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BLAST Results

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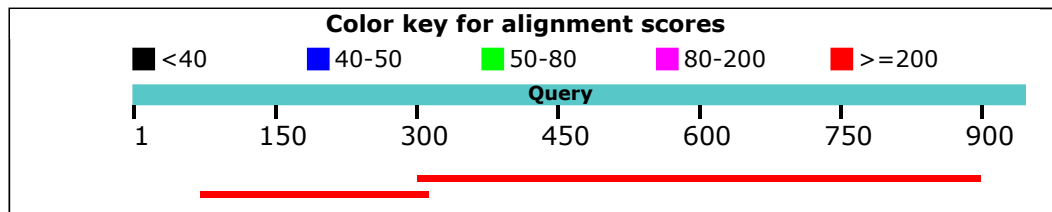
Blast 2 sequences

Job title: Nucleotide Sequence (915 letters)

RID	VZFXTTAK113 (Expires on 10-13 05:25 am)	Subject ID	4799 subjects
Query ID	lcl Query_241221	Description	▶ See details
Description	None	Molecule type	nucleic acid
Molecule type	nucleic acid	Subject Length	4343931
Query Length	915	Program	BLASTN 2.8.1+

Graphic Summary

Distribution of the top 2 Blast Hits on 2 subject sequences



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
MHIKLPCM_01506 Lipopolysaccharide core heptose(I) kinase RfaP	1026	1026	64%	0.0	98%	Query_242728
MHIKLPCM_01505 Lipopolysaccharide core biosynthesis protein RfaG	435	435	25%	4e-122	100%	Query_242727

Alignments

MHIKLPCM_01506 Lipopolysaccharide core heptose(I) kinase RfaP

Sequence ID: Query_242728 Length: 798 Number of Matches: 1

Range 1: 1 to 578

Score	Expect	Identities	Gaps	Strand	Frame
1026 bits(555)	0.0()	577/586(98%)	8/586(1%)	Plus/Plus	

Features:

Query	300	ATGGTTGAATTAGAAGAGCCACTTGCCACACTCTGGCGTGGTAAAGATGCCTTTGCAGAA	359
Sbjct	1	ATGGTTGAATTAGAAGAGCCACTTGCCACACTCTGGCGTGGTAAAGATGCCTTTGCAGAA	60
Query	360	GTTAAAAAACTGAATGGCGAGGTCCTCCGTGAACTGGAGACGCGTCGCACATTACGCTTT	419
Sbjct	61	GTTAAAAAACTGAATGGCGAGGTCCTCCGTGAACTGGAGACGCGTCGCACATTACGCTTT	120
Query	420	GAACTGGCCGGCAAAGTTATTTCTCAAATGGCACAAAGGGACGACCCATAAGGAGATT	479
Sbjct	121	GAACTGGCCGGCAAAGTTATTTCTCAAATGGCACAAAGGGACGACCCATAAGGAGATT	180
Query	480	ATAAAAAATCTGCTCTCATTGCGGATGCCCGTTTTAGGTGCAGACAGAGAGTGGCACGCT	539
Sbjct	181	ATAAAAAATCTGCTCTCATTGCGGATGCCCGTTTTAGGTGCAGACAGAGAGTGGCACGCT	240
Query	540	ATTCATCGACTGCATGATGTCGGTGTGATACGATGCACGGAATAGGATTTGGTGAAAAA	599
Sbjct	241	ATTCATCGACTGCATGATGTCGGTGTGATACGATGCACGGAATAGGATTTGGTGAAAAA	300
Query	600	GGGTTAAATCCATTAACCTCGCACATCATTTATTTACC GAAGATCTCACTCCCACAATT	659
Sbjct	301	GGGTTAAATCCATTAACCTCGCACATCATTTATTTACC GAAGATCTCACTCCCACAATT	360
Query	660	AGCCTTGAAGATTATTGTGCAGATTGGGCGGTCAACCCGCCGTGATGTACATATTAAGCGT	719
Sbjct	361	AGCCTTGAAGATTATTGTGCAGATTGGGCGGTCAACCCGCCGTGATGTACATATTAAGCGT	420
Query	720	ATGCTGATCGCGCGTGTGGCAACCATGGTGCACAAAAATGCATGCAGCAGGGATTAATCA	779
Sbjct	421	ATGCTGATCGCGCGTGTGGCAACCATGGTGCAC - AAAATGCATGCAGCAGGGATTAATCA	479
Query	780	CCGTGATTGTTATATCTGCCACTTTTTACTCCATTTGCCATTTACTGGGCCGGGAAG	839
Sbjct	480	CCGTGATTGTTATATCTGCCAC - TTTTTACTCCATTTGCCATTT - ACTGG - CC - GGGAAAG	535
Query	840	ATGAATTAAAAAATTCGGTTATCGATCTGGCACCGAGACACAGAT	885
Sbjct	536	ATGAATT - AAAAATTCGGTTATCGATCTG - CACCGGG - CACAGAT	578

MHIKLPCM_01505 Lipopolysaccharide core biosynthesis protein RfaG

Sequence ID: Query_242727 Length: 1125 Number of Matches: 1

Range 1: 891 to 1125

Score	Expect	Identities	Gaps	Strand	Frame
435 bits(235)	4e-122()	235/235(100%)	0/235(0%)	Plus/Plus	

Features:

Query	73	GTTGACGACTGCGGTATGCGGATACGCACACTATATCACAGATGCTAATTGTGGAACGGT	132
Sbjct	891	GTTGACGACTGCGGTATGCGGATACGCACACTATATCACAGATGCTAATTGTGGAACGGT	950

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Query 133  CATCGCTGAACCTTTCTCCCAGGAACAATTAAATGACGTTTTACGTAAAGCGTTAACTCA 192
Sbjct 951  CATCGCTGAACCTTTCTCCCAGGAACAATTAAATGACGTTTTACGTAAAGCGTTAACTCA 1010
Query 193  ATCTCCATTGCGCATGGCCTGGGCGGAGAAATGCTCGGTATTACGCCGATACTCAGGATTT 252
Sbjct 1011 ATCTCCATTGCGCATGGCCTGGGCGGAGAAATGCTCGGTATTACGCCGATACTCAGGATTT 1070
Query 253  ATACAGCCTGCCGGAGAAAAGCGGCAGATATCATTACAGGTGGTTTAGATGGTTGA 307
Sbjct 1071 ATACAGCCTGCCGGAGAAAAGCGGCAGATATCATTACAGGTGGTTTAGATGGTTGA 1125

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