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BLAST Results

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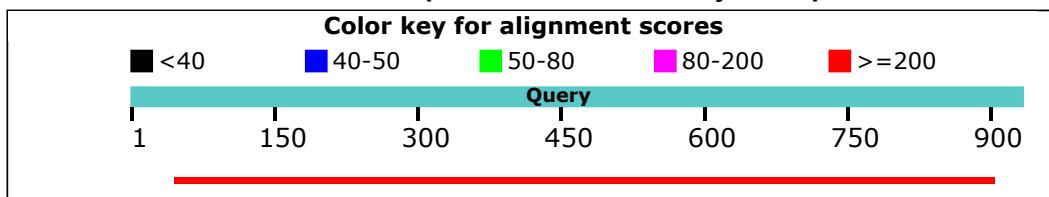
Blast 2 sequences

Job title: Nucleotide Sequence (905 letters)

RID	VZFZM8S2113 (Expires on 10-13 05:26 am)	Subject ID	4799 subjects
Query ID	lcl Query_243571	Description	▶ See details
Description	None	Molecule type	nucleic acid
Molecule type	nucleic acid	Subject Length	4343931
Query Length	905	Program	BLASTN 2.8.1+

Graphic Summary

Distribution of the top 1 Blast Hits on 1 subject sequences



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
MHIKLPCM_01505 Lipopolysaccharide core biosynthesis protein RfaG	1520	1520	93%	0.0	99%	Query_245077

Alignments

MHIKLPCM_01505 Lipopolysaccharide core biosynthesis protein RfaG

Sequence ID: Query_245077 Length: 1125 Number of Matches: 1

Range 1: 58 to 899

Score	Expect	Identities	Gaps	Strand	Frame
1520 bits(823)	0.0()	840/847(99%)	5/847(0%)	Plus/Minus	

Features:

Query	46	GTCGTCAACACAGGTAATCCCGCGGCAATTGCC	105
Sbjct	899	GTCGTCAACACAGGTAATCCCGCGGCAATTGCC	840
Query	106	TGATAAGCGGGATGCATTAATAAATCAGCGGCTGCCATTAATTCAGACACATCATTCCGC	165
Sbjct	839	TGATAAGCGGGATGCATTAATAAATCAGCGGCTGCCATTAATTCAGACACATCATTCCGC	780
Query	166	CCGGAAGAAATGCACCTTACTACGCACACCGAGTTTTCTGCCAGCACTTCAAATTTA	225
Sbjct	779	CCGGAAGAAATGCACCTTACTACGCACACCGAGTTTTCTGCCAGCACTTCAAATTTA	720
Query	226	CGCGGTTTATCCTGGCCAACAACAACAACGTAATTATGGCGTAACGATTCTGGTAAC	285
Sbjct	719	CGCGGTTTATCCTGGCCAACAACAACAACGTAATTATGGCGTAACGATTCTGGTAAC	660
Query	286	GATGCCAAAGCTTCAATTGAGCGATCCACACCTTACGACCAAAATCTGAACCAACCTGC	345
Sbjct	659	GATGCCAAAGCTTCAATTGAGCGATCCACACCTTACGACCAAAATCTGAACCAACCTGC	600
Query	346	AGCAATAAGTTTTGTTGTTGAGTGCATTTTTCTGGCGATAAAATTTACGACTGTTT	405
Sbjct	599	AGCAATAAGTTTTGTTGTTGAGTGCATTTTTCTGGCGATAAAATTTACGACTGTTT	540
Query	406	GGGATTTGCGCGTGTATTTCTGTGAGGATAGATACCAGGGGGAAGAAATTTGAAAACGT	465
Sbjct	539	GGGATTTGCGCGTGTATTTCTGTGAGGATAGATACCAGGGGGAAGAAATTTGAAAACGT	480
Query	466	TCTGGTTCAGTTTGGTAAATGCTTCTGAAAATCGGCGATTTGCTTATCGGTCAACATCATA	525
Sbjct	479	TCTGGTTCAGTTTGGTAAATGCTTCTGAAAATCGGCGATTTGCTTATCGGTCAACATCATA	420
Query	526	AGTTTCGTCGATTTACCATGTTTCGAAAGTCGCTCGCTCGAATGCAGCATAATGGCGATAG	585
Sbjct	419	AGTTTCGTCGATTTACCATGTTTCGAAAGTCGCTCGCTCGAATGCAGCATAATGGCGATAG	360
Query	586	CGCGATGTTAAACGATAGAAAAATCCCTTTTCTTGCGCCACTTTCTCGGCATAACAGACA	645
Sbjct	359	CGCGATGTTAAACGATAGAAAAATCCCTTTTCTTGCGCCACTTTCTCGGCATAACAGACA	300
Query	646	TCGGCGGCAAAATAAACATCCAGCCAGGCATCTTATTAAGCCAAACAACGCGATCAGCG	705
Sbjct	299	TCGGCGGCAAAATAAACATCCAGCCAGGCATCTTATTAAGCCAAACAACGCGATCAGCG	240
Query	706	GGATGTGCTTCAGATGGTTTTGAACCCAGGCATAAATTTCTGCATTACGTCCATGGTTA	765
Sbjct	239	GGATGTGCTTCAGATGGTTTTGAACCCAGGCATAAATTTCTGCATTACGTCCATGGTTA	180
Query	766	GTATGGGATTTAACCGGTACGCGAATAAGCTCAAATGCTTCCGGGCAATCGCCTTCCCAC	825
Sbjct	179	GTATGGGATTTAACCGGTACGCGAATAAGCTCAAATGCTTCCGGGCAATCGCCTTCCCAC	120
Query	826	GACTGTGTATATACCCCGAAACATGGGTGGCCCCGTGCGGCAACTGATGAGGTAATACGT	885
Sbjct	119	GACTGTGTATATACCC-GAA-CAT-GGTGGCCCCGTGCGGCAACTGTTGAGGCAATACG-	64
Query	886	CATTTAA 892	
Sbjct	63	CAT-AAA 58	

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