

Basic Local Alignment Search Tool

NCBI/ [BLAST](#)/ [blastn suite](#)/ **Formatting Results - Y0S9YKD4014**

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AGCT

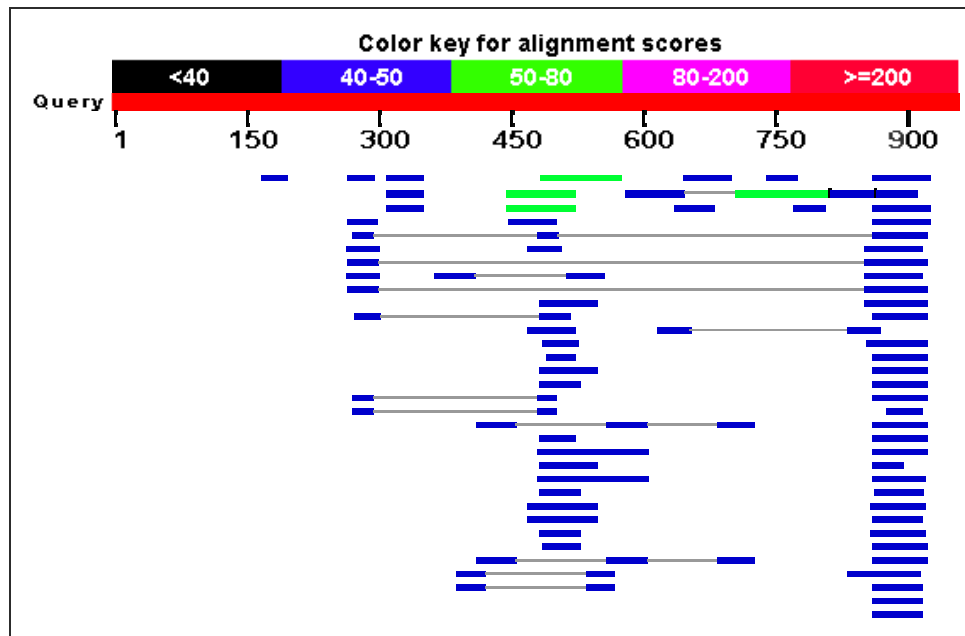
RID [Y0S9YKD4014](#) (Expires on 08-06 12:44 pm)

Query ID lc|63699
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 92 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Human DNA sequence from clone RP11-974F22 on chromosome 9, complete sequence	57.2	57.2	9%	3e-04	76%	AL772363.15
Mus musculus BAC clone RP23-470G3 from chromosome 16, complete sequence	53.6	53.6	8%	0.004	76%	AC162305.5
Mus musculus BAC clone RP23-50A18 from 16, complete sequence	53.6	53.6	8%	0.004	76%	AC145550.3
78G03_SfBAC_fin, Spodoptera frugiperda BAC, egg DNA	51.8	190	28%	0.015	74%	FP340419.1
Mus musculus chromosome 5, clone RP23-88A22, complete sequence	48.2	48.2	6%	0.18	77%	AC019028.13
Mus musculus chromosome 5, clone RP23-149H20, complete sequence	48.2	48.2	6%	0.18	77%	AC138101.8
Mus musculus chromosome 5, clone RP23-232H18, complete sequence	48.2	48.2	6%	0.18	77%	AC013622.12
Mouse DNA sequence from clone RP23-421E12 on chromosome 4, complete sequence	48.2	133	11%	0.18	80%	AL611985.22
Zebrafish DNA sequence from clone CH73-149H14 in linkage group 2, complete sequence	46.4	46.4	5%	0.62	79%	FP089540.8
Mus musculus strain C57BL6/J chromosome 5 clone RP23-280D18, complete sequence	46.4	46.4	6%	0.62	78%	AC068663.5
Mus musculus BAC clone RP23-10P23 from 16, complete sequence	46.4	89.1	10%	0.62	78%	AC126280.4
Mus musculus chromosome 5, clone RP23-185N2, complete sequence	46.4	46.4	6%	0.62	78%	AC113541.10
Mus musculus BAC clone RP23-424C5 from chromosome 16, complete sequence	46.4	89.1	10%	0.62	78%	AC163720.2
Mus musculus BAC clone RP23-467E1 from chromosome 13, complete sequence	46.4	46.4	7%	0.62	75%	AC159195.2
Homo sapiens BAC clone RP11-1288H11 from 2, complete sequence	46.4	46.4	3%	0.62	94%	AC142116.2
Mouse DNA sequence from clone RP23-130H14 on chromosome 4, complete sequence	46.4	46.4	4%	0.62	88%	AL732497.15
Lynx environmental sample clone NC4 control region, partial sequence; mitochondrial	44.6	44.6	4%	2.2	85%	JF298194.1
Lynx environmental sample clone NC2 control region, partial sequence; mitochondrial	44.6	44.6	4%	2.2	85%	JF298192.1
Homo sapiens B-cell CLL/lymphoma 2 (BCL2), RefSeqGene on chromosome 18	44.6	44.6	6%	2.2	80%	NG_009361.1
MACACA MULATTA BAC clone CH250-521P20 from chromosome 2, complete sequence	44.6	87.3	9%	2.2	83%	AC200644.3
Zebrafish DNA sequence from clone CH211-231H20 in linkage group 23, complete sequence	44.6	44.6	3%	2.2	86%	CR381544.22
Pongo abelii chromosome UNK clone CH276-15H12, complete sequence	44.6	87.3	7%	2.2	78%	AC188094.1
Salmo salar clone Alu224 microsatellite sequence	44.6	89.1	6%	2.2	86%	AY543787.1

Lynx canadensis isolate D2 mitochondrial D-loop, partial sequence	44.6	44.6	4%	2.2	85%	AY319497.1
Mus musculus BAC clone RP23-377M1 from chromosome 8, complete sequence	44.6	44.6	5%	2.2	79%	AC137157.3
Human DNA sequence from clone RP3-402H5 on chromosome 6p12.3-21.1, complete sequence	44.6	89.1	7%	2.2	89%	AL161622.12
Mus musculus 10 BAC RP24-339G14 (Roswell Park Cancer Institute (C57BL/6J Male) Mouse BAC Library) complete sequence	44.6	44.6	7%	2.2	74%	AC157089.5
Homo sapiens B-cell CLL/lymphoma 2 (BCL2) gene, complete cds	44.6	44.6	6%	2.2	80%	AY220759.1
Homo sapiens chromosome 18, clone RP11-299P2, complete sequence	44.6	44.6	6%	2.2	80%	AC022726.13
PREDICTED: Chelonia mydas eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa (EIF2S2), mRNA	42.8	42.8	4%	7.6	81%	XM_007057154.1
Fusarium fujikuroi IMI 58289 draft genome, chromosome FFUJ_chr06	42.8	42.8	3%	7.6	87%	HF679028.1
PREDICTED: Heterocephalus glaber ADP-ribosyltransferase 1 (Art1), mRNA	42.8	42.8	3%	7.6	91%	XM_004881735.1
Mus musculus BAC clone RP23-149P22 from chromosome 18, complete sequence	42.8	42.8	7%	7.6	78%	AC243907.3
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Tmem144:tm1a(EUCOMM)Wtsi; transgenic	42.8	42.8	5%	7.6	79%	JN963590.1
Mus musculus targeted non-conditional, lacZ-tagged mutant allele Itgb3:tm1e(KOMP)Wtsi; transgenic	42.8	42.8	6%	7.6	79%	JN959240.1
Mus musculus targeted non-conditional, lacZ-tagged mutant allele Rnf207:tm1e(KOMP)Wtsi; transgenic	42.8	85.5	4%	7.6	100%	JN954891.1
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Rnf207:tm1a(KOMP)Wtsi; transgenic	42.8	85.5	4%	7.6	100%	JN954890.1
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Itgb3:tm1a(KOMP)Wtsi; transgenic	42.8	42.8	6%	7.6	79%	JN951273.1
Candida glabrata CBS 138 hypothetical protein partial mRNA	42.8	128	14%	7.6	84%	XM_445412.2
Volvox carteri f. nagariensis male mating type locus, complete sequence	42.8	42.8	4%	7.6	84%	GU784916.1
Leptodactylus chaquensis clone Lchaqu16 microsatellite sequence	42.8	42.8	4%	7.6	88%	GU591326.1
Homo sapiens FOSMID clone ABC10-45517300G10 from chromosome unknown, complete sequence	42.8	42.8	13%	7.6	71%	AC235030.3
Mus musculus chromosome 18, clone RP23-468F3, complete sequence	42.8	42.8	7%	7.6	78%	AC225095.1
Astatotilapia burtoni clone BAC 20D21 platelet-derived growth factor receptor beta b (pdgfrbb) and colony-stimulating factor 1 receptor b (csf1rb) genes, complete cds	42.8	42.8	5%	7.6	77%	DQ386647.1
Homo sapiens chromosome 19 clone PC28130, complete sequence	42.8	42.8	13%	7.6	71%	AC002511.1
Mus musculus chromosome 8, clone RP24-178B9, complete sequence	42.8	42.8	3%	7.6	89%	AC119190.7
Yarrowia lipolytica YALI0E12639p (YALI0E12639g) mRNA, complete cds	42.8	42.8	3%	7.6	93%	XM_503872.1
Mus musculus chromosome 18, clone RP24-372A6, complete sequence	42.8	42.8	6%	7.6	79%	AC157910.4

Mus musculus BAC clone RP24-185D21 from chromosome 9, complete sequence	42.8	42.8	6%	7.6	78%	AC140387.2
Mus musculus chromosome 3, clone RP23-231L12, complete sequence	42.8	42.8	5%	7.6	79%	AC119162.12
Homo sapiens PAC clone RP5-1157F16 from 7, complete sequence	42.8	42.8	8%	7.6	74%	AC009296.2
Mus musculus chromosome 5, clone RP23-132D5, complete sequence	42.8	42.8	3%	7.6	86%	AC100382.22
Mus musculus chromosome 9, clone RP23-475J16, complete sequence	42.8	42.8	6%	7.6	78%	AC136903.6
Pan troglodytes BAC clone RP43-83L19 from chromosome 7, complete sequence	42.8	42.8	8%	7.6	74%	AC145394.1
Mus musculus, clone RP23-415L22, complete sequence	42.8	42.8	3%	7.6	89%	AC137844.8
Oryzias latipes hox gene cluster, complete cds, contains hoxDb	42.8	42.8	6%	7.6	78%	AB232924.1
Mus musculus BAC clone RP23-321H9 from chromosome 3, complete sequence	42.8	42.8	5%	7.6	79%	AC159281.3
Mus musculus chromosome 1, clone RP23-6F21, complete sequence	42.8	42.8	4%	7.6	82%	AC116380.14
Human DNA sequence from clone RP4-668J24 on chromosome 6p25.1-25.3, complete sequence	42.8	42.8	5%	7.6	80%	AL034346.31
Candida glabrata strain CBS138 chromosome C complete sequence	42.8	128	14%	7.6	84%	CR380949.1
Homo sapiens BAC clone RP11-725F20 from 2, complete sequence	42.8	42.8	4%	7.6	83%	AC112699.3
Homo sapiens chromosome X clone RP5-1015P16A, complete sequence	42.8	85.5	6%	7.6	91%	AC093545.1
Mus musculus BAC clone RP23-425F13 from chromosome 5, complete sequence	42.8	42.8	3%	7.6	86%	AC152721.3
Mus musculus chromosome 1, clone RP23-242C11, complete sequence	42.8	42.8	6%	7.6	76%	AC165413.16
Mus musculus BAC clone RP23-422D12 from chromosome 6, complete sequence	42.8	42.8	5%	7.6	79%	AC173480.1
Mus musculus chromosome 1, clone RP24-278B15, complete sequence	42.8	42.8	6%	7.6	76%	AC145691.5
Mus musculus BAC clone RP24-492M8 from 5, complete sequence	42.8	42.8	6%	7.6	78%	AC134523.5
Mouse DNA sequence from clone RP24-460H24 on chromosome 11, complete sequence	42.8	42.8	6%	7.6	79%	BX000996.4
Mouse DNA sequence from clone RP23-150J22 on chromosome 15, complete sequence	42.8	42.8	8%	7.6	75%	AL513354.14
Homo sapiens genomic DNA, chromosome 21q, section 89/105	42.8	42.8	5%	7.6	84%	AP001745.1
Homo sapiens genomic DNA, chromosome 21, clone:KB1430A10, MX1-D21S171 region, complete sequence	42.8	42.8	5%	7.6	84%	AP001622.1
Homo sapiens genomic DNA, chromosome 21, clone:KB1342D7, MX1-D21S171 region, complete sequence	42.8	42.8	5%	7.6	84%	AP001621.1
Homo sapiens clone DJ1015P16A, complete sequence	42.8	85.5	6%	7.6	91%	AC007486.1

Alignments

Human DNA sequence from clone RP11-974F22 on chromosome 9, complete sequence

Sequence ID: **emb|AL772363.15|** Length: 121478 Number of Matches: 1
Range 1: 28781 to 28867

Score	Expect	Identities	Gaps	Strand	Frame
57.2 bits(62)	3e-04()	71/93(76%)	6/93(6%)	Plus/Plus	
Features:					
Query	482	TGTGTCTCTGCCATGTGTGTCTCTGCTACTTGTGTCTCTGCTACTGTAGCATGAATGTGT			541
Sbjct	28781	TGTGTCTCTGTC--TGTGTGTGTCTGCGCCGTGTGTCTCTGTGTCTGT-GTATG--TGTGT			28835
Query	542	CTCTGCTACTGTAGCATGAAATGTGTGTCTCTG		574	
Sbjct	28836	CTCTGTGTCCGT-GTCTGTACTGTGTGTCTCTG		28867	

Mus musculus BAC clone RP23-470G3 from chromosome 16, complete sequence

Sequence ID: **gb|AC162305.5|** Length: 208504 Number of Matches: 1
Range 1: 142686 to 142764

Score	Expect	Identities	Gaps	Strand	Frame
53.6 bits(58)	0.004()	61/80(76%)	4/80(5%)	Plus/Minus	
Features:					
Query	445	ATGTGTGTCTCTGCTACTCGCGCTATATATATCAATGTGTGTCTCTGCCATGTGTGTCTC			504
Sbjct	142764	ATGTGTGTCTCTGTCTCTCTGTCTCTATGTCTCTATGTATGTCTCTGTCTCTGTCTCTC			142706
Query	505	TG---CTACTTGTGTCTCTG		521	
Sbjct	142705	TGTCTCTATGTGTGTCTCTG		142686	

Mus musculus BAC clone RP23-50A18 from 16, complete sequence

Sequence ID: **gb|AC145550.3|** Length: 146370 Number of Matches: 1
Range 1: 117198 to 117276

Score	Expect	Identities	Gaps	Strand	Frame
53.6 bits(58)	0.004()	61/80(76%)	4/80(5%)	Plus/Plus	
Features:					
Query	445	ATGTGTGTCTCTGCTACTCGCGCTATATATATCAATGTGTGTCTCTGCCATGTGTGTCTC			504
Sbjct	117198	ATGTGTGTCTCTGTCTCTCTGTCTCTATGTCTCTATGTATGTCTCTGTCTCTGTCTCTC			117256
Query	505	TG---CTACTTGTGTCTCTG		521	
Sbjct	117257	TGTCTCTATGTGTGTCTCTG		117276	

78G03_SfBAC_fin, Spodoptera frugiperda BAC, egg DNA

Sequence ID: **emb|FP340419.1|** Length: 132114 Number of Matches: 4
Range 1: 95824 to 95919

Score	Expect	Identities	Gaps	Strand	Frame
51.8 bits(56)	0.015()	79/107(74%)	13/107(12%)	Plus/Minus	
Features:					
Query	701	ATATCGTGCATATCATGTGTGTCTCTGCTACTCGCGCTATATATATCAT-TATATCGTGC			759
Sbjct	95919	ATATCGTGCATCTCATGCATGTC-CTGCATCTCGTGC-----ATATCGTGCATATCGTGC			95866
Query	760	ATATTGTGTCTCTGCTAC-TGTAGCATGAATTATATCGTGCATATCA		805	
Sbjct	95865	ATATCATGCATCTCCTGCATGT--CAT---TCATATCGTGCATATCA		95824	

Range 2: 95858 to 95919

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	53/68(78%)	7/68(10%)	Plus/Minus	
Features:					
Query	791	ATATCGTGCATATCATGTGTGTCTCTGCTACTCGCGCTATATATATCAT-TATATCGTGC			849
Sbjct	95919	ATATCGTGCATCTCATGCATGTC-CTGCATCTCGTGC-----ATATCGTGCATATCGTGC			95866
Query	850	ATATCATG		857	
Sbjct	95865	ATATCATG		95858	

Range 3: 95858 to 95919

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	53/68(78%)	7/68(10%)	Plus/Minus	
Features:					
Query	578	ATATCGTGCATATCATGTGTGTCTCTGCTACTCGCGCTATATATATCATT-ATATCGTGC	636		
Sbjct	95919	ATATCGTGCATCTCATGCATGTC-CTGCATCTCGTGC-----ATATCGTGCATATCGTGC	95866		
Query	637	ATATCATG	644		
Sbjct	95865	ATATCATG	95858		

Range 4: 95858 to 95919

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	52/66(79%)	5/66(7%)	Plus/Minus	
Features:					
Query	841	ATATCGTGCATATCATGTGTGTCTCTGCTACTATGTGTGTCTC-TGCTTATATCGTGCAT	899		
Sbjct	95919	ATATCGTGCATCTCATGCATGTC-CTGCATCTC-GTGCATATCGTGC--ATATCGTGCAT	95864		
Query	900	ATCATG	905		
Sbjct	95863	ATCATG	95858		

Mus musculus chromosome 5, clone RP23-88A22, complete sequence

Sequence ID: **gb|AC019028.13|** Length: 264425 Number of Matches: 1

Range 1: 35207 to 35269

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	50/65(77%)	2/65(3%)	Plus/Minus	
Features:					
Query	856	TGTGTGTCTCTGCTACTATGTGTGTCTCTGCTTATATCGTGCATATCATGTGTGTCTCTG	915		
Sbjct	35269	TGTGTGTCTCTGTGTGTGTGTGTGTCTCTGTGTACATAGT--ATGTCATGTGTGTCTTAG	35212		
Query	916	CTACT	920		
Sbjct	35211	TTACT	35207		

Mus musculus chromosome 5, clone RP23-149H20, complete sequence

Sequence ID: **gb|AC138101.8|** Length: 211521 Number of Matches: 1

Range 1: 114667 to 114729

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	50/65(77%)	2/65(3%)	Plus/Minus	
Features:					
Query	856	TGTGTGTCTCTGCTACTATGTGTGTCTCTGCTTATATCGTGCATATCATGTGTGTCTCTG	915		
Sbjct	114729	TGTGTGTCTCTGTGTGTGTGTGTGTCTCTGTGTACATAGT--ATGTCATGTGTGTCTTAG	114672		
Query	916	CTACT	920		
Sbjct	114671	TTACT	114667		

Mus musculus chromosome 5, clone RP23-232H18, complete sequence

Sequence ID: **gb|AC013622.12|** Length: 240821 Number of Matches: 1

Range 1: 13419 to 13481

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	50/65(77%)	2/65(3%)	Plus/Plus	
Features:					
Query	856	TGTGTGTCTCTGCTACTATGTGTGTCTCTGCTTATATCGTGCATATCATGTGTGTCTCTG	915		
Sbjct	13419	TGTGTGTCTCTGTGTGTGTGTGTGTCTCTGTGTACATAGT--ATGTCATGTGTGTCTTAG	13476		
Query	916	CTACT	920		
Sbjct	13477	TTACT	13481		

Mouse DNA sequence from clone RP23-421E12 on chromosome 4, complete sequence

Sequence ID: **emb|AL611985.22|** Length: 219205 Number of Matches: 3

Range 1: 184440 to 184497

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	48/60(80%)	2/60(3%)	Plus/Minus	

Features:

```
Query   856      TGTGTGTCTCTGCTACTATGTGTGTCTCTGCTTATATCGTGCATATCATGTGTGTCTCTG   915
          |||
Sbjct   184497  TGTGTGTGTGTGTGTCTATGTGTGTCTCTGATTGTGTC-TGTATCT-ATGTGTGTCTCTG   184440
```

Range 2: 68841 to 68863

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

Features:

```
Query   272      ATGTGTGTCTCTGCCATGTGTGT   294
          |||
Sbjct   68841  ATGTGTGTCTCTGCCATGTGTGT   68863
```

Range 3: 68841 to 68863

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

Features:

```
Query   479      ATGTGTGTCTCTGCCATGTGTGT   501
          |||
Sbjct   68841  ATGTGTGTCTCTGCCATGTGTGT   68863
```

Zebrafish DNA sequence from clone CH73-149I14 in linkage group 2, complete sequence

Sequence ID: **emb|FP089540.8|** Length: 81999 Number of Matches: 1

Range 1: 44217 to 44273

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	45/57(79%)	1/57(1%)	Plus/Minus	

Features:

```
Query   446      TGTGTGTCTCTGCTACTCG-CGCTATATATATCAATGTGTGTCTCTGCCATGTGTGT   501
          |||
Sbjct   44273  TGTGTGTGTCTGCGTGTCTACGCTATGTATGTGTGTGTGTGTCTGTGCCATGTGTGT   44217
```

Mus musculus strain C57BL6/J chromosome 5 clone RP23-280D18, complete sequence

Sequence ID: **gb|AC068663.5|** Length: 221134 Number of Matches: 1

Range 1: 151616 to 151682

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	52/67(78%)	2/67(2%)	Plus/Minus	

Features:

```
Query   846      GTGCATATCATGTGTGTCTCTGCTACTATGTGTGTCTCTGCTTATATC-GTGCATATC-A   903
          |||
Sbjct   151682  GTGTATGTCAATTTGTGTGTGCTTATGTGTGTCTCTGTGTATGTCTGTGTGTATCTA   151623

Query   904      TGTGTGT   910
          |||
Sbjct   151622  TGTGTGT   151616
```

Mus musculus BAC clone RP23-10P23 from 16, complete sequence

Sequence ID: **gb|AC126280.4|** Length: 211237 Number of Matches: 2

Range 1: 158072 to 158133

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	54/69(78%)	7/69(10%)	Plus/Plus	

Features:

```

Query   847      TGCATATCATGTGTGTCTCTGCTACTATGTGTGTCTCTGCTTATATCGTGCATATCATGT   906
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct   158072    TGTATAT-ATGTGTGTCTCTG-----TATGTGTGTCTCTGTCTGTAAC-TGTATCT-ATGT   158124

Query   907      GTGTCTCTG   915
          ||| ||| ||| |||
Sbjct   158125    GTGTCTGTG   158133

```

Range 2: 158072 to 158105

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

Features:

```

Query   265      TGCATTTATGTGTGTCTCTGCCATGTGTGTCTCTG   299
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct   158072    TGTATATATGTGTGTCTCTG-TATGTGTGTCTCTG   158105

```

Mus musculus chromosome 5, clone RP23-185N2, complete sequence

Sequence ID: **gb|AC113541.10|** Length: 210222 Number of Matches: 1

Range 1: 45696 to 45762

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	52/67(78%)	2/67(2%)	Plus/Plus	

Features:

```

Query   846      GTGCATATCATGTGTGTCTCTGCTACTATGTGTGTCTCTGCTTATATC-GTGCATATC-A   903
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct   45696    GTGTATGTCAATTTGTGTGTGTGCTTATGTGTGTGTCTCTGTGTATGTCTGTGTGTATCTA   45755

Query   904      TGTGTGT   910
          ||| ||| ||| |||
Sbjct   45756    TGTGTGT   45762

```

Mus musculus BAC clone RP23-424C5 from chromosome 16, complete sequence

Sequence ID: **gb|AC163720.2|** Length: 206284 Number of Matches: 2

Range 1: 158170 to 158231

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	54/69(78%)	7/69(10%)	Plus/Minus	

Features:

```

Query   847      TGCATATCATGTGTGTCTCTGCTACTATGTGTGTCTCTGCTTATATCGTGCATATCATGT   906
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct   158231    TGTATAT-ATGTGTGTCTCTG-----TATGTGTGTCTCTGTCTGTAAC-TGTATCT-ATGT   158179

Query   907      GTGTCTCTG   915
          ||| ||| ||| |||
Sbjct   158178    GTGTCTGTG   158170

```

Range 2: 158198 to 158231

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

Features:

```

Query   265      TGCATTTATGTGTGTCTCTGCCATGTGTGTCTCTG   299
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct   158231    TGTATATATGTGTGTCTCTG-TATGTGTGTCTCTG   158198

```

Mus musculus BAC clone RP23-467E1 from chromosome 13, complete sequence

Sequence ID: **gb|AC159195.2|** Length: 194915 Number of Matches: 1

Range 1: 20358 to 20437

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	60/80(75%)	10/80(12%)	Plus/Minus	

Features:

```

Query   846      GTGCATATCA-TGTGTGTCTCTGCTACTATGTGTG--TCTCTGCTTATATC-----GTG   896
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct   20437    GTGTATATCTCTGTGTGTATCTGTGACTATGTGTGTATCTCTGTGTATATCATCTCTGTG   20378

Query   897      CATATC-ATGTGTGTCTCTG   915

```


Sbjct 20377 AATATCTCTGTGTGTATCTG 20358

Homo sapiens BAC clone RP11-1288H11 from 2, complete sequence

Sequence ID: **gb|AC142116.2|** Length: 21376 Number of Matches: 1

Range 1: 12779 to 12809

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	30/32(94%)	1/32(3%)	Plus/Plus	

Features:

```
Query 265      TGCATTTATGTGTGTCTCTGCCATGTGTGTCT 296
                |||
Sbjct 12779    TGCATGTATGTGTGTCTCTG-CATGTGTGTCT 12809
```

Mouse DNA sequence from clone RP23-130H14 on chromosome 4, complete sequence

Sequence ID: **emb|AL732497.15|** Length: 208663 Number of Matches: 1

Range 1: 129071 to 129109

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	35/40(88%)	1/40(2%)	Plus/Plus	

Features:

```
Query 467      CTATATATATCAATGTGTGTCTCTGCCATGTGTGTCTCTG 506
                |||
Sbjct 129071    CTATATATATCTATGTGTGTCTGT-CTATGTGTGTGTCTG 129109
```

Lynx environmental sample clone NC4 control region, partial sequence; mitochondrial

Sequence ID: **gb|JF298194.1|** Length: 446 Number of Matches: 1

Range 1: 260 to 298

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	35/41(85%)	2/41(4%)	Plus/Plus	

Features:

```
Query 310      TATATATATCACGTCACGCGTACTATGCTTATATCGTGCAT 350
                |||
Sbjct 260      TATATATATCACATAAGGCATACTATG--TATATCGTGCAT 298
```

Lynx environmental sample clone NC2 control region, partial sequence; mitochondrial

Sequence ID: **gb|JF298192.1|** Length: 469 Number of Matches: 1

Range 1: 240 to 278

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	35/41(85%)	2/41(4%)	Plus/Plus	

Features:

```
Query 310      TATATATATCACGTCACGCGTACTATGCTTATATCGTGCAT 350
                |||
Sbjct 240      TATATATATCACATAAGGCATACTATG--TATATCGTGCAT 278
```

Homo sapiens B-cell CLL/lymphoma 2 (BCL2), RefSeqGene on chromosome 18

Sequence ID: **ref|NG_009361.1|** Length: 203035 Number of Matches: 1

Range 1: 125520 to 125575

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	48/60(80%)	4/60(6%)	Plus/Plus	

Features:

```
Query 856      TGTGTGTCTCTGCTACTATGTGTGTCTCTGCTTATATCGTGCATATCATGTGTGTCTCTG 915
                |||
Sbjct 125520    TGTGTGTCTCTGTGTCTATGTGTGTCTGTG--TATGTC-TGTGTGTC-TGTGTGTCTCTG 125575
```

MACACA MULATTA BAC clone CH250-521P20 from chromosome 2, complete sequence

Sequence ID: **gb|AC200644.3|** Length: 176707 Number of Matches: 2

Range 1: 36590 to 36634

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	38/46(83%)	1/46(2%)	Plus/Plus	
Features:					
Query	362	CACTGTGTCTCTGCTACTGTAGCATGAATGTGTCTCTGCTACTGTA	407		
Sbjct	36590	CAGTGTGTCTCTGCTACTAGAGGAAGAATGTG-GTCTGCCACTGTA	36634		

Range 2: 36593 to 36634

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	36/43(84%)	1/43(2%)	Plus/Plus	
Features:					
Query	512	TGTGTCTCTGCTACTGTAGCATGAATGTGTCTCTGCTACTGTA	554		
Sbjct	36593	TGTGTCTCTGCTACTAGAGGAAGAATGTG-GTCTGCCACTGTA	36634		

Zebrafish DNA sequence from clone CH211-231H20 in linkage group 23, complete sequence

Sequence ID: **emb|CR381544.22|** Length: 146827 Number of Matches: 1

Range 1: 116636 to 116672

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	32/37(86%)	0/37(0%)	Plus/Minus	
Features:					
Query	736	GCTATATATATCATTATATCGTGCATATTGTGTCTCT	772		
Sbjct	116672	GCTTTATATATCATTATATGTTGCATAATATGTCTCT	116636		

Pongo abelii chromosome UNK clone CH276-15H12, complete sequence

Sequence ID: **gb|AC188094.1|** Length: 205234 Number of Matches: 2

Range 1: 92330 to 92395

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	53/68(78%)	3/68(4%)	Plus/Plus	
Features:					
Query	480	TGTGTGTCTCTGCCATGTGTGTCTCTGCTACTTGTGTCTCTGCTACTGT-AGCATGAATG	538		
Sbjct	92330	TGTGTGTGTCTGTC-ATGTGTGTCTCTG-TGTGTGTGTCTCTGTGTGTGTCTGTATGTGTG	92387		
Query	539	TGTCTCTG	546		
Sbjct	92388	TGTCTCTG	92395		

Range 2: 92153 to 92220

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	53/69(77%)	3/69(4%)	Plus/Plus	
Features:					
Query	480	TGTGTGTCTCTGCCATGTGTGTCTCTG-CTACTTGTGTCTCTGCTACTGT-AGCATGAAT	537		
Sbjct	92153	TGTGTGTGTCTGTC-ATGTGTGTCTCTGTGTGTGTGTGTCTCTGTGTGTCTGTATGTGT	92211		
Query	538	GTGTCTCTG	546		
Sbjct	92212	GTGTCTCTG	92220		

Salmo salar clone Alu224 microsatellite sequence

Sequence ID: **gb|AY543787.1|** Length: 331 Number of Matches: 2

Range 1: 198 to 234

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

Query 480 TGTGTGTCTCTGCCATGTGTGTCTCTGCTACTTGTGT 516
 |||||
 Sbjct 198 TGTGTGTCTCTGCTGTGTGTGTCTCTGCTGTGTGTGT 234

Range 2: 198 to 226

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

Features:

Query 273 TGTGTGTCTCTGCCATGTGTGTCTCTGCT 301
 |||||
 Sbjct 198 TGTGTGTCTCTGCTGTGTGTGTCTCTGCT 226

Lynx canadensis isolate D2 mitochondrial D-loop, partial sequence

Sequence ID: **gb|AY319497.1|** Length: 552 Number of Matches: 1
 Range 1: 211 to 249

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	35/41(85%)	2/41(4%)	Plus/Plus	

Features:

Query 310 TATATATATCACGTCACGCGTACTATGCTTATATCGTGCAT 350
 |||||
 Sbjct 211 TATATATATCACATAAGGCATACTATG--TATATCGTGCAT 249

Mus musculus BAC clone RP23-377M11 from chromosome 8, complete sequence

Sequence ID: **gb|AC137157.3|** Length: 187666 Number of Matches: 1
 Range 1: 49353 to 49408

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	44/56(79%)	2/56(3%)	Plus/Plus	

Features:

Query 468 TATATATATCAATGTGTGTCTCTGCCATGTGTGTC--TCTGCTACTTGTGTCTCTG 521
 |||||
 Sbjct 49353 TATGTATATGTATGTGTGTCTCTGTGTTGTCTGTCTGTCTGTTATGTGTGTCTCTG 49408

Human DNA sequence from clone RP3-402H5 on chromosome 6p12.3-21.1, complete sequence

Sequence ID: **emb|AL161622.12|** Length: 131967 Number of Matches: 2
 Range 1: 4483 to 4518

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

Features:

Query 828 TATATATATCAT-TATATCGTGCATATCATGTGTGT 862
 |||||
 Sbjct 4518 TATGTATATCATGTATATCATGTATATCATGTGTGT 4483

Range 2: 4483 to 4518

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

Features:

Query 615 TATATATATCAT-TATATCGTGCATATCATGTGTGT 649
 |||||
 Sbjct 4518 TATGTATATCATGTATATCATGTATATCATGTGTGT 4483

Mus musculus 10 BAC RP24-339G14 (Roswell Park Cancer Institute (C57BL/6J Male) Mouse BAC Library) complete sequence

Sequence ID: **gb|AC157089.5|** Length: 160723 Number of Matches: 1
 Range 1: 43122 to 43194

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	56/76(74%)	12/76(15%)	Plus/Minus	

Features:

Query 849 CATATCATGTGTGTCTCTGCTACTATGTGTGTCTCTGCTTATATCGTG-----CAT 899
 |||||
 Sbjct 43194 CATATAATGTGTGTCTCTG--TGTGTGTGTGTCTCTGTATATAT-GTGTATGTATGTCAT 43138
 |||||
 Query 900 ATCATGTGTGTCTCTG 915
 |||||
 Sbjct 43137 ACAATGTGTGTCTCTG 43122
 |||||

Homo sapiens B-cell CLL/lymphoma 2 (BCL2) gene, complete cds
 Sequence ID: **gb|AY220759.1|** Length: 198051 Number of Matches: 1
 Range 1: 120969 to 121024

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	48/60(80%)	4/60(6%)	Plus/Plus	

Features:

Query 856 TGTGTGTCTCTGCTACTATGTGTGTCTCTGCTTATATCGTGCATATCATGTGTGTCTCTG 915
 |||||
 Sbjct 120969 TGTGTGTCTCTGTGTCTATGTGTGTCTGTG--TATGTC-TGTGTGTC-TGTGTGTCTCTG 121024
 |||||

Homo sapiens chromosome 18, clone RP11-299P2, complete sequence
 Sequence ID: **gb|AC022726.13|** Length: 146688 Number of Matches: 1
 Range 1: 57093 to 57148

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	48/60(80%)	4/60(6%)	Plus/Plus	

Features:

Query 856 TGTGTGTCTCTGCTACTATGTGTGTCTCTGCTTATATCGTGCATATCATGTGTGTCTCTG 915
 |||||
 Sbjct 57093 TGTGTGTCTCTGTGTCTATGTGTGTCTGTG--TATGTC-TGTGTGTC-TGTGTGTCTCTG 57148
 |||||

PREDICTED: Chelonia mydas eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa (EIF2S2), mRNA
 Sequence ID: **ref|XM_007057154.1|** Length: 1295 Number of Matches: 1
 Range 1: 69 to 111

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

Features:

Query 484 TGTCTCTGCCATGTGTGTCTCTGCTACTTGTGTCTCTGCTACT 526
 |||||
 Sbjct 111 TGTTCCTGACAACTGTGTCTCTTCTGCTTGTGTCTCTCCTCCT 69
 |||||

Fusarium fujikuroi IMI 58289 draft genome, chromosome FFUJ_chr06
 Sequence ID: **emb|HF679028.1|** Length: 4234805 Number of Matches: 1
 Range 1: 3136120 to 3136156

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

Features:

2861 bp at 5' side: related to RAM1-protein farnesyltransferase, beta subunit591 bp at 3' side: uncharacterized protein

Query 766 TGTCTCTGCTACTGTAGCATGAATTATATCGTGCATAT 803
 |||||
 Sbjct 3136156 TGTCTCGGCTA-TGTACCATGGATGATATCGTGCATAT 3136120
 |||||

PREDICTED: Heterocephalus glaber ADP-ribosyltransferase 1 (Art1), mRNA
 Sequence ID: **ref|XM_004881735.1|** Length: 978 Number of Matches: 1

► See 1 more title(s)
 Range 1: 11 to 42

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

Features:

Query 489 CTGCCATGTGTGTCTCTGCTACTTGTGTCTCTG 521
 |||||
 Sbjct 11 CTGCCATGC-TGTCTCTGCTACTTGTGTCTGTG 42

Mus musculus BAC clone RP23-149P22 from chromosome 18, complete sequence
 Sequence ID: **gb|AC243907.3|** Length: 188186 Number of Matches: 1
 Range 1: 150047 to 150110

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	53/68(78%)	5/68(7%)	Plus/Plus	

Features:

Query 480 TGTGTGTCTCTGC-CATGTGTGTCTCTGCTACTTGTGTCTCTGCTACTGTAGCATGAATG 538
 |||||
 Sbjct 150047 TGTGTGTCTCTTTGCATGTGTGTCTCTG-TA--TGTGTATCTGTGCATGT-GCATGTGTG 150102
 Query 539 TGTCTCTG 546
 |||||
 Sbjct 150103 TGTCTGTG 150110

Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Tmem144:tm1a(EUCOMM)Wtsi; transgenic
 Sequence ID: **gb|JN963590.1|** Length: 37932 Number of Matches: 1
 Range 1: 14152 to 14199

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	38/48(79%)	0/48(0%)	Plus/Plus	

Features:

Query 481 GTGTGTCTCTGCCATGTGTGTCTCTGCTACTTGTGTCTCTGCTACTGT 528
 |||||
 Sbjct 14152 GTGTGTCTCACATACGTGTGTCTCACATACGTGTGTCTCTGCGACTGT 14199

Mus musculus targeted non-conditional, lacZ-tagged mutant allele Itgb3:tm1e(KOMP)Wtsi; transgenic
 Sequence ID: **gb|JN959240.1|** Length: 39336 Number of Matches: 1
 Range 1: 26931 to 26988

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	48/61(79%)	4/61(6%)	Plus/Minus	

Features:

Query 856 TGTGTGTCTCTGCTACTATGTGTGTCTCTGCTTATAT-CGTGCATATCATGTGTGTCTCT 914
 |||||
 Sbjct 26988 TGTGTGTCTCTGAGTCTCTGTGTGTCTCTGTGTGTGTACCTG--TATC-TGTGTGTCTCT 26932
 Query 915 G 915
 |
 Sbjct 26931 G 26931

Mus musculus targeted non-conditional, lacZ-tagged mutant allele Rnf207:tm1e(KOMP)Wtsi; transgenic
 Sequence ID: **gb|JN954891.1|** Length: 37885 Number of Matches: 2
 Range 1: 5074 to 5096

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

Features:

Query 479 ATGTGTGTCTCTGCCATGTGTGT 501
 |||||
 Sbjct 5096 ATGTGTGTCTCTGCCATGTGTGT 5074

Range 2: 5074 to 5096

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

Features:

Query 272 ATGTGTGTCTCTGCCATGTGTGT 294
 |||||
 Sbjct 5096 ATGTGTGTCTCTGCCATGTGTGT 5074

Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Rnf207:tm1a(KOMP)Wtsi; transgenic
Sequence ID: **gb|JN954890.1|** Length: 37941 Number of Matches: 2
Range 1: 5074 to 5096

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

Features:

```

Query   479   ATGTGTGTCTCTGCCATGTGTGT   501
          |||||
Sbjct   5096  ATGTGTGTCTCTGCCATGTGTGT   5074

```

Range 2: 5074 to 5096

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

Features:

```

Query   272   ATGTGTGTCTCTGCCATGTGTGT   294
          |||||
Sbjct   5096  ATGTGTGTCTCTGCCATGTGTGT   5074

```

Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Itgb3:tm1a(KOMP)Wtsi; transgenic
Sequence ID: **gb|JN951273.1|** Length: 39390 Number of Matches: 1
Range 1: 26985 to 27042

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	48/61(79%)	4/61(6%)	Plus/Minus	

Features:

```

Query   856   TGTGTGTCTCTGCTACTATGTGTGTCTCTGCTTATAT-CGTGCATATCATGTGTGTCTCT   914
          |||||
Sbjct   27042  TGTGTGTCTCTGAGTCTCTGTGTGTCTCTGTGTGTGTACCTG--TATC-TGTGTGTCTCT   26986

Query   915   G   915
          |
Sbjct   26985  G   26985

```

Candida glabrata CBS 138 hypothetical protein partial mRNA
Sequence ID: **ref|XM_445412.2|** Length: 1203 Number of Matches: 3
Range 1: 48 to 90

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	38/45(84%)	2/45(4%)	Plus/Minus	

Features:

```

Query   680   ATGAAATGTGTGTCTCTGCTTATATCGTGCATATCATGTGTGTCT   724
          |||||
Sbjct   90   ATGAAATGTGTCTCTCTGTGTATATC-TGTATGTC-TGTGTGTCT   48

```

Range 2: 48 to 90

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	38/45(84%)	2/45(4%)	Plus/Minus	

Features:

```

Query   557   ATGAAATGTGTGTCTCTGCTTATATCGTGCATATCATGTGTGTCT   601
          |||||
Sbjct   90   ATGAAATGTGTCTCTCTGTGTATATC-TGTATGTC-TGTGTGTCT   48

```

Range 3: 48 to 90

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	38/45(84%)	2/45(4%)	Plus/Minus	

Features:

```

Query   410   ATGAAATGTGTGTCTCTGCTTATATCGTGCATATCATGTGTGTCT   454
          |||||
Sbjct   90   ATGAAATGTGTCTCTCTGTGTATATC-TGTATGTC-TGTGTGTCT   48

```

Volvox carteri f. nagariensis male mating type locus, complete sequence
Sequence ID: **gb|GU784916.1|** Length: 1173476 Number of Matches: 1
Range 1: 734757 to 734799

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	36/43(84%)	1/43(2%)	Plus/Plus	
Features:					
Query	480	TGTGTGTCTCTGCCATGTGTGTCTCTGCTACT-TGTGTCTCTG			521
Sbjct	734757	TGTGTGTCTCTGTTCTGTGTGTCTCTGTGTCTGTGTGTCTCTG			734799

Leptodactylus chaquensis clone Lchaqu16 microsatellite sequence
Sequence ID: **gb|GU591326.1|** Length: 383 Number of Matches: 1
Range 1: 95 to 133

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/40(88%)	2/40(5%)	Plus/Minus	
Features:					
Query	872	TATGTGTGTCTCTGCTTATATC-GTGCATATCATGTGTGT			910
Sbjct	133	TATGTGTGTGCCTGCTTATATCTGTGCATAT-GTGTGTGT			95

Homo sapiens FOSMID clone ABC10-45517300G10 from chromosome unknown, complete sequence
Sequence ID: **gb|AC235030.3|** Length: 42222 Number of Matches: 1
Range 1: 20639 to 20754

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	90/127(71%)	12/127(9%)	Plus/Minus	
Features:					
Query	479	ATGTGTGTCTCTGCCATGTGTGTCTCTGCTACTTGTGTCTCTGCTACTGTAGCATGAATG			538
Sbjct	20754	ATGTGTGTCTCTGCGGTGTGTGTGTGT-CTGTGTGTGTGTCTGTGTATGTATC-TGTGTG			20697
Query	539	TGTCTCTGCTACTGTAGCATG-AAATGTGTGTCTCTGCTTATATCGTGCATATCATGTGT			597
Sbjct	20696	TGTGTCTCTCTGT-GCATGTCTGTGTGTGTCTCTGTGTGT---GTGTACCTC-TGTGT			20646
Query	598	GTCTCTG			604
Sbjct	20645	GTCTCTG			20639

Mus musculus chromosome 18, clone RP23-468F3, complete sequence
Sequence ID: **gb|AC225095.1|** Length: 39673 Number of Matches: 1
Range 1: 30111 to 30174

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	53/68(78%)	5/68(7%)	Plus/Minus	
Features:					
Query	480	TGTGTGTCTCTGC-CATGTGTGTCTCTGCTACTTGTGTCTCTGCTACTGTAGCATGAATG			538
Sbjct	30174	TGTGTGTCTCTTTGCATGTGTGTCTCTG-TA--TGTGTATCTGTGCATGT-GCATGTGTG			30119
Query	539	TGTCTCTG			546
Sbjct	30118	TGTCTGTG			30111

Astatotilapia burtoni clone BAC 20D21 platelet-derived growth factor receptor beta b (pdgfrbb) and colony-stimulating factor 1 receptor b (csf1rb) genes, complete cds
Sequence ID: **gb|DQ386647.1|** Length: 144596 Number of Matches: 1
Range 1: 84772 to 84828

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	44/57(77%)	2/57(3%)	Plus/Plus	
Features:					

Query 643 TGTGTGTCTCTGCTACTTGTGTCTCTGCTACTGTAGC--ATGAAATGTGTGTCTCTG 697
 |||||
 Sbjct 84772 TGTGTGTCTCTGATGTTTGTGTGTCTGACATTTGAGCGTCTGAAGTGTGTGTCTCTG 84828

Homo sapiens chromosome 19 clone PC28130, complete sequence

Sequence ID: **gb|AC002511.1|** Length: 98713 Number of Matches: 1
 Range 1: 39446 to 39561

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	90/127(71%)	12/127(9%)	Plus/Plus	

Features:

Query 479 ATGTGTGTCTCTGCCATGTGTGTCTCTGCTACTTGTGTCTCTGCTACTGTAGCATGAATG 538
 |||||
 Sbjct 39446 ATGTGTGTCTCTGCGGTGTGTGTGTGT-CTGTGTGTGTGTCTGTGTATGTATC-TGTGTG 39503
 |||||
 Query 539 TGTCTCTGCTACTGTAGCATG-AAATGTGTGTCTCTGCTTATATCGTGCATATCATGTGT 597
 |||||
 Sbjct 39504 TGTGTCT-----CTGT-GCATGTCTGTGTGTGTCTCTGTGTGT---GTGTACCTC-TGTGT 39554
 |||||
 Query 598 GTCTCTG 604
 |||||
 Sbjct 39555 GTCTCTG 39561

Mus musculus chromosome 8, clone RP24-178B9, complete sequence

Sequence ID: **gb|AC119190.7|** Length: 139843 Number of Matches: 1
 Range 1: 58071 to 58104

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

Features:

Query 265 TGCATTTATGTGTGTCTCTGCCATGTGTGTCTCTG 299
 |||||
 Sbjct 58104 TGCATCTGTGTGTGTCTCTGTCT-TGTGTGTCTCTG 58071

Yarrowia lipolytica YALIOE12639p (YALIOE12639g) mRNA, complete cds

Sequence ID: **ref|XM_503872.1|** Length: 1005 Number of Matches: 1
 Range 1: 41 to 69

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

Features:

Query 169 ATACGCAAACACACATGTGTGTCTCTGCTA 198
 |||||
 Sbjct 41 ATACTCAAACACA-ATGTGTGTCTCTGCTA 69

Mus musculus chromosome 18, clone RP24-372A6, complete sequence

Sequence ID: **gb|AC157910.4|** Length: 180725 Number of Matches: 1
 Range 1: 136418 to 136475

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	48/61(79%)	4/61(6%)	Plus/Minus	

Features:

Query 856 TGTGTGTCTCTGCTACTATGTGTGTCTCTGCTTATATCGTGCATATC-ATGTGTGTCTCT 914
 |||||
 Sbjct 136475 TGTGTGTCTTTGTTTCTCTGTGTGTCTCTG--TCTCTC-TGCCTGTCTCTGTGTGTCTCT 136419
 |||||
 Query 915 G 915
 |
 Sbjct 136418 G 136418

Mus musculus BAC clone RP24-185D21 from chromosome 9, complete sequence

Sequence ID: **gb|AC140387.2|** Length: 158741 Number of Matches: 1
 Range 1: 25489 to 25546

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

Features:

Query 856 TGTGTGTCTCTGCTACTATGTGTGTCTCTGCTTATATCGTGCATATCATGTGTGTCTCTG 915
Sbjct 25546 TGTGTGTCCATGTGTGTATGTGTGTCTCTGTGTATAT-GAGCATAT-GTGTGTGTGTCTG 25489

Mus musculus chromosome 3, clone RP23-231L12, complete sequence

Sequence ID: **gb|AC119162.12|** Length: 201218 Number of Matches: 1
Range 1: 135197 to 135244

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	38/48(79%)	0/48(0%)	Plus/Plus	

Features:

Query 481 GTGTGTCTCTGCCATGTGTGTCTCTGCTACTTGTGTCTCTGCTACTGT 528
Sbjct 135197 GTGTGTCTCACATACGTGTGTCTCACATACGTGTGTCTCTGCGACTGT 135244

Homo sapiens PAC clone RP5-1157F16 from 7, complete sequence

Sequence ID: **gb|AC009296.2|** Length: 33223 Number of Matches: 1
Range 1: 9259 to 9339

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	61/82(74%)	3/82(3%)	Plus/Plus	

Features:

Query 468 TATATATATCAATGTGTGTCTCTGC-CATGTGTGTCTCTG-CTACTTGTGTCTCTGCTAC 525
Sbjct 9259 TATATATGTCTGTGTGTATGTGTTTCATGTGTGTCTCTGTGTGAGTGTGTCTCTGTGTT 9318
Query 526 TGTAGCATGAATGTGTCTCTGC 547
Sbjct 9319 TGT-GTCTGTGTGTGTCTCTGC 9339

Mus musculus chromosome 5, clone RP23-132D5, complete sequence

Sequence ID: **gb|AC100382.22|** Length: 190712 Number of Matches: 1
Range 1: 122228 to 122262

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	32/37(86%)	2/37(5%)	Plus/Plus	

Features:

Query 264 ATGCATTTATGTGTGTCTCTGCCATGTGTGTCTCTGC 300
Sbjct 122228 ATGCAT--ATGTGTGTCTGTGTCATGTGTGTCTGTGC 122262

Mus musculus chromosome 9, clone RP23-475J16, complete sequence

Sequence ID: **gb|AC136903.6|** Length: 180530 Number of Matches: 1
Range 1: 151266 to 151323

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

Features:

Query 856 TGTGTGTCTCTGCTACTATGTGTGTCTCTGCTTATATCGTGCATATCATGTGTGTCTCTG 915
Sbjct 151323 TGTGTGTCCATGTGTGTATGTGTGTCTCTGTGTATAT-GAGCATAT-GTGTGTGTGTCTG 151266

Pan troglodytes BAC clone RP43-83L19 from chromosome 7, complete sequence

Sequence ID: **gb|AC145394.1|** Length: 144147 Number of Matches: 1
Range 1: 72359 to 72439

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	61/82(74%)	3/82(3%)	Plus/Plus	

Features:

Query 468 TATATATATCAATGTGTGTCTCTGC-CATGTGTGTCTCTG-CTACTTGTGTCTCTGCTAC 525
Sbjct 151323 TATATATATCAATGTGTGTCTCTGC-CATGTGTGTCTCTG-CTACTTGTGTCTCTGCTAC 525

Sbjct 72359 TATATATGTCTGTGTGTATGTGTTTCATGTGTGTCTCTGTGTGAGTGTGTCTCTGTGTT 72418
 Query 526 TGTAGCATGAATGTGTCTCTGC 547
 Sbjct 72419 TGT-GTCTGTGTGTGTCTCTGC 72439

Mus musculus, clone RP23-415L22, complete sequence

Sequence ID: **gb|AC137844.8|** Length: 188189 Number of Matches: 1
 Range 1: 80965 to 80997

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	31/35(89%)	2/35(5%)	Plus/Minus	

Features:

Query 856 TGTGTGTCTCTGCTACTATGTGTGTCTCTGCTTAT 890
 Sbjct 80997 TGTGTGTCTCTGCA--TATGTGTGTCTCTGCATAT 80965

Oryzias latipes hox gene cluster, complete cds, contains hoxDb

Sequence ID: **dbj|AB232924.1|** Length: 220448 Number of Matches: 1
 Range 1: 171107 to 171165

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

Features:

Query 856 TGTGTGTCTCTGCTACTATGTGTGTCTCTGCTTATATCGTG-CATATCATGTGTGTCTCT 914
 Sbjct 171107 TGTGTGTCTCTGTTCCCTGTGTGTGTCTCTGGTCTTGT-GTGTAATGTCCTGTGTGTGTCT 171165

Mus musculus BAC clone RP23-321H9 from chromosome 3, complete sequence

Sequence ID: **gb|AC159281.3|** Length: 229114 Number of Matches: 1
 Range 1: 191403 to 191450

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	38/48(79%)	0/48(0%)	Plus/Minus	

Features:

Query 481 GTGTGTCTCTGCCATGTGTGTCTCTGCTACTTGTGTCTCTGCTACTGT 528
 Sbjct 191450 GTGTGTCTCTACATACGTGTGTCTCACATACGTGTGTCTCTGCGACTGT 191403

Mus musculus chromosome 1, clone RP23-6F21, complete sequence

Sequence ID: **gb|AC116380.14|** Length: 232429 Number of Matches: 1
 Range 1: 88552 to 88595

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

Features:

Query 484 TGTCTCTGCCATGTGTGTCTCTGCTACTTGTGTCTCTGCTACTGT 528
 Sbjct 88595 TGTCTCTTCCCTGTCTGTCTCTGTCTCTGTGTCTCTGCT-CTGT 88552

Human DNA sequence from clone RP4-668J24 on chromosome 6p25.1-25.3, complete sequence

Sequence ID: **emb|AL034346.31|** Length: 120429 Number of Matches: 1
 Range 1: 46830 to 46881

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	45/56(80%)	4/56(7%)	Plus/Minus	

Features:

Query 857 GTGTGTCTCTGCTACTATGTGTGTCTCTGCTTATATCGTGCATATCATGTGTGTCT 912
 Sbjct 46881 GTGTGTCTGTGC--CTATGTGTGTCTGTGTCTATGTC-TGCATGT-GTGTGTGTCT 46830

Sequence ID: **emb|CR380949.1** Length: 558804 Number of Matches: 3
Range 1: 524597 to 524639

Features:

Range 2: 524597 to 524639

Features:

Range 3: 524597 to 524639

Features:

Sequence ID: **gb|AC112699.3|** Length: 60933 Number of Matches: 1
Range 1: 11959 to 12005

Features:

Sequence ID: **gb|AC093545.1** Length: 174725 Number of Matches: 2
Range 1: 151045 to 151077

Features:

Range 2: 151045 to 151077

Features:

Mus musculus BAC clone RP23-425F13 from chromosome 5, complete sequence

Sequence ID: **gb|AC152721.3|** Length: 221637 Number of Matches: 1
Range 1: 21850 to 21884

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	32/37(86%)	2/37(5%)	Plus/Minus	

Features:

```
Query 264 ATGCATTTATGTGTGTCTCTGCCATGTGTGTCTCTGC 300
      |||
Sbjct 21884 ATGCAT--ATGTGTGTCTGTGTCTATGTGTGTCTGTGC 21850
```

Mus musculus chromosome 1, clone RP23-242C11, complete sequence

Sequence ID: **gb|AC165413.16|** Length: 186380 Number of Matches: 1
Range 1: 180408 to 180473

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	50/66(76%)	5/66(7%)	Plus/Plus	

Features:

```
Query 854 CATGTGTGTCTCTGCTACTATGTG--TGTCTCTGCTTATAT---CGTGCATATCATGTGT 908
      |||
Sbjct 180408 CATGTGTGTCTGTGTCTCTATGTGTCTGTATGTGCATATATGTGCATGCATGTCGTGTGT 180467

Query 909 GTCTCT 914
      |||
Sbjct 180468 GTTTCT 180473
```

Mus musculus BAC clone RP23-422D12 from chromosome 6, complete sequence

Sequence ID: **gb|AC173480.1|** Length: 185966 Number of Matches: 1
Range 1: 86745 to 86800

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	45/57(79%)	2/57(3%)	Plus/Minus	

Features:

```
Query 855 ATGTGTGTCTCTGCTACTATGTGTGTCTCTGCTTATATCGTGCAT-ATCATGTGTGT 910
      |||
Sbjct 86800 ATGTGTATATTTGTGTCTATGTGTGTCTCTGTGTATAT-GTGTATGTTTCATGTGTGT 86745
```

Mus musculus chromosome 1, clone RP24-278B15, complete sequence

Sequence ID: **gb|AC145691.5|** Length: 164151 Number of Matches: 1
Range 1: 24984 to 25049

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	50/66(76%)	5/66(7%)	Plus/Plus	

Features:

```
Query 854 CATGTGTGTCTCTGCTACTATGTG--TGTCTCTGCTTATAT---CGTGCATATCATGTGT 908
      |||
Sbjct 24984 CATGTGTGTCTGTGTCTCTATGTGTCTGTATGTGCATATATGTGCATGCATGTCGTGTGT 25043

Query 909 GTCTCT 914
      |||
Sbjct 25044 GTTTCT 25049
```

Mus musculus BAC clone RP24-492M8 from 5, complete sequence

Sequence ID: **gb|AC134523.5|** Length: 178801 Number of Matches: 1
Range 1: 87624 to 87683

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	50/64(78%)	8/64(12%)	Plus/Minus	

Features:

```
Query 856 TGTGTG--TCTCTGCTACTATGTGTGTCTCTGCTTATAT-CGTGCATATC-ATGTGTGTC 911
      |||
Sbjct 87683 TGTGTGCATCTCTG-----TATGTGTGTCTCTGTGTGTATGTGTGCATCTCTGTGTGTGTC 87628

Query 912 TCTG 915
      |||
Sbjct 87627 TCTG 87624
```

Mouse DNA sequence from clone RP24-460H24 on chromosome 11, complete sequence

Sequence ID: **emb|BX000996.4|** Length: 84095 Number of Matches: 1

Range 1: 27931 to 27988

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	48/61(79%)	4/61(6%)	Plus/Minus	

Features:

```
Query   856      TGTGTGTCTCTGCTACTATGTGTGTCTCTGCTTATAT-CGTGCATATCATGTGTGTCTCT   914
          |||
Sbjct   27988    TGTGTGTCTCTGAGTCTCTGTGTGTCTCTGTGTGTGTACCTG--TATC-TGTGTGTCTCT   27932

Query   915      G      915
          |
Sbjct   27931    G      27931
```

Mouse DNA sequence from clone RP23-150J22 on chromosome 15, complete sequence

Sequence ID: **emb|AL513354.14|** Length: 227073 Number of Matches: 1

Range 1: 165379 to 165455

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	61/81(75%)	4/81(4%)	Plus/Minus	

Features:

```
Query   828      TATATATATCATTATATCGTGCATATCATGTGTGTCTCTGCTACTATGTGTGTCTCTGCT   887
          |||
Sbjct   165455    TATATATGTGTGTGTAT-GTGTATAT-ATGTGTGTATGTGTATATATGTGTGTCTGTGTG   165398

Query   888      TATATCGTGCATATCATGTGT   908
          |||
Sbjct   165397    TATAT-GTGTATAT-ATGTGT   165379
```

Homo sapiens genomic DNA, chromosome 21q, section 89/105

Sequence ID: **dbj|AP001745.1|** Length: 336578 Number of Matches: 1

Range 1: 330988 to 331036

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	48/57(84%)	8/57(14%)	Plus/Minus	

Features:

```
Query   855      ATGTGTGTCTCTGCTACTATGTGTGTCTCTGCTTATATCGTGCATATCATGTGTGTC   911
          |||
Sbjct   331036    ATGTGTGTCTCTG-TA-TATGTGTGTCTCTG--TATAT-GTG--TGTC-TGTGTGTC   330988
```

Homo sapiens genomic DNA, chromosome 21, clone:KB1430A10, MX1-D21S171 region, complete sequence

Sequence ID: **dbj|AP001622.1|** Length: 149850 Number of Matches: 1

Range 1: 20679 to 20727

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	48/57(84%)	8/57(14%)	Plus/Minus	

Features:

```
Query   855      ATGTGTGTCTCTGCTACTATGTGTGTCTCTGCTTATATCGTGCATATCATGTGTGTC   911
          |||
Sbjct   20727    ATGTGTGTCTCTG-TA-TATGTGTGTCTCTG--TATAT-GTG--TGTC-TGTGTGTC   20679
```

Homo sapiens genomic DNA, chromosome 21, clone:KB1342D7, MX1-D21S171 region, complete sequence

Sequence ID: **dbj|AP001621.1|** Length: 144087 Number of Matches: 1

Range 1: 95244 to 95292

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	48/57(84%)	8/57(14%)	Plus/Minus	

Features:

```
Query   855      ATGTGTGTCTCTGCTACTATGTGTGTCTCTGCTTATATCGTGCATATCATGTGTGTC   911
          |||
Sbjct   95292    ATGTGTGTCTCTG-TA-TATGTGTGTCTCTG--TATAT-GTG--TGTC-TGTGTGTC   95244
```

Homo sapiens clone DJ1015P16A, complete sequence

Sequence ID: **gb|AC007486.1|AC007486** Length: 174725 Number of Matches: 2

Range 1: 151045 to 151077

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

Features:

Query	534	GAATGTGT-CTCTGCTACTGTAGCATGAAATGT	565
Sbjct	151077	GAATGTGTACTCTGCTGCTGTTGCATGAAATGT	151045

Range 2: 151045 to 151077

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

Features:

Query	387	GAATGTGT-CTCTGCTACTGTAGCATGAAATGT	418
Sbjct	151077	GAATGTGTACTCTGCTGCTGTTGCATGAAATGT	151045