

Basic Local Alignment Search Tool

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GACT

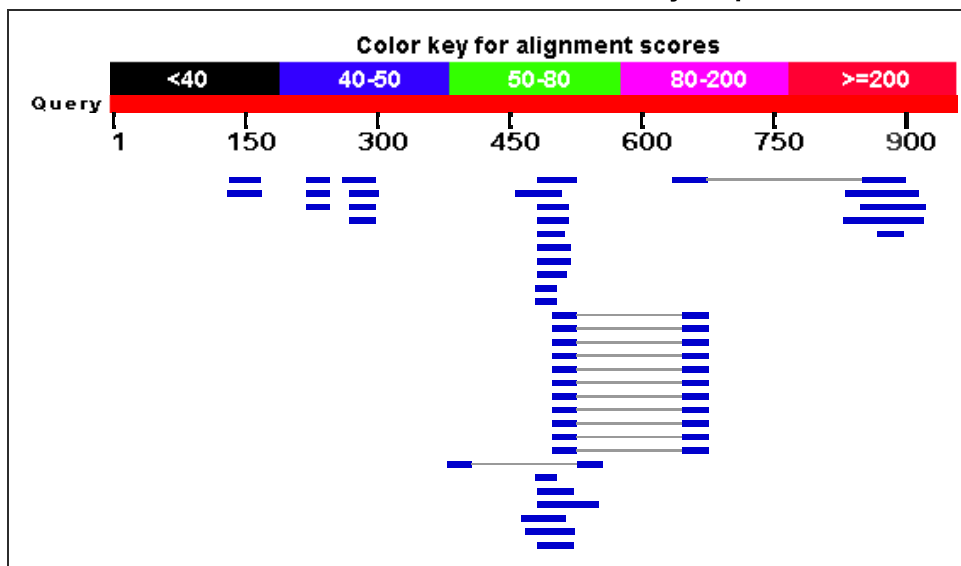
RID [Y0U1108Y01R](#) (Expires on 08-06 13:14 pm)

Query ID lc|238147
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 59 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Oryza minuta clone OM__Ba0028A17, complete sequence	46.4	46.4	3%	0.62	89%	AC229794.1
Human DNA sequence from clone RP11-655H13 on chromosome 10, complete sequence	46.4	90.9	8%	0.62	89%	AL356476.13
MACACA MULATTA BAC clone CH250-201N11 from chromosome 12, complete sequence	44.6	44.6	8%	2.2	76%	AC201936.3
Mus musculus chromosome 3, clone RP23-36H15, complete sequence	44.6	89.1	4%	2.2	81%	AC136712.9
Mus musculus BAC clone RP24-472P16 from chromosome 12, complete sequence	44.6	44.6	5%	2.2	81%	AC159618.2
Loxodonta africana clone VMRC15-151E6, complete sequence	44.6	44.6	3%	2.2	86%	AC153760.3
Human DNA sequence from clone RP11-393I2 on chromosome 6, complete sequence	44.6	44.6	7%	2.2	72%	AL139274.17
Loxodonta africana clone VMRC15-169D19, complete sequence	44.6	44.6	3%	2.2	86%	AC153764.3
Oryza sativa Japonica Group genomic DNA, chromosome 6, BAC clone:B1026E06	44.6	44.6	3%	2.2	88%	AP006860.2
Oryza sativa Japonica Group genomic DNA, chromosome 7, BAC clone:OJ1058_B11	44.6	44.6	3%	2.2	86%	AP003864.4
Oryza sativa Japonica Group genomic DNA, chromosome 7, PAC clone:P0038F10	44.6	44.6	3%	2.2	86%	AP004266.3
Oryza sativa Japonica Group genomic DNA, chromosome 6, BAC clone:B1066D09	44.6	44.6	3%	2.2	88%	AP005761.2
Mus musculus BAC clone RP24-466F1 from chromosome 9, complete sequence	44.6	44.6	9%	2.2	75%	AC162375.2
Elaeophora elaphi genome assembly E_elaphi ,scaffold EEL_contig0001608	42.8	42.8	2%	7.6	93%	LL713916.1
Solanum lycopersicum chromosome ch04, complete genome	42.8	85.5	2%	7.6	100%	HG975516.1
Solanum pennellii chromosome ch04, complete genome	42.8	85.5	2%	7.6	100%	HG975443.1
PREDICTED: Monodelphis domestica transmembrane protein 63C (TMEM63C), transcript variant X13, mRNA	42.8	85.5	5%	7.6	93%	XM_007472762.1
PREDICTED: Monodelphis domestica transmembrane protein 63C (TMEM63C), transcript variant X11, mRNA	42.8	85.5	5%	7.6	93%	XM_007472760.1
PREDICTED: Monodelphis domestica transmembrane protein 63C (TMEM63C), transcript variant X10, mRNA	42.8	85.5	5%	7.6	93%	XM_007472759.1
PREDICTED: Monodelphis domestica transmembrane protein 63C (TMEM63C), transcript variant X9, mRNA	42.8	85.5	5%	7.6	93%	XM_007472758.1
PREDICTED: Monodelphis domestica transmembrane protein 63C (TMEM63C), transcript variant X8, mRNA	42.8	85.5	5%	7.6	93%	XM_007472757.1
PREDICTED: Monodelphis domestica transmembrane protein 63C (TMEM63C), transcript variant X7, mRNA	42.8	85.5	5%	7.6	93%	XM_007472756.1

PREDICTED: Monodelphis domestica transmembrane protein 63C (TMEM63C), transcript variant X6, mRNA	42.8	85.5	5%	7.6	93%	XM_007472755.1
PREDICTED: Monodelphis domestica transmembrane protein 63C (TMEM63C), transcript variant X5, mRNA	42.8	85.5	5%	7.6	93%	XM_007472754.1
PREDICTED: Monodelphis domestica transmembrane protein 63C (TMEM63C), transcript variant X4, mRNA	42.8	85.5	5%	7.6	93%	XM_007472753.1
PREDICTED: Monodelphis domestica transmembrane protein 63C (TMEM63C), transcript variant X2, mRNA	42.8	85.5	5%	7.6	93%	XM_007472751.1
PREDICTED: Monodelphis domestica transmembrane protein 63C (TMEM63C), transcript variant X1, mRNA	42.8	85.5	5%	7.6	93%	XM_007472750.1
Wolbachia endosymbiont of Drosophila simulans wHa, complete genome	42.8	85.5	5%	7.6	93%	CP003884.1
Ashbya gossypii FDAG1 chromosome VI, complete sequence	42.8	42.8	2%	7.6	96%	CP002710.1
Eremothecium cymbalariae DBVPG#7215 chromosome 1, complete sequence	42.8	42.8	3%	7.6	87%	CP002497.1
Ashbya gossypii ATCC 10895 chromosome VI, complete sequence	42.8	42.8	2%	7.6	96%	AE016819.5
S.lycopersicum DNA sequence from clone SL_MboI-63I3 on chromosome 4, complete sequence	42.8	42.8	2%	7.6	100%	CU457449.8
Sulfurimonas denitrificans DSM 1251, complete genome	42.8	42.8	3%	7.6	89%	CP000153.1
Mus musculus BAC clone RP23-146N3 from 3, complete sequence	42.8	42.8	4%	7.6	83%	AC125410.4
Oryza sativa chromosome 3 BAC OSJNB0033J23 genomic sequence, complete sequence	42.8	42.8	4%	7.6	85%	AC137507.3
Homo sapiens BAC clone RP11-481H16 from 4, complete sequence	42.8	42.8	3%	7.6	91%	AC112717.5
Homo sapiens BAC clone RP11-423L1 from 4, complete sequence	42.8	42.8	3%	7.6	91%	AC093834.3
Pan troglodytes chromosome 22 clone:RP43-150L08, map 22, complete sequences	42.8	42.8	7%	7.6	76%	BS000109.1
Zebrafish DNA sequence from clone BUSM1-221D18 in linkage group 19 Contains the gene for a novel zinc finger domain containing protein, a novel gene and a CpG island, complete sequence	42.8	42.8	5%	7.6	81%	AL591170.5
Homo sapiens BAC clone RP11-3E14 from 2, complete sequence	42.8	42.8	5%	7.6	78%	AC009297.4
Mus musculus BAC clone RP23-346L16 from 6, complete sequence	42.8	85.5	4%	7.6	83%	AC140287.3
Ashbya gossypii ATCC 10895 AFR047Wp (AGOS_AFR047W) mRNA, complete cds	42.8	42.8	2%	7.6	96%	NM_210948.1

Alignments

Oryza minuta clone OM__Ba0028A17, complete sequence
Sequence ID: **gb|AC229794.1|** Length: 160706 Number of Matches: 1
Range 1: 69333 to 69369

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	33/37(89%)	1/37(2%)	Plus/Plus	
Features:					
Query	135	TGCATGCATGCATGTATCGATGCAGTCGA-TGATAGT	170		

Sbjct 69333 TGCATGCATGCATGTATCGATGGAGTGGAGAGATAGT 69369

Human DNA sequence from clone RP11-655H13 on chromosome 10, complete sequence

Sequence ID: **emb|AL356476.13|** Length: 184510 Number of Matches: 2

Range 1: 181404 to 181439

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	33/37(89%)	1/37(2%)	Plus/Minus	

Features:

```
Query 634      TACGTGTCGTATATATCTCTACTGCTTATATCTCTAC 670
              |||
Sbjct 181439   TACGTGTCGTATATCTCTGTA-TGCTTATATCTATAC 181404
```

Range 2: 181397 to 181439

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	39/47(83%)	4/47(8%)	Plus/Minus	

Features:

```
Query 847      TACGTGTCGTATATATCTCTACTGCTGTATATATCTCTACTTGTGTC 893
              |||
Sbjct 181439   TACGTGTCGTATATCTCTGTA-TGCT---TATATCTATACCTGTGTC 181397
```

MACACA MULATTA BAC clone CH250-201N11 from chromosome 12, complete sequence

Sequence ID: **gb|AC201936.3|** Length: 212726 Number of Matches: 1

Range 1: 88344 to 88422

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	62/82(76%)	4/82(4%)	Plus/Minus	

Features:

```
Query 828      TGTGTGTGTCGTTGTGTCATACGTGTCGTATATATCTCTACTGCTGTATATATCTCTACT 887
              |||
Sbjct 88422    TGTGTATGTATGTGTGT-ATATTTGT-GTATATATCTCTGTGTGTGTATATATCTCTGTG 88365
Query 888      TGTGT-CATACGTGTCGTATAT 908
              |||
Sbjct 88364    TGTGTATATATGTGT-GTATAT 88344
```

Mus musculus chromosome 3, clone RP23-36H15, complete sequence

Sequence ID: **gb|AC136712.9|** Length: 201139 Number of Matches: 2

Range 1: 155094 to 155140

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	38/47(81%)	0/47(0%)	Plus/Minus	

Features:

```
Query 480      TATATATCTCTACCGTATATATCTCTACTGCTTATATCTCTACTGCT 526
              |||
Sbjct 155140   TATATATCTCCCTTGTTTATATCTCCCTGCTTATATCTCCCTGCT 155094
```

Range 2: 157650 to 157696

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	38/47(81%)	0/47(0%)	Plus/Minus	

Features:

```
Query 480      TATATATCTCTACCGTATATATCTCTACTGCTTATATCTCTACTGCT 526
              |||
Sbjct 157696   TATATATCTCCCTTGTTTATATCTCCCTGCTTATATCTCCCTGCT 157650
```

Mus musculus BAC clone RP24-472P16 from chromosome 12, complete sequence

Sequence ID: **gb|AC159618.2|** Length: 170146 Number of Matches: 1

Range 1: 62585 to 62635

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	43/53(81%)	3/53(5%)	Plus/Plus	

Features:

Query 457 ACTGCTCACACTGTGTGTGTCGGTATATATCTCT-ACCGTATATATCTCTACT 508
Sbjct 62585 ACTGCACACACTGTGTGTGT--GTAAATATATATAACAGTATATAACTCTTCT 62635

Loxodonta africana clone VMRC15-151E6, complete sequence

Sequence ID: **gb|AC153760.3|** Length: 130127 Number of Matches: 1

Range 1: 116557 to 116593

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	32/37(86%)	0/37(0%)	Plus/Minus	

Features:

Query 480 TATATATCTCTACCGTATATATCTCTACTGCTTATAT 516
Sbjct 116593 TATATATCTCTACGGCATATATATCTACAGCATATAT 116557

Human DNA sequence from clone RP11-393I2 on chromosome 6, complete sequence

Sequence ID: **emb|AL139274.17|** Length: 163481 Number of Matches: 1

Range 1: 9062 to 9133

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	56/78(72%)	12/78(15%)	Plus/Plus	

Features:

Query 844 TCATACGTGTCGTATATATCTCTA-----CTGCTGTATATATCTCTACTTGTGTCATAC 897
Sbjct 9062 TCATATATGTCGTATATATCTATATCATATATGTCGTATATATCTATA-----TCATAT 9115
Query 898 GTGTCGTATATATCTCTA 915
Sbjct 9116 ATGTCGTATATATCTATA 9133

Loxodonta africana clone VMRC15-169D19, complete sequence

Sequence ID: **gb|AC153764.3|** Length: 147688 Number of Matches: 1

Range 1: 4123 to 4159

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	32/37(86%)	0/37(0%)	Plus/Minus	

Features:

Query 480 TATATATCTCTACCGTATATATCTCTACTGCTTATAT 516
Sbjct 4159 TATATATCTCTACGGCATATATATCTACAGCATATAT 4123

Oryza sativa Japonica Group genomic DNA, chromosome 6, BAC clone:B1026E06

Sequence ID: **dbj|AP006860.2|** Length: 162784 Number of Matches: 1

Range 1: 63991 to 64024

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	30/34(88%)	0/34(0%)	Plus/Minus	

Features:

Query 480 TATATATCTCTACCGTATATATCTCTACTGCTTA 513
Sbjct 64024 TATATATCTCTATCTTCTCTATCTCTACTGCTTA 63991

Oryza sativa Japonica Group genomic DNA, chromosome 7, BAC clone:OJ1058_B11

Sequence ID: **dbj|AP003864.4|** Length: 102824 Number of Matches: 1

Range 1: 10919 to 10955

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	32/37(86%)	0/37(0%)	Plus/Minus	

Features:

Query 480 TATATATCTCTACCGTATATATCTCTACTGCTTATAT 516
Sbjct 10955 TATATATCTCTATCTTCTCTATCTCTACTACTTATAT 10919

Oryza sativa Japonica Group genomic DNA, chromosome 7, PAC clone:P0038F10

Sequence ID: **dbj|AP004266.3|** Length: 153929 Number of Matches: 1

Range 1: 148566 to 148602

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	32/37(86%)	0/37(0%)	Plus/Minus	

Features:

```
Query   480      TATATATCTCTACCGTATATATCTCTACTGCTTATAT   516
          |||
Sbjct   148602  TATATATCTCTATCTTCTCTATCTCTACTACTTATAT   148566
```

Oryza sativa Japonica Group genomic DNA, chromosome 6, BAC clone:B1066D09

Sequence ID: **dbj|AP005761.2|** Length: 183999 Number of Matches: 1

Range 1: 24084 to 24117

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	30/34(88%)	0/34(0%)	Plus/Minus	

Features:

```
Query   480      TATATATCTCTACCGTATATATCTCTACTGCTTA   513
          |||
Sbjct   24117  TATATATCTCTATCTTCTCTATCTCTACTGCTTA   24084
```

Mus musculus BAC clone RP24-466F1 from chromosome 9, complete sequence

Sequence ID: **gb|AC162375.2|** Length: 164119 Number of Matches: 1

Range 1: 62796 to 62882

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	68/91(75%)	6/91(6%)	Plus/Plus	

Features:

```
Query   826      ACTGTGTGTGTCGTTGTGTCATAC-GTGTTCGTATATATCTCTACTGCTGTATATATCTCT   884
          |||
Sbjct   62796  ACTGTGTGTGTCCTCTGTGCTTTCTGTGTC-TCTTTGTCTCTA--TCTGTGTCTATCTGA   62852

Query   885      ACTTGTGTC-ATACGTGTCGTATATATCTCT   914
          |||
Sbjct   62853  ACTTGTGTCTGTCTTTGTC-TATCTATCTCT   62882
```

Elaeophora elaphi genome assembly E_elaphi ,scaffold EEL_contig0001608

Sequence ID: **emb|LL713916.1|** Length: 4880 Number of Matches: 1

Range 1: 615 to 642

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

Features:

```
Query   864      TCTACTGCTGTATATATCTCTACTTGTG   891
          |||
Sbjct   642      TCTACTGCTGTACATATTCTACTTGTG   615
```

Solanum lycopersicum chromosome ch04, complete genome

Sequence ID: **emb|HG975516.1|** Length: 64069666 Number of Matches: 2

Range 1: 45977893 to 45977915

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

Features:

```
Query   478      GGTATATATCTCTACCGTATATA   500
          |||
Sbjct   45977915  GGTATATATCTCTACCGTATATA   45977893
```

Range 2: 46180728 to 46180750

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	23/23(100%)	0/23(0%)	Plus/Minus	
Features:					
Query	478	GGTATATATCTCTACCGTATATA	500		
Sbjct	46180750	GGTATATATCTCTACCGTATATA	46180728		

Solanum pennellii chromosome ch04, complete genome

Sequence ID: **emb|HG975443.1|** Length: 77197300 Number of Matches: 2

Range 1: 56164635 to 56164657

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	23/23(100%)	0/23(0%)	Plus/Minus	
Features:					
Query	478	GGTATATATCTCTACCGTATATA	500		
Sbjct	56164657	GGTATATATCTCTACCGTATATA	56164635		

Range 2: 57024309 to 57024331

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	23/23(100%)	0/23(0%)	Plus/Minus	
Features:					
Query	478	GGTATATATCTCTACCGTATATA	500		
Sbjct	57024331	GGTATATATCTCTACCGTATATA	57024309		

PREDICTED: Monodelphis domestica transmembrane protein 63C (TMEM63C), transcript variant X13, mRNA

Sequence ID: **ref|XM_007472762.1|** Length: 5680 Number of Matches: 2

Range 1: 5203 to 5230

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	26/28(93%)	0/28(0%)	Plus/Plus	
Features:					
Query	497	TATATCTCTACTGCTTATATCTCTACTG	524		
Sbjct	5203	TATATCTTACTGCTTATATCTTACTG	5230		

Range 2: 5203 to 5230

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	26/28(93%)	0/28(0%)	Plus/Plus	
Features:					
Query	645	TATATCTCTACTGCTTATATCTCTACTG	672		
Sbjct	5203	TATATCTTACTGCTTATATCTTACTG	5230		

PREDICTED: Monodelphis domestica transmembrane protein 63C (TMEM63C), transcript variant X11, mRNA

Sequence ID: **ref|XM_007472760.1|** Length: 6150 Number of Matches: 2

Range 1: 5673 to 5700

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	26/28(93%)	0/28(0%)	Plus/Plus	
Features:					
Query	497	TATATCTCTACTGCTTATATCTCTACTG	524		
Sbjct	5673	TATATCTTACTGCTTATATCTTACTG	5700		

Range 2: 5673 to 5700

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

```

Query    645      TATATCTCTACTGCTTATATCTCTACTG      672
          |||||  |||||  |||||  |||||  |||||
Sbjct    5673     TATATCTATACTGCTTATATCTATACTG      5700

```

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

Query	497	TATATCTCTACTGCTTATATCTCTACTG	524
Sbjct	5655	TATATCTATACTGCTTATATCTATACTG	5682

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

```

Query    645      TATATCTCTACTGCTTATATCTCTACTG      672
          |||||
Sbjct    5655     TATATCTATACTGCTTATATCTATACTG      5682

```

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

```

Query   497      TATATCTCTACTGCTTATATCTCTACTG      524
          |||||  |||||  |||||  |||||  |||||
Sbjct   5824     TATATCTATACTGCTTATATCTATACTG      5851

```

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

```

Query    645      TATATCTCTACTGCTTATATCTCTACTG      672
          ||| ||| ||| ||| ||| ||| ||| |||
Sbjct    5824     TATATCTATACTGCTTATATCTATACTG     5851

```

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

```

Query    497      TATATCTCTACTGCTTATATCTCTACTG      524
          |||
Sbjct    5770     TATATCTATACTGCTTATATCTATACTG      5797

```

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

Query 645 TATATCTCTACTGCTTATATCTCTACTG 672

Sbjct 5770 TATATCTATACTGCTTATATCTATACTG 5797

PREDICTED: Monodelphis domestica transmembrane protein 63C (TMEM63C), transcript variant X7, mRNA
Sequence ID: **reflXM_007472756.1** Length: 6457 Number of Matches: 2
Range 1: 5980 to 6007

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

Features:

Query 497 TATATCTCTACTGCTTATATCTCTACTG 524
Sbjct 5980 TATATCTATACTGCTTATATCTATACTG 6007

Range 2: 5980 to 6007

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

Features:

Query 645 TATATCTCTACTGCTTATATCTCTACTG 672
Sbjct 5980 TATATCTATACTGCTTATATCTATACTG 6007

PREDICTED: Monodelphis domestica transmembrane protein 63C (TMEM63C), transcript variant X6, mRNA
Sequence ID: **reflXM_007472755.1** Length: 6433 Number of Matches: 2
Range 1: 5956 to 5983

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

Features:

Query 497 TATATCTCTACTGCTTATATCTCTACTG 524
Sbjct 5956 TATATCTATACTGCTTATATCTATACTG 5983

Range 2: 5956 to 5983

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

Features:

Query 645 TATATCTCTACTGCTTATATCTCTACTG 672
Sbjct 5956 TATATCTATACTGCTTATATCTATACTG 5983

PREDICTED: Monodelphis domestica transmembrane protein 63C (TMEM63C), transcript variant X5, mRNA
Sequence ID: **reflXM_007472754.1** Length: 6441 Number of Matches: 2
Range 1: 5964 to 5991

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

Features:

Query 497 TATATCTCTACTGCTTATATCTCTACTG 524
Sbjct 5964 TATATCTATACTGCTTATATCTATACTG 5991

Range 2: 5964 to 5991

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

Features:

Query 645 TATATCTCTACTGCTTATATCTCTACTG 672
Sbjct 5964 TATATCTATACTGCTTATATCTATACTG 5991

PREDICTED: Monodelphis domestica transmembrane protein 63C (TMEM63C), transcript variant X4, mRNA
Sequence ID: **ref|XM_007472753.1|** Length: 6095 Number of Matches: 2
Range 1: 5618 to 5645

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

Features:

```

Query   497   TATATCTCTACTGCTTATATCTCTACTG   524
          |||||  |||||  |||||  |||||  |||||
Sbjct   5618  TATATCTTATACTGCTTATATCTATACTG   5645

```

Range 2: 5618 to 5645

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

Features:

```

Query   645   TATATCTCTACTGCTTATATCTCTACTG   672
          |||||  |||||  |||||  |||||  |||||
Sbjct   5618  TATATCTTATACTGCTTATATCTATACTG   5645

```

PREDICTED: Monodelphis domestica transmembrane protein 63C (TMEM63C), transcript variant X2, mRNA
Sequence ID: **ref|XM_007472751.1|** Length: 6210 Number of Matches: 2
Range 1: 5733 to 5760

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

Features:

```

Query   497   TATATCTCTACTGCTTATATCTCTACTG   524
          |||||  |||||  |||||  |||||  |||||
Sbjct   5733  TATATCTTATACTGCTTATATCTATACTG   5760

```

Range 2: 5733 to 5760

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

Features:

```

Query   645   TATATCTCTACTGCTTATATCTCTACTG   672
          |||||  |||||  |||||  |||||  |||||
Sbjct   5733  TATATCTTATACTGCTTATATCTATACTG   5760

```

PREDICTED: Monodelphis domestica transmembrane protein 63C (TMEM63C), transcript variant X1, mRNA
Sequence ID: **ref|XM_007472750.1|** Length: 6262 Number of Matches: 2
Range 1: 5785 to 5812

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

Features:

```

Query   497   TATATCTCTACTGCTTATATCTCTACTG   524
          |||||  |||||  |||||  |||||  |||||
Sbjct   5785  TATATCTTATACTGCTTATATCTATACTG   5812

```

Range 2: 5785 to 5812

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

Features:

```

Query   645   TATATCTCTACTGCTTATATCTCTACTG   672
          |||||  |||||  |||||  |||||  |||||
Sbjct   5785  TATATCTTATACTGCTTATATCTATACTG   5812

```

Range 1: 602309 to 602336

Features:

Query 478 GGTATATATCTCTACCGTATATA 500
 |||||
 Sbjct 69906 GGTATATATCTCTACCGTATATA 69884

Sulfurimonas denitrificans DSM 1251, complete genome

Sequence ID: **gb|CP000153.1|** Length: 2201561 Number of Matches: 1
 Range 1: 125101 to 125134

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	31/35(89%)	1/35(2%)	Plus/Plus	

Features:

Query 269 TTTGTATATATCTCTACCGTATATATCTCTACTGC 303
 |||||
 Sbjct 125101 TTTGTATATC-CTCTGCTGTATATATCTCTACTGC 125134

Mus musculus BAC clone RP23-146N3 from 3, complete sequence

Sequence ID: **gb|AC125410.4|** Length: 213701 Number of Matches: 1
 Range 1: 166017 to 166057

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	34/41(83%)	0/41(0%)	Plus/Plus	

Features:

Query 480 TATATATCTCTACCGTATATATCTCTACTGCTTATATCTCT 520
 |||||
 Sbjct 166017 TATATATCTCTCCTGTTTATATCTCCCCTGTTTATATATCT 166057

Oryza sativa chromosome 3 BAC OSJNBb0033J23 genomic sequence, complete sequence

Sequence ID: **gb|AC137507.3|** Length: 126862 Number of Matches: 1
 Range 1: 43400 to 43439

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	34/40(85%)	1/40(2%)	Plus/Plus	

Features:

Query 133 AGTGCATGCATGCATGTATCGATGCAGT-CGATGATAGTG 171
 |||||
 Sbjct 43400 AGTGCATGCATGCATGCATGGAGGCAGTGCTATGCTAGTG 43439

Homo sapiens BAC clone RP11-481H16 from 4, complete sequence

Sequence ID: **gb|AC112717.5|** Length: 189406 Number of Matches: 1
 Range 1: 161138 to 161169

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	29/32(91%)	2/32(6%)	Plus/Minus	

Features:

Query 269 TTTGTATATATCTCTACC--GTATATATCTCT 298
 |||||
 Sbjct 161169 TTTGTATATATCTCTAGCATGTATATATCTCT 161138

Homo sapiens BAC clone RP11-423L1 from 4, complete sequence

Sequence ID: **gb|AC093834.3|** Length: 177582 Number of Matches: 1
 Range 1: 154906 to 154937

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	29/32(91%)	2/32(6%)	Plus/Minus	

Features:

Query 269 TTTGTATATATCTCTACC--GTATATATCTCT 298
 |||||
 Sbjct 154937 TTTGTATATATCTCTAGCATGTATATATCTCT 154906

Pan troglodytes chromosome 22 clone:RP43-150L08, map 22, complete sequences

Sequence ID: **dbj|BS000109.1** Length: 157620 Number of Matches: 1
Range 1: 77222 to 77294

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	57/75(76%)	7/75(9%)	Plus/Plus	

Features:

```
Query   480      TATATATCTCTACCGTATATATCTCTACTGCT-TATATCTCTACTGC---TATG-ACGTA   534
          |||
Sbjct   77222    TATACATCTCTAC--TATACATCTATAACATCTGTATATCTCTACTGAACATCTGTATATC   77279
          |||
Query   535      GGTATATCTCTACTG   549
          |||
Sbjct   77280    TGTATATCTCTACTG   77294
          |||
```

Zebrafish DNA sequence from clone BUSM1-221D18 in linkage group 19 Contains the gene for a novel zinc finger domain containing protein, a novel gene and a CpG island, complete sequence

Sequence ID: **emb|AL591170.5** Length: 100871 Number of Matches: 1
Range 1: 85085 to 85127

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	39/48(81%)	5/48(10%)	Plus/Plus	

Features:

```
Query   464      ACACTGTGTGTGTCGGTATATATCTCTACCGTATATATCTCTACTGCT   511
          |||
Sbjct   85085    ACACTGTGTGTGT--GTATATATATATA---TATATATATATACTGCT   85127
          |||
```

Homo sapiens BAC clone RP11-3E14 from 2, complete sequence

Sequence ID: **gb|AC009297.4** Length: 91745 Number of Matches: 1
Range 1: 81884 to 81937

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	43/55(78%)	1/55(1%)	Plus/Minus	

Features:

```
Query   468      TGTGTGTGTCGGTATATATCTCTACCGTATATATCTCTACTGCTTATATCTCTAC   522
          |||
Sbjct   81937    TGTGTGTGTGTGTATATATATATATA-TATATATCTCTACTGGGTGTATATATAC   81884
          |||
```

Mus musculus BAC clone RP23-346L16 from 6, complete sequence

Sequence ID: **gb|AC140287.3** Length: 213473 Number of Matches: 2
Range 1: 120466 to 120506

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	34/41(83%)	0/41(0%)	Plus/Minus	

Features:

```
Query   480      TATATATCTCTACCGTATATATCTCTACTGCTTATATCTCT   520
          |||
Sbjct   120506    TATATATCTCCCTTGTTTATATCTCCCTGCTTATATCTCT   120466
          |||
```

Range 2: 122774 to 122814

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	34/41(83%)	0/41(0%)	Plus/Minus	

Features:

```
Query   480      TATATATCTCTACCGTATATATCTCTACTGCTTATATCTCT   520
          |||
Sbjct   122814    TATATATCTCCCTTGTTTATATCTCCCTGCTTATATCTCT   122774
          |||
```

Ashbya gossypii ATCC 10895 AFR047Wp (AGOS_AFR047W) mRNA, complete cds

Sequence ID: **ref|NM_210948.1** Length: 777 Number of Matches: 1
Range 1: 526 to 551

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	25/26(96%)	0/26(0%)	Plus/Plus	

Features:

Query	222	TACCCGCGCAACGTGTACTACGTGCT	247
Sbjct	526	TACACGCGCAACGTGTACTACGTGCT	551