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BLAST Results

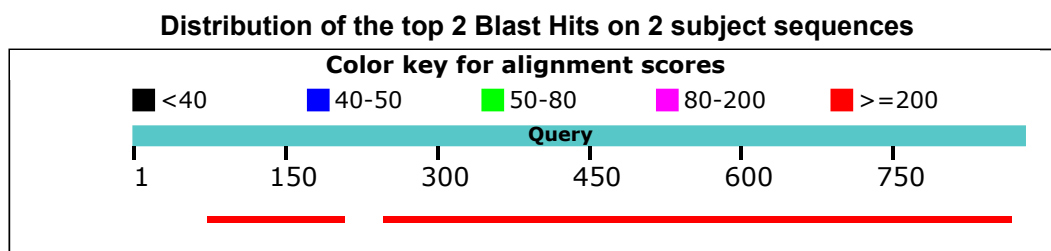
[Questions/comments](#)

Blast 2 sequences

Job title: 901E-R

RID	8RXAVK2D114 (Expires on 03-17 02:56 am)	Subject ID	4799 subjects
Query ID	lcl Query_145899	Description	See details
Description	901E-R	Molecule type	nucleic acid
Molecule type	nucleic acid	Subject Length	4343931
Query Length	858	Program	BLASTN 2.9.0+

[Graphic Summary.](#)



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
MHIKLPCM_01515 Lipopolysaccharide heptosyltransferase 1	1046	1046	71%	0.0	97.10%	Query_147415
MHIKLPCM_01514 hypothetical protein	246	246	15%	2e-65	100.00%	Query_147414

Alignments

MHIKLPCM_01515 Lipopolysaccharide heptosyltransferase 1
 Sequence ID: Query_147415 Length: 957 Number of Matches: 1
 Range 1: 338 to 957

Score	Expect	Identities	Gaps	Strand	Frame
1046 bits(566)	0.0()	603/621(97%)	8/621(1%)	Plus/Minus	

Features:

Query	245	TCAGGAATTGATTTTATTAAATACCGTTTTCTGCAGTCAGATGAGCAAGATCTTTATCTGG	304
Sbjct	957	TCAGGAATTGATTTTATTAAATACCGTTTTCTGCAGTCAGATGAGCAAGATCTTTATCTGG	898
Query	305	TGCCCTACAAACCACCTGATTCTTCCCATATCCGCCAATTAATCCCGGATCGGTTGGTCC	364
Sbjct	897	TGCCCTACAAACCACCTGATTCTTCCCATATCCGCCAATTAATCCCGGATCGGTTGGTCC	838
Query	365	ATAAACCGTGATATTCGGTCGATCCAGTGCTGCAGTTAAATGACTTAACCCAGTGTCTAC	424
Sbjct	837	ATAAACCGTGATATTCGGTCGATCCAGTGCTGCAGTTAAATGACTTAACCCAGTGTCTAC	778
Query	425	CGATACCACGAATTTTCGCTCCGGCCAGCACACGGGCAACACSTTCCAGACTCATCTTCGG	484
Sbjct	777	CGATACCACGAATTTTCGCTCCGGCCAGCACACGGGCAACACSTTCCAGACTCATCTTCGG	718
Query	485	CAATACTTCAACATAAGCAAATCCTTCCGCCAGTCGTTTCGCCCGTTTTTCTCATGCGG	544
Sbjct	717	CAATACTTCAACATAAGCAAATCCTTCCGCCAGTCGTTTCGCCCGTTTTTCTCATGCGG	658
Query	545	CGCACCCACGGAAGTTTAAATGCGAATCCCTGAATCTGCCAGTAAACCAATCAATTCTCG	604
Sbjct	657	CGCACCCACGGAAGTTTAAATGCGAATCCCTGAATCTGCCAGTAAACCAATCAATTCTCG	598
Query	605	CCAGTGTTCTTCCGGCCAGTGTTTATCATCACGGGTCGTCGCATGAAGAAATACGGCATA	664
Sbjct	597	CCAGTGTTCTTCCGGCCAGTGTTTATCATCACGGGTCGTCGCATGAAGAAATACGGCATA	538
Query	665	TTCCGCCAGCATCTGTAGGCAGGTTTCGTCAGAAAATGCTGTGCGATAGCATAATCGCCCTG	724
Sbjct	537	TTCCGCCAGCATCTGTAGGCAGGTTTCGTCAGAAAATGCTGTGCGATAGCATAATCGCCCTG	478
Query	725	GGTTTGCGGTT-GCTATAGCCAGACTTTTTGGGCAAAAAGTTCSCGGATGCGTCTTACGG	783
Sbjct	477	GGTTTGCGGTTGCTATAGCCAGACTTTT-GGCAAAAAGTTCGCGGATGCGTCTTACGG	419
Query	784	CGTGCTGCTGTTT-GCA-TATGATG-TTACGATTGTAAAACAG-CTGGCT-AAGTTTCGC	838
Sbjct	418	CGTGCTGCTGTTTGTCAATATGATGTTACGATTGTAAAACAGGCTGGCTAAAGGTTTCGC	359
Query	839	GAGCG-TTGCCAGTYCATT	858
Sbjct	358	GAGCGTTTGCCAGTCCATT	338

MHIKLPCM_01514 hypothetical protein
 Sequence ID: Query_147414 Length: 1218 Number of Matches: 1
 Range 1: 1 to 133

Score	Expect	Identities	Gaps	Strand	Frame
246 bits(133)	2e-65()	133/133(100%)	0/133(0%)	Plus/Minus	

Features:

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Query 74  GTATAGATATGATGTGTTTATAACGGGTTATACCATCAAGGAAAAAGGTTGCAATAAAGA 133
Sbjct 133  GTATAGATATGATGTGTTTATAACGGGTTATACCATCAAGGAAAAAGGTTGCAATAAAGA 74
Query 134  GGAATACCAACGCTTTATTCCAGTACGGTTTCCACTTTTCTTTATTACGTAGCGCCAGCG 193
Sbjct 73  GGAATACCAACGCTTTATTCCAGTACGGTTTCCACTTTTCTTTATTACGTAGCGCCAGCG 14
Query 194  AGGCTGTTAACAT 206
Sbjct 13  AGGCTGTTAACAT 1

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