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BLAST Results

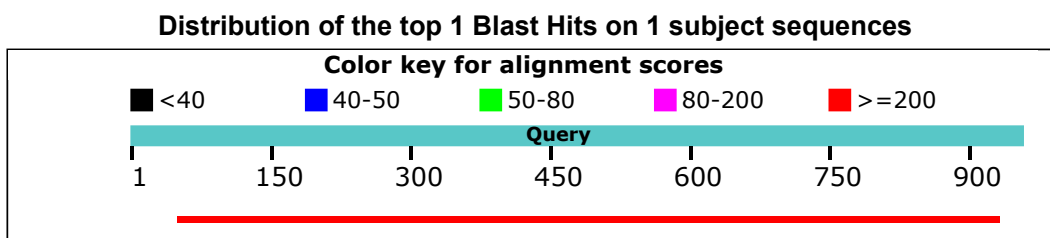
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Blast 2 sequences

Job title: 24,854-2R

RID	77X77U0T114 (Expires on 02-26 21:00 pm)	Subject ID	4799 subjects
Query ID	lcl Query_170599	Description	See details
Description	24,854-2R	Molecule type	nucleic acid
Molecule type	nucleic acid	Subject Length	4343931
Query Length	926	Program	BLASTN 2.8.1+

[Graphic Summary](#)



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
MHIKPCM_03836 Na(+)/H(+) antiporter NhaA	1410	1410	93%	0.0	96.31%	Query_174436

Alignments

MHIKPCM_03836 Na(+)/H(+) antiporter NhaA

Sequence ID: Query_174436 Length: 1167 Number of Matches: 1

Range 1: 270 to 1113

Score	Expect	Identities	Gaps	Strand	Frame
1410 bits(763)	0.0()	836/868(96%)	24/868(2%)	Plus/Minus	

Features:

Query	51	AGAGATAGAACCGACCAGGATACCGAGTTTCGCTCAGWTAATCAGTTCTGGATCTACGCT	110
Sbjct	1113	AGAGATAGAACCGACCAGGATACCGAGTTTCGCCAGTTAATCAGTTCTGGATCTACGCT	1054
Query	111	ACCAAAGGCCAGGCTGGCAATAAAGATAGACATAGTAAAACCGATACCGCACAGGATCCC	170
Sbjct	1053	ACCAAAGGCCAGGCTGGCAATAAAGATAGACATAGTAAAACCGATACCGCACAGGATCCC	994
Query	171	CACCGCCATAAATTTGCTGATAAGTCGTTCCCTCMSGCAGATGCGCCAGTTTCAAACGCAG	230
Sbjct	993	CACCGCCATAAATTTGCTGATAAGTCGTTCCCTCAGGCAGATGCGCCAGTTTCAAACGCAG	934
Query	231	CGCCAACACAGCAGAACAGACTAATCCCCAGCGGTTTGCCAATCAGCAAGCCAGCGATGAT	290
Sbjct	933	CGCCAACACAGCAGAACAGACTAATCCCCAGCGGTTTGCCAATCAGCAAGCCAGCGATGAT	874
Query	291	CCCCAATGGCAGAATGGAGGTCAAGCCATCCAGCGTGACGCCTTGCAGAGAAACGCCAGC	350
Sbjct	873	CCCCAATGGCAGAATGGAGGTCAAGCCATCCAGCGTGACGCCTTGCAGAGAAACGCCAGC	814
Query	351	ATTAGCGAATGCAAAACAGCGGCAAAATCAGATACGCCACCCACGGGTGCAACACATGCTC	410
Sbjct	813	ATTAGCGAATGCAAAACAGCGGCAAAATCAGATACGCCACCCACGGGTGCAACACATGCTC	754
Query	411	CAGTCGCTTCGWTTGGAGAACGCCCATGCTTCTCTTTCAAAGGAATAAAGAAGCCGACAAT	470
Sbjct	753	CAGTCGCTTCGWTTGGAGAACGCCCATGCTTCTCTTTCAAAGGAATAAAGAAGCCGACAAT	694
Query	471	TACCCCGCCAGAGTTGCGTGAACCCCGATTTCAACACCGCAGTCCACAACACTACGCC	530
Sbjct	693	TACCCCGCCAGAGTTGCGTGAACCCCGATTTCAACACCGCAGTCCACAACACTACGCC	634
Query	531	AACCGAATATAGACGCCCGTGCAGCGTACACCACACAGATTCATACCGCGAGTACCGC	590
Sbjct	633	AACCGAATATAGACGCCCGTGCAGCGTACACCACACAGATTCATACCGCGAGTACCGC	574
Query	591	AATTGCTACAGCCGCGACGCCAAGAGAGGCCATCGATAAAGTCATTAGTGTAGAACAATG	650
Sbjct	573	AATTGCTACAGCCGCGACGCCAAGAGAGGCCATCGATAA-GTCATTAGTGTAGAACAATG	515
Query	651	CGATGATAATGATGGCCCCAAGATCGTCGATAATAGCCAGAGCCATCAAAAAGATCTTCA	710
Sbjct	514	CGATGATAATGATGGCCCCAAGATCGTCGATAATAGCCAGAGCCATCAAAAAGATCTTCA	455
Query	711	GCGCTAACGGAAACACGACTTCCAATAGCGCCAGCACACCTAGTGTGAAGGCAATGGTCA	770
Sbjct	454	GCGCTAACGGAAACACGACTTCCAATAGCGCCAGCACACCAAGTCAAAAGGCAATG-TCA	396
Query	771	GTAGCCGCGGGATCGCCACCCCTTCGCGGGTAAATCGGAATCGGGCATAGTTAAAAGC	830
Sbjct	395	GTAGCCGCGGGATCGCCACCC-TCGCGGGTAA-TCGGA-TC-GGCATAGTTAAAAGC	340
Query	831	CCAGAATAGAGTAATGCCCGGCACCAATCCATYCCACCAACTAGCTGGCCGAATAAACT	890
Sbjct	339	C-AG-ATAGAGTAATGCC-GGCAC-AATC-AT-CCCACCAA-TAGC-GGC-GA-TAA-CT	291
Query	891	GGGAAAATGCCCGGACCTGGACCGTAAG	918
Sbjct	290	GG-AAA-TGC--GG-CCTGG-C-GTAAG	270

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