

Basic Local Alignment Search Tool

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TGCA

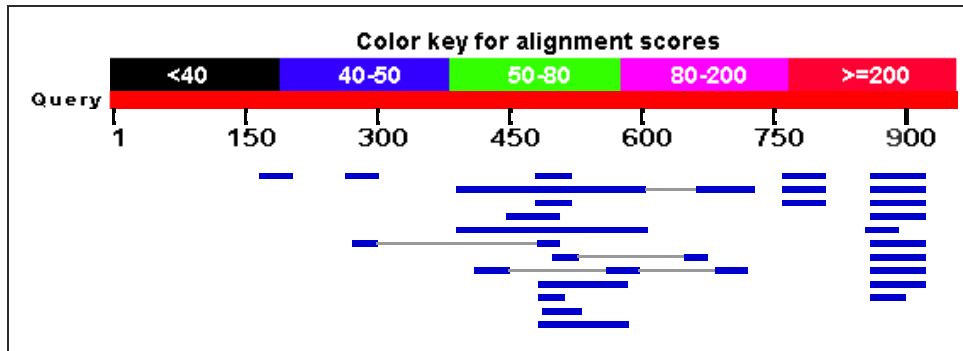
RID [Y0VJ2CE501R](#) (Expires on 08-06 13:40 pm)

Query ID lc|80171
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 41 Blast Hits on the Query Sequence



☰ Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Plasmodium vivax SaI-1 hypothetical protein partial mRNA	46.4	90.9	4%	0.62	84%	XM_001613023.1
Salmo salar clone Rsa212 microsatellite sequence	46.4	221	29%	0.62	70%	AY543913.1
Plasmodium vivax YAC 1H14, complete sequence	46.4	46.4	4%	0.62	84%	AY003872.1
Mouse DNA sequence from clone RP23-145N4 on chromosome 11, complete sequence	46.4	46.4	3%	0.62	90%	AL844147.9
Rattus norvegicus 11 BAC CH230-4O6 (Children's Hospital Oakland Research Institute) complete sequence	44.6	44.6	6%	2.2	77%	AC094784.13
Salmo salar microsatellite Rsa189 sequence	44.6	130	22%	2.2	69%	AF271595.1
PREDICTED: Anolis carolinensis forkhead box L2 (foxL2), mRNA	42.8	85.5	5%	7.6	96%	XM_008106355.1
Mus musculus targeted non-conditional, lacZ-tagged mutant allele Olig2:tm1e(EUCOMM)Hmgu; transgenic	42.8	85.5	6%	7.6	77%	JN956598.1
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Dennd1c:tm1a(EUCOMM)Wtsi; transgenic	42.8	42.8	6%	7.6	78%	JN953900.1
Mus musculus targeted deletion, lacZ-tagged mutant allele Tubb4:tm1(KOMP)Wtsi; transgenic	42.8	42.8	6%	7.6	78%	JN949088.1
Mus musculus targeted non-conditional, lacZ-tagged mutant allele Dennd1c:tm1e(EUCOMM)Wtsi; transgenic	42.8	42.8	6%	7.6	78%	JN946054.1
Homo sapiens GRB2 associated, regulator of MAPK1 (GAREM), RefSeqGene on chromosome 18	42.8	42.8	5%	7.6	81%	NG_030329.1
Pig DNA sequence from clone CH242-456J9 on chromosome X, complete sequence	42.8	42.8	3%	7.6	86%	FP085383.6
Branchiostoma floridae hypothetical protein, mRNA	42.8	85.5	5%	7.6	93%	XM_002589730.1
Rhesus Macaque BAC CH250-310K20 () complete sequence	42.8	128	11%	7.6	86%	AC200467.5
Mouse DNA sequence from clone RP24-116C19 on chromosome 17, complete sequence	42.8	42.8	6%	7.6	78%	CT571247.13
Branchiostoma floridae clone CH302-60C21, complete sequence	42.8	42.8	6%	7.6	79%	AC150412.2
Mus musculus chromosome 18, clone RP24-111I16, complete sequence	42.8	42.8	10%	7.6	73%	AC119181.11
Mus musculus chromosome 16, clone RP23-428P5, complete sequence	42.8	85.5	6%	7.6	77%	AC034116.10
Mus musculus BAC clone RP23-190G10 from chromosome 16, complete sequence	42.8	85.5	6%	7.6	77%	AC152503.5
Gibberella zeae PH-1 hypothetical protein partial mRNA	42.8	42.8	3%	7.6	90%	XM_389278.1
Homo sapiens chromosome 18, clone RP11-344B2, complete sequence	42.8	42.8	5%	7.6	81%	AC015563.11
Homo sapiens, clone RP11-12F2, complete sequence	42.8	42.8	5%	7.6	81%	AC013630.12

Homo sapiens chromosome 8, clone RP11-531A24, complete sequence	42.8	42.8	4%	7.6	81%	AC022893.6
Zebrafish DNA sequence from clone DKEY-276L17 in linkage group 14 Contains the gene for a novel protein similar to human KAT protein, the gene for a novel protein (zgc:153146), the gene for a novel protein similar to vertebrate sorbin and SH3 domain containing 2 (SORBS2), the pdlim3b gene for PDZ and LIM domain 3b, the 3' end of the gene for a novel protein similar to vertebrate odd Oz/ten-m homolog 2 (Drosophila) (ODZ2) and a novel gene, complete sequence	42.8	42.8	3%	7.6	87%	BX537102.13
Mus musculus BAC clone RP24-251M20 from 9, complete sequence	42.8	42.8	3%	7.6	84%	AC154406.2
Mus musculus chromosome 18, clone RP24-403E17, complete sequence	42.8	42.8	10%	7.6	73%	AC116857.11

Alignments

Plasmodium vivax Sal-1 hypothetical protein partial mRNA

Sequence ID: [ref|XM_001613023.1|](#) Length: 11088 Number of Matches: 2

Range 1: 9892 to 9934

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/43(84%)	0/43(0%)	Plus/Plus	

Features:

```

Query  478  TTAGAGAGACACAGCCTAGAGAGACACAGCATCAAGAGACACA  520
          |||
Sbjct  9892  TTAGAGAGACACATGCTAGAGAGACACATGCTAGAGAGACACA  9934

```

Range 2: 9908 to 9949

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	35/42(83%)	0/42(0%)	Plus/Plus	

Features:

```

Query  479  TAGAGAGACACAGCCTAGAGAGACACAGCATCAAGAGACACA  520
          |||
Sbjct  9908  TAGAGAGACACATGCTAGAGAGACACATGCTAGAGAGACACA  9949

```

Salmo salar clone Rsa212 microsatellite sequence

Sequence ID: [gb|AY543913.1|](#) Length: 644 Number of Matches: 5

Range 1: 16 to 210

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	150/214(70%)	33/214(15%)	Plus/Minus	

Features:

```

Query  403  CAGATGCTAGTTT TAGAGAGACACAGCAATA---TACGAGCTATACT--AGAGAGACACAG  457
          |||
Sbjct  210  CAGAT--TACTGTAGAGAGACACCACATTACAATAC-AGAT-TACTGTAGAGAGACACAA  155

Query  458  CATCACGCGCATATATATACT-TAGAGAGACACAGCCTAGAGAGAC-ACAGCATCAAGAG  515
          |||
Sbjct  154  CAATAC-----AGAT-TACTGTAGAGAGACACAACA-ATACAGATTACTGTAG--AGAG  105

Query  516  ACACAGCAT--CAGATGCTAGTT-AGAGACACAGCAT--CAGATGCTAGTTT TAGAGAGAC  570
          |||
Sbjct  104  ACACAACAATACAGATTACTGTAGAGAGACACAACAATACAGAT--TACTGTAGAGAGAC  47

Query  571  ACAGCAATATACGAGCTATAC--TAGAGAGACAC  602
          |||
Sbjct  46  ACAACA--ATACGAGAT-TACTGTAGAGAGACAC  16

```

Range 2: 16 to 108

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	76/103(74%)	13/103(12%)	Plus/Minus	

Features:

```

Query 390 AGAGACACAGCAT--CAGATGCTAGTTTAGAGAGACACAGCAATATACGAGCTATACTAG 447
          |||
Sbjct 108 AGAGACACAACAATACAGAT--TACTGTAGAGAGACACAACAATACA-GA-TTACTGTAG 53
          |||
Query 448 AGAGACACAGCATCACGCGCATATATATACT-TAGAGAGACAC 489
          |||
Sbjct 52 AGAGACACAACAATACGAG-AT-----TACTGTAGAGAGACAC 16
          |||
    
```

Range 3: 16 to 80

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	55/70(79%)	9/70(12%)	Plus/Minus	

Features:

```

Query 660 AGAGACACAGCAT--CAGATGCTAGTTTAGAGAGACACAGCAATATACGAGCTATACT--T 715
          |||
Sbjct 80 AGAGACACAACAATACAGAT--TACTGTAGAGAGACACAACA--ATACGAGAT-TACTGT 26
          |||
Query 716 AGAGAGACAC 725
          |||
Sbjct 25 AGAGAGACAC 16
          |||
    
```

Range 4: 44 to 136

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	76/104(73%)	14/104(13%)	Plus/Minus	

Features:

```

Query 390 AGAGACACAGCAT--CAGATGCTAGTTTAGAGAGACACAGCAATATACGAGCTATACTAG 447
          |||
Sbjct 136 AGAGACACAACAATACAGAT--TACTGTAGAGAGACACAACAATACA-GA-TTACTGTAG 81
          |||
Query 448 AGAGACACAGCATCACGCGCATATATATACT-TAGAGAGACACA 490
          |||
Sbjct 80 AGAGACACAACAATA----CAGAT---TACTGTAGAGAGACACA 44
          |||
    
```

Range 5: 72 to 164

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	76/104(73%)	14/104(13%)	Plus/Minus	

Features:

```

Query 390 AGAGACACAGCAT--CAGATGCTAGTTTAGAGAGACACAGCAATATACGAGCTATACTAG 447
          |||
Sbjct 164 AGAGACACAACAATACAGAT--TACTGTAGAGAGACACAACAATACA-GA-TTACTGTAG 109
          |||
Query 448 AGAGACACAGCATCACGCGCATATATATACT-TAGAGAGACACA 490
          |||
Sbjct 108 AGAGACACAACAATA----CAGAT---TACTGTAGAGAGACACA 72
          |||
    
```

Plasmodium vivax YAC 1H14, complete sequence

Sequence ID: **gb|AY003872.1|** Length: 199866 Number of Matches: 1
 Range 1: 149759 to 149801

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/43(84%)	0/43(0%)	Plus/Minus	

Features:

```

Query 478 TTAGAGAGACACAGCCTAGAGAGACACAGCATCAAGAGACACA 520
          |||
Sbjct 149801 TTAGAGAGACACATGCTAGAGAGACACATGCTAGAGAGACACA 149759
          |||
    
```

Mouse DNA sequence from clone RP23-145N4 on chromosome 11, complete sequence

Sequence ID: **emb|AL844147.9|** Length: 228444 Number of Matches: 1
 Range 1: 30271 to 30308

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	35/39(90%)	2/39(5%)	Plus/Plus	

Features:

```

Query 169 TATCGCTTTTCTC-TCTAGAGAGACACAGCATCAGATGCT 206
          |||
Sbjct 30271 TATCGCTTTGTCTCTTAGAGAGACACAGC-TCAGCTGCT 30308
          |||
    
```