

Basic Local Alignment Search Tool

NCBI/ [BLAST](#)/ [blastn suite](#)/ Formatting Results - Y0S5K2VV015

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ACTG

RID [Y0S5K2VV015](#) (Expires on 08-06 12:42 pm)

Query ID lc|10357

Description None

Molecule type nucleic acid

Query Length 952

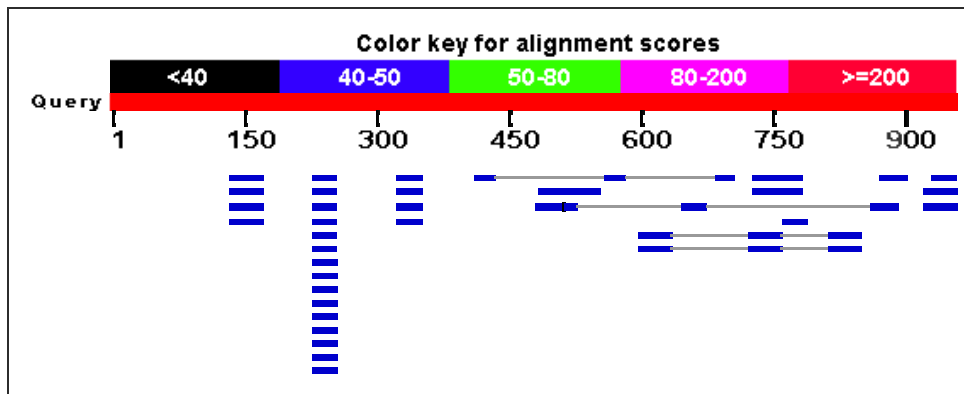
Database Name nr

Description Nucleotide collection (nt)

Program BLASTN 2.2.29+

 [Graphic Summary](#)

Distribution of 45 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 CH73-228J22 in linkage group 22, complete sequence	48.2	48.2	5%	0.18	81%	CU928218.7
Zebrafish DNA sequence from clone CH211-126J24 in linkage group 22, complete sequence	48.2	48.2	5%	0.18	81%	BX088728.23
Brucella ovis ATCC 25840 chromosome I, complete sequence	46.4	178	11%	0.62	93%	CP000708.1
Oryza sativa genomic DNA, chromosome 4, BAC clone: H0818E04, complete sequence	44.6	44.6	4%	2.2	87%	CR855170.1
Oryza sativa Japonica Group Os04g0450000 (Os04g0450000) mRNA, complete cds	44.6	44.6	4%	2.2	87%	NM_001059470.1
Oryza sativa genomic DNA, chromosome 4, BAC clone: OSJNBa0086B14, complete sequence	44.6	44.6	4%	2.2	87%	AL606615.4
Oryza sativa Japonica Group cDNA clone:002-142-G09, full insert sequence	44.6	44.6	4%	2.2	87%	AK108406.1
Cochliobolus sativus ND90Pr hypothetical protein mRNA	42.8	128	7%	7.6	100%	XM_007707580.1
PREDICTED: Cricetus griseus cyclin-T2-like (LOC103160072), partial mRNA	42.8	42.8	2%	7.6	93%	XM_007614704.1
PREDICTED: Cricetus griseus cyclin T2 (Ccnt2), transcript variant X2, mRNA	42.8	42.8	2%	7.6	93%	XM_007616241.1
PREDICTED: Cricetus griseus cyclin T2 (Ccnt2), transcript variant X1, mRNA	42.8	42.8	2%	7.6	93%	XM_003497706.2
Zebrafish DNA sequence from clone CH1073-96K14 in linkage group 25, complete sequence	42.8	85.5	2%	7.6	93%	FP102902.3
PREDICTED: Peromyscus maniculatus bairdii cyclin T2 (Ccnt2), transcript variant X3, mRNA	42.8	42.8	2%	7.6	93%	XM_006992977.1
PREDICTED: Peromyscus maniculatus bairdii cyclin T2 (Ccnt2), transcript variant X2, mRNA	42.8	42.8	2%	7.6	93%	XM_006992976.1
PREDICTED: Peromyscus maniculatus bairdii cyclin T2 (Ccnt2), transcript variant X1, mRNA	42.8	42.8	2%	7.6	93%	XM_006992975.1
PREDICTED: Rattus norvegicus cyclin T2 (Ccnt2), transcript variant X4, mRNA	42.8	42.8	2%	7.6	93%	XM_006249689.1
PREDICTED: Rattus norvegicus cyclin T2 (Ccnt2), transcript variant X3, mRNA	42.8	42.8	2%	7.6	93%	XM_006249688.1
PREDICTED: Rattus norvegicus cyclin T2 (Ccnt2), transcript variant X2, mRNA	42.8	42.8	2%	7.6	93%	XM_006249687.1
PREDICTED: Rattus norvegicus cyclin T2 (Ccnt2), transcript variant X1, mRNA	42.8	42.8	2%	7.6	93%	XM_006249686.1
PREDICTED: Microtus ochrogaster cyclin T2 (Ccnt2), transcript variant X2, mRNA	42.8	42.8	2%	7.6	93%	XM_005348238.1
PREDICTED: Microtus ochrogaster cyclin T2 (Ccnt2), transcript variant X1, mRNA	42.8	42.8	2%	7.6	93%	XM_005348237.1
PREDICTED: Mesocricetus auratus cyclin T2 (Ccnt2), transcript variant X2, mRNA	42.8	42.8	2%	7.6	93%	XM_005079881.1
PREDICTED: Mesocricetus auratus cyclin T2 (Ccnt2), transcript variant X1, mRNA	42.8	42.8	2%	7.6	93%	XM_005079880.1
Bifidobacterium thermophilum RBL67, complete genome	42.8	42.8	3%	7.6	88%	CP004346.1

Sinorhizobium fredii USDA257, complete genome	42.8	42.8	2%	7.6	93%	CP003563.1
Rattus norvegicus cyclin T2 (Ccnt2), mRNA	42.8	42.8	2%	7.6	93%	NM_001107171.1
Takifugu rubripes frMUT, frGPR136L1, and frGPR136L2 genes, complete sequence; frRUNX2 (frRUNX2) gene, complete cds; and frCLIC5, frENPP5, frPHIP, frIRAK1BP1, and frTBX18 genes, complete sequence	42.8	128	11%	7.6	89%	AY739093.1
Oryza sativa Japonica Group chromosome 10 clone OSJNBa0046L02, complete sequence	42.8	42.8	3%	7.6	90%	AC079632.4
Oryza sativa Japonica Group chromosome 10 clone Pseudo10p0.0-10p4.4, complete sequence	42.8	42.8	3%	7.6	90%	AC145127.1
Oryza sativa Japonica Group chromosome 10 clone OJA1136E01, complete sequence	42.8	42.8	3%	7.6	90%	AC166065.1
Takifugu rubripes transcription factor runx2 (runx2) gene, 5' flanking region	42.8	128	11%	7.6	89%	AF477382.1
Genomic sequence for (japonica cultivar-group) cultivar Nipponbare clone OJ1136E01, from chromosome 10, complete sequence	42.8	42.8	3%	7.6	90%	AC108883.1
Zebrafish DNA sequence from clone CH211-146A1 in linkage group 18, complete sequence	42.8	42.8	3%	7.6	87%	BX248320.3
Zebrafish DNA sequence from clone DKEY-227K11 in linkage group 18 Contains the gene for a novel protein similar to vertebrate sirtuin [silent mating type information regulation 2 homolog] 2 (S. cerevisiae) (SIRT2), the gene for a novel protein (zgc:64098), the 3' end of the rfx4 gene for regulatory factor X, 4, the 3' end of the gene for a novel protein similar to vertebrate carbohydrate (keratan sulfate Gal-6) sulfotransferase (CHST1), a novel gene and three CpG islands, complete sequence	42.8	42.8	3%	7.6	87%	BX571971.4
Homo sapiens chromosome 16 clone RP11-483N11, complete sequence	42.8	42.8	7%	7.6	74%	AC136837.1

Alignments

Zebrafish DNA sequence from clone CH73-228J22 in linkage group 22, complete sequence

Sequence ID: **emb|CU928218.7|** Length: 101850 Number of Matches: 1

Range 1: 79934 to 79990

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	47/58(81%)	2/58(3%)	Plus/Plus	
Features:					
Query	723	TGTGCTGATGCTCTCTGAGAGAGTAGGAGAGTC-GCTAGAGGCGCGTGTGCTGATGC	779		
Sbjct	79934	TGTGCTAATGTCTGTGAGAGAGAAAAGGAGTGTGTGCTA-ATGTGTGTGTGCTGATGC	79990		

Zebrafish DNA sequence from clone CH211-126J24 in linkage group 22, complete sequence

Sequence ID: **emb|BX088728.23|** Length: 168184 Number of Matches: 1

Range 1: 22370 to 22426

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	47/58(81%)	2/58(3%)	Plus/Minus	
Features:					
Query	723	TGTGCTGATGCTCTCTGAGAGAGTAGGAGAGTC-GCTAGAGGCGCGTGTGCTGATGC	779		
Sbjct	22426	TGTGCTAATGTCTGTGAGAGAGAAAAGGAGTGTGTGCTA-ATGTGTGTGTGCTGATGC	22370		

Sequence ID: **gb|CP000708.1|** Length: 211370 Number of Matches: 4
Range 1: 1310950 to 1310979

Features:

Range 2: 1310950 to 1310979

Features:

Range 3: 1310949 to 1310979

Features:

Range 4: 1310950 to 1310980

Features:

Sequence ID: **emb|CR855170.1|** Length: 146307 Number of Matches: 1
Range 1: 77866 to 77903

Features:

Sequence ID: **ref|NM_001059470.1|** Length: 994 Number of Matches: 1
Range 1: 144 to 181

Features:

```

Query    135  GATCGATCGATCGAGCGTACGATCAGTACGACGCAGATC  173
          |||||
Sbjct    181  GATCGATCGATCGATCG-ATGATCAGTACGCCGCCGATC  144

```

Oryza sativa genomic DNA, chromosome 4, BAC clone: OSJNBa0086B14, complete sequence

Sequence ID: **emb|AL606615.4|** Length: 175698 Number of Matches: 1

Range 1: 3994 to 4031

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	34/39(87%)	1/39(2%)	Plus/Minus	

Features:

```
Query 135  GATCGATCGATCGAGCGTACGATCAGTACGACGCAGATC 173
           |||
Sbjct 4031  GATCGATCGATCGATCG-ATGATCAGTACGCCGCCGATC 3994
```

Oryza sativa Japonica Group cDNA clone:002-142-G09, full insert sequence

Sequence ID: **dbj|AK108406.1|** Length: 998 Number of Matches: 1

Range 1: 148 to 185

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	34/39(87%)	1/39(2%)	Plus/Minus	

Features:

```
Query 135  GATCGATCGATCGAGCGTACGATCAGTACGACGCAGATC 173
           |||
Sbjct 185  GATCGATCGATCGATCG-ATGATCAGTACGCCGCCGATC 148
```

Cochliobolus sativus ND90Pr hypothetical protein mRNA

Sequence ID: **ref|XM_007707580.1|** Length: 1947 Number of Matches: 3

Range 1: 35 to 57

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	23/23(100%)	0/23(0%)	Plus/Plus	

Features:

```
Query 410  AGCAAAGCGCGCGTGTGCTGGAG 432
           |||
Sbjct 35   AGCAAAGCGCGCGTGTGCTGGAG 57
```

Range 2: 35 to 57

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	23/23(100%)	0/23(0%)	Plus/Plus	

Features:

```
Query 557  AGCAAAGCGCGCGTGTGCTGGAG 579
           |||
Sbjct 35   AGCAAAGCGCGCGTGTGCTGGAG 57
```

Range 3: 35 to 57

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	23/23(100%)	0/23(0%)	Plus/Plus	

Features:

```
Query 680  AGCAAAGCGCGCGTGTGCTGGAG 702
           |||
Sbjct 35   AGCAAAGCGCGCGTGTGCTGGAG 57
```

PREDICTED: Cricetulus griseus cyclin-T2-like (LOC103160072), partial mRNA

Sequence ID: **ref|XM_007614704.1|** Length: 2894 Number of Matches: 1

Range 1: 1593 to 1620

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	26/28(93%)	0/28(0%)	Plus/Plus	

Features:

```
Query 228  TATCCTAGAGCTGCTAGATGAGCTAGCA 255
           |||
Sbjct 1593 TACCCTAGAGCTGCTAGATGAGCTAACA 1620
```

Sequence ID: **ref|XM_007616241.1|** Length: 2138 Number of Matches: 1
Range 1: 762 to 789

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	26/28(93%)	0/28(0%)	Plus/Plus	

Features:

```
Query    228   TATCCTAGAGCTGCTAGATGAGCTAGCA      255
          |||||
Sbjct    762   TACCCTAGAGCTGCTAGATGAGCTAACA      789
```

PREDICTED: *Cricetulus griseus* cyclin T2 (Ccnt2), transcript variant X1, mRNA

Sequence ID: **ref|XM_003497706.2|** Length: 4569 Number of Matches: 1
Range 1: 762 to 789

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	26/28(93%)	0/28(0%)	Plus/Plus	

Features:

```
Query    228   TATCCTAGAGCTGCTAGATGAGCTAGCA      255
          |||||
Sbjct    762   TACCCTAGAGCTGCTAGATGAGCTAACA      789
```

Zebrafish DNA sequence from clone CH1073-96K14 in linkage group 25, complete sequence

Sequence ID: **emb|FP102902.3|** Length: 32620 Number of Matches: 2
Range 1: 19272 to 19299

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	26/28(93%)	0/28(0%)	Plus/Plus	

Features:

```
Query   924      CTGAGAGAGAGTAGATGTCTCTGAGAGA    951
          |||||
Sbjct  19272    CTGAGAGAGACTAGAAAGTCTCTGAGAGA    19299
```

Range 2: 20963 to 20990

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	26/28(93%)	0/28(0%)	Plus/Plus	

Features:

```

Query   924      CTGAGAGAGAGTAGATGTCTCTGAGAGA   951
          |||||
Sbjct   20963    CTGAGAGAGACTAGAAGTCTCTGAGAGA   20990

```

PREDICTED: *Peromyscus maniculatus bairdii* cyclin T2 (Ccnt2), transcript variant X3, mRNA

Sequence ID: [ref|XM_006992977.1|](#) Length: 6412 Number of Matches: 1
Range 1: 368 to 395

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	26/28(93%)	0/28(0%)	Plus/Plus	

Features:

```
Query    228   TATCCTAGAGCTGCTAGATGAGCTAGCA      255
        ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct    368   TACCCTAGAGCTGCTAGATGAGCTAACA      395
```

PREDICTED: *Peromyscus maniculatus bairdii* cyclin T2 (Ccnt2), transcript variant X2, mRNA

Sequence ID: **ref|XM_006992976.1|** Length: 2097 Number of Matches: 1
Range 1: 696 to 723

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	26/28(93%)	0/28(0%)	Plus/Plus	

Features:

```

Query  228  TATCCTAGAGCTGCTAGATGAGCTAGCA  255
      |||||||||||||||||||||
Sbjct  696  TACCCTAGAGCTGCTAGATGAGCTAACA  723

```

PREDICTED: *Peromyscus maniculatus bairdii* cyclin T2 (Ccnt2), transcript variant X1, mRNA

Sequence ID: [ref|XM_006992975.1|](#) Length: 6740 Number of Matches: 1

Range 1: 696 to 723

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	26/28(93%)	0/28(0%)	Plus/Plus	

Features:

```

Query  228  TATCCTAGAGCTGCTAGATGAGCTAGCA  255
      |||||||||||||||||||||
Sbjct  696  TACCCTAGAGCTGCTAGATGAGCTAACA  723

```

PREDICTED: Rattus norvegicus cyclin T2 (Ccnt2), transcript variant X4, mRNA

Sequence ID: [ref|XM_006249689.1|](#) Length: 7836 Number of Matches: 1

Range 1: 1749 to 1776

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	26/28(93%)	0/28(0%)	Plus/Plus	

Features:

```

Query  228      TATCCTAGAGCTGCTAGATGAGCTAGCA      255
          |||
Sbjct  1749     TACCCTAGAGCTGCTAGATGAGCTAACA      1776

```

PREDICTED: Rattus norvegicus cyclin T2 (Ccnt2), transcript variant X3, mRNA

Sequence ID: [ref|XM_006249688.1|](#) Length: 6435 Number of Matches: 1

Range 1: 348 to 375

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	26/28(93%)	0/28(0%)	Plus/Plus	

Features:

```

Query  228  TATCCTAGAGCTGCTAGATGAGCTAGCA  255
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Sbjct  348  TACCCTAGAGCTGCTAGATGAGCTAACA  375

```

PREDICTED: Rattus norvegicus cyclin T2 (Cnt2), transcript variant X2, mRNA

Sequence ID: **ref|XM_006249687.1|** Length: 8500 Number of Matches: 1

Range 1: 2413 to 2440

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	26/28(93%)	0/28(0%)	Plus/Plus	

Features:

```
Query   228      TATCCTAGAGCTGCTAGATGAGCTAGCA    255
          |||||
Sbjct   2413     TACCCTAGAGCTGCTAGATGAGCTAACA    2440
```

PREDICTED: Rattus norvegicus cyclin T2 (Cnt2), transcript variant X1, mRNA

Sequence ID: **ref|XM_006249686.1|** Length: 6723 Number of Matches: 1

Range 1: 734 to 761

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	26/28(93%)	0/28(0%)	Plus/Plus	

Features:

```

Query  228  TATCCTAGAGCTGCTAGATGAGCTAGCA  255
          |||
Sbjct  734  TACCCTAGAGCTGCTAGATGAGCTAACA  761

```

PREDICTED: *Microtus ochrogaster* cyclin T2 (Cnt2), transcript variant X2, mRNA

Range 1: 712 to 739

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	26/28(93%)	0/28(0%)	Plus/Plus	

Features:

Query	228	TATCCTAGAGCTGCTAGATGAGCTAGCA	255
Sbjct	712	TACCCTAGAGCTGCTAGATGAGCTAACA	739

PREDICTED: *Microtus ochrogaster* cyclin T2 (Ccnt2), transcript variant X1, mRNA

Sequence ID: [ref|XM_005348237.1|](#) Length: 4597 Number of Matches: 1

Range 1: 712 to 739

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	26/28(93%)	0/28(0%)	Plus/Plus	

Features:

```

Query  228  TATCCTAGAGCTGCTAGATGAGCTAGCA  255
      |||||
Sbjct  712  TACCCTAGAGCTGCTAGATGAGCTAACA  739

```

PREDICTED: Mesocricetus auratus cyclin T2 (Ccnt2), transcript variant X2, mRNA

Sequence ID: **ref|XM_005079881.1|** Length: 2782 Number of Matches: 1

Range 1: 697 to 724

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	26/28(93%)	0/28(0%)	Plus/Plus	

Features:

```

Query  228  TATCCTAGAGCTGCTAGATGAGCTAGCA  255
          |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Sbjct  697  TACCCTAGAGCTGCTAGATGAGCTAACA  724

```

PREDICTED: *Mesocricetus auratus* cyclin T2 (Ccnt2), transcript variant X1, mRNA

Sequence ID: [ref|XM_005079880.1|](#) Length: 2547 Number of Matches: 1

Range 1: 702 to 729

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	26/28(93%)	0/28(0%)	Plus/Plus	

Features:

```

Query  228  TATCCTAGAGCTGCTAGATGAGCTAGCA  255
      |||||
Sbjct  702  TACCCTAGAGCTGCTAGATGAGCTAACA  729

```

Bifidobacterium thermophilum RBL67, complete genome

Sequence ID: **gb|CP004346.1** Length: 2291643 Number of Matches: 1

Range 1: 990272 to 990304

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	29/33(88%)	0/33(0%)	Plus/Minus	

Features:

Query	865	TGCTGATGAGCGCGCGTGTGCTGGAGAGTCGCT	897
Sbjct	990304	TGCTGATGAGCGCGCGTGCATGGCGACTCGCT	990272

Sinorhizobium fredii USDA 257, complete genome

Sequence ID: **gb|CP003563.1** Length: 6476459 Number of Matches: 1

Range 1: 5274391 to 5274418

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	26/28(93%)	0/28(0%)	Plus/Minus	

Features:

shikimate kinase AroK

```
Query 756      CGCTAGAGGCGCGTGTGCTGATGCGACT 783
Sbjct 5274418  CGCTAGAGGCGCGGGTGTGCTGAAGCGACT 5274391
```

Rattus norvegicus cyclin T2 (Ccnt2), mRNA

Sequence ID: **ref|NM_001107171.1|** Length: 5652 Number of Matches: 1
Range 1: 719 to 746

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	26/28(93%)	0/28(0%)	Plus/Plus	

Features:

```
Query 228      TATCCTAGAGCTGCTAGATGAGCTAGCA 255
Sbjct 719      TACCCTAGAGCTGCTAGATGAGCTAACA 746
```

Takifugu rubripes frMUT, frGPR136L1, and frGPR136L2 genes, complete sequence; frRUNX2 (frRUNX2) gene, complete cds; and frCLIC5, frENPP5, frPHIP, frIRAK1BP1, and frTBX18 genes, complete sequence

Sequence ID: **gb|AY739093.1|** Length: 235024 Number of Matches: 3
Range 1: 84181 to 84215

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	33/37(89%)	2/37(5%)	Plus/Minus	

Features:

```
Query 808      GCGCGTGTGCTGATGTCTCTGAGAGAGAGTAGGAGAG 844
Sbjct 84215    GCGCGTGTG-TG-TGTCTGTGAGAGAGAGTAAGAGAG 84181
```

Range 2: 84181 to 84215

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	33/37(89%)	2/37(5%)	Plus/Minus	

Features:

```
Query 718      GCGCGTGTGCTGATGTCTCTGAGAGAGAGTAGGAGAG 754
Sbjct 84215    GCGCGTGTG-TG-TGTCTGTGAGAGAGAGTAAGAGAG 84181
```

Range 3: 84181 to 84215

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	33/37(89%)	2/37(5%)	Plus/Minus	

Features:

```
Query 595      GCGCGTGTGCTGATGTCTCTGAGAGAGAGTAGGAGAG 631
Sbjct 84215    GCGCGTGTG-TG-TGTCTGTGAGAGAGAGTAAGAGAG 84181
```

Oryza sativa Japonica Group chromosome 10 clone OSJNBa0046L02, complete sequence

Sequence ID: **gb|AC079632.4|** Length: 142381 Number of Matches: 1
Range 1: 5305 to 5335

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	28/31(90%)	0/31(0%)	Plus/Plus	

Features:

```
Query 322      CGTATCTCGATGAGCTGGAGAGTCGCTAGAG 352
Sbjct 5305     CGTATCTCGATCACCTGGAGAGGCGCTAGAG 5335
```

Oryza sativa Japonica Group chromosome 10 clone Pseudo10p0.0-10p4.4, complete sequence

Sequence ID: **gb|AC145127.1|** Length: 2331000 Number of Matches: 1
Range 1: 19409 to 19439

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

42.8 bits(46) 7.6() 28/31(90%) 0/31(0%) Plus/Plus

Features:

```
Query 322 CGTATCTCGATGAGCTGGAGAGTCGCTAGAG 352
          |||
Sbjct 19409 CGTATCTCGATCACCTGGAGAGGCGCTAGAG 19439
```

Oryza sativa Japonica Group chromosome 10 clone OJA1136E01, complete sequence

Sequence ID: **gb|AC166065.1|** Length: 105139 Number of Matches: 1

Range 1: 24548 to 24578

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	28/31(90%)	0/31(0%)	Plus/Plus	

Features:

```
Query 322 CGTATCTCGATGAGCTGGAGAGTCGCTAGAG 352
          |||
Sbjct 24548 CGTATCTCGATCACCTGGAGAGGCGCTAGAG 24578
```

Takifugu rubripes transcription factor runx2 (runx2) gene, 5' flanking region

Sequence ID: **gb|AF477382.1|AF477382S1** Length: 58521 Number of Matches: 3

Range 1: 54453 to 54487

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	33/37(89%)	2/37(5%)	Plus/Minus	

Features:

```
Query 808 GCGCGTGTGCTGATGTCTCTGAGAGAGTAGGAGAG 844
          |||
Sbjct 54487 GCGCGTGTG-TG-TGTCTGTGAGAGAGTAAGAGAG 54453
```

Range 2: 54453 to 54487

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	33/37(89%)	2/37(5%)	Plus/Minus	

Features:

```
Query 718 GCGCGTGTGCTGATGTCTCTGAGAGAGTAGGAGAG 754
          |||
Sbjct 54487 GCGCGTGTG-TG-TGTCTGTGAGAGAGTAAGAGAG 54453
```

Range 3: 54453 to 54487

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	33/37(89%)	2/37(5%)	Plus/Minus	

Features:

```
Query 595 GCGCGTGTGCTGATGTCTCTGAGAGAGTAGGAGAG 631
          |||
Sbjct 54487 GCGCGTGTG-TG-TGTCTGTGAGAGAGTAAGAGAG 54453
```

Genomic sequence for (japonica cultivar-group) cultivar Nipponbare clone OJ1136E01, from chromosome 10, complete sequence

Sequence ID: **gb|AC108883.1|** Length: 113856 Number of Matches: 1

Range 1: 94418 to 94448

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	28/31(90%)	0/31(0%)	Plus/Minus	

Features:

```
Query 322 CGTATCTCGATGAGCTGGAGAGTCGCTAGAG 352
          |||
Sbjct 94448 CGTATCTCGATCACCTGGAGAGGCGCTAGAG 94418
```

Zebrafish DNA sequence from clone CH211-146A1 in linkage group 18, complete sequence

Sequence ID: **emb|BX248320.3|** Length: 54960 Number of Matches: 1

Range 1: 40223 to 40259

Score	Expect	Identities	Gaps	Strand	Frame
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Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	33/38(87%)	1/38(2%)	Plus/Minus	
Features:					
Query	915	CTGATGTCTCTGAGAGAGAGTAGATGTCTCTGAGAGAG	952		
Sbjct	40259	CTGATGTC-CTGAGAGAGACTAGTGATCTCTGAGAGAG	40223		

Zebrafish DNA sequence from clone DKEY-227K11 in linkage group 18 Contains the gene for a novel protein similar to vertebrate sirtuin [silent mating type information regulation 2 homolog] 2 (S. cerevisiae) (SIRT2), the gene for a novel protein (zgc:64098), the 3' end of the rfx4 gene for regulatory factor X, 4, the 3' end of the gene for a novel protein similar to vertebrate carbohydrate (keratan sulfate Gal-6) sulfotransferase (CHST1), a novel gene and three CpG islands, complete sequence
Sequence ID: **emb|BX571971.4|** Length: 153139 Number of Matches: 1
Range 1: 98809 to 98845

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	33/38(87%)	1/38(2%)	Plus/Minus	
Features:					
Query	915	CTGATGTCTCTGAGAGAGAGTAGATGTCTCTGAGAGAG	952		
Sbjct	98845	CTGATGTC-CTGAGAGAGACTAGTGATCTCTGAGAGAG	98809		

Homo sapiens chromosome 16 clone RP11-483N11, complete sequence
Sequence ID: **gb|AC136837.1|** Length: 65756 Number of Matches: 1
Range 1: 28859 to 28924

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	53/72(74%)	8/72(11%)	Plus/Plus	
Features:					
Query	483	CGCGTGTGCTT--AGCGCGCGTGTGCTGATGGCGCGTGTGCTGATGCGACTAGCAAGCGC	540		
Sbjct	28859	CGCGTGTGGATGTAACGCGTGTGCTGATGTCACGTGTGGATG-----TCACGCGT	28912		
Query	541	GTGTGCTGATGC	552		
Sbjct	28913	GTGTGCTGATGC	28924		