



The site is secure.
The [https://](#) ensures that you are connecting to the official website and that any information you provide is encrypted and transmitted securely.
[Access keys](#) [NCBI Homepage](#) [MyNCBI Homepage](#) [Main Content](#) [Main Navigation](#)

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 lc|Query_4248615
Description [unnamed_protein_product...](#)
Molecule type amino acid
Query Length 1020

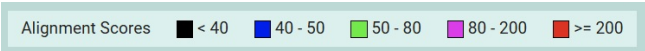
Descriptions

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

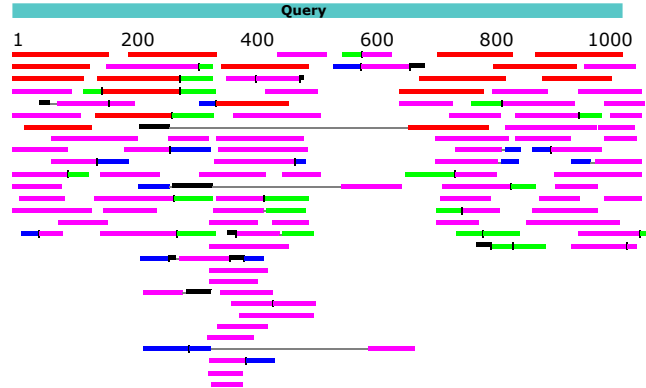
Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
SRX202160	178	233	13%	5e-55	82.18%	415	SRA:SRR610305.152419.2
SRX202160	188	188	14%	1e-54	60.99%	430	SRA:SRR610305.124202.2
SRX202160	186	186	11%	4e-54	70.09%	400	SRA:SRR610305.150040.2
SRX202160	184	240	17%	6e-53	55.41%	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	SFPPKCI	RECAKVS	PEHGKVN	APSGNM	IEGATLRF	SCDSPYYLIGQETLTCQNGQWSG	249	
Sbjct	13	AFHPKCI	RECSMVSS	LEHGKVN	SPSADLIE	GATLRF	SCDSPYYLIGQETLTCQNGQWSG	192	
Query	250	QIPQCK	KLVFCD	LDPVN	HAEHQVK	IGVEQKYG	QFPQGT	EVITYTCSGNYFLMGFNTLKCN	309
Sbjct	193	QIPQCK	KLVFCD	LDPVN	HAEHQVK	IGVEQKYG	QFPQGT	EVITYTCSGNYFLMGFNTLKCN	372
Query	310	PDGSWS	GSPSCVK	VADRE	VDCDSKA			335	
Sbjct	373	PDGSWS	GTPSCVK	VADRE	VNCDSKA			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	LEIHVNP	NYDPGNLNFDIALIQLKTPVTLTRVQICLPDITTREHLKEGT	LAVVTGWG	908	
Sbjct	462	LEIHVNP	NYDPGNLNFDIALIQLKTSVALTTRVQIPCTDITRENLKEGALAVVTGWG	283		
Query	909	LNENNTYSEMIQ	QAVLPVVAASTCEEYKEADLPLVTENMFCAGYKKGRYDACSGD	SGG	968	
Sbjct	282	LNENNTYSEMIQ	QAVLPVVAASTCEEYQDGLPLVTENMFCAGYQGRYDACSGD	SGG	103	
Query	969	PLVFADDSRTERRRWLEGVISWGS	992			
Sbjct	102	PLVFADDSRTRRRWLEGVIS*GT	31			

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	DFLDDVGEPVRIHCPAGCSLTAGTVMGTAIYHELSSVCRAAIHAGKLPNSGGAVHVVNNG				396
Sbjct	1	DFLDDVGEVRIHCPAGCSLTAGVMTAGIYHELSSVCRAAIHAGK+PNSGGAVHVVNNG				180
Query	397	PYSDFLGSDLNGIKSEELKSLARSFRFDYVSSSTAGRSGCPDGWFEVEENCYVVTSKQRA				456
Sbjct	181	PYSDFLSDNGIKSEELKSLARSFRFDYV S + +SGCPDGMFE+HENCYVVTSKQRA				357
Query	457	WERAQGVCTNMAARLAVLDKDLI	479			
Sbjct	358	WERAQGVCTNMAARLAVLDKDI	426			

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 VLASFLVSLVLGL+LAQQM PVQSRGVDLGLCD+TRFECKCGDPGY FNVP KQCTYFYR 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++PQTIDYSCSPGFKLKGVARI+CLPNGQWSSFPKICIR	209			
Query	198	ECAKVSSPEHGKVNAPSGNMIEGATLRFSCDSPYYLIGQETLTCQNGQWSGQIPQCKKL	257			
Sbjct	210	EC+ VSS EHGKVN+PS ++IEGATLRFSCDSPYYLIGQETLTCQNGQWSGQIPQC+KL	389			
Query	258	VFCPDLDPVNHAEH 271				
Sbjct	390	VFCPDLDPV+HAEH 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	VPCD	262		
Sbjct	57	SDPQVQEVKNPPN---DPQTIDYSCSPGFKLKGVARITCLPNGQWSSFPKICIRE--CSM		221		
Query	263	LDPVNHAEHQVKIGVEQKYGFPGTEVYTCSGNYFLMGFNTLKCNPDGWSGSGQSPSCV	+ + H + V +G + ++C Y+L+G TL C +G WSG P C	322		
Sbjct	222	VLSSEHGK-----VNPSADLIEGATLRFSCDSPYYLIGQETLTCQNGQWSGQIPQCQ		383		
Query	323	KVA 325				
Sbjct	384	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+LLEKWI+TAACHVTYSATAEIIDPSQFK YLGKYYRDD				218
Query	837	SrdddyVQVREAEIHHVNPNDPGNLFNFDIALIQLKTPVTLTTRVOPICLPTDITREHL				896
Sbjct	219	S+DDDYVQVREA+EIHHVNPNDPGNLFNFDIALIQLKT V LTTTRVOPICLPTD+TTRE+L				398
Query	897	KEGT LAVVTGWGLNEN 912				
Sbjct	399	KEG LAVVTGWGLNEN 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	SSQPSTVDLASKVKLPEGHYRVGSRAIYTCESRYELLGSGQRRCDNNGNSGRPASCIP		750		
Sbjct	19	S+ PSTVDL+SKVKLPEG YRVGS+AIYTCESRYELLGSGQRRCDNNG NSGRPASCIP		198		
Query	751	VCGRSDSPRSPFIWNGNSTEIGQWPWQAGISRWLADHNMFLLQCGGSLLEKWIITAAHC		810		
Sbjct	199	VCGRSDSPRSPFI NGNSTEIGQWPWQAGISRWLADHNMFLLQCGG+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	LKGCPLLPDSQVQEVNRNPPDNPTIDYSCSPGFKLKGVARISCLPNGQWSSFPPKCIRE		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	LDPVNHAHQVIGVEQKYGFQPGTEVYTCSGNYFLMGFNTLKCNDGSGWSQSPSCV		322		
Sbjct	209	V+ EH +G+ + ++C Y+L+G TL C +G WSG P C		39		
Query	323	KVA 325				
Sbjct	38	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	MVLASFVSLVGLGILAQQMRPVQSRGVDLGLCD+TRFECKGDPGYVFNPMKQCTYFY		60		
		MVLASFVSLVGLG+LAQQM PVQSRGVDLGLCD+TRFECKGDPGYVFNVP KQCTYFY				

Sbjct 381 MVLASFVLVSGLVGLLAQQMHPVQSRGVDLGLCDDTRFECKCGDPGYVFNPAKQCTYFY 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	KVPNSGGAVHVVNNGPYSDFL SDLNGIKS+ELKSLA+SFRFDYVSSSTA	G+SGCPDGM	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	CEILKGCPLLPSDSQVQEVNRNPPDNPQTIDYSCSPGFKLKGVARISCLPNGQWSSFPPKC	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	SDPQVQEVKNPPN---DPQTIDYSCSPGFKLKGMARITCLPNGQWSSFPPKCIR-----E	182				
Query 263	LDPVNHAHQVIGVEQKYGFQPGTEVTYTCSGNYFLMGFNTLKCNDGWSGSPSCV	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	PPSRTNSISRVGSPFLrlprlpllaraakpppkprSSQPSTVDLASKVKLPEGHYRVGS					714
Sbjct 1	PPSRTNSISRVGSPFLRLPLPLARAA PPPKPRS+ PSTVDL+SKVKLPEGHYRVG					180
Query 715	RAIYTCESRYVELLGSQGRCDSDNGNWSGRPASCIPVCGRSDSPRSPFIWNGNSTEIGQW					774
Sbjct 181	+AIYTCESRYVELLGSQGRCDSDNG 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	YDPGNLNFIDIALIQKTPVTLTTRVQPTICLPTDITTREHLKEGTAVVTGWGLNENNTYS					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	WSAPKPRCIKVITCONPPVPSYGSVEIKPPSRTNSISRVGSPFLrlprlpllaraakpp					686
Sbjct 10	WSAPKPRCIKVITCQ PPVPSYGSV+IKPPSRTNSISRVGSPFLRLPLPLARAA PP					189
Query 687	pkprSSQPSTVDLASKVKLPEGHYRVGSRAIYTCESRYVELLGSQGRCDSDNGNWSGRPA					746
Sbjct 190	PKPRS+ PSTVDL+SKVKLPEGHYRVGS+AIYTCESRYVELLGSQGRCDSDNG 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	MVLASFLVSGLVGLLAQQMRPVQSRGVDLGLCD+TRFECKCGDPGYVFNPMKQCTYFY					60
Sbjct 379	MVLASFLVSGLVGL+LAQQM PVQSRGVDLGLCD+TRFECKCGDPGYVFNVP KQCTYF					200
Query 61	RWRPYCKPCDDLEAKDICPKYKRCQECKAGLDSCVTCPNNKYGTWCSGECQCKNGGI					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	EGAHCEILKGCPLLPSDSQVQE		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++PQTIDYSCSPGFKLK+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	IKPPSRNTSISRVGSPFLrlplrlplaraakppkprSSQPSTVDLASKVKLPEGHYRV		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	MPKQCTYFYRWRPYCKPCDDLEAKDICPKY	81			
Sbjct 127	PVQSRGVD+GLCD+TRFECKCGDPGYVFNVP+KQCTYFYRWRPYCKPCD	LEAKD+CPKY				
Query 82	KRCQECKAGLDSCVTCPPNKGWTCGECQCKNGGICDQRTGACTCRD	129				
Sbjct 307	KRCQEC+AGLDSCV CPPN+YGTWCSGECQCKNG + GACTCRD	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	MPKQCTYFY	60			
Sbjct 66	MVL SFLVLSGLVLG+LAQQMRPVQSRGVD+GLCD+TRFECK G	DPGYVFNVP+KQCTYFY				
Query 61	RWRPYCKPCDDLEAKDICPKYKRCQECKAGLDSCVTCPPNKGWTCGEC	110				
Sbjct 246	RWRPYCKPCD LEAKD+CPKYKRCQEC+AGLDSCV CPPN+YGTWCSGEC	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	MWFLQCGGSLNNEKWIITAHCVTYSATAEIIDPSQFKIYLGKyynddsrdddyVQVREA	848				
Sbjct 357	+WF+ CGGSLNNEK++TAHCVTYS+TA +I+PSQFKIYLGKYR+D +DD+YVQ++E	178				
Query 849	LEIHVNPYDPGNLNFIDIALIQLKTPVLTITRVQPICLPTDITTREHLKEGTLAVVTGW	907				
Sbjct 177	ETHVNP YDP N DIALI+LK PV LTTRV+P+CLPTD+TTRE+LKEGT AVVTGW	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 +	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+	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	QQAVLPVVAASTCEEYKEADLPLTVTENMFCAGYKGRYDACSGDSGGPLVFADDSRTE					979
Sbjct 3	QQAVLPVVAASTCE+GY+++ PLTVTENMFCAGYK+GRYDACSGDSGGPLVFADDSRT+ QQAVLPVVAASTCEQGYQDSGSLTVTENMFCAGYKGRYDACSGDSGGPLVFADDSRTD					182
Query 980	RRWVLEGIVSWGSPSGCGKANQYGGFTKVNVLFSWIRQFI*			1020		
Sbjct 183	RRWVLEGIVSWGSPSGCGK NQYGGFTKVNVLFSWIRQFI* RRWVLEGIVSWGSPSGCGKPNQYGGFTKVNVLFSWIRQFI*			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	KAVDFLDDVGEPVRIHCPAGCSLTAGTVWGTAIYHELSSVCRAAIHAGKLPNSGGAVHVV					393
Sbjct 22	KA++ LDDVGEP+RIHCPAGCSLT G+VWGT IY ELSSVCRAAIH+G + NSGG+V V+ KAIELDDVGEPIRIHCPAGCSLTLSGVWGTVIYRELSSVCRAAIHSGIISNSGGSVQVI					201
Query 394	NNGPYSDfLGSDLNGIKSEELKSLARSFRFDYVSSSTAGR-SGCPDGFVEVEENCVVTS					452
Sbjct 202	NNGPYSDf+ S+ GI S+ L+S A SFR + G+ CP GW+++E C Y+TS NNGPYSDfVASNAYGISSKVLRSQAVSfRLVSTETQHNGKPKCEPPGWYQIENKCFYITS					381
Query 453	KQRAWERAQGVCTNMAARLAVLDKDL 478 K R+W R QGVC+NMA+ LAVLD +					
Sbjct 382	KXR5WNRVQGVCNMASSLAVLDSAV 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	PSQFKIYLGKyyrddsrdddyVQVREALEIHVNPNDPGLNFDIALIQLKTPVTLTTRV					881
Sbjct 3	PSQFK YLGKYYRDDS+DDDYVQVREALEIHVNPNDPGLNFDIALIQLKT + LTTRV PSQFKFYLKGYYRDDSKDDDYVQVREALEIHVNPNDPGLNFDIALIQLKTSIALTTRV					182
Query 882	QPICLPTDITTREHLKEGT LAVVTGWGLNENNTYSEMIQQA 922 QPICLPTD+TTRE+LKEGT LAVVTGWGLNENNTYSEMIQQ+					
Sbjct 183	QPICLPTDLTTRENKEGTLAVVTGWGLNENNTYSEMIQQS 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	QAVLPVVAASTCEEYKEADLPLTVTE-NMFCAGYKKG 957 +AVLPVVAASTCE+GY+++ PLTVTE N +CAGY +G					
Sbjct 301	KAVLPVVAASTCEQGYQDSGSLTVTENNSYCAGYNQG 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	CKPCDDLEAKDICPKYKRCQCECKAGLDSCVTCPPNKYGTWCSGECQCKNGGICDQRTGAC					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	VDLASKVKLPPEGHYRVGSRAITYTCESRYELLGSGRRCDSENGWNGRASCIPVCGRSD					756
Sbjct 394	V+ ++ LP+GHY VG++A YTCES+YY+LLGS+GRRCS+G W GRPASCIPVCGRSD					215
Query 757	SPRSPFIWNGNSTEIGQWPWQAGISRWLADHNMFQCGGSLLEKWIWTAACHVTY					813
Sbjct 214	SPRSPFI NG T+IGQWPW AGI+RW + +WF+ CGGSLLEKWIWTAACHVTY					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	IGVEQKYGQFPQGTETVYTCSGNYFLMG 302					
Sbjct 363	+ EQ+YGO+POG+ 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	GQFPQGTETVYTCSGNYFLMGFNTLKCNPDGWSGSPSCVKV 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	KTPVTLTTRVQPICLPTDITTREHLKE-----GTLAVVTGWGLNENNTYSEMIQOAV					923
Sbjct 182	KT V LTTTRVQPICLPTD+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 RAIYTCESRYVELLGSQGRRCDSNGNWSGRPASCIPVCGRSDSPRSPFIWNGNSTEIGQW 774
+AIYTCESRYVELLGSQGRRC+SNG WSGRPASCIPVCGRSDSPRSPFI NGNSTEIGQW
Sbjct 1 QAIYTCESRYVELLGSQGRRCNSNGKWSGRPASCIPVCGRSDSPRSPFIWNGNSTEIGQW 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	MVLASFLVSLVGLGILAQQMRPVQSRGVDLGLCDETRFECKCGDPGYVFNVP	60				
Sbjct 82	MVLASFLVSLVGLG+LAQQM PVQSRGVDLGLCD+TRFECKCGDPGYVFNVP 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+C+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 QPSCVKVA++ ++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	KLVFCDLDPVNHAHQVIGVEQKYGFQPGTEVITYTCSGN 297					
	+LVFCDLDPV+HAEHQVIG+EQKYGQ POGTEVITYC+GN					
Sbjct 220	ELVFCDLDPVSHAEHQVIGLEQKYGQSPQTEVITYTCTGN 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	NGQWSGQIPQCKKLVFCDLDPVNHAHQVIGVEQKYGFQPGTEVITYTCSGNYFLMGF 303					
	NGQWS Q V C + + H + V +G + ++C Y+L+G					
Sbjct 5	NGQWSFSTQ-MLFVECSMVSSLEHGK-----VNSPSADLIEGATLRFSCDSPYYLIGQ 163					
Query 304	NTLKCNPDGSGWSGQSPSC 321					
	TL C +G WSG P C					
Sbjct 164	ETLTQGNQWSGQIPQC 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	WIGLHRLDADNHFIIWELMDR 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	VYIWSKIQLQPWVKTKSCFQPSFVCMMDLSKKNKAKCNDPGPLENGHAKLHGQSIDGF 188					
Query 598	YAGSSIRYSCEVLHYLSGtetvtcttngtWSAPKPRCIK 636					
	YAGSS+RYSCEVLHYLSGTETV+CT+NGTWSAPKPRCIK					
Sbjct 189	YAGSSVRYSCVLHYLSGTETVSCTSNGTWSAPKPRCIK 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	CPDLDPVNHAHQVIGVEQKYGFQPGTEVTYTCSGNYFLMGFNTLKCNDPGSGWSGSP				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-RSGCPDGFVEEENCVVYTSKORAW				458	
	DF+ S+ GI S+ L+S A SFR + G + CP GW+++E C Y+TSK R+W					
Sbjct 220	DFVASNAYGISKVLRSQAVSFRLVSTETQHNGNQKECPPGWYQIENKCFYITSKHSWN				399	
Query 459	RAQGVCTNMAARLAVLD 475					
	RA GVC+N A+ LAVLD					
Sbjct 400	RALGVCNXASSLAVLD 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+DVGE+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	RAQGVCTNMA+ LA				
Sbjct 262	LRSQAVSFRFLVSTETQHNGNQKECP	PGWYQIENKCFYITSKHSWNRAQGVCSNMASSLA	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	464			
	LNGIKS+ELKSLA+SFRFDYVSSSTAGR SGCPD	GWFE+EENCVVYT+KQRAWERAQGVCTNMAARLA				
Sbjct 3	LNGIKSDELKSLAQSFYVSSSTAGRSGCPD	GWFEIEENCVVYTKQRAWERAQGVCTNMAARLA	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				
	+TAAHCVTYSATAEIIDPSQFK					
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	MVLASFLVSGVLGILAQOMRPVQSRGVDLGLCDETRFECKCGDPGYVFNVP	MPKQCTYFY	60			
	MVLASFLVSGVLG+LAQOM PVQSRGVDLGLCD+TRFECKCGDPGYVFNVP	KQCTYFY				
Sbjct 144	MVLASFLVSGVLGLLAQOMHPVQSRGVDLGLCDDTRFECKCGDPGYVFNVP	AKQCTYFY	323			
Query 61	RWRPYCKPCDDLEAKDICPKYKRCQCEKAG	90				
	RWRPYCKPCD LEAKD+CPKYKRCQEC+AG					
Sbjct 324	RWRPYCKPCDKLEAKDVC PKYKRCQECRAG	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	EILKGCPLLPDSQVQEVARNPPDNPTIDYSCSPGFK - 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	VCGRSDSPRSPFIWNGNSTEIGQWPWQAGISRWLADHNWML 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	KGCPLLPDSQVQEVNPPDNPTIDYSCSPGFKLKGVARISCLPNGQWSSFPKCIREC	199				
	KGC L S+ V E R P NPOTI YSC PGFKL+G +RI CLP+GOW++ PP CI+C					
Sbjct 367	KGCLLPQSNPGVIEERKPKVNPQTISYSCLPGFKLQGPSRIICLPSCGQWTLNPPSCIQQC	188				
Query 200	AKVSSPEHGKVNAPSGNMIEGATLRFSCDSPYYLIGQETLTCQNGQWSGQIPQCKKLVF	259				
	A++S+PEHG+V +++EGAT FSCD YYLIG+ETL+C GOW G IP C+KL+F					
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	IEGATLRFSCDSPYYLIGQETLTCQNGQWSGQIPQCKKLVFCDLPVNHAEHQVKIGV	277				
	+ T+ +SC + L G + C +GOW+ P C + C L H E V					
Sbjct 310	VNPQTISYSCLPGFKLQGPSRIICLPSCGQWTLNPPSC--IQQCARLSAPEHGE-----V	155				
Query 278	EQKYGFPGQTEVTYTCSGNYFLMGFNTLKCNPDGWSGSGQPSCKVK	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	TAGTVWGTATYHELSSVCRAAIHAGKLPNSGGAVHVVNNGPYSDFLGSDLNIGKSEELKS	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	QAVSFRVLSTETQHNGNQKECPGWYQIENKCFYITSKHSRWNRAQGVCSNMASLAVLD	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 KFYLGKYYRDSKDDYVQVREAIEIHVNPYDPGNLNFIDIALIQLKTSVALTTTRVQPIC 181
Query 886 LPTDITTREHLKEGT LAVVTGWGLNENNT 914
LPTD+TTRE+LKEG LAVVTGWGLNENNT
Sbjct 182 LPTDLTTRENLEKALAVVTGWGLNENNT 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	MVLASFLVSGLVGLLAQOMRPVQSRGVDLGLCDETRFECKCGDPGYVFNVP	60				
	MVLASFLVSGLVGL+LAQOM PVQSRGVD GLCD+TRFECKCGDPGYVFNVP KQCTYFY					
Sbjct 366	MVLASFLVSGLVGLLAQOMHPVQSRGVDPLCDDTRFECKCGDPGYVFNVP	187				
	MVLASFLVSGLVGLLAQOMHPVQSRGVDPLCDDTRFECKCGDPGYVFNVP					
Query 61	RWRPYCKPCDDLEAKDICPKYKRCQECK 88					
	RWRPYCKPCD LEAKD+CPKYKRCQEC+					
Sbjct 186	RWRPYCKPCDKLEAKDVCPKYKRCQECR 103					
	RWRPYCKPCDKLEAKDVCPKYKRCQECR					

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	PSTNDVKSAGLDSCVSCPPNKYGTWCSGECQCKNGGICDQR 3					
	PSTNDVKSAGLDSCVSCPPNKYGTWCSGECQCKNGGICDQR					

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	VGSRAIYTCESRYELLGSGRRCDNSGNWSGRPASCIPVCGRSDSPRSPFIWNGNSTEI 771					
	VGS+AIYTCESRYELLGSGRRCDNSG WSGRPASCIPVCGRSDSPRSPFI NGNSTEI					
Sbjct 210	VGSQAIYTCESRYELLGSGRRCDNSGNWSGRPASCIPVCGRSDSPRSPFIWNGNSTEI 31					
	VGSQAIYTCESRYELLGSGRRCDNSGNWSGRPASCIPVCGRSDSPRSPFIWNGNSTEI					
Query 772	GQNPWQAGIS 781					
	GQNPWQAGIS					
Sbjct 30	GQNPWQAGIS 1					
	GQNPWQAGIS					

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	VITCQNPVPVPSYGSVEIKPP-SRTNSISRVGSPFlr1pr1plplaraakpppkprSSQPS 695					
	VITCQ PPVPSYGSV+ P + N V L + + LPLARAA PPPKPRS+ PS					
Sbjct 431	VITCQTPPVPSYGSVDXNPQVDKLNQSCWVA--ILEVATVTLPLARAAGPPPKPRSAPPS 258					
	VITCQTPPVPSYGSVDXNPQVDKLNQSCWVA--ILEVATVTLPLARAAGPPPKPRSAPPS					
Query 696	TVDLASKVKLPEGHYRVGSR 715					
	T+DL+SKVKLPEGHYR G +					
Sbjct 257	TMDLSSKVKLPEGHYRWGLK 198					
	TMDLSSKVKLPEGHYRWGLK					

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 VKLPEGHYRVGSRAIYTCESRYVELLGSQGRCDNNGWNGRGPASCIPVCGRSDSPRSPF 762
+ LP+GHY VG++A YTCES+YY+LLGS+GRRCS+G W GRPASCIPVCGRSDSPRSPF
Sbjct 445 IVLKPGHYHVGTAQSYTCESQYKLLGSKGRRCESSGTWGRGPASCIPVCGRSDSPRSPF 266

Query 763 IWNNGNSTEIGQWPWQAGISRWLADHNMWFLQCGGSLLENEKWIVTAAHCVT 812
I NG T+IGQWPW AGI+RW + +WF+ CGGS K HC T
Sbjct 265 IINGVVTDIGQWPWHAGIARWYPEQEVNFIICGGSFTE*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	LLNEKWIVTAAHCVTYSATAEIIDPSOFKTYLGKyynddsrdddyVOVREALE				850	
Sbjct 159	LLNEKW++TAAHCVTVS+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	DCDSKAVDFLDDVGEPVRIHCPAGCSLTAGTVMGTAIYHELSSVCRAAIHAGKLPNSGGA				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	KCIRECAKVSSPEHGKVNAPSGNMIEGATLRFSCDSPYYLIGQETLTCQNGQWSGQIPQ				253	
Sbjct 183	CI++CA++S+PEHG+V +++EGAT FSCD YYLIG+ETL+C GQW G IP				362	
Query 254	CKKLVFCP 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	TLRFSCDSPYYLIGQETLTCQNGQWSGQIPQCKKLVFCPDLPVNHAEHQVIGVEQKY				281	
Sbjct 90	T+ +SC + L G + C +GQW+ P C + C L H E V +				245	
Query 282	GQFPQGETVYTCSGNYFLMGFNTLKNPDGWSGSGQSPCVK 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	QVKIGVEQKYGFPGTEVTY	292				
	++ + EQ+YGQ+PG+ 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	PQCKKLVFCPDLDPVNHAHQVK	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	QVKIGVEQKYGFPGTEVTYTCSGNYFLMGFNTLKCNPDGSHSGSQPSCVKVADREVDC	331				
	+V + EQ+YGQ+PG+ VT+ CS N++L+G +++ C PDGSHSG QPSCVKVA+ ++C					
Sbjct 55	KVDVSFEQQYGYPPQGSNVTFKCSLNHYLIGKSSITCKPDGSHSGRQPSCVKVAENVINC	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					
Sbjct 65	C++GYK A LPLVTENM CA 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	REALETHVNPYDPGNLNFDIQLK 872					
Sbjct 322	+E EIHVP YDP N DI LIQLK KEVREIHVNPFYDPATFNSDITLIQLK 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	PVVAASTCEEYKADLPLVTENMFCAGYKKGRYDACSGGGLVFADDSRTERRWVL	984	PVV+ASTC++GYK A LPLVTENM CAGYK+G+ DAC GDSGGPLVFAD S+ ER WVL			
Sbjct 247	PVVSASTCQQGYKNASLPLVTENMICAGYKEGKTACGGDSGGPLVFADYSQREVRWVL	68				
Query 985	EGIVSWGSPSGCGKANQYGGFT 1006					
Sbjct 67	EGIVSWGSPSGCG NQYGGFT 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					
Sbjct 183	+V V+NNGPYSD+ S+ GI S+ K + FR 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	NTNGNQKECPPGWYQIENKCFYITSKHRSWNRALGVCNMASSLAVLD	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	KNMICAGYKEGKTACGGDSGGPLVFADYSQRRVWVLEGIVSWGSPSGCGHPNQYGGFT	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	TRFECKCGDPGYVFNVP	MPKQCTYFYRWRPYCKPCDDLE	73		
Sbjct 111	I + PVQSRGVDLGLCD+TRFECKCGDPGYVFNVP	KQCTYFYRWRPYCKPCD LE	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	GRYDACSGDSGGPLVFADDSRTERRWLEGIV	SWGSPSGCGKANQYGGFTKVN	VFLSWIR	1016		
Sbjct 1	GRYDACSGDSGGPLVFADDSRT+RRWLEGIVSWGSP+GCGK+NQYGGFTKVN	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
-------	--------	--------	------------	-----------	------	-------

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+VMGT IY ELSSVCRAAIH+G + NSGG INCDTKAIELLDDVGEPRIHCPAGCSLTGSGVMGTVIYRELSSVCRAAIHSGIISNSGG	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+VMGT IY ELSSVCRAAIH+G + NSGG+V V+NNGPY LDDVGEPRIHCPAGRSLTLGSGVMGTVIYRELSSVCRAAIHSGIISNSGGSVQVINNGPY				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	GTEVITYTCSGNYFLMGFNTLKCNPDGWSGSPSCVKVA 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	YVSSSTAGRSGCPDGWFEVEENCVVYTSKORAWERAQGVCTNMAARLAVLDKDLIPSSLT				484
Sbjct	228	Y +S+ + CP G +++E C Y+TSK R+W RAQGV+C+NMA+ LAVLD + SL+ Y*NSTQWNQKECPGXQYQIENKCFYITSKHSWNRAQGVCSNMASSLAVLDGAVAQQSL5				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	WYQIENKCFYITSKHRSWNRALGVCSNMASSLAVLDSAVAQQLSDILNKKGLVKIWIIGL					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	VNPVDQIILPKGHYHVGTSQSYTCESQYKLLGSKGRRCESSGTWGRPPASCIPVCGRSD					222
Query 757	SPRSPFIWNGNSTEIGQWPP 776					
	SPRSPFI NG T IGQWPP					
Sbjct 223	SPRSPFIINGVVTGIGQWPP 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	MVLASFLVSGVLVLGILAQMRPVQSR-----GVDLGLCDETRFECKGDPGVVFN					50
	++L+S + + I P+S GVD LCD+ F C CG PGY F+					
Sbjct 425	IMLSSLFIIWFISIAG*SGMPRRSTSGFGKLLGNIGVD-KLCDKIFICACGKPGVTFH					249
Query 51	VPMKQCT---YFYRWRYCKPCDDLEAKDICPKYKRCQECKAGLDSCVTCPPNKGWTC					107
	+P+KQC F W C+PC+D+ +D+CPKYK+C ECK LD CV+CPPN+YG WC+					
Sbjct 248	IPIKQCISIDKFKFWETSCEPCNDISPEDVCPKYKQCLECKHNLDRCVSCPPNRYGDWCN					69
Query 108	GEQCKNGGICDQRTGACTCRD 129					
	G C CKNGG C+Q TG C CR+					
Sbjct 68	GVCDCKNGGTCNQETGECFCRE 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	DPGNLNFIDIALIQLKTPVTLTTRVQPICLPTDITTREHLKEGT LAVVTGWLNNNTYSE					917
Sbjct 68	DPGNLNFIDIALIQLKT V LTTRVQPICLPTD 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	+GRRRC+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+RYSCEVLHYLSG	TETV+CT+NGTWSAPKPRCIKVITCQ PPVPSY					
Sbjct 439	LHGQSIDGFYAGSSVRYSC	EVLYLSG	TETVSC	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	EVLYLSG	TETVSC	TNGTWSAPKPRCIKVITCQTPPVPSYGSVDIKPPSRT	227	
Query 280	KYGQFP--QGTEV	290				
K+ P G EV						
Sbjct 226	KFSAVPVKSGDEV	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	QKYGQFPQGTETVYTC	SGNYFLMGFNTLKCNPDGSHWSGSQPSCVKV	324			
Q F G+ V Y+C ++L G T+ C +G+WS +P C+KV						
Sbjct 430	QSIDGFYAGSSVRYSC	EVLYLSG	TETVSC	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	SDSQVQEV	RNPDPN	QTDYSC	PGFKLKG	VARISCL
Sbjct 33	LKGC L	S+ V E R P	NPOTI YSC	PGF+L+G	+RI CLP+G	OW++ PP CI++
Query 199	CAKVSSPE	HGKVNAP	SGNMIE	GATLRF	SCDSPY	YLIG 235
Sbjct 213	CA++S+P	EHG+V	+++EGAT	FSCD	YYLIG	
	CARLSA	PEHGEV	TRFGKDL	LEGATAT	FSCDRTY	YLIG 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	RDQLQPV	WKTKSCF	QPSFAC	MMDLS	DRNKA	KCDPGL
Sbjct 74	KNQFEPV	WRTSSCS	QPAAFM	CMIGF	SNRNEA	RCEDTG
Query 604	RYSCEVL	HYLSG	tetvtct	tngtWS	APKPRC	IKVIT 639
Sbjct 254	YSCKEL	HYPSG	SSVQTCT	TNGTW	STIKPR	CIKIT 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	KVITCON	PPVPSY	SGSVEI	KPPSR	TNS 661	
Sbjct 351	KLLPSES	PPVPAY	GLVEIK	TPERIS	S 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	NDNLTF	WASGEP	GNETNC	VYLDI	RDLQ	LPVWKTK
Sbjct 4	NDNLTF	WATEEP	NMENVC	VYLD	AKSV*AS	MEDIILF

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	WSAPKPR	CIKVITC	QNPVPS	YSGSVE	IKPPSR	TNSISR
Sbjct 255	WSAPKPR	CIKVITC	QNPVPS	YSGSVE	IKPPSR	TNSISR
Query 687	pkprSSQ	PSTVDL	ASKVKL	PEGHYR	711	
Sbjct 75	PKRSS	PSTVDL	ASKVKL	PEGHYR	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	FQPSSFACMMDLSDRNKAKCDDPGPLENGHATLHGQSIDGFYAGSSIRYSCEVLHYLSG					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	YLDIRDQLQPWVWTKSCFQPSFACMMD		567			
	YLDI+DQLQPWVWTKSCFQPSF C+ D					
Sbjct 3	YLDIQDQLQPWVWTKSCFQPSF-CLYD		83			

Follow NCBI

Please use the feedback button near the bottom-right of your screen to let us know about your experience with CD-Search. You may need to do a hard refresh to replace outdated cached data and ensure proper function of this new user interface in your browser; the previous user interface will be available [here](#) for a short period of time.

CD-Search > Navigate results

Conserved domains on [1cl|SEQMD5]

d2a8521273f934deafb44229a8e21a87

[Find similar domain architectures](#)

Live BLAST, RID = J4RWUS8T016

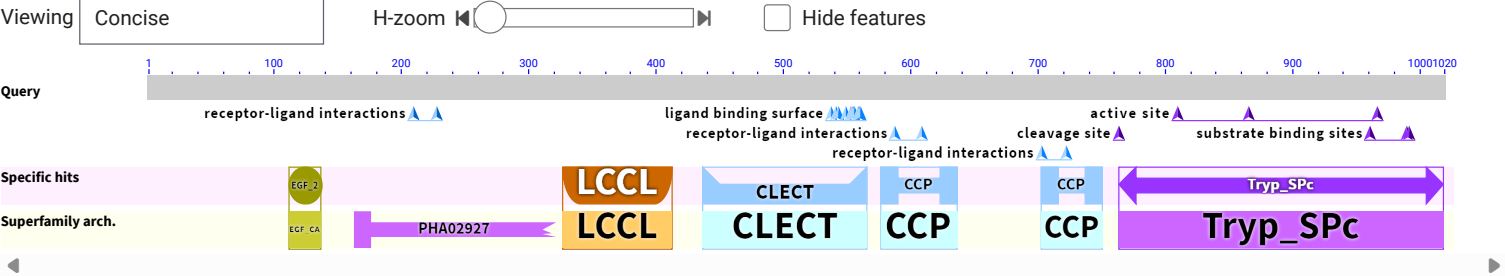
Database: CDSEARCH/cdd

E-value cut off: 0.01

Composition-based adjustment: yes

Low-complexity filter: no

[Refine parameters and search again](#)



 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}

FOLLOW NCBI



Connect with NLM

National Library of
Medicine
8600 Rockville Pike
Bethesda, MD 20894

Web Policies
FOIA
HHS Vulnerability
Disclosure

Help
Accessibility
Careers

NLM NIH HHS USA.gov

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

The site is secure.
The https:// ensures that you are connecting to the official website and that any information you provide is encrypted and transmitted securely.
[Access keys](#) [NCBI Homepage](#) [MyNCBI Homepage](#) [Main Content](#) [Main Navigation](#)

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	Id 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	KRTKI	PRLHIPGCGKRKVNVDITTVGRSGSPILPPISTQDLKGGRIIAGGV	EAKIGAW	281		
Query 160	PWMAAV	FVKNF	GIGRFHCAGSIISNKYILSAAHAF	LIGGRKLTPTRLAVRVGGHYIKRGQ	219	
Sbjct 282	PWMAAV	FVKNF	GIGRFHCAGSIIS+KYILSAAHAF	IGGRKLTPTRLAVRVGGHY+K GQ	461	
Query 220	EYPVKD	VIIHPHYVEK	235			
Sbjct 462	EYHVEX	VIIHPDYVER	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+V	VLAT	272
Query 60	LKDSFPVVC	SWNGRFQPIVCCP	Daippvttt	avtviSTKEPKL	PRLHISGCGK	RVKI 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+V	VLAT	249
Query 60	LKDSFPVVC	SWNGRFQPIVCCP	Daippvttt	avtviSTKEPKL	PRLHISGCGK	RVKI 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+V	VLAT	245
Query 60	LKDSFPVVC	SWNGRFQPIVCCP	Daippvttt	avtviSTKEPKL	PRLHISGCGK	RVKI 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	CCPDAiappv	ttt	avtviSTKEPKL	PRLHISGCGK	RVKI 129
Sbjct 499	WNGRFQPIV	CCPDA AP TT V TKE K+PRLHI	G KRVK +DITT+GRSGS			323
Query 130	PILPPISTP	ONSTGGRGIIAGG	VEAKIGAWPMAAV	VKNFVIGIRFHC	AGSIISKYI	LS 189
Sbjct 322	PILPPIST	QDLKGGRGIIAGG	VEAKIGAWPMAAV	VKNFVIGIRFHC	AGSIISKYI	FS 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	ILSAAHAFLIGGRKLTPTRLAVRVGGHYIKRGQEYPVKDVIIHPHYVEKE	236				
Sbjct 150	FLSAAHAFLIGGRKLTPTRLAVRVGGHY+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	NFGIGRFHCAGSIISNKYILSAAHAFLIGGRK	200				
Sbjct 98	NFGIGRFHCAGSII +KYILSAAHAFLIGGRK	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	IAIIELKEELNFTDLVNPITCLDPETVTDPLKDRIVTAAGWGLDFSGPRSQVLREVSTP	300				
Sbjct 1	IAII LKEELNFTDLV PTCLDPDE TD LK R VT AGWGLDF+GPRSQ P	180				
Query 301	VVPVDKCDQAYEKLNTPSLKNGITNNFLCAGLEEGGKDACQGDSSGGLMLVNNTRWIVVG	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-ECTARGGLKGSCSLIDCPVLAT	59				
Sbjct 333	M WICVITLFFALAS+TL NKVSRVG++FPKT+NDN +CTA+GGLKGSCSL DCP+VLAT	154				
Query 60	LKDSFPVVCSSWNGRFQPIVCCPDaiappvtttaviSTKEPKLPRLHISG	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 FALVSSTLSNKVSRVGI	IIFPKTQNDNKQCTAKGGLKG	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	ICVITCLLTSSSTLSNKVSRVGI	IIFPKTQNDNKQCTAKGGLKG	SCKSLTDCPAVLATLKD	146		
Query 63	SFPVVC	SWNGRFQPIVCCPDaiappvttttavtvi	STKEPKLRLHISG 111			
	SFPVVC	SWNGRFQPIVCCPD A P VTTT T++ TKE K+PRLHI G				
Sbjct 145	SFPVVC	SWNGRFQPIVCCPD-AAAPSVTTTIVPTKETKIPRLHIPG	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	VTDPLKDRIVTAAGWGLD	FSGPRSQVLREVSI	PVVPVVKCDQAYEKL	NTPSLKNGITNN 326		
	V K R VT GWGD F G +S+VL++	VSIPVV C+++Y K+ GIT				
Sbjct 371	VQQDFKGREVTVTGWGDT	FFGGAKSKVLQQVSI	PVVSNAKCNKSYSK	VALSKYPQGITRG 192		
Query 327	FLCAGLEEGGKDACQGD	SGGPLMLVNNTRWIV	GVVSFGHKCAEEGYP	GVYSRVASYLDW 386		
	+CAGL EGGKDACQGD	SGGPL+L + RW +VG+VSFG CAE GYPGVY+RV+ Y+ W				
Sbjct 191	QICAGLSEGGKDACQGD	SGGPLVLEESGRWTL	VGIVSFLNCAEPGYP	GVYTRVSHYIRW 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	FLCAGLEEGGKDACQGD	SGGPLMLVNNTRWIV	GVVSFGHKCAEEGYP	GVYSRVASYLDW 386		
	F+CAGLEEGGKDACQGD	SGGPLMLVNN+ WIV GVVSFGHKCAEEG+PGVY+RV SYL+W				
Sbjct 300	FICAGLEEGGKDACQGD	SGGPLMLVNNSSWIV	GVVSFGHKCAEEGYP	GVYTRVVSYLEW 121		
Query 387	IAKVTNSLDHAVTN*	401				
	IAKVTNSLD AVTN*					
Sbjct 120	IAKVTNSLDQAVTN*	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	LKDRIVTAAGWGLD	FSGPRSQVLREVSI	PVVPVVKCDQAYEKL	NTPSLKNGITNNFLCA 330		
	LK R VT AGWGLDF+GPR	SQVLREVSI	PVVP+ C++AY+KLNT +LKNGIT +			

Sbjct 467 LKGRRTVAGWGLDFAGPRSQLREVSIIPVPIGDCNKAYQKLTALKNGITKSLFVL 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	RVGVLPFKTRNDN-ECTARGGLKG	SCSKSLIDCP	SVLAT	59
Sbjct 70	MWICVITL	FALAS+TL NKVSR	VG++FPKT+NDN +CTA+GGLKG	SCSKSL DCP+VLAT		249
Query 60	LKDSFPV	CSWNGRFQ		76		
Sbjct 250	LKDSFPV	CSWNGRFQ		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	RVGVLPFKTRNDN-ECTARGGLKG	SCSKSLIDCP	SVLATLKDSFPV	67
Sbjct 303	V FALASSTL	SNKVS	RVGIIFPKTQNDNKQCTAKGGLKG	SCSKSLTDCP	AVLATLKDSFPV	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 I HP + +	YNDIA++ L + + F++ + PICLP P L+++I T GWG +				204
Query 286	FSGPRSQVL	REVSIIPVVPDKDQAYEKLNTPSLKNGITNNFLCAGLEEGKDACQGD				345
Sbjct 205	+ G S VLREVS	IP+ D+CD+ + + IT FLCAG + G KD+CQGD				360
Query 346	GPLML-VN	NRWIVGVVSFGHKCAEEGYPGV		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	RVGVLPFKTRNDN-ECTARGGLKG	SCSKSLIDCP	SVLATLKDSFPV	70
Sbjct 161	LAS+TL NKVSR	VG++FPKT+NDN +CTA+GGLKG	SCSKSL DCP+VLATLKDSFPV			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	appvvttt	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	EVIPV	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	EVIPV	VDKCDQ	AYEKLNT	PSLKN	GITNNFLCAGLE
Sbjct 2	+S+VL++	VSIPV C+++Y	K+ GIT +CAGL	EGGKDACQGD	SGGPLM	349
Query 350	LVNNT	RWIVGV	SFGHKCA	EEGYP	GVYSRV	ASYLWDIAKVTN
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	EVIPV	304
Query 305	DKCQAYE	KLNTPSL	KNGITNNFLCAGLE	EGGKDACQGD	SGGPLM	-VNNT
Sbjct 293	EECNNT	FVQT-----	TTNVFLCAGSKNGDK	SCQGD	SGGPLMWEAP	NNRNTLVGIVS

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				
Sbjct 255	V+DVIIPH YVE+ENYNDIAII LKEELNFTDLV VTD LK R VT AGWG	76				
Query 283	DLD FSGPRSQVLREVSI PVVPDKC	307				
Sbjct 75	DLD F+GPRSQVLREVSI PVVP+ C	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				
Sbjct 420	WM + +NFG+ RF C G++IS++Y++SAAH F + ++P+ RVGGH +K G	244				
Query 220	EYPVKDVIIPHYPHYVEKENYNDIAIIELKEELNFTDLVNPICLPDPETVTDPLKDRIVTAA	279				
Sbjct 243	Y V+DVI+H HY +NY+DIA+++K E+ D V P+CLP P V K R VT	64				
Query 280	GWGDLDF-SGPRSQVLREVSI	299				
Sbjct 63	GWGD F + +VL++VSI	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				
Sbjct 502	L + + + V PIC+P+ + L ++ V GWG + + VLRE+ +PVV +	323				
Query 306	KCDQAYEKLNTPS LKNGITNNFLCAGLEEGGKDACQGD SGGPLMLVNNT--RWI VVGVS	363				
Sbjct 322	C++Y+ ++ L GIT++ +CAG +EGG+D+C+GDSGGPLM + T R +VGVS	143				
Query 364	FGHKCAEEGYPGVYSRVASYLDWIAKVT	391				
Sbjct 142	FG CA +PGVYR++SY +W KVT	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-ECTARGGLKGCKSLIDCP SVLATLKDSFPVVC SWNGRFQPIVCCPD	82				
Sbjct 264	+G++FPKT+NDN +CTA+GGLKGCKSL DCP+VLATLKDSFPVVC SWNGRFQPIVCCPD	85				

Query 83 aiapppvttttavtviSTKEPKLRLHISG 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	FQPIVCCPDaiapppvttttavtviSTKEPKLRLHISG 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
-------	--------	--------	------------	-----------	------	-------

118 bits(296)		2e-31()		Compositional matrix adjust		54/120(45%)		77/120(64%)		1/120(0%)		-2	
Query	168	KNFGIG-RFHCAGSIISNKYILSAAHAFBIGGRKLTPTRLAVRVGGHYIKRGQEYPVKDV										226	
		+NFG+ RF C G++IS++Y++SAAH F + ++P+ RVGGH +K G Y V+DV											
Sbjct	410	QNFGLSERFLCGGALISSRYVISAAHCFKTSNKPISPSVYTRFVGGHTLKDGTNYDVEDV										231	
Query	227	IIHPHYVEKENYNDIAIIELKEELNFTDLVNPICLPDPETVTDPLKDRIVTAAGWGDLDF										286	
		I+H Y +NY+DIA+++K E+ D V P+CLP P V K R VT GWGD F											
Sbjct	230	IVHERYQPSQNYHDI AVLKVKGEVRLNDKVKPVCLPKPSFVGQDFKGREVTVTWGDTFF										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	KDACQGDSSGGLMLVNNTRWIVVGVVSGHKKAEEGYPGVYSRVASYLDWIAKVTNSLDH				396
Sbjct	363	+DACQGDSSGGLMLVNN+ IV GVVSGHKKAEEG+PGVY+RV SYL+WIAKVTNSLD				
		EDACQGDSSGGLMLVNNSSGIVTGVVSGHKKAEEGFPGVYTRVWSYLEWIAKVTNSLDQ				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	MTWICVITLFFALASATLGNKVS RVGVLF PKTRNDN-ECTARGGLKGSKSLIDCPVSLAT				59
		M WICVITLFFALAS+TL NKVSRVG++FPKT+NDN +CTA+GGLKGSKSL DCP+VLAT				
Sbjct	128	MAWICVITLFFALASSTLSNKVSRVGIIFFPKTQNDNKQCTAKGGLKGSKSLTDCPAVLAT				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	FSGPRSQVLREVSI PVVPVDKCDQAYEK-LNTPSLKNGITNNFLCAGLEEGKDACQGD				344
		F+GP S VLRREV +P+ + C QAYEK LN ITN ++CAG +GGKDACQGD				
Sbjct	296	FNGPSSAVLREVQLPIWGHPCRQAYEKDLN-----ITNVYMCAGYADGGKDACQGD				138
Query	345	GGPLMLVNNT-RWIVVGVVSGHKKAEEGYPGVYSRVASYLDWIA				388
		GGP+ML + + + +VG+VSFG KCA G+PGVY++V +LDWIA				
Sbjct	137	GGPMMLPDKSGNFYLVGIVSFGKKCALPGFPGVYTKVTEFLDWIA				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	VTAAGWGDLDFSGPRSQVLREVSI PVVPVDKCDQAYEKLNTPSLKNGITNNFLCAGLEEG			335		
		V GWG + + + VLR+ +PVV + C+++Y+ ++ L GIT++ +CAG +EG					
Sbjct	1	VWVIGWGVTERGEKYNVLRLELPPVTNELCNKSYQTISFSGLNRGITDDMICAGVQEG			180		
Query	336	GKDACQGDSGGPLMLVNNT--RWIVVGVVSGHKKAEEGYPGVYSRVASYLDWIAKV			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	VSIIPVVPVKCDQAYEKLNTPSLKNGITNNFLCAGLEEGGKDACQDSDGGPLMLVNNT--					354
Sbjct 191	+ +PVV + C+++Y+ ++ L GIT++ +CAG +EGG+D+C+GDSGGPLM + T					370
Query 355	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	KGSCKSLIDCPVLATLKDSFPVVCWNGRFQPIVCCPD	82				
	KGSCKSL DCP+VLATLKDSFPVV SWNGRFQPIVCCPD					
Sbjct 261	KGSCKSLTDCPAVLATLKDSFPVVYSWNGRFQPIVCCPD	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	MTWICVITLALASATLGNKVS RVG	25				
	M WICVITLALAS+TL NKVS RVG					
Sbjct 127	MAWICVITLALASSTLSNKVS 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	KVS RVGLFPKTRNDN-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

[Top](#)

[Follow NCBI](#)

Please use the feedback button near the bottom-right of your screen to let us know about your experience with CD-Search. You may need to do a hard refresh to replace outdated cached data and ensure proper function of this new user interface in your browser; the previous user interface will be available [here](#) for a short period of time.

CD-Search > Navigate results

Conserved domains on [1cl|SEQMD5(ref|XP_013784210)]

a3bcf7e0998de82a8ba9ecc91eb2eedf (clotting factor B)

[Find similar domain architectures](#)

Precomputed, cdd.v.3.21

Database: CDSEARCH/cdd

E-value cut off: 0.01

Composition-based adjustment: yes

Low-complexity filter: no

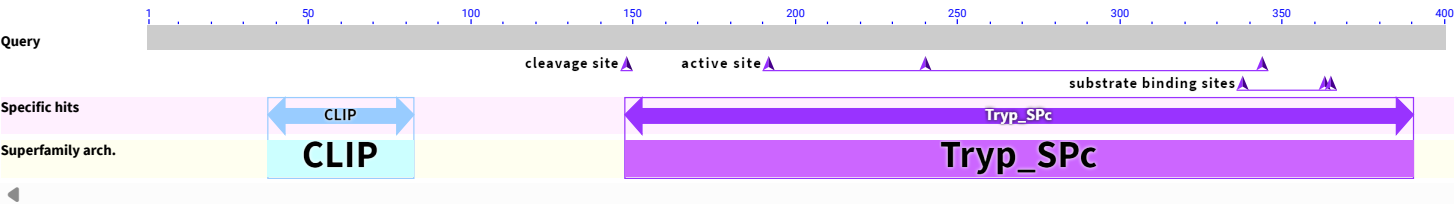
[Refine parameters and search again](#)

Viewing

Concise

H-zoom 

☐ Hide features



 Name	Accession	Description	Interval	E-value
+ 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}

FOLLOW NCBI

Feedback



Connect with NLM

National Library of
Medicine
8600 Rockville Pike
Bethesda, MD 20894

Web Policies
FOIA
HHS Vulnerability
Disclosure

Help
Accessibility
Careers

NLM NIH HHS USA.gov

Note: T.t proclotting factor used for database query was derived from NCBI nucleotide sequence Accession: M58366

The site is secure.
The https:// ensures that you are connecting to the official website and that any information you provide is encrypted and transmitted securely.
[Access keys](#) [NCBI Homepage](#) [MyNCBI Homepage](#) [Main Content](#) [Main Navigation](#)

BLAST® » **tblastn-SRA** » results for RID-J1TWKTSF016

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

Job Title [Protein Sequence...](#)
RID [J1TWKTSF016](#) Search expires on 11-23 05:28 am
Program TBLASTN
Database SRA
Query ID Id|Query_4221373
Description [unnamed_protein_product...](#)
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	YSTDDDSNP	206			
Sbjct 3	IKQGGIRSVQCGGALVTNRHVITASHCVVNS GTDVM ADVFSVRLGEHNL	YST+D S+P				
Query 207	IDFAVTSVKHHEHFVLATYLNDAIILTLNDTVTFTDRIRPICLPYRKLR	YDDLAMRKPF	266			
Sbjct 183	IDFAVTSVKHHE+FVLATYLNDAIIL LNDTVTFT +I+PICLPY LRY	+DLAMR PF+				
Query 267	TGWGTTAFNGPSSAVLREVQLPIWEHEACRQAY		299			
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	YDDLAMRKPF	I		266
Sbjct 387	IDFAVTSVKHHEFVLATYLN	DIAILTLNDTVFT +I+PICLPY LRY+DLAMR	PF+			208
Query 267	TGWGTTAFNGPSSAVLREVQ	LPIWEHEACRQAYEKDLNITNV	VMCAGFADGGKDACQ	GDS		326
Sbjct 207	AGWGTTAFNGPSSAVLREVQ	LPIW HE CRQAYEKDLNITNV	VMCAG+ADGGKDACQ	GDS		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	YDDLAMRKPFITGWGTTAFNGPSSAVLREVQ	LPIWEHEACRQAYEKD			302
Sbjct 304	QIKPICLPYESLRYEDLAMRNP	FVAGWGTTAFNGPSSAVLREVQ	LPIWGHEPCRQAYEKD			125
Query 303	LNITNVVMCAGFADGGKD	ACQDGGPMMLPVKTGEFY	LIG 343			
Sbjct 124	LNITNVVMCAG+ADGGKD	ACQDGGPMMLP 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	GTDVMPADVFSVRLGEHN	LYSTDDSNPIDFAVTSVKHHEFVLATYLN	DIAILTLNDTV			238
Sbjct 495	GTDVM ADVFSVRLGEHN	LYST+D S+PIDFAVTSVKHHEFVLATYLN	DIAIL LNDTV			316
Query 239	TFTDRIRPIC	248				
Sbjct 315	TFT ++	286				

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	NSAGTDVMPADVFSVRLGEHN	LYSTDDSNPIDFAVTSVKHHEFVLATYLN	DIAILTLN			235
Sbjct 3	NS GTDVM ADVFSVRLGEHN	LYST+D S+PIDFAVTSVKHHEFVLATYLN	DIAIL LN			182
Query 236	DTVTFTDRIRPICLPYRKLR	YDDLAMRKPFITGWGTTAFNGPSSAVLREVQ	LPIWEHEAC			295
Sbjct 183	DTVTFT +I+PTICLPY LRY+DLAMR	PF+ GWGTTAFNGPSSAVLREVQ	LPIW HE C			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 T+G CK+VL+CR LLQ KN Y +LK	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	SVQCGGALVTNRHVITASHCVVNSAGTDVMPADVFSVRLGEHNLYSTDDSNPIDFAVTS	213				
Sbjct 3	SVQCGGALVTNRHVITASHCVVNS GTDVM ADVFSVRLGEHNLYST+D S+PIDFAVTS	182				
Query 214	VKHHEFVLATYLNIDIAILNDTVTFTDRIRPICLPYRKLRYDDLAMRKPFITGWGTTA	273				
Sbjct 183	VKHHEFVLATYLNIDIAILNDTVTFT +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 DTVTFTDRIRPICLPYRKLR 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 GPMMLPVKTGEFYLGIVSFGKKCALPGFPGVYTKVTEFLDWIAEHMV* 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	VLREVQLPIW HE CRQAYEKDLNITNVYMCAG+ADGGKDACQGD SGGPMMLP K+G FY	252		
Sbjct 431	VLREVQLPIWGHPCRCRQAYEKDLNITNVYMCAGYADGGKDACQGD SGGPMMLPXXSGNFY					
Query 341	LIGIVSFGKKCALPGFPGVYTKVTEFLDWIAEHMV* 376					
Sbjct 251	L+GIVSFGKKCALPGFPGVYTKVTEFLDWIA +MV* 144					
	LVGIVSFGKKCALPGFPGVYTKVTEFLDWIAVNMV*					

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	M AVYIKQGGIRSVQCGGALVTNRHVITASHCVVNS GTDVM ADVFSVRLGEHNLYST+			
Sbjct 1	MAAVYIKQGGIRSVQCGGALVTNRHVITASHCVVNSLGTDMRADVFSVRLGEHNLYSTN	180				
Query 202	DDSNPIDFAVTSVKHHEHFVLATYLNDAIILTLND 236					
Sbjct 181	D S+PIDFAVTSVKHHE+FVLATYLNDAIIL LND 285					
	DSSDPIDFAVTSVKHHEFVLATYLNDAIILKLND					

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	++ GR+ + P W+ ++Y KQGGIRSVQCGGALVTNRHVITASHCVVNS GTDVM AD			
Sbjct 337	LLEGRKQHLEPGPGWLLSIY-KQGGIRSVQCGGALVTNRHVITASHCVVNSLGTDMRAD	161				
Query 187	VFSVRLGEHNLYSTDDDSNPIDFAVTSVKHHEHFVLATYLNDAIILTLNDTVT 239					
Sbjct 160	VFSVRLGEHNLYST+D S+PIDFAVTSVKHHE+FVLATYLNDAIIL LNDTVT 2					
	VFSVRLGEHNLYSTNDSSDPIDFAVTSVKHHEFVLATYLNDAIILKLNDTVT					

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+ 276					
	RIPSNLPKQCGNRNITTTTRIIGGQATPGAWPWMAAVYIQ					

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	CRQAYEKDLNITNVVMCAGFADGGKDACQGD	SGGPMMLPVKTGEFYLIGIVSFGKKCALP	354			
Sbjct 76	CRQAYEKDLNITNVVMCAG+ADGGKDACQGD	SGGPMMLP K+G FYL+GIVSFGKKCALP	255			
Query 355	GFPGVYTKVTEFLDWIAEHMV*	376				
Sbjct 256	GFPGVYTKVTEFLDWIA +MV*	321				

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				

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	TTAFNGPSSAVLREVQLPIWEHEACRQAYEKDLNITNVVMCAGFADGGKDACQGD	SGGPM 330				
Sbjct 3	TTAFNGPSSAVLREVQLPIW HE CRQAYEKDLNITNVVMCAG+ADGGKDACQGD	SGGPM 182				
Query 331	MLPVKTGEFYLIGIVSFGKKCAL-PGFP	GVYTKVTEFLDWIAEHMV* 376				
Sbjct 183	MLP K+G FYL+GIVSFGKK + F G K FLDWIA +MV*	323				

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	HEACRQAYEKDLNITNVVMCAGFADGGKDACQGD	SGGPMMLPVKTGEFYLIGIVSFGKKC 351				
Sbjct 6	HE CRQAYEKDLNITNVVMCAG+ADGGKDACQGD	SGGPMMLP K+G FYL+GIVSFGKKC 185				
Query 352	ALPGFPGVYTKVTEFLDWIAEHMV*	376				
Sbjct 186	ALPGFPGVYTKVTEFLDWIA +MV*	260				

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	FNGPSSAVLREVQLPIWEHEACRQAYEKDLNITNVVMCAGFADGGKDACQGD	SGGPMMLP 333				
Sbjct 13	FNGPSSAVLREVQLPIW HE CRQAYEKDLNITNVVMCAG+ADGGKDACQGD	SGGPMMLP 192				
Query 334	VKTGEFYLIGIVSFGKKCALPGFP	357				
Sbjct 193	K+G FYL+GIVSFGK LPGFP	264				

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	ACRQAYEKDLNITNVYMCAGFADGGKDACQGDSSGGMMLPVKTGEFYLGIVSFGKKCAL					353
	+CRQAYEKDLNITNVYMCAG+ADGGKDACQGDSSGGMMLP K+G FYL+GIVSFGKKCAL					
Sbjct 3	SCRQAYEKDLNITNVYMCAGYADGGKDACQGDSSGGMMLPDKSGNFYLVGIVSFGKKCAL					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	QIPPNLPEVCGIHNTTTRIIIGREAPIGAWPMTAVYIKQGGIRSVQCGGALVTRHVI					168
	+IP NLP+ CG N TTRII G+EA GAWPMT AVYIKQGGIRSVQCGGALVTRHVI					
Sbjct 278	RIPSNLPKQCGNRIITTRIIEGQAXPGAWPMAAVYIKQGGIRSVQCGGALVTRHVI					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	TTAFNGPSSAVLREVQLPIWEHEACRQAYEKDLNITNVYMCAGFADGGKDACQGDSSGGM					330
	TTAFNGPSSAVLREVQLPIW HE CRQAY KDLNITNVYMCAG+ADGGKDACQGDSSGGM					
Sbjct 3	TTAFNGPSSAVLREVQLPIWGHEPCRQAYEKDLNITNVYMCAGYADGGKDACQGDSSGGM					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	LPGFPGVYTKVTVLDWI 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	TTAFNGPSSAVLREVQLPIWEHEACRQAYEKDLNITNVYMCAGFADGGKDACQGDSSGGM					330
	TTAFNGPSSAVLREVQLPIW HE CRQAYEKDLNITNVYMCAG+ADGGKDACQGDSSGGM					
Sbjct 3	TTAFNGPSSAVLREVQLPIWGHEPCRQAYEKDLNITNVYMCAGYADGGKDACQGDSSGGM					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 - TNVYMCAGFADGGKDACQGDSGGPM		330			
	TAFNGPSSAVLREVQLPIW HE CRQAYEKD I NVYMCAG+ADGGKDACQGDSGGPM					
Sbjct 8	TAFNGPSSAVLREVQLPIWGHEPCRQAYEKDFKILQNVYMCAGYADGGKDACQGDSGGPM		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	GTTAFNGPSSAVLREVQLPIWEHEACRQAYEKDLNITNVYMCAGFADGGKDACQGDSGGP		329			
	GTTAFNGPSSAVLREVQLPIW HE CRQAYEKDLNITNVYMCAG+ADGGKDACQGDSGGP					
Sbjct 1	GTTAFNGPSSAVLREVQLPIWGHEPCRQAYEKDLNITNVYMCAGYADGGKDACQGDSGGP		180			
Query 330	MMLPVKTGEFYLLIGIVSFGKKCALPGFPGVYTKVTEF 366					
	MMLP K G F + + + ++ + PGVYTKVTEF					
Sbjct 181	MMLPKAGTFISLELC - 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+ GNGTTAFNGPSSAVLREVQLPIW					
Sbjct 1	ILKLNDTVTFTTHKIKPICLPYESLRHEDLAMRNPFAVGNGTTAFNGPSSAVLREVQLPIW		180			
Query 291	EHEACRQAYEKDLNITNVYMC 311					
	HE CRQAYEKDLNITNVYMC					
Sbjct 181	GHEPCRQAYEKDLNITNVYMC 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+ 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				
	+K G F + + FGKKCALPGFPGVYTKVTEFLDWIA +M					
Sbjct 193	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	QIPPNLFEVCGIHTTTTTRIIGGREAPIGAWPMTAVYIKGGIRSVQCGGALVTNRHVI	168				
	+IP NLP+ CG N TTTTRIIG+EA GAWPMM AVYIKGGIRSVQCGGALVTNRHVI					
Sbjct 67	RIPSNLPKQCGNRNITTTTRIIGGQATPGAWPMAAVYIKGGIRSVQCGGALVTNRHVI	246				
Query 169	TASHCIVNS 177					
	TASHCIVNS					
Sbjct 247	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				
	GTDVM ADVFSVRLGEHNLYST+D S+PIDFAVTSVKHHE					
Sbjct 278	GTDVMRADVFSVRLGEHNLYSTNDSIDPIDFAVTSVKHHE	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	MLVNNVFSLLCFPLLMVVRCSLRSRQRFVFPDEEELCSNRFTEEGTCKNVLDRCILL	60				
	MLVNN+FSLLCF LLMS+ CS+L RRRQRFVFPD+EE CSNRF +G CK+VL+CR LL					
Sbjct 96	MLVNNMFSLLCFSLLMFMFSCSSLRQRRQRFVFPDDEESCSNRFNDGICKDVLNCRDLL	275				
Query 61	QKNDYNLLKESICGFEGITPKVCCPKSS 88					
	QKNDYNLLKESIC F GITPK PK S					
Sbjct 276	QKNDYNLLKESICFRGITPKFVLPKQS 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				
	KDLNITNVVMCAG+ADGGKDACQGDSSGGMMLP K+G FYL+GIVSFGKKCALPGFPGVY					
Sbjct 1	KDLNITNVVMCAGYADGGKDACQGDSSGGMMLPKSGNFYLVGIVSFGKKCALPGFPGVY	180				

Query 361 TKVTEFLDWIAEHMV* 376
TKVTEFLDWIA +MV*
Sbjct 181 TKVTEFLDWIAVNMV* 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	DVMPADVFSVRLGEHNLYSTDDSDNPIDFAVTSVKHHEHFLATYLNDAIILTLNDTVTF					240
	DV+P DVFSVRLGEHNLYST+D S+PIDFAVTSVKHHE+FVLATYLNDAIIL LNDTVTF					
Sbjct 238	DVLP-DVFSVRLGEHNLYSTNDSSDPIDFAVTSVKHHEHFLATYLNDAIILKLNLDTVTF					62
Query 241	TDRIRPICLPYRKLYDDLA 260					
	T +I+PICLPY LRV+DLA					
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	HHEHFVLATYLNDAIILTLNDTVTFDRIRPICLPYRKLYDDLAMRPFITGWGTTAFN					275
	+H F +Y NDIA+L L V F++ I+PICLP+ + DL + +TGWT ++					
Sbjct 40	NHPDFDKVSYNDIALRLAKPVAFEFIQPICLPHPR---HDLRNKIATVTGWGTVSYG					210
Query 276	GPSAVLREVQLPIWEHEACRQAYEKDLNITNVYMCAGFADGGKDACQDSDGGPMMLPVK					335
	G SS VLREV +PIW ++ C + + + NIT V++CAG +G KD+CQDSDGGP+M					
Sbjct 211	GASSNVLREVSIPWNNDECDFTFTQ--NITKVFLCAGSKNGDKDSCQDSDGGPLMWEAP					384
Query 336	TGEFYLIGIVSFGKKCALPGFPGV 359					
	+ L+GIVS+G +CA P FPGV					
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
	+G CK+VL+CR LLQKNDYNLLKESICGFEGITPKVCCPK S V T+APP+TTTTTERP					
Sbjct 3	DGICKDVLNCRDLLQKNDYNLLKESICGFEGITPKVCCPKQSVNPITEAPPKTTTTTERP					182
Query 107	pKQIPPNLPEVCGIHNTTTTTRIIGGREAPIGAWPMMTAVYIK 148					
	P +IP NLP+ CG N TTTTRIIGG+EA GAWPMM AVYIK					
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	MCAGFADGGKDACQDSDGGPMMLPVKTGEFYLIGIVSFGKKCALPGFPGVYTKVTEFLDW					369
	MCAG+ADGGKDACQDSDGGPMMLP K+G FYL+GIVSFGKKCALPGFPGVYTKVTEFLDW					
Sbjct 345	MCAGYADGGKDACQDSDGGPMMLPDKSGNFYLVGIVSFGKKCALPGFPGVYTKVTEFLDW					166
Query 370	IAEHMV* 376					
	IA +MV*					

11/21/25, 5:32 PM

Sbjct 165 IAVNMV* 145

NCBI Blast:Protein Sequence

[Top](#)

Follow NCBI

Please use the feedback button near the bottom-right of your screen to let us know about your experience with CD-Search. You may need to do a hard refresh to replace outdated cached data and ensure proper function of this new user interface in your browser; the previous user interface will be available [here](#) for a short period of time.

CD-Search > Navigate results

Conserved domains on [lcl|SEQMD5(ref|XP_013783518)]

b187f25563c9036c5e5833b53d571b67 (proclotting enzyme-like)

[Find similar domain architectures](#)

Precomputed, cdd.v.3.21

Database: CDSEARCH/cdd

E-value cut off: 0.01

Composition-based adjustment: yes

Low-complexity filter: no

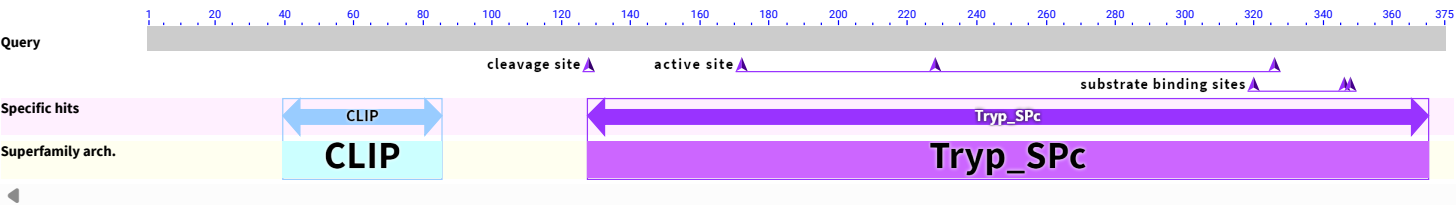
[Refine parameters and search again](#)

Viewing

Concise

H-zoom 

☐ Hide features



 Name	Accession	Description	Interval	E-value
+ Tryp_SPc	cd00190	Trypsin-like serine protease	128-370	4.42×10^{-95}
+ CLIP	smart00680	Clip or disulphide knot domain	40-85	7.18×10^{-7}

FOLLOW NCBI

 Feedback



Connect with NLM

National Library of
Medicine
8600 Rockville Pike
Bethesda, MD 20894

Web Policies
FOIA
HHS Vulnerability
Disclosure

Help
Accessibility
Careers

NLM NIH HHS USA.gov