

[BLAST®](#) » [blastn suite-2sequences](#) » RID-Z0P8CZAN114

BLAST Results

Blast 2 sequences

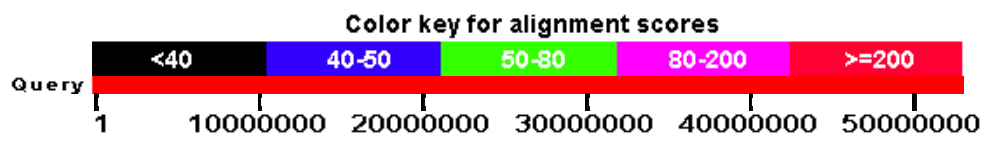
ref|NC_005111| (52716770 letters)

RID	Z0P8CZAN114 (Expires on 10-03 08:47 am)	Subject ID	NM_018984.3
Query ID	NC_005111.4	Description	Homo sapiens slingshot protein phosphatase 1 (SSH1), transcript variant 1, mRNA
Description	Rattus norvegicus strain mixed chromosome 12, Rnor_6.0		See details
Molecule type	dna	Molecule type	nucleic acid
Query Length	52716770	Subject Length	8537
		Program	BLASTN 2.5.0+

Graphic Summary

Distribution of 101 Blast Hits on the Query Sequence

Mouse over to see the define, click to show alignments



Description	Max score	Total score	Query cover	E value	Ident	Accession
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Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Homo sapiens slingshot protein phosphatase 1 (SSH1), transcript variant 1, mRNA	977	72495	0%	0.0	78%	NM_018984.3

Alignments

Homo sapiens slingshot protein phosphatase 1 (SSH1), transcript variant 1, mRNA

Sequence ID: **NM_018984.3** Length: 8537 Number of Matches: 1562

Range 1: 1976 to 3238

Score	Expect	Identities	Gaps	Strand	Frame
977 bits(2504)	0.0()	996/1273(78%)	53/1273(4%)	Plus/Plus	
Features:					
Query 48445554	TGCAGCGTGATGCGGTGTTTGGGATCCTCAGCAAAGTGAAGCCTCCCTATACATCCTGTG	48445613			
Sbjct 1976	TGGAGGATGATGCTATATTTGGGATCCTTACCAAAGTGAAGCCTTCCTATAAATCCTGTG	2035			
Query 48445614	CCGACTGCATGTACCC--AGC-AGCTGGGGCTCCTGAGGCCCTCATGGAGCGGCATGAA	48445669			
Sbjct 2036	CCGACTGCATGTACCTACAGCCAGC-GGGGCTCCTGAGGCCCTCAGGGAGCGATGTGAG	2094			
Query 48445670	GACCCCA--GCTCCTCTGCCATCTGCACCCAGCCGACCTTCCTCCCCACGTCACGTCTT	48445727			
Sbjct 2095	GACCCCAATGCTCC-C-GCCATCTGCACCCAGCCAGCCTTCCTACCCACATCACGTCTT	2152			
Query 48445728	CCCCAATGGCCACACAGCAATAGGTCCCAGCTCCGGAGAGGCCAACCTCAGGTCCAG	48445787			
Sbjct 2153	CCCCTGTGGCCCACTTGGCCAGCAGGTCCCGTGTCCGGAGAAGCCAGCCTCTGGCCCAA	2212			
Query 48445788	CTAACACCTCTCCA-TTCCTACTACCAGCGGGCTCCAGGAAGCCAGATGTGAGTGGTTCT	48445846			
Sbjct 2213	CCGA-ACCTCCCCCGTTCTTACCACCAGCAGGCTCCAGGAGGGCAGACACCAAGTGGCCCT	2271			
Query 48445847	GGAGCCGGGGTTGCCCCGAACACCAGCAAGCCTTCCAGAGCCTTCCAGAGAGACCTCG	48445906			
Sbjct 2272	GGGGCTGGAGCTGCCCTAGAGCCACCAGCCAGCCTTTTGGAACTTCCAGAGAGACCCCA	2331			
Query 48445907	AAAGCCCTTCAGAAATCTCTCCTGTGGAAGAAATCCCAGTGTGATAAGAACGCAGCCAAT	48445966			
Sbjct 2332	AAAGTCTTGCCAAAGTCCCTCCTTTTGAAGAAATTCACCTGTGATAAGAACCTCCAGC	2391			
Query 48445967	ACGGAGGCGGGCGGCAAGGAAGAAGTGTGACCAAGAAAGATCCGAAGCCCTCAAAGGAC	48446026			
Sbjct 2392	ACAGAAGTGGTAATAAAGGAAGAATCGTCACCCAAGAAAGATATGAAGCCAGCCAAGGAC	2451			
Query 48446027	CTGAGGCTCCTGTTTCACTCAAGAGGGGGAGAAGCCGACCGCCAATAGCTACCTGATGCAA	48446086			
Sbjct 2452	CTGAGGCTTCTGTTTCACTAATGAATCTGAGAAGCCGACAACCAACAGCTACCTGATGCAG	2511			
Query 48446087	CATCAGGAGTCCATTATCCAGTTGCAGAAGGCAGGCCTGGTCCGAAAGCACACCAAGAG	48446146			
Sbjct 2512	CACCAGGAGTCCATCATTAGCTGCAGAAGGCAGGCTTGGTCCGCAAGCACACCAAGAG	2571			
Query 48446147	CTGGAGAGGTTGAAGAGCCTGCCTTTCAGACTCACCATCTACTTGCCGGGACAGTGCCGCC	48446206			
Sbjct 2572	CTAGAGCGGCTGAAGAGCGTGCCCTGCAGACCCAGCACCTCCCTCCAGGGATGGCCCTGCC	2631			
Query 48446207	AGCAGGCTGGAGGCCAGCATCCCCGAGGAGGGTCAGGAGCCTG-CACAC-CCA-----	48446257			
Sbjct 2632	AGCAGGCTGGAGGCCAGCATCCCCGAGGAGAGCCAGGATCCAGCCGCGCTCCACGAGCTG	2691			
Query 48446258	-GCCC-----TA-G-ACAGCCAAGCTGGAAGTGAAGAGAAG-----CCTG--	48446294			
Sbjct 2692	GGCCCCCTGGTTATGCCAGCCAGGCCGGGAGTGATGAGAAGTCAGAGGCCGCCCGCT	2751			
Query 48446295	----TGGGCGGAGCCTCACAGAAGAGCCCTCCGCCCTACCTCCTCCTCCGCTAGATCAC	48446350			

Sbjct	2752	TCATTGGAAGGAGGCTCACTGAAGAGCCCCCTCCT---TTCTTCTACCGCTGGACCAC	2808
Query	48446351	ACCAGTAAAGACTTCTCTAAAGACTTCTGAAGTCCGCGTGCTACACTCCCACCCCTCC	48446410
Sbjct	2809	ACCAGT--AG-TTTCTCAAAAGACTTTCTGAAGACCATCTGCTACACCCCCACCTCCTCT	2865
Query	48446411	TCCATCAGCTCCAACCTGACCCGGAGCTCCAGCAGCGACAGCATCCACAGTGTCGAGGG	48446470
Sbjct	2866	TCCATGAGCTCCAACCTGACCCGGAGCTCCAGCAGCGATAGCATCCACAGTGTCGAGGG	2925
Query	48446471	AAGCCAGGGCTGGTGAAGCAGCGGGCGAGGAGATCGAGACGCGGCTCCGCTGGCCGGT	48446530
Sbjct	2926	AAGCCCGGGCTGGTGAAGCAGCGGACACAGGAGATTGAGACCCGGCTCCGCTGGCGGGC	2985
Query	48446531	CTCACTGTGTCTCCCACTGAAACGTTCCCATTCCTCGCCAAGCTGGGAAGTCTCAAC	48446590
Sbjct	2986	CTCACGCTCTCTCCCACTGAAGCGCTCACACTCTCTGCCAAGCTGGGAGTCTCACC	3045
Query	48446591	TTCTCCACGGAGGACCTGTCCAGTGAGGCTGACACGTCAACCATCGCCGACTCACAGGAT	48446650
Sbjct	3046	TTCTCAACGGGAAGACCTGTCCAGTGAGGCTGACCCGTCCACGTCGCTGACTCCAGGAC	3105
Query	48446651	GCCAAGTGACTCTCTCTCTCTCTTCTTCTGCCCCAACCAGGCGCACCTAGGAACCCCTCT	48446710
Sbjct	3106	ACCACCTTGAGTGAACTCTTCTCTCTTGCATGAGCCCCAGGGAACCCGAGGGACCCAGCT	3165
Query	48446711	GCGACCTCCAAACCATCAGGGAATCCGCCCCAGAGAACTTGAAAAATCCAGTGAGGGTG	48446770
Sbjct	3166	GCAACCTCCAAACCATCAGGGAATCCGCCCCAGAAAACTTAAAGAGCCCTTCGTGGATG	3225
Query	48446771	AACAAAAGCTGAC	48446783
Sbjct	3226	AGCAAAAAGCTGAC	3238

Range 2: 7690 to 8532

Score	Expect	Identities	Gaps	Strand	Frame
299 bits(763)	3e-79()	612/888(69%)	102/888(11%)	Plus/Plus	

Features:

Query	48451362	AGA-CACACAG-CCTCTGCCGCCCTGGCCCCCTGGCCTCGCTGCATGAGAAGACAGCTGC	48451419
Sbjct	7690	AGATCAC-CAGTCCTCCACTGTCTT-CCTGTGGCCTTGTGCTGATGAGAAGATAGCTGC	7747
Query	48451420	TTCTCTCC-----TC-TACCCCGTAATTATCTTTTACAACAGTGCCTTAATAATCGT	48451472
Sbjct	7748	TTCTCTCTCTTTTCTACACTGTAAATTATGTTTACAATTGAGTGCCTTAATAATAGT	7807
Query	48451473	TTACAAATACTGTGTATTTATGCGCAGCGTTTACGCTCTCATCTTTCGTGGCTGGGTACT	48451532
Sbjct	7808	TTACAAATACTATGTATTTATGCAAACTGTTAAAGTCTCATCTGTTATGATTGGATACT	7867
Query	48451533	TCGGTC----CCG--GTGGTTAAGATTAGCACCTGAGCTCGTCCCTACCCCCCATCCACG	48451586
Sbjct	7868	T-GGTCTGTGAGTAGTGGTCAGCATTTGGTTGTGAGCTTGTCCTACTCC--AT--ACG	7921
Query	48451587	TGTGTCACTCTGCTATGCAGTTG-ACATCCTGGGTCTCTGA-CTACTCCACCCAGCCT-GC	48451643
Sbjct	7922	TGTTTATC-CTGCTATGCAGTTTACATTGTGTGTTACATCTATTCCAAGGAGCCTTGC	7980
Query	48451644	T-GAATCCCCACAGGC---TA-TGC-GGACAT-C-GGCAAA--CCC---C-GAAAACTG	48451689
Sbjct	7981	TAGAAACAACACTGGCGGTTCTGCAAGGCCAGGCAGGCATTGGCCCATGCTGTGTCCCAT	8040
Query	48451690	AGGTAGGTAGTGAAGGA-CG-AGATTGGTTTGCCAGGCAGCCGAGAGGTGGTGCAGGCC	48451747
Sbjct	8041	AGG-AGCCAATGAAAGAACGTAGCTT-GGTCTGCTAGCCAGCCGTGGGGTGGCGCAGGCC	8098
Query	48451748	CAGCGTTCCTGAACCACAGCCCAAGACCACACCA--CCTGAACCTCTCAAGGTGCGCCT	48451805
Sbjct	8099	AGGCAGCCTCTGCACCAGAGTCCAGCACCTGCCCATTCCTCAGTCACACAA--TCATACT	8156
Query	48451806	CTAGTTT-ACAGAGGCTTGCCAACG-CCTACCCTCCACCCCTTCACACTCCCTCCTCTTC	48451863
Sbjct	8157	CTTCTTTCATAGAGATTTATTACCACCTAGAC--CACCC--T---AGTTT-TCCTCT-C	8207
Query	48451864	TGCCTGTGTCTGAGTCTCTT-GCTACA---TG--GGTACAGCTCACTCCAGAGGAGGAG	48451917
Sbjct	8208	TGTTAGTGTCTGAGCTCTTTTGCAACAAAATGTAGGTACAGACCAATCCCT--GTCCCT	8265
Query	48451918	TGGC--ACCAG-A---CCGCATCTTCACCT--TCAAACGCCCGCAGCCACCACCGTGC	48451969
Sbjct	8266	TCCCAATCAGGAGCTCCACA-CCATGAGTGTGTTGGTTTTCCAGAAGCTGCCA--GTG-	8321
Query	48451970	CGGATTCCTTCGTCA---CATTACAACCTCGATGGTTTTTTTTTTTattgtattgtttt	48452025
Sbjct	8322	-GG-TTCC--CGTGAATTGCGTTAAGATATCGATGATTTTTTTT---ATTGT-TT-TTCT	8372
Query	48452026	tcttgTTTTTT-atattatatatttAGAGGCGAGTATCTTTTGTACTGTGAATTTTCAGT	48452084
Sbjct	8373	TCTTGTTTTTTAAATAATATATTTAA-AGGCAGTATCTTTTGTACTGTGAATTTGCAGT	8431
Query	48452085	AGAAGAGGCATAGTGACATTTTTTTTTTTTACTTCTGTTGGTGTGTACTGTACATAATAG	48452144
Sbjct	8432	AGAAGATGCAGAAATGCAC---TTTTTTTTTACTTCTGTTGGTGTGTATTGT--AT-ATAG	8485

Query 48452145 TCTGCGTGCTTCTCGTGATGAGAATAAACACTTCCTTTATACATGTCC 48452192
 Sbjct 8486 TGTGTGTGCTTCTTGTGATGAAAATAAACTTTTCTTTATAAAT-TCC 8532

Range 3: 1485 to 1981

Score	Expect	Identities	Gaps	Strand	Frame
284 bits(723)	1e-74()	382/527(72%)	33/527(6%)	Plus/Plus	
Features:					
Query 48441982	CCAGCAGCCGGCAGATGACACCATAGCAGAGCCCAGTGAGTTCTTGCCAGAGACCTTGG	48442041			
Sbjct 1485	CCAGCAGCCTGTGGATGAC-CC-T-GCAGGACCTGGCGACTTCTTGCCAGAGACCCAGA	1541			
Query 48442042	TGGCGCCCTGGATACTCAGCTGCCCTGTTTGGAGATGCCACCCACCCCGGGCTCCCGAG	48442101			
Sbjct 1542	TGGACCCCGGAAAGCCAGCTGCCCTTCTTGGATGATGCCGCCAGCCC-GGCT---TAG	1597			
Query 48442102	AAGCCTGCCCTCGGGAGGACCTCTCTCCCTGTTGTTTCCGAAGACTCTCGGACCCCT	48442161			
Sbjct 1598	--G---GCCC-----CCC---CTCCCTGCTGTTTCCGGCGACTCTCAGACCCCT	1640			
Query 48442162	CCT-CCTTCCCAACCGTGATGGTGCGGGTGGCTGGTCCACTTAGAAGACCTTGAGAGGG	48442220			
Sbjct 1641	TCTGCCTTCCCTGAG-GATGAAACTGGCAGCTTGGTCCACCTGGAGGATCCGGAGAGGG	1699			
Query 48442221	ATGCTCTGTTAGAGGATGAGGCTCAGCCAGTGAGGTCGCAAGCTGGTCCCGA-GTTCC	48442279			
Sbjct 1700	AGGCTCTGTTGGAGGAAGCTGCTCCACCTGCAGAGGTGCACAGGCCGG-CCAGACAGCCC	1758			
Query 48442280	CAGGAAGGTGACAGGCTGTGTGAAAGGATGTAAAGAGGAACTGGAGTTTGGGAGCCCC	48442339			
Sbjct 1759	CAGCAAGGTTCCGGACTCTGTGAGAAGGATGTGAAGAAGAACTAGAGTTTGGGAGTCCC	1818			
Query 48442340	AAAGCCCGCAGCGGCTCCTTGCTCAGGTGGAGGAGCTGGAGAAGGATGGCAGCCCAAGA	48442399			
Sbjct 1819	AAAGGTGCGAGCGGCTCCTTGCTGCAGGTGGAGGAGACGGAAGGGAGGAGGGCTGGGA	1878			
Query 48442400	CCGGGGAGGTGGAGGCGGGCTCC-ACGCAGCTGGAGAGAGGTTTGCTTGACCAGGAAAA	48442458			
Sbjct 1879	GCAGGGAGGTGGGGGC-AGCTTCCAACCCAGCTCGATCAAAACCTGCTCAACTCGGAGAA	1937			
Query 48442459	CCTAATAACAACAACAGCAAGAGGAGCTGTCCCGATGACTTTGAGG	48442505			
Sbjct 1938	CCTA---AACAACAACAGCAAGAGGAGCTGTCCCAACGGCATGGAGG	1981			

Range 4: 623 to 819

Score	Expect	Identities	Gaps	Strand	Frame
246 bits(626)	3e-63()	179/197(91%)	0/197(0%)	Plus/Plus	
Features:					
Query 48430242	GGTCTGCCTTGCAAGTGCTTCAACAAGGCCTGTGAAGTGGCTCGGAGACATAACTACTTCC	48430301			
Sbjct 623	GGTCTGCCCTGCAGGTGCTTCAACAAGGCCTGCGAAGTGGCCGGAGGCACAACACTTCC	682			
Query 48430302	CGGGGGGAGTGGCACTCATCTGGGCCACCTACTATGAGAGCTGCATCAGCTCGGAGCAGA	48430361			
Sbjct 683	CCGGGGGTGTAGCTCTCATCTGGGTACCTACTATGAGAGCTGCATCAGCTCCGAGCAGA	742			
Query 48430362	GCTGCATCAATGAATGGAACGCCATGCAGGACCTGGAGTCCACGAGGCCCGACTCCCCCG	48430421			
Sbjct 743	GCTGCATCAACGAGTGAACGCCATGCAGGACCTGGAGTCTACGCGGCCCGACTCCCCCG	802			
Query 48430422	CGCTGTTCTGTGGACAAG	48430438			
Sbjct 803	CGCTATTTGTGGACAAG	819			

Range 5: 1237 to 1436

Score	Expect	Identities	Gaps	Strand	Frame
233 bits(593)	2e-59()	177/200(89%)	0/200(0%)	Plus/Plus	
Features:					
Query 48439006	AGGAACCAATCCAAGTGCCTGGTCCATTGCAAGATGGGCGTGAGCCGGTCTGCATCCACG	48439065			
Sbjct 1237	AGGAACCAATCCAAGTGCCTGGTGCATTGCAAAATGGGCGTGAGTCTCGCTCGGCCTCCACA	1296			
Query 48439066	GTCATAGCGTACGCCATGAAGGAGTTGGCTGGCCCTGGAGAAAGCGTTTAACTATGTG	48439125			
Sbjct 1297	GTCAATAGCTATGCAATGAAGGAATTCGGCTGGCCCTGGAAAAAGCATATAACTATGTA	1356			
Query 48439126	AAACAGAAGCGCAGCATCACGCGGCCAACGCAGGCTTTATGAGGCAGCTGTGAGAGTAT	48439185			
Sbjct 1357	AAGCAGAAGCGCAGCATCACGCGGCCAACGCAGGCTTTATGAGGCAGCTGTCTGAGTAT	1416			

Query 48439186 GAAGGTATCCTGGATGCAAG 48439205
 Sbjct 1417 GAAGGCATCTTGGATGCAAG 1436

Range 6: 4957 to 5602

Score	Expect	Identities	Gaps	Strand	Frame
212 bits(540)	4e-53()	450/670(67%)	57/670(8%)	Plus/Plus	
Features:					
Query 48449092	CCACAGCTCCATCCTGCGGTTGGCTGGTT	CAGCCAGAC - AGTTC	CGTGAGACCACAACAT	48449150	
Sbjct 4957	CCACAATTCATCTTGCCCTCAGCTGGGTC	CGCCAGATTA	ACTCAGTGAAACCAGAAAGC	5016	
Query 48449151	CTTTAAGGATACGGTGTGTCTGGAAGT	ACACGGATGGGGG	CCTCCACCG --- CACTGGT	48449207	
Sbjct 5017	CTTCAAGGACCAGCTGAATTTCTGAAAGT	G - AGTGA - GTGAGCCATCATCTTA	ACATTGGC	5074	
Query 48449208	TAGAACGGAGT - CTCAAAACGGCCATC	CTGGTGAACGCC - A - - AGTG - TCT	CTAGGATC	48449262	
Sbjct 5075	CAGAACTGTGTTCCCAAA - - GCTATT	CTAGAAAGCACCCAGGAGGGATCTGC	AGGAAC	5132	
Query 48449263	TAGGCCAGTTC - TCTTTTCATTCTCT - TGGGG - - - GTC	TTTGTGAGC - TC - TGTCTC - AG		48449314	
Sbjct 5133	AAGGCTAGTTTCATATTTT - A - - CCT	AGTGAGCACAGTTTTTGCAAAAATCCTCC	TCCAG	5189	
Query 48449315	AACTCT - TCTACCTGGCGTGAC	tttttttttttttttAATACATGTGCGT	TATTTTACAG	48449373	
Sbjct 5190	GACTTTGTCTCCTTGAGTGA - - - - -	TTTTTAAAAATACATA - - CATTACTTT	TATAG	5239	
Query 48449374	GGCTTTATTTTCCCACTACTGTCAATGG	CAGTCACCTTAAAAAGCGATCATCCACT	TTTTT	48449433	
Sbjct 5240	GGAGCTGTTTTCCCACTAGTGTCAATT	AAAAACACCTTAAAAGGTGATTATCCACT	TATT	5299	
Query 48449434	CCTGAAACCTGTGGGTTCTTCTATTCT	CCCCTCGGCCAACAAAAGC	aaaaaaaaaaaa	48449493	
Sbjct 5300	CCTAAACCTGTGGG - TTGTTCCCCCT	TTCCCTCAGCCAACAAAAGCATAGCCT	CAAAA	5358	
Query 48449494	aaaaaaGGCCAAGT - AATATATGT	CGCCAAGTCAATTTACATGGTGGG	CAATTTTT	48449552	
Sbjct 5359	AATA - - - TCAAGTTCGGTATGTTTT	GCCAAATCAAATTTATGTGGTAGAT	CAATTTTT	5414	
Query 48449553	GTGTCAAAATAATTCCTAGATTTGGTA	ATGATAGGCTTCCGCTGCGTTTTTT	AATCCCA	48449612	
Sbjct 5415	GTGTCAAAATAATCTTTTAAATTTAGT	GATGACAGGCTTTTGTTG - GTTTTTT	AACCACG	5473	
Query 48449613	TC - - TGTAAGAG - CGGCAGGATTTT	TGAAAACCTCATTTTGAAAAGCCGTAA - - TTTCT		48449667	
Sbjct 5474	TCTATGTATGAGAATGATATATTTT	TGAAAACCTTAATTTTG - AAAGCCATAATTTTCT		5532	
Query 48449668	GTTC - AAAGAGTCAGGACAGGAGGG	CAAACTGGAG - G - A - - - - - GGTCTCTGGATG		48449718	
Sbjct 5533	TATCTAAAGAGTTGGGGGTTGGGGTGT	GGAATCTGGAGAGTACAAGTTGGTCTTT	GGCTT	5592	
Query 48449719	CTGGCAGACT	48449728			
Sbjct 5593	CTGGCAAACT	5602			

Range 7: 1084 to 1236

Score	Expect	Identities	Gaps	Strand	Frame
165 bits(418)	7e-39()	132/153(86%)	1/153(0%)	Plus/Plus	
Features:					
Query 48437241	TCAGGG - TCGACTACATTTTAAATGT	CACTAGAGAAATCGACAATTTTTT	CCCTGGCCTG	48437299	
Sbjct 1084	TCAGGGGTTGATTACATTTTAAATGTT	ACCAGAGAAATCGATAATTTTTT	TCCTGGCTTA	1143	
Query 48437300	TTTGCATACCATAACATCCGAGTATAT	GACGAGGAGACCACGGACCTTCTTG	CCCACTGG	48437359	
Sbjct 1144	TTTGCATATCATAACATCCGAGTCT	ACGATGAAGAGACCACAGACCTCCT	CGCCACTGG	1203	
Query 48437360	AATGAGGCCTATCAGTTCA	AAACAAAGCGAAG	48437392		
Sbjct 1204	AATGAAGCGTATCATT	TATAAAACAAAGCGAAG	1236		

Range 8: 363 to 488

Score	Expect	Identities	Gaps	Strand	Frame
153 bits(387)	3e-35()	113/126(90%)	0/126(0%)	Plus/Plus	
Features:					
Query 48413128	GCAGGCCGTGCGCCTAGAGAGCGTCTGG	ACTGACCGTGCCGCTACATGGTTGTGGT	GTA	48413187	

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Sbjct  363      GCTGGCAGTGC GCCTGGAGAGCGCCTGGGCGGACCGGGTCCGGTACATGGTGGTGGTGTA 422
Query  48413188  CACCAGCGGGCGCCAGGACACCGAGGAGAACATCTTGTCTGGGAGTTGACTTTTCCAGTAA 48413247
Sbjct  423      CAGCAGCGGGCGCCAGGACACCGAGGAGAAATATCTTGTCTGGGAGTTGACTTTTCCAGTAA 482
Query  48413248  GGAGAG 48413253
Sbjct  483      GGAAAG 488

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Range 9: 8395 to 8532

Score	Expect	Identities	Gaps	Strand	Frame
146 bits(370)	3e-33()	125/146(86%)	8/146(5%)	Plus/Plus	

Features:

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Query  48452289  tttAAGAGGCAGTATCTTTTGTACTGTGAATTTTCAGTAGAAGAGGCATAGTGCACtttt 48452348
Sbjct  8395      TTTAA-AGGCAGTATCTTTTGTACTGTGAATTTGCAGTAGAAGATGCAGATGCAC---T 8450
Query  48452349  ttttttttACTTCTGTTGGTGTGTACTGTACATAATAGTCTGCGTGCTTCTCGTGATGAG 48452408
Sbjct  8451      TTTTTTTTACTTCTGTTGGTGTGTATTGT--AT-ATAGTGTGTGTGCTTCTTGTGATGAA 8507
Query  48452409  AATAAACACTTCCTTTATACATGTCC 48452434
Sbjct  8508      AATAAACTTTTCTTTATAAAT-TCC 8532

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Range 10: 195 to 305

Score	Expect	Identities	Gaps	Strand	Frame
140 bits(354)	2e-31()	101/111(91%)	0/111(0%)	Plus/Plus	

Features:

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Query  48408436  CAGCTTGAGCGAGAGCTTTTTTCATGGTGAAAGGAGCGGCCCTCTTCTTACAGCAGGGAAA 48408495
Sbjct  195      CAGCTTAAGTGAGAGCTTTTTTCATGGTGAAAGGCGCAGCCCTCTTCTTACAACAGGGAAG 254
Query  48408496  CAGCCCGCAGGGCCAGCGGAGTCTTCAGCACCCCTCACAAGCATGCAGGTGA 48408546
Sbjct  255      CAGCCCTCAAGGCCAGCGGAGTCTTCAGCACCCCTCACAAGCATGCAGGTGA 305

```

Range 11: 911 to 1040

Score	Expect	Identities	Gaps	Strand	Frame
124 bits(313)	2e-26()	107/130(82%)	0/130(0%)	Plus/Plus	

Features:

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Query  48433262  AGATCCGAAATGAGCTGGAGAAGCAAATGAACTGCAACCTGAAAGAGTTCAAGGAGTTCA 48433321
Sbjct  911      AGATTCTGAATGAATTAGAGAAACAGATGAATTGTAACCTGAAGGAACCAAGGAATTTA 970
Query  48433322  TCGATAACGAGATGCTGCTCATCTTGGGCCAGATGGACAAGCCCTCCCTTATCTTTGACC 48433381
Sbjct  971      TAGACAATGAGATGCTACTTATCTTGGGACAGATGGACAAGCCCTCCCTTATCTTCGATC 1030
Query  48433382  ATCTTTATCT 48433391
Sbjct  1031      ATCTTTATCT 1040

```

Range 12: 819 to 911

Score	Expect	Identities	Gaps	Strand	Frame
94.9 bits(237)	1e-17()	78/93(84%)	0/93(0%)	Plus/Plus	

Features:

```

Query  48431653  GCCGACAGAAGGAGAAAGAACTGAGCGTCTCATTAAAGCCAAACTCCGGAGTATCATGAT 48431712
Sbjct  819      GCCCACTGAAGGGGAAAGGACCGAGCGCCTCATCAAAGCCAAGCTCCGAAGCATCATGAT 878
Query  48431713  GAGCCAGGACCTTGAGAAATGTGACTTCTAAGGA 48431745
Sbjct  879      GAGCCAGGATCTAGAAAATGTGACTTCCAAGA 911

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Range 13: 559 to 625

Score	Expect	Identities	Gaps	Strand	Frame
85.9 bits(214)	6e-15()	61/67(91%)	0/67(0%)	Plus/Plus	

Features:

Query 48419955 GGGTTTCAGTGTGAGCACGGCGGGCAGGATGCACATATTCAGCCGGTGTCTGTCCAGGCC 48420014
 Sbjct 559 GGGTTTCAGCGTGAGCACAGCAGGAAGGATGCACATATTTAAGCCTGTGTCTGTCCAGGCC 618
 Query 48420015 ATGTGGT 48420021
 Sbjct 619 ATGTGGT 625

Range 14: 559 to 625

Score	Expect	Identities	Gaps	Strand	Frame
85.9 bits(214)	6e-15()	61/67(91%)	0/67(0%)	Plus/Plus	

Features:

Query 48426812 GGGTTTCAGTGTGAGCACGGCGGGCAGGATGCACATATTCAGCCGGTGTCTGTCCAGGCC 48426871
 Sbjct 559 GGGTTTCAGCGTGAGCACAGCAGGAAGGATGCACATATTTAAGCCTGTGTCTGTCCAGGCC 618
 Query 48426872 ATGTGGT 48426878
 Sbjct 619 ATGTGGT 625

Range 15: 299 to 367

Score	Expect	Identities	Gaps	Strand	Frame
78.5 bits(195)	1e-12()	60/69(87%)	0/69(0%)	Plus/Plus	

Features:

Query 48412654 CAGGTGACCTGCCTCAGCACCTGCAAGTGATGATCAACCTCCTGCGCTGTGAAGACAGAA 48412713
 Sbjct 299 CAGGTGATCTGCCTCAACATCTTCAGGTGATGATCAACCTTCTGCGTTGCGAAGACAGAA 358
 Query 48412714 TCAAACCTGG 48412722
 Sbjct 359 TCAAGCTGG 367

Range 16: 487 to 557

Score	Expect	Identities	Gaps	Strand	Frame
78.1 bits(194)	1e-12()	61/71(86%)	0/71(0%)	Plus/Plus	

Features:

Query 48418985 AGCAAAAGCTGTACAATCGGGATGGTCTTCGACTGTGGAGCGACACCAAGATCCACCTT 48419044
 Sbjct 487 AGTAAAAGCTGCACCATTTGGGATGGTCTTCGACTGTGGAGCGACACGAAAATCCACCTT 546
 Query 48419045 GATGGGGACGG 48419055
 Sbjct 547 GATGGAGATGG 557

Range 17: 487 to 557

Score	Expect	Identities	Gaps	Strand	Frame
78.1 bits(194)	1e-12()	61/71(86%)	0/71(0%)	Plus/Plus	

Features:

Query 48425650 AGCAAAAGCTGTACAATCGGGATGGTCTTCGACTGTGGAGCGACACCAAGATCCACCTT 48425709
 Sbjct 487 AGTAAAAGCTGCACCATTTGGGATGGTCTTCGACTGTGGAGCGACACGAAAATCCACCTT 546
 Query 48425710 GATGGGGACGG 48425720
 Sbjct 547 GATGGAGATGG 557

Range 18: 5804 to 5919

Score	Expect	Identities	Gaps	Strand	Frame
77.0 bits(191)	3e-12()	89/117(76%)	9/117(7%)	Plus/Minus	

Features:

Query 47166601 GAGACAGGGTTTTTCCCTGTAGCCCTGGCTGTTCTGGAATC---AC---AGA-GATCCG 47166653
 Sbjct 5919 GAGACGGGGTTTCACCATGTTGGCCAGGCTGGTCTAGAATCCTGACCTCAGATGATCCG 5860
 Query 47166654 CCTGCCTCTGCCT-CATGAGTGCTGGGATTAAAGGCGTGTGCCACCACTCCCAGCC 47166709
 Sbjct 5859 CCTGCCTCGGCCTCCCAAAGTGCTAGGATTACAGGCGTGAGCCACC-GCGCCCGGCC 5804

Range 19: 5805 to 5884

Score	Expect	Identities	Gaps	Strand	Frame
77.0 bits(191)	3e-12()	69/82(84%)	4/82(4%)	Plus/Minus	

Features:

Query 24796491 AGAACTCCTGGACTCA-ATCGATCCTCTGTCTCAGCCTCCCGA-GTAGCTGGGACTACA 24796548
 Sbjct 5884 AGAACTCCTGACCTCAGAT-GATCCGCCTGCCTCGGCCTCCCAAAGT-GCTAGGATTACA 5827
 Query 24796549 GGC GTGCGCCACCGCGCCCGGC 24796570
 Sbjct 5826 GGC GTGAGCCACCGCGCCCGGC 5805

Range 20: 5787 to 5936

Score	Expect	Identities	Gaps	Strand	Frame
75.4 bits(187)	9e-12()	108/152(71%)	5/152(3%)	Plus/Plus	

Features:

Query 16900925 AAAAGGCTAGGTG-TGGGGCCGGGCTTGGTGGCACATGCCTTTAATCCCAGCAC-TAGGG 16900982
 Sbjct 5787 AAAATGCTGTATGATGGGGCCGGGCGCGGTGGCTCACGCCTGTAATCCTAGCACTTTGGG 5846
 Query 16900983 AGGCTGACTCAGGCCGATCCGGGTAGGTTTGAAG-CCAAGTTCTAGCAAGGGCTACATAG 16901041
 Sbjct 5847 AGGCCGAGGCAGGCGGATCATCTGAGGTCAAGGAGTTCTAG-ACCAGCCTGGCCAACATGG 5905
 Query 16901042 AGAGACCCCTGTCTCaaaaaacaacaaaaa 16901073
 Sbjct 5906 TGAAACCCCGTCTCTACTAA-AAATACAAAAA 5936

Range 21: 5802 to 5895

Score	Expect	Identities	Gaps	Strand	Frame
74.6 bits(185)	2e-11()	75/94(80%)	8/94(8%)	Plus/Plus	

Features:

Query 31265302 GGAGCTGGGCGTGGTGGCGCACGCCCTTCAATCCCAGCACTT-GGGAGGCAGAAGCAGGCG 31265360
 Sbjct 5802 GGGGCCGGGCGCGGTGGCTCACGCCTGTAATCCTAGCACTTTGGGAGGCCGAGGCAGGCG 5861
 Query 31265361 GATC-TCT---GT---GAGTTCGAGGCCAGCCTG 31265387
 Sbjct 5862 GATCATCTGAGGTCAGGAGTTCTAGACCAGCCTG 5895

Range 22: 5791 to 5884

Score	Expect	Identities	Gaps	Strand	Frame
73.8 bits(183)	3e-11()	77/96(80%)	9/96(9%)	Plus/Minus	

Features:

Query 7353822 AGAACTCCTGGACTCAAGA-GATCCTCCTGTCTCAGCCTCCCGA-GTAGCTGGGACTACA 7353879
 Sbjct 5884 AGAACTCCTGACCTCA-GATGATCCGCCTGCCTCGGCCTCCCAAAGT-GCTAGGATTACA 5827
 Query 7353880 GGC GTGCGCCACCGCGCCCGC-----T-ATACAGCA 7353910
 Sbjct 5826 GGC GTGAGCCACCGCGCCCGGCCCATCATACAGCA 5791

Range 23: 5791 to 5884

Score	Expect	Identities	Gaps	Strand	Frame
73.8 bits(183)	3e-11()	77/96(80%)	9/96(9%)	Plus/Minus	

Features:

Query 7116010 AGAACTCCTGGACTCAAGA-GATCCTCCTGTCTCAGCCTCCCGA-GTAGCTGGGACTACA 7116067
 Sbjct 5884 AGAACTCCTGACCTCA-GATGATCCGCCTGCCTCGGCCTCCCAAAGT-GCTAGGATTACA 5827
 Query 7116068 GGCGTGCGCCACCGCGCCAGC----T-ATACAGCA 7116098
 Sbjct 5826 GGCGTGAGCCACCGCGCCCGGCCCATCATACAGCA 5791

Range 24: 5889 to 6004

Score	Expect	Identities	Gaps	Strand	Frame
73.1 bits(181)	5e-11()	89/118(75%)	6/118(5%)	Plus/Plus	

Features:

Query 13735213 CAGCCAGGGGTACACAGTGAAACCCCGTCTTTa-aaaaaaTGCAACAGCAT-GTTGTGCG 13735270
 Sbjct 5889 CAGCCTGGCCAACATGGTGAAACCCCGTCTCTACTAAAAATACAAAAACTTAGCTG-GGT 5947
 Query 13735271 GTGGTGGCGCATACCTTTTCATCCAGC-ACTCAGGAGGCTGAGGCAGGCAG-ATCTCT 13735326
 Sbjct 5948 GTGGTAGTGCCTGCCTGTAACTCTAGCTACTTAGGAGGCTGAGGCAGG-AGAATCGCT 6004

Range 25: 5814 to 5909

Score	Expect	Identities	Gaps	Strand	Frame
72.7 bits(180)	6e-11()	75/96(78%)	10/96(10%)	Plus/Minus	

Features:

Query 11857902 TTTACTCTGTAGACCAGGCTGACCTAGAACTC-----AGA-GATCCGCCTGCCTCTG 11857952
 Sbjct 5909 TTCACCATGTTGGCCAGGCTGGTCTAGAATCCTGACCTCAGATGATCCGCCTGCCTCGG 5850
 Query 11857953 CCTCCCGA-GTGCTAGGATTAAAGGCGTGCGCCACC 11857987
 Sbjct 5849 CCTCCCAAAGTGCTAGGATTACAGGCGTGAGCCACC 5814

Range 26: 5756 to 5936

Score	Expect	Identities	Gaps	Strand	Frame
71.9 bits(178)	1e-10()	137/197(70%)	28/197(14%)	Plus/Plus	

Features:

Query 8496325 TTG-ATGTAAACTGCAGGCAC----CT-TTGAAAAGGAGCCATCAGGGTG--GGGCAGTG 8496376
 Sbjct 5756 TTGCATGTAAACAGATGGCACATGGCTATTTAAATGCTGTATGATGGGGCCGGGC-GCG 5814
 Query 8496377 GTGGCACACGCCTTTAATCCTAGCAC-TTGGGAGGCAGAGGCGGGTGAATCTATATGAGT 8496435
 Sbjct 5815 GTGGCTACGCCTGTAACTCCTAGCACTTTGGGAGGCCGAGGCAGGCGGATC-ATCTGAGG 5873
 Query 8496436 TCAGAGCCAGCCTGGAGTTCTAGCACAGACCATAAGGGCTACACGGAGAAACCC--TATC 8496493
 Sbjct 5874 TC-A-----GGAGTTCTAGACCAG-CC-T--GGCCAACATGGTGAAACCCCGTCTC 5919
 Query 8496494 T-CAAAAAACAGATAAA 8496509
 Sbjct 5920 TACTAAAAATACAAAAA 5936

Range 27: 5803 to 5908

Score	Expect	Identities	Gaps	Strand	Frame
71.9 bits(178)	1e-10()	82/107(77%)	8/107(7%)	Plus/Minus	

Features:

Query 24965146 TCACTATGTAGAACAGGCTGGTCTTGAACCTCC--A---CAGA-GATTTGCCTTCCTCTGC 24965199
 Sbjct 5908 TCACCATGTTGGCCAGGCTGGTCTAGAATCCTGACCTCAGATGATCCGCCTGCCTCGGC 5849
 Query 24965200 CATCCC-AAGCGTGGGATTAAAGGCGTGCGCCACCAACCC 24965245
 Sbjct 5848 C-TCCCAAAGTGCTAGGATTACAGGCGTGAGCCACCGCGCCCGGCC 5803

Range 28: 5829 to 6007

Score	Expect	Identities	Gaps	Strand	Frame
71.9 bits(178)	1e-10()	127/180(71%)	32/180(17%)	Plus/Plus	

Features:

Query	11382985	TAATCCTAGCACCT- GGGAGGCAGAGGCAG	----	A-CAT	----	AG-T-AGGAATTTTAGAC	11383033
Sbjct	5829	TAATCCTAGCACTTTGGGAGGCCGAGGCAGGCGGATCATCTGAGGTCAGGAGTTCTAGAC					5888
Query	11383034	CAGCCTAGGCTACA---TGA-----GTCTCTA--AAAA-----GAAAACT----				TGGGCA	11383074
Sbjct	5889	CAGCCTGGCCAACATGGTGAAACCCCGTCTCTACTAAAAATACAAAAACTTAGCTGGGTG					5948
Query	11383075	TGGTGGTGAATGCCTTTATCCCAG-TACTTGGGAGGCAGAGGCAGGTGGATCTCTGTGA					11383133
Sbjct	5949	TGGTAGTGCGTGCCTGTAATCCTAGCTACTTAGGAGGCTGAGGCAGGAGAATCGCT-TGA					6007

Range 29: 5785 to 5908

Score	Expect	Identities	Gaps	Strand	Frame
70.3 bits(174)	3e-10()	91/124(73%)	9/124(7%)	Plus/Minus	

Features:

Query	47782634	TCACTTTGTAGACCAGGCTAGCCTTGAACCTC---AC---AGA-GATCCGCCTGCCTCTGC					47782686
Sbjct	5908	TCACCATGTTGGCCAGGCTGGTCTAGAACTCCTGACCTCAGATGATCCGCCTGCCTCGGC					5849
Query	47782687	CT-CCACAGCGCTGGGATTAAAGGCGTGCACCACAGCACCTGACCTGGTC-TGCAGTTTT					47782744
Sbjct	5848	CTCCCAAAGTGCTAGGATTACAGGCGTGAGCCACCGCGCCCGGCCCCATCATACAGCATT					5789
Query	47782745	TTAA					47782748
Sbjct	5788	TTAA					5785