

BLAST ®

Basic Local Alignment Search Tool

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ATCG

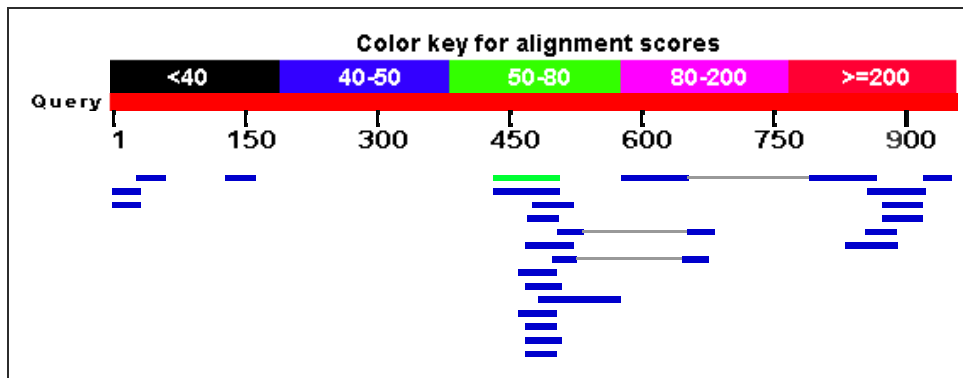
RID [Y0SET9SD01R](#) (Expires on 08-06 12:47 pm)

Query ID lc||57195
Description None
Molecule type nucleic acid
Query Length 952

Database Name nr
Description Nucleotide collection (nt)
Program BLASTN 2.2.29+

[Graphic Summary](#)

Distribution of 28 Blast Hits on the Query Sequence



☰ Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Zebrafish DNA sequence from clone DKEY-156K2 in linkage group 4, complete sequence	51.8	51.8	7%	0.015	78%	BX890613.22
Zebrafish DNA sequence from clone DKEYP-30D6 in linkage group 3, complete sequence	50.0	50.0	7%	0.051	77%	CR792416.16
CH251-10A4, complete sequence	50.0	50.0	4%	0.051	84%	CT573269.3
Dicentrarchus labrax chromosome sequence corresponding to linkage group 1, top part, complete sequence	48.2	48.2	3%	0.18	91%	FQ310506.3
Phaeosphaeria nodorum SN15 hypothetical protein partial mRNA	48.2	48.2	3%	0.18	94%	XM_001790817.1
Astyanax fasciatus ultra conserved element locus 65101 genomic sequence	44.6	44.6	3%	2.2	89%	JQ719265.1
Salmo salar clone ssal-rgb2-580-283 DmX-like protein 2 putative mRNA, complete cds	44.6	44.6	3%	2.2	88%	BT057450.1
Rhodospseudomonas palustris BisB5, complete genome	44.6	89.1	6%	2.2	93%	CP000283.1
Rattus norvegicus 1 BAC CH230-229J7 (Children's Hospital Oakland Research Institute) complete sequence	44.6	87.3	15%	2.2	75%	AC105487.6
PREDICTED: Astyanax mexicanus fibronectin leucine rich transmembrane protein 3 (flrt3), mRNA	42.8	42.8	6%	7.6	77%	XM_007238508.1
PREDICTED: Neolamprologus brichardi lethal(2) giant larvae protein homolog 1-like (LOC102796592), transcript variant X2, mRNA	42.8	42.8	4%	7.6	82%	XM_006798020.1
PREDICTED: Neolamprologus brichardi lethal(2) giant larvae protein homolog 1-like (LOC102796592), transcript variant X1, mRNA	42.8	42.8	4%	7.6	82%	XM_006798019.1
Podiceps auritus voucher LSUMZ:B19296 ultra conserved element locus chr2_8655 genomic sequence	42.8	42.8	5%	7.6	78%	KC381929.1
Mycobacterium chubuense NBB4 plasmid pMYCCH.01, complete sequence	42.8	85.5	5%	7.6	93%	CP003054.1
Verticillium albo-atrum VaMs.102 transferase family protein, mRNA	42.8	42.8	3%	7.6	88%	XM_003000541.1
Homo sapiens regulator of G-protein signaling 9 (RGS9), RefSeqGene on chromosome 17	42.8	42.8	4%	7.6	84%	NG_013021.1
Danio rerio cDNA clone IMAGE:8008437, **** WARNING: chimeric clone ****	42.8	42.8	4%	7.6	85%	BC159195.1
Nematostella vectensis predicted protein (NEMVEDRAFT_v1g59262) partial mRNA	42.8	42.8	9%	7.6	72%	XM_001620433.1
Callithrix jacchus BAC clone CH259-75H12 from chromosome unknown, complete sequence	42.8	42.8	6%	7.6	76%	AC187533.2
Homo sapiens chromosome 17, clone RP11-169I9, complete sequence	42.8	42.8	4%	7.6	84%	AC060771.8
Homo sapiens chromosome 3 clone RP11-72H11, complete sequence	42.8	42.8	3%	7.6	88%	AC092035.2
Homo sapiens 12 BAC RP11-902D13 (Roswell Park Cancer Institute Human BAC Library) complete sequence	42.8	42.8	3%	7.6	88%	AC026122.14

Phaeosphaeria nodorum SN15 hypothetical protein partial mRNA

Sequence ID: **ref|XM_001790817.1|** Length: 2364 Number of Matches: 1

Range 1: 1458 to 1488

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	29/31(94%)	0/31(0%)	Plus/Minus	

Features:

```
Query 914  GTCGACGCTCTCGAGAGAGAGCAGACGCTCT 944
          |||
Sbjct 1488  GTCGACGCGTTCGAGAGAGAGCAGACGCTCT 1458
```