 273

Score	Expect	Method	Identities	Positives	Gaps	Frame
122 bits(306)	3e-32()	Compositional matrix adjust.	53/73(73%)	65/73(89%)	0/73(0%)	+1

Query 327 REVDGCDKAVDFLDDVGEPVRIHCPAGCSLTAGTVWGTAIYHELSSVCRAAIHAGKLPNS 386
+ ++CD+KA++ LDDVGEP+RIHCPAGCSLT G+VWGT IY ELSSVCRAAIH+G + NS
Sbjct 55 KVINCDTKAIELLDDVGEPIRIHCPAGCSLTGSGVWGTIVYRELSSVCRAAIHSGIISNS 234

Query 387 GGAVHVVNNGPYS 399
GG+V V+NNGPYS
Sbjct 235 GGSVQVINNGPYS 273

SRX202160
Sequence ID: **SRA:SRR610305.677355.2** Length: 344 Number of Matches: 2
Range 1: 2 to 196

Score	Expect	Method	Identities	Positives	Gaps	Frame
102 bits(254)	3e-31(2)	Compositional matrix adjust.	45/65(69%)	53/65(81%)	0/65(0%)	-2
Query 728	LGSQGRRCDSNGNWSGRPASCI	PVCGRSDSPRSPFIWNGNSTEIGQWPWQAGISRWLADH	787			
	L +GRRC+S+G W GRPASCI	PVCGRSDSPRSPFI NG T+IGQWPW AGI+RW +				
Sbjct 196	LDQKGRRCESG	TWGGRPASCI	PVCGRSDSPRSPFIINGVVTDIGQWPWHAGIARWYPEQ	17		
Query 788	NMWFL	792				
	+WF+					
Sbjct 16	EVWFI	2				

Range 2: 186 to 308

Score	Expect	Method	Identities	Positives	Gaps	Frame
51.2 bits(121)	3e-31(2)	Composition-based stats.	22/41(54%)	34/41(82%)	2/41(4%)	-1
Query 693	QPS	TVDL--ASKVKLPEGHYRVGSRAIYTCESRYELLGSQ	731			
	+PS+++ ++ LP+GHY VG+RA YTCES+YY+LLGS+					
Sbjct 308	KPSSLNVNPDQIILPKGHYHVG	TRAS	YTCESQYKLLGSK	186		

SRX202160
Sequence ID: **SRA:SRR610305.49279.2** Length: 442 Number of Matches: 3
Range 1: 224 to 439

Score	Expect	Method	Identities	Positives	Gaps	Frame
120 bits(301)	7e-31()	Compositional matrix adjust.	66/72(92%)	70/72(97%)	0/72(0%)	-1
Query 589	LHGQSIDGFYAGSSIRYSCEVLHYLSG	tetvtcttngtWSAPKPRCIKVITCQNPVPSY	648			
	LHGQSIDGFYAGSS+RYSCEVLHYLSGTETV+CT+NGTWSAPKPRCIKVITCQ	PPVPSY				
Sbjct 439	LHGQSIDGFYAGSSVRYSC	EVLYLSGTETVSC	TNGTWSAPKPRCIKVITCQTPPVPSY	260		
Query 649	GSVEIKPPSRTN	660				
	GSV+IKPPSRT					
Sbjct 259	GSVDIKPPSRTK	224				

Range 2: 188 to 406

Score	Expect	Method	Identities	Positives	Gaps	Frame
48.1 bits(113)	1e-05()	Compositional matrix adjust.	24/73(33%)	39/73(53%)	2/73(2%)	-1
Query 220	GATLRFSCDSPYYLIGQETLTCQGNQWSGQIPQCKKL	VFCPLDPVNHAHQVKIGVEQ	279			
	G+++R+SC+ +YL G ET++C NG WS P+C K++ C ++ +K					
Sbjct 406	GSSVRYSC	EVLYLSGTETVSC	TNGTWSAPKPRCIKVITCQTPPVPSYGSVDIKPPSRT	227		
Query 280	KYGQFP--QGTEV	290				
	K+ P G EV					
Sbjct 226	KFSAPVKSGDEV	188				

Range 3: 293 to 430

Score	Expect	Method	Identities	Positives	Gaps	Frame
40.4 bits(93)	0.006()	Compositional matrix adjust.	17/46(37%)	26/46(56%)	0/46(0%)	-1
Query 279	QKYGQFPQGTETVYTCSGNYFLMGFNTLKCNP	DGSHSGSQPSVVKV	324			
	Q F G+ V Y+C ++L G T+ C +G+WS +P C+KV					
Sbjct 430	QSIDGFYAGSSVRYSC	EVLYLSGTETVSC	TNGTWSAPKPRCIKV	293		

SRX202160

Sequence ID: **SRA:SRR610305.180913.2** Length: 400 Number of Matches: 1
Range 1: 33 to 323

Score	Expect	Method	Identities	Positives	Gaps	Frame
119 bits(299)	1e-30()	Compositional matrix adjust.	56/97(58%)	72/97(74%)	0/97(0%)	+3
Query 139	LKGCPLLP	SDSQVQEVNPPDNPTIDYSCSPGFKLKGVARISCLPNGQWSSFPPKCIRE	198			
Sbjct 33	LKGC L S+ V E R P NPOTI YSC PGF+L+G +RI CLP+GOW++ PP CI++	LKGC L P QSNPGVIEERKPKVNPOTISYSCLPGFRLQGPSRIICLP SGQWTLNLPSCIQQ	212			
Query 199	CAKVSSPEHGKVNAPSGNMIEGATLRFSCDSPYYLIG	235				
Sbjct 213	CA++S+PEHG+V +++EGAT FSCD YYLIG	CARLSAPEHGEVTRFGKDLLEGATATFSCDRTYYLIG	323			

SRX202160

Sequence ID: **SRA:SRR610305.219525.2** Length: 434 Number of Matches: 3
Range 1: 74 to 361

Score	Expect	Method	Identities	Positives	Gaps	Frame
116 bits(291)	2e-30(2)	Compositional matrix adjust.	58/96(60%)	74/96(77%)	0/96(0%)	+2
Query 544	RDQLQPVWTKSCFQPSFACMMDLSDRNKAACDDPGPLENGHATLHGQSIDGFYAGSSI	603				
Sbjct 74	++Q +PVW+T SC QP++F CM+ S+RN+A+C+D G LENG+A LHGO GFYAG +I	KNQFEPVWRTSSCSQPAAFMCMIGFSNRNEARCEDTGSLENGYAKLHGQSFYAGLTI	253			
Query 604	RYSCEVLHYLSGtetvtcttngtWSAPKPRCIKVIT	639				
Sbjct 254	YSC+ LHY SG+ TCTTNGTWS KPRCIK+ T	SYSCKELHYPSGSSVQTCTTNGTWSTIKPRCIKIT	361			

Range 2: 351 to 428

Score	Expect	Method	Identities	Positives	Gaps	Frame
34.7 bits(78)	2e-30(2)	Composition-based stats.	14/26(54%)	20/26(76%)	0/26(0%)	+3
Query 636	KVITCONPPVPSYGSVEIKPPSRTNS	661				
Sbjct 351	K++ ++PPVP+YG VEIK P R +S	KLLPSESPPVPAYGLVEIKTPERISS	428			

Range 3: 4 to 129

Score	Expect	Method	Identities	Positives	Gaps	Frame
42.4 bits(98)	0.001()	Composition-based stats.	20/42(48%)	24/42(57%)	0/42(0%)	+1
Query 521	NDNLTFWASGEPGNETNCVYLDIRDQLQPVWTKSCFQPSF	562				
Sbjct 4	NDNLTFWA+ EP E CVYLD + + + F SSF	NDNLTFWATEEPNMENVCVYLDAKKSV*ASMEDIILFSTSSF	129			

SRX202160

Sequence ID: **SRA:SRR610305.33690.2** Length: 271 Number of Matches: 1
Range 1: 1 to 255

Score	Expect	Method	Identities	Positives	Gaps	Frame
117 bits(292)	2e-30()	Compositional matrix adjust.	80/85(94%)	82/85(96%)	0/85(0%)	-2
Query 627	WSAPKPRCIKVITCONPPVPSYGSVEIKPPSRTNSISRVSFPFlr1pr1plplaraakpp	686				
Sbjct 255	WSAPKPRCIKVITCO PPVPSYGSV+IKPPSRTNSISR+GSPFLRLPLPLARAAPKPP	76				
Query 687	pkprSSQPSTVDLASKVKLPEGHYR	711				
Sbjct 75	PK' RSS 'PSTVDLASKVKLPEGHYR	1				

SRX202160
Sequence ID: **SRA:SRR610305.624115.2** Length: 245 Number of Matches: 2
Range 1: 55 to 231

Score	Expect	Method	Identities	Positives	Gaps	Frame
115 bits(288)	6e-30()	Compositional matrix adjust.	51/59(86%)	54/59(91%)	0/59(0%)	+1
Query 557	FQPSSSFACMMDLSDRNKAKCDDPGPLENGHATLHGQSIDGFYAGSSIRYSCEVLHYLSG					615
	F P F CMMDLSD+NKAKC+DPGPLENGHA LHGQSIDGFYAGSS+RYSCEVLHYLSG					
Sbjct 55	FNQVVFVCMMDLSDKNKAKCNDPGPLENGHAKLHGQSIDGFYAGSSVRYSCCEVLHYLSG					231

Range 2: 3 to 83

Score	Expect	Method	Identities	Positives	Gaps	Frame
52.0 bits(123)	2e-07()	Compositional matrix adjust.	24/28(86%)	26/28(92%)	1/28(3%)	+3
Query 540	YLDIRDQLQPVWKTSCFQPSFACMMD		567			
	YLDI+DQLQPVWKTSCFQPSF C+ D					
Sbjct 3	YLDIQDQLQPVWKTSCFQPSF-CLYD		83			

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d2a8521273f934deafb44229a8e21a87

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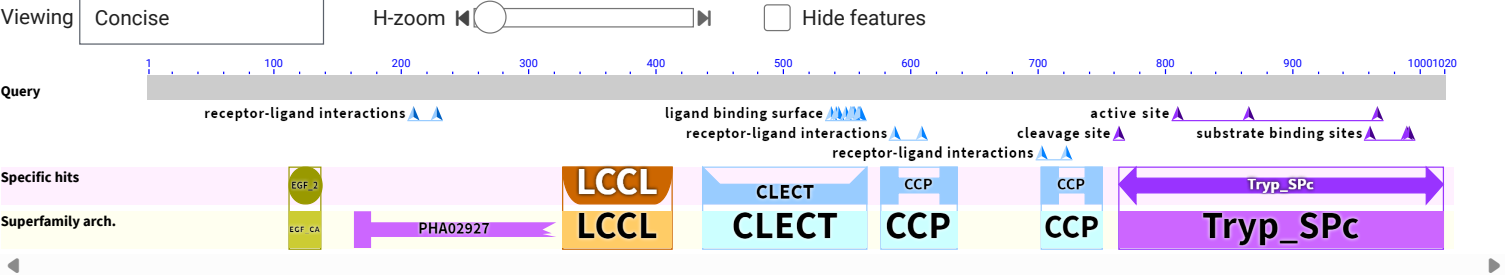
Database: CDSEARCH/cdd

E-value cut off: 0.01

Composition-based adjustment: yes

Low-complexity filter: no

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 Name	Accession	Description	Interval	E-value
+ Tryp_SPc	cd00190	Trypsin-like serine protease	764-1018	2.18×10^{-81}
+ LCCL	smart00603	LCCL domain	327-412	9.81×10^{-36}
+ CLECT	smart00034	C-type lectin (CTL) or carbohydrate-recognition domain (CRD)	437-565	2.90×10^{-18}
+ PHA02927	PHA02927	secreted complement-binding protein	163-321	2.15×10^{-12}
+ CCP	cd00033	Complement control protein (CCP) modules (aka short consensus repeats SCRs or SUSHI repeats) have been identified in several proteins of the complement system	577-636	3.06×10^{-10}

 Feedback

 Name	Accession	Description	Interval	E-value
+ CCP	cd00033	Complement control protein (CCP) modules (aka short consensus repeats SCRs or SUSHI repeats) have been identified in several proteins of the complement system	703-750	1.52×10^{-6}
+ EGF_2	pfam07974	EGF-like domain	112-136	3.61×10^{-3}

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T.t protein seq used for tblastn query was derived from translation of Accession: D14701

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BLAST® >> **tblastn-SRA** >> results for RID-J1UTAWZA016

Important update
The **ClusteredNR** database is now the **default** Protein BLAST database. [Learn more about ClusteredNR](#)

Job Title	Protein Sequence...
RID	J1UTAWZA016 Search expires on 11-23 05:43 am
Program	TBLASTN
Database	SRA
Query ID	Ic Query_4535419
Description	unnamed_protein_product...
Molecule type	amino acid
Query Length	401

Descriptions

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
▼	▼	▼	▼	▼	▼	▼	
SRX202160	239	239	34%	1e-77	85.29%	509	SRA:SRR610305.171358.2
SRX202160	226	226	37%	1e-72	75.50%	511	SRA:SRR610305.115428.2
SRX202160	187	187	34%	8e-58	69.34%	478	SRA:SRR610305.157061.2
SRX202160	174	174	30%	1e-52	72.13%	428	SRA:SRR610305.255262.2
SRX202160	172	264	42%	1e-51	61.25%	499	SRA:SRR610305.214510.2
SRX202160	165	165	23%	6e-50	88.04%	280	SRA:SRR610305.45659.2
SRX202160	166	166	36%	1e-49	60.27%	439	SRA:SRR610305.201975.2
SRX202160	162	162	28%	1e-48	73.21%	378	SRA:SRR610305.607373.2
SRX202160	152	152	20%	1e-44	85.54%	363	SRA:SRR610305.241420.2
SRX202160	145	145	27%	3e-42	68.81%	327	SRA:SRR610305.737708.2
SRX202160	145	145	30%	4e-42	56.56%	376	SRA:SRR610305.140124.2
SRX202160	143	236	33%	1e-40	88.00%	467	SRA:SRR610305.146939.2
SRX202160	141	141	19%	3e-40	85.71%	365	SRA:SRR610305.145522.2
SRX202160	137	137	18%	6e-39	85.33%	320	SRA:SRR610305.605162.2
SRX202160	137	137	38%	2e-38	45.39%	458	SRA:SRR610305.243191.2
SRX202160	134	134	18%	2e-37	86.11%	448	SRA:SRR610305.358932.2
SRX202160	132	132	28%	3e-37	63.06%	334	SRA:SRR610305.604182.2
SRX202160	132	132	32%	9e-37	49.22%	446	SRA:SRR610305.181294.2
SRX202160	126	126	26%	1e-34	57.28%	390	SRA:SRR610305.109827.2
SRX202160	127	127	34%	1e-34	46.72%	505	SRA:SRR610305.225432.2
SRX202160	124	124	21%	2e-34	74.12%	259	SRA:SRR610305.531623.2
SRX202160	127	127	35%	2e-34	43.97%	505	SRA:SRR610305.148321.2
SRX202160	125	125	36%	2e-33	41.89%	529	SRA:SRR610305.96962.2

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
SRX202160	122	122	22%	2e-33	68.54%	296	SRA:SRR610305.353544.2
SRX202160	119	158	20%	9e-33	82.35%	434	SRA:SRR610305.220615.2
SRX202160	118	118	24%	5e-32	63.27%	293	SRA:SRR610305.385163.2
SRX202160	118	118	17%	8e-32	83.82%	338	SRA:SRR610305.468223.2
SRX202160	118	118	30%	2e-31	45.00%	423	SRA:SRR610305.73348.2
SRX202160	116	116	16%	6e-31	84.62%	384	SRA:SRR610305.517531.2
SRX202160	115	115	16%	1e-30	83.08%	327	SRA:SRR610305.414191.2
SRX202160	115	115	26%	3e-30	56.19%	406	SRA:SRR610305.115187.2
SRX202160	115	115	29%	6e-30	46.61%	520	SRA:SRR610305.127978.2
SRX202160	113	113	26%	8e-30	55.24%	374	SRA:SRR610305.598174.2
SRX202160	113	113	33%	1e-29	46.97%	388	SRA:SRR610305.62354.2
SRX202160	113	113	35%	2e-29	40.85%	437	SRA:SRR610305.126966.2
SRX202160	113	113	26%	2e-29	55.66%	421	SRA:SRR610305.617893.2
SRX202160	80.1	165	20%	7e-29	92.31%	414	SRA:SRR610305.504278.2
SRX202160	108	108	27%	3e-28	51.75%	335	SRA:SRR610305.737967.2
SRX202160	108	108	26%	9e-28	53.33%	436	SRA:SRR610305.267540.2
SRX202160	109	109	34%	9e-28	45.00%	492	SRA:SRR610305.296720.2
SRX202160	108	108	25%	1e-27	53.47%	413	SRA:SRR610305.112981.2
SRX202160	108	108	36%	2e-27	37.24%	445	SRA:SRR610305.137483.2
SRX202160	105	105	19%	2e-27	69.74%	244	SRA:SRR610305.732562.2
SRX202160	108	108	24%	4e-27	50.00%	527	SRA:SRR610305.201015.2
SRX202160	85.9	139	29%	5e-27	62.90%	454	SRA:SRR610305.188779.2
SRX202160	104	154	22%	9e-27	73.24%	285	SRA:SRR610305.103135.2
SRX202160	105	105	24%	1e-26	56.12%	431	SRA:SRR610305.393406.2
SRX202160	105	105	24%	3e-26	52.53%	491	SRA:SRR610305.216960.2
SRX202160	104	104	37%	6e-26	34.90%	499	SRA:SRR610305.130106.2
SRX202160	102	102	18%	9e-26	65.28%	327	SRA:SRR610305.71831.2
SRX202160	102	102	26%	1e-25	45.79%	368	SRA:SRR610305.29509.2
SRX202160	102	102	26%	1e-25	45.79%	368	SRA:SRR610305.20998.2
SRX202160	102	102	22%	1e-25	52.27%	373	SRA:SRR610305.183648.2
SRX202160	102	102	16%	2e-25	73.13%	386	SRA:SRR610305.403595.2
SRX202160	101	101	20%	2e-25	58.33%	343	SRA:SRR610305.600452.2
SRX202160	102	102	37%	4e-25	32.21%	498	SRA:SRR610305.207366.2
SRX202160	101	101	30%	1e-24	40.16%	509	SRA:SRR610305.191995.2
SRX202160	97.4	97.4	14%	1e-24	82.14%	182	SRA:SRR610305.33895.2
SRX202160	100	100	37%	2e-24	39.22%	442	SRA:SRR610305.744412.2
SRX202160	93.2	129	17%	3e-24	87.50%	205	SRA:SRR610305.78486.2
SRX202160	98.6	98.6	20%	4e-24	58.33%	394	SRA:SRR610305.407901.2
SRX202160	96.7	96.7	16%	5e-24	68.75%	226	SRA:SRR610305.175549.2
SRX202160	96.7	96.7	16%	7e-24	68.75%	268	SRA:SRR610305.170455.2
SRX202160	96.7	96.7	16%	7e-24	68.75%	272	SRA:SRR610305.294718.2
SRX202160	96.7	96.7	16%	7e-24	68.75%	274	SRA:SRR610305.134560.2
SRX202160	96.7	96.7	16%	8e-24	68.75%	283	SRA:SRR610305.142868.2
SRX202160	96.7	96.7	16%	8e-24	68.75%	283	SRA:SRR610305.25527.2
SRX202160	96.7	96.7	16%	8e-24	68.75%	286	SRA:SRR610305.151142.2
SRX202160	96.7	96.7	16%	8e-24	68.75%	288	SRA:SRR610305.103811.2
SRX202160	96.7	96.7	16%	8e-24	68.75%	288	SRA:SRR610305.16200.2

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
SRX202160	96.7	96.7	16%	8e-24	68.75%	291	SRA:SRR610305.222319.2
SRX202160	96.7	96.7	16%	8e-24	68.75%	291	SRA:SRR610305.144937.2
SRX202160	96.7	96.7	16%	8e-24	68.75%	293	SRA:SRR610305.99698.2
SRX202160	96.7	96.7	16%	8e-24	68.75%	293	SRA:SRR610305.85009.2
SRX202160	96.7	96.7	16%	8e-24	68.75%	293	SRA:SRR610305.52731.2
SRX202160	96.7	96.7	16%	8e-24	68.75%	292	SRA:SRR610305.35520.2
SRX202160	99.0	99.0	32%	9e-24	39.53%	511	SRA:SRR610305.136408.2
SRX202160	96.7	96.7	16%	9e-24	68.75%	296	SRA:SRR610305.228512.2
SRX202160	96.3	96.3	16%	9e-24	68.75%	283	SRA:SRR610305.110393.2
SRX202160	96.3	96.3	16%	1e-23	68.75%	281	SRA:SRR610305.226576.2
SRX202160	60.5	147	36%	1e-23	34.83%	472	SRA:SRR610305.293621.2
SRX202160	70.9	127	16%	2e-23	83.78%	467	SRA:SRR610305.199721.2
SRX202160	95.9	95.9	14%	2e-23	78.95%	331	SRA:SRR610305.487971.2
SRX202160	95.1	95.1	16%	3e-23	67.19%	291	SRA:SRR610305.97919.2
SRX202160	94.4	94.4	16%	5e-23	67.19%	281	SRA:SRR610305.127990.2
SRX202160	94.4	94.4	16%	5e-23	67.19%	292	SRA:SRR610305.35811.2
SRX202160	95.9	95.9	20%	6e-23	58.33%	447	SRA:SRR610305.289470.2
SRX202160	95.1	95.1	30%	8e-23	38.21%	399	SRA:SRR610305.145801.2
SRX202160	94.0	94.0	16%	8e-23	68.25%	292	SRA:SRR610305.132920.2
SRX202160	93.6	93.6	16%	1e-22	68.25%	292	SRA:SRR610305.59360.2
SRX202160	94.0	94.0	24%	2e-22	49.49%	408	SRA:SRR610305.237604.2
SRX202160	92.4	92.4	16%	3e-22	67.19%	291	SRA:SRR610305.142595.2
SRX202160	94.7	94.7	27%	3e-22	46.85%	495	SRA:SRR610305.140318.2
SRX202160	94.0	165	27%	3e-22	65.75%	462	SRA:SRR610305.720352.2
SRX202160	92.0	92.0	16%	3e-22	66.67%	282	SRA:SRR610305.98030.2
SRX202160	93.2	93.2	23%	4e-22	47.87%	408	SRA:SRR610305.146245.2
SRX202160	90.5	90.5	15%	9e-22	67.21%	266	SRA:SRR610305.54493.2
SRX202160	93.2	93.2	37%	1e-21	33.99%	507	SRA:SRR610305.210909.2
SRX202160	91.7	133	20%	1e-21	59.30%	382	SRA:SRR610305.422514.2
SRX202160	83.6	120	25%	1e-21	53.57%	302	SRA:SRR610305.480569.2

Graphic Summary

Alignment Scores < 40 40 - 50 50 - 80 80 - 200 >= 200



Alignments

Alignment view Pairwise ☐ CDS feature Restore defaults

SRX202160

Sequence ID: **SRA:SRR610305.171358.2** Length: 509 Number of Matches: 1
Range 1: 102 to 509

Score	Expect	Method	Identities	Positives	Gaps	Frame
239 bits(609) 1e-77() Compositional matrix adjust. 116/136(85%) 124/136(91%) 0/136(0%) +3						
Query 100	KEPKL	PRLHISGCGKRKVKIDITTVGRSGSPILPPISTPQNSTGGRGIIAGGV	EAKIGAW	159		
Sbjct 102	K K+PRLHI	GCGKRKV +DITT+GRSGSPILPPIST Q+ GGRGIIAGGV	EAKIGAW	281		
Query 160	PWMAAVFVK	NFGIGRFHCAGSIISNKYILSAAHAF	LIGGRKLTPTRLAVRVGGHYIKRGQ	219		
Sbjct 282	PWMAAVFVK	NFGIGRFHCAGSIIS+KYILSAAHAF IGGRKLTPTRLAVRVGGHY+K GQ	PWMAAVFVK	461		
Query 220	EYPVKD	VIIHPHYVEK	235			
Sbjct 462	EY V+ VIIHP	VVE+ EYHVEXVIIHPDYVER	509			

SRX202160

Sequence ID: **SRA:SRR610305.115428.2** Length: 511 Number of Matches: 1
Range 1: 2 to 451

Score	Expect	Method	Identities	Positives	Gaps	Frame
226 bits(576)	1e-72()	Compositional matrix adjust.	121/151(80%)	134/151(88%)	2/151(1%)	-1
Query 1	MTWICVITL	FALASATLGNKVS	RVGLFPKTRNDN-ECTARGGLKG	SCKSLIDCP	SVLAT	59
Sbjct 451	M WICVITL	FALAS+TL NKVSRV	G++FPKT+NDN +CTA+GGLKG	SCKSL DCP+VLAT		272
Query 60	LKDSFPVVC	SWNGRFQPIVCCP	Daippvttt	avtviSTKEPKL	PRLHISGCGK	RVKVI 119
Sbjct 271	LKDSFPVVC	SWNGRFQPIVCCP	A P VTTT T++ TKE K+PRLHI	GCGKRV +		95
Query 120	DITTVGRSG	SILPPISTPONST	GGRGIIAG	150		
Sbjct 94	DITT+GRSG	SILPPIST Q+ GGRGIIAG		2		

SRX202160

Sequence ID: **SRA:SRR610305.157061.2** Length: 478 Number of Matches: 1
Range 1: 70 to 477

Score	Expect	Method	Identities	Positives	Gaps	Frame
187 bits(476)	8e-58()	Compositional matrix adjust.	102/137(74%)	118/137(86%)	2/137(1%)	+1
Query 1	MTWICVITL	FALASATLGNKVS	RVGLFPKTRNDN-ECTARGGLKG	SCKSLIDCP	SVLAT	59
Sbjct 70	M WICVITL	FALAS+TL NKVSRV	G++FPKT+NDN +CTA+GGLKG	SCKSL DCP+VLAT		249
Query 60	LKDSFPVVC	SWNGRFQPIVCCP	Daippvttt	avtviSTKEPKL	PRLHISGCGK	RVKVI 119
Sbjct 250	LKDSFPVVC	SWNGRFQPIVCCP	A P VTTT T++ TKE K+ ++ + K+KV +			426
Query 120	DITTVGRSG	SILPPIST	136			
Sbjct 427	DITT+GRSG	SILPPIST	477			

SRX202160

Sequence ID: **SRA:SRR610305.255262.2** Length: 428 Number of Matches: 1
Range 1: 66 to 428

Score	Expect	Method	Identities	Positives	Gaps	Frame
174 bits(440)	1e-52()	Compositional matrix adjust.	95/122(78%)	106/122(86%)	2/122(1%)	+3
Query 1	MTWICVITL	FALASATLGNKVS	RVGLFPKTRNDN-ECTARGGLKG	SCKSLIDCP	SVLAT	59
Sbjct 66	M WICVITL	FALAS+TL NKVSRV	G++FPKT+NDN +CTA+GGLKG	SCKSL DCP+VLAT		245
Query 60	LKDSFPVVC	SWNGRFQPIVCCP	Daippvttt	avtviSTKEPKL	PRLHISGCGK	RVKVI 119
Sbjct 246	LKDSFPVVC	SWNGRFQPIVCCP	A P VTTT T++ TKE K+PRLHI	GCGK K +		422
Query 120	DI	121				
Sbjct 423	DI	428				

SRX202160

Sequence ID: **SRA:SRR610305.214510.2** Length: 499 Number of Matches: 2
Range 1: 23 to 499

Score	Expect	Method	Identities	Positives	Gaps	Frame
172 bits(436)	1e-51()	Compositional matrix adjust.	104/160(65%)	113/160(70%)	8/160(5%)	-1
Query 70	WNGRFQPIV	CCP	Daippvttt	avtviSTKEPKL	PRLHISGCGK	RVKIIDITTVGRSGS 129
Sbjct 499	WNGRFQPIV	CCPDA AP TT V TKE K+PRLHI	G KRVK +DITT+GRSGS			323
Query 130	PILPPISTP	ONSTGGRGIIAGG	VEAKIGAWPMAAV	FKNFGIGRFH	CAGSIISKYI	LS 189
Sbjct 322	PILPPIST	QDLKGGRGIIAGG	VEAKIGAWPMAAV	FKNFGIGRFH	CAGSIISKYI	FSV 143

Query 190 AAHAFLIGGRKLTPTRLA-----VRVGGHYIKRGQ-EYP 222
F K P L+ +R G I G+ +YP
Sbjct 142 CCPRFPHWRSKADPNLSLSCPRRRRLRKDGSRISCGRCDP 23

Range 2: 1 to 150

Score	Expect	Method	Identities	Positives	Gaps	Frame
92.0 bits(227)	3e-21()	Compositional matrix adjust.	43/50(86%)	46/50(92%)	0/50(0%)	-2
Query 187	ILSAAHAFLIGGRKLTPTRLAVRVGGHYIKRGQEYPVKDVIHHPHYVEKE	236				
Sbjct 150	LSAAHAFLIGGRKLTPTRLAVRVGGHY+K GQEY V+DVIIHP YVE+E	1				

SRX202160

Sequence ID: **SRA:SRR610305.45659.2** Length: 280 Number of Matches: 1
Range 1: 3 to 278

Score	Expect	Method	Identities	Positives	Gaps	Frame
165 bits(418)	6e-50()	Compositional matrix adjust.	81/92(88%)	86/92(93%)	0/92(0%)	-3
Query 109	ISGCGKRKVKIDITTVGRSGSPILPPISTPQNSTGGRGIIAGGVEAKIGAWPWMAAVFK	168				
Sbjct 278	I GCGKRKV +DITT+GRSGSPILPPIST Q+ GGRGIIAGGVEAKIGAWPWMAAVFV+	99				
Query 169	NFGIGRFHCAGSIISNKYILSAHAFLIGGRK	200				
Sbjct 98	NFGIGRFHCAGSII +KYILSAHAFLIGGRK	3				

SRX202160

Sequence ID: **SRA:SRR610305.201975.2** Length: 439 Number of Matches: 1
Range 1: 1 to 438

Score	Expect	Method	Identities	Positives	Gaps	Frame
166 bits(420)	1e-49()	Compositional matrix adjust.	88/146(60%)	95/146(65%)	0/146(0%)	+1
Query 241	IAIIELKEELNFTDLVNPITCLDPETVTDPLKDRIVTAAGWGDLDFSGPRSQVLREVSTP	300				
Sbjct 1	IAII LKEELNFTDLV PTCLDPDE TD LK R VT AGWGDLDF+GPRSQ P	180				
Query 301	VVPVDKCDQAYEKLNTPSLKNGITNNFLCAGLEEGGKDACQGDSGGPLMLVNNTRWIVVG	360				
Sbjct 181	Q+ + P CAGLEEGGK PLMLVNN+ WIV G	360				
Query 361	VVSFGHKCAEEGPGVYSRVASYLDW	386				
Sbjct 361	VVSFGHKCAEEG+PGVY+RV SYL+W	438				

SRX202160

Sequence ID: **SRA:SRR610305.607373.2** Length: 378 Number of Matches: 1
Range 1: 1 to 333

Score	Expect	Method	Identities	Positives	Gaps	Frame
162 bits(411)	1e-48()	Compositional matrix adjust.	89/112(79%)	99/112(88%)	2/112(1%)	-1
Query 1	MTWICVITLFFALASATLGNKVS RVGLFPKTRNDN-ECTARGGLKGSCSKSLIDCPVLAT	59				
Sbjct 333	M WICVITLFFALAS+TL NKVSRVG++FPKT+NDN +CTA+GGLKGSCSKSL DCP+VLAT	154				
Query 60	LKDSFPVVCSSWNGRFQPIVCCPDaiappvtttattvstKEPKLPRLHISG	111				
Sbjct 153	LKDSFPVVCSSWNGRFQPIVCCPD A P VTTT T++ TKE K+PRLHI G	1				

SRX202160

Sequence ID: **SRA:SRR610305.241420.2** Length: 363 Number of Matches: 1
Range 1: 70 to 318

Score	Expect	Method	Identities	Positives	Gaps	Frame
152 bits(385)	1e-44()	Compositional matrix adjust.	71/83(86%)	78/83(93%)	1/83(1%)	+1
Query 1	MTWICVITL	FALASATLGNKVS	RVGVLFPKTRNDN-ECTARGGLKG	SCKSLIDCPSVLAT	59	
	M WICVITL	FAL S+TL NKVSRVG++FPKT+NDN	+CTA+GGLKG	SCKSL DCP+VLAT		
Sbjct 70	MAWICVITL	FALVSSTLSNKVSRVGII	FPKTQNDNKQCTAKGGLKG	SCKSLTDCPAVLAT	249	
Query 60	LKDSFPVVC	SWNGRFQPIVCCPD	82			
	LKDSFPVVC	SWNGRFQPIVCCPD				
Sbjct 250	LKDSFPVVC	SWNGRFQPIVCCPD	318			

SRX202160

Sequence ID: **SRA:SRR610305.737708.2** Length: 327 Number of Matches: 1
Range 1: 2 to 325

Score	Expect	Method	Identities	Positives	Gaps	Frame
145 bits(367)	3e-42()	Compositional matrix adjust.	82/109(75%)	92/109(84%)	2/109(1%)	-3
Query 4	ICVITL	FALASATLGNKVS	RVGVLFPKTRNDN-ECTARGGLKG	SCKSLIDCPSVLATLKD	62	
	ICVIT S+TL	NKVSRVG++FPKT+NDN	+CTA+GGLKG	SCKSL DCP+VLATLKD		
Sbjct 325	ICVITCLLT	SSTLSNKVSRVGII	FPKTQNDNKQCTAKGGLKG	SCKSLTDCPAVLATLKD	146	
Query 63	SFPVVC	SWNGRFQPIVCCPDaiappvttttavtvi	STKEPKL	PRLHISG	111	
	SFPVVC	SWNGRFQPIVCCPD A P VTTT T++	TKE K+PRLHI	G		
Sbjct 145	SFPVVC	SWNGRFQPIVCCPD-AAAPSVTTT	TVTTIVPTKET	KIPRLHIPG	2	

SRX202160

Sequence ID: **SRA:SRR610305.140124.2** Length: 376 Number of Matches: 1
Range 1: 6 to 371

Score	Expect	Method	Identities	Positives	Gaps	Frame
145 bits(367)	4e-42()	Compositional matrix adjust.	69/122(57%)	85/122(69%)	0/122(0%)	-3
Query 267	VTDPLK	DRIVTAAGWGLD	FSGPRSQVLREV	SIPVVPVVKCDQAYEKL	NTPSLKNGITNN	326
	V K R VT	GWGD F G +S+VL++VSIPV	C+++Y K+	GIT		
Sbjct 371	VQQDFK	GREVTVTGWGDTFFGGAKSKVL	QQVSIPVVS	NKACNKSYSKVALSKYPQGITRG	192	
Query 327	FLCAGL	EEGGKDACQGD	SGGPLMLVNNTRWIVVGV	SFGHKCAEEGYPGVY	SRVASYLDW	386
	+CAGL	EEGGKDACQGD	SGGPL+L + RW +VG+VSFG	CAE GYPGVY+RV+ Y+ W		
Sbjct 191	QICAGL	EEGGKDACQGD	SGGPLVLEESGRWTLVGIVS	FLNCAEPGYPGVYTRVSHYIRW	12	
Query 387	IA	388				
	IA					
Sbjct 11	IA	6				

SRX202160

Sequence ID: **SRA:SRR610305.146939.2** Length: 467 Number of Matches: 2
Range 1: 76 to 300

Score	Expect	Method	Identities	Positives	Gaps	Frame
143 bits(360)	1e-40()	Compositional matrix adjust.	66/75(88%)	71/75(94%)	0/75(0%)	-3
Query 327	FLCAGL	EEGGKDACQGD	SGGPLMLVNNTRWIVVGV	SFGHKCAEEGYPGVY	SRVASYLDW	386
	F+CAGL	EEGGKDACQGD	SGGPLMLVNN+ WIV GVVS	FGHKCAEEG+PGVY+RV SYL+W		
Sbjct 300	FICAGL	EEGGKDACQGD	SGGPLMLVNNSSWIVTGV	SFGHKCAEEGYPGVYTRVVSYLEW	121	
Query 387	IAKVTNSL	DHAVTN*	401			
	IAKVTNSL	AVTN*				
Sbjct 120	IAKVTNSL	DQAVTN*	76			

Range 2: 267 to 467

Score	Expect	Method	Identities	Positives	Gaps	Frame
92.8 bits(229)	1e-21()	Compositional matrix adjust.	44/67(66%)	53/67(79%)	0/67(0%)	-1
Query 271	LKDRIVTA	AGWGLD	FSGPRSQVLREV	SIPVVPVVKCDQAYEKL	NTPSLKNGITNNFLCA	330
	LK R VT	AGWGLD	F+GPRSQVLREV	SIPVVP+ C++AY+KLNT	+LKNGIT +	

Sbjct 467 LKGRRTVAGWGLDFAGPRSQLREVSIIPVPIGDCNKAYQKLNTLALKNGITKSLFVL 288
Query 331 GLEEGGK 337
++ GK
Sbjct 287 DWKKVGK 267

SRX202160
Sequence ID: **SRA:SRR610305.145522.2** Length: 365 Number of Matches: 1
Range 1: 70 to 300

Score	Expect	Method	Identities	Positives	Gaps	Frame
141 bits(355)	3e-40()	Compositional matrix adjust.	66/77(86%)	73/77(94%)	1/77(1%)	+1
Query 1	MTWICVITL	FALASATLGNKVS	RVGVLFPKTRNDN-ECTARGGLKG	SCSKSLIDCPSVLAT		59
Sbjct 70	M WICVITL	FALAS+TL NKVSRV	G++FPKT+NDN +CTA+GGLKG	SCSKSL DCP+VLAT		249
Query 60	LKDSFPVVC	SWNGRFQ 76				
Sbjct 250	LKDSFPVVC	SWNGRFQ 300				

SRX202160
Sequence ID: **SRA:SRR610305.605162.2** Length: 320 Number of Matches: 1
Range 1: 79 to 303

Score	Expect	Method	Identities	Positives	Gaps	Frame
137 bits(344)	6e-39()	Compositional matrix adjust.	64/75(85%)	72/75(96%)	1/75(1%)	-3
Query 9	L FALASATL	GNKVS	RVGVLFPKTRNDN-ECTARGGLKG	SCSKSLIDCPSVLATLKDSFPVV		67
Sbjct 303	V FALASSTL	SNKVS	RVGIIFPKTQNDNKQCTAKGGLKG	SCSKSLTDCPAVLATLKDSFPVV		124
Query 68	CSWNGRFQ	PIVCCPD 82				
Sbjct 123	CSWNGRFQ	PIVCCPD 79				

SRX202160
Sequence ID: **SRA:SRR610305.243191.2** Length: 458 Number of Matches: 1
Range 1: 34 to 456

Score	Expect	Method	Identities	Positives	Gaps	Frame
137 bits(345)	2e-38()	Compositional matrix adjust.	69/152(45%)	96/152(63%)	12/152(7%)	+1
Query 226	VIIHPHYVE	KENYNDIAIIELKEELNFTDLVNPICLPDPETVTDPLKDRIVTAAGWGLD				285
Sbjct 34	I IHP + +	YNDIA++ L + + F++ + PICLP P L+++I T GWG +				204
Query 286	FSGPRSQVL	REVSIIPVVPDKDQAYEKLNTPSLKNGITNNFLCAGLEEGGDACQGDG				345
Sbjct 205	+ G S VLREVS	IP+ D+CD+ + + IT FLCAG + G KD+CQGDG				360
Query 346	GPLML-VNN	TRWIVGVVSFGHKCAEEGYPGV 376				
Sbjct 361	GPLM N RW	+VG+VS+G +CAE +PGV 456				

SRX202160
Sequence ID: **SRA:SRR610305.358932.2** Length: 448 Number of Matches: 1
Range 1: 161 to 376

Score	Expect	Method	Identities	Positives	Gaps	Frame
134 bits(337)	2e-37()	Compositional matrix adjust.	62/72(86%)	69/72(95%)	1/72(1%)	+2
Query 12	LASATLGNK	VS	RVGVLFPKTRNDN-ECTARGGLKG	SCSKSLIDCPSVLATLKDSFPVVC	SW 70	
Sbjct 161	LAS+TL NKV	SRV	G++FPKT+NDN +CTA+GGLKG	SCSKSL DCP+VLATLKDSFPVVC	SW 340	
Query 71	NGRFQ	PIVCCPD 82				

Sbjct 341 NGRFQPIVCCPD
NGRFQPIVCCPD 376

SRX202160

Sequence ID: **SRA:SRR610305.604182.2** Length: 334 Number of Matches: 1
Range 1: 1 to 330

Score	Expect	Method	Identities	Positives	Gaps	Frame
132 bits(333)	3e-37()	Compositional matrix adjust.	77/111(69%)	85/111(76%)	1/111(0%)	-2
Query 1	MTWICVITL	FALASATLGNKVS	RVGVLPFKTRND	NECTARGGLKGS	CKSLIDCP	SVLATL 60
Sbjct 330	M WICVITL	FALAS+TL K+ L T +C	A+GGLKGSCKSL	DCP+VLATL		151
Query 61	KDSFPVCS	WNGRFP	IVCCPDai	appvttt	avtvi	ISTKEPKL
Sbjct 150	KDSFPVCS	WNGRFP	IVCCPD A P	VTTT T++	TKE K+PRLHI	G 1

SRX202160

Sequence ID: **SRA:SRR610305.181294.2** Length: 446 Number of Matches: 1
Range 1: 61 to 444

Score	Expect	Method	Identities	Positives	Gaps	Frame
132 bits(333)	9e-37()	Compositional matrix adjust.	63/128(49%)	82/128(64%)	0/128(0%)	+1
Query 216	KRGQEYP	VKDVI	IHPHYVEKENY	NDIAIIE	KEELNFT	DLVNPICLP
Sbjct 61	K Q Y V	+DVI+H Y +NY	+DIA++++K E+ D V	P+CLP P V K R		240
Query 276	VTAAGWD	LDFSGPR	SQVLR	EVSVV	VDKCDQ	AYEKLNT
Sbjct 241	VT GWGD	F G +S	+VL++VSIPV C+++Y	K+ GIT +CAGL	EG	420
Query 336	GKDACQGD		343			
Sbjct 421	GKDACQGD		444			

SRX202160

Sequence ID: **SRA:SRR610305.109827.2** Length: 390 Number of Matches: 1
Range 1: 2 to 310

Score	Expect	Method	Identities	Positives	Gaps	Frame
126 bits(317)	1e-34()	Compositional matrix adjust.	59/103(57%)	76/103(73%)	0/103(0%)	+2
Query 290	RSQVLR	EVSVV	VDKCDQ	AYEKLNT	PSLKN	GITNNFLCAGLE
Sbjct 2	+S+VL++	VSIPV C+++Y	K+ GIT +CAGL	EGGKDACQGD	SGGPL+	181
Query 350	LNNTR	WIVGV	SFGHKCA	EEGYP	GVYSRV	ASYLDWIAKVTN
Sbjct 182	L + RW	+VG+VSFG CAE	GYPGVY+RV+ Y+ WIA T+			310

SRX202160

Sequence ID: **SRA:SRR610305.225432.2** Length: 505 Number of Matches: 1
Range 1: 122 to 499

Score	Expect	Method	Identities	Positives	Gaps	Frame
127 bits(320)	1e-34()	Compositional matrix adjust.	64/137(47%)	88/137(64%)	12/137(8%)	+2
Query 245	ELKEELN	FTDLVNPICLP	DPETVTDPLK	DRIVTAAG	WGLDFSGPR	SQVLR
Sbjct 122	+ K+ +	++D + PICLPDP +	L+ ++ T GWG + + G	S VLR	EVSVV	181
Query 305	DKCQAYE	KLNTPSL	KNGITNNFLCAGLE	EGGKDACQGD	SGGPLML	-VNNTR
Sbjct 293	EECNNT	FVQT-----	TTNVFLCAGSK	NGDKDSCQGD	SGGPLM	WEPNRRWTL

Query 364 FGHKCAEEGYPGVYSRV 380
+G +CAE YPGVY+RV
Sbjct 449 WGI RCAPE NYPGVYTRV 499

SRX202160
Sequence ID: **SRA:SRR610305.531623.2** Length: 259 Number of Matches: 1
Range 1: 1 to 255

Score	Expect	Method	Identities	Positives	Gaps	Frame
124 bits(312)	2e-34()	Compositional matrix adjust.	63/85(74%)	67/85(78%)	0/85(0%)	-2
Query 223	VKDVIIPHYPHYVEKENYNDIAIIELKEELNFTDLVNPICLPDPETVTDPLKDRIVTAAGWG	282				
	V+DVIIPH YVE+ENYNDIAII LKEELNFTDLV VTD LK R VT AGWG					
Sbjct 255	VEDVIIHPDYVERENYNDIAIIVLKEELNFTDLVRQSVSLTQGAVTDSLKGRRVTVAGWG	76				
Query 283	DLD FSGPRSQVLREVSI PVVPDKC 307					
	DLD F+GPRSQVLREVSI PVVP+ C					
Sbjct 75	DLD FAGPRSQVLREVSI PVVPISDC 1					

SRX202160
Sequence ID: **SRA:SRR610305.148321.2** Length: 505 Number of Matches: 1
Range 1: 1 to 420

Score	Expect	Method	Identities	Positives	Gaps	Frame
127 bits(319)	2e-34()	Compositional matrix adjust.	62/141(44%)	90/141(63%)	3/141(2%)	-2
Query 161	WMAAVFVKNF GIG- RFHCAGSIISNKYILSAAHAF LIGGRKLTPTRLAVRVGGHYIKRGQ	219				
	WM + +NFG+ RF C G++IS++Y++SAAH F + ++P+ RVGGH +K G					
Sbjct 420	WMVGI-SQN FGLSERFLCGGALISSRVVISA AHCFTSNKPI SPVYTSRVGGHTLKDGT	244				
Query 220	EYPVKDVIIPHYPHYVEKENYNDIAIIELKEELNFTDLVNPICLPDPETVTDPLKDRIVTAA	279				
	Y V+DVI+H HY +NY+DIA+++K E+ D V P+CLP P V K R VT					
Sbjct 243	NYDVEDVIVHEHYQPSQNYHDI AVLKVKGEVRLNDKVKPVCLPKPSFVGQDFKGREVTVT	64				
Query 280	GWGDLDF-SGPRSQVLREVSI 299					
	GWGD F + +VL++VSI					
Sbjct 63	GWGDTFFWRCEKVKVLQQVSI 1					

SRX202160
Sequence ID: **SRA:SRR610305.96962.2** Length: 529 Number of Matches: 1
Range 1: 59 to 502

Score	Expect	Method	Identities	Positives	Gaps	Frame
125 bits(313)	2e-33()	Compositional matrix adjust.	62/148(42%)	95/148(64%)	2/148(1%)	-1
Query 246	LKEELNFTDLVNPICLPDPETVTDPLKDRIVTAAGWGD LDFSGPRSQVLREVSI PVVPVD	305				
	L + + + V PIC+P+ + L ++ V GWG + + VLRE+ +PVV +					
Sbjct 502	LSKPIEYNYKVQPICIPELNKLNVLNNKEVVVIGWGVTERGSEKYNVLRLELPVVTNE	323				
Query 306	KCDQAYEKLNTPSLKNGITNNFLCAGLEE GGDACQGD SGGPLMLVNNT--RWI VVGVS	363				
	C++Y+ ++ L GIT++ +CAG +EGG+D+C+GDSGGPLM + T R +VGVVS					
Sbjct 322	LCNKSYQTISFSGLNRGITDDMICAGYQEGGRDSC EGD SGGPLMYHDP TTGRV ELVGVS	143				
Query 364	FGHKCAEEGYPGVYSRVASYLDWIAKVT 391					
	FG CA +PGVY+R++SY +W KVT					
Sbjct 142	FGFGCARPNFPGVYTRLSSYGNWFQKVT 59					

SRX202160
Sequence ID: **SRA:SRR610305.353544.2** Length: 296 Number of Matches: 1
Range 1: 1 to 264

Score	Expect	Method	Identities	Positives	Gaps	Frame
122 bits(305)	2e-33()	Compositional matrix adjust.	68/89(76%)	78/89(87%)	2/89(2%)	-3
Query 24	VGVLFPKTRNDN-ECTARGGLKGSKSLIDCPSVLATLKDSFPVVC SWNGRFQPIVCCPD	82				
	+G++FPKT+NDN +CTA+GGLKGSKSL DCP+VLATLKDSFPVVC SWNGRFQPIVCCPD					
Sbjct 264	MGII FPKTQNDNKQCTAKGGLKGSKSLTDCPAVLATLKDSFPVVC SWNGRFQPIVCCPD	85				

Query 83 aiapppvtttvtviSTKEPKLRLHISG 111
A P VTTT T++ TKE K+PRLHI G
Sbjct 84 -AAAPSVTTTIVPTKETKIPRLHIPG 1

SRX202160
Sequence ID: **SRA:SRR610305.220615.2** Length: 434 Number of Matches: 2
Range 1: 172 to 375

Score	Expect	Method	Identities	Positives	Gaps	Frame
119 bits(297)	9e-33(2)	Compositional matrix adjust.	56/68(82%)	63/68(92%)	1/68(1%)	+1
Query 1	MTWICVITL FALASATLGNKVS RVGLFPKTRNDN-ECTARGGLKG SCKSLIDCPSVLAT	59				
	M WICVITLF LAS+TL NKVSRVG++FPKT+NDN +CTA+GGLKG SCKSL DCP+VLAT					
Sbjct 172	MAWICVITLFTLASSTLSNKVSRVGIIFPKTQNDNKQCTAKGGLKG SCKSL TDCPAVLAT	351				
Query 60	LKDSFPVV 67					
	LKDSFPVV					
Sbjct 352	LKDSFPVV 375					

Range 2: 363 to 419

Score	Expect	Method	Identities	Positives	Gaps	Frame
39.3 bits(90)	9e-33(2)	Compositional matrix adjust.	16/19(84%)	16/19(84%)	0/19(0%)	+3
Query 64	FPVVC SWNGRFQPIVCCPD 82					
	FP CSWNGRFQPIVC PD					
Sbjct 363	FPCRCSWNGRFQPIVCXPD 419					

SRX202160
Sequence ID: **SRA:SRR610305.385163.2** Length: 293 Number of Matches: 1
Range 1: 2 to 292

Score	Expect	Method	Identities	Positives	Gaps	Frame
118 bits(296)	5e-32()	Compositional matrix adjust.	69/98(70%)	77/98(78%)	1/98(1%)	-2
Query 14	SATLGNKVS RVGLFPKTRNDN ECTARGGLKG SCKSLIDCPSVLATLKDSFPVVC SWNGR	73				
	S+TL NKVSR G T +CTA+GGLKG SCKSL DCP+VLATLKDSFPVVC SWNGR					
Sbjct 292	SSTLSNKVSRWGSSS* DTERYKQCTAKGGLKG SCKSLTDCPAVLATLKDSFPVVC SWNGR	113				
Query 74	FQPIVCCPDaiapppvtttvtviSTKEPKLRLHISG 111					
	FQPIVCCPD A P VTTT T++ TKE K+PRLH+ G					
Sbjct 112	FQPIVCCPD-AAAPSVTTTIVPTKETKIPRLHVP G 2					

SRX202160
Sequence ID: **SRA:SRR610305.468223.2** Length: 338 Number of Matches: 1
Range 1: 129 to 332

Score	Expect	Method	Identities	Positives	Gaps	Frame
118 bits(296)	8e-32()	Compositional matrix adjust.	57/68(84%)	63/68(92%)	1/68(1%)	+3
Query 1	MTWICVITL FALASATLGNKVS RVGLFPKTRNDN-ECTARGGLKG SCKSLIDCPSVLAT	59				
	M WICVITL FALAS+TL NKVSRVG++FPKT+NDN +CTA+GGLKG SCKSL DCPS LAT					
Sbjct 129	MAWICVITL FALASSTLSNKVSRVGIIFPKTQNDNKQCTAKGGLKG SCKSLTDCPSCLAT	308				
Query 60	LKDSFPVV 67					
	LKDSFPVV					
Sbjct 309	LKDSFPVV 332					

SRX202160
Sequence ID: **SRA:SRR610305.73348.2** Length: 423 Number of Matches: 1
Range 1: 51 to 410

Score	Expect	Method	Identities	Positives	Gaps	Frame
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118 bits(296) 2e-31() Compositional matrix adjust. 54/120(45%) 77/120(64%) 1/120(0%) -2									
Query	168	KNFGIG-RFH	CAGSIISNKYILSAAH	FLIGGRKLTPTRLAVRVGGHYIKRGQEYPVKDV	226				
		+NFG+	RF C G++IS++Y++SAAH F + ++P+ RVGGH +K G Y V+DV						
Sbjct	410	QNFGLSERFL	CGGALISSRYVISAAHCFKTSNKPISPSVYTFRVGGHTLKDGTNYDVEDV	231					
Query	227	IIHPHYVEKENYNDIAII	IELKEELNFTDLVNPICLPDPETVTDPLKDRIVTAAGWGDLDF	286					
		I+H Y +NY+DIA+++K E+ D V P+CLP P V K R VT GWGD F							
Sbjct	230	IVHERYQPSQNYHDI	AVLKVKGVEVRLNDKVKPVCLPKPSFVGQDFKGREVTVTGWGDTFF	51					

SRX202160
Sequence ID: **SRA:SRR610305.517531.2** Length: 384 Number of Matches: 1
Range 1: 169 to 363

Score	Expect	Method	Identities	Positives	Gaps	Frame
116 bits(291) 6e-31() Compositional matrix adjust. 55/65(85%) 60/65(92%) 0/65(0%) -1						
Query	337	KDACQGD	SGGPLMLVNNTRWIVVGVVSGHKKAE	EGYPGVYSRVASYLDWIAKVTNSLDH	396	
		+DACQGD	SGGPLMLVNN+ IV GVVSGHKKAE	EG+PGVY+RV SYL+WIAKVTNSLD		
Sbjct	363	EDACQGD	SGGPLMLVNNSSGIVTGVVSGHKKAE	EGFPGVYTRVWSYLEWIAKVTNSLDQ	184	
Query	397	AVTN*	401			
		AVTN*				
Sbjct	183	AVTN*	169			

SRX202160
Sequence ID: **SRA:SRR610305.414191.2** Length: 327 Number of Matches: 1
Range 1: 128 to 322

Score	Expect	Method	Identities	Positives	Gaps	Frame
115 bits(287) 1e-30() Composition-based stats. 54/65(83%) 61/65(93%) 1/65(1%) +2						
Query	1	MTWICVITL	FALASATLGNKVS	RVGVLF	FPKTRNDN-ECTARGGLKG	SCSLIDCPSVLAT 59
		M WICVITL	FALAS+TL NKVSRV	G++FPKT+NDN +CTA+GGLKG	SCSKL DCP+VLAT	
Sbjct	128	MAWICVITL	FALASSTLSNKVSRVGIIFPKTQNDNKQCTAKGGLKG	SCSKL TDCPAVLAT	307	
Query	60	LKDSF	64			
		LKDSF				
Sbjct	308	LKDSF	322			

SRX202160
Sequence ID: **SRA:SRR610305.115187.2** Length: 406 Number of Matches: 1
Range 1: 3 to 296

Score	Expect	Method	Identities	Positives	Gaps	Frame
115 bits(287) 3e-30() Compositional matrix adjust. 59/105(56%) 76/105(72%) 9/105(8%) -3						
Query	286	FSGPRSQVL	REVSI	PVVPVDKCDQAYEK-LNTPSLKNGITNNFLCAGLEEGKDACQGD	344	
		F+GP S VLR	EV +P+ + C QAYEK LN ITN ++CAG +GGKDACQGD			
Sbjct	296	FNGPSSAVL	REVQLPIWGHPC	QAYEKDLN-----ITNVYMCAGYADGGKDACQGD	138	
Query	345	GGPLMLV	NNT-RWIVVGVVSGHKKAE	EGYPGVYSRVASYLDWIA	388	
		GGP+ML + + + +VG+VSFG KCA G+PGVY++V +LDWIA				
Sbjct	137	GGPMMLPDKSGNF	LVGIVSFGKKCALPGFPGVYTKVTEFLDWIA	3		

SRX202160
Sequence ID: **SRA:SRR610305.127978.2** Length: 520 Number of Matches: 1
Range 1: 1 to 354

Score	Expect	Method	Identities	Positives	Gaps	Frame
115 bits(288) 6e-30() Compositional matrix adjust. 55/118(47%) 80/118(67%) 2/118(1%) +1						
Query	276	VTAAGWGD	LDFSGPRSQVLREVSI	PVVPVDKCDQAYEKLNTPSLKNGITNNFLCAGLEEG	335	
		V GWG + + + VLR	+ +PVV + C+++Y+ ++ L GIT++ +CAG +EG			
Sbjct	1	VWVIGWGV	TERGEKYNVLRLEL	PVVTNELCNKSYQTISFSGLN	RGITDDMICAGVQEG 180	
Query	336	GKDACQGD	SGGPLMLVNNT--RWIVVGVVSGHKKAE	EGYPGVYSRVASYLDWIAKVT	391	

Sbjct 181 G+D+C+GDSGGPLM + T R +VGVSFSG CA +PGVY++SY +W KVT
GRDSCGDSGGPLMYHDPITGRVELVGVSFGFGCARPNFPGVYTRLSSYGNWFQKVT 354

SRX202160

Sequence ID: **SRA:SRR610305.598174.2** Length: 374 Number of Matches: 1
Range 1: 12 to 305

Score	Expect	Method	Identities	Positives	Gaps	Frame
113 bits(283)	8e-30()	Compositional matrix adjust.	58/105(55%)	75/105(71%)	9/105(8%)	+3
Query 286	FSGPRSQVLREVSIPVVPVKCDQAYEK-LNTPSLKNGITNNFLCAGLEEGGKDACQGDS					344
Sbjct 12	F+GP S VLREV +P+ + C QAYEK LN ITN ++CAG +G KDACQGDS					170
Query 345	GGPLMLVNNT-RWIVVGVSFGHKCAEEGYPGVYSRVASYLDWIA					388
Sbjct 171	GGP+ML + + + +VG+VSFG KCA G+PGVY++V +LDWIA					305

SRX202160

Sequence ID: **SRA:SRR610305.62354.2** Length: 388 Number of Matches: 1
Range 1: 10 to 384

Score	Expect	Method	Identities	Positives	Gaps	Frame
113 bits(283)	1e-29()	Compositional matrix adjust.	62/132(47%)	80/132(60%)	8/132(6%)	-2
Query 220	EYPVKDVIIHPHYEKENYNDIAIIELKEELNFTDLVNPICLPDPETVTDPLKDRIVTAA					279
Sbjct 384	++ V V H ++V NDIAI++L + + FT + PICLP + L R A					205
Query 280	GWGDLDFSGPRSQVLREVSIPVVPVKCDQAYEK-LNTPSLKNGITNNFLCAGLEEGGKD					338
Sbjct 204	GWG F+GP S VLREV +P+ + C QAYEK LN ITN ++CAG +GGKD					46
Query 339	ACQGDSDGGPLML 350					
Sbjct 45	ACQGDSDGGP+ML 10					

SRX202160

Sequence ID: **SRA:SRR610305.126966.2** Length: 437 Number of Matches: 1
Range 1: 11 to 436

Score	Expect	Method	Identities	Positives	Gaps	Frame
113 bits(283)	2e-29()	Compositional matrix adjust.	58/142(41%)	89/142(62%)	2/142(1%)	+2
Query 237	NYNDIAIIELKEELNFTDLVNPICLPDPETVTDPLKDRIVTAAGWDLDFSGPRSQVLRE					296
Sbjct 11	+Y DI +I L + + + V PIC+P+ + L ++ V GWG + + VLRE					190
Query 297	VSIPVVPVKCDQAYEKLNTPSLKNGITNNFLCAGLEEGGKDACQDSDGGPLMLVNNT--					354
Sbjct 191	+ +PVV + C+++Y+ ++ L GIT++ +CAG +EGG+D+C+GDSGGPLM + T					370
Query 355	LELPVVTNELCNKSYQTISFSGLNRGITDDMICAGYQEGGRDSCGDSGGPLMYHDPITG					
Query 371	RWIVVGVSFGHKCAEEGYPGV 376					
Sbjct 371	R +VGVSFSG CA +PGV 436					

SRX202160

Sequence ID: **SRA:SRR610305.617893.2** Length: 421 Number of Matches: 1
Range 1: 115 to 411

Score	Expect	Method	Identities	Positives	Gaps	Frame
113 bits(282)	2e-29()	Compositional matrix adjust.	59/106(56%)	74/106(69%)	10/106(9%)	-2
Query 286	FSGPRSQVLREVSIPVVPVKCDQAYEK-LNTPSLKNGITNNFLCAGLEEGGKDACQGDS					344
Sbjct 411	F+GP S VLREV +P+ + C QAYEK LN ITN ++CAG +GGKDACQGDS					253

Query 345 GGPLMLVNNTR--WIVVGVVSFGHKCAEEGYPGVYSRVASYLDWIA 388
GGP+ML + R +I + VSFG KCA G+PGVY++V +LDWIA
Sbjct 252 GGPMMLPDKKRELFISLEFVSFGKKCALPGFPGVYTKVTEFLDWIA 115

SRX202160
Sequence ID: **SRA:SRR610305.504278.2** Length: 414 Number of Matches: 3
Range 1: 261 to 377

Score	Expect	Method	Identities	Positives	Gaps	Frame
80.1 bits(196)	7e-29(3)	Compositional matrix adjust.	36/39(92%)	37/39(94%)	0/39(0%)	+3
Query 44	KGSCSKSLIDCPSVLATLKDSFPVVCWNGRFQPIVCCPD	82				
	KGSCSKSL DCP+VLATLKDSFPVV SWNGRFQPIVCCPD					
Sbjct 261	KGSCSKSLTDCPAVLATLKDSFPVVYSWNGRFQPIVCCPD	377				

Range 2: 127 to 201

Score	Expect	Method	Identities	Positives	Gaps	Frame
47.8 bits(112)	7e-29(3)	Compositional matrix adjust.	22/25(88%)	23/25(92%)	0/25(0%)	+1
Query 1	MTWICVITLFFALASATLGNKVS RVG	25				
	M WICVITLFFALAS+TL NKVS RVG					
Sbjct 127	MAWICVITLFFALASSTLSNKVS RVG	201				

Range 3: 185 to 262

Score	Expect	Method	Identities	Positives	Gaps	Frame
37.7 bits(86)	7e-29(3)	Compositional matrix adjust.	17/26(65%)	22/26(84%)	1/26(3%)	+2
Query 20	KVSRVGVLFPPKTRNDN-ECTARGGLK	44				
	K+ G++FPKTRNDN +CTA+GGLK					
Sbjct 185	KLVEWGIIFPKTRNDNKQCTAKGGLK	262				

SRX202160
Sequence ID: **SRA:SRR610305.737967.2** Length: 335 Number of Matches: 1
Range 1: 3 to 311

Score	Expect	Method	Identities	Positives	Gaps	Frame
108 bits(271)	3e-28()	Compositional matrix adjust.	59/114(52%)	74/114(64%)	16/114(14%)	+3
Query 280	WGDLDFSGPRSQVLREVSIPVVPDKCDQAYEK-LNTPSLKNGITNNFLCAGLEEGGKD	338				
	WG F+GP S VLREV +P+ + C QAYEK LN ITN ++CAG +GGKD					
Sbjct 3	WGTTAFNGPSSAVLREVQLPIWGHEPCRQAYEKDLN-----ITNVYMCAGYADGGKD	161				
Query 339	ACQGDSSGGPLMLVNN-----TRWIVVGVVSFGHKCAEEGYPGVYSRVASYLDWIA	388				
	ACQGDSSGGP+ML + +RW V F +CA G+PGVY++V +LDWIA					
Sbjct 162	ACQGDSSGGPMMLPDKAGLLSRWNCV----FSEECALPGFPGVYTKVTEFLDWIA	311				

SRX202160
Sequence ID: **SRA:SRR610305.267540.2** Length: 436 Number of Matches: 1
Range 1: 141 to 434

Score	Expect	Method	Identities	Positives	Gaps	Frame
108 bits(270)	9e-28()	Compositional matrix adjust.	56/105(53%)	73/105(69%)	9/105(8%)	-3
Query 281	WGDLDFSGPRSQVLREVSIPVVPDKCDQAYEK-LNTPSLKNGITNNFLCAGLEEGGKDA	339				
	WG F+GP S VLREV +P+ + C QAYEK LN ITN ++CAG +GGKDA					
Sbjct 434	WGTTAFNGPSSAVLREVQLPIWGHEPCRQAYEKDLN-----ITNVYMCAGYADGGKDA	276				
Query 340	CQGDSSGGPLMLVNNTR-RWIVVGVVSFGHKCAEEGYPGVYSRVASY	383				
	CQGDSSGGP+ML + + + +VG+VSFG KCA G+PGVY++V +					
Sbjct 275	CQGDSSGGPMMLPDKSGNFYLVGIVSFGKKCALPGFPGVYTKVTEF	141				

SRX202160

Sequence ID: **SRA:SRR610305.296720.2** Length: 492 Number of Matches: 1
Range 1: 5 to 385

Score	Expect	Method	Identities	Positives	Gaps	Frame
109 bits(272) 9e-28() Compositional matrix adjust. 63/140(45%) 87/140(62%) 16/140(11%) +2						
Query 243	I I E L K E E L N - F T D L V N P I C L P D P E T V T D P L K D R I V T A A G W G D L D F S G P R S Q V L R E V S I P V					301
	++ L+ +LN F L+ + +T+ +P AGWG F+GP S VLREV +P+					
Sbjct 5	L L R L R T K L N Q F V Y L M * S L R Y E G S K T M R N P F - - - - - V A G W G T T A F N G P S S A V L R E V Q L P I					166
Query 302	V P V D K C D Q A Y E K - L N T P S L K N G I T N N F L C A G L E E G G K D A C Q G D S G G P L M L V N N T - R W I V V					359
	+ C Q A Y E K L N I T N ++CAG +G G K D A C Q G D S G G P + M L + + + + V					
Sbjct 167	W G H E P C R Q A Y E K D L N - - - - - I T N V Y M C A G Y A D G G K D A C Q G D S G G P M M L P D K S G N F Y L V					325
Query 360	G V V S F G H K C A E E G Y P G V Y S R					379
	G+VSFG KCA G+PGV +					
Sbjct 326	G I V S F G K K C A L P G F P G V L H K					385

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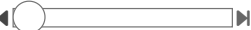
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Composition-based adjustment: yes

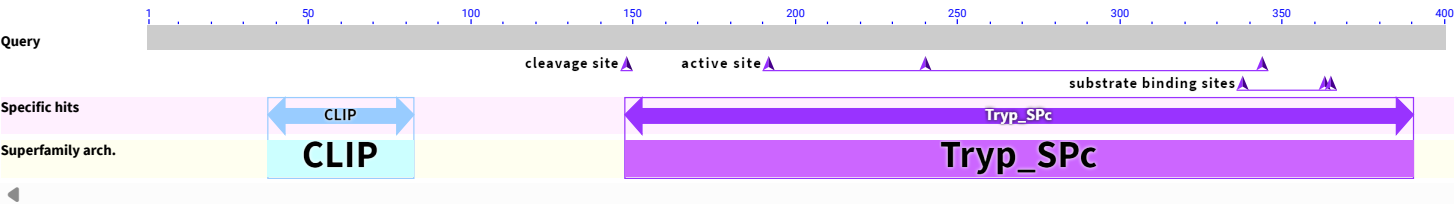
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+ Tryp_SPc	cd00190	Trypsin-like serine protease	148-390	3.78×10^{-91}
+ CLIP	smart00680	Clip or disulphide knot domain	38-82	5.10×10^{-6}

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Molecule type amino acid
Query Length 376

Descriptions

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
▼	▼	▼	▼	▼	▼	▼	
SRX202160	285	285	41%	2e-96	88.24%	462	SRA:SRR610305.97090.2
SRX202160	246	246	34%	1e-81	88.37%	388	SRA:SRR610305.62354.2
SRX202160	193	312	44%	8e-79	85.15%	495	SRA:SRR610305.140318.2
SRX202160	233	288	40%	1e-75	85.83%	473	SRA:SRR610305.104315.2
SRX202160	209	253	43%	2e-66	76.64%	492	SRA:SRR610305.124826.2
SRX202160	204	204	28%	5e-65	90.57%	374	SRA:SRR610305.598174.2
SRX202160	205	295	41%	6e-65	80.65%	472	SRA:SRR610305.184275.2
SRX202160	199	251	34%	8e-63	91.09%	406	SRA:SRR610305.115187.2
SRX202160	198	273	38%	4e-62	84.55%	492	SRA:SRR610305.296720.2
SRX202160	196	196	26%	9e-62	92.86%	436	SRA:SRR610305.267540.2
SRX202160	195	251	36%	4e-61	85.32%	461	SRA:SRR610305.159521.2
SRX202160	190	190	28%	2e-59	85.98%	421	SRA:SRR610305.617893.2
SRX202160	186	186	29%	3e-58	83.49%	335	SRA:SRR610305.737967.2
SRX202160	187	187	26%	5e-58	90.62%	431	SRA:SRR610305.393406.2
SRX202160	184	184	25%	1e-57	91.58%	287	SRA:SRR610305.606681.2
SRX202160	179	240	35%	5e-55	79.65%	401	SRA:SRR610305.254076.2
SRX202160	169	222	28%	1e-51	91.46%	343	SRA:SRR610305.600452.2
SRX202160	168	168	28%	3e-51	79.44%	341	SRA:SRR610305.376727.2
SRX202160	165	165	23%	1e-49	90.59%	447	SRA:SRR610305.289470.2
SRX202160	162	162	22%	5e-49	88.10%	264	SRA:SRR610305.503368.2
SRX202160	162	162	22%	2e-48	90.36%	394	SRA:SRR610305.407901.2
SRX202160	159	159	24%	1e-47	84.78%	329	SRA:SRR610305.487009.2
SRX202160	158	197	26%	2e-47	90.12%	305	SRA:SRR610305.640026.2

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
SRX202160	156	211	27%	1e-46	78.12%	302	SRA:SRR610305.480569.2
SRX202160	152	152	21%	1e-45	86.25%	247	SRA:SRR610305.718598.2
SRX202160	152	152	26%	3e-45	76.29%	319	SRA:SRR610305.373614.2
SRX202160	151	151	22%	6e-45	83.95%	245	SRA:SRR610305.534301.2
SRX202160	151	218	28%	7e-45	87.50%	317	SRA:SRR610305.482196.2
SRX202160	120	197	29%	1e-44	84.06%	431	SRA:SRR610305.352700.2
SRX202160	147	147	23%	7e-43	76.14%	372	SRA:SRR610305.163349.2
SRX202160	147	147	20%	9e-43	90.79%	418	SRA:SRR610305.182165.2
SRX202160	144	144	21%	3e-42	83.75%	310	SRA:SRR610305.295524.2
SRX202160	140	140	38%	6e-40	47.22%	458	SRA:SRR610305.243191.2
SRX202160	136	136	27%	4e-39	66.67%	309	SRA:SRR610305.195167.2
SRX202160	135	135	18%	2e-38	89.55%	346	SRA:SRR610305.726966.2
SRX202160	135	135	22%	2e-38	75.00%	399	SRA:SRR610305.700005.2
SRX202160	135	135	34%	6e-38	50.00%	505	SRA:SRR610305.225432.2
SRX202160	133	133	18%	1e-37	89.39%	316	SRA:SRR610305.298799.2
SRX202160	129	129	16%	1e-36	93.44%	185	SRA:SRR610305.180820.2
SRX202160	129	129	21%	2e-36	79.75%	269	SRA:SRR610305.616637.2
SRX202160	126	126	17%	1e-35	90.77%	199	SRA:SRR610305.518418.2
SRX202160	127	127	19%	2e-35	79.17%	322	SRA:SRR610305.348725.2
SRX202160	125	125	19%	2e-35	81.69%	219	SRA:SRR610305.483431.2
SRX202160	125	125	30%	1e-34	48.33%	376	SRA:SRR610305.140124.2
SRX202160	124	124	16%	2e-34	93.44%	292	SRA:SRR610305.707164.2
SRX202160	124	124	39%	1e-33	39.60%	499	SRA:SRR610305.130106.2
SRX202160	121	181	26%	4e-33	70.51%	300	SRA:SRR610305.285510.2
SRX202160	82.8	218	27%	7e-33	78.26%	379	SRA:SRR610305.361489.2
SRX202160	120	120	17%	3e-32	88.89%	446	SRA:SRR610305.14547.2
SRX202160	119	119	26%	5e-32	54.55%	413	SRA:SRR610305.112981.2
SRX202160	118	174	23%	1e-31	86.89%	407	SRA:SRR610305.376954.2
SRX202160	119	119	26%	1e-31	63.54%	482	SRA:SRR610305.118091.2
SRX202160	114	194	28%	2e-30	89.09%	332	SRA:SRR610305.503276.2
SRX202160	111	111	20%	9e-30	73.08%	231	SRA:SRR610305.410890.2
SRX202160	113	113	41%	3e-29	38.71%	498	SRA:SRR610305.207366.2
SRX202160	112	112	26%	3e-29	51.55%	491	SRA:SRR610305.216960.2
SRX202160	90.5	143	34%	3e-28	54.43%	454	SRA:SRR610305.188779.2
SRX202160	110	110	37%	4e-28	36.30%	529	SRA:SRR610305.96962.2
SRX202160	105	105	16%	1e-27	78.33%	199	SRA:SRR610305.331792.2
SRX202160	107	159	21%	6e-27	87.27%	499	SRA:SRR610305.182264.2
SRX202160	105	164	21%	6e-27	90.74%	421	SRA:SRR610305.360300.2
SRX202160	103	103	14%	7e-27	88.46%	223	SRA:SRR610305.660101.2
SRX202160	95.1	137	43%	1e-26	38.14%	487	SRA:SRR610305.113694.2
SRX202160	105	105	36%	1e-26	36.50%	457	SRA:SRR610305.151653.2
SRX202160	104	104	25%	1e-26	48.51%	390	SRA:SRR610305.109827.2
SRX202160	104	104	36%	2e-26	38.52%	410	SRA:SRR610305.136853.2
SRX202160	102	102	14%	2e-26	88.46%	246	SRA:SRR610305.367693.2
SRX202160	104	104	35%	2e-26	37.41%	437	SRA:SRR610305.126966.2
SRX202160	102	102	14%	3e-26	88.46%	300	SRA:SRR610305.727575.2
SRX202160	103	103	23%	3e-26	52.87%	408	SRA:SRR610305.146245.2

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
SRX202160	102	102	14%	8e-26	90.20%	317	SRA:SRR610305.336205.2
SRX202160	100	100	14%	1e-25	88.24%	230	SRA:SRR610305.627753.2
SRX202160	102	102	42%	1e-25	35.44%	450	SRA:SRR610305.151617.2
SRX202160	100	100	14%	2e-25	88.24%	300	SRA:SRR610305.713722.2
SRX202160	100	100	14%	2e-25	88.24%	301	SRA:SRR610305.712751.2
SRX202160	100	100	14%	2e-25	88.24%	300	SRA:SRR610305.497770.2
SRX202160	100	100	14%	2e-25	88.24%	302	SRA:SRR610305.366843.2
SRX202160	99.8	99.8	14%	4e-25	86.54%	298	SRA:SRR610305.345310.2
SRX202160	98.6	98.6	13%	4e-25	91.84%	183	SRA:SRR610305.637166.2
SRX202160	98.6	98.6	14%	8e-25	86.27%	252	SRA:SRR610305.587030.2
SRX202160	99.8	99.8	14%	1e-24	87.04%	401	SRA:SRR610305.209764.2
SRX202160	100	100	38%	1e-24	36.91%	507	SRA:SRR610305.210909.2
SRX202160	100	100	28%	2e-24	41.23%	520	SRA:SRR610305.127978.2
SRX202160	97.1	97.1	13%	3e-24	86.00%	247	SRA:SRR610305.350431.2
SRX202160	86.7	129	28%	3e-24	60.94%	467	SRA:SRR610305.146939.2
SRX202160	98.2	98.2	26%	4e-24	51.02%	408	SRA:SRR610305.237604.2
SRX202160	81.3	128	18%	5e-24	77.27%	239	SRA:SRR610305.296329.2
SRX202160	95.1	95.1	13%	6e-24	89.80%	149	SRA:SRR610305.371887.2
SRX202160	97.1	162	24%	6e-24	89.80%	320	SRA:SRR610305.534797.2
SRX202160	94.7	94.7	12%	8e-24	93.48%	140	SRA:SRR610305.607386.2
SRX202160	97.1	97.1	37%	2e-23	36.43%	440	SRA:SRR610305.53396.2
SRX202160	96.7	96.7	37%	2e-23	36.43%	414	SRA:SRR610305.696422.2
SRX202160	96.7	96.7	31%	2e-23	37.10%	446	SRA:SRR610305.181294.2
SRX202160	95.9	95.9	14%	4e-23	88.24%	414	SRA:SRR610305.366389.2
SRX202160	95.1	95.1	26%	4e-23	43.81%	368	SRA:SRR610305.29509.2
SRX202160	95.1	95.1	26%	4e-23	43.81%	368	SRA:SRR610305.20998.2
SRX202160	96.3	96.3	43%	5e-23	30.06%	504	SRA:SRR610305.217492.2
SRX202160	94.0	94.0	14%	1e-22	86.27%	399	SRA:SRR610305.731254.2
SRX202160	93.6	93.6	29%	1e-22	47.32%	366	SRA:SRR610305.95861.2
SRX202160	92.8	92.8	18%	2e-22	59.70%	327	SRA:SRR610305.71831.2

Graphic Summary

Alignment Scores < 40 40 - 50 50 - 80 80 - 200 >= 200

Distribution of the top 126 Blast Hits on 100 subject sequences



Alignments

Alignment view Pairwise ☐ CDS feature Restore defaults

SRX202160
Sequence ID: **SRA:SRR610305.97090.2** Length: 462 Number of Matches: 1
Range 1: 3 to 461

Score	Expect	Method	Identities	Positives	Gaps	Frame
285 bits(729) 2e-96() Compositional matrix adjust. 135/153(88%) 142/153(92%) 0/153(0%) +3						
Query 147	IKQGGIRSVQCGGALVTNRHVITASHCVVNSAGTDVMPADVFSVRLGEHNL	YSTDDSNP	206			
Sbjct 3	IKQGGIRSVQCGGALVTNRHVITASHCVVNS GTDVM ADVFSVRLGEHNL	YST+D S+P				
	IKQGGIRSVQCGGALVTNRHVITASHCVVNSLGTDMRADVFSVRLGEHNL	YSTNDSSDP	182			
Query 207	IDFAVTSVKHHEHFVLATYLNDAIILTLNDTVTFTDRIRPICLPYRKLR	YDDLAMRKPF	266			
Sbjct 183	IDFAVTSVKHHE+FVLATYLNDAIIL LNDTVTFT +I+PICLPY LRY+DLAMR	PF+				
	IDFAVTSVKHHENFVLATYLNDAIILKLN	DTVTFTHKIKPICLPYESLRYEDLAMRNP	362			
Query 267	TGWGTTAFNGPSSAVLREVQLPIWEHEACRQAY	299				
	GWGTTAFNGPSSAVLREVQLPIW HE CRQAY					
Sbjct 363	AGWGTTAFNGPSSAVLREVQLPIWGHEPCRQAY	461				

SRX202160
Sequence ID: **SRA:SRR610305.62354.2** Length: 388 Number of Matches: 1
Range 1: 1 to 387

Score	Expect	Method	Identities	Positives	Gaps	Frame
246 bits(629) 1e-81() Compositional matrix adjust. 114/129(88%) 120/129(93%) 0/129(0%) -2						
Query 207	IDFAVTSVKHHEFVLATYLN	DIAILTLNDTVFTDRIRPICLPYRKLR	YDDLAMRKPFI	266		
Sbjct 387	IDFAVTSVKHHEFVLATYLN	DIAILTLNDTVFT +I+PICLPY LRY+DLAMR PF+	IDFAVTSVKHHEFVLATYLN	DIAILTLNDTVFTTHKIKPICLPYESLRYEDLAMRNPFV	208	
Query 267	TGWGTTAFNGPSSAVLREVQLPIWEHEACRQAYEKDLNITNVYMCAGFADGGKDACQGDS	326				
Sbjct 207	AGWGTTAFNGPSSAVLREVQLPIW HE CRQAYEKDLNITNVYMCAG+ADGGKDACQGDS	28				
Query 327	GGPMMLPVK 335					
Sbjct 27	GGPMMLP K 1					

SRX202160
Sequence ID: **SRA:SRR610305.140318.2** Length: 495 Number of Matches: 2
Range 1: 2 to 304

Score	Expect	Method	Identities	Positives	Gaps	Frame
193 bits(491) 8e-79(2) Compositional matrix adjust. 86/101(85%) 93/101(92%) 0/101(0%) -3						
Query 243	RIRPICLPYRKLR	YDDLAMRKPFI	TGWGTTAFNGPSSAVLREVQLPIWEHEACRQAYEKD	302		
Sbjct 304	QIKPICLPYESLRYEDLAMRNPFVAGWGTTAFNGPSSAVLREVQLPIWGHEPCRQAYEKD	125				
Query 303	LNITNVYMCAGFADGGKDACQGDSGGPMMLPVKTGEFYLI	343				
Sbjct 124	LNITNVYMCAG+ADGGKDACQGDSGGPMMLP K+G FYL+G	2				

Range 2: 286 to 495

Score	Expect	Method	Identities	Positives	Gaps	Frame
118 bits(296) 8e-79(2) Compositional matrix adjust. 57/70(81%) 62/70(88%) 0/70(0%) -1						
Query 179	GTDVMPADVFSVRLGEHNLYSTDDSNPIDFAVTSVKHHEFVLATYLN	DIAILTLNDTV	238			
Sbjct 495	GTDVM ADVFSVRLGEHNLYST+D S+PIDFAVTSVKHHEFVLATYLN	DIAIL TLNDTV	316			
Query 239	TFTDRIRPIC 248					
Sbjct 315	TFT ++					

SRX202160
Sequence ID: **SRA:SRR610305.104315.2** Length: 473 Number of Matches: 2
Range 1: 3 to 383

Score	Expect	Method	Identities	Positives	Gaps	Frame
233 bits(593) 1e-75() Compositional matrix adjust. 109/127(86%) 116/127(91%) 0/127(0%) +3						
Query 176	NSAGTDVMPADVFSVRLGEHNLYSTDDSNPIDFAVTSVKHHEFVLATYLN	DIAILTLN	235			
Sbjct 3	NSLGTDM ADVFSVRLGEHNLYST+D S+PIDFAVTSVKHHEFVLATYLN	DIAIL LN	182			
Query 236	DTVTFTDRIRPICLPYRKLR	YDDLAMRKPFI	TGWGTTAFNGPSSAVLREVQLPIWEHEAC	295		
Sbjct 183	DTVTFTTHKIKPICLPYESLRYEDLAMRNPFVAGWGTTAFNGPSSAVLREVQLPIWGHEPC	362				
Query 296	RQAYEKD 302					
Sbjct 363	RQAYEKD 383					

Range 2: 356 to 457

Score	Expect	Method	Identities	Positives	Gaps	Frame
55.5 bits(132)	1e-08()	Compositional matrix adjust.	25/34(74%)	28/34(82%)	0/34(0%)	+2
Query 294	ACRQAYEKDLNITNVVMCAGFADGGKDACQGD	327				
Sbjct 356	ALQAGLREGLNITNVVMCAGYADGGKDACQGD	457				

SRX202160
Sequence ID: **SRA:SRR610305.124826.2** Length: 492 Number of Matches: 2
Range 1: 3 to 413

Score	Expect	Method	Identities	Positives	Gaps	Frame
209 bits(532)	2e-66()	Compositional matrix adjust.	115/137(84%)	121/137(88%)	0/137(0%)	-2
Query 62	KNDYNLLKESICGFEGITPKVCCPKSSHVISSTQAppetttterppKQIPPNLPEVCGIH	121				
Sbjct 413	KNDYNLLKESICGFEGITPKVCCPKS V T+APP+TTTTERPP +IP NLP+ CG	234				
Query 122	NTTTTRIIGGREAPIGAWPWMTAVYIKQGGIRSVQCGGALVTNRHVITASHCVVNSAGTD	181				
Sbjct 233	N TTTTRIIGG+EA GAWPW+ AVYIKQGGIRSVQCGGALVTNRHVITASHCVVNS GTD	54				
Query 182	VMPADVFSVRLGEHNLY 198					
Sbjct 53	VM ADVFSVRLGEHNLY 3					

Range 2: 368 to 490

Score	Expect	Method	Identities	Positives	Gaps	Frame
44.3 bits(103)	1e-04()	Compositional matrix adjust.	23/41(56%)	28/41(68%)	7/41(17%)	-3
Query 36	EEELCSNRFTEEGTCKNVLD CRILLQ-----KNDYNLLK 69					
Sbjct 490	+EE CSNRF +G CK+VL+CR LLQ KN Y +LK					
	DEESCSNRF+NDGICKDVLNCRDLLQKMIIY*KNQYAVLK 368					

SRX202160
Sequence ID: **SRA:SRR610305.598174.2** Length: 374 Number of Matches: 1
Range 1: 3 to 320

Score	Expect	Method	Identities	Positives	Gaps	Frame
204 bits(519)	5e-65()	Compositional matrix adjust.	96/106(91%)	100/106(94%)	0/106(0%)	+3
Query 271	TTAFNGPSSAVLREVQLPIWEHEACRQAYEKDLNITNVVMCAGFADGGKDACQGD	330				
Sbjct 3	TTAFNGPSSAVLREVQLPIW HE CRQAYEKDLNITNVVMCAG+ADG KDACQGD	182				
Query 331	MLPVKTGEFYLGIVSFGKKCALPGFPGVYTKVTEFLDWIAEHMV* 376					
Sbjct 183	MLP K+G FYL+GIVSFGKKCALPGFPGVYTKVTEFLDWIA +MV* 320					

SRX202160
Sequence ID: **SRA:SRR610305.184275.2** Length: 472 Number of Matches: 2
Range 1: 3 to 374

Score	Expect	Method	Identities	Positives	Gaps	Frame
205 bits(521)	6e-65()	Compositional matrix adjust.	100/124(81%)	107/124(86%)	0/124(0%)	+3
Query 154	SVQCGGALVTNRHVITASHCVVNSAGTDVMPADVFSVRLGEHNLYSTDDSDNPIDFAVTS	213				
Sbjct 3	SVQCGGALVTNRHVITASHCVVNS GTDVM ADVFSVRLGEHNLYST+D S+PIDFAVTS	182				
Query 214	VKHHEHFLATYLNIDIAILTLNDTVTF+TDRIRPICLPYRKLRYDDLAMRKPFITGWGTTA	273				
Sbjct 183	VKHHEHFLATYLNIDIAILKLNLDTVTF+I+PICLPY LRY+DLAMR PF G +	362				
Query 274	FNGP 277					

Sbjct 363 I*WP 374

Range 2: 337 to 471

Score	Expect	Method	Identities	Positives	Gaps	Frame
89.7 bits(221)	9e-21()	Compositional matrix adjust.	40/45(89%)	41/45(91%)	0/45(0%)	+1
Query 265	FITGWGTTAFNGPSSAVLREVQLPIWEHEACRQAYEKDLNITNVY					309
	+ GWTGTTAFNGPSSAVLREVQLPIW HE CRQAYEKDLNITNVY					
Sbjct 337	LVAGWGTTAFNGPSSAVLREVQLPIWGHEPCRQAYEKDLNITNVY					471

SRX202160

Sequence ID: **SRA:SRR610305.115187.2** Length: 406 Number of Matches: 2
Range 1: 3 to 305

Score	Expect	Method	Identities	Positives	Gaps	Frame
199 bits(506)	8e-63()	Compositional matrix adjust.	92/101(91%)	96/101(95%)	0/101(0%)	-3
Query 271	TTAFNGPSSAVLREVQLPIWEHEACRQAYEKDLNITNVYMCAGFADGGKDACQGDSSGGPM					330
	T+ FNGPSSAVLREVQLPIW HE CRQAYEKDLNITNVYMCAG+ADGGKDACQGDSSGGPM					
Sbjct 305	TSLFNGPSSAVLREVQLPIWGHEPCRQAYEKDLNITNVYMCAGYADGGKDACQGDSSGGPM					126
Query 331	MLPVKTGEFYLGIVSFGKKCALPGFPGVYTKVTEFLDWIA					371
	MLP K+G FYL+GIVSFGKKCALPGFPGVYTKVTEFLDWIA					
Sbjct 125	MLPDKSGNFYLVGIVSFGKKCALPGFPGVYTKVTEFLDWIA					3

Range 2: 304 to 384

Score	Expect	Method	Identities	Positives	Gaps	Frame
51.6 bits(122)	2e-07()	Compositional matrix adjust.	20/27(74%)	22/27(81%)	0/27(0%)	-2
Query 246	PICLPYRKLRYDDLAMRKPFITGWGTT					272
	PICLPY LRY+DLAMR PF+ GWTG					
Sbjct 384	PICLPYESLRYEDLAMRNPFVAGWGTTN					304

SRX202160

Sequence ID: **SRA:SRR610305.296720.2** Length: 492 Number of Matches: 3
Range 1: 56 to 385

Score	Expect	Method	Identities	Positives	Gaps	Frame
198 bits(503)	4e-62()	Compositional matrix adjust.	93/110(85%)	98/110(89%)	1/110(0%)	+2
Query 254	LRYD-DLAMRKPFITGWGTTAFNGPSSAVLREVQLPIWEHEACRQAYEKDLNITNVYMC					312
	LRY+ MR PF+ GWTGTTAFNGPSSAVLREVQLPIW HE CRQAYEKDLNITNVYMC					
Sbjct 56	LRYEGSKTRNPFVAGWGTTAFNGPSSAVLREVQLPIWGHEPCRQAYEKDLNITNVYMC					235
Query 313	GFADGGKDACQGDSSGGPMMLPVKTGEFYLGIVSFGKKCALPGFPGVYTK					362
	G+ADGGKDACQGDSSGGPMMLP K+G FYL+GIVSFGKKCALPGFPGV K					
Sbjct 236	GYADGGKDACQGDSSGGPMMLPDKSGNFYLVGIVSFGKKCALPGFPGVLHK					385

Range 2: 300 to 428

Score	Expect	Method	Identities	Positives	Gaps	Frame
38.1 bits(87)	0.013()	Compositional matrix adjust.	20/43(47%)	25/43(58%)	0/43(0%)	+3
Query 334	VKTGEFYLGIVSFGKKCALPGFPGVYTKVTEFLDWIAEHMV*					376
	+K G F + + + F G YTKVTEFLDWIA +MV*					
Sbjct 300	IKAGTFISLELCLSERNARCLDFLGFTKVTEFLDWIAVNMV*					428

Range 3: 1 to 60

Score	Expect	Method	Identities	Positives	Gaps	Frame
37.0 bits(84)	0.042()	Compositional matrix adjust.	15/20(75%)	18/20(90%)	0/20(0%)	+1

Query 236 DTVTFDRIRPICLPYRKLR 255
DTVTFT +I+PICLPY KL+
Sbjct 1 DTVTFTHKIKPICLPYVKLK 60

SRX202160
Sequence ID: **SRA:SRR610305.267540.2** Length: 436 Number of Matches: 1
Range 1: 141 to 434

Score	Expect	Method	Identities	Positives	Gaps	Frame
196 bits(499)	9e-62()	Compositional matrix adjust.	91/98(93%)	94/98(95%)	0/98(0%)	-3
Query 269	WGTTAFNGPSSAVLREVQLPIWEHEACRQAYEKDLNITNVYMCAGFADGGKDACQGDSSGG					328
Sbjct 434	WGTTAFNGPSSAVLREVQLPIW HE CRQAYEKDLNITNVYMCAG+ADGGKDACQGDSSGG					255
Query 329	PMMLPVKTGEFYILIGIVSFGKKCALPGFPGVYTKVTEF 366					
Sbjct 254	PMMLP K+G FYL+GIVSFGKKCALPGFPGVYTKVTEF 141					

SRX202160
Sequence ID: **SRA:SRR610305.159521.2** Length: 461 Number of Matches: 2
Range 1: 51 to 377

Score	Expect	Method	Identities	Positives	Gaps	Frame
195 bits(496)	4e-61()	Compositional matrix adjust.	93/109(85%)	99/109(90%)	1/109(0%)	+3
Query 206	PIDF-AVTSVKHHEFVLATYLNDAIILTLNDTVTFTDRIRPICLPYRKLRDYDDLAMRKP					264
Sbjct 51	PI F +VTSVKHHE+FVLATYLNDAIIL LNDTVTFT +I+PICLPY LRY+DLAMR P					230
Query 265	FITGWGTTAFNGPSSAVLREVQLPIWEHEACRQAYEKDLNITNVYMCAG 313					
Sbjct 231	F+ GWGTTAFNGPSSAVLREVQLPIW HE CRQAYEKDLNITNVYMCAG					377

Range 2: 376 to 459

Score	Expect	Method	Identities	Positives	Gaps	Frame
55.5 bits(132)	2e-08()	Compositional matrix adjust.	24/28(86%)	26/28(92%)	0/28(0%)	+1
Query 313	GFADGGKDACQGDSSGPMMLPVKTGEFY 340					
Sbjct 376	G+ADGGKDACQGDSSGPMMLP K+G FY					459

SRX202160
Sequence ID: **SRA:SRR610305.617893.2** Length: 421 Number of Matches: 1
Range 1: 100 to 420

Score	Expect	Method	Identities	Positives	Gaps	Frame
190 bits(483)	2e-59()	Compositional matrix adjust.	92/107(86%)	97/107(90%)	1/107(0%)	-2
Query 271	TTAFNGPSSAVLREVQLPIWEHEACRQAYEKDLNITNVYMCAGFADGGKDACQGDSSGPM					330
Sbjct 420	TTAFNGPSSAVLREVQLPIW HE CRQAYEKDLNITNVYMCAG+ADGGKDACQGDSSGPM					241
Query 331	MLPVKTGEFYL-IGIVSFGKKCALPGFPGVYTKVTEFLDWIAEHMV* 376					
Sbjct 240	MLP K E ++ + VSFGKKCALPGFPGVYTKVTEFLDWIA +MV*					100

SRX202160
Sequence ID: **SRA:SRR610305.737967.2** Length: 335 Number of Matches: 1
Range 1: 3 to 326

Score	Expect	Method	Identities	Positives	Gaps	Frame
186 bits(473)	3e-58()	Compositional matrix adjust.	91/109(83%)	95/109(87%)	1/109(0%)	+3

Query 268 GWGTTAFNGPSSAVLREVQLPIWEHEACRQAYEKDLNITNVYMCAGFADGGKDACQGD SG 327
Sbjct 3 GWGTTAFNGPSSAVLREVQLPIW HE CRQAYEKDLNITNVYMCAG+ADGGKDACQGD SG 182
Query 328 GPMMLPVKTGEFYLIGIVSFGKKCALPGFPGVYTKVTEFLDWIAEHMV* 376
Sbjct 183 GPMMLP K G V F ++CALPGFPGVYTKVTEFLDWIA +MV* 326
GPMMLPDKAGLLSRWNCV-FSEECALPGFPGVYTKVTEFLDWIAVNMV*

SRX202160
Sequence ID: **SRA:SRR610305.393406.2** Length: 431 Number of Matches: 1
Range 1: 144 to 431

Score	Expect	Method	Identities	Positives	Gaps	Frame
187 bits(474)	5e-58()	Compositional matrix adjust.	87/96(91%)	91/96(94%)	0/96(0%)	-1
Query 281	VLREVQLPIWEHEACRQAYEKDLNITNVYMCAGFADGGKDACQGD SGGPMMLPVKTGEFY	340				
Sbjct 431	VLREVQLPIW HE CRQAYEKDLNITNVYMCAG+ADGGKDACQGD SGGPMMLP K+G FY	252				
Query 341	LIGIVSFGKKCALPGFPGVYTKVTEFLDWIAEHMV* 376					
Sbjct 251	L+GIVSFGKKCALPGFPGVYTKVTEFLDWIA +MV* 144					

SRX202160
Sequence ID: **SRA:SRR610305.606681.2** Length: 287 Number of Matches: 1
Range 1: 1 to 285

Score	Expect	Method	Identities	Positives	Gaps	Frame
184 bits(468)	1e-57()	Composition-based stats.	87/95(92%)	90/95(94%)	0/95(0%)	+1
Query 142	MTAVYIKQGGIRSVQCGGALVTNRHVITASHCVVNSAGTDVMPADVFSVRLGEHNLYSTD	201				
Sbjct 1	M AVYIKQGGIRSVQCGGALVTNRHVITASHCVVNS GTDVM ADVFSVRLGEHNLYST+ MAAVYIKQGGIRSVQCGGALVTNRHVITASHCVVNSLGTDMRADVFSVRLGEHNLYSTN	180				
Query 202	DDSNPIDFAVTSVKHHEHFVLATYLNDAIILTLND 236					
Sbjct 181	D S+PIDFAVTSVKHHE+FVLATYLNDAIIL LND DSSDPIDFAVTSVKHHEFVLATYLNDAIILKLND 285					

SRX202160
Sequence ID: **SRA:SRR610305.254076.2** Length: 401 Number of Matches: 2
Range 1: 2 to 337

Score	Expect	Method	Identities	Positives	Gaps	Frame
179 bits(453)	5e-55()	Compositional matrix adjust.	90/113(80%)	100/113(88%)	2/113(1%)	-2
Query 128	IIGGREAPIGAWP-WMTAVYIKQGGIRSVQCGGALVTNRHVITASHCVVNSAGTDVMPAD	186				
Sbjct 337	++ GR+ + P W+ ++Y KQGGIRSVQCGGALVTNRHVITASHCVVNS GTDVM AD LLEGRKQHLEPGPGWLLSIY-KQGGIRSVQCGGALVTNRHVITASHCVVNSLGTDMRAD	161				
Query 187	VFSVRLGEHNLYSTDDDSNPIDFAVTSVKHHEHFVLATYLNDAIILTLNDTVT 239					
Sbjct 160	VFSVRLGEHNLYST+D S+PIDFAVTSVKHHE+FVLATYLNDAIIL LNDTVT VFSVRLGEHNLYSTNDSSDPIDFAVTSVKHHEFVLATYLNDAIILKLNDTVT 2					

Range 2: 276 to 395

Score	Expect	Method	Identities	Positives	Gaps	Frame
61.6 bits(148)	6e-11()	Compositional matrix adjust.	28/40(70%)	32/40(80%)	0/40(0%)	-1
Query 109	QIPPNLPEVCGIHNTTTTTRIIGGREAPIGAWPWMTAVYIK 148					
Sbjct 395	+IP NLP+ CG- N TTTTRIIGG+EA GAWPMM AVYI+ RIPSNLPKQCGNRNITTTTRIIGGQATPGAWPWMAAVYIQ 276					

SRX202160
Sequence ID: **SRA:SRR610305.600452.2** Length: 343 Number of Matches: 2
Range 1: 76 to 321

Score	Expect	Method	Identities	Positives	Gaps	Frame
169 bits(429)	1e-51()	Composition-based stats.	75/82(91%)	79/82(96%)	0/82(0%)	+1
Query 295	CRQAYEKDLNITNVVMCAGFADGGKDACQGDSDGGPMMLPVKTGEFYLGIVSFGKKCALP					354
Sbjct 76	CRQAYEKDLNITNVVMCAG+ADGGKDACQGDSDGGPMMLP K+G FYL+GIVSFGKKCALP					255
Query 355	GFPGVYTKVTEFLDWIAEHMV*		376			
Sbjct 256	GFPGVYTKVTEFLDWIA +MV*		321			
	GFPGVYTKVTEFLDWIAVNMV*					

Range 2: 3 to 128

Score	Expect	Method	Identities	Positives	Gaps	Frame
52.8 bits(125)	6e-08()	Composition-based stats.	25/42(60%)	28/42(66%)	1/42(2%)	+3
Query 271	TTAFNGPSSAVLREVQLPIWEHEACRQAYEKDLN-ITNVVMC			311		
Sbjct 3	TTAFNGPSSAVLREVQLPIW HE + + VY+C			128		
	TTAFNGPSSAVLREVQLPIWGHEPLQAGLREGFKYKRVYVC					

SRX202160

Sequence ID: **SRA:SRR610305.376727.2** Length: 341 Number of Matches: 1
Range 1: 3 to 323

Score	Expect	Method	Identities	Positives	Gaps	Frame
168 bits(426)	3e-51()	Compositional matrix adjust.	85/107(79%)	90/107(84%)	1/107(0%)	+3
Query 271	TTAFNGPSSAVLREVQLPIWEHEACRQAYEKDLNITNVVMCAGFADGGKDACQGDSDGGPM			330		
Sbjct 3	TTAFNGPSSAVLREVQLPIW HE CRQAYEKDLNITNVVMCAG+ADGGKDACQGDSDGGPM			182		
	TTAFNGPSSAVLREVQLPIWGHEPCRQAYEKDLNITNVVMCAGYADGGKDACQGDSDGGPM					
Query 331	MLPVKTGEFYLGIVSFGKKCAL-PGFPGVYTKVTEFLDWIAEHMV*		376			
Sbjct 183	MLP K+G FYL+GIVSFGKK + F G K FLDWIA +MV*		323			
	MLPDKSGNFYLVGIVSFGKKWRVCLDFLGFTQK*P*FLDWIASNMV*					

SRX202160

Sequence ID: **SRA:SRR610305.289470.2** Length: 447 Number of Matches: 1
Range 1: 6 to 260

Score	Expect	Method	Identities	Positives	Gaps	Frame
165 bits(418)	1e-49()	Compositional matrix adjust.	77/85(91%)	81/85(95%)	0/85(0%)	+3
Query 292	HEACRQAYEKDLNITNVVMCAGFADGGKDACQGDSDGGPMMLPVKTGEFYLGIVSFGKKC			351		
Sbjct 6	HE CRQAYEKDLNITNVVMCAG+ADGGKDACQGDSDGGPMMLP K+G FYL+GIVSFGKKC			185		
	HEPCRQAYEKDLNITNVVMCAGYADGGKDACQGDSDGGPMMLPDKSGNFYLVGIVSFGKKC					
Query 352	ALPGFPGVYTKVTEFLDWIAEHMV*		376			
Sbjct 186	ALPGFPGVYTKVTEFLDWIA +MV*		260			
	ALPGFPGVYTKVTEFLDWIAVNMV*					

SRX202160

Sequence ID: **SRA:SRR610305.503368.2** Length: 264 Number of Matches: 1
Range 1: 13 to 264

Score	Expect	Method	Identities	Positives	Gaps	Frame
162 bits(409)	5e-49()	Compositional matrix adjust.	74/84(88%)	77/84(91%)	0/84(0%)	+1
Query 274	FNGPSSAVLREVQLPIWEHEACRQAYEKDLNITNVVMCAGFADGGKDACQGDSDGGPMMLP			333		
Sbjct 13	FNGPSSAVLREVQLPIW HE CRQAYEKDLNITNVVMCAG+ADGGKDACQGDSDGGPMMLP			192		
	FNGPSSAVLREVQLPIWGHEPCRQAYEKDLNITNVVMCAGYADGGKDACQGDSDGGPMMLP					
Query 334	VKTGEFYLGIVSFGKKCALPGFP		357			
Sbjct 193	K+G FYL+GIVSFGK LPGFP		264			
	DKSGNFYLVGIVSFGKNATLPGFP					

SRX202160
Sequence ID: **SRA:SRR610305.407901.2** Length: 394 Number of Matches: 1
Range 1: 3 to 251

Score	Expect	Method	Identities	Positives	Gaps	Frame
162 bits(409)	2e-48()	Compositional matrix adjust.	75/83(90%)	80/83(96%)	0/83(0%)	+3
Query 294	ACRQAYEKDLNITNVYMCAGFADGGKDACQGDSSGGPMMLPVKTGEFYLGIVSFGKKCAL					353
	+CRQAYEKDLNITNVYMCAG+ADGGKDACQGDSSGGPMMLP K+G FYL+GIVSFGKKCAL					
Sbjct 3	SCRQAYEKDLNITNVYMCAGYADGGKDACQGDSSGGPMMLPDKSGNFYLVGIVSFGKKCAL					182
Query 354	PGFPGVYTKVTEFLDWIAEHMV* 376					
	PGFPGVYTKVTEFLDWIA +MV*					
Sbjct 183	PGFPGVYTKVTEFLDWIAVMV* 251					

SRX202160
Sequence ID: **SRA:SRR610305.487009.2** Length: 329 Number of Matches: 1
Range 1: 3 to 278

Score	Expect	Method	Identities	Positives	Gaps	Frame
159 bits(402)	1e-47()	Compositional matrix adjust.	78/92(85%)	81/92(88%)	0/92(0%)	-1
Query 109	QIPPNLPEVCGIHNTTTTRIIGGREAPIGAWPMTAVYIKQGGIRSVQCGGALVTNRHVI					168
	+IP NLP+ CG N TTTRII G+EA GAWPWM AVYIKQGGIRSVQCGGALVTNRHVI					
Sbjct 278	RIPSNLPKQCGNRIITTTRIIEGQEXPGAWPWMAAVYIKQGGIRSVQCGGALVTNRHVI					99
Query 169	TASHCCVNSAGTDVMPADVFSVRLGEHNLST 200					
	TASHCCVNS GTDVM ADVFSVRLGEHNLST					
Sbjct 98	TASHCCVNSLGTDMRADVFSVRLGEHNLST 3					

SRX202160
Sequence ID: **SRA:SRR610305.640026.2** Length: 305 Number of Matches: 2
Range 1: 3 to 245

Score	Expect	Method	Identities	Positives	Gaps	Frame
158 bits(399)	2e-47()	Compositional matrix adjust.	73/81(90%)	76/81(93%)	0/81(0%)	+3
Query 271	TTAFNGPSSAVLREVQLPIWEHEACRQAYEKDLNITNVYMCAGFADGGKDACQGDSSGGPM					330
	TTAFNGPSSAVLREVQLPIW HE CRQAY KDLNITNVYMCAG+ADGGKDACQGDSSGGPM					
Sbjct 3	TTAFNGPSSAVLREVQLPIWGHEPCRQAYEKDLNITNVYMCAGYADGGKDACQGDSSGGPM					182
Query 331	MLPVKTGEFYLGIVSFGKKC 351					
	MLP K+G FYL+GIVSFGKKC					
Sbjct 183	MLPDKSGNFYLVGIVSFGKKC 245					

Range 2: 251 to 304

Score	Expect	Method	Identities	Positives	Gaps	Frame
38.9 bits(89)	0.003()	Composition-based stats.	16/18(89%)	16/18(88%)	0/18(0%)	+2
Query 353	LPGFPGVYTKVTEFLDWI 370					
	LPGFPGVYTKVT LDWI					
Sbjct 251	LPGFPGVYTKTVVLDWI 304					

SRX202160
Sequence ID: **SRA:SRR610305.480569.2** Length: 302 Number of Matches: 2
Range 1: 3 to 290

Score	Expect	Method	Identities	Positives	Gaps	Frame
156 bits(394)	1e-46()	Compositional matrix adjust.	75/96(78%)	79/96(82%)	0/96(0%)	+3
Query 271	TTAFNGPSSAVLREVQLPIWEHEACRQAYEKDLNITNVYMCAGFADGGKDACQGDSSGGPM					330
	TTAFNGPSSAVLREVQLPIW HE CRQAYEKDLNITNVYMCAG+ADGGKDACQGDSSGGPM					
Sbjct 3	TTAFNGPSSAVLREVQLPIWGHEPCRQAYEKDLNITNVYMCAGYADGGKDACQGDSSGGPM					182
Query 331	MLPVKTGEFYLGIVSFGKKCALPGFPGVYTKVTEF 366					

Sbjct 183 MLP K+G FYL+GIVSFG+ F G K F
MLPDKSGNFYLVGIVSFGRNARCLDFLGFTQK*PSF 290

Range 2: 230 to 301

Score	Expect	Method	Identities	Positives	Gaps	Frame
55.5 bits(132)	5e-09()	Composition-based stats.	23/24(96%)	23/24(95%)	0/24(0%)	+2
Query 347	FGKKCALPGFPGVYTKVTEFLDWI		370			
	F KKCALPGFPGVYTKVTEFLDWI					
Sbjct 230	FRKKCALPGFPGVYTKVTEFLDWI		301			

SRX202160

Sequence ID: **SRA:SRR610305.718598.2** Length: 247 Number of Matches: 1
Range 1: 8 to 247

Score	Expect	Method	Identities	Positives	Gaps	Frame
152 bits(385)	1e-45()	Composition-based stats.	69/80(86%)	72/80(90%)	1/80(1%)	+2
Query 272	TAFNGPSSAVLREVQLPIWEHEACRQAYEKDLNI - TNVVMCAGFADGGKDACQGDSGGPM		330			
	TAFNGPSSAVLREVQLPIW HE CRQAYEKD I NVVMCAG+ADGGKDACQGDSGGPM					
Sbjct 8	TAFNGPSSAVLREVQLPIWGHEPCRQAYEKDFKILQNVVMCAGYADGGKDACQGDSGGPM		187			
Query 331	MLPVKTGEFYLLIGIVSFGKK 350					
	MLP K+G FYL+GIVSFGKK					
Sbjct 188	MLPDKSGNFYLVGIVSFGKK 247					

SRX202160

Sequence ID: **SRA:SRR610305.373614.2** Length: 319 Number of Matches: 1
Range 1: 1 to 288

Score	Expect	Method	Identities	Positives	Gaps	Frame
152 bits(385)	3e-45()	Compositional matrix adjust.	74/97(76%)	80/97(82%)	1/97(1%)	+1
Query 270	GTTAFNGPSSAVLREVQLPIWEHEACRQAYEKDLNITNVVMCAGFADGGKDACQGDSGGP		329			
	GTTAFNGPSSAVLREVQLPIW HE CRQAYEKDLNITNVVMCAG+ADGGKDACQGDSGGP					
Sbjct 1	GTTAFNGPSSAVLREVQLPIWGHEPCRQAYEKDLNITNVVMCAGYADGGKDACQGDSGGP		180			
Query 330	MMLPVKTGEFYLLIGIVSFGKKCALPGFPGVYTKVTEF 366					
	MMLP K G F + + ++ + PGVYTKVTEF					
Sbjct 181	MMLPDKAGTFISLELC - LSERMRVAWIPGVYTKVTEF 288					

SRX202160

Sequence ID: **SRA:SRR610305.534301.2** Length: 245 Number of Matches: 1
Range 1: 1 to 243

Score	Expect	Method	Identities	Positives	Gaps	Frame
151 bits(381)	6e-45()	Compositional matrix adjust.	68/81(84%)	73/81(90%)	0/81(0%)	+1
Query 231	ILTLNDTVTFTDIRIPICLPYRKLYDDLAMRKPFITGWGTTAFNGPSSAVLREVQLPIW		290			
	IL LNDTVTFT +I+PICLPY LR++DLAMR PF+ GWGTTAFNGPSSAVLREVQLPIW					
Sbjct 1	ILKLNDTVTFTTHKIKPICLPYESLRHEDLAMRNPFVAGWGTTAFNGPSSAVLREVQLPIW		180			
Query 291	EHEACRQAYEKDLNITNVVMC 311					
	HE CRQAYEKDLNITNVVMC					
Sbjct 181	GHEPCRQAYEKDLNITNVVMC 243					

SRX202160

Sequence ID: **SRA:SRR610305.482196.2** Length: 317 Number of Matches: 2
Range 1: 3 to 242

Score	Expect	Method	Identities	Positives	Gaps	Frame
151 bits(382)	7e-45()	Compositional matrix adjust.	70/80(88%)	74/80(92%)	0/80(0%)	+3

Query 271 TTAfNGPSSAVLREVQLPIWEHEACRQAYEKDLNITNVVMCAGFADGGKDACQGDSSGGPM 330
Sbjct 3 TTAfNGPSSAVLREVQLPIW HE CRQAYEKDLN TNVVMCAG+ADGGKDACQGDSSGGPM 182

Query 331 MLPVKTGEFYLIIGIVSFGKK 350
Sbjct 183 MLP K+G FYL+GIVSF K+ MLPDKSGNFYLVGIVSFRKE 242

Range 2: 193 to 315

Score	Expect	Method	Identities	Positives	Gaps	Frame
66.6 bits(161)	6e-13()	Composition-based stats.	29/41(71%)	33/41(80%)	0/41(0%)	+1
Query 334	VKTGEFYLIIGIVSFGKKCALPGFPGVYTKVTEFLDWIAEHM	374				
Sbjct 193	+K G F + + FGKKCALPGFPGVYTKVTEFLDWIA +M IKAGTFISLELCLFGKKCALPGFPGVYTKVTEFLDWIAVNM	315				

SRX202160

Sequence ID: **SRA:SRR610305.352700.2** Length: 431 Number of Matches: 2
Range 1: 67 to 273

Score	Expect	Method	Identities	Positives	Gaps	Frame
120 bits(302)	1e-44(2)	Compositional matrix adjust.	58/69(84%)	61/69(88%)	0/69(0%)	+1
Query 109	QIPPNLFEVCGIHTTTTTTRIIGGREAPIGAWPMTAVYIKGGIRSVQCGGALVTNRHVI	168				
Sbjct 67	+IP NLP+ CG N TTTTRIIGG+EA GAWPMM AVYIKGGIRSVQCGGALVTNRHVI RIPS NLPKQCGNRNITTTTRIIGGQATPGAWPMAAVYIKGGIRSVQCGGALVTNRHVI	246				
Query 169	TASHCIVNS 177					
Sbjct 247	TASHCIVNS TASHCIVNS 273					

Range 2: 278 to 397

Score	Expect	Method	Identities	Positives	Gaps	Frame
77.0 bits(188)	1e-44(2)	Compositional matrix adjust.	36/40(90%)	38/40(95%)	0/40(0%)	+2
Query 179	GTDVMPADVFSVRLGEHNLYSTDDSNPIDFAVTSVKHHE	218				
Sbjct 278	GTDVM ADVFSVRLGEHNLYST+D S+PIDFAVTSVKHHE GTDVMRADVFSVRLGEHNLYSTNDSDPIDFAVTSVKHHE	397				

SRX202160

Sequence ID: **SRA:SRR610305.163349.2** Length: 372 Number of Matches: 1
Range 1: 96 to 359

Score	Expect	Method	Identities	Positives	Gaps	Frame
147 bits(371)	7e-43()	Composition-based stats.	67/88(76%)	74/88(84%)	0/88(0%)	+3
Query 1	MLVNNVFSLLCFPLLMVVRCSLRSRQRFVFPDEEELCSNRFTEEGTKCNVLCRILL	60				
Sbjct 96	MLVNN+FSLLCF LLMS+ CS+L RRRQRFVFPD+EE CSNRF +G CK+VL+CR LL MLVNNMFSLLCFSLLMMSFSCSSLGRQRRQRFVFPDDEESCSNRF TNDGICKDVLNCRDLL	275				
Query 61	QKNDYNLLKESICGFEGITPKVCCPKSS 88					
Sbjct 276	QKNDYNLLKESIC F GITPK PK S QKNDYNLLKESICRFRGITPKFVLPKQS	359				

SRX202160

Sequence ID: **SRA:SRR610305.182165.2** Length: 418 Number of Matches: 1
Range 1: 1 to 228

Score	Expect	Method	Identities	Positives	Gaps	Frame
147 bits(371)	9e-43()	Compositional matrix adjust.	69/76(91%)	73/76(96%)	0/76(0%)	+1
Query 301	KDLNITNVVMCAGFADGGKDACQGDSSGGMMLPVKTGEFYLIIGIVSFGKKCALPGFPGVY	360				
Sbjct 1	KDLNITNVVMCAG+ADGGKDACQGDSSGGMMLP K+G FYL+GIVSFGKKCALPGFPGVY KDLNITNVVMCAGYADGGKDACQGDSSGGMMLPKSGNFYLVGIVSFGKKCALPGFPGVY	180				

Query 361 TKVTEFLDWIAEHMV* 376
Sbjct 181 TKVTEFLDWIA +MV* 228

SRX202160
Sequence ID: **SRA:SRR610305.295524.2** Length: 310 Number of Matches: 1
Range 1: 2 to 238

Score	Expect	Method	Identities	Positives	Gaps	Frame
144 bits(364)	3e-42()	Composition-based stats.	67/80(84%)	74/80(92%)	1/80(1%)	-1
Query 181	DVMPADVFSVRLGEHNLYSTDDDSNPIDFAVTSVKHHEHFLATYLNDAIILTLNDTVTF	240				
Sbjct 238	DVLP-DVFSVRLGEHNLYSTNDSSDPIDFAVTSVKHHEHFLATYLNDAIILTLNDTVTF	62				
Query 241	TDRIRPICLPYRKLYDDLA	260				
Sbjct 61	THKIKPICLPYESLRYEDLA	2				

SRX202160
Sequence ID: **SRA:SRR610305.243191.2** Length: 458 Number of Matches: 1
Range 1: 40 to 456

Score	Expect	Method	Identities	Positives	Gaps	Frame
140 bits(354)	6e-40()	Compositional matrix adjust.	68/144(47%)	95/144(65%)	5/144(3%)	+1
Query 216	HHEHFVFLATYLNDAIILTLNDTVTFDRIRPICLPYRKLYDDLAMRPFITGWGTTAFN	275				
Sbjct 40	NHPDFDKVSYNDIALRLAKPVAFEFIQPICLPHPR---HDLRNKIATVTGWGTVSYG	210				
Query 276	GPSAVLREVQLPIWEHEACRQAYEKDLNITNVYMCAGFADGGKDACQDSDGGPMMLPVK	335				
Sbjct 211	GASSNVLREVSIPWNNDECDFTQ--NITKVFLCAGSKNGDKDSCQDSDGGPLMWEAP	384				
Query 336	TGEFYLGIVSFGKKCALPGFPGV	359				
Sbjct 385	NRRWTLVGIVSWGIRCAEPKFPGV	456				

SRX202160
Sequence ID: **SRA:SRR610305.195167.2** Length: 309 Number of Matches: 1
Range 1: 3 to 308

Score	Expect	Method	Identities	Positives	Gaps	Frame
136 bits(343)	4e-39()	Compositional matrix adjust.	78/102(76%)	86/102(84%)	0/102(0%)	+3
Query 47	EGTCKNVLDRCRILLQKNDYNLLKESICGFEGITPKVCCPKSSHVISSTQAppettttterp	106				
Sbjct 3	DGICKDVLNCRDLLQKNDYNLLKESICGFEGITPKVCCPKSIVNPITEAPPKTTTTTERP	182				
Query 107	pKQIPPNLPEVCGIHNTTTTTRIIGGREAPIGAWPMMTAVYIK	148				
Sbjct 183	PIRIPSNLPKQCGNRNITTTTRIIGGQEATPGAWPMAAVYIK	308				

SRX202160
Sequence ID: **SRA:SRR610305.726966.2** Length: 346 Number of Matches: 1
Range 1: 145 to 345

Score	Expect	Method	Identities	Positives	Gaps	Frame
135 bits(340)	2e-38()	Composition-based stats.	60/67(90%)	64/67(95%)	0/67(0%)	-2
Query 310	MCAGFADGGKDACQDSDGGPMMLPVKTGEFYLGIVSFGKKCALPGFPGVYTKVTEFLDW	369				
Sbjct 345	MCAGYADGGKDACQDSDGGPMMLPDKSGNFYLVGIVSFGKKCALPGFPGVYTKVTEFLDW	166				
Query 370	IAEHMV*	376				
	IA +MV*					

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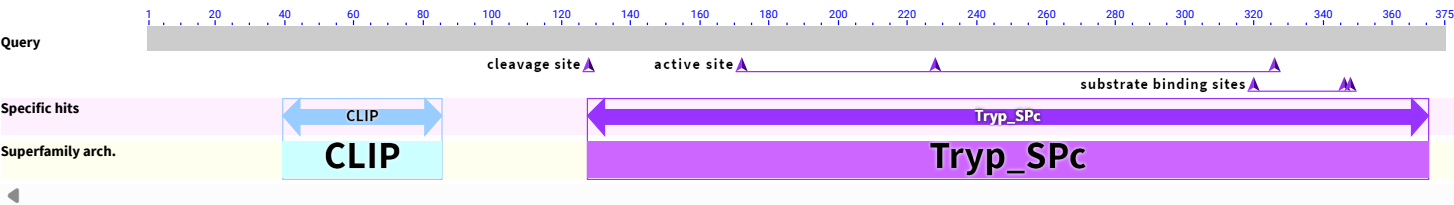
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