

Basic Local Alignment Search Tool

[NCBI/ BLAST/ blastx/](#) **Formatting Results - B8BHYJXD014**

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Nucleotide Sequence (605 letters)

RID [B8BHYJXD014](#) (Expires on 02-06 12:08 pm)

Query ID lcl|Query_59009

Description None

Molecule type nucleic acid

Query Length 605

Database Name nr

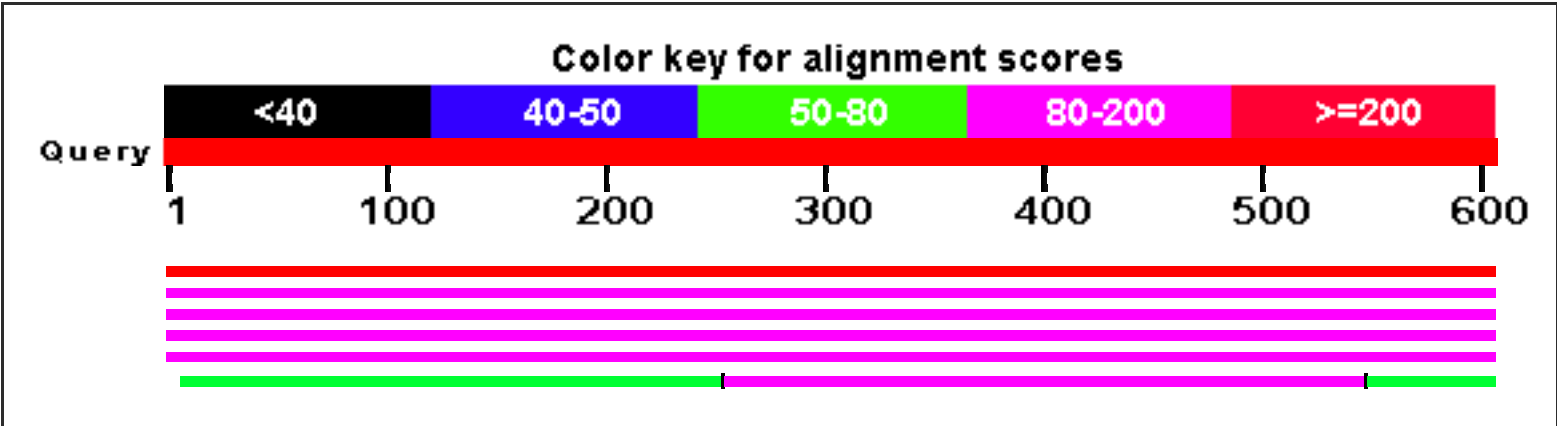
Description All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF
excluding environmental samples from
WGS projects

Program BLASTX 2.3.1+

[Graphic Summary](#)

No putative conserved domains have been detected

Distribution of 166 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
mucin 14A [Drosophila melanogaster]	205	20186	99%	2e-56	97%	NP_727928.3
GD17263 [Drosophila simulans]	131	1119	99%	5e-31	71%	XP_002105717.1
uncharacterized protein Dere_GG27179 [Drosophila erecta]	115	1353	99%	1e-25	69%	XP_015011493.1
uncharacterized protein Dyak_GE27476 [Drosophila yakuba]	98.6	247	99%	4e-21	68%	XP_015044596.1
uncharacterized protein Dyak_GE28509 [Drosophila yakuba]	99.8	309	99%	8e-21	67%	XP_015045967.1
uncharacterized protein Dsimw501_GD28225 [Drosophila simulans]	100	215	98%	1e-20	75%	KMZ10072.1

Alignments

mucin 14A [Drosophila melanogaster]
Sequence ID: **ref|NP_727928.3|** Length: 16223 Number of Matches: 129

See 1 more title(s)
Range 1: 5349 to 5549

Score	Expect	Method	Identities	Positives	Gaps	Frame
205 bits(522)	2e-56()	Compositional matrix adjust.	195/201(97%)	196/201(97%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaaeqtaqeetsEHSKSLPQL				425
Sbjct	5349	NIFSSPSLNEDNISQEDTRTL ISVPQSIATANSLLTGSSAEEQTAQEETSEHSKSLPQL				5408
Query	424	TTeesssfqessaeENQMTEVPWtlstslsqsssQAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct	5409	TTEESSSFQESSAEENQ TEVPWTLSTSLSQSSSQAKNIFSS SLNEDNISQEDTRT SI				5468
Query	244	SVPQSIATANSLLTGssaaeqtaqeetsEHSKSLPQLTTeesssfqessaeENQMTEVPW				65
Sbjct	5469	SVPQSIATANSLLTGSSAEEQTAQEETSEHSKSLPQLTTEESSSFQ+SSAEENQMTEVPW				5528
Query	64	tlstslsqsssQAKNIFSSPS 2				
Sbjct	5529	TLSTSLSQSSSQAKNIFSS S 5549				

Range 2: 5737 to 5937

Score	Expect	Method	Identities	Positives	Gaps	Frame
201 bits(511)	7e-55()	Compositional matrix adjust.	192/201(96%)	195/201(97%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaaeqtaqeetsEHSKSLPQL				425
Sbjct	5737	NIFSSPSLNEDNISQEDTRTL ISVPQSIATANSLLTGSSAEEQTAQEETSEHSKSLPQL				5796
Query	424	TTeesssfqessaeENQMTEVPWtlstslsqsssQAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct	5797	TTEESSSFQESSAEENQMTEVPWTLSTSLSQSSS+ KNIFSS S+NED SQEDTRTLSI				5856
Query	244	SVPQSIATANSLLTGssaaeqtaqeetsEHSKSLPQLTTeesssfqessaeENQMTEVPW				65
Sbjct	5857	SVPQSIATANSLLTGSSAEEQTAQEETSE SKSLPQLTTEESSSFQ+SSAEENQMTEVPW				5916

Query 64 tlstslsqsssqAKNIFSSPS 2
Sbjct 5917 TLSTSLSQSSSQAKNIFSSPS 5937

Range 3: 6553 to 6753

Score	Expect	Method	Identities	Positives	Gaps	Frame
201 bits(511)	7e-55()	Compositional matrix adjust.	192/201(96%)	194/201(96%)	0/201(0%)	-2
Features:						
Query 604		NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeegtaqeetsEHKSLPQL				425
Sbjct 6553		NIFSSPSLNEDNISQEDTRTL ISVPQSIATANSLLTGSSAEEQTAQEETSEHKS				6612
Query 424		TTeesssffqessaeENQMTEVPWtlstslsqsssqAKNIFSSPSLNEDNISQEDTRTL				245
Sbjct 6613		TTEESSSFFQESSAEENQMTEVPWTLSTSLSQSSSQKNIFSSQSLNEDNISQEDTRTL				6672
Query 244		SVPQSIATANSLLTGssaeegtaqeetsEHKSLPQLTTeesssffqessaeENQMTEVPW				65
Sbjct 6673		SVPQSIATANSLLTGSSAEEQTAQEETSEHKS				6732
Query 64		tlstslsqsssqAKNIFSSPS 2				
Sbjct 6733		TLSTS SQSSSQKNIFSSPS 6753				

Range 4: 5834 to 6034

Score	Expect	Method	Identities	Positives	Gaps	Frame
197 bits(502)	1e-53()	Compositional matrix adjust.	188/201(94%)	191/201(95%)	0/201(0%)	-2
Features:						
Query 604		NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeegtaqeetsEHKSLPQL				425
Sbjct 5834		NIFSS S+NED SQEDTRTLSISVPQSIATANSLLTGSSAEEQTAQEETSE SKSLPQL				5893
Query 424		TTeesssffqessaeENQMTEVPWtlstslsqsssqAKNIFSSPSLNEDNISQEDTRTL				245
Sbjct 5894		TTEESSSFFQSSAEENQMTEVPWTLSTSLSQSSSQAKNIFSSPS NEDNISQEDTRTL				5953
Query 244		SVPQSIATANSLLTGssaeegtaqeetsEHKSLPQLTTeesssffqessaeENQMTEVPW				65
Sbjct 5954		SVPQSIATANSLLTGSSAEEQTAQEETSEHKS				6013
Query 64		tlstslsqsssqAKNIFSSPS 2				
Sbjct 6014		T+ TSLSQSSSQKNIFSS S 6034				

Range 5: 7678 to 7878

Score	Expect	Method	Identities	Positives	Gaps	Frame
197 bits(502)	1e-53()	Compositional matrix adjust.	188/201(94%)	191/201(95%)	0/201(0%)	-2
Features:						
Query 604		NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeegtaqeetsEHKSLPQL				425
Sbjct 7678		NIFSSPS NEDNISQEDTRTL ISVPQSIATANSLLTGSSAEEQTAQEETSEHKS				7737
Query 424		TTeesssffqessaeENQMTEVPWtlstslsqsssqAKNIFSSPSLNEDNISQEDTRTL				245
Sbjct 7738		TTEESSSFFQESSAEENQMTEVPWT+ TSLSQSSSQKNIFSS S+NED SQEDTRTL				7797
Query 244		SVPQSIATANSLLTGssaeegtaqeetsEHKSLPQLTTeesssffqessaeENQMTEVPW				65
Sbjct 7798		SVPQSIATANSLLTGSSAEEQTAQEETSE S SLPQLTTEESSSFFQSSAEENQMTEVPW				7857
Query 64		tlstslsqsssqAKNIFSSPS 2				
Sbjct 7858		TLSTSLSQSSSQAKNIFSSPS 7878				

Range 6: 5446 to 5646

Score	Expect	Method	Identities	Positives	Gaps	Frame
196 bits(499)	3e-53()	Compositional matrix adjust.	191/201(95%)	193/201(96%)	0/201(0%)	-2

Features:

Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaaeqtaqeetsEH	425
Sbjct	5446	NIFSS SLNEDNISQEDTRT SISVPQSIATANSLLTGSSAAEQTAQEETSEH	5505
Query	424	TTeesssffgessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTL	245
Sbjct	5506	TTEESSSFFQ+SSAEENQMTEVPWTLSTSLSQSSSQAKNIFSS SLNEDNISQEDTRT SI	5565
Query	244	SVPQSIATANSLLTGssaaeqtaqeetsEH	65
Sbjct	5566	SVPQSIATANSLLTGSSAAEQTAQEETSEH	5625
Query	64	tlstslsqssssQAKNIFSSPS 2	
Sbjct	5626	TLSTS SQSSS+ KNIFSS S 5646	

Range 7: 6028 to 6228

Score	Expect	Method	Identities	Positives	Gaps	Frame
196 bits(498)	4e-53()	Compositional matrix adjust.	190/201(95%)	193/201(96%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaaeqtaqeetsEH SKSLPQL				425
Sbjct	6028	NIFSS S+NED SQEDTRTLSISVPQSIATANSLLTGSSAAEQTAQEETSE S SLPQL				6087
Query	424	TTeesssffgessaeENQMTEVPWtlstslsqsssqAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct	6088	TTEESSSFFQ+SSAEENQMTEVPWTLSTSLSQSSSQAKNIFSS SLNEDNISQEDTRT SI				6147
Query	244	SVPQSIATANSLLTGssaaeqtaqeetsEH SKSLPQLTTeesssffgessaeENQMTEVPW				65
Sbjct	6148	SVPQSIATANSLLTGSSAAEQTAQEETSEH SKSLPQLTTEESSSFFQ+SSAEENQMTEVPW				6207
Query	64	tlstslsqsssqAKNIFSSPS		2		
Sbjct	6208	TLSTSLSQSSSQAKNIFSS S				
		TLSTSLSQSSSQAKNIFSSQS		6228		

Range 8: 7775 to 7975

Score	Expect	Method	Identities	Positives	Gaps	Frame
195 bits(496)	7e-53()	Compositional matrix adjust.	186/201(93%)	188/201(93%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaaeqtaqeetsEH SKSLPQL				425
Sbjct	7775	NIFSS S+NED SQEDTRTLSISVPQSIATANSLLTGSSAAEQTAQEETSE S SLPQL				7834
Query	424	TTeesssffgessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct	7835	TTEESSSFFQ+SSAEENQMTEVPWTLSTSLSQSSSQAKNIFSSPS NEDNISQEDTRTL I				7894
Query	244	SVPQSIATANSLLTGssaaeqtaqeetsEH SKSLPQLTTeesssffgessaeENQMTEVPW				65
Sbjct	7895	SVPQSIATANSLLTGSSAAEQTAQEETSEH SKSLPQLTTEE SS QESSAEENQMTEVPW				7954
Query	64	tlstslsqssssQAKNIFSSPS		2		
Sbjct	7955	TLSTS QSSSQAKN FSS S				
		TLSTSQFQSSSQAKNTFSSQS		7975		

Range 9: 5931 to 6131

Score	Expect	Method	Identities	Positives	Gaps	Frame
194 bits(493)	2e-52()	Compositional matrix adjust.	187/201(93%)	190/201(94%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaaeqtaqeetsEH	425			
Sbjct	5931	NIFSSPS NEDNISQEDTRTL ISVPQSIATANSLLTGSSAAEQTAQEETSEH	5990			
Query	424	TTeesssffgessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTL	245			
Sbjct	5991	TTEESSSFFQESSAEENQMTEVPWT+ TSLSQSSS KNIFSS S+NED SQEDTRTL	6050			
Query	244	SVPQSIATANSLLTGssaaeqtaqeetsEH	65			
Sbjct	6051	SVPQSIATANSLLTGSSAAEQTAQEETSE S SLPQLTTEESSSFFQ+SSAEENQMTEVPW	6110			

Query 64 tlstslsqssssQAKNIFSSPS 2
TLSTSLSQSSSQAKNIFSS S
Sbjct 6111 TLSTSLSQSSSQAKNIFSSQS 6131

Range 10: 4767 to 4967

Score	Expect	Method	Identities	Positives	Gaps	Frame
194 bits(493)	2e-52()	Compositional matrix adjust.	189/201(94%)	190/201(94%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPOS IATANSLLTGssaeegtaqeetsEH SKSLPQL				425
Sbjct	4767	NIFSS S+NED SQEDTRTL ISVPOS IAT NSLLTGSSAEEQTAQEETSEH SKSLPQL				4826
Query	424	TTeesssfqessaeENQMTEVPWtlstslsqss sQAKNIFSSPSLNEDNISQEDTRTL SI				245
Sbjct	4827	TTEESSSF ESSAEENQ TEVPWTLSTSL SQSS QAKNIFSSPSLNEDNISQEDTRTL I				4886
Query	244	SVPOS IATANSLLTGssaeegtaqeetsEH SKSLPQLTTeesssfqessaeENQMTEVPW				65
Sbjct	4887	SVPOS IATANSLLTGSSAEEQTAQEETSEH SKSLPQLTTEESSSFQESSAEENQ TEVPW				4946
Query	64	tlstslsqss sQAKNIFSSPS		2		
Sbjct	4947	TLSTSL SQSSSQAKNIFSS S		4967		

Range 11: 5252 to 5452

Score	Expect	Method	Identities	Positives	Gaps	Frame
194 bits(493)	2e-52()	Compositional matrix adjust.	189/201(94%)	190/201(94%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeegtaqeetsEH NIFSS S+NED SQEDTRTL ISVPQSIAT NSLLTGSSAEEQTAQEETSEH				425
Sbjct	5252	NIFSSQSVNEDKTSQEDTRTLPISVPQSIATTNSLLTGSSAEEQTAQEETSEH				5311
Query	424	TTeesssfqessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTL TTEESSSF ESSAEENQ TEVPWTLSTSLSQSS QAKNIFSSPSLNEDNISQEDTRTL I				245
Sbjct	5312	TTEESSSFLESSAEENQTTEVPWTLSTSLSQSSSLQAKNIFSSPSLNEDNISQEDTRTLPI				5371
Query	244	SVPQSIATANSLLTGssaeegtaqeetsEH SVPQSIATANSLLTGSSAEEQTAQEETSEH SVPQSIATANSLLTGSSAEEQTAQEETSEH				65
Sbjct	5372	SVPQSIATANSLLTGSSAEEQTAQEETSEH SVPQSIATANSLLTGSSAEEQTAQEETSEH SVPQSIATANSLLTGSSAEEQTAQEETSEH				5431
Query	64	tlstslsqssssQAKNIFSSPS 2				
Sbjct	5432	TLSTSLSQSSSQAKNIFSS S 5452				

Range 12: 6125 to 6325

Score	Expect	Method	Identities	Positives	Gaps	Frame
193 bits(491)	4e-52()	Compositional matrix adjust.	190/201(95%)	192/201(95%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeegtaqeetsEH NIFSS SLNEDNISQEDTRT SISVPQSIATANSLLTGSSAEEQTAQEETSEH				425
Sbjct	6125	NIFSSQSLNEDNISQEDTRTPSISVPQSIATANSLLTGSSAEEQTAQEETSEH				6184
Query	424	TTeesssfqessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTL TTEESSSFQ+SSAEENQMTEVPWTLSTSLSQSSSQAKNIFSS SLNEDNISQEDTRT SI				245
Sbjct	6185	TTEESSSFQKSSAEENQMTEVPWTLSTSLSQSSSQAKNIFSSQSLNEDNISQEDTRTPSI				6244
Query	244	SVPQSIATANSLLTGssaeegtaqeetsEH SVPQSIATANSLLTGSSAEEQTAQEETSEHSL QLTTEESSSFQESSAEENQ TEVPW				65
Sbjct	6245	SVPQSIATANSLLTGSSAEEQTAQEETSEHSLAQLTTEESSSFQESSAEENQTTEVPW				6304
Query	64	tlstslsqssssQAKNIFSSPS		2		
		TLSTS SQSSS+ KNIFSS S				
Sbjct	6305	TLSTSPSQSSSKTKNIFSSQS		6325		

Range 13: 8454 to 8654

Score	Expect	Method	Identities	Positives	Gaps	Frame
191 bits(485)	2e-51()	Compositional matrix adjust.	182/201(91%)	186/201(92%)	0/201(0%)	-2

Features:

Query	604	NIFSSPSLNEDNISQEDTRTLSISVPOSIATANSLLTGssaaeqtageetsEHSKSLPQL	425
Sbjct	8454	NIFSS S+NED SQEDTRTLSISVPQS ATANSLLTGSSAEEQTAQEETSEHSKSLPQL NIFSSQSVNEDKTSQEDTRTLSISVPQSFATANSLLTGSSAEEQTAQEETSEHSKSLPQL	8513
Query	424	TTeesssffqessaeENQMTEVPWtlstslsqsssQAKNIFSSPSLNEDNISQEDTRTLSI	245
Sbjct	8514	TTEESSSSFQESSAEENQMTEVPWT+ TSLSQSSS KNIFSS S+NED SQEDTRTLSI TTEESSSFQESSAEENQMTEVPWTVLTSLSQSSSITKNIFSSQSVNEDKTSQEDTRTLSI	8573
Query	244	SVPOSIATANSLLTGssaaeqtageetsEHSKSLPQLTTeesssffqessaeENQMTEVPW	65
Sbjct	8574	SVPQS ATANSLLTGSSAEEQTAQEETSEHSKSLPQLTTEESSSSFQESSAEENQMTEVPW SVPQSFATANSLLTGSSAEEQTAQEETSEHSKSLPQLTTEESSSFQESSAEENQMTEVPW	8633
Query	64	tlstslsqsssQAKNIFSSPS 2	
Sbjct	8634	T+ TSLSQSSS KNIFSS S TVLTSLSQSSSITKNIFSSQS 8654	

Range 14: 4670 to 4870

Score	Expect	Method	Identities	Positives	Gaps	Frame
191 bits(485)	2e-51()	Compositional matrix adjust.	185/201(92%)	188/201(93%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPOSIATANSLLTGssaaeqtageetsEHSKSLPQL NIFSSPSLNEDNISQEDTRTL ISVPOSIATA+SLLTGSSAEEQTAQEETSEHSKSLPQL				425
Sbjct	4670	NIFSSPSLNEDNISQEDTRTLPI SVPOSIATAHSLLTGSSAEEQTAQEETSEHSKSLPQL				4729
Query	424	TTeesssffqessaeENQMTEVPWtlstslsqsssQAKNIFSSPSLNEDNISQEDTRTLSI TTEESSSF ESSAEENQ TEVPWTLSTS SQSSS+ KNIFSS S+NED SQEDTRTL I				245
Sbjct	4730	TTEESSSFLESSAEENQTTEVPWTLSTSPSQSSSKTKNIFSSQSVNEDKTSQEDTRTLPI				4789
Query	244	SVPOSIATANSLLTGssaaeqtageetsEHSKSLPQLTTeesssffqessaeENQMTEVPW SVPOSIAT NSLLTGSSAEEQTAQEETSEHSKSLPQLTTEESSSF ESSAEENQ TEVPW				65
Sbjct	4790	SVPQSIATTNSLLTGSSAEEQTAQEETSEHSKSLPQLTTEESSSFLESSAEENQTTEVPW				4849
Query	64	tlstslsqsssQAKNIFSSPS		2		
		TLSTSLSQSS QAKNIFSSPS				
Sbjct	4850	TLSTSLSQSSLQAKNIFSSPS		4870		

Range 15: 8648 to 8848

Score	Expect	Method	Identities	Positives	Gaps	Frame
191 bits(484)	3e-51()	Compositional matrix adjust.	181/201(90%)	186/201(92%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPOSIATANSLLTGssaaeqtageetsEHSKSLPQL				425
Sbjct	8648	NIFSS S+NED SQEDTRTLSISVPQS AT N LLTGSSAEEQTAQEETSEHSKSLPQL				8707
Query	424	TTeesssffqessaeENQMTEVPWtlstslsqsssQAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct	8708	TTEE SS QESSAEENQMTEVPWT+ TSLSQSSS+ KNIFSS S+NED SQEDTRTLSI				8767
Query	244	SVPOSIATANSLLTGssaaeqtageetsEHSKSLPQLTTeesssffqessaeENQMTEVPW				65
Sbjct	8768	SVPOSIATANSLLTGSSAEEQTAQEETSE S SLPQLTTEESSSFQ+SSAEENQMTEVPW				8827
Query	64	tlstslsqsssQAKNIFSSPS		2		
Sbjct	8828	TLSTSLSQSSSQAKNIFSSPS		8848		

Range 16: 8842 to 9042

Score	Expect	Method	Identities	Positives	Gaps	Frame
190 bits(483)	3e-51()	Compositional matrix adjust.	186/201(93%)	188/201(93%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPOSIATANSLLTGssaaeqtageetsEHSKSLPQL				425
Sbjct	8842	NIFSSPS NEDNISQEDTRTL ISVPOSIATANSLLTGSSAEEQTAQEETSEHSKSLPQL				8901
Query	424	TTeesssffqessaeENQMTEVPWtlstslsqsssQAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct	8902	TTEESSSFQESSAEENQ TEVPWTLSTSLSQSSS+ KNIFSS S+NED SQEDTRTLSI				8961
Query	244	SVPOSIATANSLLTGssaaeqtageetsEHSKSLPQLTTeesssffqessaeENQMTEVPW				65
Sbjct	8962	SVPQS AT N LLTGSSAEEQTAQEETSEHSKSLPQLTTEE SS QESSAEENQMTEVPW				9021
Query	64	tlstslsqsssQAKNIFSSPS		2		
Sbjct	9022	TLSTSLSQSSSQAKNIFSS S		9042		

Range 17: 8163 to 8363

Score	Expect	Method	Identities	Positives	Gaps	Frame
190 bits(483)	4e-51()	Compositional matrix adjust.	186/201(93%)	189/201(94%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPOS	ATANSLLTGssaeegtaqeetsEHSKSLPQL	425		
Sbjct	8163	NIFSSPS NEDNISQEDTRTL ISVPOS	ATANSLLTGSSAEEQTAQEETSEHSKSLPQL	8222		
Query	424	TTeesssffgessaeENQMTEVPWtlstslsqsssQAKNIFSSPSLNEDNISQEDTRTLSI	245			
Sbjct	8223	TTEESSSFFQESSAEENQ TEVPWTLSTSLSQSSS+ KNIFSS S+NED SQEDTRTLSI	8282			
Query	244	SVPOS	ATANSLLTGssaeegtaqeetsEHSKSLPQLTTeesssffgessaeENQMTEVPW	65		
Sbjct	8283	SVPOS	AT NSLLTGSSAEEQTAQEETSEHSKSLPQLTTEESSSFFQESSAEENQMTEVPW	8342		
Query	64	tlstslsqsssQAKNIFSSPS	2			
Sbjct	8343	T+ TSLSQSSS KNIFSS S	8363			

Range 18: 4864 to 5064

Score	Expect	Method	Identities	Positives	Gaps	Frame
190 bits(482)	6e-51()	Compositional matrix adjust.	188/201(94%)	190/201(94%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPOS	ATANSLLTGssaeegtaqeetsEHSKSLPQL	425		
Sbjct	4864	NIFSSPSLNEDNISQEDTRTL ISVPOS	ATANSLLTGSSAEEQTAQEETSEHSKSLPQL	4923		
Query	424	TTeesssffgessaeENQMTEVPWtlstslsqsssQAKNIFSSPSLNEDNISQEDTRTLSI	245			
Sbjct	4924	TTEESSSFFQESSAEENQ TEVPWTLSTSLSQSSSQAKNIFSS SLNED SQEDTRT SI	4983			
Query	244	SVPOS	ATANSLLTGssaeegtaqeetsEHSKSLPQLTTeesssffgessaeENQMTEVPW	65		
Sbjct	4984	SVPOS	ATA+SLLTGSSAEEQTAQEETSEHSKSLPQLTTEESSSFF ESSAEENQ TEVPW	5043		
Query	64	tlstslsqsssQAKNIFSSPS	2			
Sbjct	5044	TLSTS SQSSS+ KNIFSS S	5064			

Range 19: 8551 to 8751

Score	Expect	Method	Identities	Positives	Gaps	Frame
189 bits(481)	6e-51()	Compositional matrix adjust.	178/201(89%)	183/201(91%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPOS	ATANSLLTGssaeegtaqeetsEHSKSLPQL	425		
Sbjct	8551	NIFSS S+NED SQEDTRTLSISVPOS	ATANSLLTGSSAEEQTAQEETSEHSKSLPQL	8610		
Query	424	TTeesssffgessaeENQMTEVPWtlstslsqsssQAKNIFSSPSLNEDNISQEDTRTLSI	245			
Sbjct	8611	TTEESSSFFQESSAEENQMTEVPWT+ TSLSQSSS KNIFSS S+NED SQEDTRTLSI	8670			
Query	244	SVPOS	ATANSLLTGssaeegtaqeetsEHSKSLPQLTTeesssffgessaeENQMTEVPW	65		
Sbjct	8671	SVPOS	AT N LLTGSSAEEQTAQEETSEHSKSLPQLTTEE SS QESSAEENQMTEVPW	8730		
Query	64	tlstslsqsssQAKNIFSSPS	2			
Sbjct	8731	T+ TSLSQSSS+ KNIFSS S	8751			

Range 20: 9133 to 9333

Score	Expect	Method	Identities	Positives	Gaps	Frame
189 bits(481)	7e-51()	Compositional matrix adjust.	186/201(93%)	189/201(94%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPOS	TAN LLTGS A+EQTAQEETSE SKSLPQL	425		

Sbjct	9133	NIFSSQSLNEDNISQEDTRTPSISV PQSSTTANRLLTG SIAKEQTAQEETSELSKSLPQL	9192
Query	424	TTeesssffgessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTL SI	245
Sbjct	9193	TTEESSSFFQESS EENQMTEVPWTLSTSLSQSSS+ KNIFSSPSL EDNISQEDTRTL SI	9252
Query	244	SVPQSIATANSLLTGssaeegtaqeetsEHSKSLPQLTTeesssffgessaeENQMTEVPW	65
Sbjct	9253	SVPQSIATANSLLTGSSAAEQTAQEETSE S SLPQLTTEESSSFFQ+SSAEENQMTEVPW	9312
Query	64	tlstslsqssssQAKNIFSSPS	2
Sbjct	9313	TLSTSLSQSSSQAKNIFSSPS	9333

Range 21: 5640 to 5840

Score	Expect	Method	Identities	Positives	Gaps	Frame
189 bits(479)	1e-50()	Compositional matrix adjust.	186/201(93%)	188/201(93%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeegtaqeetsEHSKSLPQL				425
Sbjct	5640	NIFSS S+NED SQEDTRTL ISVPQSIAT NSLLTGSSAAEEQTAQEETSEHSK LPQL				5699
Query	424	TTeesssffgessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct	5700	TTEESSSFF ESSAEENQ TEVPWTLSTSLSQSS Q KNIFSSPSLNEDNISQEDTRTL I				5759
Query	244	SVPQSIATANSLLTGssaeegtaqeetsEHSKSLPQLTTeesssffgessaeENQMTEVPW				65
Sbjct	5760	SVPQSIATANSLLTGSSAAEEQTAQEETSEHSKSLPQLTTEESSSFFQESSAEENQMTEVPW				5819
Query	64	tlstslsqssssQAKNIFSSPS		2		
Sbjct	5820	TLSTSLSQSSS+ KNIFSS S		5840		

Range 22: 7872 to 8072

Score	Expect	Method	Identities	Positives	Gaps	Frame
189 bits(479)	2e-50()	Compositional matrix adjust.	179/201(89%)	181/201(90%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeegtaqeetsEHSKSLPQL				425
Sbjct	7872	NIFSSPS NEDNISQEDTRTL ISVPQSIATANSLLTGSSAAEEQTAQEETSEHSKSLPQL				7931
Query	424	TTeesssffgessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct	7932	TTEE SS QESSAEENQMTEVPWTLSTS QSSSQAKN FSS SLNED SQEDTRTLSI				7991
Query	244	SVPQSIATANSLLTGssaeegtaqeetsEHSKSLPQLTTeesssffgessaeENQMTEVPW				65
Sbjct	7992	S PQS TAN LLTGS AEEQTAQEETSE SKSLPQLTTEESSSFFQ+SSAEENQMTEVPW				8051
Query	64	tlstslsqssssQAKNIFSSPS 2				
Sbjct	8052	T+ TSLSQSSS KNIFSS S				
		TVLTSLSQSSSITKNIFSSQS 8072				

Range 23: 8066 to 8266

Score	Expect	Method	Identities	Positives	Gaps	Frame
188 bits(478)	2e-50()	Compositional matrix adjust.	188/201(94%)	191/201(95%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeegtaqeetsEHSKSLPQL				425
Sbjct	8066	NIFSS S+NED SQEDTRTLSISVPQSIATANSLLTGSSAAEEQTAQEETSE S SLPQL				8125
Query	424	TTeesssffgessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct	8126	TTEESSSFFQ+SSAEENQMTEVPWTLSTSLSQSSSQAKNIFSSPS NEDNISQEDTRTL I				8185
Query	244	SVPQSIATANSLLTGssaeegtaqeetsEHSKSLPQLTTeesssffgessaeENQMTEVPW				65
Sbjct	8186	SVPQSIATANSLLTGSSAAEEQTAQEETSEHSKSLPQLTTEESSSFFQESSAEENQ TEVPW				8245
Query	64	tlstslsqssssQAKNIFSSPS		2		
		TLSTSLSQSSS+ KNIFSS S				
Sbjct	8246	TLSTSLSQSSSKTKNIFSSQS		8266		

Range 24: 8357 to 8557

Score	Expect	Method	Identities	Positives	Gaps	Frame
188 bits(478)	2e-50()	Compositional matrix adjust.	180/201(90%)	183/201(91%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTG	ssaeeqtaqeets	EH	SKSLPQL	425
Sbjct	8357	NIFSS S+NED SQEDTRTLSISVPQS AT N LLTGSSAEEQTAQEETSE	EH	SKSLPQL		8416
Query	424	TTeesssffgessaeENQMTEVPWtlstslsqsssQAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct	8417	TTEE SS QESSAEENQMTEVPWTLSTSLSQSSS KNIFSS S+NED SQEDTRTLSI				8476
Query	244	SVPQSIATANSLLTGssaeeqtaqeetsEH	SKSLPQLTTeesssffgessaeENQMTEVPW			65
Sbjct	8477	SVPQS ATANSLLTGSSAEEQTAQEETSE	EH	SKSLPQLTTEESSSFFQESSAEENQMTEVPW		8536
Query	64	tlstslsqsssQAKNIFSSPS	2			
Sbjct	8537	T+ TSLSQSSS KNIFSS S				
		TVLTSLSQSSSITKNIFSSQS	8557			

Range 25: 8745 to 8945

Score	Expect	Method	Identities	Positives	Gaps	Frame
188 bits(478)	2e-50()	Compositional matrix adjust.	188/201(94%)	191/201(95%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTG	ssaeeqtaqeets	EH	SKSLPQL	425
Sbjct	8745	NIFSS S+NED SQEDTRTLSISVPQSIATANSLLTGSSAEEQTAQEETSE S SLPQL				8804
Query	424	TTeesssffgessaeENQMTEVPWtlstslsqsssQAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct	8805	TTEESSSFFQ+SSAEENQMTEVPWTLSTSLSQSSSQAKNIFSSPS NEDNISQEDTRTL I				8864
Query	244	SVPQSIATANSLLTGssaeeqtaqeetsEH	SKSLPQLTTeesssffgessaeENQMTEVPW			65
Sbjct	8865	SVPQSIATANSLLTGSSAEEQTAQEETSE	EH	SKSLPQLTTEESSSFFQESSAEENQ TEVPW		8924
Query	64	tlstslsqsssQAKNIFSSPS	2			
Sbjct	8925	TLSTSLSQSSS+ KNIFSS S				
		TLSTSLSQSSSKTKNIFSSQS	8945			

Range 26: 7113 to 7313

Score	Expect	Method	Identities	Positives	Gaps	Frame
188 bits(478)	2e-50()	Compositional matrix adjust.	185/201(92%)	190/201(94%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTG	ssaeeqtaqeets	EH	SKSLPQL	425
Sbjct	7113	NIFSS S+NED SQEDTRTLSISVPQSIAT NSLLTGSSAEEQTAQEETSE SKSLPQL				7172
Query	424	TTeesssffgessaeENQMTEVPWtlstslsqsssQAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct	7173	TTEESSSFFQ+SSAEENQMTEVPWTLSTSLSQSSS+ KNIFSS SLNEDNISQEDTRTLSI				7232
Query	244	SVPQSIATANSLLTGssaeeqtaqeetsEH	SKSLPQLTTeesssffgessaeENQMTEVPW			65
Sbjct	7233	SVPQ IATANSLLTGSSAEEQTAQEE SE	HSKSLPQLTTEESSSFFQESSAEENQMTEVPW			7292
Query	64	tlstslsqsssQAKNIFSSPS	2			
Sbjct	7293	TLSTSLSQSSS+ KNIFS+ S				
		TLSTSLSQSSSKTKNIFSNQS	7313			

Range 27: 8260 to 8460

Score	Expect	Method	Identities	Positives	Gaps	Frame
188 bits(477)	2e-50()	Compositional matrix adjust.	180/201(90%)	183/201(91%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTG	ssaeeqtaqeets	EH	SKSLPQL	425
Sbjct	8260	NIFSS S+NED SQEDTRTLSISVPQSIAT NSLLTGSSAEEQTAQEETSE	EH	SKSLPQL		8319
Query	424	TTeesssffgessaeENQMTEVPWtlstslsqsssQAKNIFSSPSLNEDNISQEDTRTLSI				245

Sbjct	8320	TTESSSSFQESSAEENQMTEVPWT+ TSLSQSSS KNIFSS S+NED SQEDTRTLSI	8379
Query	244	SVPOS IATANSLLTGssaeeqtaqeetsEHSKSLPQLTTeesssfqessaeENQMTEVPW	65
Sbjct	8380	SVPOS AT N LLTGSSAEEQTAQEETSEHSKSLPQLTTEE SS QESSAEENQMTEVPW	8439
Query	64	tlstslsqssssQAKNIFSSPS 2	
Sbjct	8440	TLSTSLSQSSS KNIFSS S	
		TLSTSLSQSSSITKNIFSSQS 8460	

Range 28: 7210 to 7410

Score	Expect	Method	Identities	Positives	Gaps	Frame
187 bits(475)	4e-50()	Compositional matrix adjust.	185/201(92%)	190/201(94%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeeqtaqeetsEHSKSLPQL				425
Sbjct	7210	NIFSS SLNEDNISQEDTRTLSISVPQ IATANSLLTGSSAEEQTAQEE SEHSKSLPQL				7269
Query	424	TTeesssfqessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct	7270	TTESSSSFQESSAEENQMTEVPWTLSTSLSQSSS+ KNIFS+ S+NED SQEDTRTLSI				7329
Query	244	SVPQSIATANSLLTGssaeeqtaqeetsEHSKSLPQLTTeesssfqessaeENQMTEVPW				65
Sbjct	7330	SVPQSIAT NSLLTGSSAEEQTAQEETSE SKSLPQLTTESSSSFQ+SSAEENQMTEVPW				7389
Query	64	tlstslsqssssQAKNIFSSPS		2		
Sbjct	7390	TLSTSLSQSSS+ KNIFSS S				
		TLSTSLSQSSSEPKNIFSSOS		7410		

Range 29: 6222 to 6421

Score	Expect	Method	Identities	Positives	Gaps	Frame
187 bits(475)	5e-50()	Compositional matrix adjust.	186/200(93%)	188/200(94%)	0/200(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeeqtaqeetsEHSKSLPQL				425
Sbjct	6222	NIFSS SLNEDNISQEDTRT SISVPQSIATANSLLTGSSAEEQTAQEETSEHSKSL QL				6281
Query	424	TTeesssfqessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct	6282	TTESSSSFQESSAEENQ TEVPWTLSTS SQSSS+ KNIFSS S+NED SQEDTRTL I				6341
Query	244	SVPOS IATANSLLTGssaeeqtaqeetsEHSKSLPQLTTeesssfqessaeENQMTEVPW				65
Sbjct	6342	SVPOS IAT NSLLTGSSAEEQTAQEETSEHSKSLPQLTTESSSSFQESSAEENQMTEVPW				6401
Query	64	tlstslsqssssQAKNIFSSP		5		
Sbjct	6402	TLSTSLSQSS QAKNIFSSP				
		TLSTSLSQSSLQAKNIFSSP		6421		

Range 30: 8939 to 9139

Score	Expect	Method	Identities	Positives	Gaps	Frame
187 bits(474)	7e-50()	Compositional matrix adjust.	183/201(91%)	185/201(92%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeeqtaqeetsEHSKSLPQL				425
Sbjct	8939	NIFSS S+NED SQEDTRTLSISVPQS AT N LLTGSSAEEQTAQEETSEHSKSLPQL				8998
Query	424	TTeesssfqessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct	8999	TTEE SS QESSAEENQMTEVPWTLSTSLSQSSSQAKNIFSS SLNEDNISQEDTRT SI				9058
Query	244	SVPOS IATANSLLTGssaeeqtaqeetsEHSKSLPQLTTeesssfqessaeENQMTEVPW				65
Sbjct	9059	SVPOS TAN LLTGS AEEQTAQEETSEHSKSLPQLTTEESSSFQESSAEENQMTEVPW				9118
Query	64	tlstslsqssssQAKNIFSSPS		2		
Sbjct	9119	TLSTSLSQSSS+ KNIFSS S				
		TLSTSLSQSSSEPKNIFSSQS		9139		

Range 31: 9230 to 9428

Score	Expect	Method	Identities	Positives	Gaps	Frame
186 bits(473)	8e-50()	Compositional matrix adjust.	186/199(93%)	190/199(95%)	0/199(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaaeqtagaetsEH SKSLPQL				425
Sbjct	9230	NIFSSPSL EDNISQEDTRTLSISVPQSIATANSLLTGSSAEEQTAQEETSE S SLPQL				9289
Query	424	TTeesssffqessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct	9290	TTEESSSFFQ+SSAEENQMTEVPWTLSTSLSQSSSQAKNIFSSPSLNEDNISQEDTRTL I				9349
Query	244	SV PQSIATANSLLTGssaaeqtagaetsEH SKSLPQLTTeesssffqessaeENQMTEVPW				65
Sbjct	9350	SV PQSIATANSLLTGSSAEEQTAQEETSE S SLPQLTTEESSSFFQESSAEENQ T++PW				9409
Query	64	tlstslsqssssQAKNIFSS 8				
Sbjct	9410	TLSTSLSQSSS+ KNIFSS 9428				

Range 32: 6456 to 6656

Score	Expect	Method	Identities	Positives	Gaps	Frame
186 bits(472)	1e-49()	Compositional matrix adjust.	186/201(93%)	188/201(93%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaaeqtagaetsEH SKSLPQL				425
Sbjct	6456	NIFSS SLNEDNISQEDTRT SISV QS TAN LLTGS AEEQTAQEETSEH SKSLPQL				6515
Query	424	TTeesssffqessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct	6516	TTEESSSFFQESSAEENQ TEVPWTLSTS SQSSS+ KNIFSSPSLNEDNISQEDTRTL I				6575
Query	244	SV PQSIATANSLLTGssaaeqtagaetsEH SKSLPQLTTeesssffqessaeENQMTEVPW				65
Sbjct	6576	SV PQSIATANSLLTGSSAEEQTAQEETSEH SKSLPQLTTEESSSFFQESSAEENQMTEVPW				6635
Query	64	tlstslsqssssQAKNIFSSPS 2				
Sbjct	6636	TLSTSLSQSSS+ KNIFSS S 6656				

Range 33: 5543 to 5743

Score	Expect	Method	Identities	Positives	Gaps	Frame
184 bits(468)	3e-49()	Compositional matrix adjust.	184/201(92%)	186/201(92%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaaeqtagaetsEH SKSLPQL				425
Sbjct	5543	NIFSS SLNEDNISQEDTRT SISVPQSIATANSLLTGSSAEEQTAQEETSEH SKSLPQL				5602
Query	424	TTeesssffqessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct	5603	TTEESSSFFQESSAEENQ TEVPWTLSTS SQSSS+ KNIFSS S+NED SQEDTRTL I				5662
Query	244	SV PQSIATANSLLTGssaaeqtagaetsEH SKSLPQLTTeesssffqessaeENQMTEVPW				65
Sbjct	5663	SV PQSIAT NSLLTGSSAEEQTAQEETSEH SK LPQLTTEESSSFF ESSAEENQ TEVPW				5722
Query	64	tlstslsqssssQAKNIFSSPS 2				
Sbjct	5723	TLSTSLSQSS Q KNIFSSPS 5743				

Range 34: 4379 to 4579

Score	Expect	Method	Identities	Positives	Gaps	Frame
184 bits(467)	5e-49()	Compositional matrix adjust.	181/201(90%)	187/201(93%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaaeqtagaetsEH SKSLPQL				425
Sbjct	4379	NIFSS S+NED SQEDTRTL ISVPQSIATANSLLTGSSAEEQTAQEETSE SKSLPQL				4438
Query	424	TTeesssffqessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct	4439	TTEESSSFFQESSAEENQMTEVPWT+STSLSQS S+ KNIFSS S+NED SQEDTRTLSI				4498

Query	244	SV PQSIATANSLLTGSSAEEQTAQEETSEH SKSLPQLTTEESSSfQESSAEENQMTEVPW	65
Sbjct	4499	SV PQSIATANSLLTGSSAEEQTAQEETSE SKSLPQLTTEESSSfQESSAEENQMTEVPW	4558
Query	64	tlstslsqssSQAKNIFSSPS 2	
Sbjct	4559	TVSTSLSQSRSKTKNIFSSQS 4579	

Range 35: 5155 to 5355

Score	Expect	Method	Identities	Positives	Gaps	Frame
184 bits(466)	7e-49()	Compositional matrix adjust.	182/201(91%)	186/201(92%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGSSAEEQTAQEETSEH SKSLPQL	425			
Sbjct	5155	NIFSSQSVNEDKTSQEDTRTLPI SV PQSIATANSLLTGSSAEEQTAQEETSKH SKSLPQL	5214			
Query	424	TTEESSSfQESSAEENQMTEVPWtlstslsqssSQAKNIFSSPSLNEDNISQEDTRTLSI	245			
Sbjct	5215	TTEESSSfQESSAEENQTEVPWTLSTS SQSSS+ KNIFSS S+NED SQEDTRTL I	5274			
Query	244	SV PQSIATANSLLTGSSAEEQTAQEETSEH SKSLPQLTTEESSSfQESSAEENQMTEVPW	65			
Sbjct	5275	SV PQSIAT NSLLTGSSAEEQTAQEETSEH SKSLPQLTTEESSSfQESSAEENQTEVPW	5334			
Query	64	tlstslsqssSQAKNIFSSPS 2				
Sbjct	5335	TLSTSLSQSS QAKNIFSSPS	5355			

Range 36: 1633 to 1833

Score	Expect	Method	Identities	Positives	Gaps	Frame
183 bits(465)	1e-48()	Compositional matrix adjust.	185/201(92%)	192/201(95%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGSSAEEQTAQEETSEH SKSLPQL	425			
Sbjct	1633	NIFSSQSVNEDNISQEDTRTLSISVPQSIAT NSLLTGSSAEEQTAQEETSE SKSLPQL	1692			
Query	424	TTEESSSfQESSAEENQMTEVPWtlstslsqssSQAKNIFSSPSLNEDNISQEDTRTLSI	245			
Sbjct	1693	TTEESSSfQESSAEENQMTEVPWTLSTSLSS+SSS+ +NIFSS S+NEDNISQEDTRT SI	1752			
Query	244	SV PQSIATANSLLTGSSAEEQTAQEETSEH SKSLPQLTTEESSSfQESSAEENQMTEVPW	65			
Sbjct	1753	SV PQSIATANSLLTGSSAEEQTAQEETSEH SKSLPQLTTEESSSfQESSAEENQMTEVPW	1812			
Query	64	tlstslsqssSQAKNIFSSPS 2				
Sbjct	1813	TL+TSLSQSSS+ KNIFSS S	1833			

Range 37: 4476 to 4676

Score	Expect	Method	Identities	Positives	Gaps	Frame
182 bits(462)	2e-48()	Compositional matrix adjust.	180/201(90%)	186/201(92%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGSSAEEQTAQEETSEH SKSLPQL	425			
Sbjct	4476	NIFSSQSVNEDKTSQEDTRTLSISVPQSIATANSLLTGSSAEEQTAQEETSEH SKSLPQL	4535			
Query	424	TTEESSSfQESSAEENQMTEVPWtlstslsqssSQAKNIFSSPSLNEDNISQEDTRTLSI	245			
Sbjct	4536	TTEESSSfQESSAEENQMTEVPWT+STSLSQS S+ KNIFSS S+NED SQEDTRT SI	4595			
Query	244	SV PQSIATANSLLTGSSAEEQTAQEETSEH SKSLPQLTTEESSSfQESSAEENQMTEVPW	65			
Sbjct	4596	SV PQSIATANSLLTGSSAEEQTAQEETSEH SKSLPQLT EESSSfQ+SSAEE+Q TEVPW	4655			
Query	64	tlstslsqssSQAKNIFSSPS 2				
Sbjct	4656	TLS SLSQSS QAKNIFSSPS	4676			

Range 38: 4573 to 4773

Score	Expect	Method	Identities	Positives	Gaps	Frame
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182 bits(461) 4e-48() Compositional matrix adjust. 181/201(90%) 186/201(92%) 0/201(0%) -2

Features:

Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaaeqtageetsEH	425
Sbjct	4573	NIFSS S+NED SQEDTRT SISVPQSIATANSLLTGSSAEEQTAQEETSE SKSLPQL	4632
Query	424	TTeesssffgessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTL	245
Sbjct	4633	TREESSSFQKSSAEEHQTEVPWTLSISLSQSSSQAKNIFSSPSLNEDNISQEDTRTLPI	4692
Query	244	SVPQSIATANSLLTGssaaeqtageetsEH	65
Sbjct	4693	SVPQSIATA+SLLTGSSAEEQTAQEETSEH	4752
Query	64	tlstslsqssssQAKNIFSSPS 2	
Sbjct	4753	TLSTS SQSSS+ KNIFSS S 4773	

Range 39: 9036 to 9236

Score	Expect	Method	Identities	Positives	Gaps	Frame
181 bits(460) 4e-48() Compositional matrix adjust.	182/201(91%)	185/201(92%)	0/201(0%)	-2		
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaaeqtageetsEH	425			
Sbjct	9036	NIFSS SLNEDNISQEDTRT SISVPQS TAN LLTGS AEEQTAQEETSEH	9095			
Query	424	TTeesssffgessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTL	245			
Sbjct	9096	TTEESSSFQESSAEENQMTEVPWTLSTSLSQSSS+ KNIFSS SLNEDNISQEDTRT SI	9155			
Query	244	SVPQSIATANSLLTGssaaeqtageetsEH	65			
Sbjct	9156	SVPQS TAN LLTGS A+EQTAQEETSE SKSLPQLTTEESSSFQESS EENQMTEVPW	9215			
Query	64	tlstslsqssssQAKNIFSSPS 2				
Sbjct	9216	TLSTSLSQSSS+ KNIFSSPS 9236				

Range 40: 7969 to 8169

Score	Expect	Method	Identities	Positives	Gaps	Frame
181 bits(459) 6e-48() Compositional matrix adjust.	179/201(89%)	183/201(91%)	0/201(0%)	-2		
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaaeqtageetsEH	425			
Sbjct	7969	N FSS SLNED SQEDTRTLSIS PQS TAN LLTGS AEEQTAQEETSE SKSLPQL	8028			
Query	424	TTeesssffgessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTL	245			
Sbjct	8029	TTEESSSFQ+SSAEENQMTEVPWT+ TSLSQSSS KNIFSS S+NED SQEDTRTL	8088			
Query	244	SVPQSIATANSLLTGssaaeqtageetsEH	65			
Sbjct	8089	SVPQSIATANSLLTGSSAEEQTAQEETSE S SLPQLTTEESSSFQ+SSAEENQMTEVPW	8148			
Query	64	tlstslsqssssQAKNIFSSPS 2				
Sbjct	8149	TLSTSLSQSSSQAKNIFSSPS 8169				

Range 41: 7307 to 7507

Score	Expect	Method	Identities	Positives	Gaps	Frame
180 bits(456) 2e-47() Compositional matrix adjust.	184/201(92%)	189/201(94%)	0/201(0%)	-2		
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaaeqtageetsEH	425			
Sbjct	7307	NIFS+ S+NED SQEDTRTLSISVPQSIAT NSLLTGSSAEEQTAQEETSE SKSLPQL	7366			
Query	424	TTeesssffgessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTL	245			
Sbjct	7367	TTEESSSFQ+SSAEENQMTEVPWTLSTSLSQSSS+ KNIFSS SLNEDNISQEDTRTL I	7426			
Query	244	SVPQSIATANSLLTGssaaeqtageetsEH	65			

```
Sbjct 7427 SVPQSIATANSLLTGSSAEEQTAQEETSE SKSLPQLTTEESSSSFQESSAEENQ TEVPW 7486
Query 64 tlstslsqssssQAKNIFSSPS 2
TLSTSLSQSSS+ KNIFSS S
Sbjct 7487 TLSTSLSQSSSKTKNIFSSQS 7507
```

Range 42: 2060 to 2260

Score	Expect	Method	Identities	Positives	Gaps	Frame
179 bits(455)	2e-47()	Compositional matrix adjust.	185/201(92%)	191/201(95%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISV	PQSIATANSLLTGssaeegtaqeetsE	HSKSLPQL		425
Sbjct	2060	NIFSS S+NEDNISQEDTRT SISV	PQSIATANSLLTGSSAEEQTAQEETSE	SKSLPQL		2119
Query	424	TTeesssffqessaeENQMTEVPW	tlstslsqssssQAKNIFSSPSLNEDNISQEDTRTL	SI		245
Sbjct	2120	TTEESSS QESSAEEN+MTEVPW	TLSTSLSQSSS+ KNIFSS S+NEDNISQEDTRT	SI		2179
Query	244	SVPQSIATANSLLTGssaeegtaqeetsE	HSKSLPQLTTeesssffqessaeENQMTEVPW		65	
Sbjct	2180	SVPQSIATANSLLTGSSAEEQTAQEETSE	SKSLPQLTTEESSSSFQESSAEENQMTEVPW		2239	
Query	64	tlstslsqssssQAKNIFSSPS 2				
Sbjct	2240	TL+TSLSQSSS+ KNIFSS S	TLTTSLSQSSSKTKNIFSSQS 2260			

Range 43: 9948 to 10148

Score	Expect	Method	Identities	Positives	Gaps	Frame
179 bits(455)	2e-47()	Compositional matrix adjust.	184/201(92%)	189/201(94%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISV	PQSIATANSLLTGssaeegtaqeetsE	HSKSLPQL		425
Sbjct	9948	NIFSS S+NEDNISQEDTRT SISV	PQSIATANSLLTGSSAEEQTAQEETSE	SKSLPQL		10007
Query	424	TTeesssffqessaeENQMTEVPW	tlstslsqssssQAKNIFSSPSLNEDNISQEDTRTL	SI		245
Sbjct	10008	TTEESSS QESSAEEN+MTEVPW	TLSTSLSQSSS+ KNIFSS S+NEDNISQEDTRT	SI		10067
Query	244	SVPQSIATANSLLTGssaeegtaqeetsE	HSKSLPQLTTeesssffqessaeENQMTEVPW		65	
Sbjct	10068	SVPQSIATANSLLTGSSAEEQTAQEETSE	SKSLPQLTTEESSS QESSAEENQMTEVPW		10127	
Query	64	tlstslsqssssQAKNIFSSPS 2				
Sbjct	10128	TLSTSLSQSSS+ NIFSS S	TLSTSLSQSSSKTMNIFSSQS 10148			

Range 44: 9851 to 10051

Score	Expect	Method	Identities	Positives	Gaps	Frame
178 bits(452)	6e-47()	Compositional matrix adjust.	184/201(92%)	190/201(94%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISV	PQSIATANSLLTGssaeegtaqeetsE	HSKSLPQL		425
Sbjct	9851	NIFSS S+NEDNISQEDTRT SISV	PQSIATANSLLTGSSAEEQTAQEETSE	SKSLPQL		9910
Query	424	TTeesssffqessaeENQMTEVPW	tlstslsqssssQAKNIFSSPSLNEDNISQEDTRTL	SI		245
Sbjct	9911	TTEESSS QESSAEEN+MTEVPW	TLSTSLSQSSS+ KNIFSS S+NEDNISQEDTRT	SI		9970
Query	244	SVPQSIATANSLLTGssaeegtaqeetsE	HSKSLPQLTTeesssffqessaeENQMTEVPW		65	
Sbjct	9971	SVPQSIATANSLLTGSSAEEQTAQEETSE	SKSLPQLTTEESSS QESSAEEN+MTEVPW		10030	
Query	64	tlstslsqssssQAKNIFSSPS 2				
Sbjct	10031	TLSTSLSQSSS+ KNIFSS S	TLSTSLSQSSSKTKNIFSSQS 10051			

Range 45: 1536 to 1736

Score	Expect	Method	Identities	Positives	Gaps	Frame
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178 bits(452) 6e-47() Compositional matrix adjust. 182/201(91%) 190/201(94%) 0/201(0%) -2

Features:

Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeegtaqeetsEH	425
Sbjct	1536	NIFSS S+NED SQEDTRTLSISVPQSIATANSLLTGSSAEEQTAQEETSE S+SLPQL	1595
Query	424	TTeesssffgessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI	245
Sbjct	1596	TTEESSSFFQESSA+EN MTEVPWTLSTSLSQSSS+ KNIFSS S+NEDNISQEDTRTLSI	1655
Query	244	SVPQSIATANSLLTGssaeegtaqeetsEH	65
Sbjct	1656	SVPQSIAT NSLLTGSSAEEQTAQEETSE SKSLPQLTTEESSSFFQESSAEENQMTEVPW	1715
Query	64	tlstslsqssssQAKNIFSSPS 2	
Sbjct	1716	TLSTSLS+SSS+ +NIFSS S	1736

Range 46: 2627 to 2827

Score	Expect	Method	Identities	Positives	Gaps	Frame
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178 bits(451) 6e-47() Compositional matrix adjust. 184/201(92%) 186/201(92%) 0/201(0%) -2

Features:

Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeegtaqeetsEH	425
Sbjct	2627	NIFSS S+NEDNISQEDTRTL ISVPQS TAN LLTGS AEEQTAQEETSEH	2686
Query	424	TTeesssffgessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI	245
Sbjct	2687	TTEESSSFFQESSAEENQMTEVPWTLSTSLSQSSSQAKNIFSS SLNEDNISQEDTRT SI	2746
Query	244	SVPQSIATANSLLTGssaeegtaqeetsEH	65
Sbjct	2747	SVPQS TAN LLTGSSAEE TAQEETSE SKSLPQLTTEESSSFFQESSAEENQMTEVPW	2806
Query	64	tlstslsqssssQAKNIFSSPS 2	
Sbjct	2807	TLSTSLSQSSS+ KNIFSS S	2827

Range 47: 6919 to 7119

Score	Expect	Method	Identities	Positives	Gaps	Frame
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178 bits(451) 8e-47() Compositional matrix adjust. 182/201(91%) 186/201(92%) 0/201(0%) -2

Features:

Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeegtaqeetsEH	425
Sbjct	6919	NIFSS S+NED SQEDTRTLSISVPQSIAT NSLLTGSSAEEQTAQEETSEH	6978
Query	424	TTeesssffgessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI	245
Sbjct	6979	TTEESSSFFQESSAEENQMTEVPWTLSTSLSQSSS+ KNIFSS S+NED SQEDTRTLSI	7038
Query	244	SVPQSIATANSLLTGssaeegtaqeetsEH	65
Sbjct	7039	SVPQSIAT NSLLTGSSAEEQTAQEETSE SKSLPQLTTEESSSFFQESSAEENQ TEVPW	7098
Query	64	tlstslsqssssQAKNIFSSPS 2	
Sbjct	7099	T STS SQSSS+ KNIFSS S	7119

Range 48: 7016 to 7216

Score	Expect	Method	Identities	Positives	Gaps	Frame
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178 bits(451) 8e-47() Compositional matrix adjust. 180/201(90%) 185/201(92%) 0/201(0%) -2

Features:

Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeegtaqeetsEH	425
Sbjct	7016	NIFSS S+NED SQEDTRTLSISVPQSIAT NSLLTGSSAEEQTAQEETSE SKSLPQL	7075
Query	424	TTeesssffgessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI	245
Sbjct	7076	TTEESSSFFQESSAEENQ TEVPWT STS SQSSS+ KNIFSS S+NED SQEDTRTLSI	7135
Query	244	SVPQSIATANSLLTGssaeegtaqeetsEH	65
		SVPQSIAT NSLLTGSSAEEQTAQEETSE SKSLPQLTTEESSSFFQ+SSAEENQMTEVPW	

Sbjct 7136 SVPQSIATTNSLLTGSSAEEQTAQEETSEDSKSLPQLTTEESSSSFQKSSAEENQMTEVPW 7195

Query 64 **tlstslsqss**QAKNIFSSPS 2
TLSTSLSQSSS+ KNIFSS S

Sbjct 7196 TLSTSLSQSSSEPKNIFSSQS 7216

Range 49: 2351 to 2551

Score	Expect	Method	Identities	Positives	Gaps	Frame
178 bits(451)	8e-47()	Compositional matrix adjust.	184/201(92%)	190/201(94%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTG ssaeeqtaqeets EH SKSLPQL				425
Sbjct	2351	NIFSS S+NEDNISQEDTRT SISVPQSIATA SLLTGSSAEEQTAQEETSE SKSLPQL NIFSSLSVNEDNISQEDTRTPSISVPQSIATAKSLLTGSSAEEQTAQEETSEL SKSLPQL				2410
Query	424	T Teesssfqessae ENQMTEVPW tlstslsqss QAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct	2411	TTEESSSFQESSAEENQMTEVPWTLSTS SQSSS+ KNIFSS S+N+DNISQEDTRTLSI TTEESSSFQESSAEENQMTEVPWTLSTSRSQSSSKTKNIFSSQSVNDDNISQEDTRTLSI				2470
Query	244	SVPQSIATANSLLTG ssaeeqtaqeets EH SKSLPQLT Teesssfqessae ENQMTEVPW				65
Sbjct	2471	SVPQSIAT NSLLTGSSAEEQTAQEETSE SKSLPQLTTEESSSFQESSAEENQMTEVPW SVPQSIATTNSLLTGSSAEEQTAQEETSEL SKSLPQLTTEESSSFQESSAEENQMTEVPW				2530
Query	64	tlstslsqss QAKNIFSSPS 2 TL+TSLSQSSS+ KNIFSS S				
Sbjct	2531	TLTTSLSQSSSKTKNIFSSQS 2551				

Range 50: 1245 to 1445

Score	Expect	Method	Identities	Positives	Gaps	Frame
177 bits(450)	9e-47()	Compositional matrix adjust.	184/201(92%)	190/201(94%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTG ssaeeqtaqeets EH SKSLPQL				425
Sbjct	1245	NIFSS S+NEDNISQEDTRTLSISVPQSIATANSLLTGSSAEE TAQEETSE SKSLPQL NIFSSLSVNEDNISQEDTRTLSISVPQSIATANSLLTGSSAEEHTAQEETSEL SKSLPQL				1304
Query	424	T Teesssfqessae ENQMTEVPW tlstslsqss QAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct	1305	TTEESSSFQESSAEENQMTEVPWTL+TSLSQSSS+ KNIFSS S+NEDNISQEDTRT SI TTEESSSFQESSAEENQMTEVPWTLTTSLSQSSSKTKNIFSSLSVNEDNISQEDTRTPSI				1364
Query	244	SVPQSIATANSLLTG ssaeeqtaqeets EH SKSLPQLT Teesssfqessae ENQMTEVPW				65
Sbjct	1365	SVPQSIATANSLLTGSSAEEQTAQEETSE SKSLPQLTTEESSSFQESSA+EN MTEV W SVPQSIATANSLLTGSSAEEQTAQEETSEL SKSLPQLTTEESSSFQESSAKENHMTEVSW				1424
Query	64	tlstslsqss QAKNIFSSPS 2 TLSTSLSQSSS+ KNIFSS S				
Sbjct	1425	TLSTSLSQSSSKTKNIFSSQS 1445				

Range 51: 1730 to 1928

Score	Expect	Method	Identities	Positives	Gaps	Frame
177 bits(449)	1e-46()	Compositional matrix adjust.	182/199(91%)	190/199(95%)	0/199(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTG ssaeeqtaqeets EH SKSLPQL				425
Sbjct	1730	NIFSS S+NEDNISQEDTRT SISVPQSIATANSLLTGSSAEEQTAQEETSE SKSLPQL NIFSSQSVNEDNISQEDTRTPSISVPQSIATANSLLTGSSAEEQTAQEETSEL SKSLPQL				1789
Query	424	T Teesssfqessae ENQMTEVPW tlstslsqss QAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct	1790	TTEESSSFQESSAEENQMTEVPWTL+TSLSQSSS+ KNIFSS S+NEDNISQEDTRT SI TTEESSSFQESSAEENQMTEVPWTLTTSLSQSSSKTKNIFSSQSVNEDNISQEDTRTPSI				1849
Query	244	SVPQSIATANSLLTG ssaeeqtaqeets EH SKSLPQLT Teesssfqessae ENQMTEVPW				65
Sbjct	1850	SVPQSIATANSLLTGSSAEEQTAQEETSE S+SLPQLTTEESSSFQESSA+EN MTEVPW SVPQSIATANSLLTGSSAEEQTAQEETSELSESLPQLTTEESSSFQESSAKENHMTEVPW				1909
Query	64	tlstslsqss QAKNIFSS 8 TLSTSLS+SSS+ KNIFSS				
Sbjct	1910	TLSTSLSKSSSKTKNIFSS 1928				

Range 52: 2157 to 2355

Score	Expect	Method	Identities	Positives	Gaps	Frame
177 bits(449)	1e-46()	Compositional matrix adjust.	182/199(91%)	190/199(95%)	0/199(0%)	-2

Features:

Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaaeqtaqeetsEH	425
Sbjct	2157	NIFSS S+NEDNISQEDTRT SISVPQSIATANSLLTGSSAEEQTAQEETSE SKSLPQL	2216
Query	424	TTeesssffgessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI	245
Sbjct	2217	TTEESSSFFQESSAEENQMTEVPWTL+TSLSQSSS+ KNIFSS S+NEDNISQEDTRT SI	2276
Query	244	SVPQSIATANSLLTGssaaeqtaqeetsEH	65
Sbjct	2277	SVPQSIATANSLLTGSSAEEQTAQEETSE S+SLPQLTTEESSSFFQESSA+EN MTEVPW	2336
Query	64	tlstslsqssssQAKNIFSS	8
Sbjct	2337	TLSTSLS+SSS+ KNIFSS	2355

Range 53: 4088 to 4286

Score	Expect	Method	Identities	Positives	Gaps	Frame
177 bits(448)	2e-46()	Compositional matrix adjust.	181/199(91%)	186/199(93%)	0/199(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaaeqtaqeetsEH SKSLPQL				425
Sbjct	4088	NIFSS S+NED SQEDTRTLSISVPQSIATANSLLTGSSAEEQTAQEETSE SKSLPQL				4147
Query	424	TTeesssffgessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct	4148	TTEESSSFFQESSAEENQ TEVPWTLSTSLSQSSS+ KNIFSS S+NEDNISQEDTRT SI				4207
Query	244	SVPQSIATANSLLTGssaaeqtaqeetsEH SKSLPQLTTeesssffgessaeENQMTEVPW				65
Sbjct	4208	SVPQS TAN LLTGSSAEE TAQEETSE SKSLPQLTTEESSSFFQ+SSAEENQMTEVPW				4267
Query	64	tlstslsqssssQAKNIFSS		8		
Sbjct	4268	TLSTSLSQSSS+AKNIFSS		4286		

Range 54: 5058 to 5258

Score	Expect	Method	Identities	Positives	Gaps	Frame
176 bits(445)	4e-46()	Compositional matrix adjust.	179/201(89%)	184/201(91%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaaeqtaqeetsEH NIFSS S+NED SQEDTRTL ISVPQSIAT NSLLTGSSAEEQTAQEETSEH				425
Sbjct	5058	NIFSSQSVNEDKTSQEDTRTLPI NIFSSQSVNEDKTSQEDTRTLPI				5117
Query	424	TTeesssffgessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI TTEESSSF ESSAEENQ TEVPWTLSTS SQSSS+ KNIFSS S+NED SQEDTRTL I				245
Sbjct	5118	TTEESSSFLESSAEENQTTEVPWTLSTSPSQSSSKTKNIFSSQSVNEDKTSQEDTRTLPI				5177
Query	244	SVPQSIATANSLLTGssaaeqtaqeetsEH SVPQSIATANSLLTGSSAEEQTAQEETS+H SVPQSIATANSLLTGSSAEEQTAQEETSKH				65
Sbjct	5178	SVPQSIATANSLLTGSSAEEQTAQEETS+H SVPQSIATANSLLTGSSAEEQTAQEETSKH				5237
Query	64	tlstslsqssssQAKNIFSSPS		2		
Sbjct	5238	TLSTS SQSSS+ KNIFSS S		5258		

Range 55: 2254 to 2454

Score	Expect	Method	Identities	Positives	Gaps	Frame
175 bits(443)	9e-46()	Compositional matrix adjust.	182/201(91%)	189/201(94%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaaeqtaqeetsEH	SKSLPQL	425		
Sbjct	2254	NIFSS S+NEDNISQEDTRT SISVPQSIATANSLLTGSSAEEQTAQEETSE S+SLPQL		2313		
Query	424	TTeesssffgessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI		245		
Sbjct	2314	TTEESSSFFQESSA+EN MTEVPWTLSTSLS+SSS+ KNIFSS S+NEDNISQEDTRT SI		2373		
Query	244	SVPQSIATANSLLTGssaaeqtaqeetsEH	SKSLPQLTTeesssffgessaeENQMTEVPW	65		
Sbjct	2374	SVPQSIATA SLLTGSSAEEQTAQEETSE SKSLPQLTTEESSSFFQESSAEENQMTEVPW		2433		

Query 64 tlstslsqssssQAKNIFSSPS 2
TLSTS SQSSS+ KNIFSS S
Sbjct 2434 TLSTSRSQSSSKTKNIFSSQS 2454

Range 56: 7598 to 7781

Score	Expect	Method	Identities	Positives	Gaps	Frame
174 bits(442)	1e-45()	Compositional matrix adjust.	169/201(84%)	173/201(86%)	17/201(8%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeegtaqeetsEH				425
Sbjct	7598	NIFSS S+NE+ SQEDTRTLSISVPQSIAT NSLLTGSSAEEQTAQEETSE SKSLPQL				7657
Query	424	TTeesssffqessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTL				245
Sbjct	7658	TTEESSSFFQ+SSAEENQMTE NIFSSPS NEDNISQEDTRTL I				7700
Query	244	SVPQSIATANSLLTGssaeegtaqeetsEH				65
Sbjct	7701	SVPQSIATANSLLTGSSAEEQTAQEETSEH				7760
Query	64	tlstslsqssssQAKNIFSSPS 2				
Sbjct	7761	T+ TSLSQSSS KNIFSS S				

Range 57: 1439 to 1639

Score	Expect	Method	Identities	Positives	Gaps	Frame
174 bits(442)	1e-45()	Compositional matrix adjust.	182/201(91%)	190/201(94%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeegtaqeetsEH				425
Sbjct	1439	NIFSS S+N+DNISQEDTRT SISVPQSIATANSLLTGSSAEEQTAQEETSE SKSLPQL				1498
Query	424	TTeesssffqessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTL				245
Sbjct	1499	TTEESSSFFQESSAEENQMTEVPWTL+TSLSQSSS+ KNIFSS S+NED SQEDTRTL				1558
Query	244	SVPQSIATANSLLTGssaeegtaqeetsEH				65
Sbjct	1559	SVPQSIATANSLLTGSSAEEQTAQEETSE S+SLPQLTTEESSSFFQESSA+EN MTEVPW				1618
Query	64	tlstslsqssssQAKNIFSSPS 2				
Sbjct	1619	TLSTSLSQSSS+ KNIFSS S				

Range 58: 6319 to 6559

Score	Expect	Method	Identities	Positives	Gaps	Frame
174 bits(441)	1e-45()	Compositional matrix adjust.	187/241(78%)	190/241(78%)	40/241(16%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeegtaqeetsEH				425
Sbjct	6319	NIFSS S+NED SQEDTRTL ISVPQSIAT NSLLTGSSAEEQTAQEETSEH				6378
Query	424	TTeesssffqessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTL				245
Sbjct	6379	TTEESSSFFQESSAEENQMTEVPWTLSTSLSQSS QAKNIFSSP+LNEDNISQEDTRTL				6438
Query	244	SVPQSIATANS-----LLTGssae				185
Sbjct	6439	SVPQSIATANS LLTGS AEE				6498
Query	184	gtaqeetsEH				5
Sbjct	6499	QTAQEETSEH				6558
Query	4	S 2				
Sbjct	6559	S 6559				

Range 59: 4961 to 5161

Score	Expect	Method	Identities	Positives	Gaps	Frame
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174 bits(441) 2e-45() Compositional matrix adjust. 179/201(89%) 183/201(91%) 0/201(0%) -2

Features:

Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeegtaqeetsEHKSLPQL	425
Sbjct	4961	NIFSS SLNED SQEDTRT SISVPQSIATA+SLLTGSSAEEQTAQEETSEHKSLLPQL NIFSSQSLNEDKTSQEDTRTPSISVPQSIATAHSLLTGSSAEEQTAQEETSEHKSLLPQL	5020
Query	424	TTeesssffgessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI	245
Sbjct	5021	TTEESSSF ESSAEENQ TEVPWTLSTS SQSSS+ KNIFSS S+NED SQEDTRTL I TTEESSSFLESSAEENQTTEVPWTLSTSPSQSSSKTKNIFSSQSVNEDKTSQEDTRTLPI	5080
Query	244	SVPQSIATANSLLTGssaeegtaqeetsEHKSLPQLTTeesssffgessaeENQMTEVPW	65
Sbjct	5081	SVPQSIAT NSLLTGSSAEEQTAQEETSEHKSLLPQLTTEESSSF ESSAEENQ TEVPW SVPQSIATTNSLLTGSSAEEQTAQEETSEHKSLLPQLTTEESSSFLESSAEENQTTEVPW	5140
Query	64	tlstslsqssssQAKNIFSSPS 2	
Sbjct	5141	TLSTS SQSSS+ KNIFSS S TLSTSPSQSSSKTKNIFSSQS 5161	

Range 60: 6650 to 6808

Score	Expect	Method	Identities	Positives	Gaps	Frame
174 bits(441)	2e-45()	Compositional matrix adjust.	151/159(95%)	152/159(95%)	0/159(0%)	-2

Features:

Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeegtaqeetsEHKSLPQL	425
Sbjct	6650	NIFSS SLNEDNISQEDTRTL ISVPQSIATANSLLTGSSAEEQTAQEETSEHKSLLPQL NIFSSQSLNEDNISQEDTRTLPI SVVPQSIATANSLLTGSSAEEQTAQEETSEHKSLLPQL	6709
Query	424	TTeesssffgessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI	245
Sbjct	6710	TTEESSSFQESSAEENQ TEVPWTLSTS SQSSS+ KNIFSSPSLNEDNISQEDTRTL I TTEESSSFQESSAEENQTTEVPWTLSTSPSQSSSKTKNIFSSPSLNEDNISQEDTRTLPI	6769
Query	244	SVPQSIATANSLLTGssaeegtaqeetsEHKSLPQLTT	128
Sbjct	6770	SVPQSIATANSLLTGSSAEEQTAQEETSE SKSLPQLTT SVPQSIATANSLLTGSSAEEQTAQEETSESKSLPQLTT	6808

Range 61: 1342 to 1540

Score	Expect	Method	Identities	Positives	Gaps	Frame
173 bits(439)	3e-45()	Compositional matrix adjust.	182/199(91%)	189/199(94%)	0/199(0%)	-2

Features:

Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeegtaqeetsEHKSLPQL	425
Sbjct	1342	NIFSS S+NEDNISQEDTRT SISVPQSIATANSLLTGSSAEEQTAQEETSE SKSLPQL NIFSSLSVNEDNISQEDTRTPSISVPQSIATANSLLTGSSAEEQTAQEETSELSKSLPQL	1401
Query	424	TTeesssffgessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI	245
Sbjct	1402	TTEESSSFQESSA+EN MTEV WTLSTSLSQSSS+ KNIFSS S+N+DNISQEDTRT SI TTEESSSFQESSAKENHMTESVWTLSTSLSQSSSKTKNIFSSQSVNDDNISQEDTRTPSI	1461
Query	244	SVPQSIATANSLLTGssaeegtaqeetsEHKSLPQLTTeesssffgessaeENQMTEVPW	65
Sbjct	1462	SVPQSIATANSLLTGSSAEEQTAQEETSE SKSLPQLTTEESSSFQESSAEENQMTEVPW SVPQSIATANSLLTGSSAEEQTAQEETSELSKSLPQLTTEESSSFQESSAEENQMTEVPW	1521
Query	64	tlstslsqssssQAKNIFSS 8	
Sbjct	1522	TL+TSLSQSSS+ KNIFSS TLTTSLSQSSSKTKNIFSS 1540	

Range 62: 7404 to 7604

Score	Expect	Method	Identities	Positives	Gaps	Frame
173 bits(439)	3e-45()	Compositional matrix adjust.	181/201(90%)	185/201(92%)	0/201(0%)	-2

Features:

Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeegtaqeetsEHKSLPQL	425
Sbjct	7404	NIFSS SLNEDNISQEDTRTL ISVPQSIATANSLLTGSSAEEQTAQEETSE SKSLPQL NIFSSQSLNEDNISQEDTRTLPI SVVPQSIATANSLLTGSSAEEQTAQEETSELSKSLPQL	7463
Query	424	TTeesssffgessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI	245
Sbjct	7464	TTEESSSFQESSAEENQ TEVPWTLSTSLSQSSS+ KNIFSS S+NED SQEDTRT SI TTEESSSFQESSAEENQTTEVPWTLSTSLSQSSSKTKNIFSSQSVNEDKTSQEDTRTPSI	7523
Query	244	SVPQSIATANSLLTGssaeegtaqeetsEHKSLPQLTTeesssffgessaeENQMTEVPW	65
Sbjct	7524	SVPQS ATAN LLTGSSA+EQTAQEETSEHKSLLPQLTTEESSSFQESSAEENQ TEVPW SVPQSSATANRLLTGSSAKEQTAQEETSEHKSLLPQLTTEESSSFQESSAEENQTTEVPW	7583
Query	64	tlstslsqssssQAKNIFSSPS 2	
		T STS SQSSS+ KNIFSS S	

Sbjct 7584 TPSTSPSQSSSKTKNIFSSQS 7604

Range 63: 3118 to 3318

Score	Expect	Method	Identities	Positives	Gaps	Frame
172 bits(436)	8e-45()	Compositional matrix adjust.	179/201(89%)	185/201(92%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeegtaqeetsEHSKSLPQL				425
Sbjct	3118	NIFSS S+NEDNISQEDTRT SISVPQS TAN LLTGSSAEE TAQEETSE SKSLPQL				
Query	424	TTeesssfgessaeENQMTEVPWtlstslsqsssQAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct	3178	TTEESSSFQESSAEE+Q TEVPWTLSTSLSQSSS+AKNIFSS S+NEDNISQEDTRTL I				3237
Query	244	SVPQSIATANSLLTGssaeegtaqeetsEHSKSLPQLTTeesssfgessaeENQMTEVPW				65
Sbjct	3238	SVPOS TAN LLTGS AEEQTAQEETSEHSKSLPQLTTEESSSFQESSAEE+Q TEVPW				3297
Query	64	tlstslsqsssQAKNIFSSPS 2				
Sbjct	3298	TLSTSLSQSSS+AKNIFSS S TLSTSLSQSSSEAKNIFSSQS 3318				

Range 64: 10045 to 10243

Score	Expect	Method	Identities	Positives	Gaps	Frame
171 bits(434)	1e-44()	Compositional matrix adjust.	179/199(90%)	184/199(92%)	0/199(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeegtaqeetsEHSKSLPQL				425
Sbjct	10045	NIFSS S+NEDNISQEDTRT SISVPQSIATANSLLTGSSAEEQTAQEETSE SKSLPQL				
Query	424	TTeesssfgessaeENQMTEVPWtlstslsqsssQAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct	10105	TTEESSS QESSAEEENQMTEVPWTLSTSLSQSSS+ NIFSS S+ ED QEDTRT SI				10164
Query	244	SVPQSIATANSLLTGssaeegtaqeetsEHSKSLPQLTTeesssfgessaeENQMTEVPW				65
Sbjct	10165	SVPQSIATANSLLTGSSAEEQTAQEETSE SKSLPQLTTEESSSFQESSAE+NQMTEVPW				10224
Query	64	tlstslsqsssQAKNIFSS 8				
Sbjct	10225	TLSTSLSQSSS+ NIFSS TLSTSLSQSSSKTMNIFSS 10243				

Range 65: 3021 to 3221

Score	Expect	Method	Identities	Positives	Gaps	Frame
171 bits(434)	1e-44()	Compositional matrix adjust.	179/201(89%)	185/201(92%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeegtaqeetsEHSKSLPQL				425
Sbjct	3021	NIFSS S+NEDNISQEDTRTL ISVPQS TAN LLTGS AEEQTAQEETSEHSKSLPQL				
Query	424	TTeesssfgessaeENQMTEVPWtlstslsqsssQAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct	3081	TTEESSSFQESSAEE+Q TEVPWTLSTSLSQSSS+AKNIFSS S+NEDNISQEDTRT SI				3140
Query	244	SVPQSIATANSLLTGssaeegtaqeetsEHSKSLPQLTTeesssfgessaeENQMTEVPW				65
Sbjct	3141	SVPOS TAN LLTGSSAEE TAQEETSE SKSLPQLTTEESSSFQESSAEE+Q TEVPW				3200
Query	64	tlstslsqsssQAKNIFSSPS 2				
Sbjct	3201	TLSTSLSQSSS+AKNIFSS S TLSTSLSQSSSEAKNIFSSQS 3221				

Range 66: 3409 to 3609

Score	Expect	Method	Identities	Positives	Gaps	Frame
171 bits(432)	2e-44()	Compositional matrix adjust.	180/201(90%)	184/201(91%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeegtaqeetsEHSKSLPQL				425

Sbjct	3409	NIFSS S+NEDNISQEDTRT SISVPQS TAN LLTGSSAEE TAQEETSE SKSLPQL NIFSSQSVNEDNISQEDTRTPSISVPQSSTTANRLLTGSSAEEPTAQEETSELSKSLPQL	3468
Query	424	TTeesssffqessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTL SI TTEESSSFQESSAEENQMTEVPWTLSTSLSQSSS+ KNIFSS S+NEDNISQEDTRT SI	245
Sbjct	3469	TTEESSSFQESSAEENQMTEVPWTLSTSLSQSSSKTKNIFSSQSVNEDNISQEDTRTPSI	3528
Query	244	SVPQSIATANSLLTGssaeegtaqeetsEHKSLPQLTTeesssffqessaeENQMTEVPW SVPQS TAN LLTGSAEE TAQEETSE SKSLPQLTTEESSSFQESSAEENQMTEVPW	65
Sbjct	3529	SVPQSSTTANRLLTGSGAEEPTAQEETSELSKSLPQLTTEESSSFQESSAEENQMTEVPW	3588
Query	64	tlstslsqssssQAKNIFSSPS 2 TLSTSLSQSSS+AKNIFSS S	
Sbjct	3589	TLSTSLSQSSSEAKNIFSSQS 3609	

Range 67: 3215 to 3415

Score	Expect	Method	Identities	Positives	Gaps	Frame
170 bits(431)	3e-44()	Compositional matrix adjust.	179/201(89%)	184/201(91%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeegtaqeetsEHKSLPQL				425
Sbjct	3215	NIFSS S+NEDNISQEDTRTL ISVPQS TAN LLTGS AEEQTAQEETSEHSLPQL NIFSSQSVNEDNISQEDTRTLPISVPQSSTTANRLLTGSAEEQTAQEETSEHSLPQL				3274
Query	424	TTeesssffqessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct	3275	TTEESSSFQESSAEE+Q TEVPWTLSTSLSQSSS+AKNIFSS S+NEDNISQEDTRT SI TTEESSSFQESSAEEHQTEVPWTLSTSLSQSSSEAKNIFSSQSVNEDNISQEDTRTPSI				3334
Query	244	SVPQSIATANSLLTGssaeegtaqeetsEHKSLPQLTTeesssffqessaeENQMTEVPW				65
Sbjct	3335	SVPQS TAN LLTGSSAEE TAQEETSE SKSLPQLT EESSSFQESSAEENQMTEVPW SVPQSSTTANRLLTGSSAEEPTAQEETSELSKSLPQLTAEESSSFQESSAEENQMTEVPW				3394
Query	64	tlstslsqssssQAKNIFSSPS		2		
		TLSTSLSQSSS+ KNIFSS S				
Sbjct	3395	TLSTSLSQSSSKTKNIFSSQS		3415		

Range 68: 4282 to 4482

Score	Expect	Method	Identities	Positives	Gaps	Frame
170 bits(430)	4e-44()	Compositional matrix adjust.	176/201(88%)	182/201(90%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeegtaqeetsEHKSLPQL				425
Sbjct	4282	NIFSS +NED SQEDTRT SISVPQS TANSLLTGSSAEEQTAQEETSE SKSLPQL NIFSSQIVNEDKTSQEDTRTPSISVPQSSTTANSLLTGSSAEEQTAQEETSELSKSLPQL				4341
Query	424	TTeesssffqessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct	4342	TTEESSSFQESSAEENQ TEVPWT+ TSLSQSSS+ KNIFSS S+NED SQEDTRTL I				4401
Query	244	SVPQSIATANSLLTGssaeegtaqeetsEHKSLPQLTTeesssffqessaeENQMTEVPW				65
Sbjct	4402	SVPQSIATANSLLTGSSAEEQTAQEETSE SKSLPQLTTEESSSFQESSAEENQMTEVPW				4461
Query	64	tlstslsqssssQAKNIFSSPS		2		
Sbjct	4462	T+STSLSQS S+ KNIFSS S				
		TVSTSLSQSRSKTKNIFSSQS		4482		

Range 69: 6828 to 7022

Score	Expect	Method	Identities	Positives	Gaps	Frame
169 bits(428)	9e-44()	Compositional matrix adjust.	177/195(91%)	181/195(92%)	0/195(0%)	-2
Features:						
Query	586	SLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeegtaqeetsEHKSLPQLTTeess				407
Sbjct	6828	S+NED SQEDTRTLSISVPQSIAT NSLLTGSSAEEQTAQEETSE SKSLPQLTTEESS SVNEDKTSQEDTRTLSISVPQSIATTNSLLTGSSAEEQTAQEETSEDSKSLPQLTTEESS				6887
Query	406	sfqessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSISVPQSI				227
Sbjct	6888	SFQESSAEENQ TEVPWT STS SQSSS+ KNIFSS S+NED SQEDTRTLSISVPQSI SFQESSAEENQTEVPWTPSTSPSQSSSKTKNIFSSQSVNEDKTSQEDTRTLSISVPQSI				6947
Query	226	ATANSLLTGssaeegtaqeetsEHKSLPQLTTeesssfqessaeENQMTEVPWtlstsl				47
Sbjct	6948	AT NSLLTGSSAEEQTAQEETSEHSLPQLTTEESSSFQESSAEENQMTEVPWTLSTSL ATTNSLLTGSSAEEQTAQEETSEHSLPQLTTEESSSFQESSAEENQMTEVPWTLSTSL				7007
Query	46	sqssssQAKNIFSSPS 2				
Sbjct	7008	SQSSS+ KNIFSS S SQSSSKTKNIFSSQS 7022				

Range 70: 4185 to 4385

Score	Expect	Method	Identities	Positives	Gaps	Frame
168 bits(426)	1e-43()	Compositional matrix adjust.	176/201(88%)	182/201(90%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaaeeqtaqeetsEHSKSLPQL				425
Sbjct	4185	NIFSS S+NEDNISQEDTRT SISVPQS TAN LLTGSSAEE TAQEETSE SKSLPQL				4244
Query	424	TTeesssffgessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct	4245	TTEESSSSFQ+SSAEENQMTEVPWTLSTLSQSSS+AKNIFSS +NED SQEDTRT SI				4304
Query	244	SVPQSIATANSLLTGssaaeeqtaqeetsEHSKSLPQLTTeesssffgessaeENQMTEVPW				65
Sbjct	4305	SVPQS TANSLLTGSSAEEQTAQEETSE SKSLPQLTTEESSSSFQESSAEENQ TEVPW				4364
Query	64	tlstslsqssssQAKNIFSSPS 2				
Sbjct	4365	T+ TSLSQSSS+ KNIFSS S				
		TVLTSLSQSSSKTKNIFSSQS 4385				

Range 71: 3894 to 4094

Score	Expect	Method	Identities	Positives	Gaps	Frame
168 bits(425)	2e-43()	Compositional matrix adjust.	176/201(88%)	183/201(91%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaaeeqtaqeetsEHSKSLPQL				425
Sbjct	3894	NIFSS S+NED ISQEDTRTLSISV QS TAN LLTGS AEEQTAQEETSE SKSLPQL				3953
Query	424	TTeesssffgessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct	3954	TTEESSSSFQ+SSAEENQMTEVPWTLSTLSQSSS+AKNIFSS +NED SQEDTRT SI				4013
Query	244	SVPQSIATANSLLTGssaaeeqtaqeetsEHSKSLPQLTTeesssffgessaeENQMTEVPW				65
Sbjct	4014	SVPQS TANSLLTGSSAEEQTAQEETSE SKSLPQLTTEESSSSFQ+SSAEENQMTEVPW				4073
Query	64	tlstslsqssssQAKNIFSSPS 2				
Sbjct	4074	T+STSLSQSSS+ KNIFSS S				
		TVSTSLSQSSSKTKNIFSSQS 4094				

Range 72: 3991 to 4191

Score	Expect	Method	Identities	Positives	Gaps	Frame
168 bits(425)	2e-43()	Compositional matrix adjust.	179/201(89%)	185/201(92%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaaeeqtaqeetsEHSKSLPQL				425
Sbjct	3991	NIFSS +NED SQEDTRT SISVPQS TANSLLTGSSAEEQTAQEETSE SKSLPQL				4050
Query	424	TTeesssffgessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct	4051	TTEESSSSFQ+SSAEENQMTEVPWT+STSLSQSSS+ KNIFSS S+NED SQEDTRTLSI				4110
Query	244	SVPQSIATANSLLTGssaaeeqtaqeetsEHSKSLPQLTTeesssffgessaeENQMTEVPW				65
Sbjct	4111	SVPQSIATANSLLTGSSAEEQTAQEETSE SKSLPQLTTEESSSSFQESSAEENQ TEVPW				4170
Query	64	tlstslsqssssQAKNIFSSPS 2				
Sbjct	4171	TLSTSLSQSSS+ KNIFSS S				
		TLSTSLSQSSSKTKNIFSSQS 4191				

Range 73: 2918 to 3124

Score	Expect	Method	Identities	Positives	Gaps	Frame
166 bits(421)	7e-43()	Compositional matrix adjust.	178/207(86%)	187/207(90%)	6/207(2%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQS-----IATANSLLTGssaaeeqtaqeetsEHS				443
Sbjct	2918	NIFSS S+NEDNISQEDTRTL ISVPQS + TANSLLTGSSAEEQTAQEETSE S				2977
		NIFSSQSVNEDNISQEDTRTLPI SVPQSSTTANRLLTANSLLTGSSAEEQTAQEETSELS				

Query	442	KSLPQLTTeesssfqessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQED	263
Sbjct	2978	+SLPQLTTEESSSFQESSA+EN MTEVPWTLSTSL+SSS+ KNIFSS S+NEDNISQED ESLPQLTTEESSSFQESSAKENHMTTEVPWTLSTSLSKSSSKTKNIFSSSLSVNEDNISQED	3037
Query	262	TRTLSISVPQSIATANSLLTGssaeeqtagaetsEHSKSLPQLTTeesssfqessaeENQ	83
Sbjct	3038	TRTL ISVPQS TAN LLTGS AEEQTAQEETSEHSKSLPQLTTEESSSFQESSAEE+Q TRTLPISVPQSSTTANRLLTGSI AEEQTAQEETSEHSKSLPQLTTEESSSFQESSAEEHQ	3097
Query	82	MTEVPWtlstslsqssssQAKNIFSSPS	2
Sbjct	3098	TEVPWTLSTSLSQSSS+AKNIFSS S TTEVPWTLSTSLSQSSSEAKNIFSSQS	3124

Range 74: 2545 to 2730

Score	Expect	Method	Identities	Positives	Gaps	Frame
<hr/>						
165 bits(418)	2e-42()	Compositional matrix adjust.	167/201(83%)	172/201(85%)	15/201(7%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeeqtagaetsEHSKSLPQL				425
Sbjct	2545	NIFSS S+NEDNISQEDTRT SISVPQSIATANSLL GSSAEEQTAQEETSE SKSLPQL NIFSSQSVNEDNISQEDTRTPSISVPQSIATANSLLAGSSAEEQTAQEETSELSKSLPQL				2604
Query	424	TTeesssfqessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct	2605	TTEESSSFQ+ SAEENQ ++ KNIFSS S+NEDNISQEDTRTL I TTEESSSFQKFSAEENQSSKT-----KNIFSSQSVNEDNISQEDTRTLP I				2649
Query	244	SVQSIATANSLLTGssaeeqtagaetsEHSKSLPQLTTeesssfqessaeENQMTEVPW				65
Sbjct	2650	SVPOS TAN LLTGS AEEQTAQEETSEHSKSLPQLTTEESSSFQESSAEEENQMTEVPW SVPQSSTTANRLLTGSI AEEQTAQEETSEHSKSLPQLTTEESSSFQESSAEEENQMTEVPW				2709
Query	64	tlstslsqssssQAKNIFSSPS				2
Sbjct	2710	TLSTSLSQSSSQAKNIFSS S TLSTSLSQSSSQAKNIFSSOS				2730

Range 75: 3603 to 3803

Score	Expect	Method	Identities	Positives	Gaps	Frame
164 bits(416)	3e-42()	Compositional matrix adjust.	174/201(87%)	181/201(90%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeeqtagaetsEHSKSLPQL NIFSS S+N+D SQEDTRT SISVPQS TAN LLTGSSAEE TAQEETSEHSKSLPQL				425
Sbjct	3603	NIFSSQSVNDDKTSQEDTRTPSISVPQSSTTANRLLTGSSAEEPTAQEETSEHSKSLPQL				3662
Query	424	TTeesssfqessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI TTEESSSFQESSAEE+Q TEVPWTLSTS SQSSS+ KNIFSS S+NED ISQEDTRTLSI				245
Sbjct	3663	TTEESSSFQESSAEEHQTEVPWTLSTSPSQSSSKTKNIFSSQSVNEDKISQEDTRTLSI				3722
Query	244	SVPQSIATANSLLTGssaeeqtagaetsEHSKSLPQLTTeesssfqessaeENQMTEVPW SV QS TAN LLTGS AEEQTAQEETSE SKSLPQLTTEESSSFQ+SSAEEENQMTEVPW				65
Sbjct	3723	SVSQSSTTANRLLTGSI AEEQTAQEETSELSKSLPQLTTEESSSFQKSSAEEENQMTEVPW				3782
Query	64	tlstslsqssssQAKNIFSSPS		2		
		TLSTSLSQSSS+AKNIFSS S				
Sbjct	3783	TLSTSLSQSSSEAKNIFSSQS		3803		

Range 76: 2724 to 2924

Score	Expect	Method	Identities	Positives	Gaps	Frame
164 bits(416)	3e-42()	Compositional matrix adjust.	179/201(89%)	183/201(91%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeeqtagaetsEHSKSLPQL				425
Sbjct	2724	NIFSS SLNEDNISQEDTRT SISVPQS TAN LLTGSSAEE TAQEETSE SKSLPQL NIFSSQSLNEDNISQEDTRTPSISVPQSSTTANRLLTGSSAEEPTAQEETSELSKSLPQL				2783
Query	424	TTeesssfqessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct	2784	TTEESSSFQESSAEEENQMTEVPWTLSTSLSQSSS+ KNIFSS S+NEDNISQEDTRT SI TTEESSSFQESSAEEENQMTEVPWTLSTSLSQSSSKTKNIFSSQSVNEDNISQEDTRTPSI				2843
Query	244	SVQSIATANSLLTGssaeeqtagaetsEHSKSLPQLTTeesssfqessaeENQMTEVPW				65
Sbjct	2844	SVPOS TAN LLTGSSAEE TAQEETSE SKSLPQLTTEESSSFQESSAEE+Q TEVPW SVPQSSTTANRLLTGSSAEEPTAQEETSELSKSLPQLTTEESSSFQESSAEEHQTEVPW				2903
Query	64	tlstslsqssssQAKNIFSSPS		2		
Sbjct	2904	TLSTSLSQSSS+ KNIFSS S				
		TLSTSLSQSSSEPKNIFSSQS		2924		

Range 77: 3506 to 3706

Score	Expect	Method	Identities	Positives	Gaps	Frame
164 bits(416)	3e-42()	Compositional matrix adjust.	175/201(87%)	181/201(90%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaaeqtaqeetsEH	SKSLPQL	425		
Sbjct	3506	NIFSS S+NEDNISQEDTRT SISVPQS TAN LLTGS AEE TAQEETSE SKSLPQL		3565		
Query	424	TTEesssffqessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTL	SI	245		
Sbjct	3566	TTEESSSFFQESSAEENQMTEVPWTLSTSLSQSSS+AKNIFSS S+N+D SQEDTRT SI		3625		
Query	244	SVPQSIATANSLLTGssaaeqtaqeetsEH	SKSLPQLTTEesssffqessaeENQMTEVPW	65		
Sbjct	3626	SVPQS TAN LLTGSSAEE TAQEETSEH	SKSLPQLTTEESSSFFQESSAEE+Q TEVPW	3685		
Query	64	tlstslsqssssQAKNIFSSPS	2			
Sbjct	3686	TLSTS SQSSS+ KNIFSS S	3706			

Range 78: 3312 to 3512

Score	Expect	Method	Identities	Positives	Gaps	Frame
164 bits(416)	3e-42()	Compositional matrix adjust.	179/201(89%)	183/201(91%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaaeqtaqeetsEH	SKSLPQL	425		
Sbjct	3312	NIFSS S+NEDNISQEDTRT SISVPQS TAN LLTGSSAEE TAQEETSE SKSLPQL		3371		
Query	424	TTEesssffqessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTL	SI	245		
Sbjct	3372	T EESSSFFQESSAEENQMTEVPWTLSTSLSQSSS+ KNIFSS S+NEDNISQEDTRT SI		3431		
Query	244	SVPQSIATANSLLTGssaaeqtaqeetsEH	SKSLPQLTTEesssffqessaeENQMTEVPW	65		
Sbjct	3432	SVPQS TAN LLTGSSAEE TAQEETSE SKSLPQLTTEESSSFFQESSAEENQMTEVPW		3491		
Query	64	tlstslsqssssQAKNIFSSPS	2			
Sbjct	3492	TLSTSLSQSSS+ KNIFSS S	3512			

Range 79: 3700 to 3900

Score	Expect	Method	Identities	Positives	Gaps	Frame
164 bits(415)	5e-42()	Compositional matrix adjust.	174/201(87%)	182/201(90%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaaeqtaqeetsEH	SKSLPQL	425		
Sbjct	3700	NIFSS S+NED ISQEDTRTLSISV QS TAN LLTGS AEEQTAQEETSE SKSLPQL		3759		
Query	424	TTEesssffqessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTL	SI	245		
Sbjct	3760	TTEESSSFFQ+SSAEENQMTEVPWTLSTSLSQSSS+AKNIFSS S+N+D SQEDTRT SI		3819		
Query	244	SVPQSIATANSLLTGssaaeqtaqeetsEH	SKSLPQLTTEesssffqessaeENQMTEVPW	65		
Sbjct	3820	SVPQS TANSLLTGSSAEEQTAQEETSE SKSLPQLTTEESSSFFQ+SSAEE+Q TEVPW		3879		
Query	64	tlstslsqssssQAKNIFSSPS	2			
Sbjct	3880	TLSTS SQSSS+ KNIFSS S	3900			

Range 80: 3797 to 3995

Score	Expect	Method	Identities	Positives	Gaps	Frame
163 bits(413)	7e-42()	Compositional matrix adjust.	173/199(87%)	181/199(90%)	0/199(0%)	-2

Features:

Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaaeqtaqeetsEH	SKSLPQL	425		
Sbjct	3797	NIFSS S+N+D SQEDTRT SISVPQS TANSLLTGSSAEEQTAQEETSE SKSLPQL		3856		
Query	424	TTEesssffqessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTL	SI	245		

Sbjct	3857	TTEESSSSFQ+SSAEE+Q TEVPWTLSTS SQSSS+ KNIFSS S+NED ISQEDTRTLSI	3916
Query	244	SV PQSIATANSLLTGssaeeqtaqeetsEH SKSLPQLTTeesssfqessaeENQMTEVPW	65
Sbjct	3917	SV QS TAN LLTGS AEEQTAQEETSE SKSLPQLTTEESSSSFQ+SSAEENQMTEVPW	3976
		SVSQSSTTANRLLTGSI AEEQTAQEETSELSKSLPQLTTEESSSSFQKSSAEENQMTEVPW	
Query	64	tlstslsqssssQAKNIFSS 8	
		TLSTSLSQSSS+AKNIFSS	
Sbjct	3977	TLSTSLSQSSSEAKNIFSS 3995	

Range 81: 2448 to 2633

Score	Expect	Method	Identities	Positives	Gaps	Frame
162 bits(410)	2e-41()	Compositional matrix adjust.	166/201(83%)	174/201(86%)	15/201(7%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeeqtaqeetsEH SKSLPQL				425
Sbjct	2448	NIFSS S+N+DNISQEDTRTLSISVPQSIAT NSLLTGSSAEEQTAQEETSE SKSLPQL				2507
		NIFSSQSVNDDNISQEDTRTLSISVPQSIATTNSLLTGSSAEEQTAQEETSELSKSLPQL				
Query	424	TTeesssfqessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct	2508	TTEESSSFQESSAEENQMTEVPWTL+TSLSQSSS+ KNIFSS S+NEDNISQEDTRT SI				2567
		TTEESSSFQESSAEENQMTEVPWTLTTSLSQSSSKTKNIFSSQSVNEDNISQEDTRTPSI				
Query	244	SV PQSIATANSLLTGssaeeqtaqeetsEH SKSLPQLTTeesssfqessaeENQMTEVPW				65
Sbjct	2568	SV PQSIATANSLL GSSAEEQTAQEETSE SKSLPQLTTEESSSSFQ+ SAEENQ ++				2625
		SV PQSIATANSLLAGSSAEEQTAQEETSELSKSLPQLTTEESSSSFQKFAEENQSSKT--				
Query	64	tlstslsqssssQAKNIFSSPS 2				
		KNIFSS S				
Sbjct	2626	-----KNIFSSQS 2633				

Range 82: 7501 to 7684

Score	Expect	Method	Identities	Positives	Gaps	Frame
160 bits(406)	7e-41()	Compositional matrix adjust.	163/201(81%)	169/201(84%)	17/201(8%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeeqtaqeetsEH SKSLPQL				425
Sbjct	7501	NIFSS S+NED SQEDTRT SISVPQS ATAN LLTGSSA+EQTAQEETSEH SKSLPQL				7560
		NIFSSQSVNEDKTSQEDTRTPSISVPQSSATANRLLTGSSAKEQTAQEETSEH SKSLPQL				
Query	424	TTeesssfqessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct	7561	TTEESSSFQESSAEENQ TEVPWT STS SQSSS+ KNIFSS S+NE+ SQEDTRTLSI				7620
		TTEESSSFQESSAEENQTEVPWTPSTSPSQSSSKTKNIFSSQSVNEEKTSQEDTRTLSI				
Query	244	SV PQSIATANSLLTGssaeeqtaqeetsEH SKSLPQLTTeesssfqessaeENQMTEVPW				65
Sbjct	7621	SV PQSIAT NSLLTGSSAEEQTAQEETSE SKSLPQLTTEESSSSFQ+SSAEENQMTE				7677
		SV PQSIATTNSLLTGSSAEEQTAQEETSEDSKSLPQLTTEESSSSFQKSSAEENQMTE---				
Query	64	tlstslsqssssQAKNIFSSPS 2				
		NIFSSPS				
Sbjct	7678	-----NIFSSPS 7684				

Range 83: 2821 to 3025

Score	Expect	Method	Identities	Positives	Gaps	Frame
158 bits(399)	6e-40()	Compositional matrix adjust.	175/205(85%)	184/205(89%)	6/205(2%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeeqtaqeetsEH SKSLPQL				425
Sbjct	2821	NIFSS S+NEDNISQEDTRT SISVPQS TAN LLTGSSAEE TAQEETSE SKSLPQL				2880
		NIFSSQSVNEDNISQEDTRTPSISVPQSSTTANRLLTGSSAEEPTAQEETSELSKSLPQL				
Query	424	TTeesssfqessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct	2881	TTEESSSFQESSAEE+Q TEVPWTLSTSLSQSSS+ KNIFSS S+NEDNISQEDTRTL I				2940
		TTEESSSFQESSAEEHQTEVPWTLSTSLSQSSSEPKNIFSSQSVNEDNISQEDTRTLPI				
Query	244	SV PQS-----IATANSLLTGssaeeqtaqeetsEH SKSLPQLTTeesssfqessaeENQ				83
Sbjct	2941	SV PQS + TANSLLTGSSAEEQTAQEETSE S+SLPQLTTEESSSFQESSA+EN				3000
		SV PQSSTTANRLLTANSLLTGSSAEEQTAQEETSELSKSLPQLTTEESSSFQESSAKENH				
Query	82	MTEVPWtlstslsqssssQAKNIFSS 8				
		MTEVPWTLSTSLS+SSS+ KNIFSS				
Sbjct	3001	MTEVPWTLSTSLSKSSSKTKNIFSS 3025				

Range 84: 1924 to 2163

Score	Expect	Method	Identities	Positives	Gaps	Frame
157 bits(398)	9e-40()	Compositional matrix adjust.	183/240(76%)	188/240(78%)	39/240(16%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaaeqtageetsEH	SKSLPQL	425		
Sbjct	1924	NIFSS S+NEDNISQEDTRT SISVPQSIATA SLLTGSSAEEQTAQEETSE	SKSLPQL	1983		
Query	424	TTeesssfqessaeE-----	NQMTEV	362		
Sbjct	1984	TTEESSSFQESSA NQMTEV		2043		
Query	361	PWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaaeq		182		
Sbjct	2044	PWTLSTSLSQSSS+ KNIFSS S+NEDNISQEDTRT SISVPQSIATANSLLTGSSAEEQ		2103		
Query	181	tageetsEH	SKSLPQLTTeesssfqessaeENQMTEVPWtlstslsqssssQAKNIFSSPS	2		
Sbjct	2104	TAQEETSE SKSLPQLTTEESSS QESSAEEN+MTEVPWTLSTSLSQSSS+ KNIFSS S		2163		

Range 85: 1827 to 1985

Score	Expect	Method	Identities	Positives	Gaps	Frame
156 bits(395)	2e-39()	Compositional matrix adjust.	144/159(91%)	150/159(94%)	0/159(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaaeqtageetsEH	SKSLPQL	425		
Sbjct	1827	NIFSS S+NEDNISQEDTRT SISVPQSIATANSLLTGSSAEEQTAQEETSE S+SLPQL		1886		
Query	424	TTeesssfqessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI		245		
Sbjct	1887	TTEESSSFQESSA+EN MTEVPWTLSTSL+SSS+ KNIFSS S+NEDNISQEDTRT SI		1946		
Query	244	SV	PQSIATANSLLTGssaaeqtageetsEH	SKSLPQLTT 128		
Sbjct	1947	SV	PQSIATA SLLTGSSAEEQTAQEETSE SKSLPQLTT	1985		

Range 86: 9756 to 9954

Score	Expect	Method	Identities	Positives	Gaps	Frame
154 bits(389)	1e-38()	Compositional matrix adjust.	170/201(85%)	180/201(89%)	2/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaaeqtageetsEH	SKSLPQL	425		
Sbjct	9756	NIFSS S+NED +S EDTRTLS S QSI NSLLT S+E+QT QEETSE S+SLPQL		9813		
Query	424	TTeesssfqessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI		245		
Sbjct	9814	TTEE SSFQESSA+ENQMTEVPWTLSTSLSQSSS+ KNIFSS S+NEDNISQEDTRT SI		9873		
Query	244	SV	PQSIATANSLLTGssaaeqtageetsEH	SKSLPQLTTeesssfqessaeENQMTEVPW	65	
Sbjct	9874	SV	PQSIATANSLLTGSSAEEQTAQEETSE SKSLPQLTTEESSS QESSAEEN+MTEVPW	9933		
Query	64	tlstslsqssssQAKNIFSSPS	2			
Sbjct	9934	TLSTSLSQSSS+ KNIFSS S	9954			

Range 87: 6747 to 6925

Score	Expect	Method	Identities	Positives	Gaps	Frame
152 bits(384)	6e-38()	Compositional matrix adjust.	163/201(81%)	166/201(82%)	22/201(10%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaaeqtageetsEH	SKSLPQL	425		
Sbjct	6747	NIFSSPSLNEDNISQEDTRTL ISVPQSIATANSLLTGSSAEEQTAQEETSE SKSLPQL		6806		
Query	424	TTeesssfqessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI		245		
Sbjct	6807	TTEESSSFQESSAEENQ T + S+NED SQEDTRTLSI		6844		
Query	244	SV	PQSIATANSLLTGssaaeqtageetsEH	SKSLPQLTTeesssfqessaeENQMTEVPW	65	
Sbjct	6845	SV	PQSIAT NSLLTGSSAEEQTAQEETSE SKSLPQLTTEESSSFQESSAEENQ TEVPW	6904		

Query 64 tlstslsqsssqAKNIFSSPS 2
T STS SQSSS+ KNIFSS S
Sbjct 6905 TPSTSPSQSSSKTKNIFSSQS 6925

Range 88: 1168 to 1346

Score	Expect	Method	Identities	Positives	Gaps	Frame
133 bits(335)	1e-31()	Compositional matrix adjust.	157/179(88%)	165/179(92%)	0/179(0%)	-2
Features:						
Query	544	LSISVPQSIATANSLLTGssaeegtag	eeetsEHSKSLPQLTTeesssfqessae	ENQMTE		365
Sbjct	1168	L I +PQS TA+SLLT SAE QT QEETSE S+S	SLPQLTTEESSSFQESSAEENQMTE			1227
Query	364	VPWtlstslsqsssqAKNIFSSPSLNEDNISQEDTR	TL	LSISVPQSIATANSLLTGssae		185
Sbjct	1228	VPWTL+TSLSQSSS+ KNIFSS S+NEDNISQEDTR	TL	LSISVPQSIATANSLLTGSSAE		1287
Query	184	gtag	eeetsEHSKSLPQLTTeesssfqessae	ENQMTEVPWtlstslsqsssqAKNIFSS		8
Sbjct	1288	HTAQEETSELSKSLPQLTTEESSSFQESSAEENQMTEVPWTL+TSLSQSSS+ KNIFSS				1346

Range 89: 11199 to 11395

Score	Expect	Method	Identities	Positives	Gaps	Frame
120 bits(302)	3e-27()	Compositional matrix adjust.	150/201(75%)	160/201(79%)	4/201(1%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPOSIATANSLLTGssaeegtag eeets EHSKSLPQL				425
Sbjct	11199	NIFSS S+NED +S EDTRTLS S QSI NSLLT SAE+QT QEETSE SKSLPQL				11256
		NIFSSQSVNEDKVSLEDTRTLSTS--QSITITNSLLTDLSAEDQTNQEETSELSKSLPQL				
Query	424	TTeesssfq essae ENQMTEVPWtlstslsqsssqAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct	11257	TTEES SFQESSAE+NQMTE PWTLSTS QSSS+ IFSS S+NED S EDTRTLS				11316
		TTEESISFQESSAEQNQMTEEPWTLSTSPPPQSSSKTNIIFSSQSVNEDKTSLEDTRTLST				
Query	244	SVPOSIATANSLLTGssaeegtag eeets EHSKSLPQLTTeesssfq essae ENQMTEVPW				65
Sbjct	11317	S QSI NSLLT SAE+QT QEETSE S S+PQLTTEES SFQESSAE+NQMTE PW				11374
		S--QSITITNSLLTDLSAEDQTNQEETSELSNSVPQLTTEESISFQESSAEQNQMTEEPW				
Query	64	tlstslsqsssqAKNIFSSPS 2				
Sbjct	11375	TLSTS QSSS+ KNIFSS S				
		TLSTSPPOSSSKTKNIFSSQS 11395				

Range 90: 10582 to 10778

Score	Expect	Method	Identities	Positives	Gaps	Frame
120 bits(302)	4e-27()	Compositional matrix adjust.	147/201(73%)	162/201(80%)	4/201(1%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVQPQSIATANSLLTGssaeegtagaeesEHSKSLPQL				425
Sbjct	10582	NIFSS S+NED +S E+TRTLS S QSI NSLLT SAE+QT QEETSE S S+PQL				10639
Query	424	TTeesssfqessaeENQMTEVPWtlstslsqsssqAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct	10640	TTEES SFQESSA++NQ+TE PWTLS QSSS+ KNIFSS S+NED +S EDTRTLS				10699
Query	244	SVQPQSIATANSLLTGssaeegtagaeesEHSKSLPQLTTeesssfqessaeENQMTEVPW				65
Sbjct	10700	S--QSITITNSLLTDLSAEDQTNQEETSELSNSVPQLTTEESISFQESSAEQNQMTEEPW				10757
Query	64	tlstslsqsssqAKNIFSSPS 2				
Sbjct	10758	TLSTS QSSS+ KNIFSS S TLSTSPSQSSSKTKNIFSSQS 10778				

Range 91: 14869 to 15063

Score	Expect	Method	Identities	Positives	Gaps	Frame
120 bits(302)	4e-27()	Compositional matrix adjust.	150/199(75%)	158/199(79%)	4/199(2%)	-2
Features:						
Query	598	FSSPSLNEDNISQEDTRTLSISVPSIATANSLLTGssaeegtagaeesEHSKSLPQLTT				419
		FSS S+NED S EDTRTLSIS QSI NSLLT SAE+QT QEETSE SKSLPQLTT				

Sbjct 14869 FSSQSVNEDKTSLEDTRTLSIS--QSITMTNSLLTDLSEAEDQTNQEETSELSKSLPQLTT 14926

Query 418 eesssfgessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSISV 239
EES SFQESSAE+NQMTE PWTLSLSTL QSSS+ NIFSS S+NED S EDTRTLS S

Sbjct 14927 EESISFQESSAEQNQMTEEPWTLSTSLPQSSSKTNNIFSSQSVNEDKTSLEDTRTLSTSQ 14986

Query 238 PQSIATANSLLTGssaeegtagaetsEHKSLPQLTTeesssfgessaeENQMTEVPWtl 59
P I NS LT SAE+QT QEETS SKSLPQLTTEES SFQESSAE+NQMTE PWT

Sbjct 14987 P--ITITNSPLTDLSEAEDQTNQEETSVLSKSLPQLTTEESISFQESSAEQNQMTEEPWTL 15044

Query 58 stslsqssssQAKNIFSSPS 2
STS QSSS+ KNIFSS S

Sbjct 15045 STSPPQSSSKTKNIFSSQS 15063

Range 92: 10142 to 10274

Score	Expect	Method	Identities	Positives	Gaps	Frame
119 bits(298)	1e-26()	Compositional matrix adjust.	109/133(82%)	114/133(85%)	0/133(0%)	-2
Features:						
Query 604		NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeegtagaetsEHKSLPQL				425
Sbjct 10142		NIFSS S+ ED QEDTRT SISVPQSIATANSLLTGSSAEEQTAQEETSE SKSLPQL				10201
Query 424		TTeesssfgessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct 10202		TTEESSSFQESSAE+NQMTEVPWTLSTSLSQSSS+ NIFSS ++ ED QEDTRT SI				10261
Query 244		SVQSIATANSL 206				
Sbjct 10262		S PQS ANSL 10274				

Range 93: 10677 to 10871

Score	Expect	Method	Identities	Positives	Gaps	Frame
118 bits(296)	2e-26()	Compositional matrix adjust.	151/199(76%)	163/199(81%)	4/199(2%)	-2
Features:						
Query 604		NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeegtagaetsEHKSLPQL				425
Sbjct 10677		NIFSS S+NED +S EDTRTLS S QSI NSLLT SAE+QT QEETSE S S+PQL				10734
Query 424		TTeesssfgessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct 10735		TTEES SFQESSAE+NQMTE PWTLSLST QSSS+ KNIFSS S+NED +S EDTRTLSI				10794
Query 244		SVQSIATANSLLTGssaeegtagaetsEHKSLPQLTTeesssfgessaeENQMTEVPW				65
Sbjct 10795		S QSI NS LT SAE+QT QEETSE S S+PQLTTEESSSFQESS EEN +TEVPW				10852
Query 64		tlstslsqssssQAKNIFSS 8				
Sbjct 10853		TLSTSLSQSSS+ KNIFSS 10871				

Range 94: 11770 to 11965

Score	Expect	Method	Identities	Positives	Gaps	Frame
118 bits(295)	3e-26()	Compositional matrix adjust.	149/200(75%)	159/200(79%)	4/200(2%)	-2
Features:						
Query 601		IFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeegtagaetsEHKSLPQLT				422
Sbjct 11770		IFSS S+NED S EDTRTLS S QSI NSLLT S+E+QT QEETSE SKSLPQLT				11827
Query 421		TeesssfgessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSIS				242
Sbjct 11828		TEES SFQESSAE+ QMTE PWTLSLST QSSS+ IFSS S+NED S EDTRTLS S				11887
Query 241		VPQSIATANSLLTGssaeegtagaetsEHKSLPQLTTeesssfgessaeENQMTEVPWtl				62
Sbjct 11888		QSI NSLLT S+E+QT QEETSE SKSLPQLTTEES SFQESSAEENQMTE PWT				11945
Query 61		lstslsqssssQAKNIFSSPS 2				
Sbjct 11946		LSTS +QSSS+ KNIFSS S 11965				

Range 95: 14298 to 14493

Score	Expect	Method	Identities	Positives	Gaps	Frame
117 bits(293)	6e-26()	Compositional matrix adjust.	151/200(76%)	160/200(80%)	4/200(2%)	-2
Features:						
Query	601	IFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaaeqtagaetsEH	SKSLPQLT	422		
Sbjct	14298	IFSS S+NED S DTRTLSIS QSI NSLLT SAE+QT QEETSE SKSLPQLT	IFSSQSVNEDKTS	14355		
Query	421	TeesssfqessaeENQMTEVPWtlstslsqss	QAKNIFSSPSLNEDNISQEDTRTLSIS	242		
Sbjct	14356	TEES SFQESSAE+NQMTE PWTLSL Q+SS+ IFSS S+NED S EDTRTLSIS	TEESISFQESSAEQNQMTEEPWTLSTSLPQTSSKTNIIFSSQSVNEDKTSLEDTRTLSIS	14415		
Query	241	VPQSIATANSLLTGssaaeqtagaetsEH	SKSLPQLTTeesssfqessaeENQMTEVPWt	62		
Sbjct	14416	QSI NS LT SAE+QT QEETSE SKSLPQLTTEES SFQESSAE+NQMTE PWT	--QSITMTNSPLTDL	14473		
Query	61	lstslsqss	QAKNIFSSPS 2			
Sbjct	14474	LSTSL QSSS+ NIFSS S	LSTSLPQSSSKTNNIFSSQS 14493			

Range 96: 14962 to 15137

Score	Expect	Method	Identities	Positives	Gaps	Frame
117 bits(292)	8e-26()	Compositional matrix adjust.	133/180(74%)	142/180(78%)	4/180(2%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaaeqtagaetsEH	SKSLPQL	425		
Sbjct	14962	NIFSS S+NED S EDTRTLS S P I NS LT SAE+QT QEETS SKSLPQL	NIFSSQSVNEDKTSLEDTRTLSTSQP--ITITNSPLTDL	15019		
Query	424	TTeesssfqessaeENQMTEVPWtlstslsqss	QAKNIFSSPSLNEDNISQEDTRTLSI	245		
Sbjct	15020	TTEES SFQESSAE+NQMTE PWTLS TS QSSS+ KNIFSS S+NE+ S EDTRTLSI	TTEESISFQESSAEQNQMTEEPWTLSTSP	15079		
Query	244	SVPQSIATANSLLTGssaaeqtagaetsEH	SKSLPQLTTeesssfqessaeENQMTEVPW	65		
Sbjct	15080	S QS A NSLLT SAE+QT +EE SE SKSLPQLTTEES SFQESSAE+NQMTE PW	S--QSR	15137		

Range 97: 11865 to 12060

Score	Expect	Method	Identities	Positives	Gaps	Frame
116 bits(290)	1e-25()	Compositional matrix adjust.	149/200(75%)	158/200(79%)	4/200(2%)	-2
Features:						
Query	601	IFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaaeqtagaetsEH	SKSLPQLT	422		
Sbjct	11865	IFSS S+NED S EDTRTLS S QSI NSLLT S+E+QT QEETSE SKSLPQLT	IFSSQSVNEDKTSLEDTRTLSTS--QSITITNSLLTDL	11922		
Query	421	TeesssfqessaeENQMTEVPWtlstslsqss	QAKNIFSSPSLNEDNISQEDTRTLSIS	242		
Sbjct	11923	TEES SFQESSAEENQMTE PWTLS TS +QSSS+ KNIFSS S+NED S EDTRTL S	TEESISFQESSAEENQMTEEPWTLSTSPAQSSSKTKNIFSSQSVNEDKTSLEDTRTLLTS	11982		
Query	241	VPQSIATANSLLTGssaaeqtagaetsEH	SKSLPQLTTeesssfqessaeENQMTEVPWt	62		
Sbjct	11983	QSI NSLLT SAE+QT QEETSE S SLPQLTTEES SFQESSAE+NQMTE PWT	--QSITITNSLLTELSAEDQTNQEETSELSNSLPQLTTEESISFQESSAEQNQMTEEPWT	12040		
Query	61	lstslsqss	QAKNIFSSPS 2			
Sbjct	12041	LSTS QSSS+ IFSS S	LSTSP	12060		

Range 98: 9327 to 9457

Score	Expect	Method	Identities	Positives	Gaps	Frame
116 bits(290)	1e-25()	Compositional matrix adjust.	110/134(82%)	115/134(85%)	3/134(2%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaaeqtagaetsEH	SKSLPQL	425		
Sbjct	9327	NIFSSPSLNEDNISQEDTRTL ISVPQSIATANSLLTGSSAEEQTAQEETSE S SLPQL	NIFSSPSLNEDNISQEDTRTLPI	9386		
Query	424	TTeesssfqessaeENQMTEVPWtlstslsqss	QAKNIFSSPSLNEDNISQEDTRTLSI	245		
Sbjct	9387	TTEESSSFQESSAEENQ T++PWTLS TS SQSSS+ KNIFSS ++ ED QEDT SI	TTEESSSFQESSAEENQTTKMPWTLSTSPSQSSSKTKNIFSSQNVKEDKTFQEDT---SI	9443		
Query	244	SVPQSIATANSLLT	203			
Sbjct	9444	S PQS ANS LT	SFPQSSTKANSFLT 9457			

Range 99: 11580 to 11775

Score	Expect	Method	Identities	Positives	Gaps	Frame
115 bits(287)	3e-25()	Compositional matrix adjust.	146/200(73%)	158/200(79%)	4/200(2%)	-2
Features:						
Query	601	IFSSPSLNEDNISQEDTRTLSISVPOSIATANSLLTGssaeegtaqeetsEHKSLPQLT				422
Sbjct	11580	IFSS S+NED S EDTRTLS S QSI NSLLT SAE+QT QEETSE S S+PQLT				11637
Query	421	TeesssfqessaeENQMTEVPWtlstslsgssssQAKNIFSSPSLNEDNISQEDTRTLSIS				242
Sbjct	11638	TEES SFQESSAE+NQMTE PWTLS TS QSSS+ KNIFSS S+NED +S EDTRTLS S				11697
Query	241	VPQSIATANSLLTGssaeegtaqeetsEHKSLPQLTTeesssfqessaeENQMTEVPWt				62
Sbjct	11698	QSI NSLLT SAE+QT QEETSE S S+PQLTTEES SFQESSAE+NQMTE PWT				11755
Query	61	lstslsgssssQAKNIFSSPS 2				
Sbjct	11756	STSL Q+SS+ IFSS S PSTSLPQTSSKTNIIFSSQS 11775				

Range 100: 11295 to 11469

Score	Expect	Method	Identities	Positives	Gaps	Frame
114 bits(286)	5e-25()	Compositional matrix adjust.	133/179(74%)	143/179(79%)	4/179(2%)	-2
Features:						
Query	601	IFSSPSLNEDNISQEDTRTLSISVPOSIATANSLLTGssaeegtaqeetsEHKSLPQLT				422
Sbjct	11295	IFSS S+NED S EDTRTLS S QSI NSLLT SAE+QT QEETSE S S+PQLT				11352
Query	421	TeesssfqessaeENQMTEVPWtlstslsgssssQAKNIFSSPSLNEDNISQEDTRTLSIS				242
Sbjct	11353	TEES SFQESSAE+NQMTE PWTLS TS QSSS+ KNIFSS S+NED +S EDTRTLS S				11412
Query	241	VPQSIATANSLLTGssaeegtaqeetsEHKSLPQLTTeesssfqessaeENQMTEVPW				65
Sbjct	11413	QSI NSLLT SAE+QT QEETSE S S+PQLTTEES SFQESSAE+NQMTE PW				11469

Range 101: 13241 to 13435

Score	Expect	Method	Identities	Positives	Gaps	Frame
114 bits(285)	6e-25()	Compositional matrix adjust.	150/199(75%)	159/199(79%)	4/199(2%)	-2
Features:						
Query	598	FSSPSLNEDNISQEDTRTLSISVPOSIATANSLLTGssaeegtaqeetsEHKSLPQLTT				419
Sbjct	13241	FSS S+NED S EDTRTLSIS QSI NS LT SAE+QT QEETSE SKSLPQLTT				13298
Query	418	eesssfqessaeENQMTEVPWtlstslsgssssQAKNIFSSPSLNEDNISQEDTRTLSISV				239
Sbjct	13299	EES SFQESSAE+NQMTE PWT STSL QSSS+ NIFSS S+NED S DTRT SIS				13357
Query	238	PQSIATANSLLTGssaeegtaqeetsEHKSLPQLTTeesssfqessaeENQMTEVPWtl				59
Sbjct	13358	QS A NSLLT SAE+QT QEETSE SKSLPQLTTEES SFQESSAE+NQMTE PWT				13416
Query	58	stslsgssssQAKNIFSSPS 2				
Sbjct	13417	STSLSQ+SS+ NIFSS S STSLSQTSKTNIFSSQS 13435				

Range 102: 13334 to 13509

Score	Expect	Method	Identities	Positives	Gaps	Frame
114 bits(285)	6e-25()	Compositional matrix adjust.	137/180(76%)	145/180(80%)	4/180(2%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPOSIATANSLLTGssaeegtaqeetsEHKSLPQL				425
Sbjct	13334	NIFSS S+NED S DTRT SIS QS A NSLLT SAE+QT QEETSE SKSLPQL				13391
Query	424	TTeesssfqessaeENQMTEVPWtlstslsgssssQAKNIFSSPSLNEDNISQEDTRTL				245
Sbjct	13392	TTEES SFQESSAE+NQMTE PWTLS TSLSQ+SS+ NIFSS S+ ED S EDTRTL				13451

Query	244	SV PQSIATANSLLTGssaeegtaqeetsEH SKSLPQLTTeesssfqessaeENQMTEVPW	65
		S QSI NSLLT SAE+QT QEETSE SKSLPQLTTEES SFOESSAE+NQMTE PW	
Sbjct	13452	S--QSITITNSLLTDLSAEDQTNQEETSELSKSLPQLTTEESISFQESSAEQNQMTEEPW	13509

Range 103: 14393 to 14567

Score	Expect	Method	Identities	Positives	Gaps	Frame
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113 bits(283) 1e-24() Compositional matrix adjust. 135/179(75%) 142/179(79%) 4/179(2%) -2

Features:

Query	601	IFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeegtaqeetsEH SKSLPQLT	422
		IFSS S+NED S EDTRTLSIS QSI NS LT SAE+QT QEETSE SKSLPQLT	
Sbjct	14393	IFSSQSVNEDKTSLEDTRTLSIS--QSITMTNSPLTDLSAEDQTNQEETSELSKSLPQLT	14450

Query	421	TeesssfqessaeENQMTEVPWtlstslsqssSQAKNIFSSPSLNEDNISQEDTRTLSIS	242
		TEES SFOESSAE+NQMTE PWTLSLSTL QSSS+ NIFSS S+NED S DTRTLSIS	
Sbjct	14451	TEESISFQESSAEQNQMTEEPWTLSTSLPQSSSKTNIFSSQSVNEDKTS LGDTRTLSIS	14510

Query	241	VPQSIATANSLLTGssaeegtaqeetsEH SKSLPQLTTeesssfqessaeENQMTEVPW	65
		QS NSLLT SAE+QT QEETSE SKSLPQLTTEES SFOESSAE+NQMTE PW	
Sbjct	14511	--QSREITNSLLTDLSAEDQTNQEETSELSKSLPQLTTAESISFQESSAEQNQMTEEPW	14567

Range 104: 11486 to 11680

Score	Expect	Method	Identities	Positives	Gaps	Frame
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112 bits(280) 3e-24() Compositional matrix adjust. 147/199(74%) 157/199(78%) 4/199(2%) -2

Features:

Query	598	FSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeegtaqeetsEH SKSLPQLTT	419
		FSS S+N+D S EDTRTLSIS QSI NS LT SAE+QT QEETSE SKSLPQLTT	
Sbjct	11486	FSSQSVNKDKTSLEDTRTLSIS--QSITMTNSPLTDLSAEDQTNQEETSELSKSLPQLTT	11543

Query	418	eesssfqessaeENQMTEVPWtlstslsqssSQAKNIFSSPSLNEDNISQEDTRTLSISV	239
		EES SFOESSAE+NQMTE PWTLSLSTL QSSS+ IFSS S+NED S EDTRTLS S	
Sbjct	11544	EESISFQESSAEQNQMTEEPWTLSTSPQSSSKTNIFSSQSVNEDKTSLEDTRTLSTLST-	11602

Query	238	PQSIATANSLLTGssaeegtaqeetsEH SKSLPQLTTeesssfqessaeENQMTEVPWtl	59
		QSI NSLLT SAE+QT QEETSE S S+PQLTTEES SFOESSAE+NQMTE PWTL	
Sbjct	11603	-QSITITNSLLTDLSAEDQTNQEETSELSNSVPQLTTEESISFQESSAEQNQMTEEPWTL	11661

Query	58	stslsqssSQAKNIFSSPS 2	
		STS QSSS+ KNIFSS S	
Sbjct	11662	STSPQSSSKTKNIFSSQS 11680	

Range 105: 12573 to 12748

Score	Expect	Method	Identities	Positives	Gaps	Frame
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112 bits(280) 3e-24() Compositional matrix adjust. 135/180(75%) 143/180(79%) 4/180(2%) -2

Features:

Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeegtaqeetsEH SKSLPQL	425
		NIFSS S+NED S DTRTLSIS QS NSLLT SAE+QT QEETSE SKSLPQL	
Sbjct	12573	NIFSSQSVNEDKTS LGDTRTLSIS--QSREITNSLLTDLSAEDQTNQEETSELSKSLPQL	12630

Query	424	TTeesssfqessaeENQMTEVPWtlstslsqssSQAKNIFSSPSLNEDNISQEDTRTLSI	245
		TTEES SFOESSAE+NQMTE PWTLSLSTLSQ+SS+ NIFSS S+NED S DTRTLSI	
Sbjct	12631	TTEESISFQESSAEQNQMTEEPWTLSTLSQTSSKTNIFSSQSVNEDKTS LGDTRTLSI	12690

Query	244	SV PQSIATANSLLTGssaeegtaqeetsEH SKSLPQLTTeesssfqessaeENQMTEVPW	65
		S QSI NS LT SAE+QT QEETSE SKSLPQLTTEES SFOESSAE+NQMTE PW	
Sbjct	12691	S--QSITMTNSPLTDLSAEDQTNQEETSELSKSLPQLTTAESISFQESSAEQNQMTEEPW	12748

Range 106: 12246 to 12419

Score	Expect	Method	Identities	Positives	Gaps	Frame
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111 bits(277) 7e-24() Compositional matrix adjust. 134/178(75%) 141/178(79%) 4/178(2%) -2

Features:

Query	598	FSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeegtaqeetsEH SKSLPQLTT	419
		FSS S+NED S EDTRTLSIS QSI NS LT SAE+QT QEETSE SKSLPQLTT	
Sbjct	12246	FSSQSVNEDKTSLEDTRTLSIS--QSITMTNSPLTDLSAEDQTNQEETSELSKSLPQLTT	12303

Query	418	eesssfqessaeENQMTEVPWtlstslsqssSQAKNIFSSPSLNEDNISQEDTRTLSISV	239
		EES SFOESSAE+NQMTE PWT STSL QSSS+ NIFSS S+NED S DTRTLSIS	

Sbjct 12304 EESISFQESSAEQNQMTEEPWTPSTSLPQSSSKTNNIFSSQSVNEDKTS LGDTRTLSIS- 12362

Query 238 PQSIATANSLLTGssaaeqtaqeetsEHSKSLPQLTTeesssfqessaeENQMTEVPW 65

Sbjct 12363 -QSREITNSLLTDLSAEDQTNQEETSELSKSLPQLTTEESISFQESSAEQNQMTEEPW 12419

Range 107: 11674 to 11870

Score	Expect	Method	Identities	Positives	Gaps	Frame
110 bits(276)	9e-24()	Compositional matrix adjust.	145/201(72%)	157/201(78%)	4/201(1%)	-2
Features:						
Query 604		NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaaeqtaqeetsEHSKSLPQL				425
Sbjct 11674		NIFSS S+NED +S EDTRTLS S QSI NSLLT SAE+QT QEETSE S S+PQL				11731
Query 424		TTeesssfqessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct 11732		TTEES SFQESSAE+NQMTE PWT STSL Q+SS+ IFSS S+NED S EDTRTLS				11791
Query 244		SVPQSIATANSLLTGssaaeqtaqeetsEHSKSLPQLTTeesssfqessaeENQMTEVPW				65
Sbjct 11792		S QSI NSLLT S+E+QT QEETSE SKSLPQLTTEES SFQESSAE+ QMTE PW				11849
Query 64		tlstslsqssssQAKNIFSSPS 2				
Sbjct 11850		TLSTS QSSS+ IFSS S TLSTSPPPQSSSKTNIIFSSQS 11870				

Range 108: 11389 to 11585

Score	Expect	Method	Identities	Positives	Gaps	Frame
109 bits(273)	3e-23()	Compositional matrix adjust.	145/201(72%)	157/201(78%)	4/201(1%)	-2
Features:						
Query 604		NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaaeqtaqeetsEHSKSLPQL				425
Sbjct 11389		NIFSS S+NED +S EDTRTLS S QSI NSLLT SAE+QT QEETSE S S+PQL				11446
Query 424		TTeesssfqessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct 11447		TTEES SFQESSAE+NQMTE PWT STSL Q+SS+ FSS S+N+D S EDTRTLSI				11506
Query 244		SVPQSIATANSLLTGssaaeqtaqeetsEHSKSLPQLTTeesssfqessaeENQMTEVPW				65
Sbjct 11507		S QSI NS LT SAE+QT QEETSE SKSLPQLTTEES SFQESSAE+NQMTE PW				11564
Query 64		tlstslsqssssQAKNIFSSPS 2				
Sbjct 11565		TLSTS QSSS+ IFSS S TLSTSPPPQSSSKTNIIFSSQS 11585				

Range 109: 12339 to 12514

Score	Expect	Method	Identities	Positives	Gaps	Frame
109 bits(272)	3e-23()	Compositional matrix adjust.	133/180(74%)	141/180(78%)	4/180(2%)	-2
Features:						
Query 604		NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaaeqtaqeetsEHSKSLPQL				425
Sbjct 12339		NIFSS S+NED S DTRTLSIS QS NSLLT SAE+QT QEETSE SKSLPQL				12396
Query 424		TTeesssfqessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct 12397		TTEES SFQESSAE+NQMTE PWT LST L Q+SS+ FSS S+NED S EDTRTLSI				12456
Query 244		SVPQSIATANSLLTGssaaeqtaqeetsEHSKSLPQLTTeesssfqessaeENQMTEVPW				65
Sbjct 12457		S QSI NS LT SAE+QT QEETSE SKSLPQLTTEES SFQESSAE+NQMTE PW				12514

Range 110: 13596 to 13790

Score	Expect	Method	Identities	Positives	Gaps	Frame
109 bits(272)	3e-23()	Compositional matrix adjust.	146/199(73%)	156/199(78%)	4/199(2%)	-2
Features:						
Query 598		FSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaaeqtaqeetsEHSKSLPQLTT				419

Sbjct	13596	FSS S+NED S EDTRTLSIS QSI NS LT SAE+QT QEETSE SKSLPQLTT FSSQSVNEDKTSLEDTRTLSIS--QSITMTNSPLTDLSAEDQTNQEETSELSKSLPQLTT	13653
Query	418	eesssfqessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSISV EES SFQESSAE+NQMTE PWT STSL Q+SS+ FSS S+ ED S EDTRTLSIS	239
Sbjct	13654	EESISFQESSAEQNQMTEEPWTPSTSLPQTSSKTNITFSSQSVYEDKTSLEDTRTLSIS-	13712
Query	238	PQSIATANSLLTGssaeeqtageetsEHSKSLPQLTTeesssfqessaeENQMTEVPWtl QSI NS LT SAE+QT QEETSE SKSLPQLTTEES SFQESSAE+NQMTE PWT	59
Sbjct	13713	-QSIAMTNSPLTDLSAEDQTNQEETSELSKSLPQLTTEESISFQESSAEQNQMTEEPWTL	13771
Query	58	stslsqssssQAKNIFSSPS 2 STSL Q+SS+ N FSS S	
Sbjct	13772	STSLPQTSSKTNNTFSSQS 13790	

Range 111: 14014 to 14208

Score	Expect	Method	Identities	Positives	Gaps	Frame
108 bits(270)	5e-23()	Compositional matrix adjust.	148/199(74%)	158/199(79%)	4/199(2%)	-2

Features:

Query	598	FSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeeqtageetsEHSKSLPQLTT	419
Sbjct	14014	FSS S+NED S EDTRTLSIS QSI NS LT SAE+QT QEETSE SKSLPQLTT FSSQSVNEDKTSLEDTRTLSIS--QSITMTNSPLTDLSAEDQTNQEETSELSKSLPQLTT	14071
Query	418	eesssfqessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSISV EES SFQESSAE+NQMTE PWTSTSL Q+SS+ FSS S+NED S EDTRTLSIS	239
Sbjct	14072	EESISFQESSAEQNQMTEEPWTLSTSLPQTSSKTNITFSSQSVNEDKTSLEDTRTLSIS-	14130
Query	238	PQSIATANSLLTGssaeeqtageetsEHSKSLPQLTTeesssfqessaeENQMTEVPWtl QSI NS LT SAE+QT QEETSE SKSLPQLTTEES SFQESSAE+NQMTE PWT	59
Sbjct	14131	-QSITMTNSPLTDLSAEDQTNQEETSELSKSLPQLTTEESISFQESSAEQNQMTEEPWTL	14189
Query	58	stslsqssssQAKNIFSSPS 2 STSLSQ+SS+ IFSS S	
Sbjct	14190	STSLSQTSSKTNIIIFSSQS 14208	

Range 112: 14203 to 14398

Score	Expect	Method	Identities	Positives	Gaps	Frame
108 bits(269)	8e-23()	Compositional matrix adjust.	146/200(73%)	157/200(78%)	4/200(2%)	-2

Features:

Query	601	IFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeeqtageetsEHSKSLPQLT	422
Sbjct	14203	IFSS S+NED S +TRTLSIS QSI NS LT SAE+QT QEE SE SKSLPQLT IFSSQSVNEDKTS LGNTRTLSIS--QSITMTNSPLTDLSAEDQTNQEEASELSKSLPQLT	14260
Query	421	TeesssfqessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSIS TEES SFQESSAE+NQMTE PWTSTSL Q+SS+ IFSS S+NED S DTRTLSIS	242
Sbjct	14261	TEESISFQESSAEQNQMTEEPWTLSTSLPQTSSKTNIIIFSSQSVNEDKTS LGDTRTLSIS	14320
Query	241	VPQSIATANSLLTGssaeeqtageetsEHSKSLPQLTTeesssfqessaeENQMTEVPWt QSI NSLLT SAE+QT QEETSE SKSLPQLTTEES SFQESSAE+NQMTE PWT	62
Sbjct	14321	--QSITITNSLLTDLSAEDQTNQEETSELSKSLPQLTTEESISFQESSAEQNQMTEEPWT	14378
Query	61	lstslsqssssQAKNIFSSPS 2 LSTSL Q+SS+ IFSS S	
Sbjct	14379	LSTSLPQTSSKTNIIIFSSQS 14398	

Range 113: 14487 to 14662

Score	Expect	Method	Identities	Positives	Gaps	Frame
107 bits(266)	2e-22()	Compositional matrix adjust.	132/180(73%)	140/180(77%)	4/180(2%)	-2

Features:

Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeeqtageetsEHSKSLPQL	425
Sbjct	14487	NIFSS S+NED S DTRTLSIS QS NSLLT SAE+QT QEETSE SKSLPQL NIFSSQSVNEDKTS LGDTRTLSIS--QSREITNSLLTDLSAEDQTNQEETSELSKSLPQL	14544
Query	424	TTeesssfqessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI TT ES SFQESSAE+NQMTE PWTSTSL Q+SS+ FSS S+ ED S EDTRTLSI	245
Sbjct	14545	TTAESISFQESSAEQNQMTEEPWTLSTSLPQTSSKTNITFSSQSVYEDKTSLEDTRTLSI	14604
Query	244	SVQSIATANSLLTGssaeeqtageetsEHSKSLPQLTTeesssfqessaeENQMTEVPW S QSI NS LT SAE+QT QEETSE SKSLPQLTTEES SFQESSAE+NQMTE PW	65
Sbjct	14605	S--QSITMTNSPLTDLSAEDQTNQEETSELSKSLPQLTTEESISFQESSAEQNQMTEKPW	14662

Range 114: 12668 to 12843

Score Expect Method Identities Positives Gaps Frame

106 bits(264) 3e-22() Compositional matrix adjust. 132/180(73%) 140/180(77%) 4/180(2%) -2

Features:

Query	604	NIFSSPSLNEDNISQEDTRTLSISVPOSIATANSLLTGssaeegtagaetsEH	425
Sbjct	12668	NIFSS S+NED S DTRTLSIS QSI NS LT SAE+QT QEETSE SKSLPQL	12725
Query	424	TTeesssfgessaeENQMTEVPWtlstslsqsssQAKNIFSSPSLNEDNISQEDTRTLSI	245
Sbjct	12726	TT ES SFQESSAE+NQMTE PWTLSLSTL Q+SS+ FSS S+ ED S EDTRTLSI	12785
Query	244	SVPOSIATANSLLTGssaeegtagaetsEH	65
Sbjct	12786	S QSI NS LT SAE+QT QEETSE SKSLPQLTTEES SFQESSAE+NQMTE PW	12843

Range 115: 14109 to 14303

Score Expect Method Identities Positives Gaps Frame

105 bits(262) 6e-22() Compositional matrix adjust. 146/199(73%) 157/199(78%) 4/199(2%) -2

Features:

Query	598	FSSPSLNEDNISQEDTRTLSISVPOSIATANSLLTGssaeegtagaetsEH	419
Sbjct	14109	FSS S+NED S EDTRTLSIS QSI NS LT SAE+QT QEETSE SKSLPQLTT	14166
Query	418	eesssfgessaeENQMTEVPWtlstslsqsssQAKNIFSSPSLNEDNISQEDTRTLSISV	239
Sbjct	14167	EES SFQESSAE+NQMTE PWTLSLSTLSQ+SS+ IFSS S+NED S +TRTLSIS	14225
Query	238	PQSIATANSLLTGssaeegtagaetsEH	59
Sbjct	14226	QSI NS LT SAE+QT QEE SE SKSLPQLTTEES SFQESSAE+NQMTE PWTL	14284
Query	58	stslsqsssQAKNIFSSPS 2	
Sbjct	14285	STSL Q+SS+ IFSS S STSLPQTSSKTNIIIFSSQS 14303	

Range 116: 9679 to 9857

Score Expect Method Identities Positives Gaps Frame

105 bits(261) 7e-22() Compositional matrix adjust. 138/181(76%) 151/181(83%) 2/181(1%) -2

Features:

Query	544	LSISVPOSIATANSLLTGssaeegtagaetsEH	365
Sbjct	9679	L I +PQS TA+SLLT SAE+QT QEETSE S S+PQLTTEES SFQESSAE+NQMTE	9738
Query	364	VPWtlstslsqsssQAKNIFSSPSLNEDNISQEDTRTLSISVPOSIATANSLLTGssae	185
Sbjct	9739	PWTLSLST QSSS+ KNIFSS S+NED +S EDTRTLS S QSI NSLLT S+E+	9796
Query	184	qtagaetsEH	5
Sbjct	9797	QT QEETSE S+SLPQLTTEE SSFQESSA+ENQMTEVPWTLSTSLSQSSS+ KNIFSS	9856
Query	4	S 2	
Sbjct	9857	S 9857	

Range 117: 13051 to 13224

Score Expect Method Identities Positives Gaps Frame

105 bits(261) 8e-22() Compositional matrix adjust. 131/178(74%) 139/178(78%) 4/178(2%) -2

Features:

Query	598	FSSPSLNEDNISQEDTRTLSISVPOSIATANSLLTGssaeegtagaetsEH	419
Sbjct	13051	FSS S+NED S EDTRTLSIS QSI NS LT SAE+QT QEETSE SKSLPQLTT	13108
Query	418	eesssfgessaeENQMTEVPWtlstslsqsssQAKNIFSSPSLNEDNISQEDTRTLSISV	239
Sbjct	13109	ES SFQESSAE+NQMTE PWTLSLSTL Q+SS+ FSS S+ ED S EDTRTLSIS	13167
Query	238	PQSIATANSLLTGssaeegtagaetsEH	65
Sbjct	13168	QSI NS LT SAE+QT QEETSE SKSLPQLTTEES SFQESSAE+NQMTE PW	13224

Range 118: 11959 to 12155

Score	Expect	Method	Identities	Positives	Gaps	Frame
104 bits(260)	1e-21()	Compositional matrix adjust.	144/201(72%)	154/201(76%)	4/201(1%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTSLISVPOSIATANSLLTGssaeegtaqeetsEHSKSLPQL				425
Sbjct	11959	NIFSS S+NED S EDTRTL S QSI NSLLT SAE+QT QEETSE S SLPQL				12016
Query	424	TTeesssfgessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTSLI				245
Sbjct	12017	TTEES SFQESSAE+NQMTE PWTLS TS QSSS+ IFSS S+NE+ S EDTRTSL				12076
Query	244	SVPOSIATANSLLTGssaeegtaqeetsEHSKSLPQLTTeesssfgessaeENQMTEVPW				65
Sbjct	12077	S QSI NSLLT SAE+QT QEETSE S S+PQLTTEES SFQES AE+NQMTE PW				12134
Query	64	tlstslsqssssQAKNIFSSPS 2				
Sbjct	12135	TLSTS QSSS+ IFSS S TLSTSPPOSSSKTNIIFSSQS 12155				

Range 119: 14679 to 14852

Score	Expect	Method	Identities	Positives	Gaps	Frame
102 bits(255)	5e-21()	Compositional matrix adjust.	130/178(73%)	138/178(77%)	4/178(2%)	-2
Features:						
Query	598	FSSPSLNEDNISQEDTRTSLISVPOSIATANSLLTGssaeegtaqeetsEHSKSLPQLTT				419
Sbjct	14679	FSS S+ ED S EDTRTSLIS QS NSLLT SAE+QT QEETSE SKSLPQLTT				14736
Query	418	eeesssfgessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTSLISV				239
Sbjct	14737	ES SFQESSAE+NQMTE PWTLS TS Q+SS+ FSS S+ ED S EDTRTSLIS				14795
Query	238	POSIATANSLLTGssaeegtaqeetsEHSKSLPQLTTeesssfgessaeENQMTEVPW				65
Sbjct	14796	QSI NS LT SAE+QT QEETSE SKSLPQLTTEES SFQESSAE+NQMTE PW				14852

Range 120: 12055 to 12229

Score	Expect	Method	Identities	Positives	Gaps	Frame
101 bits(251)	2e-20()	Compositional matrix adjust.	127/179(71%)	139/179(77%)	4/179(2%)	-2
Features:						
Query	601	IFSSPSLNEDNISQEDTRTSLISVPOSIATANSLLTGssaeegtaqeetsEHSKSLPQLT				422
Sbjct	12055	IFSS S+NE+ S EDTRTSL S QSI NSLLT SAE+QT QEETSE S S+PQLT				12112
Query	421	TeesssfgessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTSLIS				242
Sbjct	12113	TEES SFQES AE+NQMTE PWTLS TS QSSS+ IFSS S+NE+ S EDTRTSL S				12172
Query	241	VPOSIATANSLLTGssaeegtaqeetsEHSKSLPQLTTeesssfgessaeENQMTEVPW				65
Sbjct	12173	QSI NSLLT SAE+QT QE+TSE S S+PQLTTEES SFQESSAE+NQMTE PW				12229

Range 121: 10505 to 10683

Score	Expect	Method	Identities	Positives	Gaps	Frame
100 bits(250)	2e-20()	Compositional matrix adjust.	133/181(73%)	146/181(80%)	2/181(1%)	-2
Features:						
Query	544	LSISVPOSIATANSLLTGssaeegtaqeetsEHSKSLPQLTTeesssfgessaeENQMTE				365
Sbjct	10505	L I +POS TA+SLLT SAE QT QEETSE SKSLPQLTTEE SSFQESSA+EN MTE				10564
Query	364	VPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTSLISVPOSIATANSLLTGssae				185
Sbjct	10565	PWTLS TS QSSS+ KNIFSS S+NED +S E+TRTSL S QSI NSLLT SAE+				10622
Query	184	qtageetsEHSKSLPQLTTeesssfgessaeENQMTEVPWtlstslsqssssQAKNIFSSP				5
		QT QEETSE S S+PQLTTEES SFQESSA++NQ+TE PWTLS TS QSSS+ KNIFSS				

Sbjct 10623 QTNQEETSELSNSVLPQLTTEESISFQESSAKQNQITEEPWTLSTSPQSSSKTKNIFSSQ 10682

Query 4 S 2

Sbjct 10683 S 10683

Range 122: 11122 to 11300

Score	Expect	Method	Identities	Positives	Gaps	Frame
100 bits(248)	4e-20()	Compositional matrix adjust.	135/181(75%)	145/181(80%)	2/181(1%)	-2
Features:						
Query	544	LSISVPOS	IATANSLLTGssaeegtag	eetSEH	SKSLPQLTTeesssfqessae	ENQMTE 365
Sbjct	11122	LYIYLPQSSTTAHSL	LLTDLSAENQTNQEETSELSNSVLPQLTTEESISFQESSAEQNQMTE			11181
Query	364	VPWtlstslsqss	QAKNIFSSPSLNEDNISQEDTRT	LSISVPOS	IATANSLLTGssae	185
Sbjct	11182	EPWTLSTSPQSSSKTKNIFSSQSVNEDKVSLEDTRTLSTS--Q	SITITNSLLTDLSAED			11239
Query	184	qtageetSEH	SKSLPQLTTeesssfqessae	ENQMTEVPWtlstslsqss	QAKNIFSSP	5
Sbjct	11240	QTNQEETSELSKSLPQLTTEESISFQESSAEQNQMTEEPWTLSTSPQSSSKTNIIFSSQ				11299
Query	4	S 2				
Sbjct	11300	S 11300				

Range 123: 13691 to 13843

Score	Expect	Method	Identities	Positives	Gaps	Frame
98.6 bits(244)	1e-19()	Compositional matrix adjust.	116/157(74%)	123/157(78%)	4/157(2%)	-2
Features:						
Query	598	FSSPSLNEDNISQEDTRT	LSISVPOS	IATANSLLTGssaeegtag	eetSEH	SKSLPQLTT 419
Sbjct	13691	FSSQSVYEDKTSLEDTRT	LSIS--QSIAMTNSPLTDLSAEDQTNQEETSELSKSLPQLTT			13748
Query	418	eesssfqessae	ENQMTEVPWtlstslsqss	QAKNIFSSPSLNEDNISQEDTRT	LSISV	239
Sbjct	13749	EESISFQESSAEQNQMTEEPWTLSTSLPQTSSKTNNTFSSQSVNEDKTSLEDTRT	LSIS-			13807
Query	238	POSIATANSLLTGssaeegtag	eetSEH	SKSLPQLTT	128	
Sbjct	13808	-QSI NS LT SAE+QT QEETSE SKSLPQLTT			13843	

Range 124: 12765 to 12935

Score	Expect	Method	Identities	Positives	Gaps	Frame
98.6 bits(244)	2e-19()	Compositional matrix adjust.	130/175(74%)	138/175(78%)	4/175(2%)	-2
Features:						
Query	598	FSSPSLNEDNISQEDTRT	LSISVPOS	IATANSLLTGssaeegtag	eetSEH	SKSLPQLTT 419
Sbjct	12765	FSSQSVYEDKTSLEDTRT	LSIS--QSI NS LT SAE+QT QEETSE SKSLPQLTT			12822
Query	418	eesssfqessae	ENQMTEVPWtlstslsqss	QAKNIFSSPSLNEDNISQEDTRT	LSISV	239
Sbjct	12823	EESISFQESSAEQNQMTEEPWTLSTSLPQTSSKTNITFSSQSVNEDKTSLEDTRT	LSIS-			12881
Query	238	POSIATANSLLTGssaeegtag	eetSEH	SKSLPQLTTeesssfqessae	ENQMTE	74
Sbjct	12882	-QSI NS LT SAE+QT QEETSE SKSLPQLTTEES SFQESSAE+NQMTE			12935	

Range 125: 12860 to 13034

Score	Expect	Method	Identities	Positives	Gaps	Frame
97.1 bits(240)	5e-19()	Compositional matrix adjust.	124/179(69%)	133/179(74%)	5/179(2%)	-2
Features:						
Query	598	FSSPSLNEDNISQEDTRT	LSISVPOS	IATANSLLTGssaeegtag	eetSEH	SKSLPQLTT 419
Sbjct	12860	FSSQSVNEDKTSLEDTRT	LSIS--QSI NS LT SAE+QT QEETSE SKSLPQLTT			12917
Query	418	eesssfqessae	ENQMTEVPWtlstslsqss	QAKNI-FSSPSLNEDNISQEDTRT	LSIS	242

EES SFQESSAE+NQMTE++ +S NI FSS S+ ED S EDTRTLSIS

Sbjct 12918 EESISFQESSAEQNQMTEGGRGHLSTSLPQTSSKTNITFSSQSVYEDKTSLEDTRTLSIS 12977

Query 241 VPQSIATANSLLTGssaeegtagaetsEHKSLPQLTTeesssfqessaeENQMTEVPW 65

Sbjct 12978 --QSI NS LT SAE+QT QEETSE SKSLPQLTTEES SFQESSAE+NQMTE PW 13034

Range 126: 13784 to 13997

Score	Expect	Method	Identities	Positives	Gaps	Frame
88.2 bits(217) 4e-16() Compositional matrix adjust. 133/218(61%) 141/218(64%) 42/218(19%) -2						
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeegtagaetsEHKSLPQ-				428
Sbjct	13784	N FSS S+NED S EDTRTLSIS QSI NS LT SAE+QT QEETSE SKSLPQ				13841
Query	427	-----LTTeesssfqessaeENQMTEVP				359
Sbjct	13842	TTEESISFQESSPLTDLAEDQTNQEETSELSKSLPQLTTEESISFQESSAEQNQMTEEP				13901
Query	358	WtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeegt				179
Sbjct	13902	WTLSTSL Q+SS+ FSS S+ ED S EDTRTLSIS QSI NS LT SAE+QT				13959
Query	178	ageetsEHKSLPQLTTeesssfqessaeENQMTEVPW 65				
Sbjct	13960	QEETSE SKSLPQLTTEES SFQESSAE+NQMTE PW 13997				

Range 127: 10772 to 10900

Score	Expect	Method	Identities	Positives	Gaps	Frame
85.1 bits(209) 4e-15() Compositional matrix adjust. 96/134(72%) 104/134(77%) 5/134(3%) -2						
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeegtagaetsEHKSLPQL				425
Sbjct	10772	NIFSS S+NED +S EDTRTLSIS QSI NS LT SAE+QT QEETSE S S+PQL				10829
Query	424	TTeesssfqessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct	10830	TTEESSSFQESS EEN +TEVPWTLSTSLSQSSS+ KNIFSS ++ ED QEDT SI				10886
Query	244	SVPQSIATANSLLT 203				
Sbjct	10887	S PQS ANS LT SFPQSSTKANSFLT 10900				

Range 128: 13550 to 13674

Score	Expect	Method	Identities	Positives	Gaps	Frame
80.9 bits(198) 1e-13() Compositional matrix adjust. 98/127(77%) 104/127(81%) 2/127(1%) -2						
Features:						
Query	445	SKSLPQLTTeesssfqessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQE				266
Sbjct	13550	SKSLPQLTTEES SFQESSAE+NQMTE PWTLSTSL Q+SS+ FSS S+NED S E				13609
Query	265	DTRTLSISVPQSIATANSLLTGssaeegtagaetsEHKSLPQLTTeesssfqessaeEN				86
Sbjct	13610	DTRTLSIS QSI NS LT SAE+QT QEETSE SKSLPQLTTEES SFQESSAE+N				13667
Query	85	QMTEVPW 65				
Sbjct	13668	QMTE PW 13674				

Range 129: 12551 to 12674

Score	Expect	Method	Identities	Positives	Gaps	Frame
77.0 bits(188) 2e-12() Compositional matrix adjust. 95/126(75%) 101/126(80%) 2/126(1%) -2						
Features:						
Query	379	NQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTG				200
Sbjct	12551	NQMTE PWT STSL QSSS+ NIFSS S+NED S DTRTLSIS QS NSLLT				12608

Query 199 ssaeeqtageetsEHSKSLPQLTTeesssfqessaeENQMTEVPWtlstslsqssssQAKN 20
SAE+QT QEETSE SKSLPQLTTEES SFOESSAE+NQMTE PWTlSTSLSQ+SS+ N
Sbjct 12609 LSAEDQTNQEETSELSKSLPQLTTEESISFQESSAEQNQMTEEPWTlSTSLSQTSSTNN 12668

Query 19 IFSSPS 2
IFSS S
Sbjct 12669 IFSSQS 12674

GD17263 [Drosophila simulans]
Sequence ID: **ref[XP_002105717.1]** Length: 995 Number of Matches: 11

► **See 1 more title(s)**
Range 1: 628 to 810

Score	Expect	Method	Identities	Positives	Gaps	Frame
131 bits(329)	5e-31()	Compositional matrix adjust.	136/191(71%)	146/191(76%)	19/191(9%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeeqtageetsEHSKSLPQ-				428
Sbjct	628	NIFSSPS+NEDNISQEDTRTLS S PQS TANSLLT SSAEE T QEETSE SK+LPQ				687
Query	427	-----LTTeesssfqessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDN				278
Sbjct	688	TT+ESSSFQESSAEENQMTEVPW + S ++ S S+NED				739
Query	277	ISQEDTRTLSISVPQSIATANSLLTGssaeeqtageetsEHSKSLPQLTTeesssfqess				98
Sbjct	740	SQEDTRTLS S PQS A+SLLT SSAE+QT +EETSE SKSLPQLTTEESSSFQESS				799
Query	97	aeENQMTEVPW 65				
Sbjct	800	AEENQMTEVPW 810				

Range 2: 434 to 634

Score	Expect	Method	Identities	Positives	Gaps	Frame
127 bits(319)	8e-30()	Compositional matrix adjust.	147/211(70%)	158/211(74%)	20/211(9%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeeqtageetsEHSKSLPQL				425
Sbjct	434	NIFSSPS+NEDNISQEDTRTLS S PQS TANSLLT SSAEE T +EETSE SK+LPQ				493
Query	424	T-----TeesssfqessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNI				275
Sbjct	494	T T + SSFQESSAEENQMTEVPW + S ++ S S+NED				545
Query	274	SQEDTRTLSISVPQSIATANSLLTGssaeeqtageetsEHSKSLPQLTTeesssfqessa				95
Sbjct	546	SQEDTRT+SIS QS T NSLLT SAE+QT QEETSE SKSLPQLTTEESSSFQESSA				603
Query	94	eENQMTEVPWtlstslsqssssQAKNIFSSPS 2				
Sbjct	604	EEN +TEVPWTLSTSL Q SS NIFSSPS				634

Range 3: 537 to 721

Score	Expect	Method	Identities	Positives	Gaps	Frame
124 bits(312)	9e-29()	Compositional matrix adjust.	142/187(76%)	149/187(79%)	13/187(6%)	-2
Features:						
Query	592	SPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeeqtageetsEHSKSLPQLTTe				413
Sbjct	537	S S+NED SQEDTRT+SIS QS T NSLLT SAE+QT QEETSE SKSLPQLTTEE				594
Query	412	sssfqessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSISVPQ				233
Sbjct	595	SSSFQESSAEEN +TEVPWTLSTSL Q SS NIFSSPS+NEDNISQEDTRTLS S PQ				654
Query	232	SIATANSLLTGssaeeqtageetsEHSKSLPQ-----LTTeesssfqessaeEN				86
Sbjct	655	S TANSLLT SSAEE T QEETSE SK+LPQ TT+ESSSFQESSAEEN				714
Query	85	QMTEVPW 65				
Sbjct	715	QMTEVPW 721				

Range 4: 732 to 918

Score	Expect	Method	Identities	Positives	Gaps	Frame
118 bits(295)	2e-26()	Compositional matrix adjust.	143/197(73%)	155/197(78%)	10/197(5%)	-2
Features:						
Query	592	SPSLNEDNISQEDTRTLSISVPOSIATANSLLTGssaeegtagaetsEHSKSLPQLTTe				413
Sbjct	732	S S+NED SQEDTRTLS S PQS A+SLLT SSAE+QT +EETSE SKSLPQLTTEE				791
Query	412	sssfqessaeENQMTEVPWtlstslsqsssQAKNIFSSPSLNEDNISQEDTRTLSISVPQ				233
Sbjct	792	SSSFQESSAEENQMTEVPWT S+ ++ S S+NED SQEDTRT+SIS Q				841
Query	232	SIATANSLLTGssaeegtagaetsEHSKSLPQLTTeesssfqessaeENQMTEVPWtlst				53
Sbjct	842	S T NSLLT SAE+QT QEETSE SKSLPQLTTEESSSFQESSAEEN +TEVPWT+ST				901
Query	52	slsqsssQAKNIFSSPS 2				
Sbjct	902	SL Q SS NIFSSPS 918				

Range 5: 17 to 201

Score	Expect	Method	Identities	Positives	Gaps	Frame
114 bits(285)	4e-25()	Compositional matrix adjust.	139/195(71%)	152/195(77%)	10/195(5%)	-2
Features:						
Query	592	SPSLNEDNISQEDTRTLSISVPOSIATANSLLTGssaeegtagaetsEHSKSLPQLTTe				413
Sbjct	17	S S+NED SQEDTRTLS S PQS A+SLLT SSAE+QT +EETSE SKSLPQLTTEE				76
Query	412	sssfqessaeENQMTEVPWtlstslsqsssQAKNIFSSPSLNEDNISQEDTRTLSISVPQ				233
Sbjct	77	SSSFQESSAEENQMTEVPW + S ++ S S+NED SQEDTRT+SIS Q				126
Query	232	SIATANSLLTGssaeegtagaetsEHSKSLPQLTTeesssfqessaeENQMTEVPWtlst				53
Sbjct	127	S T NSLLT SAE+QT QEET+E SKSLPQLTTEESSSFQESSAEEN +TEVPWT+ST				186
Query	52	slsqsssQAKNIFSS 8				
Sbjct	187	SL Q SS NIFSS 201				

Range 6: 346 to 526

Score	Expect	Method	Identities	Positives	Gaps	Frame
112 bits(280)	1e-24()	Compositional matrix adjust.	133/183(73%)	143/183(78%)	12/183(6%)	-2
Features:						
Query	583	LNEDNISQEDTRTLSISVPOSIATANSLLTGssaeegtagaetsEHSKSLPQLTTe				404
Sbjct	346	+N++ SQEDTR + IS QS T NSLLT SAE+QT QEETSE SKSLPQLTTEESSS				403
Query	403	fqessaeENQMTEVPWtlstslsqsssQAKNIFSSPSLNEDNISQEDTRTLSISVPQ				224
Sbjct	404	FOESSAEEN +TEVPWTLSTSL Q SS NIFSSPS+NEDNISQEDTRTLS S PQS				463
Query	223	TANSLLTGssaeegtagaetsEHSKSLPQLT-----TeesssfqessaeENQMTE				74
Sbjct	464	TANSLLT SSAEE T +EETSE SK+LPQ T T + SSFQESSAEENQMTE				523
Query	73	VPW 65				
Sbjct	524	VPW 526				

Range 7: 821 to 972

Score	Expect	Method	Identities	Positives	Gaps	Frame
109 bits(272)	2e-23()	Compositional matrix adjust.	119/154(77%)	126/154(81%)	2/154(1%)	-2
Features:						
Query	592	SPSLNEDNISQEDTRTLSISVPOSIATANSLLTGssaeegtagaetsEHSKSLPQLTTe				413
Sbjct		S S+NED SQEDTRT+SIS QS T NSLLT SAE+QT QEETSE SKSLPQLTTEE				

Sbjct	821	SQSVNEDKTSQEDTRTVSIS--QSKTTTNSLLTDLSAEDQTKQEETSELSKSLPQLTTEE	878
Query	412	sssfgessaeENQMTEVPWt1stslsgssssQAKNIFSSPSLNEDNISQEDTRTLSISVPQ	233
Sbjct	879	SSSFQESSAEEN +TEVPWT+STSL Q SS NIFSSPS+NEDNISQEDTRTLS S Q	938
Query	232	SIATANSLLTGssaeeqtageetsEHSKSLPQLT	131
Sbjct	939	S TANSLLT SSAEE T QEETSE SK+LPQ T	972

Range 8: 106 to 233

Score	Expect	Method	Identities	Positives	Gaps	Frame
105 bits(262)	3e-22()	Compositional matrix adjust.	99/130(76%)	107/130(82%)	2/130(1%)	-2
Features:						
Query	592	SPSLNEDNISQEDTRTLSISVPOSIATANSLLTGssaeeqtageetsEHSKSLPQLTTEE				413
Sbjct	106	S S+NED SQEDTRT+SIS QS T NSLLT SAE+QT QEET+E SKSLPQLTTEE				163
Query	412	sssfgessaeENQMTEVPWt1stslsgssssQAKNIFSSPSLNEDNISQEDTRTLSISVPO				233
Sbjct	164	SSSFQESSAEEN +TEVPWT+STSL Q SS NIFSS ++NEDNISQEDTRTLS S PQ				223
Query	232	SIATANSLLT	203			
Sbjct	224	S TANSLLT	233			

Range 9: 912 to 972

Score	Expect	Method	Identities	Positives	Gaps	Frame
62.8 bits(151)	4e-08()	Compositional matrix adjust.	49/61(80%)	51/61(83%)	0/61(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeeqtageetsEHSKSLPQL				425
Sbjct	912	NIFSSPS+NEDNISQEDTRTLS S QS TANSLLT SSAEE T QEETSE SK+LPQ				971
Query	424	T	422			
Sbjct	972	T	972			

Range 10: 197 to 233

Score	Expect	Method	Identities	Positives	Gaps	Frame
58.9 bits(141)	7e-07()	Compositional matrix adjust.	30/37(81%)	32/37(86%)	0/37(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLT		494		
		NIFSS ++NEDNISQEDTRTLS S PQS TANSLLT				
Sbjct	197	NIFSSQTVNEDNISQEDTRTLSTSFPQSSTTANSLLT		233		

Range 11: 346 to 440

Score	Expect	Method	Identities	Positives	Gaps	Frame
53.9 bits(128)	3e-05()	Compositional matrix adjust.	72/97(74%)	78/97(80%)	2/97(2%)	-2
Features:						
Query	292	LNEDNISQEDTRTLSISVPOSIATANSLLTGssaeeqtageetsEHSKSLPQLTTEesss	113			
Sbjct	346	+N++ SQEDTR + IS QS T NSLLT SAE+QT QEETSE SKSLPQLTTEESSS	403			
Query	112	fgessaeENQMTEVPWt1stslsgssssQAKNIFSSPS	2			
Sbjct	404	FQESSAEEN +TEVPWTLSTSL Q SS NIFSSPS	440			

Range 1: 1321 to 1495

Score	Expect	Method	Identities	Positives	Gaps	Frame
115 bits(289)	1e-25()	Compositional matrix adjust.	124/179(69%)	141/179(78%)	4/179(2%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISV PQSIATANSLLTG	ssaeeqtaqeets	EH	SKSLPQL	425
Sbjct	1321	IFSS S++ED SQE T IS PQS A NSLLT SSA +QT Q+E +E SKSLPQ				1376
Query	424	TTeesssffgessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct	1377	TT+ES SFQESS +ENQM+E+PWTLLSTS Q S++ K+ FSS S+ ED SQEDTRTLSI				1436
Query	244	SVPQSIATANSLLTG	ssaeeqtaqeets	EH	SKSLPQLTTeesssffgessaeENQMTEVP	68
Sbjct	1437	S PQS AT NSLLT SSAE+QT Q+ET+E SKSLPQ TTEES SFQESSAEENQM+EVP				1495
Sbjct		SFPQSYATENSLLTVSSAEDQTIQKETTEISKSLPQSTTEESISFQESSAEENQMSEVP				

Range 2: 796 to 971

Score	Expect	Method	Identities	Positives	Gaps	Frame
108 bits(271)	4e-23()	Compositional matrix adjust.	113/181(62%)	135/181(74%)	6/181(3%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISV PQSIATANSLLTG	ssaeeqtaqeets	EH	SKSLPQL	425
Sbjct	796	IFSS S++ED SQE T IS PQS A NSLLT SSA +QT Q+E +E SKSLPQ				851
Query	424	TTeesssffgessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI				245
Sbjct	852	TT+ES SFQESS +ENQM+E+PWTLLSTS Q S++ K+ FSS S+ ED SQEDTRTLSI				911
Query	244	SVPQSIATANSLLTG	ssaeeqtaqeets	EH	SKSLP-QLTTeesssffgessaeENQMTEVP	68
Sbjct	912	S PQS AT NSLLT S+ ++ + ++ + S S+P Q TTEE SS QESSAEENQMTE+P				970
Sbjct		SFPQSYATENSLLTVSNEDKTSQEDTRTV-SISVPQQYTTEERSSSLQESSAEENQMTEMP				
Query	67	W 65				
Sbjct	971	W 971				

Range 3: 680 to 895

Score	Expect	Method	Identities	Positives	Gaps	Frame
100 bits(250)	2e-20()	Compositional matrix adjust.	133/220(60%)	160/220(72%)	23/220(10%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISV PQSIATANSLLTG	ssaeeqtaqeets	EH	SK-----	440
Sbjct	680	+IFSS S++E+ ISQ+DTRT+SIS+PQ +TAN LLT SSAE+QT QEET+E S				739
Query	439	-----SLPQL-TTeesssffgessaeENQMTEVPWtlstslsqssssQAKNIFS				302
Sbjct	740	SLPQ TTE+SSS Q+SSAE+NQMTEVPWTL TSL QSS++ K IFS				799
Query	301	DKTSQEDTRTLSISLPQQSTTEKSSSLQSSAEKNQMTEVPWTLTSLPQSSTTKRIFS				
Query	301	SPSLNEDNISQEDTRTLSISV PQSIATANSLLTG	ssaeeqtaqeets	EH	SKSLPQLTTe	122
Sbjct	800	S S++ED SQE T IS PQS A NSLLT SSA +QT Q+E +E SKSLPQ TT+E				855
Sbjct		SQSVDDEKASQEYT----ISFPQSYAIENSLLTVSSAIDQTMQKEITEISKSLPQFTTDE				
Query	121	sssfgessaeENQMTEVPWtlstslsqssssQAKNIFSSPS		2		
Sbjct	856	S SFQESS +ENQM+E+PWTLLSTS Q S++ K+ FSS S				895
Sbjct		SISFQESSEKENQMSELPWTLSTSHHQLSTKTKSTFSSQS				

Range 4: 575 to 802

Score	Expect	Method	Identities	Positives	Gaps	Frame
99.0 bits(245)	8e-20()	Compositional matrix adjust.	125/230(54%)	150/230(65%)	31/230(13%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISV PQSIATANSLLTG	ssaeeqtaqeets	EH	-----	446
Sbjct	575	+IFSS S+ ED SQE+TRTLSIS PQS AT NSLLT S + E+				634
Query	445	SIFSSHSVEEDKTSQENTR TLSISFPQSYATENSLLTVSKESSSLQESSAEENQMTEMPW				
Query	445	--SKSLPQLTTeesssff-gessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNI				275
Sbjct	635	S SLPQL T++ QESSAEENQMTEV W + S S + ++IFSS S++E+ I				692
Sbjct		TLSTSLPQLKTKKEIRSPQESSAEENQMTEVTW--TLSTSLPQLKTESIFSSQSVDENEI				
Query	274	SQEDTRTLSISV PQSIATANSLLTG	ssaeeqtaqeets	EH	SK-----	149

Sbjct 693 SQ+DTRT+SIS+PQ +TAN LLT SSAE+QT QEET+E S 752

Query 148 SLPQL-TTeesssfgessaeENQMTEVPWtlstslsgssssQAKNIFSSPS 2

Sbjct 753 SLPQ TTE+SSS Q+SSAE+NQMTEVPWTL TSL QSS++ K IFSS S 802

Range 5: 21 to 190

Score	Expect	Method	Identities	Positives	Gaps	Frame
94.7 bits(234)	2e-18()	Compositional matrix adjust.	112/183(61%)	130/183(71%)	16/183(8%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTSLISV PQSIATANSLLTGssaeegtaqeetsEHSKSLPQL				425
Sbjct	21	+IFSS S++E+ SQ+DTRT+SIS+PQ +T NSLLT SSAE+QT Q+ET+E SKSLPQ				80
		SIFSSQSVDENETSQKDTRTISISLPQLGSTPNLLTVSSAEDQTVQKETTEISKSLPQS				
Query	424	TTeesssfgessaeENQMTEVPWtlstslsgssssQAKNIFSSPSLNEDNISQEDTRTSLI				245
Sbjct	81	TT+ESSS QE SAEENQMTEVPWTLST S P ED SQEDTRTSLI				127
		TTKESSSLQEFSAEENQMTEVPWTLST-----SLPQSKEDKSSQEDTRTSLI				
Query	244	SVP-QSIATANSLLTGssaeegtaqeetsEHSKSLPQL--TTeesssfgessaeENQMTE				74
Sbjct	128	++P QS +S L SAE E S SLPQL TT++SSS QESSAEENQMTE				187
		TLPQQSTTEESSSLQEYSAEENQMTEVQWTPSTSLPQLSTTTTKSSSLQESSAEENQMTE				
Query	73	VPW 65				
Sbjct	188	+PW				
		MPW 190				

Range 6: 1255 to 1420

Score	Expect	Method	Identities	Positives	Gaps	Frame
94.4 bits(233)	3e-18()	Compositional matrix adjust.	113/201(56%)	134/201(66%)	35/201(17%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTSLISV PQSIATANSLLTGssaeegtaqeetsEHSKSLPQL				425
Sbjct	1255	+IFSS S+ ED S+EDTRTSLIS+PQ Q				1283
		SIFSSQSVEEDKTSKEDTRTSLISLPQ-----QS				
Query	424	TTeesssfgessaeENQMTEVPWtlstslsgssssQAKNIFSSPSLNEDNISQEDTRTSLI				245
Sbjct	1284	TTE+SSS Q+SSAE+NQMTEVPWTL TSL QSS++ K IFSS S++ED SQE T I				1339
		TTEKSSSLQQSSAEKNQMTEVPWTLTSLPQSSTKTKRIFSSQSVDEDKASQEYT----I				
Query	244	SVPQSIATANSLLTGssaeegtaqeetsEHSKSLPQLTTeesssfgessaeENQMTEVPW				65
Sbjct	1340	S PQS A NSLLT SSA +QT Q+E +E SKSLPQ TT+ES SFQESS +ENQM+E+PW				1399
		SFPQSYAIENSLLTVSSAIDQTMQKEITEISKSLPQFTTDESISFQESSEKENQMSELPW				
Query	64	tlstslsgssssQAKNIFSSPS 2				
Sbjct	1400	TLSTS Q S++ K+ FSS S				
		TLSTSHHQLSTTKTKSTFSSQS 1420				

Range 7: 1828 to 2030

Score	Expect	Method	Identities	Positives	Gaps	Frame
92.0 bits(227)	2e-17()	Compositional matrix adjust.	112/205(55%)	131/205(63%)	27/205(13%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTSLISV PQSIATANSL-LTGssaeegtaqeetsEHSKSLPQ				428
Sbjct	1828	++FS S++ED SQEDT T SIS+PQ T S+ L SSAEE E S SLPQ				1887
		SLFSRQSVDEDKTSQEDTWTPSISLPQQSTTEKSISLQESSAEENQMTEVPGTLSTSLPQ				
Query	427	L-----TTeesssfgessaeENQMTEVPWtlstslsgssssQ				320
Sbjct	1888	L TTE+SSS Q+SS EENQMTEVPW LST+L Q				1945
		LKTKNEDKTSQEDARTLSISLPQQSTTEKSSSLQQSSGEENQMTEVPWALSTTLPQLK--				
Query	319	AKNIFSSPSLNEDNISQEDTRTSLISV PQSIATANSLLTGssaeegtaqeetsEHSKSLP				140
Sbjct	1946	K+I SS S+ ED SQE RTLSIS PQS AT NSLLT SSAE+Q ++E++E SKSLP				2005
		TKSILSSQSVDEDKASQEYLRTLSISFPQSYATENSLLTVSSAEDQKMRKESTEISKSLP				
Query	139	QLTTeesssfgessaeENQMTEVPW 65				
Sbjct	2006	Q TTEES S +ESSA+ENQMTE+PW				
		QSTTEESISLKESSAKENQMTELPW 2030				

Range 8: 1125 to 1327

Score	Expect	Method	Identities	Positives	Gaps	Frame
-------	--------	--------	------------	-----------	------	-------

87.8 bits(216) 4e-16() Compositional matrix adjust. 120/234(51%) 143/234(61%) 64/234(27%) -2

Features:

Query	604	NIFSSPSLNEDNISQEDTRTLSISVPSI-----	518
Sbjct	1125	+IFS+ S+ ED SQEDTRTLSI++PQ SIFSTQSVEEDKSSQEDTRTLSITLPQQSTTEESSSLQEYSAEENQMTEVQWTPSTSFPQ	1184
Query	517	--ATANSLLTGssaeeqtaqeetsEHKSLPQLTTeesssfqessaeENQMTEVPWtlst	344
Sbjct	1185	+TANSLLT SSAE+QT QEET+E SKSLPQ TT+ESSS QESSAEENQ TE+ W LST LSSTANSLLTVSSAEDQTVQEETTEISKSLPQSTTKESSSLQESSAEENQNTLQWALST	1244
Query	343	slsqsssQAKNIFSSPSLNEDNISQEDTRTLSISVPSIATANSLLTGssaeeqtaqeet	164
Sbjct	1245	SL + S++A++IFSS S+ ED S+EDTRTLSIS+PQ SLPKLSTKAESIFSSQSVEEDKTSKEDTRTLSISLPQ-----	1281
Query	163	seHKSLSLPQLTTeesssfqessaeENQMTEVPWtlstslsqsssQAKNIFSSPS 2	
Sbjct	1282	Q TTE+SSS Q+SSAE+NQMTEVPWTL TSL QSS++ K IFSS S -----QSTTEKSSSLQSSAEKNQMTEVPWTLTSLPQSSTKTKRIFSSQS 1327	

Range 9: 511 to 667

Score	Expect	Method	Identities	Positives	Gaps	Frame
80.9 bits(198)	9e-14()	Compositional matrix adjust.	96/190(51%)	108/190(56%)	43/190(22%)	-2

Features:

Query	604	NIFSSPSLNEDNISQEDTRTLSISVPSIATANSLLTGssaeeqtaqeetsEHKSLPQL	425
Sbjct	511	IFSS S++ED SQEDTRTLSI + L Q GIFSSQSVDEDKTSQEDTRTLSIFL-----LQQS	539
Query	424	TTeesssfqessaeENQMTEVPWtlstslsqsssQAKNIFSSPSLNEDNISQEDTRTLSI	245
Sbjct	540	+TE+SSS QESSAEENQMTEV WTLSTSL Q K+IFSS S+ ED SQE+TRTLSI STEKSSSLQESSAEENQMTEVTWTLSTSLPQLK--TKSIFSSHVEEDKTSQENTRTLSI	597
Query	244	SVPQSIATANSLLTGssaeeqtaqeetsEH-----SKSLPQLTTeesssf-qessa	95
Sbjct	598	S PQS AT NSLLT S + E+ S SLPQL T++ QESSA SFPQSYATENSLLTVSKESSSLQESSAEENQMTEMPWTLSTSLPQLKTKKEIRSPQESSA	657
Query	94	eENQMTEVPW 65	
Sbjct	658	EENQMTEV W EENQMTEVTW 667	

Range 10: 1 to 103

Score	Expect	Method	Identities	Positives	Gaps	Frame
77.0 bits(188)	2e-12()	Compositional matrix adjust.	72/103(70%)	89/103(86%)	0/103(0%)	-2

Features:

Query	373	MTEVPWtlstslsqsssQAKNIFSSPSLNEDNISQEDTRTLSISVPSIATANSLLTGss	194
Sbjct	1	MTEVPWTLSTSL++ S++ ++IFSS S++E+ SQ+DTRT+SIS+PQ +T NSLLT SS MTEVPWTLSTSLTKLSTKTESIFSSQSVDENETSQKDTRTISISLPQLGSTPNLLTVSS	60
Query	193	aeeqtaqeetsEHKSLPQLTTeesssfqessaeENQMTEVPW 65	
Sbjct	61	AE+QT Q+ET+E SKSLPQ TT+ESSS QE SAEENQMTEVPW AEDQTVQKETTEISKSLPQSTTKESSSLQEFSAEENQMTEVPW 103	

Range 11: 325 to 517

Score	Expect	Method	Identities	Positives	Gaps	Frame
74.7 bits(182)	8e-12()	Compositional matrix adjust.	119/226(53%)	132/226(58%)	58/226(25%)	-2

Features:

Query	604	NIFSSPSLNEDNISQEDTRTLSISVPSIAT-ANSLLTGssaeeqtaqeetsEHKSLPQ	428
Sbjct	325	IFSS S++ED SQEDTRTLSI +PQ +T +S L SSAEE E T S SLPQ GIFSSQSVDEDKTSQEDTRTLSIFLPQQSSTEKSSSLQESSAEENQMTEVTWTLSTSLPQ	384
Query	427	L-----TTeesssfqessaeENQMTEVPWtlstslsqsssQ	320
Sbjct	385	L TTEESSS QESSAEENQMTE+PWTLSL Q LKTKNEDKTSQEDTRTVSISVPQQYTTEESSSLQESSAEENQMTEMPWTLSTSLPQLK--	442
Query	319	AKNIFSSPSLNEDNISQEDTRTLSISVPSIATANSLLTGssaeeqtaqeetsEHKSLP	140
Sbjct	443	K+IFS S+ ED SQEDTRT+SIS+PQ TKSIFSRQSVGEDKTSQEDTRTVSISLPQ-----	471
Query	139	QLTTeesssfqessaeENQMTEVPWtlstslsqsssQAKNIFSSPS 2	
Sbjct	472	Q TTEESSS QESSAEENQMTE+PWTLSL QSS++ K IFSS S QSTTEESSSLQESSAEENQMTEMPWTLSTSLPQSSTKTKGIFSSQS 517	

Range 12: 110 to 331

Score	Expect	Method	Identities	Positives	Gaps	Frame
72.4 bits(176)	4e-11()	Compositional matrix adjust.	122/225(54%)	144/225(64%)	32/225(14%)	-2
Features:						
Query	589	PSLNEDNISQEDTRTLSISVPQ-SIATANSLLTGssaaeqtagaetsEHSKSLPQL--TT				419
Sbjct	110	P ED SQEDTRTLSI++PQ S +S L SAAE E S SLPQL TT				169
Query	418	eesssfqessaeENQMTEVPWtlstslsqsssQAKNIFSSPSLNEDNISQEDTRTLSISV				239
Sbjct	170	++SSS QESSAEENQMTE+PWTLSLSTL Q K+IFS S+ ED SQEDTRT+SIS+				227
Query	238	PQ-----SIATANSLLTGssaaeqtagaetsEHSKSLPQL				134
Sbjct	228	PQQTTEESSSSLQESSAEENQMTEVTWTLSTLSLSQL-KTKNEDKTSQEDTRTVSISLPPQ				286
Query	133	-TTeesssfqessaeENQMTEVPWtlstslsqsssQAKNIFSSPS		2		
Sbjct	287	TTEESSS QESSAEEN MTE+PWTLSLSTL QSS++ K IFSS S		331		

Range 13: 203 to 432

Score	Expect	Method	Identities	Positives	Gaps	Frame
70.5 bits(171)	2e-10()	Compositional matrix adjust.	117/231(51%)	139/231(60%)	52/231(22%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQ-----SIATANSL				500
Sbjct	203	+IFS S+ ED SQEDTRT+SIS+PQ +++T+ S				262
Query	499	LTGssaaeqtagaetsEHSKSLPQL-TTeesssfqessaeENQMTEVPWtlstslsqsss				323
Sbjct	263	L + E++T+QE+T S SLPQ TTEESSS QESSAEEN MTE+PWTLSLSTL QSS+				321
Query	322	QAKNIFSSPSLNEDNISQEDTRTLSISVPQSIAT-ANSLLTGssaaeqtagaetsEHSKS				146
Sbjct	322	+ K IFSS S++ED SQEDTRTLSI +PQ +T +S L SSAEE E T S S				381
Query	145	LPQL-----TTeesssfqessaeENQMTEVPW		65		
Sbjct	382	LPQL TTEESSS QESSAEENQMTE+PW		432		

Range 14: 1023 to 1261

Score	Expect	Method	Identities	Positives	Gaps	Frame
68.9 bits(167)	6e-10()	Compositional matrix adjust.	127/241(53%)	145/241(60%)	49/241(20%)	-2
Features:						
Query	583	LNEDNISQEDTRTLSISVPQSIATANSL-LTGssaaeqtagaetsEHSKSLPQL-----				425
Sbjct	1023	ED SQEDT T SIS+PQ T S+ SSAEE E S S PQL				1082
Query	424	-----TTeesssfqessaeENQMTEVPWtlstslsqsssQAKNIFSSPSLNEDNISQE				266
Sbjct	1083	TTEESSS QESSAEENQMTE+PWTLSLSTL Q K+IFS+ S+ ED SQE				1140
Query	265	DTRTLSISVPQS-----IATANSLLTGssaae				185
Sbjct	1141	DTRTLSI++PQ +TANSLLT SSAE+				1200
Query	184	tagaetsEHSKSLPQLTTeesssfqessaeENQMTEVPWtlstslsqsssQAKNIFSSP				5
Sbjct	1201	QT QEET+E SKSLPQ TT+ESSS QESSAEENQ TE+ W LSTSL + S++A++IFSS				1260
Query	4	S 2				
Sbjct	1261	S 1261				

Range 15: 1532 to 1681

Score	Expect	Method	Identities	Positives	Gaps	Frame
58.2 bits(139)	1e-06()	Compositional matrix adjust.	83/150(55%)	91/150(60%)	23/150(15%)	-2
Features:						
Query	445	SKSLPQLTTeesssf-qessaeENQMTEVPWtlstslsqsssQAKNIFSS-----				299

Sbjct	1532	S SLPQL T++ QESSAEENQMTEV WTLSTSL QSS++ K IFSS STSLPQLKTKKEIRSPQESSAEENQMTEVTWTLSTSLPQSSTKTKRIFSSQSVDEDKTSQ	1591
Query	298	-----PSLNEDNISQEDTRTLSISVPQSIAT-ANSLLTGssaeeqtageetsEHS P +ED SQEDTRT+SISVPQ T S L SSAEE E S	152
Sbjct	1592	ANTMTLSISFPQSDDEDKTSQEDTRTVSISVPQQYTTEERSSSLQESSAEENQMTEMPWTLS	1651
Query	151	KSLPQLTTeess-sfgessaeENQMTEVPW 65 SLPQL T++ S S QESSA ENQMTEVPW	
Sbjct	1652	TSLPQLKTKKQSSISLQESSAVENQMTEVPW 1681	

Range 16: 1602 to 1831

Score	Expect	Method	Identities	Positives	Gaps	Frame
57.4 bits(137) 2e-06() Compositional matrix adjust. 115/230(50%) 137/230(59%) 37/230(16%) -2						
Features:						
Query	589	PSLNEDNISQEDTRTLSISVPQSIAT-ANSLLTGssaeeqtageetsEHSKSLPQLTTe				413
Sbjct	1602	P +ED SQEDTRT+SISVPQ T S L SSAEE E S SLPQL T++				1661
PQSDDEDKTSQEDTRTVSISVPQQYTTEERSSSLQESSAEENQMTEMPWTLSSTSLPQLKTKK						
Query	412	ss-sfgessaeENQMTEVPWtlstslsqss-----				329
Sbjct	1662	S S QESSA ENQMTEVPW LSTSL QS				1721
QSSISLQESSAVENQMTEVPWALSTSLPQSKTKKESSSLQESSAEENQMTEVPGTLSTSLP						
Query	328	--ssQAKNIFSSPSLNEDNISQEDTRTLSISVPQS--IATANSLLTGssaeeqtageets				161
Sbjct	1722	++ K+I S E+N E T TLS S+PQS NSLLT SSAE+QT Q+E++				1781
QLKTKKKSISLQESSAEENQMTEVTWTLSTSLPQSSTKTKKNSLLTVSSAEDQTMQKEST						
Query	160	EHSKSLPQLTTeesssfgessaeENQMTEVPWtlstslsqssssQAKNIFS				11
Sbjct	1782	E SKSLPQ TTEE+ SFOESSA+ENQ TE+ W LSTSL + S++A+++FS				1831
EISKSLPQSTTEETISFQESSAKENQKTELQWALSTSLPKLSTKAESLFS						

uncharacterized protein Dyak_GE27476, partial [Drosophila yakuba]
Sequence ID: **ref|XP_015044596.1|** Length: 253 Number of Matches: 3

► **See 1 more title(s)**
Range 1: 21 to 221

Score	Expect	Method	Identities	Positives	Gaps	Frame
98.6 bits(244)	4e-21()	Compositional matrix adjust.	136/201(68%)	152/201(75%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPSIATANSLLTGssaeeqtageetsEHSKSLPQL IFSS S+N+D S+EDTRTLSIS QS ANSL T SAE QT QEET+E LPQ				425
Sbjct	21	RIFSSQSVNKDRTSEEDTRTLSISPFQSSTMANSLPTVPSAEIQTIQEETTEFLNPLPQS				80
Query	424	TTeesssfgessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSI TTEESSSFQESS EENQMTE PWTLS L QSS+Q ++IFSS S++ED S+EDTRTLSI				245
Sbjct	81	TTEESSSFQESSEENQMTEGPWTLS TKLPQSSTQTESIFSSQSVDEDR TSEEDTRTLSI				140
Query	244	SVPSIATANSLLTGssaeeqtageetsEHSKSLPQLTTeesssfgessaeENQMTEVPW S QS ANS T SSAE+QT +EET+E LPQ TTESSSS +ESS EENQMTEVPW				65
Sbjct	141	SNFQSSTMANSFPTVSSAEDQTIKEETTEFLTPLPQSTTEESSSLKESSEENQMTEVPW				200
Query	64	tlstslsqssssQAKNIFSSPS 2 TLST L SS+Q + IFSS S				
Sbjct	201	TLSTKLLPSSTQTERIFSSQS 221				

Range 2: 119 to 249

Score	Expect	Method	Identities	Positives	Gaps	Frame
84.3 bits(207)	3e-16()	Compositional matrix adjust.	87/131(66%)	99/131(75%)	0/131(0%)	-2
Features:						
Query	601	IFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeeqtageetsEHSKSLPQLT				422
Sbjct	119	IFSS S++ED S+EDTRTLSIS QS ANS T SSAE+QT +EET+E LPQ T IFSSQSVDEDR TSEEDTRTLSISNFQSSTMANSFPTVSSAEDQTIKEETTEFLTPLPQST				178
Query	421	TeesssfgessaeENQMTEVPWtlstslsqssssQAKNIFSSPSLNEDNISQEDTRTLSIS				242
Sbjct	179	TEESSS +ESS EENQMTEVPWTLS L SS+Q + IFSS S+N+D S+EDTRTLSIS TEESSSLKESSEENQMTEVPWTLS TKLLPSSTQTERIFSSQSVNKDRTSEEDTRTLSIS				238
Query	241	VPQSIATANSL	209			
		QS ANSL				
Sbjct	239	NFQSSTMANSL	249			

Range 3: 1 to 124

Score	Expect	Method	Identities	Positives	Gaps	Frame
64.7 bits(156)	2e-09()	Compositional matrix adjust.	86/124(69%)	95/124(76%)	0/124(0%)	-2
Features:						
Query	373	MTEVPWtlstslsqsssQAKNIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGss				194
Sbjct	1	MTEVPWTLST L SS+Q + IFSS S+N+D S+EDTRTLSIS QS ANSL T S				60
Query	193	aeeqtageetsEHSKSLPQLTTeesssfqessaeENQMTEVPWtlstslsqsssQAKNIF				14
Sbjct	61	AE QT QEET+E LPQ TTESSSSFOESS EENQMT E PWTLS L QSS+Q ++IF				120
Query	13	SSPS 2				
Sbjct	121	SS S				
		SSQS 124				

uncharacterized protein Dyak_GE28509 [Drosophila yakuba]
Sequence ID: ref|XP_015045967.1| Length: 478 Number of Matches: 4

► See 1 more title(s)
Range 1: 68 to 268

Score	Expect	Method	Identities	Positives	Gaps	Frame
99.8 bits(247)	8e-21()	Compositional matrix adjust.	134/201(67%)	155/201(77%)	0/201(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeeqtageetsEHSKSLPQL				425
Sbjct	68	+IFSS S +++ IS+EDTRTLSIS QS ANSL T SSAE +T +E+T+E LPQ				127
Query	424	TTeesssfqessaeENQMTEVPWtlstslsqsssQAKNIFSSPSLNEDNISQEDTRTL				245
Sbjct	128	TTESSSSFOESS EEN MTEVPWTLST L Q+S+Q K+IFSS S++ED S+EDTRTL				187
Query	244	SVPQSIATANSLLTGssaeeqtageetsEHSKSLPQLTTeesssfqessaeENQMTEVP				65
Sbjct	188	S QS A SL T SSAE +T +E T+E LPQ TTESSSSFOESS EENQMT E VP				247
Query	64	tlstslsqsssQAKNIFSSPS 2				
Sbjct	248	TLST L Q+S+Q K+IFSS S				
		TLSTKLPQTSTQTKSIFSSQS 268				

Range 2: 165 to 296

Score	Expect	Method	Identities	Positives	Gaps	Frame
86.7 bits(213)	3e-16()	Compositional matrix adjust.	88/132(67%)	101/132(76%)	0/132(0%)	-2
Features:						
Query	604	NIFSSPSLNEDNISQEDTRTLSISVPQSIATANSLLTGssaeeqtageetsEHSKSLPQL				425
Sbjct	165	+IFSS S++ED S+EDTRTLSIS QS A SL T SSAE +T +E T+E LPQ				224
Query	424	TTeesssfqessaeENQMTEVPWtlstslsqsssQAKNIFSSPSLNEDNISQEDTRTL				245
Sbjct	225	TTESSSSFOESS EENQMT E VPWTLST L Q+S+Q K+IFSS S++ED S+EDTRTL				284
Query	244	SVPQSIATANSL 209				
Sbjct	285	S QS ANSL				
		SPFQSSTMANSL 296				

Range 3: 27 to 171

Score	Expect	Method	Identities	Positives	Gaps	Frame
72.0 bits(175)	3e-11()	Compositional matrix adjust.	102/145(70%)	116/145(80%)	0/145(0%)	-2
Features:						
Query	436	LPQLTTeesssfqessaeENQMTEVPWtlstslsqsssQAKNIFSSPSLNEDNISQEDTR				257
Sbjct	27	LPQ TTE SSSFOESS EENQMT E VPWTLST L QSS+Q ++IFSS S +++ IS+EDTR				86
		LPQSTTEGSSSFQESSEENQMT E VPWTLSTKLPQSSQTESIFSSQSEDKNRISKEDTR				

Score	Expect	Method	Identities	Positives	Gaps	Frame	
54.7 bits(130)	2e-05()	Compositional matrix adjust.	64/82(78%)	68/82(82%)	6/82(7%)	-2	
Features:							
Query	253	LSISVPQSIATANSLLTGssaeegtaqeetsEHSKSLPQLTTeesssfqessaeENQMTE					74
Sbjct	997	LSI +PQS ATANSLLT SSAEEQT Q+ETSE SKSLPQLTTEESSSSFQE+SAEENQMTE					1056
		LSIYLPQSSATANSLLTDSSAEEQTIQKETSELSKSLPQLTTEESSSSFQETSAEENQMTE					
Query	73	VPWtlstslsqsssQAKNIFSS 8					
		VPW 0 SS+ KNIFSS					

Sbjct 1057 VPW-----KQPSSRTKNIFSS 1072