

Basic Local Alignment Search Tool

NCBI/ [BLAST](#)/ [blastn suite](#)/ **Formatting Results - Y0T7M3AJ015**

► [Formatting options](#)

► [Download](#)

[Blast report description](#)

ATGC

RID [Y0T7M3AJ015](#) (Expires on 08-06 13:00 pm)

Query ID lc|49399

Description None

Molecule type nucleic acid

Query Length 952

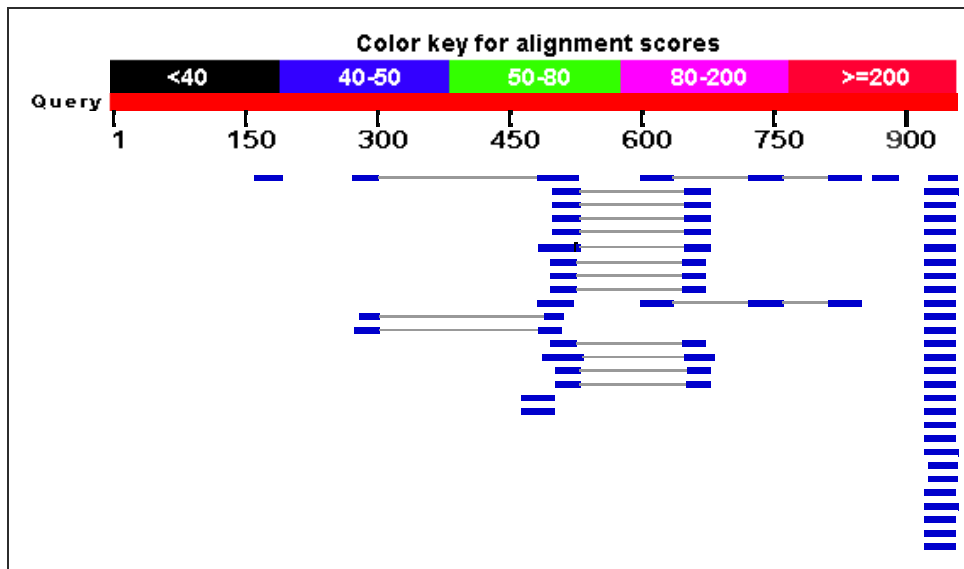
Database Name nr

Description Nucleotide collection (nt)

Program BLASTN 2.2.29+

[Graphic Summary](#)

Distribution of 71 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: <i>Astyanax mexicanus</i> POU class 6 homeobox 2 (pou6f2), mRNA	53.6	144	8%	0.004	88%	XM_007258616.1
PREDICTED: <i>Oryzteropus afer</i> myosin XVIIIa (MYO18A), transcript variant X4, mRNA	50.0	99	6%	0.051	97%	XM_007937398.1
PREDICTED: <i>Oryzteropus afer</i> myosin XVIIIa (MYO18A), transcript variant X3, mRNA	50.0	99	6%	0.051	97%	XM_007937396.1
PREDICTED: <i>Oryzteropus afer</i> myosin XVIIIa (MYO18A), transcript variant X2, mRNA	50.0	99	6%	0.051	97%	XM_007937395.1
PREDICTED: <i>Oryzteropus afer</i> myosin XVIIIa (MYO18A), transcript variant X1, mRNA	50.0	99	6%	0.051	97%	XM_007937394.1
PREDICTED: <i>Tupaia chinensis</i> myosin XVIIIa (MYO18A), mRNA	50.0	146	7%	0.051	97%	XM_006165469.1
PREDICTED: <i>Macaca fascicularis</i> sodium channel, voltage-gated, type IV, alpha subunit (SCN4A), transcript variant X1, mRNA	44.6	44.6	3%	2.2	94%	XM_005584688.1
PREDICTED: <i>Equus przewalskii</i> microtubule-associated protein 7 (MAP7), transcript variant X3, mRNA	42.8	85.5	5%	7.6	93%	XM_008528203.1
PREDICTED: <i>Equus przewalskii</i> microtubule-associated protein 7 (MAP7), transcript variant X2, mRNA	42.8	85.5	5%	7.6	93%	XM_008528196.1
PREDICTED: <i>Equus przewalskii</i> microtubule-associated protein 7 (MAP7), transcript variant X1, mRNA	42.8	85.5	5%	7.6	93%	XM_008528186.1
<i>Endocarpon pusillum</i> Z07020 hypothetical protein mRNA	42.8	42.8	4%	7.6	81%	XM_007802202.1
<i>Neofusicoccum parvum</i> UCRNP2 putative ethanolamine kinase protein mRNA	42.8	42.8	3%	7.6	88%	XM_007588770.1
<i>Neofusicoccum parvum</i> UCRNP2 putative fggy-family carbohydrate kinase protein mRNA	42.8	85.5	4%	7.6	100%	XM_007585011.1
<i>Auricularia delicata</i> TFB-10046 SS5 hypothetical protein (AURDEDRAFT_171169), partial mRNA	42.8	85.5	5%	7.6	93%	XM_007352082.1
<i>Burkholderia cenocepacia</i> H111 chromosome 1 complete genome	42.8	128	11%	7.6	84%	HG938370.1
PREDICTED: <i>Mus musculus</i> uncharacterized LOC102638393 (LOC102638393), ncRNA	42.8	42.8	3%	7.6	89%	XR_385149.1
PREDICTED: <i>Mus musculus</i> SRC kinase signaling inhibitor 1 (Srcin1), transcript variant X21, mRNA	42.8	42.8	3%	7.6	89%	XM_006533782.1
PREDICTED: <i>Mus musculus</i> SRC kinase signaling inhibitor 1 (Srcin1), transcript variant X20, mRNA	42.8	42.8	3%	7.6	89%	XM_006533781.1
PREDICTED: <i>Mus musculus</i> SRC kinase signaling inhibitor 1 (Srcin1), transcript variant X18, mRNA	42.8	42.8	3%	7.6	89%	XM_006533779.1
PREDICTED: <i>Mus musculus</i> SRC kinase signaling inhibitor 1 (Srcin1), transcript variant X16, mRNA	42.8	42.8	3%	7.6	89%	XM_006533777.1
PREDICTED: <i>Mus musculus</i> SRC kinase signaling inhibitor 1 (Srcin1), transcript	42.8	42.8	3%	7.6	89%	XM_006533776.1

variant X15, mRNA						
PREDICTED: Mus musculus SRC kinase signaling inhibitor 1 (Srcin1), transcript variant X14, mRNA	42.8	42.8	3%	7.6	89%	XM_006533775.1
PREDICTED: Mus musculus SRC kinase signaling inhibitor 1 (Srcin1), transcript variant X13, mRNA	42.8	42.8	3%	7.6	89%	XM_006533774.1
PREDICTED: Mus musculus SRC kinase signaling inhibitor 1 (Srcin1), transcript variant X12, mRNA	42.8	42.8	3%	7.6	89%	XM_006533773.1
PREDICTED: Mus musculus SRC kinase signaling inhibitor 1 (Srcin1), transcript variant X10, mRNA	42.8	42.8	3%	7.6	89%	XM_006533771.1
PREDICTED: Mus musculus SRC kinase signaling inhibitor 1 (Srcin1), transcript variant X9, mRNA	42.8	42.8	3%	7.6	89%	XM_006533770.1
PREDICTED: Mus musculus SRC kinase signaling inhibitor 1 (Srcin1), transcript variant X8, mRNA	42.8	42.8	3%	7.6	89%	XM_006533769.1
PREDICTED: Mus musculus SRC kinase signaling inhibitor 1 (Srcin1), transcript variant X7, mRNA	42.8	42.8	3%	7.6	89%	XM_006533768.1
PREDICTED: Mus musculus SRC kinase signaling inhibitor 1 (Srcin1), transcript variant X6, mRNA	42.8	42.8	3%	7.6	89%	XM_006533767.1
PREDICTED: Mus musculus SRC kinase signaling inhibitor 1 (Srcin1), transcript variant X5, mRNA	42.8	42.8	3%	7.6	89%	XM_006533766.1
PREDICTED: Mus musculus SRC kinase signaling inhibitor 1 (Srcin1), transcript variant X4, mRNA	42.8	42.8	3%	7.6	89%	XM_006533765.1
PREDICTED: Mus musculus SRC kinase signaling inhibitor 1 (Srcin1), transcript variant X3, mRNA	42.8	42.8	3%	7.6	89%	XM_006533764.1
PREDICTED: Mus musculus SRC kinase signaling inhibitor 1 (Srcin1), transcript variant X2, mRNA	42.8	42.8	3%	7.6	89%	XM_006533763.1
PREDICTED: Mus musculus SRC kinase signaling inhibitor 1 (Srcin1), transcript variant X1, mRNA	42.8	42.8	3%	7.6	89%	XM_006533762.1
PREDICTED: Mus musculus uncharacterized LOC102638393 (LOC102638393), ncRNA	42.8	42.8	3%	7.6	89%	XR_397252.1
PREDICTED: Equus caballus microtubule-associated protein 7 (MAP7), mRNA	42.8	85.5	5%	7.6	93%	XM_005596943.1
PREDICTED: Spermophilus tridecemlineatus DAB2 interacting protein (Dab2ip), transcript variant X1, mRNA	42.8	42.8	3%	7.6	90%	XM_005320919.1
Sorangium cellulosum So0157-2, complete genome	42.8	85.5	8%	7.6	80%	CP003969.1
PREDICTED: Saimiri boliviensis boliviensis MAU2 chromatid cohesion factor homolog (C. elegans) (MAU2), mRNA	42.8	42.8	3%	7.6	91%	XM_003942308.1
Sporisorium reilianum SRZ2 chromosome 9 complete DNA sequence	42.8	85.5	5%	7.6	96%	FQ311474.1
Pig DNA sequence from clone CH242-239P7 on chromosome 11, complete sequence	42.8	42.8	3%	7.6	91%	CU207380.20
Burkholderia cenocepacia J2315 chromosome 1, complete genome	42.8	128	11%	7.6	84%	AM747720.1
Cupriavidus taiwanensis str. LMG19424 chromosome 2, complete genome	42.8	85.5	5%	7.6	93%	CU633750.1
Mus musculus SRC kinase signaling inhibitor 1 (Srcin1), mRNA	42.8	42.8	3%	7.6	89%	NM_018873.2
Mus musculus BAC clone RP24-465A20						

from chromosome 17, complete sequence	42.8	42.8	3%	7.6	89%	AC126929.3
Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:D130061K21 product:unclassifiable, full insert sequence	42.8	42.8	3%	7.6	89%	AK051643.1
Homo sapiens chromosome 1 clone RP4-706A16, complete sequence	42.8	42.8	4%	7.6	85%	AC113935.2
Human DNA sequence from clone RP4-564M11 on chromosome 1p31.1, complete sequence	42.8	42.8	4%	7.6	85%	AL035409.15
Mus musculus, clone IMAGE:5692573, mRNA	42.8	42.8	3%	7.6	89%	BC048145.1
Mouse DNA sequence from clone RP23-157O10 on chromosome 11, complete sequence	42.8	42.8	3%	7.6	89%	AL596088.14

Alignments

PREDICTED: Astyanax mexicanus POU class 6 homeobox 2 (pou6f2), mRNA

Sequence ID: [reflXM_007258616.1](#) Length: 2282 Number of Matches: 3

Range 1: 794 to 835

Score	Expect	Identities	Gaps	Strand	Frame
53.6 bits(58)	0.004()	37/42(88%)	0/42(0%)	Plus/Minus	

Features:

```

Query   482  CTCTCGCGCTGGACTCTCTCGCGCTGCAGCCTCTCGCGCTGC   523
      |||
Sbjct   835  CTCTCGCGCTGCTCTCTCTCGCGCTGCTCTCTCTCGCGCTGC   794

```

Range 2: 775 to 822

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	39/48(81%)	0/48(0%)	Plus/Minus	

Features:

```

Query   480  CTCTCTCGCGCTGGACTCTCTCGCGCTGCAGCCTCTCGCGCTGCAGCT   527
      |||
Sbjct   822  CTCTCTCGCGCTGCTCTCTCTCGCGCTGCTCTCGCTCTCTCTGCTGCT   775

```

Range 3: 794 to 822

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

```

Query   273  CTCTCTCGCGCTGGACTCTCTCGCGCTGC   301
      |||
Sbjct   822  CTCTCTCGCGCTGCTCTCTCTCGCGCTGC   794

```

PREDICTED: Oryzteropus afer afer myosin XVIIIa (MYO18A), transcript variant X4, mRNA

Sequence ID: [reflXM_007937398.1](#) Length: 6515 Number of Matches: 2

Range 1: 3543 to 3572

Score	Expect	Identities	Gaps	Strand	Frame
50.0 bits(54)	0.051()	29/30(97%)	0/30(0%)	Plus/Minus	

Features:

```

Query   646  TCTCGCGCTGCAGCCTCTCGCGCTGCAGCT   675
      |||
Sbjct   3572  TCTCGCGCTGCAGCTTCTCGCGCTGCAGCT   3543

```

Range 2: 3543 to 3572

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

50.0 bits(54) 0.051() 29/30(97%) 0/30(0%) Plus/Minus

Features:

```
Query 498 TCTCGCGCTGCAGCCTCTCGCGCTGCAGCT 527
          |||
Sbjct 3572 TCTCGCGCTGCAGCTTCTCGCGCTGCAGCT 3543
```

PREDICTED: Orycteropus afer afer myosin XVIII^A (MYO18A), transcript variant X3, mRNA

Sequence ID: **ref|XM_007937396.1|** Length: 7411 Number of Matches: 2

Range 1: 4548 to 4577

Score	Expect	Identities	Gaps	Strand	Frame
50.0 bits(54)	0.051()	29/30(97%)	0/30(0%)	Plus/Minus	

Features:

```
Query 646 TCTCGCGCTGCAGCCTCTCGCGCTGCAGCT 675
          |||
Sbjct 4577 TCTCGCGCTGCAGCTTCTCGCGCTGCAGCT 4548
```

Range 2: 4548 to 4577

Score	Expect	Identities	Gaps	Strand	Frame
50.0 bits(54)	0.051()	29/30(97%)	0/30(0%)	Plus/Minus	

Features:

```
Query 498 TCTCGCGCTGCAGCCTCTCGCGCTGCAGCT 527
          |||
Sbjct 4577 TCTCGCGCTGCAGCTTCTCGCGCTGCAGCT 4548
```

PREDICTED: Orycteropus afer afer myosin XVIII^A (MYO18A), transcript variant X2, mRNA

Sequence ID: **ref|XM_007937395.1|** Length: 7564 Number of Matches: 2

Range 1: 4590 to 4619

Score	Expect	Identities	Gaps	Strand	Frame
50.0 bits(54)	0.051()	29/30(97%)	0/30(0%)	Plus/Minus	

Features:

```
Query 646 TCTCGCGCTGCAGCCTCTCGCGCTGCAGCT 675
          |||
Sbjct 4619 TCTCGCGCTGCAGCTTCTCGCGCTGCAGCT 4590
```

Range 2: 4590 to 4619

Score	Expect	Identities	Gaps	Strand	Frame
50.0 bits(54)	0.051()	29/30(97%)	0/30(0%)	Plus/Minus	

Features:

```
Query 498 TCTCGCGCTGCAGCCTCTCGCGCTGCAGCT 527
          |||
Sbjct 4619 TCTCGCGCTGCAGCTTCTCGCGCTGCAGCT 4590
```

PREDICTED: Orycteropus afer afer myosin XVIII^A (MYO18A), transcript variant X1, mRNA

Sequence ID: **ref|XM_007937394.1|** Length: 7640 Number of Matches: 2

Range 1: 4612 to 4641

Score	Expect	Identities	Gaps	Strand	Frame
50.0 bits(54)	0.051()	29/30(97%)	0/30(0%)	Plus/Minus	

Features:

```
Query 646 TCTCGCGCTGCAGCCTCTCGCGCTGCAGCT 675
          |||
Sbjct 4641 TCTCGCGCTGCAGCTTCTCGCGCTGCAGCT 4612
```

Range 2: 4612 to 4641

Score	Expect	Identities	Gaps	Strand	Frame
50.0 bits(54)	0.051()	29/30(97%)	0/30(0%)	Plus/Minus	

Features:

Query 498 TCTCGCGCTGCAGCCTCTCGCGCTGCAGCT 527
 |||||
 Sbjct 4641 TCTCGCGCTGCAGCTTCTCGCGCTGCAGCT 4612

PREDICTED: Tupaia chinensis myosin XVIIIa (MYO18A), mRNA
 Sequence ID: **ref|XM_006165469.1|** Length: 6242 Number of Matches: 3
 Range 1: 4497 to 4526

Score	Expect	Identities	Gaps	Strand	Frame
50.0 bits(54)	0.051()	29/30(97%)	0/30(0%)	Plus/Minus	

Features:

Query 646 TCTCGCGCTGCAGCCTCTCGCGCTGCAGCT 675
 |||||
 Sbjct 4526 TCTCGCGCTGCAGCTTCTCGCGCTGCAGCT 4497

Range 2: 4497 to 4526

Score	Expect	Identities	Gaps	Strand	Frame
50.0 bits(54)	0.051()	29/30(97%)	0/30(0%)	Plus/Minus	

Features:

Query 498 TCTCGCGCTGCAGCCTCTCGCGCTGCAGCT 527
 |||||
 Sbjct 4526 TCTCGCGCTGCAGCTTCTCGCGCTGCAGCT 4497

Range 3: 4487 to 4526

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	34/40(85%)	0/40(0%)	Plus/Minus	

Features:

Query 483 TCTCGCGCTGGACTCTCTCGCGCTGCAGCCTCTCGCGCTG 522
 |||||
 Sbjct 4526 TCTCGCGCTGCAGCTTCTCGCGCTGCAGCTTTTCGCGCTG 4487

PREDICTED: Macaca fascicularis sodium channel, voltage-gated, type IV, alpha subunit (SCN4A), transcript variant X1, mRNA
 Sequence ID: **ref|XM_005584688.1|** Length: 7630 Number of Matches: 1
 Range 1: 7570 to 7600

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	31/33(94%)	2/33(6%)	Plus/Minus	

Features:

Query 920 CGTGTGCACACACACGACGCGTGTGCACACAC 952
 |||||
 Sbjct 7600 CGTGTGCACACACAC-ACA-CGTGTGCACACAC 7570

PREDICTED: Equus przewalskii microtubule-associated protein 7 (MAP7), transcript variant X3, mRNA
 Sequence ID: **ref|XM_008528203.1|** Length: 4137 Number of Matches: 2
 Range 1: 1904 to 1931

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

Features:

Query 644 TCTCTCGCGCTGCAGCCTCTCGCGCTGC 671
 |||||
 Sbjct 1931 TCTCTCGCGCTGCTCCCTCTCGCGCTGC 1904

Range 2: 1904 to 1931

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

Features:

Query 496 TCTCTCGCGCTGCAGCCTCTCGCGCTGC 523
 |||||
 Sbjct 1931 TCTCTCGCGCTGCTCCCTCTCGCGCTGC 1904

PREDICTED: Equus przewalskii microtubule-associated protein 7 (MAP7), transcript variant X2, mRNA
Sequence ID: **ref|XM_008528196.1|** Length: 4180 Number of Matches: 2
Range 1: 1947 to 1974

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

Features:

```

Query   644   TCTCTCGCGCTGCAGCCTCTCGCGCTGC   671
          |||
Sbjct   1974  TCTCTCGCGCTGCTCCCTCTCGCGCTGC   1947

```

Range 2: 1947 to 1974

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

Features:

```

Query   496   TCTCTCGCGCTGCAGCCTCTCGCGCTGC   523
          |||
Sbjct   1974  TCTCTCGCGCTGCTCCCTCTCGCGCTGC   1947

```

PREDICTED: Equus przewalskii microtubule-associated protein 7 (MAP7), transcript variant X1, mRNA
Sequence ID: **ref|XM_008528186.1|** Length: 4225 Number of Matches: 2
Range 1: 1992 to 2019

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

Features:

```

Query   644   TCTCTCGCGCTGCAGCCTCTCGCGCTGC   671
          |||
Sbjct   2019  TCTCTCGCGCTGCTCCCTCTCGCGCTGC   1992

```

Range 2: 1992 to 2019

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

Features:

```

Query   496   TCTCTCGCGCTGCAGCCTCTCGCGCTGC   523
          |||
Sbjct   2019  TCTCTCGCGCTGCTCCCTCTCGCGCTGC   1992

```

Endocarpon pusillum Z07020 hypothetical protein mRNA
Sequence ID: **ref|XM_007802202.1|** Length: 3159 Number of Matches: 1
Range 1: 2262 to 2304

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/43(81%)	0/43(0%)	Plus/Plus	

Features:

```

Query   480   CTCTCTCGCGCTGGACTCTCTCGCGCTGCAGCCTCTCGCGCTG   522
          |||
Sbjct   2262  CTATCTCGTGCTGGCCTCTCTCGCGCTGATTTTCTCGCGCTG   2304

```

Neofusicoccum parvum UCRNP2 putative ethanolamine kinase protein mRNA
Sequence ID: **ref|XM_007588770.1|** Length: 1275 Number of Matches: 1
Range 1: 254 to 286

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

Features:

```

Query   163   TCATCTACAGTGAAAGAGAGACTCTCTCGCGCT   195

```

Sbjct 254 TCATCGACAGAGAAAGAGAGACTCGCTCGCACT 286

Neofusicoccum parvum UCRNP2 putative fggy-family carbohydrate kinase protein mRNA

Sequence ID: **ref|XM_007585011.1|** Length: 1791 Number of Matches: 2

Range 1: 1343 to 1365

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

Features:

Query 281 CGCTGGACTCTCTCGCGCTGCAG 303
Sbjct 1343 CGCTGGACTCTCTCGCGCTGCAG 1365

Range 2: 1343 to 1365

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

Features:

Query 488 CGCTGGACTCTCTCGCGCTGCAG 510
Sbjct 1343 CGCTGGACTCTCTCGCGCTGCAG 1365

Auricularia delicata TFB-10046 SS5 hypothetical protein (AURDEDRAFT_171169), partial mRNA

Sequence ID: **ref|XM_007352082.1|** Length: 951 Number of Matches: 2

Range 1: 740 to 767

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

Features:

Query 275 CTCTCGCGCTGGACTCTCTCGCGCTGCA 302
Sbjct 740 CTCCCGCGCTGGAATCTCTCGCGCTGCA 767

Range 2: 740 to 767

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

Features:

Query 482 CTCTCGCGCTGGACTCTCTCGCGCTGCA 509
Sbjct 740 CTCCCGCGCTGGAATCTCTCGCGCTGCA 767

Burkholderia cenocepacia H111 chromosome 1 complete genome

Sequence ID: **emb|HG938370.1|** Length: 3572953 Number of Matches: 3

Range 1: 1739808 to 1739845

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	32/38(84%)	0/38(0%)	Plus/Minus	

Features:

Non-ribosomal peptide synthetase modules

Query 809 TCTCGCGCTGCAGCGTGTGCACACACGACCACACGT 846
Sbjct 1739845 TCTCGCGCTGCAGCGTGTGCAGCCAGTCGGCCGCACGT 1739808

Range 2: 1739808 to 1739845

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	32/38(84%)	0/38(0%)	Plus/Minus	

Features:

Non-ribosomal peptide synthetase modules

Query 719 TCTCGCGCTGCAGCGTGTGCACACACGACCACACGT 756
|||||

Sbjct 1739845 TCTCGCGCTGCAGCGTGTGCAGCCAGTCGGCCGCACGT 1739808

Range 3: 1739808 to 1739845

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	32/38(84%)	0/38(0%)	Plus/Minus	

Features:

Non-ribosomal peptide synthetase modules

Query	596	TCTCGCGCTGCAGCGTGTGCACACACACGACCACACGT	633
Sbjct	1739845	TCTCGCGCTGCAGCGTGTGCAGCCAGTCGGCCGCACGT	1739808

PREDICTED: Mus musculus uncharacterized LOC102638393 (LOC102638393), ncRNA

Sequence ID: **ref|XR_385149.1|** Length: 3230 Number of Matches: 1

Range 1: 2091 to 2126

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

Features:

PREDICTED: Mus musculus SRC kinase signaling inhibitor 1 (Srcin1), transcript variant X21, mRNA

Sequence ID: [ref|XM_006533782.1|](#) Length: 7437 Number of Matches: 1

Range 1: 6534 to 6567

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

Features:

```

Query    917      CAGCGTGTGCACACACACGACAGCGTGTGCACACA      951
          |||||
Sbjct    6567     CAGCGTGTGCACACACAC-ACAGAGGCTGCACACA      6534

```

PREDICTED: Mus musculus SRC kinase signaling inhibitor 1 (Srcin1), transcript variant X20, mRNA

Sequence ID: **ref|XM_006533781.1|** Length: 7047 Number of Matches: 1

Range 1: 6144 to 6177

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

Features:

```

Query    917      CAGCGTGTGCACACACACGACAGCGTGTGCACACA      951
          |||||
Sbjct    6177     CAGCGTGTGCACACACAC-ACAGAGGCTGCACACA      6144

```

PREDICTED: Mus musculus SRC kinase signaling inhibitor 1 (Srcin1), transcript variant X18, mRNA

Sequence ID: [ref|XM_006533779.1|](#) Length: 7150 Number of Matches: 1

Range 1: 6247 to 6280

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

Features:

```

Query    917      CAGCGTGTGCACACACACGACAGCGTGTGCACACA      951
          |||||
Sbjct    6280     CAGCGTGTGCACACACAC-ACAGAGGCTGCACACA      6247

```

PREDICTED: Mus musculus SRC kinase signaling inhibitor 1 (Srcin1), transcript variant X16, mRNA

Sequence ID: **ref|XM_006533777.1|** Length: 7177 Number of Matches: 1

Range 1: 6274 to 6307

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

42.8 bits(46) 7.6() 31/35(89%) 1/35(2%) Plus/Minus

Features:

```
Query 917 CAGCGTGTGCACACACACGACAGCGTGTGCACACA 951
          |||
Sbjct 6307 CAGCGTGTGCACACACAC-ACAGAGGCTGCACACA 6274
```

PREDICTED: Mus musculus SRC kinase signaling inhibitor 1 (Srcin1), transcript variant X15, mRNA

Sequence ID: **ref|XM_006533776.1|** Length: 7216 Number of Matches: 1

Range 1: 6313 to 6346

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

Features:

```
Query 917 CAGCGTGTGCACACACACGACAGCGTGTGCACACA 951
          |||
Sbjct 6346 CAGCGTGTGCACACACAC-ACAGAGGCTGCACACA 6313
```

PREDICTED: Mus musculus SRC kinase signaling inhibitor 1 (Srcin1), transcript variant X14, mRNA

Sequence ID: **ref|XM_006533775.1|** Length: 7301 Number of Matches: 1

Range 1: 6398 to 6431

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

Features:

```
Query 917 CAGCGTGTGCACACACACGACAGCGTGTGCACACA 951
          |||
Sbjct 6431 CAGCGTGTGCACACACAC-ACAGAGGCTGCACACA 6398
```

PREDICTED: Mus musculus SRC kinase signaling inhibitor 1 (Srcin1), transcript variant X13, mRNA

Sequence ID: **ref|XM_006533774.1|** Length: 7636 Number of Matches: 1

Range 1: 6733 to 6766

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

Features:

```
Query 917 CAGCGTGTGCACACACACGACAGCGTGTGCACACA 951
          |||
Sbjct 6766 CAGCGTGTGCACACACAC-ACAGAGGCTGCACACA 6733
```

PREDICTED: Mus musculus SRC kinase signaling inhibitor 1 (Srcin1), transcript variant X12, mRNA

Sequence ID: **ref|XM_006533773.1|** Length: 9048 Number of Matches: 1

Range 1: 8145 to 8178

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

Features:

```
Query 917 CAGCGTGTGCACACACACGACAGCGTGTGCACACA 951
          |||
Sbjct 8178 CAGCGTGTGCACACACAC-ACAGAGGCTGCACACA 8145
```

PREDICTED: Mus musculus SRC kinase signaling inhibitor 1 (Srcin1), transcript variant X10, mRNA

Sequence ID: **ref|XM_006533771.1|** Length: 9072 Number of Matches: 1

Range 1: 8169 to 8202

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

Features:

```
Query 917 CAGCGTGTGCACACACACGACAGCGTGTGCACACA 951
          |||
Sbjct 8202 CAGCGTGTGCACACACAC-ACAGAGGCTGCACACA 8169
```

PREDICTED: Mus musculus SRC kinase signaling inhibitor 1 (Srcin1), transcript variant X9, mRNA
Sequence ID: **ref|XM_006533770.1|** Length: 7743 Number of Matches: 1
Range 1: 6840 to 6873

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

Features:

```
Query    917      CAGCGTGTGCACACACACGACAGCGTGTGCACACA      951
          |||||
Sbjct    6873     CAGCGTGTGCACACACAC-ACAGAGGCTGCACACA      6840
```

PREDICTED: Mus musculus SRC kinase signaling inhibitor 1 (Srcin1), transcript variant X8, mRNA
Sequence ID: **ref|XM_006533769.1|** Length: 7743 Number of Matches: 1
Range 1: 6840 to 6873

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

Features:

```

Query    917      CAGCGTGTGCACACACACGACAGCGTGTGCACACA      951
          |||||
Sbjct    6873     CAGCGTGTGCACACACAC-ACAGAGGCTGCACACA      6840

```

PREDICTED: Mus musculus SRC kinase signaling inhibitor 1 (Srcin1), transcript variant X7, mRNA
Sequence ID: **ref|XM_006533768.1|** Length: 7699 Number of Matches: 1
Range 1: 6796 to 6829

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

Features:

```

Query    917      CAGCGTGTGCACACACACGACAGCGTGTGCACACA      951
          |||||
Sbjct    6829     CAGCGTGTGCACACACAC-ACAGAGGCTGCACACA      6796

```

PREDICTED: Mus musculus SRC kinase signaling inhibitor 1 (Srcin1), transcript variant X6, mRNA
Sequence ID: **ref|XM_006533767.1|** Length: 7767 Number of Matches: 1
Range 1: 6864 to 6897

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

Features:

```

Query 917 CAGCGTGTGCACACACACGACAGCGTGTGCACACA 951
          |||||
Sbjct 6897 CAGCGTGTGCACACACAC-ACAGAGGCTGCACACA 6864

```

PREDICTED: Mus musculus SRC kinase signaling inhibitor 1 (Srcin1), transcript variant X5, mRNA
Sequence ID: **ref|XM_006533766.1|** Length: 7803 Number of Matches: 1
Range 1: 6900 to 6933

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

Features:

```

Query    917      CAGCGTGTGCACACACACGACAGCGTGTGCACACA      951
          |||||
Sbjct    6933     CAGCGTGTGCACACACAC-ACAGAGGCTGCACACA      6900

```

PREDICTED: Mus musculus SRC kinase signaling inhibitor 1 (Srcin1), transcript variant X4, mRNA
Sequence ID: **ref|XM_006533765.1|** Length: 7839 Number of Matches: 1
Range 1: 6936 to 6969

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

42.8 bits(46)	7.6()	31/35(89%)	1/35(2%)	Plus/Minus
---------------	-------	------------	----------	------------

Features:

```

Query   917   CAGCGTGTGCACACACACGACAGCGTGTGCACACA   951
          |||
Sbjct   6969  CAGCGTGTGCACACACAC-ACAGAGGCTGCACACA   6936

```

PREDICTED: Mus musculus SRC kinase signaling inhibitor 1 (Srcin1), transcript variant X3, mRNA
Sequence ID: **ref|XM_006533764.1|** Length: 7842 Number of Matches: 1
Range 1: 6939 to 6972

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

Features:

```

Query   917   CAGCGTGTGCACACACACGACAGCGTGTGCACACA   951
          |||
Sbjct   6972  CAGCGTGTGCACACACAC-ACAGAGGCTGCACACA   6939

```

PREDICTED: Mus musculus SRC kinase signaling inhibitor 1 (Srcin1), transcript variant X2, mRNA
Sequence ID: **ref|XM_006533763.1|** Length: 7863 Number of Matches: 1
Range 1: 6960 to 6993

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

Features:

```

Query   917   CAGCGTGTGCACACACACGACAGCGTGTGCACACA   951
          |||
Sbjct   6993  CAGCGTGTGCACACACAC-ACAGAGGCTGCACACA   6960

```

PREDICTED: Mus musculus SRC kinase signaling inhibitor 1 (Srcin1), transcript variant X1, mRNA
Sequence ID: **ref|XM_006533762.1|** Length: 7866 Number of Matches: 1
Range 1: 6963 to 6996

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

Features:

```

Query   917   CAGCGTGTGCACACACACGACAGCGTGTGCACACA   951
          |||
Sbjct   6996  CAGCGTGTGCACACACAC-ACAGAGGCTGCACACA   6963

```

PREDICTED: Mus musculus uncharacterized LOC102638393 (LOC102638393), ncRNA
Sequence ID: **ref|XR_397252.1|** Length: 3219 Number of Matches: 1
Range 1: 2080 to 2115

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

Features:

```

Query   917   CAGCGTGTGCACACACACG-ACAGCGTGTGCACACAC   952
          |||
Sbjct   2080  CAGAGTGTGCACACACACGCACA-CGTGCGCACACAC   2115

```

PREDICTED: Equus caballus microtubule-associated protein 7 (MAP7), mRNA
Sequence ID: **ref|XM_005596943.1|** Length: 3715 Number of Matches: 2
Range 1: 1548 to 1575

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

Features:

```

Query   644   TCTCTCGCGCTGCAGCCTCTCGCGCTGC   671
          |||
Sbjct   1575  TCTCTCGCGCTGCTCCCTCTCGCGCTGC   1548

```

Range 2: 1548 to 1575

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

Features:

Query	496	TCTCTCGCGCTGCAGCCTCTCGCGCTGC	523
Sbjct	1575	TCTCTCGCGCTGCTCCCTCTCGCGCTGC	1548

PREDICTED: *Spermophilus tridecemlineatus* DAB2 interacting protein (Dab2ip), transcript variant X1, mRNA

Sequence ID: [ref|XM_005320919.1|](#) Length: 4638 Number of Matches: 1

Range 1: 3835 to 3865

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

Features:

Sorangium cellulosum So0157-2, complete genome

Sequence ID: **gb|CP003969.1|** Length: 14782125 Number of Matches: 2

Range 1: 14133337 to 14133382

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	37/46(80%)	0/46(0%)	Plus/Minus	

Features:

hypothetical protein

Query 486 CGCGCTGGACTCTCTCGCGCTGCAGCCTCTCGCGCTGCAGCTCATG 531
Sbjct 14133382 CGAGCGGGCCGCGCTCGCCCTGCCGCCCTCGCGCTGCAGCTCCTG 14133337

Range 2: 14133337 to 14133369

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

Features:

hypothetical protein

```

Query    647      CTCGCGCTGCAGCCTCTCGCGCTGCAGCTCATG      679
          |||||
Sbjct    14133369 CTCGCCCTGCCGCCCTCGCGCTGCAGCTCCTG      14133337

```

PREDICTED: Saimiri boliviensis boliviensis MAU2 chromatid cohesion factor homolog (C. elegans) (MAU2), mRNA

Sequence ID: [ref|XM_003942308.1|](#) Length: 4848 Number of Matches: 1

Range 1: 2578 to 2612

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	32/35(91%)	2/35(5%)	Plus/Minus	

Features:

Sporisorium reilianum SRZ2 chromosome 9 complete DNA sequence

Sequence ID: **embIFQ311474.1** | Length: 670125 | Number of Matches: 2

Range 1: 483595 to 483620

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

Features:

Query 650 GCGCTGCAGCCTCTCGCGCTGCAGCT 675
 Sbjct 483620 GCGCCGCAGCCTCTCGCGCTGCAGCT 483595

Range 2: 483595 to 483620

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

Features:

Query 502 GCGCTGCAGCCTCTCGCGCTGCAGCT 527
 Sbjct 483620 GCGCCGCAGCCTCTCGCGCTGCAGCT 483595

Pig DNA sequence from clone CH242-239P7 on chromosome 11, complete sequence

Sequence ID: **emb|CU207380.20|** Length: 199852 Number of Matches: 1

Range 1: 110303 to 110334

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	30/33(91%)	1/33(3%)	Plus/Minus	

Features:

Query 920 CGTGTGCACACACACGACGCGTGTGCACACAC 952
 Sbjct 110334 CGTGTGCACACACAGCACA-CGTGTGCACACAC 110303

Burkholderia cenocepacia J2315 chromosome 1, complete genome

Sequence ID: **emb|AM747720.1|** Length: 3870082 Number of Matches: 3

Range 1: 1862840 to 1862877

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	32/38(84%)	0/38(0%)	Plus/Minus	

Features:

ornibactin biosynthesis non-ribosomal peptide synthase

Query 809 TCTCGCGCTGCAGCGTGTGCACACACGACCACACGT 846
 Sbjct 1862877 TCTCGCGCTGCAGCGTGTGCAGCCAGTCGGCCGCACGT 1862840

Range 2: 1862840 to 1862877

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	32/38(84%)	0/38(0%)	Plus/Minus	

Features:

ornibactin biosynthesis non-ribosomal peptide synthase

Query 719 TCTCGCGCTGCAGCGTGTGCACACACGACCACACGT 756
 Sbjct 1862877 TCTCGCGCTGCAGCGTGTGCAGCCAGTCGGCCGCACGT 1862840

Range 3: 1862840 to 1862877

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	32/38(84%)	0/38(0%)	Plus/Minus	

Features:

ornibactin biosynthesis non-ribosomal peptide synthase

Query 596 TCTCGCGCTGCAGCGTGTGCACACACGACCACACGT 633
 Sbjct 1862877 TCTCGCGCTGCAGCGTGTGCAGCCAGTCGGCCGCACGT 1862840

Cupriavidus taiwanensis str. LMG19424 chromosome 2, complete genome

Sequence ID: **emb|CU633750.1|** Length: 2502411 Number of Matches: 2

Range 1: 2201094 to 2201121

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

Features:

```

Query    501      CGCGCTGCAGCCTCTCGCGCTGCAGCTC      528
          |||||
Sbjct    2201094  CGCGCTGCAGCCGCTGGCGCTGCAGCTC      2201121

```

Range 2: 2201094 to 2201121

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

Features:

```

Query    649      CGCGCTGCAGCTCTCGCGCTGCAGCTC      676
          |||||
Sbjct    2201094  CGCGCTGCAGCCGCTGGCGCTGCAGCTC      2201121

```

Mus musculus SRC kinase signaling inhibitor 1 (Srcin1), mRNA

Sequence ID: [ref|NM_018873.2|](#) Length: 6965 Number of Matches: 1

Range 1: 6062 to 6095

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

Features:

```

Query    917      CAGCGTGTGCACACACACGACAGCGTGTGCACACA      951
          |||||
Sbjct    6095     CAGCGTGTGCACACACAC-ACAGAGGCTGCACACA      6062

```

Mus musculus BAC clone RP24-465A20 from chromosome 17, complete sequence

Sequence ID: **gb|AC126929.3|** Length: 168712 Number of Matches: 1

Range 1: 116762 to 116797

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

Features:

```
Query    917      CAGCGTGTGCACACACACG-ACAGCGTGTGCACACAC      952
          ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   116797   CAGAGTGTGCACACACACGCACA-CGTGCGCACACAC      116762
```

Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:D130061K21 product:unclassifiable, full insert sequence

Sequence ID: **dbj|AK051643.1** Length: 1686 Number of Matches: 1

Range 1: 790 to 823

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

Features:

```

Query    917    CAGCGTGTGCACACACACGACAGCGTGTGCACACA    951
          |||||
Sbjct    823    CAGCGTGTGCACACACAC-ACAGAGGCTGCACACA    790

```

Homo sapiens chromosome 1 clone RP4-706A16, complete sequence

Sequence ID: **gb|AC113935.2** Length: 142422 Number of Matches: 1

Range 1: 26335 to 26370

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	33/39(85%)	3/39(7%)	Plus/Plus	

Features:

```

Query    463      GTGTGCACACACGAACTCTCTCGCGCTGGACTCTCTC    501
          |||||
Sbjct    26335    GTGTGCACACACAGTACTCTCTCTCTCT---CTCTCTC    26370

```

Human DNA sequence from clone RP4-564M11 on chromosome 1p31.1, complete sequence

Sequence ID: **emb|AL035409.15** Length: 138783 Number of Matches: 1

Range 1: 8540 to 8575

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	33/39(85%)	3/39(7%)	Plus/Minus	

Features:

```

Query   463   GTGTGCACACACACGAACTCTCTCGCGCTGGACTCTCTC   501
          |||||
Sbjct   8575  GTGTGCACACACACGTACTCTCTCTCTCT---CTCTCTC   8540

```

Mus musculus, clone IMAGE:5692573, mRNA

Sequence ID: **gb|BC048145.1|** Length: 924 Number of Matches: 1

Range 1: 3 to 36

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

Features:

```

Query   917   CAGCGTGTGCACACACACGACAGCGTGTGCACACA   951
          |||||
Sbjct   36    CAGCGTGTGCACACACAC-ACAGAGGCTGCACACA   3

```

Mouse DNA sequence from clone RP23-157O10 on chromosome 11, complete sequence

Sequence ID: **emb|AL596088.14|** Length: 233204 Number of Matches: 1

Range 1: 183126 to 183159

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

Features:

```

Query   917   CAGCGTGTGCACACACACGACAGCGTGTGCACACA   951
          |||||
Sbjct   183126 CAGCGTGTGCACACACAC-ACAGAGGCTGCACACA   183159

```