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BLAST Results

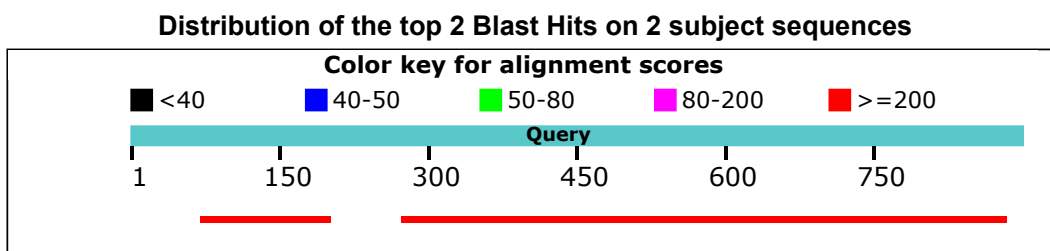
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Blast 2 sequences

Job title: 901M-R

RID	8RXWTM0X114 (Expires on 03-17 03:06 am)	Subject ID	4799 subjects
Query ID	lcl Query_145995	Description	See details
Description	901M-R	Molecule type	nucleic acid
Molecule type	nucleic acid	Subject Length	4343931
Query Length	877	Program	BLASTN 2.9.0+

[Graphic Summary](#)



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
MHIKLPCM_04538 Toxin coregulated pilus biosynthesis protein E	1014	1014	68%	0.0	97.03%	Query_150534
MHIKLPCM_04537 Toxin coregulated pilus biosynthesis protein T	237	237	14%	1e-62	100.00%	Query_150533

Alignments

MHIKLPCM_04538 Toxin coregulated pilus biosynthesis protein E

Sequence ID: Query_150534 Length: 996 Number of Matches: 1

Range 1: 1 to 601

Score	Expect	Identities	Gaps	Strand	Frame
1014 bits(549)	0.0()	589/607(97%)	8/607(1%)	Plus/Plus	

Features:

Query	270	ATGTCTCGTTACCTTGTTAATGGCGTTCGGTTATCTTATGCATTGAATGAACCTTATCAG	329
Sbjct	1	ATGTCTCGTTACCTTGTTAATGGCGTTCGGTTATCTTATGCATTGAATGAACCTTATCAG	60
Query	330	TTTACTACCGATTACGGAAAAGAAAACAACATCTTCAATTGTTATTCGTGATGTCTTG	389
Sbjct	61	TTTACTACCGATTACGGAAAAGAAAACAACATCTTCAATTGTTATTCGTGATGTCTTG	120
Query	390	CGTTCAGTCAGGAACGGGCAGAGCTTCTCTGATGCCTTGAAATTCGGGTTCTGCTGAT	449
Sbjct	121	CGTTCAGTCAGGAACGGGCAGAGCTTCTCTGATGCCTTGAAATTCGGGTTCTGCTGAT	180
Query	450	GAGATTTCAATTCCTTCAGCTGGGGAGTATTCAGGAAAACCTTATGAATCTATTGATAAT	509
Sbjct	181	GAGATTTCAATTCCTTCAGCTGGGGAGTATTCAGGAAAACCTTATGAATCTATTGATAAT	240
Query	510	ATCATACACATCAATCAGACCAAGaaaaaaTAAAAATCAGCTCTATTTGGTATTGTTTAT	569
Sbjct	241	ATCATACACATCAATCAGACCAAGAAAAAAAAAATAAAATCAGCTCTATTTGGTATTGTTTAT	300
Query	570	CCGTTAGTGCTTGTCTTAACCACCTGTTTATATTTATATATCTTTGGAAATCGGGTTGTG	629
Sbjct	301	CCGTTAGTGCTTGTCTTAACCACCTGTTTATATTTATATATCTTTGGAAATCGGGTTGTG	360
Query	630	CCTGCATTTTCTCAGGTTTTACCTGTAGAAGAGTGGCAAGGGGCCGGACGACTAATGTAC	689
Sbjct	361	CCTGCATTTTCTCAGGTTTTACCTGTAGAAGAGTGGCAAGGGGCCGGACGACTAATGTAC	420
Query	690	CATCTTGCATTGTTTGTGCAAAAATTATCTTTTGTGACGATGGTTATTGTTTTTATGATT	749
Sbjct	421	CATCTTGCATTGTTTGTGCAAAAATTATCTTTTGTGACGATGGTTATTGTTTTTATGATT	480
Query	750	tttttAWATGCATTATTGTGACATTAGGGCTGTGGGTAGGTAA-GTAAAGATGTTTTTGA	808
Sbjct	481	TTTTAT--ATGCATTATTGTGACATTAGGGCTGTGGGTAGGTAAAGGTAAAGGATGTTTTTGA	538
Query	809	ATAAGTTTCCGC-ATGAACAATTTTAWTAAAAACAGTCGTGACTTGTGATTTTCTGCCTGA	867
Sbjct	539	ATAAGTTTCCGCCATGGACAATTT-A-TAAAAACAGTCGTGGGCTGTGGTTTTCTGC-TGT	595
Query	868	CCTTTAT	874
Sbjct	596	C-TTTAT	601

MHIKLPCM_04537 Toxin coregulated pilus biosynthesis protein T

Sequence ID: Query_150533 Length: 1566 Number of Matches: 1

Range 1: 1439 to 1566

Score	Expect	Identities	Gaps	Strand	Frame
237 bits(128)	1e-62()	128/128(100%)	0/128(0%)	Plus/Plus	

Features:

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Query 71 TAACAATGGCAGAGCATGCATGGTTAAAAGTTATCAGGGGGGAAATTTCTGTTTTTGTG 130
Sbjct 1439 TAACAATGGCAGAGCATGCATGGTTAAAAGTTATCAGGGGGGAAATTTCTGTTTTTGTG 1498

Query 131 CTATTAGTAAAGTATCGCGAATAGAAAATATACCTAAAGAAAGGCGAGCGTATCTAAACG 190
Sbjct 1499 CTATTAGTAAAGTATCGCGAATAGAAAATATACCTAAAGAAAGGCGAGCGTATCTAAACG 1558

Query 191 GTCCTTTAA 198
Sbjct 1559 GTCCTTTAA 1566

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