

Basic Local Alignment Search Tool

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GCAT

RID [Y0RH1E82014](#) (Expires on 08-06 12:31 pm)

Query ID lc|40829

Description None

Molecule type nucleic acid

Query Length 952

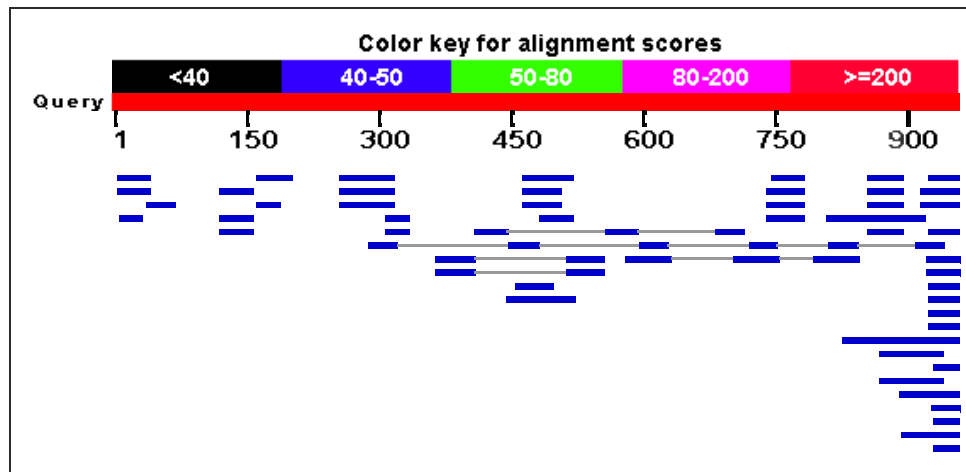
Database Name nr

Description Nucleotide collection (nt)

Program BLASTN 2.2.29+

[Graphic Summary](#)

Distribution of 64 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Homo sapiens chromosome 7qtelo BAC F6, complete sequence	48.2	48.2	3%	0.18	91%	AF104455.1
Human DNA sequence from clone RP5-878O8 on chromosome Xq21.1-21.33, complete sequence	48.2	48.2	6%	0.18	79%	AL031116.2
Human DNA sequence from clone RP1-249C1 on chromosome Xq21.1-22.2, complete sequence	48.2	48.2	6%	0.18	79%	AL022154.2
H.sapiens STS from genomic clone 249C1	48.2	48.2	6%	0.18	79%	AL021231.1
Solanum lycopersicum chromosome ch00, complete genome	46.4	46.4	2%	0.62	96%	HG975512.1
Solanum pennellii chromosome ch02, complete genome	46.4	46.4	4%	0.62	84%	HG975441.1
Solanum lycopersicum strain Heinz 1706 chromosome 0 clone slm-50i17 map 0, complete sequence	46.4	46.4	2%	0.62	96%	AC254685.3
Homo sapiens chromosome 11, clone RP11-261E12, complete sequence	46.4	46.4	4%	0.62	89%	AC026843.9
Homo sapiens BAC clone RP11-625A6 from 4, complete sequence	46.4	46.4	6%	0.62	77%	AC096763.2
Valeriana officinalis partial rpb2 gene for RNA polymerase II, exons 17-24, i-paralogue	46.4	269	20%	0.62	89%	AJ565859.1
Callorhinchus milii clone P27K07.Kidney.k16 mRNA sequence	44.6	44.6	11%	2.2	75%	JX059005.1
Mus musculus targeted non-conditional, lacZ-tagged mutant allele Adap1:tm1e(EUCOMM)Wtsi	44.6	44.6	4%	2.2	84%	JN956177.1
tm1e(EUCOMM)Hmgu; transgenic						
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Adap1:tm1a(EUCOMM)Wtsi; transgenic	44.6	44.6	4%	2.2	84%	JN951965.1
Rattus norvegicus Y Chr BAC RNECO-158J06 (Amplicon Express Rat SHR-Akr (EcoR1 Digest) BAC library) complete sequence	44.6	44.6	4%	2.2	83%	AC240651.3
Rattus norvegicus Y Chr BAC RNECO-173B17 (Amplicon Express Rat SHR-Akr (EcoR1 Digest) BAC library) complete sequence	44.6	44.6	4%	2.2	83%	AC240752.4
Homo sapiens dystrophin (DMD), RefSeqGene (LRG_199) on chromosome X	44.6	44.6	3%	2.2	92%	NG_012232.1
Mouse DNA sequence from clone RP24-365A12 on chromosome 9, complete sequence	44.6	44.6	3%	2.2	85%	CT025751.20
Mus musculus BAC clone RP24-159F5 from chromosome 9, complete sequence	44.6	44.6	3%	2.2	85%	AC162177.2
Mus musculus BAC clone RP24-232D3 from chromosome 12, complete sequence	44.6	44.6	3%	2.2	88%	AC155300.2
Mus musculus BAC clone RP24-406H23 from chromosome 12, complete sequence	44.6	44.6	3%	2.2	88%	AC155235.2
Methanosarcina barkeri str. Fusaro, complete genome	44.6	44.6	4%	2.2	85%	CP000099.1
Mus musculus BAC clone RP23-276B20						

from chromosome 5, complete sequence	44.6	44.6	4%	2.2	84%	AC140216.3
Mus musculus BAC clone RP24-226L20 from chromosome 5, complete sequence	44.6	44.6	4%	2.2	85%	AC129080.6
Mus musculus BAC clone RP23-205J6 from chromosome 5, complete sequence	44.6	44.6	4%	2.2	84%	AC161058.2
Human DNA sequence from clone RP11-460L11 on chromosome 6, complete sequence	44.6	44.6	3%	2.2	88%	AL590402.10
Human DNA sequence from clone RP11-151J4 on chromosome X, complete sequence	44.6	44.6	3%	2.2	92%	AL451144.5
Mus musculus BAC clone RP23-371A1 from 5, complete sequence	44.6	44.6	4%	2.2	85%	AC145559.4
Homo sapiens chromosome 9, clone hRPK.467_F_21, complete sequence	44.6	44.6	13%	2.2	72%	AC006239.5
Solanum lycopersicum chromosome ch06, complete genome	42.8	42.8	7%	7.6	75%	HG975518.1
Solanum lycopersicum chromosome ch04, complete genome	42.8	42.8	3%	7.6	87%	HG975516.1
PREDICTED: Aplysia californica uncharacterized LOC101860881 (LOC101860881), mRNA	42.8	42.8	3%	7.6	88%	XM_005094864.1
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Fgd3:tm1a(EUCOMM)Wtsi; transgenic	42.8	42.8	3%	7.6	93%	JN963855.1
Aminobacterium colombiense DSM 12261, complete genome	42.8	42.8	4%	7.6	82%	CP001997.1
Zebrafish DNA sequence from clone CH73-376K6 in linkage group 24, complete sequence	42.8	42.8	4%	7.6	85%	CU927887.4
Solanum lycopersicum chromosome 6 clone C06HBa0215M16, complete sequence	42.8	42.8	7%	7.6	75%	AC211063.3
Mus musculus chromosome 15, clone RP24-489M6, complete sequence	42.8	42.8	6%	7.6	76%	AC102004.7
Mus musculus BAC clone RP23-306M13 from chromosome 8, complete sequence	42.8	128	11%	7.6	89%	AC159285.3
Mus musculus chromosome 19, clone RP23-13N2, complete sequence	42.8	42.8	3%	7.6	90%	AC102655.7
Mus musculus BAC clone RP24-420M8 from chromosome 13, complete sequence	42.8	42.8	3%	7.6	93%	AC132245.3
Mus musculus BAC clone RP24-263E2 from chromosome 8, complete sequence	42.8	85.5	9%	7.6	86%	AC128663.4
Mus musculus BAC clone RP24-114G1 from 8, complete sequence	42.8	85.5	9%	7.6	86%	AC121866.2
Human DNA sequence from clone RP13-310B24 on chromosome X, complete sequence	42.8	42.8	4%	7.6	82%	AL157779.6
Human DNA sequence from clone RP13-272N16 on chromosome Xq21.2-21.33, complete sequence	42.8	42.8	4%	7.6	82%	AL137015.9
Mustela vison clone XII3C9 genomic sequence	42.8	42.8	2%	7.6	93%	DQ271791.1
Zebrafish DNA sequence from clone DKEY-18L4 in linkage group 24, complete sequence	42.8	42.8	4%	7.6	85%	CR354591.13
Zebrafish DNA sequence from clone CH211-219E17 in linkage group 12, complete sequence	42.8	42.8	4%	7.6	81%	BX005344.13
Homo sapiens BAC clone RP11-516O5 from 2, complete sequence	42.8	42.8	6%	7.6	78%	AC114778.5

Homo sapiens BAC clone RP11-309M4 from Y, complete sequence	42.8	42.8	4%	7.6	82%	AC010144.4
Mus musculus BAC clone RP24-534D6 from 13, complete sequence	42.8	42.8	3%	7.6	93%	AC140284.3
Mouse DNA sequence from clone RP23-375N8 on chromosome 2, complete sequence	42.8	128	16%	7.6	79%	AL845358.2
Zebrafish DNA sequence from clone CH211-202A8 in linkage group 24, complete sequence	42.8	42.8	4%	7.6	85%	AL929009.5
Mouse DNA sequence from clone RP23-419G22 on chromosome X, complete sequence	42.8	42.8	2%	7.6	93%	AL672180.11
Mouse DNA sequence from clone RP23-179F9 on chromosome 2, complete sequence	42.8	42.8	8%	7.6	76%	AL805958.8

Alignments

Homo sapiens chromosome 7qtelo BAC F6, complete sequence
Sequence ID: **gb|AF104455.1|** Length: 71353 Number of Matches: 1
Range 1: 61685 to 61718

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	31/34(91%)	0/34(0%)	Plus/Minus	

Features:

```

Query   919      ATACACATGTGTGTGTAGTGATACACATGTGTGT   952
          |||
Sbjct   61718  ATACACATGTGTGTGTACATATACACATGTGTGT   61685

```

Human DNA sequence from clone RP5-878O8 on chromosome Xq21.1-21.33, complete sequence
Sequence ID: **emb|AL031116.2|** Length: 130718 Number of Matches: 1
Range 1: 128803 to 128859

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	50/63(79%)	6/63(9%)	Plus/Minus	

Features:

```

Query   256      TATGTACAGTCAGTTTGTCTCTCTATATCAAGTCTCTCTATATCATGATACACATGTGTG   315
          |||
Sbjct   128859  TATGTATA-TAAATTTGTCTCTCTATAT-ATGTCTCTCTATAT----ATATGTATGTGTG   128806
Query   316      TGT   318
          |||
Sbjct   128805  TGT   128803

```

Human DNA sequence from clone RP1-249C1 on chromosome Xq21.1-22.2, complete sequence
Sequence ID: **emb|AL022154.2|** Length: 118153 Number of Matches: 1
Range 1: 85 to 141

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	50/63(79%)	6/63(9%)	Plus/Minus	

Features:

```

Query   256      TATGTACAGTCAGTTTGTCTCTCTATATCAAGTCTCTCTATATCATGATACACATGTGTG   315
          |||
Sbjct   141      TATGTATA-TAAATTTGTCTCTCTATAT-ATGTCTCTCTATAT----ATATGTATGTGTG   88
Query   316      TGT   318
          |||
Sbjct   87       TGT   85

```

H.sapiens STS from genomic clone 249C1
Sequence ID: **emb|AL021231.1|** Length: 1000 Number of Matches: 1
Range 1: 85 to 141

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

48.2 bits(52) 0.18() 50/63(79%) 6/63(9%) Plus/Minus

Features:

```
Query 256 TATGTACAGTCAGTTTGTCTCTCTATATCAAGTCTCTCTATATCATGATACACATGTGTG 315
      |||||
Sbjct 141 TATGTATA-TAAATTTGTCTCTCTATAT-ATGTCTCTCTATAT----ATATGTATGTGTG 88
Query 316 TGT 318
      |||
Sbjct 87 TGT 85
```

Solanum lycopersicum chromosome ch00, complete genome

Sequence ID: **emb|HG975512.1|** Length: 21806818 Number of Matches: 1

Range 1: 11258587 to 11258614

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	27/28(96%)	0/28(0%)	Plus/Plus	

Features:

```
Query 308 CATGTGTGTGTAGACTAGACACTGATGT 335
      |||||
Sbjct 11258587 CATGTGTGTGCAGACTAGACACTGATGT 11258614
```

Solanum pennellii chromosome ch02, complete genome

Sequence ID: **emb|HG975441.1|** Length: 59803892 Number of Matches: 1

Range 1: 11721106 to 11721150

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	38/45(84%)	1/45(2%)	Plus/Minus	

Features:

```
Query 909 CTATATCATGATACACATGTGTGTAGTG-ATACACATGTGTGT 952
      |||||
Sbjct 11721150 CTAAATCATCATACATTTGTGTGTAGTGAATACATTTGTGTGT 11721106
```

Solanum lycopersicum strain Heinz 1706 chromosome 0 clone slm-50i17 map 0, complete sequence

Sequence ID: **gb|AC254685.3|** Length: 97417 Number of Matches: 1

Range 1: 24429 to 24456

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	27/28(96%)	0/28(0%)	Plus/Minus	

Features:

```
Query 308 CATGTGTGTGTAGACTAGACACTGATGT 335
      |||||
Sbjct 24456 CATGTGTGTGCAGACTAGACACTGATGT 24429
```

Homo sapiens chromosome 11, clone RP11-261E12, complete sequence

Sequence ID: **gb|AC026843.9|** Length: 166287 Number of Matches: 1

Range 1: 104885 to 104929

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	41/46(89%)	4/46(8%)	Plus/Plus	

Features:

```
Query 910 TATATCATG-ATACACATGTGTGTGTA-GTG-ATACACATGTGTGT 952
      |||||
Sbjct 104885 TATAT-ATGTATACACATGTGTGTGTATATGTATACACATGTGTGT 104929
```

Homo sapiens BAC clone RP11-625A6 from 4, complete sequence

Sequence ID: **gb|AC096763.2|** Length: 168710 Number of Matches: 1

Range 1: 140324 to 140378

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	46/60(77%)	5/60(8%)	Plus/Minus	

Features:

Query 461 ATACACATGTGTGTGTAGGTCTCTCTATATCAAGTCTCTCTATATCATGATTCTCTATAT 520
 |||||
 Sbjct 140378 ATACACATGTGTGTGTATCTATCTATATCTAG-----CTATATCATCTATATCTATAT 140324

Valeriana officinalis partial rpb2 gene for RNA polymerase II, exons 17-24, i-paralogue

Sequence ID: **emb|AJ565859.1|** Length: 2407 Number of Matches: 6

Range 1: 91 to 125

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	31/35(89%)	0/35(0%)	Plus/Plus	

Features:

Query 446 TCTCTCTATATCATGATACACATGTGTGTAGGT 480
 |||||
 Sbjct 91 TCTCTCTATATAATGATACACATGACTGTGTACGT 125

Range 2: 91 to 122

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	29/32(91%)	0/32(0%)	Plus/Plus	

Features:

Query 288 TCTCTCTATATCATGATACACATGTGTGTGTA 319
 |||||
 Sbjct 91 TCTCTCTATATAATGATACACATGACTGTGTGTA 122

Range 3: 91 to 122

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	29/32(91%)	0/32(0%)	Plus/Plus	

Features:

Query 593 TCTCTCTATATCATGATACACATGTGTGTGTA 624
 |||||
 Sbjct 91 TCTCTCTATATAATGATACACATGACTGTGTGTA 122

Range 4: 91 to 122

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	29/32(91%)	0/32(0%)	Plus/Plus	

Features:

Query 716 TCTCTCTATATCATGATACACATGTGTGTGTA 747
 |||||
 Sbjct 91 TCTCTCTATATAATGATACACATGACTGTGTGTA 122

Range 5: 91 to 122

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	29/32(91%)	0/32(0%)	Plus/Plus	

Features:

Query 806 TCTCTCTATATCATGATACACATGTGTGTGTA 837
 |||||
 Sbjct 91 TCTCTCTATATAATGATACACATGACTGTGTGTA 122

Range 6: 91 to 122

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	29/32(91%)	0/32(0%)	Plus/Plus	

Features:

Query 904 TCTCTCTATATCATGATACACATGTGTGTGTA 935
 |||||
 Sbjct 91 TCTCTCTATATAATGATACACATGACTGTGTGTA 122

Callorhinchus milii clone P27K07.Kidney.k16 mRNA sequence

Sequence ID: **gb|JX059005.1|** Length: 419 Number of Matches: 1

Range 1: 86 to 192

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	85/114(75%)	11/114(9%)	Plus/Minus	
Features:					
Query	805	GTCTCTCT-ATATCATGATACACATGTGTGTAGTTGTGTACTCAGTGTA-GTCTCTCT			862
Sbjct	192	GTCTCTCTCAAATC-TG-TCCGCATGTGTGTGTGTGTCTGTAT---GTGTATGTCTCTCT			138
Query	863	ATATC-ATGATGTCTCTCTATATCATTTGTGTACTCAGTGT-AGTCTCTCTATAT			914
Sbjct	137	ATATCTATG-TGTGTCTATATATATATATATAC-CCGTGTGTGTGTCTCTATAT			86

Mus musculus targeted non-conditional, lacZ-tagged mutant allele Adap1:tm1e(EUCOMM)Wtsi tm1e(EUCOMM)Hmgu; transgenic
Sequence ID: **gb|JN956177.1|** Length: 38015 Number of Matches: 1
Range 1: 7545 to 7588

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	38/45(84%)	3/45(6%)	Plus/Minus	
Features:					
Query	850	GTGTAGTCTCTCTATATC--ATGATGTCTCTCTATATCATTTGTGT			892
Sbjct	7588	GTGT-GTCTCTCTATATCTGATGGTGTCTCTCTATGTCTGTGTGT			7545

Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Adap1:tm1a(EUCOMM)Wtsi; transgenic
Sequence ID: **gb|JN951965.1|** Length: 38078 Number of Matches: 1
Range 1: 7545 to 7588

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	38/45(84%)	3/45(6%)	Plus/Minus	
Features:					
Query	850	GTGTAGTCTCTCTATATC--ATGATGTCTCTCTATATCATTTGTGT			892
Sbjct	7588	GTGT-GTCTCTCTATATCTGATGGTGTCTCTCTATGTCTGTGTGT			7545

Rattus norvegicus Y Chr BAC RNECO-158J06 (Amplicon Express Rat SHR-Akr (EcoR1 Digest) BAC library) complete sequence
Sequence ID: **gb|AC240651.3|** Length: 147530 Number of Matches: 1
Range 1: 146885 to 146929

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	38/46(83%)	1/46(2%)	Plus/Minus	
Features:					
Query	461	ATACACATGTGTGTGTAGGTCTCTCTATATCAAGTCTCTCTATATC			506
Sbjct	146929	ATACATATGTGTGTGTATCTATATCTATATC-TGTCTATCTATATC			146885

Rattus norvegicus Y Chr BAC RNECO-173B17 (Amplicon Express Rat SHR-Akr (EcoR1 Digest) BAC library) complete sequence
Sequence ID: **gb|AC240752.4|** Length: 179395 Number of Matches: 1
Range 1: 11754 to 11798

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	38/46(83%)	1/46(2%)	Plus/Minus	
Features:					
Query	461	ATACACATGTGTGTGTAGGTCTCTCTATATCAAGTCTCTCTATATC			506
Sbjct	11798	ATACATATGTGTGTGTATCTATATCTATATC-TGTCTATCTATATC			11754

Homo sapiens dystrophin (DMD), RefSeqGene (LRG_199) on chromosome X
Sequence ID: **ref|NG_012232.1|** Length: 2227382 Number of Matches: 1
Range 1: 335117 to 335152

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	33/36(92%)	2/36(5%)	Plus/Minus	

Features:

Query 919 ATACACATGTGTGTGTA-GTG-ATACACATGTGTGT 952
Sbjct 335152 ATACACATATGTGTGTATGTGTATACACATGTGTGT 335117

Mouse DNA sequence from clone RP24-365A12 on chromosome 9, complete sequence

Sequence ID: **emb|CT025751.20|** Length: 176584 Number of Matches: 1
Range 1: 103311 to 103350

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	34/40(85%)	3/40(7%)	Plus/Plus	

Features:

Query 916 ATGATACACATGTGTGTGTA---GTGATACACATGTGTGT 952
Sbjct 103311 ATGATGCACATGTGTGTGTATGTGTGATGCATATGTGTGT 103350

Mus musculus BAC clone RP24-159F5 from chromosome 9, complete sequence

Sequence ID: **gb|AC162177.2|** Length: 148915 Number of Matches: 1
Range 1: 131378 to 131417

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	34/40(85%)	3/40(7%)	Plus/Plus	

Features:

Query 916 ATGATACACATGTGTGTGTA---GTGATACACATGTGTGT 952
Sbjct 131378 ATGATGCACATGTGTGTGTATGTGTGATGCATATGTGTGT 131417

Mus musculus BAC clone RP24-232D3 from chromosome 12, complete sequence

Sequence ID: **gb|AC155300.2|** Length: 176261 Number of Matches: 1
Range 1: 141593 to 141626

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

Features:

Query 919 ATACACATGTGTGTGTAGTGATACACATGTGTGT 952
Sbjct 141593 ATACATATGTGTGTGTATAGATATACATGTGTGT 141626

Mus musculus BAC clone RP24-406H23 from chromosome 12, complete sequence

Sequence ID: **gb|AC155235.2|** Length: 158341 Number of Matches: 1
Range 1: 45431 to 45464

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

Features:

Query 919 ATACACATGTGTGTGTAGTGATACACATGTGTGT 952
Sbjct 45431 ATACATATGTGTGTGTATAGATATACATGTGTGT 45464

Methanosarcina barkeri str. Fusaro, complete genome

Sequence ID: **gb|CP000099.1|** Length: 4837408 Number of Matches: 1
Range 1: 1827543 to 1827581

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	33/39(85%)	0/39(0%)	Plus/Minus	

Features:

1653 bp at 5' side: cell surface protein391 bp at 3' side: inorganic pyrophosphatase

Query 481 CTCTCTATATCAAGTCTCTCTATATCATGATTCTCTATA 519
Sbjct 1827581 CTCTCTATAAAAAGGCTCTCTCTATAGAAAGATTCTCTATA 1827543

Mus musculus BAC clone RP23-276B20 from chromosome 5, complete sequence

Sequence ID: **gb|AC140216.3|** Length: 194560 Number of Matches: 1

Range 1: 20762 to 20805

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	38/45(84%)	3/45(6%)	Plus/Plus	

Features:

```
Query   850      GTGTAGTCTCTCTATATC--ATGATGTCTCTCTATATCATTGTGT   892
          |||||
Sbjct   20762    GTGT-GTCTCTCTATATCTGATGGTGTCTCTCTATGTCTGTGTGT   20805
```

Mus musculus BAC clone RP24-226L20 from chromosome 5, complete sequence

Sequence ID: **gb|AC129080.6|** Length: 156781 Number of Matches: 1

Range 1: 32419 to 32457

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	33/39(85%)	0/39(0%)	Plus/Plus	

Features:

```
Query    6      CATACACACATGTGTGTGTAGGTACTCATGACTAGACAC   44
          |||||
Sbjct   32419    CATACACACATGTGTGTGTACATACACATATGTAGACAC   32457
```

Mus musculus BAC clone RP23-205J6 from chromosome 5, complete sequence

Sequence ID: **gb|AC161058.2|** Length: 222180 Number of Matches: 1

Range 1: 71253 to 71296

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	38/45(84%)	3/45(6%)	Plus/Minus	

Features:

```
Query   850      GTGTAGTCTCTCTATATC--ATGATGTCTCTCTATATCATTGTGT   892
          |||||
Sbjct   71296    GTGT-GTCTCTCTATATCTGATGGTGTCTCTCTATGTCTGTGTGT   71253
```

Human DNA sequence from clone RP11-460L11 on chromosome 6, complete sequence

Sequence ID: **emb|AL590402.10|** Length: 45126 Number of Matches: 1

Range 1: 22325 to 22358

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

Features:

```
Query   919      ATACACATGTGTGTGTAGTGATACACATGTGTGT   952
          |||||
Sbjct   22358    ATATACATGTGTGTGTATTCATATACATGTGTGT   22325
```

Human DNA sequence from clone RP11-151J4 on chromosome X, complete sequence

Sequence ID: **emb|AL451144.5|** Length: 100207 Number of Matches: 1

Range 1: 53664 to 53699

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	33/36(92%)	2/36(5%)	Plus/Plus	

Features:

```
Query   919      ATACACATGTGTGTGTA-GTG-ATACACATGTGTGT   952
          |||||
Sbjct   53664    ATACACATATGTGTGTATGTGTATACACATGTGTGT   53699
```

Mus musculus BAC clone RP23-371A1 from 5, complete sequence

Sequence ID: **gb|AC145559.4|** Length: 203726 Number of Matches: 1

Range 1: 185317 to 185355

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

44.6 bits(48) 2.2() 33/39(85%) 0/39(0%) Plus/Plus

Features:

```
Query 6 CATAACACATGTGTGTGTAGGTACTCATGACTAGACAC 44
      |||
Sbjct 185317 CATAACACATGTGTGTGTACATACACATATGTAGACAC 185355
```

Homo sapiens chromosome 9, clone hRPK.467_F_21, complete sequence

Sequence ID: **gb|AC006239.5|AC006239** Length: 195032 Number of Matches: 1

Range 1: 90721 to 90848

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	98/136(72%)	12/136(8%)	Plus/Plus	

Features:

```
Query 821 ATACACATGTGTGTGTAGTTGTGTACTCA-GTGTAGTCTCTCTATAT---CATGATGTCT 876
      |||
Sbjct 90721 ATACACACGTGTGTGTATATATATACACACGTGT-GTGTGTATATATACACACG-TGTGT 90778

Query 877 CTCTATATCATTGTGTACTCAGTGTAGTCTCTCTATATCATGATACACATGTGTGTGTAG 936
      |||
Sbjct 90779 GTGTATATA--TATATACAC-GTGT-GTGTGTATATAT-AT-ATACACATGTGTGTATAT 90832

Query 937 TGATACACATGTGTGT 952
      |||
Sbjct 90833 ATATATACACGTGTGT 90848
```

Solanum lycopersicum chromosome ch06, complete genome

Sequence ID: **emb|HG975518.1|** Length: 46045610 Number of Matches: 1

Range 1: 35132160 to 35132229

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	54/72(75%)	2/72(2%)	Plus/Minus	

Features:

```
Query 863 ATATCATGATGTCTCTCTATATCATTGTGTACTCAGTGTAGTCTCTCTATATCATGATAC 922
      |||
Sbjct 35132229 ATATCATGATGATTATATATATAATTTTTCAGTATAAACTGAATATAT-AT-ATAT 35132172

Query 923 ACATGTGTGTGT 934
      |||
Sbjct 35132171 ATATGTGTGTGT 35132160
```

Solanum lycopersicum chromosome ch04, complete genome

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

Range 1: 32492854 to 32492891

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	33/38(87%)	1/38(2%)	Plus/Minus	

Features:

```
Query 742 TGTGTAGTTGTGTACTCAGTG-TTCTCTATATCATGAT 778
      |||
Sbjct 32492891 TGTGTAGTTGTGTGCTATGTGGTTCTCTATATTATGAT 32492854
```

PREDICTED: Aplysia californica uncharacterized LOC101860881 (LOC101860881), mRNA

Sequence ID: **ref|XM_005094864.1|** Length: 8420 Number of Matches: 1

Range 1: 7070 to 7102

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

Features:

```
Query 40 GACACTGATGTCATACTGCTGGTAGCTCATCAC 72
      |||
Sbjct 7070 GACTCTGGTGTGCTGCTGCTGGTAGCTCACCAC 7102
```

Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Fgd3:tm1a(EUCOMM)Wtsi; transgenic

Sequence ID: **gb|JN963855.1|** Length: 38708 Number of Matches: 1

Range 1: 13491 to 13520

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	28/30(93%)	1/30(3%)	Plus/Minus	

Features:

```

Query   924      CATGTGTGTGTAGTG-ATACACATGTGTGT   952
          |||
Sbjct   13520   CATGTGTGTGTAGTGCATACACCTGTGTGT   13491

```

Aminobacterium colombiense DSM 12261, complete genome

Sequence ID: **gb|CP001997.1|** Length: 1980592 Number of Matches: 1

Range 1: 107827 to 107871

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	37/45(82%)	2/45(4%)	Plus/Minus	

Features:

```

Query   162      GCTGCTCGTGACAGGGAGAGAGTCTCTCTATATCATG--ATCTGC   204
          |||
Sbjct   107871   GCTGCTCATGACAGGGAGAGAGGCTCCCGACATCCTGGCATCTGC   107827

```

Zebrafish DNA sequence from clone CH73-376K6 in linkage group 24, complete sequence

Sequence ID: **emb|CU927887.4|** Length: 101389 Number of Matches: 1

Range 1: 14667 to 14705

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

Features:

```

Query   121      TGCAGCTCGAGTCGTGACTGACTGACTGTCTAGCTGACGT   160
          |||
Sbjct   14705   TGCAGCGCCCGTC-TGACTGACTGACTGCCTATCTGACGT   14667

```

Solanum lycopersicum chromosome 6 clone C06HBa0215M16, complete sequence

Sequence ID: **gb|AC211063.3|** Length: 101821 Number of Matches: 1

Range 1: 72265 to 72334

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	54/72(75%)	2/72(2%)	Plus/Minus	

Features:

```

Query   863      ATATCATGATGTCTCTCTATATCATTGTGTACTCAGTGTAGTCTCTCTATATCATGATAC   922
          |||
Sbjct   72334   ATATCATGATGATTATATATATAATTTTATTTCAGTATAAACTGAATATAT-AT-ATAT   72277

Query   923      ACATGTGTGTGT   934
          |||
Sbjct   72276   ATATGTGTGTGT   72265

```

Mus musculus chromosome 15, clone RP24-489M6, complete sequence

Sequence ID: **gb|AC102004.7|** Length: 164810 Number of Matches: 1

Range 1: 57018 to 57082

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	52/68(76%)	5/68(7%)	Plus/Plus	

Features:

```

Query   887      TTGTGTACTCAGTGTAGTC-TCTCTATATCATG-ATACACATGTGTGTAGTGATACAC   944
          |||
Sbjct   57018   TTATGTATTCA---TAGTCATCACTATAGAATATATACACATGTGTATGTACTCATGCAC   57074

Query   945      ATGTGTGT   952
          |||
Sbjct   57075   TTGTGTGT   57082

```

Mus musculus BAC clone RP23-306M13 from chromosome 8, complete sequence

Sequence ID: **gb|AC159285.3|** Length: 231778 Number of Matches: 3

Range 1: 112086 to 112122

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

42.8 bits(46)	7.6()	33/37(89%)	2/37(5%)	Plus/Plus
Features:				
Query	409	AGTCGGGTCTCTCTATA-TCAT-TGTGTACTCAGTGT	443	
Sbjct	112086	AGTAGGGTCTCTCTATAGTCATCTGTGTACTCATTGT	112122	

Range 2: 112086 to 112122

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	33/37(89%)	2/37(5%)	Plus/Plus	
Features:					
Query	556	AGTCGGGTCTCTCTATA-TCAT-TGTGTACTCAGTGT			590

Range 3: 112086 to 112122

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	33/37(89%)	2/37(5%)	Plus/Plus	
Features:					
Query	679	AGTCGGGTCTCTCTATA-TCAT-TGTGTACTCAGTGT			713
Sbjct	112086	AGTAGGGTCTCTCTATAGTCATCTGTGTACTCATTGT			112122

Mus musculus chromosome 19, clone RP23-13N2, complete sequence
Sequence ID: **gb|AC102655.7|** Length: 202294 Number of Matches: 1
Range 1: 120842 to 120872

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	28/31(90%)	0/31(0%)	Plus/Plus	
Features:					
Query	922	CACATGTGTGTGTAGTGATACACATGTGTGT	952		
Sbjct	120842	CACATGTGTGTGTGCTTATACACATGTGTGT	120872		

Mus musculus BAC clone RP24-420M8 from chromosome 13, complete sequence
Sequence ID: **gb|AC132245.3|** Length: 148654 Number of Matches: 1
Range 1: 24886 to 24915

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	28/30(93%)	1/30(3%)	Plus/Plus	
Features:					
Query	924	CATGTGTGTGTAGTG-ATACACATGTGTGT	952		
Sbjct	24886	CATGTGTGTGTAGTGCATACACCTGTGTGT	24915		

Mus musculus BAC clone RP24-263E2 from chromosome 8, complete sequence
Sequence ID: **gb|AC128663.4|** Length: 197679 Number of Matches: 2
Range 1: 31993 to 32034

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	38/44(86%)	3/44(6%)	Plus/Plus	
Features:					
Query	365	TCTCTATATCATGATCTG-CAGTCGGTCTCTATATCATGATCTG			407
Sbjct	31993	TCTCTATATCATG-TCTGTCTGACTGTCTCTATATCATG-TCTG			32034

Range 2: 31993 to 32034

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	38/44(86%)	3/44(6%)	Plus/Plus	
Features:					

Query 512 TCTCTATATCATGATCTG-CAGTCGGTCTCTATATCATGATCTG 554
 |||||
 Sbjct 31993 TCTCTATATCATG-TCTGTCTGACTGTCTCTATATCATG-TCTG 32034

Mus musculus BAC clone RP24-114G1 from 8, complete sequence

Sequence ID: **gb|AC121866.2|** Length: 162835 Number of Matches: 2

Range 1: 39498 to 39539

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	38/44(86%)	3/44(6%)	Plus/Minus	

Features:

Query 512 TCTCTATATCATGATCTG-CAGTCGGTCTCTATATCATGATCTG 554
 |||||
 Sbjct 39539 TCTCTATATCATG-TCTGTCTGACTGTCTCTATATCATG-TCTG 39498

Range 2: 39498 to 39539

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	38/44(86%)	3/44(6%)	Plus/Minus	

Features:

Query 365 TCTCTATATCATGATCTG-CAGTCGGTCTCTATATCATGATCTG 407
 |||||
 Sbjct 39539 TCTCTATATCATG-TCTGTCTGACTGTCTCTATATCATG-TCTG 39498

Human DNA sequence from clone RP13-310B24 on chromosome X, complete sequence

Sequence ID: **emb|AL157779.6|** Length: 99632 Number of Matches: 1

Range 1: 1601 to 1645

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	37/45(82%)	1/45(2%)	Plus/Minus	

Features:

Query 735 ACATGTGTGTGTAGTTGTGTAAGTCTCTCT-ATATCATGAT 778
 |||||
 Sbjct 1645 ACCTGTGTGTGCAGTAGTGTACTCAGTGATCTTTAATATTATTAT 1601

Human DNA sequence from clone RP13-272N16 on chromosome Xq21.2-21.33, complete sequence

Sequence ID: **emb|AL137015.9|** Length: 99527 Number of Matches: 1

Range 1: 56423 to 56467

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	37/45(82%)	1/45(2%)	Plus/Minus	

Features:

Query 735 ACATGTGTGTGTAGTTGTGTAAGTCTCTCT-ATATCATGAT 778
 |||||
 Sbjct 56467 ACCTGTGTGTGCAGTAGTGTACTCAGTGATCTTTAATATTATTAT 56423

Mustela vison clone XI3C9 genomic sequence

Sequence ID: **gb|DQ271791.1|** Length: 515 Number of Matches: 1

Range 1: 195 to 222

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

Features:

Query 163 CTGCTCGTGACAGGGAGAGAGTCTCTCT 190
 |||||
 Sbjct 222 CTGCTCCTGACATGGAGAGAGTCTCTCT 195

Zebrafish DNA sequence from clone DKEY-18L4 in linkage group 24, complete sequence

Sequence ID: **emb|CR354591.13|** Length: 218314 Number of Matches: 1

Range 1: 179922 to 179960

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	34/40(85%)	1/40(2%)	Plus/Minus	
Features:					
Query	121	TGCAGCTCGAGTCGTCGACTGACTGACTGTCTAGCTGACGT	160		
Sbjct	179960	TGCAGCGCCCGTC-TGACTGACTGACTGCCTATCTGACGT	179922		

Zebrafish DNA sequence from clone CH211-219E17 in linkage group 12, complete sequence
Sequence ID: **emb|BX005344.13|** Length: 170634 Number of Matches: 1
Range 1: 124670 to 124712

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/43(81%)	0/43(0%)	Plus/Plus	
Features:					
Query	454	TATCATGATACACATGTGTGTGTAGGTCTCTCTATATCAAGTC	496		
Sbjct	124670	TATAATAATATACATGTGTGTGTGTGTCTCTCTCTCAAATC	124712		

Homo sapiens BAC clone RP11-516O5 from 2, complete sequence
Sequence ID: **gb|AC114778.5|** Length: 187842 Number of Matches: 1
Range 1: 157467 to 157532

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	52/67(78%)	3/67(4%)	Plus/Minus	
Features:					
Query	888	TGTGTACTCAGTGTA-GTCTCTCTATATCATG-ATACACATGTGTGTGTAGTGATACACA	945		
Sbjct	157532	TGTGTTTTGAGTATATGTGTGTATATAT-ATGTATACACATGTGTGTATATGTATACACA	157474		
Query	946	TGTGTGT	952		
Sbjct	157473	TATGTGT	157467		

Homo sapiens BAC clone RP11-309M4 from Y, complete sequence
Sequence ID: **gb|AC010144.4|AC010144** Length: 166347 Number of Matches: 1
Range 1: 42247 to 42291

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	37/45(82%)	1/45(2%)	Plus/Minus	
Features:					
Query	735	ACATGTGTGTGTAGTTGTGTACTCAGTGTTCTCT-ATATCATGAT	778		
Sbjct	42291	ACCTGTGTGTGCAGTAGTGACTCAGTGATCTTTAATATTATTAT	42247		

Mus musculus BAC clone RP24-534D6 from 13, complete sequence
Sequence ID: **gb|AC140284.3|** Length: 186444 Number of Matches: 1
Range 1: 183465 to 183494

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	28/30(93%)	1/30(3%)	Plus/Plus	
Features:					
Query	924	CATGTGTGTGTAGTG-ATACACATGTGTGT	952		
Sbjct	183465	CATGTGTGTGTAGTGCATACACCTGTGTGT	183494		

Mouse DNA sequence from clone RP23-375N8 on chromosome 2, complete sequence
Sequence ID: **emb|AL845358.2|** Length: 31523 Number of Matches: 3
Range 1: 20151 to 20200

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	41/52(79%)	2/52(3%)	Plus/Plus	
Features:					

Query 577 TGTGTACTCAGTGTAGTCTCTCTATATCATGATACACATGTGTGTAGTTG 628
 |||||
 Sbjct 20151 TGTGTGCCCAGTGTAGTGTCTCCATGT--TGTCACACATGTGTGTCCAGTTG 20200

Range 2: 20151 to 20200

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	41/52(79%)	2/52(3%)	Plus/Plus	

Features:

Query 700 TGTGTACTCAGTGTAGTCTCTCTATATCATGATACACATGTGTGTAGTTG 751
 |||||
 Sbjct 20151 TGTGTGCCCAGTGTAGTGTCTCCATGT--TGTCACACATGTGTGTCCAGTTG 20200

Range 3: 20151 to 20200

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	41/52(79%)	2/52(3%)	Plus/Plus	

Features:

Query 790 TGTGTACTCAGTGTAGTCTCTCTATATCATGATACACATGTGTGTAGTTG 841
 |||||
 Sbjct 20151 TGTGTGCCCAGTGTAGTGTCTCCATGT--TGTCACACATGTGTGTCCAGTTG 20200

Zebrafish DNA sequence from clone CH211-202A8 in linkage group 24, complete sequence

Sequence ID: **emb|AL929009.5|** Length: 208279 Number of Matches: 1

Range 1: 4428 to 4466

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

Features:

Query 121 TGCAGCTCGAGTCGTGACTGACTGACTGTCTAGCTGACGT 160
 |||||
 Sbjct 4428 TGCAGCGCCCCGTC-TGACTGACTGACTGCCATCTGACGT 4466

Mouse DNA sequence from clone RP23-419G22 on chromosome X, complete sequence

Sequence ID: **emb|AL672180.11|** Length: 212659 Number of Matches: 1

Range 1: 160287 to 160314

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

Features:

Query 8 TACACACATGTGTGTGTAGGTACTCATG 35
 |||||
 Sbjct 160287 TACAAACATGTGTGTGCAGGTACTCATG 160314

Mouse DNA sequence from clone RP23-179F9 on chromosome 2, complete sequence

Sequence ID: **emb|AL805958.8|** Length: 198627 Number of Matches: 1

Range 1: 71285 to 71361

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	60/79(76%)	4/79(5%)	Plus/Minus	

Features:

Query 445 GTCTCTCTATATC-ATG-ATACACATGTGTGTAGGTCTCTCTATATCAAGTCTCTCTA 502
 |||||
 Sbjct 71361 GTCTCTGTATCTCTATACATACAAATGTGTGTATCTCTCTATCTCTCTA-TCTCTCTA 71303
 Query 503 TATCATGATTCTCTATATC 521
 |||||
 Sbjct 71302 TTTC-TATCTCTCTATCTC 71285