

[BLAST®](#) » [blastn suite-2sequences](#) » RID-6BJW20G5114

## BLAST Results

[Questions/comments](#)

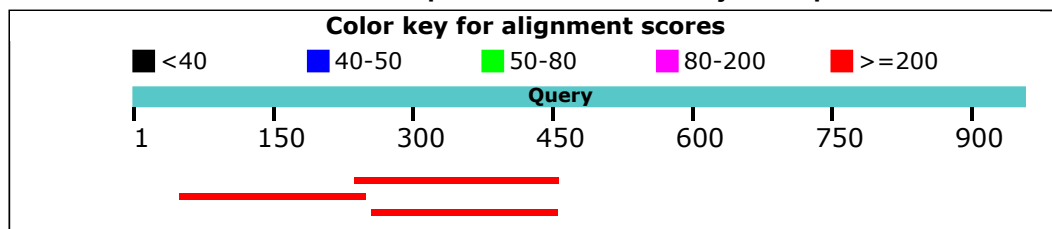
### Blast 2 sequences

Job title: 40,632-1R

<b>RID</b>	<a href="#">6BJW20G5114</a> (Expires on 02-16 03:11 am)	<b>Subject ID</b>	4799 subjects
<b>Query ID</b>	lcl Query_99005	<b>Description</b>	<a href="#">See details</a>
<b>Description</b>	40,632-1R	<b>Molecule type</b>	nucleic acid
<b>Molecule type</b>	nucleic acid	<b>Subject Length</b>	4343931
<b>Query Length</b>	936	<b>Program</b>	BLASTN 2.8.1+

## [Graphic Summary](#)

Distribution of the top 3 Blast Hits on 3 subject sequences



## Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
MHIKLPCM_04682 hypothetical protein	398	398	22%	5e-111	100.00%	Query_103688
MHIKLPCM_04534 Outer membrane lipoprotein BfpB	350	350	21%	2e-96	97.99%	Query_103540
MHIKLPCM_00759 hypothetical protein	276	276	21%	3e-74	91.88%	Query_99765

## Alignments

MHIKLPCM\_04682 hypothetical protein

Sequence ID: Query\_103688 Length: 648 Number of Matches: 1  
Range 1: 1 to 215

Score	Expect	Identities	Gaps	Strand	Frame
398 bits(215)	5e-111()	215/215(100%)	0/215(0%)	Plus/Minus	

Features:

Query	239	GGTACCGTGGAAAAATTGTC	CGTAAAGGCAGGCATCAAGTTCTGCTCCGACATGCCTGCG	298
Sbjct	215	GGTACCGTGGAAAAATTGTC	CGTAAAGGCAGGCATCAAGTTCTGCTCCGACATGCCTGCG	156
Query	299	GGCAAAGGCCACGAAAGGCCAGCTCTCCGAAAGCGCACGAACATACTACAAACTGTTGAT	358	
Sbjct	155	GGCAAAGGCCACGAAAGGCCAGCTCTCCGAAAGCGCACGAACATACTACAAACTGTTGAT	96	
Query	359	TTTGGTACACCCAGGCGACGCCCGGGCCACAACCCGGGGTAAATGTTCTTCAAAGTGAAGA	418	
Sbjct	95	TTTGGTACACCCAGGCGACGCCCGGGCCACAACCCGGGGTAAATGTTCTTCAAAGTGAAGA	36	
Query	419	CGTAAAGCTTCAGTGATCCAGGTCCGGTGTTTCAT	453	
Sbjct	35	CGTAAAGCTTCAGTGATCCAGGTCCGGTGTTTCAT	1	

MHIKLPCM\_04534 Outer membrane lipoprotein BfpB

Sequence ID: Query\_103540 Length: 1662 Number of Matches: 1  
Range 1: 515 to 713

Score	Expect	Identities	Gaps	Strand	Frame
350 bits(189)	2e-96()	195/199(98%)	1/199(0%)	Plus/Plus	

Features:

Query	51	ACTCTGGTCCATTATCAGTGTTTCTTGATMMM	TTCGTCACATTTTGACCTTGCATGGC	110
Sbjct	515	ACTCTGGTCCATTATCAGTGTTTCTTGATAA	TTTCGTCACATTTTGACCTTGCATGGC	574
Query	111	AATATGTTGATGGTCAATTATTAATATCGACAGACGAGGTCAGAAAAATTTCTATAAGCT	170	
Sbjct	575	AATATGTTGATGGTCAATTATTAATATCGACAGACGAGGTCAGAAAAATTTCTATAAGCT	634	
Query	171	CATTACCAAACAAAATCGAATCTACAAGTAGTATAGGTAGTGAAAGTAGTGGCAGTAGTG	230	
Sbjct	635	CATTACCAAACAAAATCGAATCTACAAGTAGTATAGGTAGTGAAAGTAGTGGCAGTAGTG	694	
Query	231	GTGGAGGGGGTACCG-TGG	248	
Sbjct	695	GTGGAGGGGGTACCGTGG	713	

MHIKLPCM\_00759 hypothetical protein

Sequence ID: Query\_99765 Length: 306 Number of Matches: 1  
Range 1: 1 to 197

Score	Expect	Identities	Gaps	Strand	Frame
276 bits(149)	3e-74()	181/197(92%)	0/197(0%)	Plus/Minus	
Features:					
Query 257	CCGTAAAGGCAGGCATCAAGTTCCTGCTCCGACATGCCTGCGGGCAAAGGCCACGAAAGG				316
Sbjct 197	CCGTAAAGACGGGCATCAAGTTCCTGCTCCGACATACCTGCGGGCAGAGGCCATGAAAGG				138
Query 317	CCAGCTCTCCGAAAGCGCACGAACATACTACAAACTGTTGATTTTGGTACACCCAGGCCA				376
Sbjct 137	CCAGCTTTTCGGAAGCGCACGAACATACCACAAACTGTTGATTTTGGTACGCCCAGGCCA				78
Query 377	CGCCCCGGCCACAACCCGGGGTAAATGTTCTTCAAAGTGAAGACGTAAGCTTCAGTGATC				436
Sbjct 77	CGTCCGGCCACAATCCGTGGTAAATGTTCTTCAAAGTGAAGACGTAAGCTTCAGTGATC				18
Query 437	CAGGTCGGTGTTCAT	453			
Sbjct 17	CAGGTCGGTATTCCAT	1			

BLAST is a registered trademark of the National Library of Medicine



[Support center Mailing list](#)

[YouTube](#)



- [National Library Of Medicine](#)



- [National Institutes Of Health](#)



- [U.S. Department of Health & Human Services](#)



- [USA.gov](#)

## NCBI

[National Center for Biotechnology Information](#), [U.S. National Library of Medicine](#) 8600 Rockville Pike, Bethesda MD, 20894 USA  
[Policies and Guidelines](#) | [Contact](#)