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BLAST Results

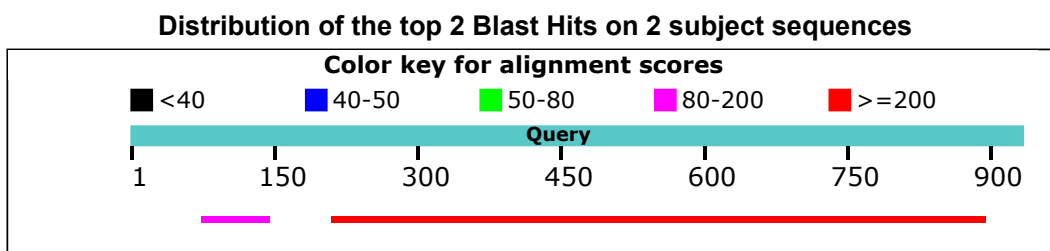
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Blast 2 sequences

Job title: 23,854-2F

| | | | |
|----------------------|---|-----------------------|-----------------------------|
| RID | 77WZACK9114 (Expires on 02-26 20:55 pm) | Subject ID | 4799 subjects |
| Query ID | lcl Query_123529 | Description | See details |
| Description | 23,854-2F | Molecule type | nucleic acid |
| Molecule type | nucleic acid | Subject Length | 4343931 |
| Query Length | 913 | Program | BLASTN 2.8.1+ |

[Graphic Summary](#)



Descriptions

Sequences producing significant alignments:

| Description | Max score | Total score | Query cover | E value | Ident | Accession |
|--|-----------|-------------|-------------|---------|--------|--------------|
| MHIKPCM_03835 Transcriptional activator protein NhaR | 1153 | 1153 | 74% | 0.0 | 97.36% | Query_127365 |
| MHIKPCM_03836 Na(+)/H(+) antiporter NhaA | 110 | 110 | 7% | 3e-24 | 95.52% | Query_127366 |

Alignments

MHIKPCM_03835 Transcriptional activator protein NhaR

Sequence ID: Query_127365 Length: 900 Number of Matches: 1

Range 1: 1 to 669

| Score | Expect | Identities | Gaps | Strand | Frame |
|----------------|--------|--------------|------------|-----------|-------|
| 1153 bits(624) | 0.0() | 663/681(97%) | 12/681(1%) | Plus/Plus | |

Features:

| | | | |
|-------|-----|---|-----|
| Query | 208 | ATGTCTCATATCAATTACAACCACCTTGTATTACTTCTGGCATGCTATAAAGAAGGTTCC | 267 |
| Sbjct | 1 | ATGTCTCATATCAATTACAACCACCTTGTATTACTTCTGGCATGCTATAAAGAAGGTTCC | 60 |
| Query | 268 | GTGGTTGGCGCAGCGGAGGCGCTTTATTTGACACCACAAACCATTACCGGACAGATCCGG | 327 |
| Sbjct | 61 | GTGGTTGGCGCAGCGGAGGCGCTTTATTTGACACCACAAACCATTACCGGACAGATCCGG | 120 |
| Query | 328 | GCTCTGGAAGAGCGCCTGCAAGGCAAATATTTAAGCGCAAGGGACGTGGTCTCGAACCC | 387 |
| Sbjct | 121 | GCTCTGGAAGAGCGCCTGCAAGGCAAATATTTAAGCGCAAGGGACGTGGTCTCGAACCC | 180 |
| Query | 388 | AGCGAGCTGGGAGAAGCTGGTCTATCGCTATGCCGATAAAATGTTACCTTAAGCCAGGAA | 447 |
| Sbjct | 181 | AGCGAGCTGGGAGAAGCTGGTCTATCGCTATGCCGATAAAATGTTACCTTAAGCCAGGAA | 240 |
| Query | 448 | ATGCTGGATATTGTGAACATCGCAAAGAATCCAATTTATTGTTTACGTTGGCGTGGCT | 507 |
| Sbjct | 241 | ATGCTGGATATTGTGAACATCGCAAAGAATCCAATTTATTGTTTACGTTGGCGTGGCT | 300 |
| Query | 508 | GATGCACCTTCCAAACGCCTGGTCAAGTGCAGTGCATGCTGCAATGCTGCAAGGCGAG | 567 |
| Sbjct | 301 | GATGCACCTTCCAAACGCCTGGTCAAGTGCAGTGCATGCTGCAATGCTGCAAGGCGAG | 360 |
| Query | 568 | CCGATTCATCTTCGCTGCTTGAATCCACCCACGAAATGCTACTGGAGCAATTAAGCCA | 627 |
| Sbjct | 361 | CCGATTCATCTTCGCTGCTTGAATCCACCCACGAAATGCTACTGGAGCAATTAAGCCA | 419 |
| Query | 628 | GCATAAACTGGATATGATCATTTCCGACTGTCCGATAGACTCTACGCAGCAGGAAGGCCT | 687 |
| Sbjct | 420 | GCATAAACTGGATATGATCATTTCCGACTGTCCGATAGACTCTACGCAGCAGGAAGGCCT | 479 |
| Query | 688 | GTTCTCCGTGAGAAWTTGGCGAATGTGGCGTGGTGTACAAATCCACCACCAG | 747 |
| Sbjct | 480 | GTTCTCCGTGAGAA-TTGGCGAATGTGGCGTGGTGTACAAATCCACCACCAG | 538 |
| Query | 748 | AAAAAACCGTTCCCGCTTGTCTGGAAGAACGGCGACTTTKGATCCCTGGGGCCGACGT | 807 |
| Sbjct | 539 | -AAAAAACCGTTCCCGCTTGTCTGGAAGAACGGCGACTTTGATTCC-TGGG-C-GACGT | 594 |
| Query | 808 | TCAATTGTTAGGGGCGCAATTTGGCTTAAGTGGTTTAACTCYCTAGGGATTCAACCGTAGA | 867 |
| Sbjct | 595 | TCAAT-GTTAGGG-CGCAAAATGCTTAAGTGGTTTAACTCCC-AGGGATTAAA-CGTAGA | 650 |
| Query | 868 | AATCCTCCGGCGAAGTTKGAT | 888 |
| Sbjct | 651 | AATCCTC-GGCGA-GTTTGAT | 669 |

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

Sequence ID: Query_127366 Length: 1167 Number of Matches: 1

Range 1: 1102 to 1167

| Score | Expect | Identities | Gaps | Strand | Frame |
|-------|--------|------------|------|--------|-------|
|-------|--------|------------|------|--------|-------|

110 bits(59) 3e-24() 64/67(96%) 1/67(1%) Plus/Plus

Features:

```

Query 76  GGTTCATCYCTTTCGGCGGTAATTGGATACAGTTGGTTACGCGTTCGTTTGCSTCCATC 135
Sbjct 1102 GGTTCATCTC-TTCGGCGGTAATTGGATACAGTTGGTTACGCGTTCGTTTGCSTCCATC 1160

Query 136  AGTTTGA 142
Sbjct 1161 AGTTTGA 1167

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