

BLAST Results

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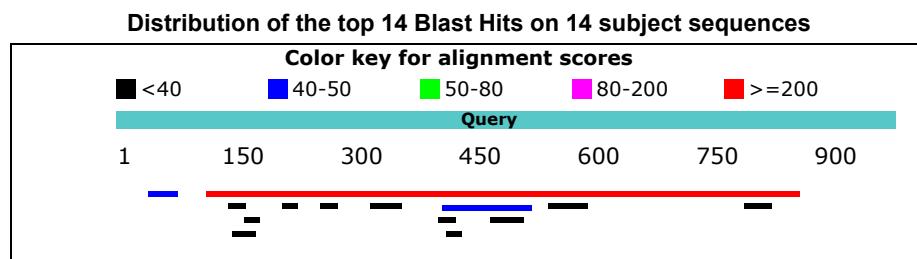
Blast 2 sequences

Job title: 35,441-1F

RID [6KCHUD1X11R](#) (Expires on 02-19 02:12 am)

Query ID Icl|Query_231363
Description 35,441-1F
Molecule type nucleic acid
Query Length 955

Subject ID 4799 subjects
Description [See details](#)
Molecule type nucleic acid
Subject Length 4343931
Program BLASTN 2.8.1+

[Graphic Summary](#)[Descriptions](#)

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
MHIKLPCM_04179 Chaperone protein FimC	1213	1213	77%	0.0	97.31%	Query_235543
MHIKLPCM_04178 putative major fimbrial subunit LpfA	45.5	45.5	3%	2e-04	88.57%	Query_235542
MHIKLPCM_03618 putative fimbrial chaperone SfmC	41.0	41.0	11%	0.002	69.44%	Query_234982
MHIKLPCM_03911 UTP--glucose-1-phosphate uridylyltransferase	35.6	35.6	4%	0.078	80.49%	Query_235275
MHIKLPCM_02587 Bifunctional aspartokinase/homoserine dehydrogenase 2	34.6	34.6	3%	0.27	83.87%	Query_233951
MHIKLPCM_02308 putative fimbrial chaperone Yral	34.6	34.6	3%	0.27	80.56%	Query_233672
MHIKLPCM_00722 Fructose-1,6-bisphosphatase 2 class 2	33.7	33.7	1%	0.27	100.00%	Query_232086
MHIKLPCM_01940 HTH-type transcriptional regulator PgrR	32.8	32.8	2%	0.95	95.00%	Query_233304
MHIKLPCM_01622 putative fimbrial chaperone YadV	31.9	31.9	4%	0.95	74.47%	Query_232986
MHIKLPCM_00300 Putative cyclic-di-GMP phosphodiesterase AdrB	31.9	31.9	1%	0.95	100.00%	Query_231664
MHIKLPCM_04027 Putative type II secretion system protein D	31.0	31.0	2%	3.3	87.50%	Query_235391
MHIKLPCM_03645 tRNA 2-selenouridine synthase	31.0	31.0	1%	3.3	94.74%	Query_235009
MHIKLPCM_02726 Enterobactin synthase component F	30.1	30.1	1%	3.3	100.00%	Query_234090
MHIKLPCM_00279 putative autotransporter	30.1	30.1	1%	3.3	100.00%	Query_231643

Alignments

MHIKPCM_04179 Chaperone protein FimC

Sequence ID: Query_23543 Length: 726 Number of Matches: 1

Range 1: 1 to 726

Score	Expect	Identities	Gaps	Strand	Frame
1213 bits(1344)	0.0()	723/743(97%)	17/743(2%)	Plus/Plus	

Features:

Query	110	GTGAGTAATAAAAACGTCAATGTAAGGAAATCGCAGGAAATAACATTCTGCTTGCTGGCA	169
Sbjct	1	GTGAGTAATAAAAACGTCAATGTAAGGAAATCGCAGGAAATAACATTCTGCTTGCTGGCA	60
Query	170	GGTATCCTGATGTTTATGGCAATGATGGTTGCCGGACGCGCTGAAGCGGGAGTGGCCTTA	229
Sbjct	61	GGTATCCTGATGTTTATGGCAATGATGGTTGCCGGACGCGCTGAAGCGGGAGTGGCCTTA	120
Query	230	GGTGCGACTCGCGTAATTTATCCGGCAGGGCAAAAACAAGTGCAACTTGCCGTGACAAAT	289
Sbjct	121	GGTGCGACTCGCGTAATTTATCCGGCAGGGCAAAAACAAGTGCAACTTGCCGTGACAAAT	180
Query	290	AATGATGAAAATAGTACCTATTTAATTCAATCATGGGTGGAAAATGCCGATGGTGTAAAG	349
Sbjct	181	AATGATGAAAATAGTACCTATTTAATTCAATCATGGGTGGAAAATGCCGATGGTGTAAAG	240
Query	350	GATGGTCGTTTTATCGTGACGCCTCCTCTGTTTGCATGAAGGGGAAAAAGAGAATACC	409
Sbjct	241	GATGGTCGTTTTATCGTGACGCCTCCTCTGTTTGCATGAAGGGGAAAAAGAGAATACC	300
Query	410	TTGCGTATTCCTGATGCAACAAATAACCAATGGCCACAGGATCGGGAAAGTTTATTCTGG	469
Sbjct	301	TTGCGTATTCCTGATGCAACAAATAACCAATGGCCACAGGATCGGGAAAGTTTATTCTGG	360
Query	470	ATGAATGTTAAAGCGATTCCGTCAATGGATAAATCAAATGACTGAGAATACGCTACAG	529
Sbjct	361	ATGAATGTTAAAGCGATTCCGTCAATGGATAAATCAAATGACTGAGAATACGCTACAG	420
Query	530	CTCGCAATATCAGCCGCATTAACCTGTACTATCGCCCGGTAAATTAGCGTTGCCACCC	589
Sbjct	421	CTCGCAATATCAGCCGCATTAACCTGTACTATCGCCCGGTAAATTAGCGTTGCCACCC	480
Query	590	GATCAGGCCGAGAAAAATTAAGATTTTCGTCTAGCGCGAATTCCTGACGCTTGATTAA	649
Sbjct	481	GATCAGGCCGAGAAAAATTAAGATTTTCGTCTAGCGCGAATTCCTGACGC-TGATTAA	539
Query	650	MCCCGACACCCTATTACCTGGACGGWAACAGAGTTGAATGCCGGGAAACCCGGGTTCTTG	709
Sbjct	540	-CCCGACACCCTATTACCT-GACGGTAACAGAGTTGAATGCCGG--AACCCGGGTTCTTG	595
Query	710	AAAATGCCTTGGTGCCTCCAATGGGGCGAAAGCACGGTTAAATGGCCTTCTGATGCGGG	769
Sbjct	596	AAAATGCCTTGGTGCCTCCAAT-GGGCGAAAGCACGGTTAAAT-GCCTTCTGATGCGGG	653
Query	770	AAGCAATATTWACTTTACCGAACAAATAAATGATTATGGTGCACCTTACCCCAAAAAAT	829
Sbjct	654	AAGCAATATT-AC-TTACCGAACAAATAAATGATTATGGTG-CA-CTTACCCCA--AAAAT	707
Query	830	GACGGGCGSGTAAWTGGGAATAA	852
Sbjct	708	GACGGG--CGTAAT--GGAATAA	726

MHIKPCM_04178 putative major fimbrial subunit LpfA

Sequence ID: Query_23542 Length: 498 Number of Matches: 1

Range 1: 466 to 498

Score	Expect	Identities	Gaps	Strand	Frame
45.5 bits(49)	2e-04()	31/35(89%)	2/35(5%)	Plus/Plus	

Features:

Query	39	GCCCAGGCCYCGTGTTCTCTTTAACCTATCAGTAA	73
Sbjct	466	GCCCAGGCCCTGGT--TCTCTTTAACCTATCAGTAA	498

MHIKPCM_03618 putative fimbrial chaperone SfmC

Sequence ID: Query_234982 Length: 693 Number of Matches: 1

Range 1: 253 to 357

Score	Expect	Identities	Gaps	Strand	Frame
41.0 bits(44)	0.002()	75/108(69%)	3/108(2%)	Plus/Plus	

Features:

Query	395	aaaaaaGAGAATACCTTGCGTATTCTTGATGCAACAAATAACCAATTGCCACAGGATCGG	454
Sbjct	253	AAAAGCGAAAATACTTTGCGTATTATTA--CACGGTCCACCGCTGGCGGAG-ATCGT	309

Query 455 GAAAGTTTATTCTGGATGAATGTTAAAGCGATTCCGTCAATGGATAAA 502
 Sbjct 310 GAGTCTCTGTTCTGGATGAATGTTAAGACGATCCCTTCGGTAGATAAA 357

MHIKLPCM_03911 UTP--glucose-1-phosphate uridylyltransferase

Sequence ID: Query_235275 Length: 909 Number of Matches: 1
 Range 1: 413 to 452

Score	Expect	Identities	Gaps	Strand	Frame
35.6 bits(38)	0.078()	33/41(80%)	1/41(2%)	Plus/Plus	

Features:

Query 461 TTATTCTGGATGAATGTTAAAGCGATTCCGTCAATGGATAA 501
 Sbjct 413 TTATTCTGGATGAATATGAATCCGATT-TGTCACAGGATAA 452

MHIKLPCM_02587 Bifunctional aspartokinase/homoserine dehydrogenase 2

Sequence ID: Query_233951 Length: 2433 Number of Matches: 1
 Range 1: 1385 to 1415

Score	Expect	Identities	Gaps	Strand	Frame
34.6 bits(37)	0.27()	26/31(84%)	0/31(0%)	Plus/Minus	

Features:

Query 766 CGGGAAGCAATATTWACTTTACCGAACAATA 796
 Sbjct 1415 CGGGAACCGATATTGCCCTTACCGAACAATA 1385

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