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## BLAST Results

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### Blast 2 sequences

Job title: 36,441-1R

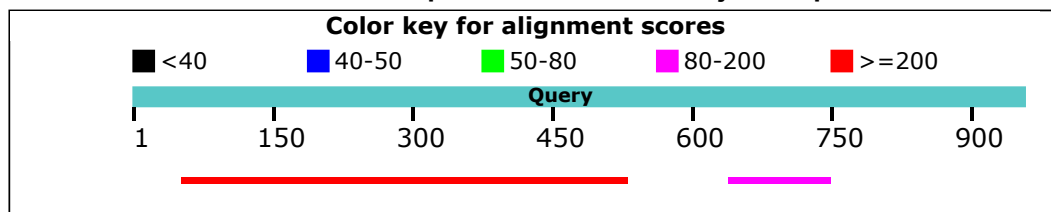
**RID** [6BGNGG4G114](#) (Expires on 02-16 02:34 am)

**Query ID** lcl|Query\_73635  
**Description** 36,441-1R  
**Molecule type** nucleic acid  
**Query Length** 934

**Subject ID** 4799 subjects  
**Description** ▶ [See details](#)  
**Molecule type** nucleic acid  
**Subject Length** 4343931  
**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_04178 putative major fimbrial subunit LpfA	846	846	50%	0.0	98.31%	Query_77814
MHIKLPCM_04177 Type-1 fimbrial protein, A chain	180	180	11%	2e-45	97.20%	Query_77813

## Alignments

MHIKLPCM\_04178 putative major fimbrial subunit LpfA

Sequence ID: Query\_77814 Length: 498 Number of Matches: 1  
Range 1: 1 to 474

Score	Expect	Identities	Gaps	Strand	Frame
846 bits(458)	0.0()	466/474(98%)	0/474(0%)	Plus/Minus	

Features:

Query	54	GGCCTGGGCATTGGCGATGCCGCCAGTMWCCCGACGCCCGGTAGCACGATATTTGGCGAT	113
Sbjct	474	GGCCTGGGCATTGGCGATGCCGCCAGTAACCCGACGCCCGGTAGCACGATATTTGGCGAT	415
Query	114	GAAATGTAKCGAAGTARAGCCTGAGTAAAGCCGTTTCCAGTTTGCTGGAGGACGATTAAT	173
Sbjct	414	GAAATGTAGCGAAGTARAGCCTGAGTAAAGCCGTTTCCAGTTTGCTGGAGGACGATTAAT	355
Query	174	CGGTACGAGGTTTCTTCATCATCAAACAACGCTACGCCAATATTGGTGGCTATCCCTGG	233
Sbjct	354	CGGTACGAGGTTTCTTCATCATCAAACAACGCTACGCCAATATTGGTGGCTATCCCTGG	295
Query	234	CCCCCTCTCCACGGAAGCACATCCGGATTTTTACCATCCGCGACACCGTGAAACGCCAC	293
Sbjct	294	CCCCCTCTCCACGGAAGCACATCCGGATTTTTACCATCCGCGACACCGTGAAACGCCAC	235
Query	294	CCCCACACGTTCACTCACCACCGTGCTACATTCCCGTAAATGAATAACAAAAGGCACCGG	353
Sbjct	234	CCCCACACGTTCACTCACCACCGTGCTACATTCCCGTAAATGAATAACAAAAGGCACCGG	175
Query	354	TGCSCTATCTTCCCCTGCCGCATGAAACCGGTTACTGCTGATTTGCCCATATTGACCGT	413
Sbjct	174	TGCGCTATCTTCCCCTGCCGCATGAAACCGGTTACTGCTGATTTGCCCATATTGACCGT	115
Query	414	CATTTGTTTATCACCGGCTTCAATCCGGCAAGTTTCYKYAATAATGACGCCCTGAAATTG	473
Sbjct	114	CATTTGTTTATCACCGGCTTCAATCCGGCAAGTTTCYKYAATAATGACGCCCTGAAATTG	55
Query	474	CATATTTCCGCGGGCAGCGTGGTATTCATTTATTTCCGGCCAGAGCAAACAT	527
Sbjct	54	CATATTTCCGCGGGCAGCGTGGTATTCATTTATTTCCGGCCAGAGCAAACAT	1

MHIKLPCM\_04177 Type-1 fimbrial protein, A chain

Sequence ID: Query\_77813 Length: 549 Number of Matches: 1  
Range 1: 445 to 549

Score	Expect	Identities	Gaps	Strand	Frame
180 bits(97)	2e-45()	104/107(97%)	2/107(1%)	Plus/Minus	

Features:

Query	634	TTATTGATACTGAACCTTGAAGGTTGCATCCGCATTAGCTGCACCCGGGGTTGCCTCGCC	693
Sbjct	549	TTATTGATACTGAACCTTGAAGGTTGCATCCGCATTAGCTGCACCCGGGGTTGCCTCGCC	490
Query	694	GATTGCATAATAACGCGCCTGGAACGGAATGGTGTTTGGGTACCATT	740
Sbjct	489	GATTGCATAATAACGCGCCTGGAACGGAATGGTGTTTGGGTACCATT	445

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