

BLAST® >> **blastn suite-2sequences** >> results for RID-6RMVKATZ114

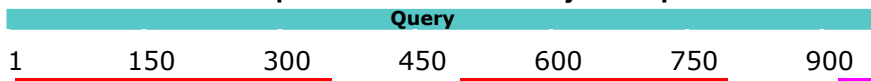
Job Title [Consensus TR1 NB/M13 R/R ...](#)
 RID [6RMVKATZ114](#) Search expires on 03-15 02:39 am
 Program Blast 2 sequences
 Query ID Icl|Query_8830 (dna)
 Query Descr [Consensus TR1 NB/M13 R/R ...](#)
 Query Length 957
 Subject ID Icl|Query_8832 and 1 more subject(s) (dna)
 Subject Descr • [See details](#)
 Subject Length 7014

Descriptions

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Ec-071	634	1110	66%	0.0	99.71%	Query_8832
pJP5603	80.5	80.5	5%	4e-18	96.00%	Query_8833

Graphic Summary

Distribution of the top 3 Blast Hits on 2 subject sequences



Alignments

Alignment view CDS feature

Ec-071
 Sequence ID: Query_8832 Length: 3888 Number of Matches: 2
 Range 1: 1275 to 1621

Score	Expect	Identities	Gaps	Strand	Frame
634 bits(343)	0.0()	346/347(99%)	1/347(0%)	Plus/Plus	
Query 10	GACGATT-ATTGATGACTGGCTATTTAGATGCCAGATCGCATTATTCATGCTAACTGTAG	68			
Sbjct 1275	GACGATTAATTGATGACTGGCTATTTAGATGCCAGATCGCATTATTCATGCTAACTGTAG	1334			
Query 69	CTTTGGGGGCTGTTATTGCGCCTCGATAGGCGGTATCAAAGCCATACAAAAGAGTCTCTG	128			
Sbjct 1335	CTTTGGGGGCTGTTATTGCGCCTCGATAGGCGGTATCAAAGCCATACAAAAGAGTCTCTG	1394			
Query 129	CCCATGCCTGATAAAGCAGACGATATAGTCGGTGTTCAGTTTTCAGGCTGTCCCAGAGTAA	188			
Sbjct 1395	CCCATGCCTGATAAAGCAGACGATATAGTCGGTGTTCAGTTTTCAGGCTGTCCCAGAGTAA	1454			
Query 189	TGGTTGCTGCATCATCAGCATAAATATTTCCGGTGACAGATGCCATATTTCTGGCAATGA	248			
Sbjct 1455	TGGTTGCTGCATCATCAGCATAAATATTTCCGGTGACAGATGCCATATTTCTGGCAATGA	1514			
Query 249	AATTTGCATTTCCACCACTCAGCCTGAATCCATCAGCAGCGTAGTGGAGACCCGGCGTTA	308			
Sbjct 1515	AATTTGCATTTCCACCACTCAGCCTGAATCCATCAGCAGCGTAGTGGAGACCCGGCGTTA	1574			
Query 309	CAGTTTTACTATTCTGTTCAAGGATTCCCATCATAGTCAGTTCACCG	355			
Sbjct 1575	CAGTTTTACTATTCTGTTCAAGGATTCCCATCATAGTCAGTTCACCG	1621			

Range 2: 1761 to 2048

Score	Expect	Identities	Gaps	Strand	Frame
475 bits(257)	4e-137()	276/290(95%)	2/290(0%)	Plus/Plus	

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Query 497  TGTKATGKGRGTGATGCCAMACTGTAWWTWAAAGTWTCTCCTATGGATAGATTAGTACT 556
           |||
Sbjct 1761  TGTATGTGCAGTGATGCCA-CCTGTAAT-TTAGTTTCTCCTATGGATAGATTAGTACT 1818
           |||
Query 557  GATAGTTTGTGTTGAAGTCAAACCAATTATTAGTAATATTTTCCCTGCAAGATTATCAAT 616
           |||
Sbjct 1819  GATAGTTTGTGTTGAAGTCAAACCAATTATTAGTAATATTTTCCCTGCAAGATTATCAAT 1878
           |||
Query 617  GTAAGCATTTTTATCGCCGATTGTGATAGCTGATTTATTTGCTGATATATTTCCCTTCAAC 676
           |||
Sbjct 1879  GTAAGCATTTTTATCGCCGATTGTGATAGCTGATTTATTTGCTGATATATTTCCCTTCAAC 1938
           |||
Query 677  ATTGGCATTGCGTGATATTGAAAAGTCAGCATTGTTCASGTGTAATGTATCAAATTTAAA 736
           |||
Sbjct 1939  ATTGGCATTGCGTGATATTGAAAAGTCAGCATTGTTCASGTGTAATGTATCAAATTTAAA 1998
           |||
Query 737  CACCCCRGTTTTCCWGTCTGGCTGATCAAATGAGGTCTGCTGATTATTAC 786
           |||
Sbjct 1999  CACCCCGTTTTCCAGTCTGGCTGATCAAATGAGGTCTGCTGATTATTAC 2048
           |||

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pJP5603

Sequence ID: Query_8833 Length: 3126 Number of Matches: 1

Range 1: 1405 to 1454

Score	Expect	Identities	Gaps	Strand	Frame
80.5 bits(43)	4e-18()	48/50(96%)	2/50(4%)	Plus/Minus	
Query 908	ATTCGAGCTCGGTACCCGGGGATCCTCTAGAGTCGAC-TGCAG-CATGCA				955
Sbjct 1454	ATTCGAGCTCGGTACCCGGGGATCCTCTAGAGTCGACCTGCAGGCATGCA				1405

Taxonomy

Reports

- Lineage
- Organism
- Taxonomy

Plot of Icl|Query_8830 vs Icl|Query_8833

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