BLAST ®

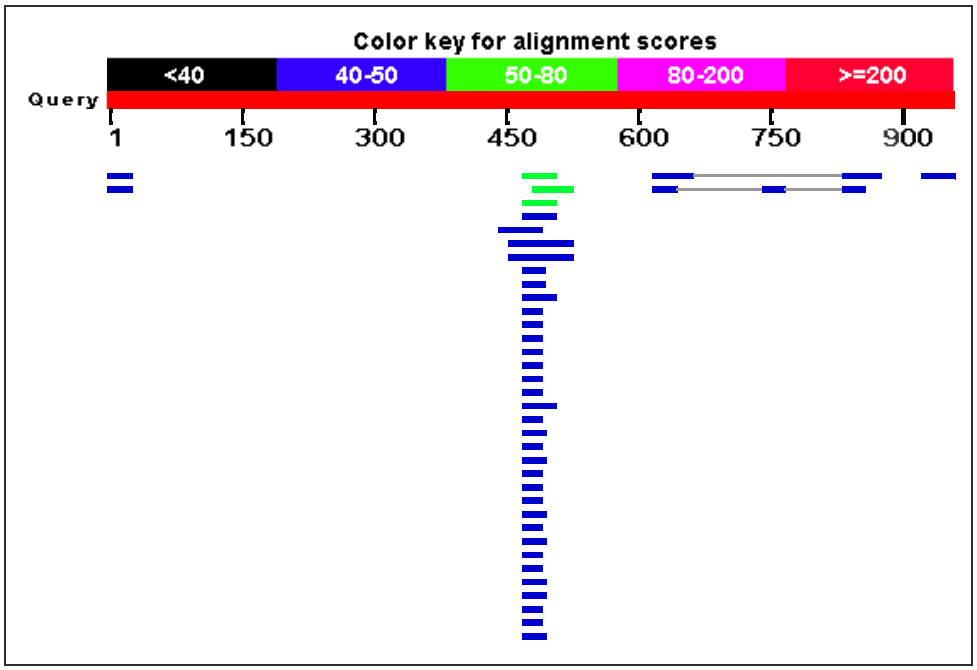
Basic Local Alignment Search Tool

TGAC

RID	Y0VB0ME0015 (Expires on 08-06 13:36 pm)		
Query ID	lcl|12039	**Database Name**	nr
Description	None	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.2.29+
Query Length	952		

Graphic Summary

Distribution of 44 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-121H17 in linkage group 21, complete sequence	55.4	55.4	4%	0.001	92%	CR382296.26
Ostreococcus lucimarinus CCE9901 chromosome 9, complete sequence	53.6	53.6	5%	0.004	86%	CP000589.1
Zebrafish DNA sequence from clone CH73-205E7 in linkage group 5, complete sequence	51.8	51.8	3%	0.015	89%	FP340311.5
Salpingoeca sp. ATCC 50818 hypothetical protein (PTSG_00954) mRNA, complete cds	48.2	96.3	9%	0.18	84%	XM_004998370.1
Zebrafish DNA sequence from clone DKEY-162H11 in linkage group 7, complete sequence	48.2	48.2	3%	0.18	89%	CR926130.14
Homo sapiens 3 BAC RP11-119P22 (Roswell Park Cancer Institute Human BAC Library) complete sequence	46.4	46.4	3%	0.62	89%	AC097105.10
Zebrafish DNA sequence from clone CH73-305A18 in linkage group 2, complete sequence	44.6	44.6	5%	2.2	81%	FP101911.9
Gadus morhua hemoglobin beta 1 (HbB1) gene, HbB1-5 allele, complete cds	44.6	44.6	7%	2.2	75%	FJ666976.1
Gadus morhua hemoglobin beta 1 (HbB1) gene, HbB1-2 allele, complete cds	44.6	44.6	7%	2.2	75%	FJ666973.1
Zebrafish DNA sequence from clone CH1073-66C17 in linkage group 23, complete sequence	44.6	44.6	2%	2.2	100%	CU571070.6
Zebrafish DNA sequence from clone DKEY-171L20 in linkage group 10, complete sequence	44.6	44.6	2%	2.2	100%	CT027796.13
Pan troglodytes BAC clone CH251-344F10 from chromosome unknown, complete sequence	44.6	44.6	3%	2.2	93%	AC183922.3
Pan troglodytes BAC clone RP43-22I12 from chromosome 7, complete sequence	44.6	44.6	3%	2.2	93%	AC140952.1
Zebrafish DNA sequence from clone CH211-203F4 in linkage group 15, complete sequence	44.6	87.3	3%	2.2	87%	BX649258.11
Zebrafish DNA sequence from clone CH211-207G17 in linkage group 16, complete sequence	42.8	42.8	2%	7.6	100%	BX537113.10
Zebrafish DNA sequence from clone DKEY-169A9 in linkage group 10, complete sequence	42.8	42.8	2%	7.6	100%	CU463258.14
Zebrafish DNA sequence from clone DKEY-20J10 in linkage group 5, complete sequence	42.8	42.8	2%	7.6	100%	BX323563.11
Zebrafish DNA sequence from clone CH73-220K24 in linkage group 3, complete sequence	42.8	42.8	2%	7.6	100%	FQ311897.4
Zebrafish DNA sequence from clone CH211-63E8 in linkage group 3, complete sequence	42.8	42.8	2%	7.6	100%	CU855917.15
Zebrafish DNA sequence from clone CH73-375G18 in linkage group 23, complete sequence	42.8	42.8	2%	7.6	100%	CU896563.7
Zebrafish DNA sequence from clone						

CH1073-234E12 in linkage group 17, complete sequence	42.8	42.8	2%	7.6	100%	CU634002.7
Vitis vinifera contig VV78X128443.7, whole genome shotgun sequence	42.8	128	8%	7.6	96%	AM428522.2
Zebrafish DNA sequence from clone CH211-136I24 in linkage group 18, complete sequence	42.8	42.8	3%	7.6	87%	CR854830.20
Zebrafish DNA sequence from clone CH73-289A15 in linkage group 23, complete sequence	42.8	42.8	2%	7.6	100%	CT573385.8
Zebrafish DNA sequence from clone CH211-232J20 in linkage group 6, complete sequence	42.8	42.8	2%	7.6	96%	CR533579.7
Zebrafish DNA sequence from clone CH211-101L11 in linkage group 1, complete sequence	42.8	42.8	2%	7.6	100%	BX950201.12
Zebrafish DNA sequence from clone CH211-9F23 in linkage group 4, complete sequence	42.8	42.8	2%	7.6	96%	CR392331.15
Zebrafish DNA sequence from clone CH211-147L19 in linkage group 21, complete sequence	42.8	42.8	2%	7.6	100%	CR759923.6
Zebrafish DNA sequence from clone DKEYP-70G1 in linkage group 5, complete sequence	42.8	42.8	2%	7.6	100%	BX323870.13
Zebrafish DNA sequence from clone DKEY-228B21 in linkage group 1, complete sequence	42.8	42.8	2%	7.6	100%	BX530018.8
Zebrafish DNA sequence from clone CH211-217M19 in linkage group 16, complete sequence	42.8	42.8	2%	7.6	96%	AL928695.23
Zebrafish DNA sequence from clone CH211-243G18 in linkage group 10, complete sequence	42.8	42.8	2%	7.6	100%	BX248511.4
Zebrafish DNA sequence from clone DKEY-3N4, complete sequence	42.8	42.8	2%	7.6	96%	BX004984.6
Zebrafish DNA sequence from clone CH211-89M19, complete sequence	42.8	42.8	2%	7.6	100%	BX004832.9
Zebrafish DNA sequence from clone CH211-232P17 in linkage group 18 Contains the 3' end of the gene for a novel protein similar to vertebrate thyroid hormone receptor interactor 12 (TRIP12), the gene for a novel protein similar to vertebrate pentaxin-related gene rapidly induced by IL-1 beta (PTX3), the 5' end of the veph gene for ventricular zone expressed PH domain protein and three CpG islands, complete sequence	42.8	42.8	2%	7.6	100%	BX255879.6
Zebrafish DNA sequence from clone DKEY-191C11, complete sequence	42.8	42.8	2%	7.6	96%	BX511214.8
Zebrafish DNA sequence from clone DKEY-28P22, complete sequence	42.8	42.8	2%	7.6	96%	AL953891.10
Zebrafish DNA sequence from clone CH211-241L3 in linkage group 21, complete sequence	42.8	42.8	2%	7.6	100%	AL935199.4
Zebrafish DNA sequence from clone CH211-227C6 in linkage group 13, complete sequence	42.8	42.8	2%	7.6	100%	AL928999.4
Zebrafish DNA sequence from clone DKEY-1M11 in linkage group 15, complete sequence	42.8	42.8	2%	7.6	96%	AL929092.4

Alignments

Zebrafish DNA sequence from clone DKEY-121H17 in linkage group 21, complete sequence
Sequence ID: **emb|CR382296.26|** Length: 137360 Number of Matches: 1

Range 1: 101486 to 101521

Score	Expect	Identities	Gaps	Strand	Frame
55.4 bits(60)	0.001()	36/39(92%)	3/39(7%)	Plus/Plus	

Features:

```
Query  468     CTCTCTCTCATTCGCGCGCACACGAATCGCGCGCACACG  506
               ||||||||||||||||||||||    ||||||||||||
Sbjct  101486  CTCTCTCTCATTCGCGCGCACACG---CGCGCGCACACG  101521
```

Ostreococcus lucimarinus CCE9901 chromosome 9, complete sequence

Sequence ID: **gb|CP000589.1|** Length: 670853 Number of Matches: 1
Range 1: 380063 to 380111

Score	Expect	Identities	Gaps	Strand	Frame
53.6 bits(58)	0.004()	43/50(86%)	3/50(6%)	Plus/Plus	

Features:

```
Query  479     TCGCGCGCACACGAATCG--CGCGCACACGACTACCGCGCACACGACTAC  526
               |||||||||||||||| ||   | ||||||||||| ||| ||||||||||| ||
Sbjct  380063  TCGCGCGCACACGAA-CGACCACGCACACGACGACCACGCACACGACGAC  380111
```

Zebrafish DNA sequence from clone CH73-205E7 in linkage group 5, complete sequence

Sequence ID: **emb|FP340311.5|** Length: 110126 Number of Matches: 1
Range 1: 88682 to 88719

Score	Expect	Identities	Gaps	Strand	Frame
51.8 bits(56)	0.015()	34/38(89%)	0/38(0%)	Plus/Minus	

Features:

```
Query  468    CTCTCTCTCATTCGCGCGCACACGAATCGCGCGCACAC  505
              |||||||||||||||| ||||| || ||||| |||||
Sbjct  88719  CTCTCTCTCATTCGCGCACACACCAAGCGCGCACACAC  88682
```

Salpingoeca sp. ATCC 50818 hypothetical protein (PTSG_00954) mRNA, complete cds

Sequence ID: **ref|XM_004998370.1|** Length: 1216 Number of Matches: 2
Range 1: 1138 to 1179

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	38/45(84%)	3/45(6%)	Plus/Minus	

Features:

```
Query  828   CTCTCTCTCATCCTCTCAGCGATCTCATCGCGCGCACACGACTAC  872
             ||||||||| |||||||     ||||| ||||||||||||||||
Sbjct  1179  CTCTCTCTCTTCCTCTCTC---TCTCAGCGCGCGCACACGACTAC  1138
```

Range 2: 1138 to 1179

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	38/45(84%)	3/45(6%)	Plus/Minus	

Features:

```
Query  615   CTCTCTCTCATCCTCTCAGCGATCTCATCGCGCGCACACGACTAC  659
             ||||||||| |||||||     ||||| ||||||||||||||||
Sbjct  1179  CTCTCTCTCTTCCTCTCTC---TCTCAGCGCGCGCACACGACTAC  1138
```

Zebrafish DNA sequence from clone DKEY-162H11 in linkage group 7, complete sequence

Sequence ID: **emb|CR926130.14|** Length: 170105 Number of Matches: 1
Range 1: 7339 to 7375

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	34/38(89%)	1/38(2%)	Plus/Minus	

Features:

```
Query  468   CTCTCTCTCATTCGCGCGCACACGAATCGCGCGCACAC  505
             ||||||||||||||||||||| || | | |||||||||
Sbjct  7375  CTCTCTCTCATTCGCGCGCACGCGCA-CACGCGCACAC  7339
```