

Basic Local Alignment Search Tool

NCBI/ [BLAST](#)/ [blastn suite](#)/ **Formatting Results - Y0TBKKEV014**

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CAGT

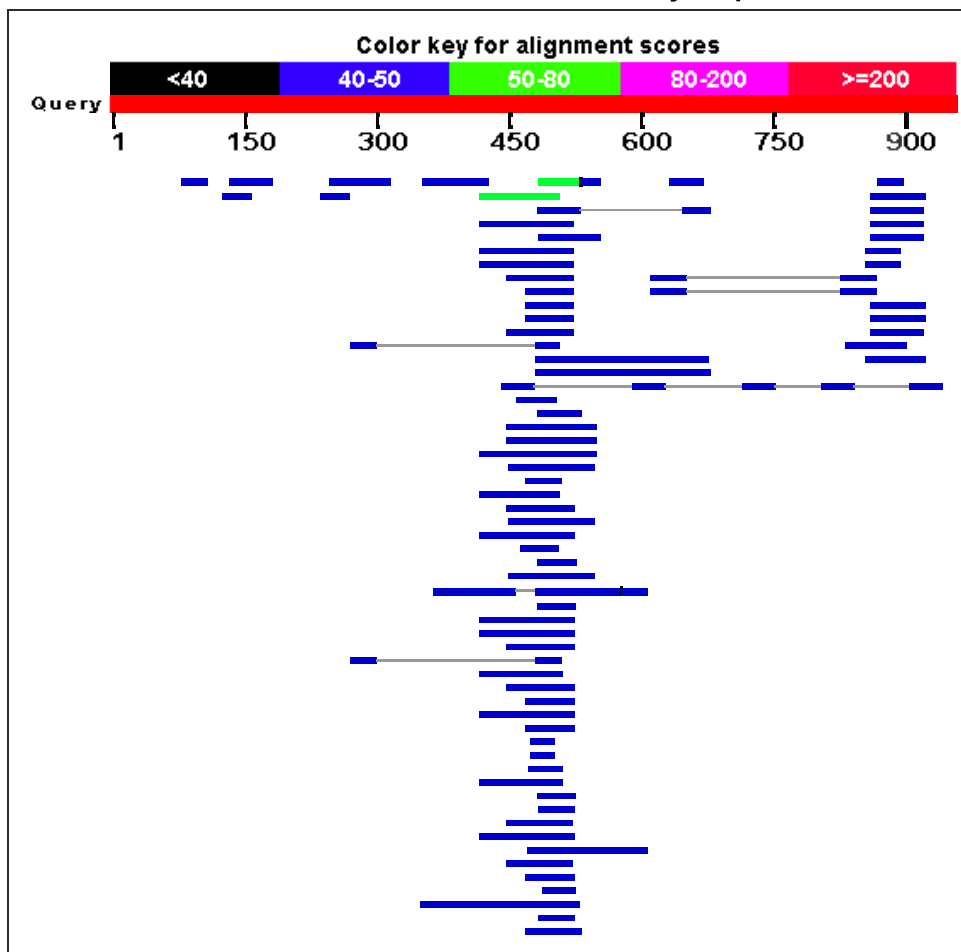
RID [Y0TBKKEV014](#) (Expires on 08-06 13:02 pm)

Query ID lc|33355
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 97 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Homo sapiens adenylate kinase 3 (AK3), RefSeqGene on chromosome 9	51.8	101	7%	0.015	87%	NG_028041.1
Homo sapiens PAC clone RP5-959C21 from 7, complete sequence	51.8	51.8	9%	0.015	73%	AC004936.2
Plasmodium knowlesi strain H chromosome 7, complete genome	50.0	94.5	8%	0.051	84%	AM910989.1
Homo sapiens 3 BAC RP11-292E2 (Roswell Park Cancer Institute Human BAC Library) complete sequence	50.0	50.0	11%	0.051	73%	AC078788.8
Human DNA sequence from clone RP11-6J24 on chromosome 9p24.1-24.3, complete sequence	50.0	50.0	7%	0.051	79%	AL136231.12
Homo sapiens 3 BAC RP11-147F23 (Roswell Park Cancer Institute Human BAC Library) complete sequence	50.0	50.0	11%	0.051	73%	AC117421.6
Homo sapiens chromosome 5 clone RP11-32D16, complete sequence	48.2	94.5	11%	0.18	72%	AC091939.3
Neospora caninum Liverpool complete genome, chromosome VIIa	46.4	46.4	7%	0.62	77%	FR823388.1
Pan troglodytes BAC clone CH251-503N9 from chromosome x, complete sequence	46.4	46.4	7%	0.62	75%	AC192729.3
Mus musculus chromosome 3, clone RP23-111L16, complete sequence	46.4	46.4	5%	0.62	81%	AC116671.14
Mus musculus chromosome 3, clone RP23-277D9, complete sequence	46.4	46.4	5%	0.62	81%	AC166331.5
Homo sapiens 12q BAC RP11-29C9 (Roswell Park Cancer Institute Human BAC Library) complete sequence	46.4	46.4	5%	0.62	80%	AC108360.3
Homo sapiens 3 BAC RP11-73N1 (Roswell Park Cancer Institute Human BAC Library) complete sequence	46.4	46.4	7%	0.62	78%	AC008082.12
Homo sapiens zinc finger, MYM-type 2 (ZMYM2), RefSeqGene on chromosome 13	44.6	44.6	7%	2.2	74%	NG_023348.2
Staphylococcus phage 6ec, complete genome	44.6	87.3	5%	2.2	93%	KJ804259.1
PREDICTED: Rattus norvegicus protein tyrosine phosphatase-like (proline instead of catalytic arginine), member a (Ptpla), transcript variant X4, mRNA	44.6	44.6	20%	2.2	66%	XM_006254295.1
PREDICTED: Rattus norvegicus protein tyrosine phosphatase-like (proline instead of catalytic arginine), member a (Ptpla), transcript variant X3, mRNA	44.6	44.6	20%	2.2	66%	XM_006254294.1
Lethenteron camtschaticum clone BAC 424C19, BAC 204J11 homeobox protein Hox-epsilon14 (Hox-epsilon14) gene, partial cds; and homeobox protein Hox-epsilon13 (Hox-epsilon13) and homeobox protein Hox-epsilon11 (Hox-epsilon11) genes, complete cds, complete sequence	44.6	222	18%	2.2	89%	KF318004.1
Tetrapisipora phaffii CBS 4417 chromosome 13, complete genome	44.6	44.6	4%	2.2	81%	HE612868.1
Spirodela polyrhiza strain 7498 chloroplast, complete genome	44.6	44.6	5%	2.2	80%	JN160603.1
Vitis vinifera, whole genome shotgun sequence, contig V78X194258.16, clone ENTAV 115	44.6	44.6	3%	2.2	93%	AM468332.1

Mus musculus chromosome 8, clone RP24-460J16, complete sequence	44.6	44.6	10%	2.2	70%	AC119279.8
Mus musculus chromosome 8, clone RP23-240K12, complete sequence	44.6	44.6	10%	2.2	70%	AC113041.9
Pan troglodytes BAC clone RP43-32E8 from chromosome 7, complete sequence	44.6	44.6	13%	2.2	70%	AC146225.2
Mus musculus BAC clone RP24-249E21 from chromosome 10, complete sequence	44.6	44.6	10%	2.2	75%	AC126242.3
Mus musculus BAC clone RP23-354J3 from chromosome 13, complete sequence	44.6	44.6	4%	2.2	85%	AC123935.4
Homo sapiens chromosome 1 clone RP11-384B12, complete sequence	44.6	44.6	9%	2.2	73%	AC093155.2
Human DNA sequence from clone RP11-110K18 on chromosome 13q12.1-12.3, complete sequence	44.6	44.6	7%	2.2	74%	AL137119.26
Mus musculus 10 BAC RP23-9N9 (Roswell Park Cancer Institute (C57BL/6J Female) Mouse BAC Library) complete sequence	44.6	44.6	10%	2.2	75%	AC159137.8
Pan troglodytes chromosome 22 clone:RP43-164H01, map 22, complete sequences	44.6	44.6	11%	2.2	71%	BS000085.1
Mus musculus chromosome 3, clone RP24-108F9, complete sequence	44.6	44.6	4%	2.2	83%	AC114627.8
Mus musculus 10 BAC RP23-349H12 (Roswell Park Cancer Institute (C57BL/6J Female) Mouse BAC Library) complete sequence	44.6	89.1	4%	2.2	82%	AC153524.3
Mus musculus strain C57BL/6J chromosome 10 clone rp23-7p15, complete sequence	44.6	44.6	10%	2.2	75%	AC092856.26
Human chromosome 14 DNA sequence BAC C-2017C7 of library CalTech-D from chromosome 14 of Homo sapiens (Human), complete sequence	44.6	133	22%	2.2	74%	AL137779.6
Homo sapiens 12 BAC RP11-72J9 (Roswell Park Cancer Institute Human BAC Library) complete sequence	44.6	44.6	4%	2.2	85%	AC092470.9
Homo sapiens genomic DNA, chromosome 21q, section 30/105	44.6	44.6	11%	2.2	71%	AP001686.1
Homo sapiens genomic DNA, chromosome 21q21.1-q21.2, clone:B677J23, LL56-APP region, complete sequence	44.6	44.6	11%	2.2	71%	AP001116.1
Homo sapiens PAC clone RP5-1198O21 from Ch22, complete sequence	44.6	44.6	7%	2.2	74%	AC005233.2
Zebrafish DNA sequence from clone CH211-201C19 in linkage group 6, complete sequence	42.8	85.5	5%	7.6	93%	AL954307.8
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Fbxl21:tm1a(KOMP)Wtsi; transgenic	42.8	42.8	9%	7.6	74%	JN950715.1
Homo sapiens BAC clone ABC8-40885900H22 from chromosome x, complete sequence	42.8	85.5	7%	7.6	74%	AC243591.3
Pan troglodytes BAC clone CH251-67E21 from chromosome 16, complete sequence	42.8	42.8	5%	7.6	80%	AC241812.3
Homo sapiens FRAS1 related extracellular matrix 1 (FREM1), RefSeqGene on chromosome 9	42.8	42.8	11%	7.6	71%	NG_017005.2
Pirellula staleyi DSM 6068, complete genome	42.8	42.8	5%	7.6	84%	CP001848.1
Pan troglodytes BAC clone CH251-641E6 from chromosome 16, complete	42.8	42.8	5%	7.6	80%	AC193196.3

sequence						
Pongo abelii BAC clone CH276-161K21 from chromosome 21, complete sequence	42.8	42.8	6%	7.6	78%	AC200441.3
Trichomonas vaginalis G3 hypothetical protein (TVAG_472960) partial mRNA	42.8	42.8	4%	7.6	85%	XM_001316797.1
Gallus gallus BAC clone CH261-144P8 from chromosome z, complete sequence	42.8	42.8	2%	7.6	96%	AC192783.2
Gallus gallus BAC clone TAM31-62C15 from chromosome z, complete sequence	42.8	42.8	2%	7.6	96%	AC188691.2
Mus musculus chromosome 5, clone wi1-1993I8, complete sequence	42.8	42.8	6%	7.6	77%	AC175377.3
Mus musculus chromosome 7, clone RP23-21B1, complete sequence	42.8	42.8	3%	7.6	88%	AC116389.12
Mus musculus BAC clone RP24-75N14 from chromosome 17, complete sequence	42.8	42.8	3%	7.6	89%	AC165953.3
Mus musculus chromosome 13, clone RP24-282A18, complete sequence	42.8	42.8	9%	7.6	74%	AC132901.11
Mus musculus BAC clone RP24-269P22 from chromosome 8, complete sequence	42.8	42.8	4%	7.6	84%	AC129206.3
Homo sapiens Chromosome 16 BAC clone CIT987SK-A-952F10, complete sequence	42.8	42.8	6%	7.6	78%	AC004787.1
Mus musculus BAC clone RP23-49D1 from 8, complete sequence	42.8	42.8	4%	7.6	85%	AC122195.4
Mus musculus chromosome 5, clone RP23-408A1, complete sequence	42.8	42.8	6%	7.6	77%	AC122546.14
Homo sapiens chromosome 8, clone RP11-641K18, complete sequence	42.8	42.8	3%	7.6	87%	AC087627.10
Homo sapiens chromosome 8, clone RP11-6I2, complete sequence	42.8	42.8	3%	7.6	87%	AC087672.7
Homo sapiens 3 BAC RP11-495D2 (Roswell Park Cancer Institute Human BAC Library) complete sequence	42.8	85.5	8%	7.6	83%	AC119037.6
Homo sapiens 3 BAC RP11-130C13 (Roswell Park Cancer Institute Human BAC Library) complete sequence	42.8	85.5	8%	7.6	83%	AC117426.3
Human DNA sequence from clone RP11-374P20 on chromosome 9, complete sequence	42.8	42.8	7%	7.6	75%	AL445931.29
Human DNA sequence from clone RP11-430G6 on chromosome 1, complete sequence	42.8	42.8	6%	7.6	77%	AL583850.5
Human DNA sequence from clone RP11-476C9 on chromosome 9, complete sequence	42.8	42.8	11%	7.6	71%	AL354672.27
Homo sapiens BAC clone RP11-499E18 from 4, complete sequence	42.8	42.8	14%	7.6	70%	AC098487.1
Human DNA sequence from clone RP11-192B18 on chromosome Xq21.1-21.33, complete sequence	42.8	42.8	7%	7.6	73%	AL590229.3
Human DNA sequence from clone RP11-373O10 on chromosome 9, complete sequence	42.8	42.8	5%	7.6	80%	AL590381.4
Human DNA sequence from clone RP11-526K24 on chromosome 20, complete sequence	42.8	42.8	6%	7.6	78%	AL161659.17
Oryza sativa Japonica Group genomic DNA, chromosome 6, PAC clone:P0001H02	42.8	42.8	3%	7.6	91%	AP004234.3
Photorhabdus luminescens subsp. laumondii TTO1 complete genome; segment 7/17	42.8	42.8	3%	7.6	90%	BX571865.1
Homo sapiens chromosome 16 clone						

RP11-292B23, complete sequence	42.8	42.8	6%	7.6	78%	AC009058.10
Papio hamadryas, clone RP41-208E11, complete sequence	42.8	42.8	3%	7.6	86%	AC117539.6
Homo sapiens BAC clone RP11-167A8 from 4, complete sequence	42.8	42.8	18%	7.6	71%	AC104790.4
Mus musculus BAC clone RP23-391P1 from 3, complete sequence	42.8	42.8	7%	7.6	78%	AC147559.5
Mus musculus BAC clone RP23-328K6 from 8, complete sequence	42.8	42.8	4%	7.6	85%	AC144944.5
Mus musculus BAC clone RP23-311O15 from 7, complete sequence	42.8	42.8	6%	7.6	76%	AC132425.3
Mouse DNA sequence from clone RP23-68O14 on chromosome 2, complete sequence	42.8	42.8	4%	7.6	82%	AL929563.15
Homo sapiens genomic DNA, chromosome 11 clone:RP11-838I13, complete sequence	42.8	42.8	7%	7.6	74%	AP001591.5
Homo sapiens genomic DNA, chromosome 11 clone:RP11-697H9, complete sequence	42.8	42.8	7%	7.6	74%	AP000753.4
Mouse DNA sequence from clone RP23-14G21 on chromosome 5, complete sequence	42.8	42.8	6%	7.6	77%	AL591865.8
Genomic sequence from Human 9q34, complete sequence	42.8	42.8	7%	7.6	75%	AC002105.1
Human DNA sequence from clone XX-H2A1KLT on chromosome 9, complete sequence	42.8	42.8	7%	7.6	75%	Z81330.1

Alignments

Homo sapiens adenylate kinase 3 (AK3), RefSeqGene on chromosome 9

Sequence ID: [ref|NG_028041.1|](#) Length: 39488 Number of Matches: 2

Range 1: 33008 to 33052

Score	Expect	Identities	Gaps	Strand	Frame
51.8 bits(56)	0.015()	41/47(87%)	2/47(4%)	Plus/Plus	

Features:

```

Query   482      TATATGTGTAGGCTATATATGTGTAGTCGTTATATGTGTAGTCGTAT      528
          |||||
Sbjct   33008    TATATGTGTAG-CTGTATATGTGTAGGTGT-ATATGTGTAGGCGTAT      33052

```

Range 2: 32980 to 33052

Score	Expect	Identities	Gaps	Strand	Frame
50.0 bits(54)	0.051()	59/75(79%)	5/75(6%)	Plus/Plus	

Features:

```

Query   482      TATATGTGTAGGCTATATATGTGTAGTCGTTATATGTGTAGTCGTATCAGC-TACCT--A      538
          |||||
Sbjct   32980    TATATGTGTAGG-TGTATATGTGTAGATGT-ATATGTGTAGCTGTATATGTGTAGGTGTA      33037

Query   539      TATGTGTAGTCGTAT      553
          |||||
Sbjct   33038    TATGTGTAGGCGTAT      33052

```

Homo sapiens PAC clone RP5-959C21 from 7, complete sequence

Sequence ID: [gb|AC004936.2|](#) Length: 139949 Number of Matches: 1

Range 1: 82157 to 82249

Score	Expect	Identities	Gaps	Strand	Frame
51.8 bits(56)	0.015()	69/94(73%)	4/94(4%)	Plus/Minus	

Features:

```

Query   416      TATATATGTGTAGTTCTCTG---ATAGCTCTGCTATATATGTGTAGTCGTGAGAGTCTCT      472
          |||||
Sbjct   82249    TATATATGTGTATATATATGTGTATATATGTG-TATATATGTGTATATATGTGTGTATAT      82191

```

```
Query    473      CTCTGCCTATATAATGTGTAGGCTATATATGTGTA      506
          ||| ||| |
Sbjct   82190     CTATGTATATATATGTGTAATATATATATGTGTA      82157
```

Plasmodium knowlesi strain H chromosome 7, complete genome

Sequence ID: **emb|AM910989.1|** Length: 1496036 Number of Matches: 2

Range 1: 498635 to 498681

Score	Expect	Identities	Gaps	Strand	Frame
50.0 bits(54)	0.051()	42/50(84%)	4/50(8%)	Plus/Plus	

Features:

Query	480	TATATATGTGTAGGCTATATATGTGTAGTCGT-TATATGTGTAGTCGTAT	528
Sbjct	498635	TATATATCTGTAC---ATATATGTGTAGTCGTATATATATATAGTCGTAT	498681

Range 2: 498648 to 498681

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	31/34(91%)	1/34(2%)	Plus/Plus	

Features:

```

Query    644      ATATATGTGTAGTCGT-TATATGTGTAGTCGTAT      676
          |||      |||      |||      |||      |||      |||      |||      |||
Sbjct    498648    ATATATGTGTAGTCGTATATATATATAGTCGTAT      498681

```

Homo sapiens 3 BAC RP11-292E2 (Roswell Park Cancer Institute Human BAC Library) complete sequence

Sequence ID: **gb|AC078788.8|** Length: 166538 Number of Matches: 1

Range 1: 117896 to 117997

Score	Expect	Identities	Gaps	Strand	Frame
50.0 bits(54)	0.051()	79/108(73%)	8/108(7%)	Plus/Minus	

Features:

Query	416	TATATATGTGTAGTTCCTCTG-ATAGCTCTGC-TATATATGTGTAGTCGTGAGAGTCTCTC	473
Sbjct	117997	TATATATGTGTATATATATGTATATATGTGTGTATATATGTGTATATATGTGTGTATATA	117938
Query	474	TCTGCCTATATATGTGTAGGCTATATATGTGTAGTCGTTATATGTGTA	521
Sbjct	117937	TATGTATATATATGTGTGA---TATATATGTGT-GT--ATATATGTGTA	117896

Human DNA sequence from clone RP11-6J24 on chromosome 9p24.1-24.3, complete sequence

Sequence ID: **emb|AL136231.12|** Length: 160012 Number of Matches: 1

Range 1: 152922 to 152994

Score	Expect	Identities	Gaps	Strand	Frame
50.0 bits(54)	0.051()	59/75(79%)	5/75(6%)	Plus/Minus	

Features:

```

Query      482      TATATGTTGTAGGCTATATATGTGTAGTCGTTATATGTGTAGTCGTATCAGC-TACCT--A      538
Sbjct     152994    TATATGTTGTAGG-TGTATATGTGTAGATGT-ATATGTGTAGCTGTATATGTGTAGGTGTA      152937

Query      539      TATGTGTAGTCGTAT      553
Sbjct     152936    TATGTGTAGGCGTAT      152922

```

Homo sapiens 3 BAC RP11-147F23 (Roswell Park Cancer Institute Human BAC Library) complete sequence

Sequence ID: **gb|AC117421.6|** Length: 113840 Number of Matches: 1

Range 1: 81895 to 81996

Score	Expect	Identities	Gaps	Strand	Frame
50.0 bits(54)	0.051()	79/108(73%)	8/108(7%)	Plus/Plus	

Features:

```

Query   416      TATATATGTGTAGTTCTCTG-ATAGCTCTGC-TATATATGTGTAGTCGTGAGAGTCTCTC   473
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct   81895     TATATATGTGTATATATATGTATATATGTGTGTATATATGTGTATATATGTGTGTATATA   81954
Query   474      TCTGCCTATATATGTGTAGGCTATATATGTGTAGTCGTTATATGTGTA   521

```

Sbjct 81955 TATGTATATATATGTGTA---TATATATGTGT-GT---ATATATGTGTA 81996

Homo sapiens chromosome 5 clone RP11-32D16, complete sequence

Sequence ID: **gb|AC091939.3|** Length: 190346 Number of Matches: 2

Range 1: 153910 to 154010

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	77/107(72%)	8/107(7%)	Plus/Minus	

Features:

```
Query 416 TATATATGTGTAGTTCTCTG-ATAGCTCTGC-TATATATGTGTAGTCGTGAGAGTCTCTC 473
          |||
Sbjct 154010 TATATATGTGTATATATGTGTATATATATGTGTATATATGTGTATATATGTGTGTATATA 153951
          |||
Query 474 TCTGCCTATATATGTGTAGGCTATATATGTGTAGTCGTTATATGTGT 520
          |||
Sbjct 153950 TATGTGTATATATGTGTA---TATATATGTGTA---TATATATGTGT 153910
          |||
```

Range 2: 153967 to 154034

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	56/76(74%)	8/76(10%)	Plus/Minus	

Features:

```
Query 446 TATATATGTGTAGTCGTGAGAGTCTCTCTCTGCCTATATATGTGTAGGCTATATATGTGT 505
          |||
Sbjct 154034 TATATATGTGTATATATGTGTATATATATGTGTATATATGTGTA---TATATATGTGT 153978
          |||
Query 506 AGTCGTTATATGTGTA 521
          |||
Sbjct 153977 A-----TATATGTGTA 153967
          |||
```

Neospora caninum Liverpool complete genome, chromosome VIIa

Sequence ID: **emb|FR823388.1|** Length: 3947736 Number of Matches: 1

Range 1: 1420868 to 1420936

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	55/71(77%)	3/71(4%)	Plus/Minus	

Features:

conserved hypothetical protein

```
Query 247 TCTAGCTA-CTGTCTGAGCTAGCTTTCTATATATGTGTAGGCTATATATGTGTAGTCGTG 305
          |||
Sbjct 1420936 TCTATCTATCTCTCT-ATCTACCTGTCTATCTATGTGTAGGC-ATATGCATGCAGTTGTG 1420879
          |||
Query 306 AGAGTCTCTCT 316
          |||
Sbjct 1420878 CGAGTATCTCT 1420868
          |||
```

Pan troglodytes BAC clone CH251-503N9 from chromosome x, complete sequence

Sequence ID: **gb|AC192729.3|** Length: 185836 Number of Matches: 1

Range 1: 158626 to 158697

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	57/76(75%)	4/76(5%)	Plus/Plus	

Features:

```
Query 446 TATATATGTGTAGTCGTGAGAGTCTCTCTCTGCCTATATATGTGTAGGCTATATATGTGT 505
          |||
Sbjct 158626 TATATATGTGTATATATGTGTGTATATATATGTGTATATATGTGTA---TATATATGTGT 158682
          |||
Query 506 AGTCGTTATATGTGTA 521
          |||
Sbjct 158683 -GTATATATATGTGTA 158697
          |||
```

Mus musculus chromosome 3, clone RP23-111L16, complete sequence

Sequence ID: **gb|AC116671.14|** Length: 207768 Number of Matches: 1

Range 1: 27528 to 27579

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	44/54(81%)	2/54(3%)	Plus/Minus	

Features:

Query 468 TCTCTCTCTGCCTATATATGTGTAGGCTATATATGTGTAGTCGTTATATGTGTA 521
 Sbjct 27579 TCTCTCTCTCCATATATATGTGT-GTATATATATGTGT-GTATATATATATGTA 27528

Mus musculus chromosome 3, clone RP23-277D9, complete sequence

Sequence ID: **gb|AC166331.5|** Length: 187537 Number of Matches: 1

Range 1: 80764 to 80815

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	44/54(81%)	2/54(3%)	Plus/Plus	

Features:

Query 468 TCTCTCTCTGCCTATATATGTGTAGGCTATATATGTGTAGTCGTTATATGTGTA 521
 Sbjct 80764 TCTCTCTCTCCATATATATGTGT-GTATATATATGTGT-GTATATATATATGTA 80815

Homo sapiens 12q BAC RP11-29C9 (Roswell Park Cancer Institute Human BAC Library) complete sequence

Sequence ID: **gb|AC108360.3|** Length: 157546 Number of Matches: 1

Range 1: 70034 to 70079

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	43/54(80%)	8/54(14%)	Plus/Minus	

Features:

Query 468 TCTCTCTCTGCCTATATATGTGTAGGCTATATATGTGTAGTCGTTATATGTGTA 521
 Sbjct 70079 TCTCTCTCTATATATATATGTGTA---TATATATGTGTA-----TATATGTGTA 70034

Homo sapiens 3 BAC RP11-73N1 (Roswell Park Cancer Institute Human BAC Library) complete sequence

Sequence ID: **gb|AC008082.12|** Length: 171619 Number of Matches: 1

Range 1: 137143 to 137214

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	59/76(78%)	4/76(5%)	Plus/Minus	

Features:

Query 352 TATAGTAGATGCGTATATGTGTAGTCGTATCAGCTACCTATATGTGTAGTCGTATCAGCT 411
 Sbjct 137214 TATA-TATATACGTATATGTGTATACGTAT-ATATACGTATATATGTATACGTAT-ATAT 137158
 Query 412 ACCCTATATATGTGTA 427
 Sbjct 137157 A-CGTATATATGTGTA 137143

Homo sapiens zinc finger, MYM-type 2 (ZMYM2), RefSeqGene on chromosome 13

Sequence ID: **ref|NG_023348.2|** Length: 140176 Number of Matches: 1

Range 1: 92907 to 92976

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	56/76(74%)	6/76(7%)	Plus/Plus	

Features:

Query 446 TATATATGTGTAGTCGTGAGAGTCTCTCTCTGCCTATATATGTGTAGGCTATATATGTGT 505
 Sbjct 92907 TATATATGTGTGTGTGTGTGTGTGTGTGTGTGTATATATATGTGTA---TATATATGTGT 92963
 Query 506 AGTCGTTATATGTGTA 521
 Sbjct 92964 A---TATATATGTGTA 92976

Staphylococcus phage 6ec, complete genome

Sequence ID: **gb|KJ804259.1|** Length: 93794 Number of Matches: 2

Range 1: 92761 to 92789

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

Features:

Query 271 TCTATATATGTGTAGGCTATATATGTGTA 299
 |||||
 Sbjct 92761 TCTATATATGTGTATGCTATATATGTGTGTA 92789

Range 2: 92762 to 92789

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

Features:

Query 479 CTATATATGTGTAGGCTATATATGTGTA 506
 |||||
 Sbjct 92762 CTATATATGTGTATGCTATATATGTGTGTA 92789

PREDICTED: Rattus norvegicus protein tyrosine phosphatase-like (proline instead of catalytic arginine), member a (Ptpla), transcript variant X4, mRNA

Sequence ID: **ref|XM_006254295.1|** Length: 2923 Number of Matches: 1
 Range 1: 2253 to 2439

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	138/208(66%)	33/208(15%)	Plus/Plus	

Features:

Query 479 CTATATATGTGTAGG----CTATATATGTGTAGTCGTTATATGTGTAGTCGTATCAGCTA 534
 |||||
 Sbjct 2253 CTATATGTGTGTAGTAGTCTCTATATGTGTAGTAGTCCCTGTGT----TTAGTAGTTC 2308
 Query 535 CCTATATGTGTAGTCGTATCAGCTACCCTATATATGT-GTAGTTCTCT-----GATAGCT 588
 |||||
 Sbjct 2309 TCTATATGTGTAGTAG-----TTCTCTATGTGTGTAGTAGTTCTCTATGTGTGTAGTA 2361
 Query 589 CTGCTATATATGTGTAGTCGTGAGAGTCTCTCTCTGCTTCTCTGATAGCTCTGCTATATA 648
 |||||
 Sbjct 2362 GTTCTCTATGTGTGTAGTAGT-----TCTCTATG--TGTGTAGTAGTTCT-CTATGTG 2411
 Query 649 TGT-GTAG-TCGTTATATGTGTAGTCGT 674
 |||||
 Sbjct 2412 TGTAGTAGTTCTTTATATGTGTAGTAGT 2439

PREDICTED: Rattus norvegicus protein tyrosine phosphatase-like (proline instead of catalytic arginine), member a (Ptpla), transcript variant X3, mRNA

Sequence ID: **ref|XM_006254294.1|** Length: 2775 Number of Matches: 1
 Range 1: 2110 to 2296

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	138/208(66%)	33/208(15%)	Plus/Plus	

Features:

Query 479 CTATATATGTGTAGG----CTATATATGTGTAGTCGTTATATGTGTAGTCGTATCAGCTA 534
 |||||
 Sbjct 2110 CTATATGTGTGTAGTAGTCTCTATATGTGTAGTAGTCCCTGTGT----TTAGTAGTTC 2165
 Query 535 CCTATATGTGTAGTCGTATCAGCTACCCTATATATGT-GTAGTTCTCT-----GATAGCT 588
 |||||
 Sbjct 2166 TCTATATGTGTAGTAG-----TTCTCTATGTGTGTAGTAGTTCTCTATGTGTGTAGTA 2218
 Query 589 CTGCTATATATGTGTAGTCGTGAGAGTCTCTCTCTGCTTCTCTGATAGCTCTGCTATATA 648
 |||||
 Sbjct 2219 GTTCTCTATGTGTGTAGTAGT-----TCTCTATG--TGTGTAGTAGTTCT-CTATGTG 2268
 Query 649 TGT-GTAG-TCGTTATATGTGTAGTCGT 674
 |||||
 Sbjct 2269 TGTAGTAGTTCTTTATATGTGTAGTAGT 2296

Lethenteron camtschaticum clone BAC 424C19, BAC 204J11 homeobox protein Hox-epsilon14 (Hox-epsilon14) gene, partial cds; and homeobox protein Hox-epsilon13 (Hox-epsilon13) and homeobox protein Hox-epsilon11 (Hox-epsilon11) genes, complete cds, complete sequence

Sequence ID: **gb|KF318004.1|** Length: 154930 Number of Matches: 5
 Range 1: 27861 to 27895

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	32/36(89%)	1/36(2%)	Plus/Minus	

Features:

Query 899 TCTGCTATATATGTGTAGTCGTGAGAGTCTCTCTCT 934
 |||||
 Sbjct 27895 TCTGCTCTATATGTGTAGT-GTGCGTGTCTCTCTCT 27861

Range 2: 27861 to 27895

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	32/36(89%)	1/36(2%)	Plus/Minus	
Features:					
Query	801	TCTGCTATATATGTGTAGTCGTGAGAGTCTCTCTCT	836		
Sbjct	27895	TCTGCTCTATATGTGTAGT-GTGCGTGTCTCTCTCT	27861		

Range 3: 27861 to 27895

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	32/36(89%)	1/36(2%)	Plus/Minus	
Features:					
Query	711	TCTGCTATATATGTGTAGTCGTGAGAGTCTCTCTCT	746		
Sbjct	27895	TCTGCTCTATATGTGTAGT-GTGCGTGTCTCTCTCT	27861		

Range 4: 27861 to 27895

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	32/36(89%)	1/36(2%)	Plus/Minus	
Features:					
Query	588	TCTGCTATATATGTGTAGTCGTGAGAGTCTCTCTCT	623		
Sbjct	27895	TCTGCTCTATATGTGTAGT-GTGCGTGTCTCTCTCT	27861		

Range 5: 27861 to 27895

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	32/36(89%)	1/36(2%)	Plus/Minus	
Features:					
Query	441	TCTGCTATATATGTGTAGTCGTGAGAGTCTCTCTCT	476		
Sbjct	27895	TCTGCTCTATATGTGTAGT-GTGCGTGTCTCTCTCT	27861		

Tetrapispora phaffii CBS 4417 chromosome 13, complete genome

Sequence ID: **emb|HE612868.1|** Length: 452480 Number of Matches: 1

Range 1: 345883 to 345929

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	38/47(81%)	4/47(8%)	Plus/Minus	
Features:					
Query	458	GTCGTGAGAGTCTCTCTCTGCCTATATATGTG----TAGGCTATATA	500		
Sbjct	345929	GTTGTGAGAGTCTCTCTATCCATATATATGTGTATTGGCTATATA	345883		

Spirodela polyrhiza strain 7498 chloroplast, complete genome

Sequence ID: **gb|JN160603.1|** Length: 168788 Number of Matches: 1

Range 1: 33725 to 33771

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	40/50(80%)	3/50(6%)	Plus/Plus	
Features:					
Query	480	TATATATGTGTAGGCTATATATGTGTAGTCGTTATATGTGTAGTCGTATC	529		
Sbjct	33725	TATATATATATA---TATATATATGTACTCCTTATATGTGTACTCCTATC	33771		

Vitis vinifera, whole genome shotgun sequence, contig VV78X194258.16, clone ENTAV 115

Sequence ID: **emb|AM468332.1|** Length: 19730 Number of Matches: 1

Range 1: 11691 to 11719

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

Features:

```

Query   863      GTGTAGTCGTCTATATATGTGTAGTTCTC   891
          |||
Sbjct   11719   GTGTAGTCGTCAATATATGTTTAGTTCTC   11691

```

Mus musculus chromosome 8, clone RP24-460J16, complete sequence

Sequence ID: **gb|AC119279.8|** Length: 139356 Number of Matches: 1

Range 1: 94300 to 94403

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	78/111(70%)	17/111(15%)	Plus/Plus	

Features:

```

Query   446      TATATATGTGTAGTCGTGAGAGTCTCTCTGCCTATATATGTGT-----AGGCTATA   498
          |||
Sbjct   94300   TATATATGTGT-GT-GTGTGTGTCTATGTATGTATATATATGTGTGTATGTGTGTCTATA   94357

Query   499      TATGTGTAGTCGTTATATGTGTAGTCGTATCAG---CTACCTATATGTGTA   546
          |||
Sbjct   94358   TATGTGTA-----TATATGTGTATGTGTATCTGTGTATATATATATGTGTA   94403

```

Mus musculus chromosome 8, clone RP23-240K12, complete sequence

Sequence ID: **gb|AC113041.9|** Length: 175827 Number of Matches: 1

Range 1: 1326 to 1429

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	78/111(70%)	17/111(15%)	Plus/Plus	

Features:

```

Query   446      TATATATGTGTAGTCGTGAGAGTCTCTCTGCCTATATATGTGT-----AGGCTATA   498
          |||
Sbjct   1326   TATATATGTGT-GT-GTGTGTGTCTATGTATGTATATATATGTGTGTATGTGTGTCTATA   1383

Query   499      TATGTGTAGTCGTTATATGTGTAGTCGTATCAG---CTACCTATATGTGTA   546
          |||
Sbjct   1384   TATGTGTA-----TATATGTGTATGTGTATCTGTGTATATATATATGTGTA   1429

```

Pan troglodytes BAC clone RP43-32E8 from chromosome 7, complete sequence

Sequence ID: **gb|AC146225.2|** Length: 171272 Number of Matches: 1

Range 1: 27464 to 27591

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	93/132(70%)	5/132(3%)	Plus/Plus	

Features:

```

Query   416      TATATATGTGTAGTTCTCTGATAGCTCTGCTATATATGTGTAGTCGTGAGAGTCTCTCTC   475
          |||
Sbjct   27464   TATATATGTGTATATATGTG-TATATGTG-TATATATGTATATATGTGTGTGTATATATA   27521

Query   476      TGCCTATATATGTGTAGGCTATATATGTGTAGTCGT-TATATGTGTAGTCGTATCAGCTA   534
          |||
Sbjct   27522   TGTATATATATGTGTGTGC-ATATATGTATATATGTGTATATATGTATATGTGT-ATATA   27579

Query   535      CCTATATGTGTA   546
          |||
Sbjct   27580   TGTATATGTGTA   27591

```

Mus musculus BAC clone RP24-249E21 from chromosome 10, complete sequence

Sequence ID: **gb|AC126242.3|** Length: 177581 Number of Matches: 1

Range 1: 149943 to 150031

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	74/99(75%)	11/99(11%)	Plus/Plus	

Features:

```

Query   448      TATATGTGTAGTCGTGAGAGTCTCTCTGCCTATATATGTGTAGGCTATATATGTGTAG   507
          |||
Sbjct   149943   TATATGTCT-GT-GTGTGTGTCTCTCTCTGGGTATATATGTG-----TATATATGTCTAG   149995

Query   508      TCGT-TATATGTGTAGTCGTATCAGCTACCTATATGTGT   545
          |||

```

Sbjct 149996 GTGTGTGTCTGTGT-GT-GTAT-ATGTATCTATGTGTGT 150031

Mus musculus BAC clone RP23-354J3 from chromosome 13, complete sequence

Sequence ID: **gb|AC123935.4|** Length: 219370 Number of Matches: 1

Range 1: 81932 to 81970

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

Features:

```
Query 468 TCTCTCTCTGCCTATATATGTGTAGGCTATATATGTGTA 506
          |||||
Sbjct 81932 TCTCTCTCTATATATATATATATATGCTATATATGTGTA 81970
```

Homo sapiens chromosome 1 clone RP11-384B12, complete sequence

Sequence ID: **gb|AC093155.2|** Length: 189760 Number of Matches: 1

Range 1: 43165 to 43253

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	67/92(73%)	5/92(5%)	Plus/Minus	

Features:

```
Query 416 TATATATGTGTAGTTCTCTG-ATAGCTCTGC-TATATATGTGTAGTCGTGAGAGTCTCTC 473
          |||||
Sbjct 43253 TATATATGTGTATATATGTGTATATATGTGTGTATATATGTGTATATATGTGTATATA 43194

Query 474 TCTGCCTATATATGTGTAGGCTATATATGTGT 505
          |||||
Sbjct 43193 TGTGTATATATATGTGTA---TATATATGTGT 43165
```

Human DNA sequence from clone RP11-110K18 on chromosome 13q12.1-12.3, complete sequence

Sequence ID: **emb|AL137119.26|** Length: 142494 Number of Matches: 1

Range 1: 114504 to 114573

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	56/76(74%)	6/76(7%)	Plus/Plus	

Features:

```
Query 446 TATATATGTGTAGTCGTGAGAGTCTCTCTCTGCCTATATATGTGTAGGCTATATATGTGT 505
          |||||
Sbjct 114504 TATATATGTGTGTGTGTGTGTGTGTGTGTGTATATATATGTGTA---TATATATGTGT 114560

Query 506 AGTCGTTATATGTGTA 521
          |||||
Sbjct 114561 A---TATATATGTGTA 114573
```

Mus musculus 10 BAC RP23-9N9 (Roswell Park Cancer Institute (C57BL/6J Female) Mouse BAC Library) complete sequence

Sequence ID: **gb|AC159137.8|** Length: 207728 Number of Matches: 1

Range 1: 15929 to 16017

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	74/99(75%)	11/99(11%)	Plus/Plus	

Features:

```
Query 448 TATATGTGTAGTCGTGAGAGTCTCTCTCTGCCTATATATGTGTAGGCTATATATGTGTAG 507
          |||||
Sbjct 15929 TATATGTCT-GT-GTGTGTGTCTCTCTCTGGGTATATATGTG-----TATATATGTCTAG 15981

Query 508 TCGT-TATATGTGTAGTCGTATCAGCTACCTATATGTGT 545
          |||||
Sbjct 15982 GTGTGTGTCTGTGT-GT-GTAT-ATGTATCTATGTGTGT 16017
```

Pan troglodytes chromosome 22 clone:RP43-164H01, map 22, complete sequences

Sequence ID: **dbj|BS000085.1|** Length: 171357 Number of Matches: 1

Range 1: 129666 to 129775

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	79/111(71%)	6/111(5%)	Plus/Plus	

Features:

Query 416 TATATATGTGTAGTTCTCTG-ATAGCTCTGC---TATATATGTGTAGTCGTGAGAGTCTC 471
 |||||
 Sbjct 129666 TATATATGTGTATATGTGTGTATATATGTGTATATCTATATGTGTATATATGTGTATATC 129725
 |||||
 Query 472 TCTCTGCCTATATATGTGTA-GGCTATATATGTGTAGTCGTTATATGTGTA 521
 |||||
 Sbjct 129726 TTTATGTGTATATATGTGTATTGATATATGTGTGTA-TAGCTATATGTGTA 129775
 |||||

Mus musculus chromosome 3, clone RP24-108F9, complete sequence

Sequence ID: **gb|AC114627.8|** Length: 152152 Number of Matches: 1

Range 1: 75693 to 75734

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

Features:

Query 461 GTGAGAGTCTCTCTCTGCCTATATATGTGTAGGCTATATATG 502
 |||||
 Sbjct 75693 GTGTGAGTCTCTCTCTGCATATATGTGTGCAGGGTGCATATG 75734
 |||||

Mus musculus 10 BAC RP23-349H12 (Roswell Park Cancer Institute (C57BL/6J Female) Mouse BAC Library) complete sequence

Sequence ID: **gb|AC153524.3|** Length: 167574 Number of Matches: 2

Range 1: 120992 to 121035

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	36/44(82%)	0/44(0%)	Plus/Minus	

Features:

Query 480 TATATATGTGTAGGCTATATATGTGTAGTCGTTATATGTGTAGT 523
 |||||
 Sbjct 121035 TATATGTGTATAGTGTATGTATGTGTAGTATGTATATGTGTAGT 120992
 |||||

Range 2: 121047 to 121090

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	36/44(82%)	0/44(0%)	Plus/Minus	

Features:

Query 480 TATATATGTGTAGGCTATATATGTGTAGTCGTTATATGTGTAGT 523
 |||||
 Sbjct 121090 TATATGTGTATAGTGTATGTATGTGTAGTATGTATATGTGTAGT 121047
 |||||

Mus musculus strain C57BL/6J chromosome 10 clone rp23-7p15, complete sequence

Sequence ID: **gb|AC092856.26|** Length: 221799 Number of Matches: 1

Range 1: 52987 to 53075

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	74/99(75%)	11/99(11%)	Plus/Minus	

Features:

Query 448 TATATGTGTAGTCGTGAGAGTCTCTCTCTGCCTATATATGTGTAGGCTATATATGTGTAG 507
 |||||
 Sbjct 53075 TATATGTCT-GT-GTGTGTGTCTCTCTCTGGGTATATATGTG-----TATATATGTCTAG 53023
 |||||
 Query 508 TCGT-TATATGTGTAGTCGTATCAGCTACCTATATGTGT 545
 |||||
 Sbjct 53022 GTGTGTGTCTGTGT-GT-GTAT-ATGTATCTATGTGTGT 52987
 |||||

Human chromosome 14 DNA sequence BAC C-2017C7 of library CalTech-D from chromosome 14 of Homo sapiens (Human), complete sequence

Sequence ID: **emb|AL137779.6|** Length: 189116 Number of Matches: 3

Range 1: 154187 to 154279

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	73/98(74%)	7/98(7%)	Plus/Minus	

Features:

Query 478 CCTATATATGTGTAGGCTATATATGTGTAGTCGTTATATGTGTAGTCGTATCAGCTA-CC 536
 |||||
 Sbjct 154279 CCTATATATGTGTGCCTATATA--TATACCTATATATGTGTCTCCT-ATAT-ATATACCC 154224
 |||||

Query 537 TATATGTGTAGTCGTAT-CAGCTACCCTATATATGTGT 573
 Sbjct 154223 TATATATGT-GTCCATATATATATACCCTATATATGTGT 154187

Range 2: 154239 to 154325

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	71/93(76%)	7/93(7%)	Plus/Minus	

Features:

Query 512 TATATGTGTAGTCGTATCAGCTACC-TATATGTGTAGTCGTATCAGCTACCCTATATATG 570
 Sbjct 154325 TATATATGT-GTCCAT-ATATACCCTATATATGT-GTCCTAT-ATATACCCTATATATG 154270
 Query 571 TGTAGTTCTCTGATAGCTCTGCTATATATGTGT 603
 Sbjct 154269 TGT-GTCCAT-ATATATACCCTATATATGTGT 154239

Range 3: 154239 to 154325

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	71/93(76%)	7/93(7%)	Plus/Minus	

Features:

Query 365 TATATGTGTAGTCGTATCAGCTACC-TATATGTGTAGTCGTATCAGCTACCCTATATATG 423
 Sbjct 154325 TATATATGT-GTCCAT-ATATACCCTATATATGT-GTCCTAT-ATATACCCTATATATG 154270
 Query 424 TGTAGTTCTCTGATAGCTCTGCTATATATGTGT 456
 Sbjct 154269 TGT-GTCCAT-ATATATACCCTATATATGTGT 154239

Homo sapiens 12 BAC RP11-72J9 (Roswell Park Cancer Institute Human BAC Library) complete sequence

Sequence ID: **gb|AC092470.9|** Length: 96100 Number of Matches: 1

Range 1: 6807 to 6846

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	35/41(85%)	1/41(2%)	Plus/Minus	

Features:

Query 481 ATATATGTGTAGGCTATATATGTGTAGTCGTTATATGTGTA 521
 Sbjct 6846 ATATATGTGTAGACTATATATGTAT-GTACATATATGTGTA 6807

Homo sapiens genomic DNA, chromosome 21q, section 30/105

Sequence ID: **dbj|AP001686.1|** Length: 340000 Number of Matches: 1

Range 1: 223916 to 224025

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	79/111(71%)	6/111(5%)	Plus/Plus	

Features:

Query 416 TATATATGTGTAGTTCTCTG-ATAGCTCTGC---TATATATGTGTAGTCGTGAGAGTCTC 471
 Sbjct 223916 TATATATGTGTATATGTGTGTATATATGTGTATATCTATATGTGTATATATGTGTATATC 223975
 Query 472 TCTCTGCCTATATATGTGTA-GGCTATATATGTGTAGTCGTTATATGTGTA 521
 Sbjct 223976 TTTATGTGTATATATGTGTATTGATATATGTGTGTA-TAGCTATATGTGTA 224025

Homo sapiens genomic DNA, chromosome 21q21.1-q21.2, clone:B677J23, LL56-APP region, complete sequence

Sequence ID: **dbj|AP001116.1|** Length: 93290 Number of Matches: 1

Range 1: 81958 to 82067

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	79/111(71%)	6/111(5%)	Plus/Plus	

Features:

Query 416 TATATATGTGTAGTTCTCTG-ATAGCTCTGC---TATATATGTGTAGTCGTGAGAGTCTC 471
 Sbjct 81958 TATATATGTGTATATGTGTGTATATATGTGTATATCTATATGTGTATATATGTGTATATC 82017
 Query 472 TCTCTGCCTATATATGTGTA-GGCTATATATGTGTAGTCGTTATATGTGTA 521
 Sbjct 82018 TTTATGTGTATATATGTGTATTGATATATGTGTGTA-TAGCTATATGTGTA 82067

Sequence ID: **gb|AC005233.2|AC005233** Length: 64359 Number of Matches: 1
Range 1: 25739 to 25808

Query	446	TATATA	GTGTAG	TCGTGAG	AGTCTCTCTCTG	CCATATAT	GTGTAGG	CTATATAT	GTGT	505
Sbjct	13854	TATATA	GTGTATAT	GTGTGTATAT	GTATATGTATATATAT	GTGT	-GTATATATAT	GTGT		13796
Query	506	AGTCGTTATATGTGTA	521							
Sbjct	13795	A---	TATATATGTGTA	13783						

Range 2: 13843 to 13914

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	56/76(74%)	4/76(5%)	Plus/Minus	
Features:					
Query	446	TATATATGTGTAGTCGTGAGAGTCTCTCTCGCCTATATATGTGTAGGCTATATATGTGT	505		
Sbjct	13914	TATATATGTGTATATGTGTATATGTATATGTATATATATATGTGT-GTATATATATGTGT	13856		
Query	506	AGTCGTTATATGTGTA	521		
Sbjct	13855	A---TATATATGTGTA	13843		

Pan troglodytes BAC clone CH251-67E21 from chromosome 16, complete sequence

Sequence ID: **gb|AC241812.3|** Length: 174880 Number of Matches: 1

Range 1: 132067 to 132120

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	45/56(80%)	4/56(7%)	Plus/Minus	
Features:					
Query	468	TCTCTCTCTGCCT--ATATATGTGTAGGCTATATATGTGTAGTCGTTATATGTGTA	521		
Sbjct	132120	TCTCTCTCTGTCTCTATATATGTGTA-AATATATATATGT-GTAAATATATGTGTA	132067		

Homo sapiens FRAS1 related extracellular matrix 1 (FREM1), RefSeqGene on chromosome 9

Sequence ID: **ref|NG_017005.2|** Length: 182571 Number of Matches: 1

Range 1: 54430 to 54521

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	75/106(71%)	14/106(13%)	Plus/Plus	
Features:					
Query	416	TATATATGTGTAGTTCTCTGATAGCTCTGCTATATATGTGTAGTCGTGAGAGTCTCTCTC	475		
Sbjct	54430	TATATATGTGTATATATGT-ATA--TATG-TATATATGTGTATATATGTGCATATATATG	54485		
Query	476	TGCCTATATATGTGTAGGCTATATATGTGTAGTCGTTATATGTGTA	521		
Sbjct	54486	TGCATATATATGTG-----TATATATGTGTA-----TATATGTGTA	54521		

Pirellula staleyi DSM 6068, complete genome

Sequence ID: **gb|CP001848.1|** Length: 6196199 Number of Matches: 1

Range 1: 5481869 to 5481915

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	41/49(84%)	3/49(6%)	Plus/Minus	
Features: phospholipid/glycerol acyltransferase					
Query	135	TCGATCGATCGATCTA-TGCATCGACTGCATCATACTCGAGCCCGCGCG	182		
Sbjct	5481915	TCGATCGA-CGATCTGCTGCAT-GAGGGGATCGTACTCGAGCCCGCGCG	5481869		

Pan troglodytes BAC clone CH251-641E6 from chromosome 16, complete sequence

Sequence ID: **gb|AC193196.3|** Length: 211576 Number of Matches: 1

Range 1: 43847 to 43900

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	45/56(80%)	4/56(7%)	Plus/Minus	
Features:					
Query	468	TCTCTCTCTGCCT--ATATATGTGTAGGCTATATATGTGTAGTCGTTATATGTGTA	521		
Sbjct	43900	TCTCTCTCTGTCTCTATATATGTGTA-AATATATATATGT-GTAAATATATGTGTA	43847		

Pongo abelii BAC clone CH276-161K21 from chromosome 21, complete sequence

Sequence ID: **gb|AC200441.3|** Length: 210028 Number of Matches: 1
Range 1: 139584 to 139641

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	47/60(78%)	2/60(3%)	Plus/Minus	

Features:

```
Query   856      TATATATGTGTAGTCGTCCTATATATGTGTAGTTCTCTGATAGCTCTGCTATATATGTGTA   915
          |||
Sbjct   139641  TATATATGTGTATGTGTGTATATATGTGTATATATGTG-TATATGTG-TATATATGTGTA   139584
```

Trichomonas vaginalis G3 hypothetical protein (TVAG_472960) partial mRNA

Sequence ID: **ref|XM_001316797.1|** Length: 963 Number of Matches: 1
Range 1: 786 to 824

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

Features:

```
Query   629      TCTGATAGCTCTGCTATATATGTGTAGTCGTTATATGTGT   668
          |||
Sbjct   786      TCTGATAGCTCTGATAT-TATTTGTTGTTCTTATATGTGT   824
```

Gallus gallus BAC clone CH261-144P8 from chromosome z, complete sequence

Sequence ID: **gb|AC192783.2|** Length: 212002 Number of Matches: 1
Range 1: 64345 to 64370

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

Features:

```
Query   474      TCTGCCTATATATGTGTAGGCTATAT   499
          |||
Sbjct   64345  TCTGCCTTATATATGTGTAGGCTATAT   64370
```

Gallus gallus BAC clone TAM31-62C15 from chromosome z, complete sequence

Sequence ID: **gb|AC188691.2|** Length: 168286 Number of Matches: 1
Range 1: 153279 to 153304

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

Features:

```
Query   474      TCTGCCTATATATGTGTAGGCTATAT   499
          |||
Sbjct   153279  TCTGCCTTATATATGTGTAGGCTATAT   153304
```

Mus musculus chromosome 5, clone wi1-1993I8, complete sequence

Sequence ID: **gb|AC175377.3|** Length: 38230 Number of Matches: 1
Range 1: 33461 to 33520

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	46/60(77%)	1/60(1%)	Plus/Minus	

Features:

```
Query   856      TATATATGTGTAGTCGTCCTATATATGTGTAGT-TCTCTGATAGCTCTGCTATATATGTGT   914
          |||
Sbjct   33520  TATATATGTGTGTATGTATATATGTGTGTGATGTGTGATATATATGCTATATATGTGT   33461
```

Mus musculus chromosome 7, clone RP23-21B1, complete sequence

Sequence ID: **gb|AC116389.12|** Length: 236139 Number of Matches: 1
Range 1: 179584 to 179616

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

Features:

Query 238 AGTAGCTCGTCTAGCTACTGTCTGAGCTAGCTT 270
 |||||
 Sbjct 179584 AGCAGCTCCTCTAGCTGCTGGCTGAGCTAGCTT 179616

Mus musculus BAC clone RP24-75N14 from chromosome 17, complete sequence
 Sequence ID: **gb|AC165953.3|** Length: 224622 Number of Matches: 1
 Range 1: 148326 to 148359

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

Features:

Query 472 TCTCTGCCCTATATATGTGTAGGCTATATATGTGTA 506
 |||||
 Sbjct 148326 TCTCTGTATATATATGTGTATG-TATATATGTGTA 148359

Mus musculus chromosome 13, clone RP24-282A18, complete sequence
 Sequence ID: **gb|AC132901.11|** Length: 187090 Number of Matches: 1
 Range 1: 91580 to 91667

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	69/93(74%)	5/93(5%)	Plus/Minus	

Features:

Query 416 TATATATGTGTAGTTCTCTGATAGCTCTGCTATATATGTGTAGTCGTGAGAGTCTCTCTC 475
 |||||
 Sbjct 91667 TATGTATGTGT-GTT-TATG-TATCTGTG-TATATATGTGTATATGTGAGTATATGTATG 91612
 Query 476 TGCCTATATATGTGTAGGCTATATATGTGTAGT 508
 |||||
 Sbjct 91611 TGTGTACATATGTGTATG-TATGTATGTGTTGT 91580

Mus musculus BAC clone RP24-269P22 from chromosome 8, complete sequence
 Sequence ID: **gb|AC129206.3|** Length: 181214 Number of Matches: 1
 Range 1: 144635 to 144678

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	37/44(84%)	3/44(6%)	Plus/Minus	

Features:

Query 481 ATATATGTGTAGGC--TATATATGTGTAGTCGT-TATATGTGTA 521
 |||||
 Sbjct 144678 ATATATGTGTATGCAATATATATGTGTATATGTATATATGTGTA 144635

Homo sapiens Chromosome 16 BAC clone CIT987SK-A-952F10, complete sequence
 Sequence ID: **gb|AC004787.1|HUAC004787** Length: 216021 Number of Matches: 1
 Range 1: 81264 to 81322

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	47/60(78%)	2/60(3%)	Plus/Minus	

Features:

Query 856 TATATATGTGTAGTCGTCTATATATGTGTAGTTCTCTG-ATAGCTCTGCTATATATGTGT 914
 |||||
 Sbjct 81322 TATATATGTGTATATGTATATATATGTGTATATATGTATATGTGTG-TATATATGTGT 81264

Mus musculus BAC clone RP23-49D1 from 8, complete sequence
 Sequence ID: **gb|AC122195.4|** Length: 204335 Number of Matches: 1
 Range 1: 104989 to 105027

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

Features:

Query 482 TATATGTGTAGGCTATATATGTGTAGTCGTTATATGTGTA 521
 |||||
 Sbjct 105027 TATATGTGTATGATATATATGTGTATTTG-TATGTGTGTA 104989

Mus musculus chromosome 5, clone RP23-408A1, complete sequence
Sequence ID: **gb|AC122546.14|** Length: 191640 Number of Matches: 1
Range 1: 184548 to 184607

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	46/60(77%)	1/60(1%)	Plus/Plus	

Features:

```

Query   856      TATATATGTGTAGTCGTCTATATATGTGTAGT-TCTCTGATAGCTCTGCTATATATGTGT   914
          |||
Sbjct   184548  TATATATGTGTGTATGTATATATGTGTGTGATATGTGTGATATATATGCTATATATGTGT   184607

```

Homo sapiens chromosome 8, clone RP11-641K18, complete sequence
Sequence ID: **gb|AC087627.10|** Length: 170211 Number of Matches: 1
Range 1: 114819 to 114855

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

Features:

```

Query   851      TCTGCTATATATGTGTAGTCGTCTATATATGTGTAGTT   888
          |||
Sbjct   114855  TCTGGTATATATGTGTA-TCGTCAATATATGTCTATTT   114819

```

Homo sapiens chromosome 8, clone RP11-612, complete sequence
Sequence ID: **gb|AC087672.7|** Length: 152061 Number of Matches: 1
Range 1: 112484 to 112520

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

Features:

```

Query   851      TCTGCTATATATGTGTAGTCGTCTATATATGTGTAGTT   888
          |||
Sbjct   112484  TCTGGTATATATGTGTA-TCGTCAATATATGTCTATTT   112520

```

Homo sapiens 3 BAC RP11-495D2 (Roswell Park Cancer Institute Human BAC Library) complete sequence
Sequence ID: **gb|AC119037.6|** Length: 200182 Number of Matches: 2
Range 1: 110555 to 110596

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/42(83%)	2/42(4%)	Plus/Minus	

Features:

```

Query   821      GTGAGAGTCTCTCTCTGCTTCTCTGATAGCTC--TGCTATAT   860
          |||
Sbjct   110596  GTGAGAGTTTCTCTCTGCTTCTAAGATAGCACCTTGATATAT   110555

```

Range 2: 110555 to 110596

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/42(83%)	2/42(4%)	Plus/Minus	

Features:

```

Query   608      GTGAGAGTCTCTCTCTGCTTCTCTGATAGCTC--TGCTATAT   647
          |||
Sbjct   110596  GTGAGAGTTTCTCTCTGCTTCTAAGATAGCACCTTGATATAT   110555

```

Homo sapiens 3 BAC RP11-130C13 (Roswell Park Cancer Institute Human BAC Library) complete sequence
Sequence ID: **gb|AC117426.3|** Length: 150601 Number of Matches: 2
Range 1: 135686 to 135727

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/42(83%)	2/42(4%)	Plus/Plus	

Features:

Query 608 GTGAGAGTCTCTCTCTGCTTCTCTGATAGCTC--TGCTATAT 647
 |||||
 Sbjct 135686 GTGAGAGTTTCTCTCTGCTTCTAAGATAGCACCTTGATATAT 135727

Range 2: 135686 to 135727

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/42(83%)	2/42(4%)	Plus/Plus	

Features:

Query 821 GTGAGAGTCTCTCTCTGCTTCTCTGATAGCTC--TGCTATAT 860
 |||||
 Sbjct 135686 GTGAGAGTTTCTCTCTGCTTCTAAGATAGCACCTTGATATAT 135727

Human DNA sequence from clone RP11-374P20 on chromosome 9, complete sequence

Sequence ID: **emb|AL445931.29|** Length: 175033 Number of Matches: 1

Range 1: 155893 to 155961

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	56/75(75%)	6/75(8%)	Plus/Minus	

Features:

Query 446 TATATATGTGTAGTCGTGAGAGTCTCTCTGCGCTATATATGTGTAGGCTATATATGTGT 505
 |||||
 Sbjct 155961 TATATATGTGTATATATGTGTGTATATATATGTGTATATATGTGTA---TATATATGTGT 155905
 Query 506 AGTCGTTATATGTGT 520
 |||||
 Sbjct 155904 -GT--GTATATGTGT 155893

Human DNA sequence from clone RP11-430G6 on chromosome 1, complete sequence

Sequence ID: **emb|AL583850.5|** Length: 165329 Number of Matches: 1

Range 1: 72079 to 72140

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	48/62(77%)	2/62(3%)	Plus/Minus	

Features:

Query 856 TATATATGTGTAGTCGTCTATATATGTGTAGTTCTCTG--ATAGCTCTG-CTATATATGTG 913
 |||||
 Sbjct 72140 TATATATGTGTATATGTGTATATATGTGTATATATGTGTATATATGTGTATATATGTG 72081
 Query 914 TA 915
 ||
 Sbjct 72080 TA 72079

Human DNA sequence from clone RP11-476C9 on chromosome 9, complete sequence

Sequence ID: **emb|AL354672.27|** Length: 65254 Number of Matches: 1

Range 1: 8006 to 8097

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	75/106(71%)	14/106(13%)	Plus/Minus	

Features:

Query 416 TATATATGTGTAGTTCTCTGATAGCTCTGCTATATATGTGTAGTCGTGAGAGTCTCTCTC 475
 |||||
 Sbjct 8097 TATATATGTGTATATATGT-ATA--TATG-TATATATGTGTATATATGTGCATATATATG 8042
 Query 476 TGCCTATATATGTGTAGGCTATATATGTGTAGTCGTTATATGTGTA 521
 |||||
 Sbjct 8041 TGCATATATATGTG-----TATATATGTGTA-----TATATGTGTA 8006

Homo sapiens BAC clone RP11-499E18 from 4, complete sequence

Sequence ID: **gb|AC098487.1|** Length: 163914 Number of Matches: 1

Range 1: 115660 to 115791

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	98/141(70%)	15/141(10%)	Plus/Plus	

Features:

Query 470 TCTCTCTGCCTATATATGTGTAGGCTATATATGTGTAGTCGT-TATATGTGTAGTCGTAT 528

```

Sbjct  115660  TCTCTCT--CTATATATGTGTAC--ATATATATACACACCTATATATGTGTATACATAT 115714
Query  529      -----CAGCTACCTATATGTGTAGTCGTATCAGCTACCCTATATATGTGTAGTTCTCTGA 583
Sbjct  115715  ATACACACCTA--TATATGTGTATACATATATACACACCTATATATGTGTGTA-TACATATA 115771
Query  584      TAGCTCTGCTATATATGTGTGTA 604
Sbjct  115772  TA-CACACCTATATATGTGTGTA 115791

```

Human DNA sequence from clone RP11-192B18 on chromosome Xq21.1-21.33, complete sequence
Sequence ID: **emb|AL590229.3|** Length: 171847 Number of Matches: 1
Range 1: 82614 to 82682

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	55/75(73%)	6/75(8%)	Plus/Plus	

Features:

```

Query  446      TATATATGTGTAGTCGTGAGAGTCTCTCTCTGCCTATATATGTGTAGGCTATATATGTGT 505
Sbjct  82614  TATATATGTGTATATATGTGTGTATATATGTGTATATATATGTGTGTA---TATATATGTGT 82670
Query  506      AGTCGTTATATGTGT 520
Sbjct  82671  A---TATATATGTGT 82682

```

Human DNA sequence from clone RP11-373O10 on chromosome 9, complete sequence
Sequence ID: **emb|AL590381.4|** Length: 182430 Number of Matches: 1
Range 1: 5852 to 5902

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	43/54(80%)	3/54(5%)	Plus/Plus	

Features:

```

Query  468      TCTCTCTCTGCCTATATATGTGTAGGCTATATATGTGTAGTCGTTATATGTGTA 521
Sbjct  5852      TCTCTCTCTG--TATATATATATATG-TATATATGTGTATATATTATATATGTA 5902

```

Human DNA sequence from clone RP11-526K24 on chromosome 20, complete sequence
Sequence ID: **emb|AL161659.17|** Length: 101789 Number of Matches: 1
Range 1: 58778 to 58835

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	47/60(78%)	2/60(3%)	Plus/Minus	

Features:

```

Query  856      TATATATGTGTAGTCGTCTATATATGTGTAGTTCTCTGATAGCTCTGCTATATATGTGTA 915
Sbjct  58835  TATATATGTGTATATGTGTATATATGTGTATATATGT-ATATATATG-TATATATGTGTA 58778

```

Oryza sativa Japonica Group genomic DNA, chromosome 6, PAC clone:P0001H02
Sequence ID: **dbj|AP004234.3|** Length: 147160 Number of Matches: 1
Range 1: 43039 to 43070

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

Features:

```

Query  127      TACGCTACTCGATCGATCGATCTATGCATCGAC 159
Sbjct  43070  TACG-TACTCGATCGATCGATCTCTGCATGGAC 43039

```

Photorhabdus luminescens subsp. laumondii TTO1 complete genome; segment 7/17
Sequence ID: **emb|BX571865.1|** Length: 348813 Number of Matches: 1
Range 1: 147158 to 147188

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

Features:

Query 81 CGATAGACTCGCCTACTGCTATTCTCTGATA 111
 |||||
 Sbjct 147158 CGATAGAATCGCGTACTGCTATTCTCTGCTA 147188

Homo sapiens chromosome 16 clone RP11-292B23, complete sequence
 Sequence ID: **gb|AC009058.10|** Length: 164844 Number of Matches: 1
 Range 1: 140631 to 140689

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	47/60(78%)	2/60(3%)	Plus/Minus	

Features:

Query 856 TATATATGTGTAGTCGTCCTATATATGTGTAGTTCTCTG-ATAGCTCTGCTATATATGTGT 914
 |||||
 Sbjct 140689 TATATATGTGTATATGTATATATATGTGTATATATGTATATGTGTG-TATATATGTGT 140631

Papio hamadryas, clone RP41-208E11, complete sequence
 Sequence ID: **gb|AC117539.6|** Length: 208592 Number of Matches: 1
 Range 1: 109923 to 109958

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	31/36(86%)	0/36(0%)	Plus/Minus	

Features:

Query 486 TGTGTAGGCTATATATGTGTAGTCGTTATATGTGTA 521
 |||||
 Sbjct 109958 TGTGTAGGATGTGTATGTGTGGTGGTTATATGTGTA 109923

Homo sapiens BAC clone RP11-167A8 from 4, complete sequence
 Sequence ID: **gb|AC104790.4|** Length: 123589 Number of Matches: 1
 Range 1: 28390 to 28558

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	135/189(71%)	29/189(15%)	Plus/Plus	

Features:

Query 349 CTCTATAGTAGATGCGTA-TATGTGTAGTCGTATCAGCTACCTATATGTGTAGTCGTATC 407
 |||||
 Sbjct 28390 CTATATACCTATATGTGTAGTATATGTACTC-TATA---TAC-TATATGTGTAGT-GTATG 28443
 Query 408 AGCTACCCATATA-----TGTGTAGTTCTCTGATAGCTCTGC-TA-TATATGTGTAGTC 460
 |||||
 Sbjct 28444 ---TACTCTATATACTATATGTGTAGTG-TATG-TA-CTCTATATACTATATGTGTAGT- 28496
 Query 461 GTGAGAGTCTCTCTCTGCCATATATGTGTAGGCTATATA-TGTGTAGTCGTTATATGTG 519
 |||||
 Sbjct 28497 GT-ATATACTCTATATAC---TATATGTGTAGTGTATATACTCTATATAC--TATATGTG 28550
 Query 520 TAGTCGTAT 528
 |||||
 Sbjct 28551 TAGT-GTAT 28558

Mus musculus BAC clone RP23-391P1 from 3, complete sequence
 Sequence ID: **gb|AC147559.5|** Length: 188305 Number of Matches: 1
 Range 1: 144902 to 144968

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	54/69(78%)	4/69(5%)	Plus/Plus	

Features:

Query 828 TCTCTCTCTGCTTCTCTG-ATAGCTCTGCTATATATGTGTAGTCGTCTATATATGTGTAG 886
 |||||
 Sbjct 144902 TCTCTCTCTTCTCTCTGTATA-CTCTG-TATATATGTGTGTGTGTATATATATATAC 144959
 Query 887 TTCT-CTGA 894
 |||||
 Sbjct 144960 TTCTGCTGA 144968

Mus musculus BAC clone RP23-328K6 from 8, complete sequence
 Sequence ID: **gb|AC144944.5|** Length: 185319 Number of Matches: 1
 Range 1: 167812 to 167850

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

Features:

```

Query   482      TATATGTGTAGGCTATATATGTGTAGTCGTTATATGTGTA   521
          |||||
Sbjct   167850  TATATGTGTATGATATATATGTGTATTTG-TATGTGTGTA   167812

```

Mus musculus BAC clone RP23-311O15 from 7, complete sequence

Sequence ID: **gb|AC132425.3|** Length: 160552 Number of Matches: 1

Range 1: 43231 to 43293

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	48/63(76%)	1/63(1%)	Plus/Plus	

Features:

```

Query   468      TCTCTCTCTGCCTATATATGTGTAGGCTATATATGTGTAGTCGT-TATATGTGTAGTCGT   526
          |||||
Sbjct   43231  TCTCTCTGTGCGTGTGCATGTGTATCATGTATATATGTACACATGTATATGTGTAGTCAT   43290

Query   527      ATC   529
          |||
Sbjct   43291  ATC   43293

```

Mouse DNA sequence from clone RP23-68O14 on chromosome 2, complete sequence

Sequence ID: **emb|AL929563.15|** Length: 113198 Number of Matches: 1

Range 1: 27475 to 27519

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

Features:

```

Query   480      TATATATGTGTAGGCTATATATGTGTA-GTCGTTATATGTGTAGT   523
          |||||
Sbjct   27475  TATATATGTGTGTGGTATGTATGTGTATGTGTATATGTGTAGT   27519

```

Homo sapiens genomic DNA, chromosome 11 clone:RP11-838I13, complete sequence

Sequence ID: **dbj|AP001591.5|** Length: 178982 Number of Matches: 1

Range 1: 137240 to 137311

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	56/76(74%)	4/76(5%)	Plus/Plus	

Features:

```

Query   446      TATATATGTGTAGTCGTGAGAGTCTCTCTCTGCCTATATATGTGTAGGCTATATATGTGT   505
          |||||
Sbjct   137240  TATATATGTGTATATATGTGTGTATATGTGTGTATATATATGTGT---GTATATATGTGT   137296

Query   506      AGTCGTTATATGTGTA   521
          |||
Sbjct   137297  -GTATATATATGTGTA   137311

```

Homo sapiens genomic DNA, chromosome 11 clone:RP11-697H9, complete sequence

Sequence ID: **dbj|AP000753.4|** Length: 184057 Number of Matches: 1

Range 1: 39930 to 40001

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	56/76(74%)	4/76(5%)	Plus/Plus	

Features:

```

Query   446      TATATATGTGTAGTCGTGAGAGTCTCTCTCTGCCTATATATGTGTAGGCTATATATGTGT   505
          |||||
Sbjct   39930  TATATATGTGTATATATGTGTGTATATGTGTGTATATATATGTGT---GTATATATGTGT   39986

Query   506      AGTCGTTATATGTGTA   521
          |||
Sbjct   39987  -GTATATATATGTGTA   40001

```

Mouse DNA sequence from clone RP23-14G21 on chromosome 5, complete sequence

Sequence ID: **emb|AL591865.8|** Length: 251952 Number of Matches: 1

Range 1: 92452 to 92520

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	53/69(77%)	3/69(4%)	Plus/Plus	
Features:					
Query	850	CTCTGCTATATATGTGTAGTCGTCCTATATATGTGTAGTTCTCT-GATA-GC-TCTGCTAT	906		
Sbjct	92452	CTCTACTATATATGTGTCTGGGGCTATATAAGTGTATATGTGTATATATGCGTCTGCTAT	92511		
Query	907	ATATGTGTA	915		
Sbjct	92512	AAATGTGTA	92520		

Genomic sequence from Human 9q34, complete sequence

Sequence ID: **gb|AC002105.1|AC002105** Length: 37909 Number of Matches: 1

Range 1: 30830 to 30898

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	56/75(75%)	6/75(8%)	Plus/Minus	
Features:					
Query	446	TATATATGTGTAGTCGTGAGAGTCTCTCTCTGCCTATATATGTGTAGGCTATATATGTGT	505		
Sbjct	30898	TATATATGTGTATATATGTGTGTATATATATGTGTATATATGTGTA---TATATATGTGT	30842		
Query	506	AGTCGTTATATGTGT	520		
Sbjct	30841	-GT--GTATATGTGT	30830		

Human DNA sequence from clone XX-H2A1KLT on chromosome 9, complete sequence

Sequence ID: **emb|Z81330.1|** Length: 21644 Number of Matches: 1

Range 1: 4242 to 4310

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	56/75(75%)	6/75(8%)	Plus/Plus	
Features:					
Query	446	TATATATGTGTAGTCGTGAGAGTCTCTCTCTGCCTATATATGTGTAGGCTATATATGTGT	505		
Sbjct	4242	TATATATGTGTATATATGTGTGTATATATATGTGTATATATGTGTA---TATATATGTGT	4298		
Query	506	AGTCGTTATATGTGT	520		
Sbjct	4299	-GT--GTATATGTGT	4310		