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## BLAST Results

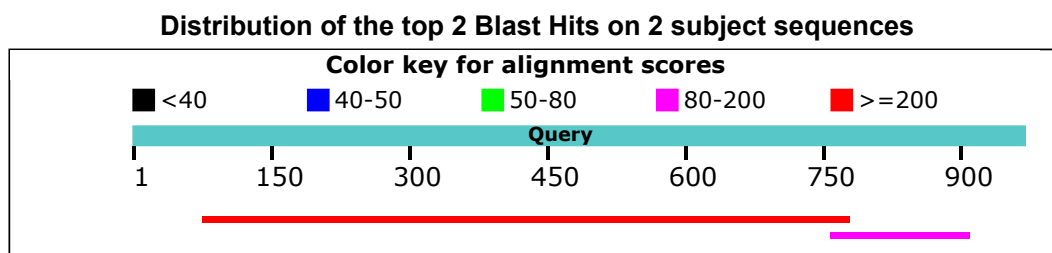
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### Blast 2 sequences

Job title: 31,316-1f

<b>RID</b>	<a href="#">6BASEY6H114</a> (Expires on 02-16 00:53 am)	<b>Subject ID</b>	4799 subjects
<b>Query ID</b>	lcl Query_60045	<b>Description</b>	<a href="#">See details</a>
<b>Description</b>	31,316-1f	<b>Molecule type</b>	nucleic acid
<b>Molecule type</b>	nucleic acid	<b>Subject Length</b>	4343931
<b>Query Length</b>	938	<b>Program</b>	BLASTN 2.8.1+

## [Graphic Summary](#)



## Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
MHIKLPCM_04540 Leader peptidase PppA	1242	1242	73%	0.0	98.84%	Query_64586
MHIKLPCM_04539 Putative type II secretion system protein E	185	185	15%	5e-47	91.10%	Query_64585

## Alignments

MHIKLPCM\_04540 Leader peptidase PppA

Sequence ID: Query\_64586 Length: 753 Number of Matches: 1  
Range 1: 1 to 691

Score	Expect	Identities	Gaps	Strand	Frame
1242 bits(672)	0.0()	684/692(99%)	1/692(0%)	Plus/Minus	

Features:

Query	76	CTTTAAGCTTGTatragkaaagaatataaaaataaatgtaactgcggaatwawtataaat	135
Sbjct	691	CTTTAAGCCTGTAT-GGTAAGAATATAAAATAAATGTAACGCGGAAATAAATAAAAT	633
Query	136	aaaagaaCTTTATCCATTCTAGCCATGCCCTGCAGCCGTGGCAAAGACAATATCCCCT	195
Sbjct	632	AAAAGAACTTTATCCATTCTAGCCATGCCCTGCAGCCGTGGCAAAGACAATATCCCCT	573
Query	196	CCGGCAATAMSATCTTCTTATGTAGAACGGaaactaaaaacatagaaaaataaaaaaca	255
Sbjct	572	CCGGCAATAAGATCTTCTTATGTAGAACGGAAACTAAAAACATAGAAAAATAAAAAACA	513
Query	256	caaaaTCTTGATACACTGCCTAAAATCTGGAAATAGGAATCATCTTCAAATGGTGAAAAT	315
Sbjct	512	CAAAATCTTGATACACTGCCTAAAATCTGGAAATAGGAATCATCTTCAAATGGTGAAAAT	453
Query	316	AAAAGACCTAACCCAGAAAAGAGGTATAGTGACAACAAAAGGCAACCATGTCTCATTATA	375
Sbjct	452	AAAAGACCTAACCCAGAAAAGAGGTATAGTGACAACAAAAGGCAACCATGTCTCATTATA	393
Query	376	TCAATAAGTGTAAAGAAAAGAAGAACAAAGAAATAGGAATATTATCCATAGTCCCTTCCCTC	435
Sbjct	392	TCAATAAGTGTAAAGAAAAGAAGAACAAAGAAATAGGAATATTATCCATAGTCCCTTCCCTC	333
Query	436	TCAATTCCGTAATAATATGCAATAACAACACAGGCAATGGCACTGAAAACTCCATAACA	495
Sbjct	332	TCAATTCCGTAATAATATGCAATAACAACACAGGCAATGGCACTGAAAACTCCATAACA	273
Query	496	GGATATATACATGGAATTTTCACTCCACACTCAGGACATTTTCTTTAGAAAAGCAAAAAG	555
Sbjct	272	GGATATATACATGGAATTTTCACTCCACACTCAGGACATTTTCTTTAGAAAAGCAAAAAG	213
Query	556	CCCAGAAATGGGTATTAGATATATCCATTTTATATTTATATGACAATTATTACATCTCGAT	615
Sbjct	212	CCCAGAAATGGGTATTAGATATATCCATTTTATATTTATATGACAATTATTACATCTCGAT	153
Query	616	GGTGGCGACCATATAGTAAGACTATCTTCAGGATCATCTCGCCAGTTTAGTTGATGAGGG	675
Sbjct	152	GGTGGCGACCATATAGTAAGACTATCTTCAGGATCATCTCGCCAGTTTAGTTGATGAGGG	93
Query	676	AGCCTGTCAACTACCAGACAAATAAACTGGTTATTACAGATCCAATCCAGAATATTGAA	735
Sbjct	92	AGCCTGTCAACTACCAGACAAATAAACTGGTTATTACAGATCCAATCCAGAATATTGAA	33
Query	736	GCATAAATAAAAAATTTATAAAGTACTGGCAT 767	
Sbjct	32	GCATAAATAAAAAATTTATAAAGTACTGGCAT 1	

MHIKLPCM\_04539 Putative type II secretion system protein E

Sequence ID: Query\_64585 Length: 978 Number of Matches: 1  
Range 1: 846 to 978

Score	Expect	Identities	Gaps	Strand	Frame
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185 bits(100)    5e-47()    133/146(91%)    13/146(8%)    Plus/Minus

## Features:

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Query 751 TTATAAAGTACTGGCATAATGAGTGTGTAATTTATTCCTTTGGATAACATAATATTCT 810
Sbjct 978 TTATAAAGTACTGGCATAATGAGTGTGTAATTTATTCCTTT-GGATAACATAATATTCT 920
Query 811 GGGGCTTCTATTTCACTAAGAAAGCTTCAAGCTTAACCCGATCTAATTTTTTAGAAA 870
Sbjct 919 GGG-CTTCTATTTCACTAAGAA-GCT-CAAGCTT-ACCCGATCTAATTTT--AGAAA 866
Query 871 ACCCATAGGAAGGCAACSGCCARCCT 896
Sbjct 865 -CC-ATAG-AAGG-AAC-GCCA-CCT 846

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