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BLAST Results

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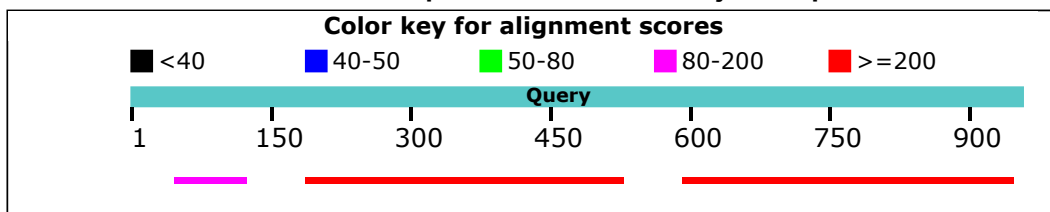
Blast 2 sequences

Job title: 32,316-1R

RID	6BAM3TAZ114 (Expires on 02-16 00:50 am)	Subject ID	4799 subjects
Query ID	lcl Query_124407	Description	See details
Description	32,316-1R	Molecule type	nucleic acid
Molecule type	nucleic acid	Subject Length	4343931
Query Length	929	Program	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
MHIKPCM_04541 hypothetical protein	621	621	36%	3e-178	100.00%	Query_128949
MHIKPCM_04542 hypothetical protein	440	440	37%	9e-124	90.31%	Query_128950
MHIKPCM_04540 Leader peptidase PppA	99.0	99.0	7%	6e-21	90.67%	Query_128948

Alignments

MHIKPCM_04541 hypothetical protein

Sequence ID: Query_128949 Length: 336 Number of Matches: 1
Range 1: 1 to 336

Score	Expect	Identities	Gaps	Strand	Frame
621 bits(336)	3e-178()	336/336(100%)	0/336(0%)	Plus/Plus	

Features:

Query	183	ATGTCGTGCATTGCTGTTGAAGGTGGCCGGATTGGGTTAGCTTCaaaaataaaaaTGGG	242
Sbjct	1	ATGTCGTGCATTGCTGTTGAAGGTGGCCGGATTGGGTTAGCTTCAAAAATAAAAAATGGG	60
Query	243	ACTGAGGATCTTGGTATTATGCAGATTAATACAGGAGCATGGCTTAAACTTGTCAAGTCGG	302
Sbjct	61	ACTGAGGATCTTGGTATTATGCAGATTAATACAGGAGCATGGCTTAAACTTGTCAAGTCGG	120
Query	303	GTCtttttttttAGGTGATAAAGAAAAGGCTTATATACGTTTAAAGGATGATGGCTGTTTT	362
Sbjct	121	GTCTTTTTTTTAGGTGATAAAGAAAAGGCTTATATACGTTTAAAGGATGATGGCTGTTTT	180
Query	363	AATATATCTGTTGGGGCATGGATACTGAGTACCTCAATCAGACAAGAGAAAAGGGGATGTA	422
Sbjct	181	AATATATCTGTTGGGGCATGGATACTGAGTACCTCAATCAGACAAGAGAAAAGGGGATGTA	240
Query	423	TGGTCAGGTGTCGGTCGGTATCATTCAAACACCCCTTTTtataaaaatagatatatttct	482
Sbjct	241	TGGTCAGGTGTCGGTCGGTATCATTCAAACACCCCTTTTATAAAAAATAGATATAATTTCT	300
Query	483	aaagttcggatataaaatacagaaaaataaatttgtaa	518
Sbjct	301	AAAGTTCGATATAAATACAGAAAAATAAATTTGTAA	336

MHIKPCM_04542 hypothetical protein

Sequence ID: Query_128950 Length: 480 Number of Matches: 1
Range 1: 1 to 323

Score	Expect	Identities	Gaps	Strand	Frame
440 bits(238)	9e-124()	317/351(90%)	29/351(8%)	Plus/Plus	

Features:

Query	580	ATGAAGAAAGAGAAGGGGATGACTCTTCTTGAAGTGTGTTGGCCCTAATAGTAACTACA	639
Sbjct	1	ATGAAGAAAGAGAAGGGGATGACTCTTCTTGAAGTGTGTTGGCCCTAATAGTAACTACA	60
Query	640	TCAGTAAATGGTTACAGTATGGTTTTCCATTCAAGGATATTATAAGATTTTATCCTTACAR	699
Sbjct	61	TCAGT-AATGGTTACAGTATGGTTTTCCATTCAAGGATATTATAAGATTTTATC-TTACA-	117
Query	700	AGAACAGTCGCCCTATACTGTCAATTAATAAGATGAACATAGCGATTYGATWACGTGtaa	759
Sbjct	118	AGAACAGTCGCCCTATACTGTCAATTAAT-AAGATGAACATAGCGATT-GAT-ACGTGTA	174
Query	760	aagcaaaagtgcctcaaaagtgcctcaaaagtgcctcaaaagtgcctcaaaagtgcctcaaaTKGTGTCA	819
Sbjct	175	AAGCAAAGTGTCAAAGTGTCAAAGTGTCAAAGTGTCAAAGT-GCTCAAT-GTGTCA	232

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Query 820 TTACCTGATATGGGTAGGCAGGTAAAAGGCCAAATYTTWCCTWATAGAGAATAGAGAKAA 879
Sbjct 233 TTA-CTGATATGGGTAG-CAG-TAAA-GG-AAAAT-TTAC-T-ATAGA-AAATAAA-AGA- 281

Query 880 CTCCTTAGCCATAAATAGGGTKGTCTATACTGCCTTGWAKGGaaaaa-aaa 929
Sbjct 282 CTC-T-AGC-ATAA-TAGGGT-GTCT-TAC-GC-TTG-ATGGAAAAATAAA 323

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MHIKLPCM_04540 Leader peptidase PppA

Sequence ID: Query_128948 Length: 753 Number of Matches: 1

Range 1: 680 to 753

Score	Expect	Identities	Gaps	Strand	Frame
99.0 bits(53)	6e-21()	68/75(91%)	2/75(2%)	Plus/Plus	

Features:

```

Query 48 ACAGGGCTTAAAGGCATTCGCTTTGCTCCTATGGGACCGSGK-TGAGTATAGGTTTTTTG 106
Sbjct 680 ACA-GGCTTAAAGGCATTCGCTTTGCTCCTATGGGCCCTCATTGAGTATAGGTTTTTTG 738

Query 107 CTATGTCTGCTGTAA 121
Sbjct 739 CTATGTCTGCTGTAA 753

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