

# BLAST ®

## Basic Local Alignment Search Tool

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CTGA

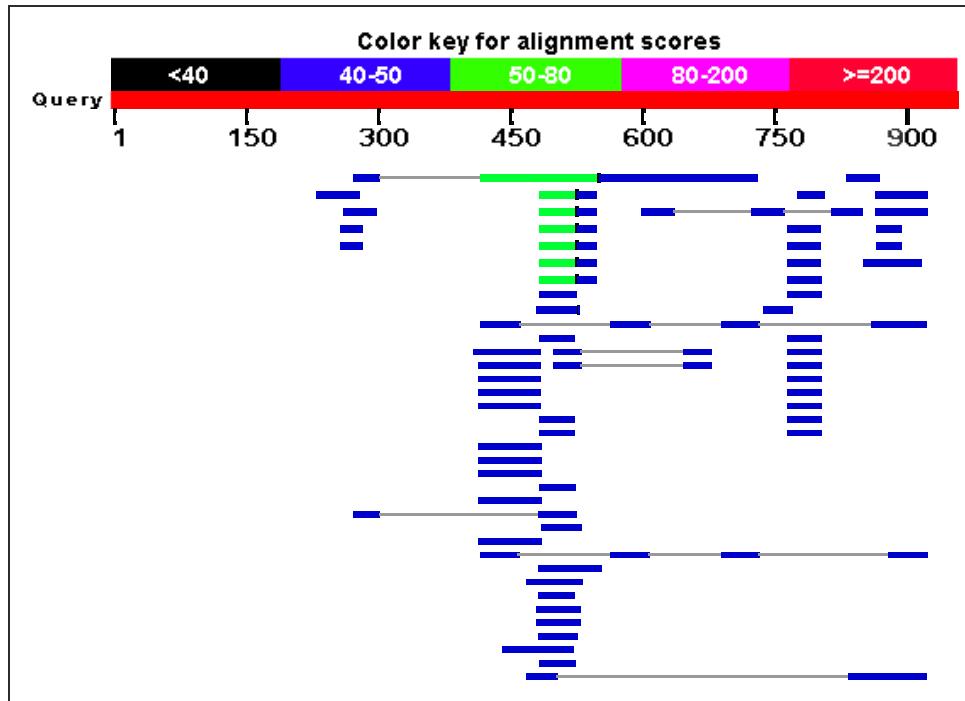
RID [Y0TWPPJ501R](#) (Expires on 08-06 13:11 pm)

Query ID Icl|212489  
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 189 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 RP13-102H20 on chromosome X, complete sequence	68.0	628	35%	2e-07	75%	<a href="#">AL590131.8</a>
Homo sapiens interferon (alpha, beta and omega) receptor 1 (IFNAR1) gene, complete cds	51.8	638	6%	0.015	90%	<a href="#">AY654286.1</a>
Homo sapiens genomic DNA, chromosome 21q22.1, segment 15/28, complete sequence	51.8	638	6%	0.015	90%	<a href="#">AP000044.1</a>
Homo sapiens genomic DNA, chromosome 21q, section 60/105	51.8	638	6%	0.015	90%	<a href="#">AP001716.1</a>
Homo sapiens genomic DNA, chromosome 21q22.1, D21S226-AML region, clone:D71A4, complete sequence	51.8	638	6%	0.015	90%	<a href="#">AP000296.1</a>
Homo sapiens genomic DNA, chromosome 21q22.1, D21S226-AML region, clone Q78C10-f32E9, segment 15/21, complete sequence	51.8	638	6%	0.015	90%	<a href="#">AP000188.1</a>
Homo sapiens genomic DNA of 21q22.1, GART and AML related, Q78C10-149C3 region, segment 15/20	51.8	638	6%	0.015	90%	<a href="#">AP000112.1</a>
Plasmodium yoelii yoelii str. 17XNL peptidyl prolyl cis-trans isomerase (PY01794) partial mRNA	50.0	99	4%	0.051	86%	<a href="#">XM_724503.1</a>
Plasmodium chabaudi chabaudi hypothetical protein (PC405113.00.00) partial mRNA	50.0	272	5%	0.051	84%	<a href="#">XM_735345.1</a>
Postia placenta clone ACWS09-E13, complete sequence	48.2	187	19%	0.18	81%	<a href="#">AC242745.1</a>
Apis mellifera mast cell-degranulating peptide (Mcdp), mRNA	48.2	48.2	4%	0.18	88%	<a href="#">NM_001011611.2</a>
Gorilla DNA sequence from clone CH255-56N15, complete sequence	48.2	48.2	8%	0.18	75%	<a href="#">CU104674.1</a>
Homo sapiens HLA class III region containing NOTCH4 gene, partial sequence, homeobox PBX2 (HPBX) gene, receptor for advanced glycosylation end products (RAGE) gene, complete cds, and 6 unidentified cds, complete sequence	48.2	48.2	7%	0.18	77%	<a href="#">U89336.1</a>
Human DNA sequence from clone DASS-39F23 on chromosome 6, complete sequence	48.2	48.2	7%	0.18	77%	<a href="#">BX284686.9</a>
Human DNA sequence from clone DAQB-143M3 on chromosome 6, complete sequence	48.2	48.2	7%	0.18	77%	<a href="#">AL845464.5</a>
Human DNA sequence from clone CH501-300A18 on chromosome 6, complete sequence	48.2	48.2	7%	0.18	77%	<a href="#">AL662884.11</a>
mast cell-degranulating peptide [Apis mellifera=worker bees, venom glands, mRNA Partial, 369 nt]	48.2	48.2	4%	0.18	88%	<a href="#">S78459.1</a>
Apis mellifera apamin protein (Apamin), mRNA	48.2	48.2	4%	0.18	88%	<a href="#">NM_001011612.1</a>
Human DNA sequence from clone DAMC-108L3 on chromosome 6, complete sequence	48.2	48.2	7%	0.18	77%	<a href="#">CR933878.7</a>
Human DNA sequence from clone DAAP-218M18 on chromosome 6, complete	48.2	48.2	7%	0.18	77%	<a href="#">CR812478.6</a>

sequence							
Human DNA sequence from clone DAMA-358M23 on chromosome 6, complete sequence	48.2	48.2	7%	0.18	77%	<a href="#">BX927239.5</a>	
Botryotinia fuckeliana T4 SupSuperContig_8_105_1 genomic supercontig	46.4	92.7	7%	0.62	89%	<a href="#">FQ790346.1</a>	
Plasmodium falciparum 3D7 conserved Plasmodium protein, unknown function (MAL4P1.163) mRNA, complete cds	46.4	46.4	6%	0.62	78%	<a href="#">XM_002808612.1</a>	
Plasmodium falciparum 3D7 chromosome 4	46.4	46.4	6%	0.62	78%	<a href="#">AL844503.1</a>	
Zebrafish DNA sequence from clone DKEY-30J9 in linkage group 25, complete sequence	46.4	46.4	3%	0.62	91%	<a href="#">CR933757.8</a>	
Homo sapiens cosmid D66B10, chromosome 21 5' of IFNAR1	46.4	755	4%	0.62	88%	<a href="#">AF039904.1</a>	
Human DNA sequence from clone CH502-105D18 on chromosome 6, complete sequence	46.4	46.4	7%	0.62	77%	<a href="#">AL662828.5</a>	
Human DNA sequence from clone RP3-418A9 on chromosome 6q21, complete sequence	46.4	89.1	7%	0.62	84%	<a href="#">Z84480.1</a>	
Oryza sativa Japonica Group genomic DNA, chromosome 9, PAC clone:P0668D04	46.4	46.4	2%	0.62	96%	<a href="#">AP005426.3</a>	
Oryza sativa Japonica Group genomic DNA, chromosome 9, PAC clone:P0701F11	46.4	46.4	2%	0.62	96%	<a href="#">AP005429.3</a>	
Plasmodium yoelii yoelii str. 17XNL hypothetical protein (PY05377) partial mRNA	46.4	46.4	4%	0.62	82%	<a href="#">XM_720735.1</a>	
Aegirocystis lacustris clone E33DIFJ02JN0T4 microsatellite sequence	44.6	44.6	6%	2.2	78%	<a href="#">GQ194915.1</a>	
Pan troglodytes BAC clone CH251-607M18 from chromosome 6, complete sequence	44.6	44.6	7%	2.2	76%	<a href="#">AC190421.3</a>	
Rattus norvegicus strain Brown Norway chromosome 6 clone RP31-263K14, complete sequence	44.6	44.6	5%	2.2	82%	<a href="#">AC079389.2</a>	
Homo sapiens chromosome 16 clone CTD-2535I10, complete sequence	44.6	178	17%	2.2	83%	<a href="#">AC093515.4</a>	
Plasmodium yoelii yoelii str. 17XNL hypothetical protein (PY07183) partial mRNA	44.6	44.6	7%	2.2	76%	<a href="#">XM_722897.1</a>	
Mouse DNA sequence from clone RP23-479D16 on chromosome X, complete sequence	44.6	44.6	6%	2.2	78%	<a href="#">AL807398.8</a>	
PREDICTED: Microtus ochrogaster anaphase promoting complex subunit 1 (Anapc1), mRNA	42.8	128	11%	7.6	86%	<a href="#">XM_005365655.1</a>	
Neospora caninum Liverpool complete genome, chromosome IX	42.8	42.8	3%	7.6	87%	<a href="#">FR823385.1</a>	
Pongo abelii BAC clone CH276-51D13 from chromosome unknown, complete sequence	42.8	42.8	4%	7.6	83%	<a href="#">AC226682.2</a>	
Plasmodium falciparum 3D7 conserved Plasmodium protein, unknown function (PF13_0148) mRNA, complete cds	42.8	42.8	5%	7.6	83%	<a href="#">XM_002808990.1</a>	
Mus musculus predicted gene 8728 (Gm8728) pseudogene on chromosome 7	42.8	42.8	3%	7.6	87%	<a href="#">NG_019220.1</a>	
Mus musculus predicted gene 8685 (Gm8685) pseudogene on chromosome 7	42.8	42.8	3%	7.6	87%	<a href="#">NG_019213.1</a>	
Mus musculus predicted gene 8486 (Gm8486) pseudogene on chromosome 7	42.8	42.8	3%	7.6	87%	<a href="#">NG_019185.1</a>	

Plasmodium falciparum 3D7 chromosome 13	42.8	42.8	5%	7.6	83%	<a href="#">AL844509.2</a>
Pan troglodytes BAC clone CH251-623J17 from chromosome x, complete sequence	42.8	42.8	4%	7.6	84%	<a href="#">AC193009.2</a>
Sus scrofa clone KVL2978 microsatellite sequence	42.8	42.8	8%	7.6	77%	<a href="#">EF132836.1</a>
Mus musculus chromosome 7, clone RP23-287I20, complete sequence	42.8	42.8	2%	7.6	96%	<a href="#">AC101716.6</a>
Apis cerana cerana mast cell degranulating peptide precursor, mRNA, complete cds	42.8	42.8	4%	7.6	85%	<a href="#">AY327447.1</a>
Mus musculus BAC clone RP23-362F11 from chromosome 7, complete sequence	42.8	42.8	3%	7.6	87%	<a href="#">AC151988.3</a>
Mus musculus BAC clone RP23-82H2 from chromosome 7, complete sequence	42.8	42.8	3%	7.6	87%	<a href="#">AC133951.3</a>
Mus musculus chromosome 1, clone RP24-228M19, complete sequence	42.8	42.8	3%	7.6	88%	<a href="#">AC161221.7</a>
Mus musculus chromosome 7, clone RP23-332G12, complete sequence	42.8	42.8	2%	7.6	96%	<a href="#">AC164001.4</a>
Mus musculus BAC clone RP23-6N4 from chromosome 7, complete sequence	42.8	42.8	3%	7.6	87%	<a href="#">AC161002.2</a>
Mus musculus BAC clone RP23-145O23 from chromosome 7, complete sequence	42.8	42.8	3%	7.6	87%	<a href="#">AC150900.5</a>
Homo sapiens chromosome 3 clone RP11-523D22, complete sequence	42.8	85.5	12%	7.6	73%	<a href="#">AC104305.2</a>
Zebrafish DNA sequence from clone CH211-280H1 in linkage group 17, complete sequence	42.8	85.5	6%	7.6	88%	<a href="#">BX469900.4</a>
Mus musculus BAC clone RP23-248K5 from chromosome 7, complete sequence	42.8	42.8	3%	7.6	87%	<a href="#">AC168909.4</a>
Mus musculus BAC clone RP24-101E7 from chromosome 7, complete sequence	42.8	42.8	3%	7.6	87%	<a href="#">AC171682.2</a>
Mus musculus BAC clone RP24-163J14 from chromosome 7, complete sequence	42.8	42.8	3%	7.6	87%	<a href="#">AC171240.3</a>
Mus musculus BAC clone RP23-170J16 from chromosome 7, complete sequence	42.8	42.8	3%	7.6	87%	<a href="#">AC168854.4</a>
Mus musculus BAC clone RP23-182D23 from chromosome 7, complete sequence	42.8	42.8	3%	7.6	87%	<a href="#">AC171196.1</a>
Mus musculus BAC clone RP23-88M21 from chromosome 7, complete sequence	42.8	42.8	3%	7.6	87%	<a href="#">AC164312.3</a>
Zebrafish DNA sequence from clone CH211-195M7, complete sequence	42.8	85.5	6%	7.6	88%	<a href="#">AL805945.5</a>

## Alignments

Human DNA sequence from clone RP13-102H20 on chromosome X, complete sequence  
Sequence ID: [emb|AL590131.8|](#) Length: 146343 Number of Matches: 13  
Range 1: 114641 to 114764

Score	Expect	Identities	Gaps	Strand	Frame
68.0 bits(74)	2e-07()	101/135(75%)	14/135(10%)	Plus/Plus	

Features:

Query 416	ATATATAGAGATG-AACACAG-TATGCACAGCATATATAGAGATGACCGAGTGTGACACAC	473
Sbjct 114641	ATATATAGAGATGGAATATAGATATATGGAAATATAGAGATG--GAATAT-AGATAT	114697

Query	474	ACA-GCCATATATAGAGATGGCATATATAGAGATGACGAATATAGAGATGACGATACTGC	532
Sbjct	114698	ATATGGAATATATAGAGATGGAATATATAGAGATG--GAATATAGATAT---ATATGGA	114751
Query	533	ATCCATATAGAGATG 547	
Sbjct	114752	AT---ATATAGAGATG 114764	

Range 2: 114374 to 114589

Score	Expect	Identities	Gaps	Strand	Frame
51.8 bits(56)	0.015()	172/255(67%)	47/255(18%)	Plus/Plus	
Features:					
Query	482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATGACGATACTGCATCCATATA	541		
Sbjct	114374	ATATATATATGGAATATATAGAGATG--GAATATAGA---GATATGGAAT---ATATA	114423		
Query	542	GAGAT-GACGATA---CTGCATCCCATATATAGAGAT-GAACACAG-TATGCACAGCATA	595		
Sbjct	114424	GAGATGGAATATAGAGATATGGAATATATAGAGATGGAATATAGATAATATGGAATA	114483		
Query	596	TATAGAGATGACGAGTGTGACACACACAGCAACACAGTATGCACAGCATATATAGAGATG	655		
Sbjct	114484	TATAGAGATG--GAATAT-AGATATA-----TATG---GAATATATAGAGATG	114525		
Query	656	ACGAATATAGAGATGACGATACTGCATCCCATATATAGAGAT-GAACACAG-TATGCACA	713		
Sbjct	114526	--GAATATAGATAT---ATA-TGGA---ATATATAGAGATGGAATATAGATATATG	114574		
Query	714	GCATATATAGAGATG 728			
Sbjct	114575	GAATATATAGAGATG 114589			

Range 3: 112919 to 112957

Score	Expect	Identities	Gaps	Strand	Frame
50.0 bits(54)	0.051()	36/41(88%)	2/41(4%)	Plus/Plus	
Features:					
Query	482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522			
Sbjct	112919	ATATAGAGATGGAATATATAGAAATG--GAATATATAGATG 112957			

Range 4: 114449 to 114717

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	214/320(67%)	58/320(18%)	Plus/Plus	
Features:					
Query	416	ATATATAGAGATG-AACACAG-TATGCACAGCATATATAGAGATGACGAGTGTGACACAC	473		
Sbjct	114449	ATATATAGAGATGGAATATAGATATATGGAATATATAGAGATG--GAATAT-AGATAT	114505		
Query	474	ACA-GCCATATATAGAGATGGCATATATAGAGATGACGAATATAGAGATGACGATACTGC	532		
Sbjct	114506	ATATGGAATATATAGAGATGGAATATAGATATATGGAATATATAGA-GA-----TGG	114558		
Query	533	ATCCATATAGAGATGACGATACTGCATCCCATATATAGAGAT-GAACACAG-TATGCACA	590		
Sbjct	114559	A---ATATAGATAT---ATA-TGGA---ATATATAGAGATGGAATATAGATATATG	114606		
Query	591	GCATATATAGAGATGACGAGTGTGACACACACAGCAACACAGTATGCACAGCATATATAG	650		
Sbjct	114607	GAATATATAGAGATG--GAATAT-AGATATA-----TATG---GAATATATAG	114648		
Query	651	AGATGACGAATATAGAGATGACGATACTGCATCCCATATATAGAGAT-GAACACAG-TAT	708		
Sbjct	114649	AGATG--GAATATAGATAT---ATA-TGGA---ATATATAGAGATGGAATATAGATAT	114697		
Query	709	GCACAGCATATATAGAGATG 728			
Sbjct	114698	ATATGGAATATATAGAGATG 114717			

Range 5: 114513 to 114617

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	79/108(73%)	6/108(5%)	Plus/Plus	
Features:					
Query	416	ATATATAGAGATG-AACACAG-TATGCACAGCATATATAGAGATGACGAGTGTGACACAC	473		
Sbjct	114513	ATATATAGAGATGGAATATAGATATATGGAATATATAGAGATG--GAATAT-AGATAT	114569		
Query	474	ACA-GCCATATATAGAGATGGCATATATAGAGATGACGAATATAGAGA 520			
Sbjct	114570	ATATGGAATATATAGAGATGGAATATAGATATATGGAATATATAGA 114617			

Range 6: 114545 to 114649

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	79/108(73%)	6/108(5%)	Plus/Plus	

Features:

Query 416	ATATATAGAGATG-AACACAG-TATGCACAGCATATATAGAGATGACGAGTGTGACACAC 	473
Sbjct 114545	ATATATAGAGATGGAATATAGATATATATGGAATATATAGAGATG--GAATAT-AGATAT	114601
Query 474	ACA-GCCATATATAGAGATGGCATATATAGAGATGACGAATATAGAGA 	520
Sbjct 114602	ATATGGAATATATAGAGATGGAATATAGATATATATGGAATATATAGA	114649

Range 7: 114577 to 114681

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	79/108(73%)	6/108(5%)	Plus/Plus	

Features:

Query 416	ATATATAGAGATG-AACACAG-TATGCACAGCATATATAGAGATGACGAGTGTGACACAC 	473
Sbjct 114577	ATATATAGAGATGGAATATAGATATATATGGAATATATAGAGATG--GAATAT-AGATAT	114633
Query 474	ACA-GCCATATATAGAGATGGCATATATAGAGATGACGAATATAGAGA 	520
Sbjct 114634	ATATGGAATATATAGAGATGGAATATAGATATATATGGAATATATAGA	114681

Range 8: 112874 to 112916

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/43(84%)	0/43(0%)	Plus/Plus	

Features:

Query 480	ATATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 	522
Sbjct 112874	ATATATATAGATGGAATATATAGATGGAATATATAGAGATG	112916

Range 9: 114705 to 114732

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

Features:

Query 273	ATATATAGAGATGGCATATATAGAGATG 	300
Sbjct 114705	ATATATAGAGATGGAATATATAGAGATG	114732

Range 10: 114387 to 114653

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	214/322(66%)	64/322(19%)	Plus/Plus	

Features:

Query 416	ATATATAGAGATG-AACACAG---TATGCACAGCATATATAGAGATGACGAGTGTGACAC 	471
Sbjct 114387	ATATATAGAGATGGAATATAGAGATATGGA---ATATATAGAGATG--GAATAT-AGAG	114439
Query 472	ACACA-GCCATATATAGAGATGGCATATATAGAGATGACGAATATAGAGATGACGATACT 	530
Sbjct 114440	ATATATGGAATATATAGAGATGGAATATAGATATATGGAATATATAGA-GA-----T	114492
Query 531	GCATCCATATAGAGATGACGATACTGCATCCCATAATAGAGAT-GAACACAG-TATGCA 	588
Sbjct 114493	GGA---ATATAGATAT---ATA-TGGA---ATATATAGAGATGGAATATAGATATA 	114540
Query 589	CAGCATATATAGAGATGACGAGTGTGACACACACAGCAACACAGTATGCACAGCATAT 	648
Sbjct 114541	TGGAATATATAGAGATG--GAATAT-AGATATA-----TATG---GAATATAT 	114582
Query 649	AGAGATGACGAATATAGAGATGACGATACTGCATCCCATAATAGAGAT-GAACACAG-T 	706
Sbjct 114583	AGAGATG--GAATATAGATAT---ATA-TGGA---ATATATAGAGATGGAATATAGAT 	114631
Query 707	ATGCACAGCATATATAGAGATG 	728
Sbjct 114632	ATATATGGAATATATAGAGATG	114653

Range 11: 112889 to 112916

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

## Features:

Query	273	ATATATAGAGATGGCATATATAGAGATG	300
Sbjct	112889	ATATATATAGATGGAATATATAGAGATG	112916

Range 12: 112904 to 112940

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/41(85%)	4/41(9%)	Plus/Plus	

## Features:

Query	480	ATATATAGAGATGGCATATATAGAGATGACGAATATAGAGA	520
Sbjct	112904	ATATATAGAGATGG--AAATATAGAGATG--GAATATATAGA	112940

Range 13: 114673 to 114776

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	79/109(72%)	8/109(7%)	Plus/Plus	

## Features:

Query	416	ATATATAGAGAT-GAACACAG-TATGCCACAGCATATATAGAGATGACGAGTGTGACACAC	473
Sbjct	114673	ATATATAGAGATGGAATATAGATATATGGAATATATAGAGATG--GAATAT-ATAGAG	114729
Query	474	ACAG-CCATATATAGAGATGGCATATATAGAGATGACGAATATAGAGAT	521
Sbjct	114730	ATGGAATATAGATATATGGAATATATAGAGATG--GACTATATAGAT	114776

Homo sapiens interferon (alpha, beta and omega) receptor 1 (**IFNAR1**) gene, complete cds

Sequence ID: **gb|AY654286.1** | Length: 35410 Number of Matches: 14

Range 1: 356 to 392

Score	Expect	Identities	Gaps	Strand	Frame
51.8 bits(56)	0.015()	37/41(90%)	4/41(9%)	Plus/Plus	

## Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522  
Sbjct 356 ATATAGAGATGCC--ATATAGAGATG--GAATATAGAGATG 392

Range 2: 454 to 490

Score	Expect	Identities	Gaps	Strand	Frame
51.8 bits(56)	0.015()	37/41(90%)	4/41(9%)	Plus/Plus	

#### Features:

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Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522
Sbjct 454 ATATAGAGATGGC--ATATAGAGATG--GAATATAGAGATG 490

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Range 3: 278 to 340

Score	Expect	Identities	Gaps	Strand	Frame
50.0 bits(54)	0.051()	53/67(79%)	5/67(7%)	Plus/Plus	

## Features:

Query	482	ATATAGAGATGGCATATATAAGAGATGACCAATATAGAGATGAC-GATACTGCATCCATAT	540
Sbjct	278	ATATAGAGATGCC--ATATAGAGATG--GCATATAGAGATGGCATATAGAGATGGCATAT	333
Query	541	AGAGATG 547	
Sbjct	334	AGAGATG 340	

Range 4: 330 to 366

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/41(88%)	4/41(9%)	Plus/Plus	

Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522  
Sbjct 330 ATATAGAGATGGC--ATATAGAGATG--GCATATAGAGATG 366

Range 5: 780 to 816

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/41(88%)	4/41(9%)	Plus/Plus	

Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522  
Sbjct 780 ATATAGAGATGG--GATATAGAGATG--GAATATAGAGATG 816

Range 6: 806 to 842

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/41(88%)	4/41(9%)	Plus/Plus	

Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522  
Sbjct 806 ATATAGAGATGG--GATATAGAGATG--GAATATAGAGATG 842

Range 7: 871 to 907

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/41(88%)	4/41(9%)	Plus/Plus	

Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522  
Sbjct 871 ATATAGAGATGGAATATAT--AGATG--GAATATAGAGATG 907

Range 8: 253 to 314

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	51/66(77%)	5/66(7%)	Plus/Plus	

Features:

Query 483 TATAGAGATGGCATATATAGAGATGACGAATATAGAGATGAC-GATACTGCATCCATATA 541  
Sbjct 253 TATAGAGATGGCATATAT--ATATG--GCATATAGAGATGGCATATAGAGATGGCATATA 308  
Query 542 GAGATG 547  
Sbjct 309 GAGATG 314

Range 9: 565 to 601

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/41(85%)	4/41(9%)	Plus/Plus	

Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522  
Sbjct 565 ATATAGAGATGG--AATATAGAGATG--GGATATAGAGATG 601

Range 10: 591 to 627

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/41(85%)	4/41(9%)	Plus/Plus	

Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522  
Sbjct 591 ATATAGAGATGG--GATATAGAGATG--GGATATAGAGATG 627

Range 11: 617 to 653

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/41(85%)	4/41(9%)	Plus/Plus	

42.8 bits(46) 7.6() 35/41(85%) 4/41(9%) Plus/Plus

Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522  
Sbjct 617 ATATAGAGATGG--GATATAGAGATG--GGATATAGAGATG 653

Range 12: 643 to 679

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/41(85%)	4/41(9%)	Plus/Plus	

Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522  
Sbjct 643 ATATAGAGATGG--GATATAGTGTG--GAATATAGAGATG 679

Range 13: 754 to 790

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/41(85%)	4/41(9%)	Plus/Plus	

Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522  
Sbjct 754 ATATAGAGATGG--AATATAGAGATG--GGATATAGAGATG 790

Range 14: 832 to 868

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/41(85%)	4/41(9%)	Plus/Plus	

Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522  
Sbjct 832 ATATAGAGATGG--GATATAGAGATG--GAATATAGTGTG 868

Homo sapiens genomic DNA, chromosome 21q22.1, segment 15/28, complete sequence

Sequence ID: **dbj|AP000044.1|** Length: 100000 Number of Matches: 14

Range 1: 45275 to 45311

Score	Expect	Identities	Gaps	Strand	Frame
51.8 bits(56)	0.015()	37/41(90%)	4/41(9%)	Plus/Plus	

Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522  
Sbjct 45275 ATATAGAGATGGC--ATATAGAGATG--GAATATAGAGATG 45311

Range 2: 45373 to 45409

Score	Expect	Identities	Gaps	Strand	Frame
51.8 bits(56)	0.015()	37/41(90%)	4/41(9%)	Plus/Plus	

Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522  
Sbjct 45373 ATATAGAGATGGC--ATATAGAGATG--GAATATAGAGATG 45409

Range 3: 45197 to 45259

Score	Expect	Identities	Gaps	Strand	Frame
50.0 bits(54)	0.051()	53/67(79%)	5/67(7%)	Plus/Plus	

Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATGAC-GATACTGCATCCAT 540  
Sbjct 45197 ATATAGAGATGGC--ATATAGAGATG--GCATATAGAGATGGCATATAGAGATGGCATAT 45252  
Query 541 AGAGATG 547  
Sbjct 45253 AGAGATG 45259

Range 4: 45249 to 45285

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/41(88%)	4/41(9%)	Plus/Plus	

## Features:

Query	482	ATATAGAGATGGCATATAAGAGATGACGAATATAGAGATG	522
Sbjct	45249	ATATAGAGATGGC--ATATAGAGATG--GCATATAGAGATG	45285

Range 5: 45699 to 45735

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/41(88%)	4/41(9%)	Plus/Plus	

## Features:

Query	482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG	522
Sbjct	45699	ATATAGAGATGG--GATATAGAGATG--GAATATAGAGATG	45735

Range 6: 45725 to 45761

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/41(88%)	4/41(9%)	Plus/Plus	

#### Features:

Query	482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG	522
Sbjct	45725	ATATAGAGATGG--GATATAGAGATG--GAATATAGAGATG	45761

Range 7: 45790 to 45826

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/41(88%)	4/41(9%)	Plus/Plus	

#### Features:

```

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522
Sbjct 45790 ATATAGAGATGAAATATAT--AGATG--GAATATAGAGATG 45826

```

Range 8: 45172 to 45233

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	51/66(77%)	5/66(7%)	Plus/Plus	

#### **Features:**

```

Query 483 TATAGAGATGGCATATATAGAGATGACGAATATAGAGATGAC-GATACTGCATCCATATA 541
Sbjct 45172 TATAGAGATGGCATATAT--ATATG--GCATATAGAGATGCCATATAGAGATGGCATATA 45227

```

Query 542 GAGATG 547  
Sbjct 45228 GAGATG 45233

Range 9: 45484 to 45520

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/41(85%)	4/41(0%)	Plus/Plus	

#### **Features:**

Query	482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG	522
Sbjct	45484	ATATAGAGATGG--AATATAGAGATG--GGATATAGAGATG	45520

Range 10: 45510 to 45546

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/41(85%)	4/41(0%)	Plus/Plus	

#### Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522

Sbjct 45510 ATATAGAGATGG--GATATAGAGATG--GGATATAGAGATG 45546

Range 11: 45536 to 45572

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/41(85%)	4/41(9%)	Plus/Plus	

Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522  
Sbjct 45536 ATATAGAGATGG--GATATAGAGATG--GGATATAGAGATG 45572

Range 12: 45562 to 45598

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/41(85%)	4/41(9%)	Plus/Plus	

Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522  
Sbjct 45562 ATATAGAGATGG--GATATAGTGTGATG--GAATATAGAGATG 45598

Range 13: 45673 to 45709

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/41(85%)	4/41(9%)	Plus/Plus	

Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522  
Sbjct 45673 ATATAGAGATGG--AATATAGAGATG--GGATATAGAGATG 45709

Range 14: 45751 to 45787

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/41(85%)	4/41(9%)	Plus/Plus	

Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522  
Sbjct 45751 ATATAGAGATGG--GATATAGAGATG--GAATATAGTGTGATG 45787

Homo sapiens genomic DNA, chromosome 21q, section 60/105

Sequence ID: **dbj|AP001716.1|** Length: 340000 Number of Matches: 14

Range 1: 271425 to 271461

Score	Expect	Identities	Gaps	Strand	Frame
51.8 bits(56)	0.015()	37/41(90%)	4/41(9%)	Plus/Plus	

Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522  
Sbjct 271425 ATATAGAGATGGC--ATATAGAGATG--GAATATAGAGATG 271461

Range 2: 271523 to 271559

Score	Expect	Identities	Gaps	Strand	Frame
51.8 bits(56)	0.015()	37/41(90%)	4/41(9%)	Plus/Plus	

Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522  
Sbjct 271523 ATATAGAGATGGC--ATATAGAGATG--GAATATAGAGATG 271559

Range 3: 271347 to 271409

Score	Expect	Identities	Gaps	Strand	Frame
50.0 bits(54)	0.051()	53/67(79%)	5/67(7%)	Plus/Plus	

Features:

Query	482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATGAC-GATACTGCATCCATAT	540
Sbjct	271347	.....     .....     .....     .....     .....     .....     .....	
Query	541	ATATAGAGATGGC--ATATAGAGATG--GCATATAGAGATGGCATATAGAGATGGCATAT	271402
Sbjct	271403	.....     .....     .....     .....     .....     .....	
	AGAGATG	547	
	AGAGATG	271409	

Range 4: 271399 to 271435

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/41(88%)	4/41(9%)	Plus/Plus	

Features:

Query	482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG	522
Sbjct	271399	.....     .....     .....     .....     .....	
	ATATAGAGATGGC--ATATAGAGATG--GCATATAGAGATG	271435	

Range 5: 271849 to 271885

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/41(88%)	4/41(9%)	Plus/Plus	

Features:

Query	482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG	522
Sbjct	271849	.....     .....     .....     .....     .....	
	ATATAGAGATGG--GATATAGAGATG--GAATATAGAGATG	271885	

Range 6: 271875 to 271911

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/41(88%)	4/41(9%)	Plus/Plus	

Features:

Query	482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG	522
Sbjct	271875	.....     .....     .....     .....     .....	
	ATATAGAGATGG--GATATAGAGATG--GAATATAGAGATG	271911	

Range 7: 271940 to 271976

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/41(88%)	4/41(9%)	Plus/Plus	

Features:

Query	482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG	522
Sbjct	271940	.....     .....     .....     .....     .....	
	ATATAGAGATGGAATATAT--AGATG--GAATATAGAGATG	271976	

Range 8: 271322 to 271383

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	51/66(77%)	5/66(7%)	Plus/Plus	

Features:

Query	483	TATAGAGATGGCATATATAGAGATGACGAATATAGAGATGAC-GATACTGCATCCATATA	541
Sbjct	271322	.....     .....     .....     .....     .....     .....	
	TATAGAGATGGCATATAT--ATATG--GCATATAGAGATGGCATATAGAGATGGCATATA	271377	

Query	542	GAGATG	547
Sbjct	271378	.....	
	GAGATG	271383	

Range 9: 271634 to 271670

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/41(85%)	4/41(9%)	Plus/Plus	

Features:

Query	482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG	522
Sbjct	271634	.....     .....     .....     .....     .....	
	ATATAGAGATGG--AATATAGAGATG--GGATATAGAGATG	271670	

Range 10: 271660 to 271696

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/41(85%)	4/41(9%)	Plus/Plus	

Features:

Query 482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG	522
Sbjct 271660		
	ATATAGAGATGG--GATATAGAGATG--GGATATAGAGATG	271696

Range 11: 271686 to 271722

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/41(85%)	4/41(9%)	Plus/Plus	

Features:

Query 482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG	522
Sbjct 271686		
	ATATAGAGATGG--GATATAGAGATG--GGATATAGAGATG	271722

Range 12: 271712 to 271748

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/41(85%)	4/41(9%)	Plus/Plus	

Features:

Query 482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG	522
Sbjct 271712		
	ATATAGAGATGG--GATATAGTGTATG--GAATATAGAGATG	271748

Range 13: 271823 to 271859

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/41(85%)	4/41(9%)	Plus/Plus	

Features:

Query 482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG	522
Sbjct 271823		
	ATATAGAGATGG--AATATAGAGATG--GGATATAGAGATG	271859

Range 14: 271901 to 271937

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/41(85%)	4/41(9%)	Plus/Plus	

Features:

Query 482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG	522
Sbjct 271901		
	ATATAGAGATGG--GATATAGAGATG--GAATATAGTGTATG	271937

Homo sapiens genomic DNA, chromosome 21q22.1, D21S226-AML region, clone:D71A4, complete sequence  
Sequence ID: [dbj|AP000296.1](#) Length: 18188 Number of Matches: 14  
Range 1: 11207 to 11243

Score	Expect	Identities	Gaps	Strand	Frame
51.8 bits(56)	0.015()	37/41(90%)	4/41(9%)	Plus/Plus	

Features:

Query 482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG	522
Sbjct 11207		
	ATATAGAGATGGC--ATATAGAGATG--GAATATAGAGATG	11243

Range 2: 11305 to 11341

Score	Expect	Identities	Gaps	Strand	Frame
51.8 bits(56)	0.015()	37/41(90%)	4/41(9%)	Plus/Plus	

Features:

Query 482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG	522
Sbjct 11305		
	ATATAGAGATGGC--ATATAGAGATG--GAATATAGAGATG	11341

Range 3: 11129 to 11191

Score	Expect	Identities	Gaps	Strand	Frame
50.0 bits(54)	0.051()	53/67(79%)	5/67(7%)	Plus/Plus	

Features:

Query 482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATGAC-GATACTGCATCCATAT	540
Sbjct 11129	ATATAGAGATGGC--ATATAGAGATG--GCATATAGAGATGGCATATAGAGATGGCATAT	11184
Query 541	AGAGATG 547	
Sbjct 11185	AGAGATG 11191	

Range 4: 11181 to 11217

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/41(88%)	4/41(9%)	Plus/Plus	

Features:

Query 482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522	
Sbjct 11181	ATATAGAGATGGC--ATATAGAGATG--GCATATAGAGATG 11217	

Range 5: 11631 to 11667

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/41(88%)	4/41(9%)	Plus/Plus	

Features:

Query 482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522	
Sbjct 11631	ATATAGAGATGG--GATATAGAGATG--GAATATAGAGATG 11667	

Range 6: 11657 to 11693

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/41(88%)	4/41(9%)	Plus/Plus	

Features:

Query 482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522	
Sbjct 11657	ATATAGAGATGG--GATATAGAGATG--GAATATAGAGATG 11693	

Range 7: 11722 to 11758

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/41(88%)	4/41(9%)	Plus/Plus	

Features:

Query 482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522	
Sbjct 11722	ATATAGAGATGGAATATAT--AGATG--GAATATAGAGATG 11758	

Range 8: 11104 to 11165

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	51/66(77%)	5/66(7%)	Plus/Plus	

Features:

Query 483	TATAGAGATGGCATATATAGAGATGACGAATATAGAGATGAC-GATACTGCATCCATA	541
Sbjct 11104	TATAGAGATGGCATATAT--ATATG--GCATATAGAGATGGCATATAGAGATGGCATATA	11159
Query 542	GAGATG 547	
Sbjct 11160	GAGATG 11165	

Range 9: 11416 to 11452

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/41(85%)	4/41(9%)	Plus/Plus	

Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522  
Sbjct 11416 ATATAGAGATGG--AATATAGAGATG--GGATATAGAGATG 11452

Range 10: 11442 to 11478

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/41(85%)	4/41(9%)	Plus/Plus	

Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522  
Sbjct 11442 ATATAGAGATGG--GATATAGAGATG--GGATATAGAGATG 11478

Range 11: 11468 to 11504

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/41(85%)	4/41(9%)	Plus/Plus	

Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522  
Sbjct 11468 ATATAGAGATGG--GATATAGAGATG--GGATATAGAGATG 11504

Range 12: 11494 to 11530

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/41(85%)	4/41(9%)	Plus/Plus	

Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522  
Sbjct 11494 ATATAGAGATGG--GATATAGTGTG--GAATATAGAGATG 11530

Range 13: 11605 to 11641

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/41(85%)	4/41(9%)	Plus/Plus	

Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522  
Sbjct 11605 ATATAGAGATGG--AATATAGAGATG--GGATATAGAGATG 11641

Range 14: 11683 to 11719

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/41(85%)	4/41(9%)	Plus/Plus	

Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522  
Sbjct 11683 ATATAGAGATGG--GATATAGAGATG--GAATATAGTGTG 11719

Homo sapiens genomic DNA, chromosome 21q22.1, D21S226-AML region, clone Q78C10-f32E9, segment 15/21, complete sequence

Sequence ID: [dbJ|AP000188.1](#) | Length: 100000 Number of Matches: 14

Range 1: 51251 to 51287

Score	Expect	Identities	Gaps	Strand	Frame
51.8 bits(56)	0.015()	37/41(90%)	4/41(9%)	Plus/Plus	

Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522  
Sbjct 51251 ATATAGAGATGG--ATATAGAGATG--GAATATAGAGATG 51287

Range 2: 51349 to 51385

Score	Expect	Identities	Gaps	Strand	Frame
51.8 bits(56)	0.015()	37/41(90%)	4/41(9%)	Plus/Plus	

51.8 bits(56) 0.015() 37/41(90%) 4/41(9%) Plus/Plus

Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522  
Sbjct 51349 ATATAGAGATGGC--ATATAGAGATG--GAATATAGAGATG 51385

Range 3: 51173 to 51235

Score	Expect	Identities	Gaps	Strand	Frame
50.0 bits(54)	0.051()	53/67(79%)	5/67(7%)	Plus/Plus	

Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATGAC-GATACTGCATCCATAT 540  
Sbjct 51173 ATATAGAGATGGC--ATATAGAGATG--GCATATAGAGATGGCATATAGAGATGGCATAT 51228  
Query 541 AGAGATG 547  
Sbjct 51229 AGAGATG 51235

Range 4: 51225 to 51261

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/41(88%)	4/41(9%)	Plus/Plus	

Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522  
Sbjct 51225 ATATAGAGATGGC--ATATAGAGATG--GCATATAGAGATG 51261

Range 5: 51675 to 51711

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/41(88%)	4/41(9%)	Plus/Plus	

Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522  
Sbjct 51675 ATATAGAGATGG--GATATAGAGATG--GAATATAGAGATG 51711

Range 6: 51701 to 51737

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/41(88%)	4/41(9%)	Plus/Plus	

Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522  
Sbjct 51701 ATATAGAGATGG--GATATAGAGATG--GAATATAGAGATG 51737

Range 7: 51766 to 51802

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/41(88%)	4/41(9%)	Plus/Plus	

Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522  
Sbjct 51766 ATATAGAGATGGAATATAT--AGATG--GAATATAGAGATG 51802

Range 8: 51148 to 51209

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	51/66(77%)	5/66(7%)	Plus/Plus	

Features:

Query 483 TATAGAGATGGCATATATAGAGATGACGAATATAGAGATGAC-GATACTGCATCCATATA 541  
Sbjct 51148 TATAGAGATGGCATATAT--ATATG--GCATATAGAGATGGCATATAGAGATGGCATATA 51203  
Query 542 GAGATG 547  
Sbjct 51204 GAGATG 51209

Range 9: 51460 to 51496

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/41(85%)	4/41(9%)	Plus/Plus	

## Features:

Query	482	ATATAGAGATGGCATATATAGAGATGACGAATATAAGAGATG	522
Sbjct	51460	ATATAGAGATGG--AAATATAGAGATG--GGATATAGAGATG	51496

Range 10: 51486 to 51522

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/41(85%)	4/41(9%)	Plus/Plus	

#### Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522  
Sbjct 51486 ATATAGAGATGG--GATATAGAGATG--GGATATAGAGATG 51522

Range 11: 51512 to 51548

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/41(85%)	4/41(9%)	Plus/Plus	

#### Features:

Query	482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG	522
Sbjct	51512	ATATAGAGATGG--GATATAGAGATG--GGATATAGAGATG	51548

Range 12: 51538 to 51574

Score	Expect	Identities	Gaps	Strand	Frame
42 8 bits(46)	7 6()	35/41(85%)	4/41(9%)	Plus/Plus	

#### **Features:**

Query	482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG	522
Subject	51538	ATATAGAGATGG--GATATAGTGTATG--GAATA TAGAGATG	51574

Range 13: 51649 to 51685

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/41(85%)	4/41(0%)	Plus/Plus	

#### **Features:**

Query	482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG	522
Sbjct	51649	ATATAGAGATGG--AATATAGAGATG--GGATATAGAGATG	51685

Range 14: 51727 to 51763

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/41(85%)	4/41(0%)	Plus/Plus	

#### **Features:**

```

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522
Sbjct 51727 ATATAGAGATGG--GATATAGAGATG--GAATA-TAGTGTATG 51763

```

Homo sapiens genomic DNA of 21q22.1, GART and AML related, Q78C10-149C3 region, segment 15/20

Sequence ID: dbJAP000112.1 | Length: 100000 Number of Matches: 14

Sequence ID: **dbJAF000**  
Range 1: 51251 to 51287

Score	Expect	Identities	Gaps	Strand	Frame
51.8 bits(56)	0.015()	37/41(90%)	4/41(9%)	Plus/Plus	

#### Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522

Sbjct 51251 ATATAGAGATGGC--ATATAGAGATG--GAATATAGAGATG 51287

Range 2: 51349 to 51385

Score	Expect	Identities	Gaps	Strand	Frame
51.8 bits(56)	0.015()	37/41(90%)	4/41(9%)	Plus/Plus	

Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522  
Sbjct 51349 ATATAGAGATGGC--ATATAGAGATG--GAATATAGAGATG 51385

Range 3: 51173 to 51235

Score	Expect	Identities	Gaps	Strand	Frame
50.0 bits(54)	0.051()	53/67(79%)	5/67(7%)	Plus/Plus	

Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATGAC-GATACTGCATCCATAT 540  
Sbjct 51173 ATATAGAGATGGC--ATATAGAGATG--GCATATAGAGATGGCATATAGAGATGGCATAT 51228  
Query 541 AGAGATG 547  
Sbjct 51229 AGAGATG 51235

Range 4: 51225 to 51261

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/41(88%)	4/41(9%)	Plus/Plus	

Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522  
Sbjct 51225 ATATAGAGATGGC--ATATAGAGATG--GCATATAGAGATG 51261

Range 5: 51675 to 51711

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/41(88%)	4/41(9%)	Plus/Plus	

Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522  
Sbjct 51675 ATATAGAGATGG--GATATAGAGATG--GAATATAGAGATG 51711

Range 6: 51701 to 51737

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/41(88%)	4/41(9%)	Plus/Plus	

Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522  
Sbjct 51701 ATATAGAGATGG--GATATAGAGATG--GAATATAGAGATG 51737

Range 7: 51766 to 51802

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/41(88%)	4/41(9%)	Plus/Plus	

Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522  
Sbjct 51766 ATATAGAGATGGAATATAT--AGATG--GAATATAGAGATG 51802

Range 8: 51148 to 51209

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	51/66(77%)	5/66(7%)	Plus/Plus	

Features:

Query	483	TATAGAGATGGCATATATAGAGATGACGAATATAGAGATGAC-GATACTGCATCCATATA	541
Sbjct	51148	TATAGAGATGGCATATAT--ATATG--GCATATAGAGATGGCATATAGAGATGGCATATA	51203
Query	542	GAGATG 547	
Sbjct	51204	GAGATG 51209	

Range 9: 51460 to 51496

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/41(85%)	4/41(9%)	Plus/Plus	

## Features:

```

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522
Sbjct 51460 ATATAGAGATGG--AATATAGAGATG--GGATATAGAGATG 51496

```

Range 10: 51486 to 51522

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/41(85%)	4/41(9%)	Plus/Plus	

## Features:

Query	482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG	522
Sbjct	51486	ATATAGAGATGG--GATATAGAGATG--GGATATAGAGATG	51522

Range 11: 51512 to 51548

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/41(85%)	4/41(9%)	Plus/Plus	

## Features:

```

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522
Sbjct 51512 ATATAGAGATGG--GATATAGAGATG--GGATATAGAGATG 51548

```

Range 12: 51538 to 51574

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/41(85%)	4/41(9%)	Plus/Plus	

## Features:

Query	482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG	522
Sbjct	51538	ATATAGAGATGG--GATATAGTGTATG--GAATATAGAGATG	51574

Range 13: 51649 to 51685

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/41(85%)	4/41(9%)	Plus/Plus	

## Features:

Query	482	ATATAGAGATGGCATATATAGAGATGACGAATATAAGAGATG	522
Sbjct	51649	ATATAGAGATGG--AATATAGAGATG--GGATATAGAGATG	51685

Range 14: 51727 to 51763

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/41(85%)	4/41(9%)	Plus/Plus	

## Features:

```

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522
Sbjct 51727 ATATAGAGATGG--GATATAGAGATG--GAATATAGTGTATG 51763

```

Score	Expect	Identities	Gaps	Strand	Frame
50.0 bits(54)	0.051()	36/42(86%)	0/42(0%)	Plus/Plus	

Features:

Query 482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATGA	523
Sbjct 2001		
	ATATAGAAATGATAAATATAGAGATGATAAATATAGAGATGA	2042

Range 2: 2016 to 2057

Score	Expect	Identities	Gaps	Strand	Frame
50.0 bits(54)	0.051()	36/42(86%)	0/42(0%)	Plus/Plus	

Features:

Query 482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATGA	523
Sbjct 2016		
	ATATAGAGATGATAAATATAGAGATGATAAATATAGGGATGA	2057

Plasmodium chabaudi chabaudi hypothetical protein (PC405113.00.0) partial mRNA

Sequence ID: [ref|XM\\_735345.1|](#) Length: 1077 Number of Matches: 6

Range 1: 551 to 595

Score	Expect	Identities	Gaps	Strand	Frame
50.0 bits(54)	0.051()	38/45(84%)	0/45(0%)	Plus/Plus	

Features:

Query 479	CATATATAGAGATGGCATATATAGAGATGACGAATATAGAGATGA	523
Sbjct 551		
	CAAATATAGGGATGACAGATATAGAGATGATAAATACAGAGATGA	595

Range 2: 521 to 571

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	42/51(82%)	1/51(1%)	Plus/Plus	

Features:

Query 479	CATATATAGAGATGGCATATATAGAGATGACGAATATAGAGATGAC-GATA	528
Sbjct 521		
	CAGATATAGAGATGATAGATAAAGGATGACAAATATAGGGATGACAGATA	571

Range 3: 494 to 535

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

Features:

Query 482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATGA	523
Sbjct 494		
	ATATAAGGATGACAAATATAGGGATGACAGATATAGAGATGA	535

Range 4: 539 to 580

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

Features:

Query 482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATGA	523
Sbjct 539		
	ATATAAGGATGACAAATATAGGGATGACAGATATAGAGATGA	580

Range 5: 506 to 551

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

Features:

Query 479	CATATATAGAGATGGCATATATAGAGATGACGAATATAGAGATGAC	524
Sbjct 506		
	CAAATATAGGGATGACAGATATAGAGATGATAGATAAAGGATGAC	551

Range 6: 566 to 608

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/43(81%)	0/43(0%)	Plus/Plus	
Features:					
Query 479	CATATATAGAGATGGCATATATAGAGATGACGAATATAAGAGAT				521
Sbjct 566	CAGATATAGAGATGTATAAACATACAGAGATGATAAAATATAGGGAT				608

*Postia* placenta clone ACWS09-E13, complete sequence

Sequence ID: **gb|AC242745.1|** Length: 36471 Number of Matches: 4  
Range 1: 291 to 353

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	52/64(81%)	4/64(6%)	Plus/Plus	
Features:					
Query 856	ATATATAGAGATG-AC-GACATATATAGAGATGAACACAGTATGCACA-GCATATATAGA				9
Sbjct 291	ATGTACAGAGATGTACAGGGATATATAGAGATGTACAGAG-ATGTACAGGGATATATAGA				3
Query 913	GATG 916				
Sbjct 350	GATG 353				

Range 2: 311 to 353

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	38/44(86%)	2/44(4%)	Plus/Plus	
Features:					
Query 416		ATATATAGAGATGAACACAGTATGCACA-GCATATATAGAGATG			458
Sbjct 311		ATATATAGAGATGTACAGAG-ATGTACAGGGATATAGAGATG			353

Range 3: 311 to 353

Range 4: 311 to 353

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	38/44(86%)	2/44(4%)	Plus/Plus	
Features:					
Query 686		ATATATAGAGATGAACACAGTATGCACA- GCATATATAAGAGATG			728
Sbjct 311		ATATATAGAGATGTACAGAG- ATGTACAGGGATATAGAGATG			353

## *Apis mellifera* mast cell-degranulating peptide (Mcdp), mRNA

Sequence ID: **ref|NM\_001011611.2|** Length: 369 Number of Matches: 1  
Range 1: 305 to 342

Gorilla DNA sequence from clone CH255-56N15. complete sequence

Sequence ID: **emb|CU104674.1|** Length: 236843 Number of Matches: 1  
Range 1: 150833 to 150906

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	58/77(75%)	3/77(3%)	Plus/Minus	
Features:					
Query 408	TGCATCCCATA TAGAGATGAAACACAGTATGCACAGCATATA TAGAGATGACGAGTGTG				467
Sbjct 150906	TGTATCGCATATA CATATA CGAACACAGCA-CACAGCATATA GGTGATTGTGACAGA-				150850
Query 468	ACACACACAGCCATATA 484				
Sbjct 150849	ACACTCACAGCCATATA 150833				

Homo sapiens HLA class III region containing NOTCH4 gene, partial sequence, homeobox PBX2 (HPBX) gene, receptor for advanced glycosylation end products (RAGE) gene, complete cds, and 6 unidentified cds, complete sequence

Sequence ID: **gb|U89336.1|HSMHC3W5A** Length: 62944 Number of Matches: 1  
Range 1: 30509 to 30575

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	54/70(77%)	3/70(4%)	Plus/Minus	
Features:					
Query 415	CATATATAGAGATGAAACACAGTATGCACAGCATATA TAGAGATGACGAGTGTGACACACA				474
Sbjct 30575	CATATATATATA CGAACACAGCA-CACAGCATATA GGTGATTGTGACAGA-ACACTCA				30519
Query 475	CAGCCATATA 484				
Sbjct 30518	CAGCCATATA 30509				

Human DNA sequence from clone DASS-39F23 on chromosome 6, complete sequence

Sequence ID: **emb|BX284686.9|** Length: 80063 Number of Matches: 1  
Range 1: 42188 to 42254

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	54/70(77%)	3/70(4%)	Plus/Plus	
Features:					
Query 415	CATATATAGAGATGAAACACAGTATGCACAGCATATA TAGAGATGACGAGTGTGACACACA				474
Sbjct 42188	CATATATATATA CGAACACAGCA-CACAGCATATA GGTGATTGTGACAGA-ACACTCA				42244
Query 475	CAGCCATATA 484				
Sbjct 42245	CAGCCATATA 42254				

Human DNA sequence from clone DAQB-143M3 on chromosome 6, complete sequence

Sequence ID: **emb|AL845464.5|** Length: 56747 Number of Matches: 1  
Range 1: 32428 to 32494

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	54/70(77%)	3/70(4%)	Plus/Plus	
Features:					
Query 415	CATATATAGAGATGAAACACAGTATGCACAGCATATA TAGAGATGACGAGTGTGACACACA				474
Sbjct 32428	CATATATATATA CGAACACAGCA-CACAGCATATA GGTGATTGTGACAGA-ACACTCA				32484
Query 475	CAGCCATATA 484				
Sbjct 32485	CAGCCATATA 32494				

Human DNA sequence from clone CH501-300A18 on chromosome 6, complete sequence

Sequence ID: **emb|AL662884.11|** Length: 137935 Number of Matches: 1  
Range 1: 85497 to 85563

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	54/70(77%)	3/70(4%)	Plus/Plus	
Features:					
Query 415	CATATATAGAGATGAAACACAGTATGCACAGCATATA TAGAGATGACGAGTGTGACACACA				474

Sbjct	85497	CATATATATACGAACACAGCA	—CACAGCATATATGGTATTGTGACAGA—ACACTCA	85553
Query	475	CAGCCATATA	484	
Sbjct	85554	CAGCCATATA	85563	

mast cell-degranulating peptide [Apis mellifera=worker bees, venom glands, mRNA Partial, 369 nt]

Sequence ID: **gb|S78459.1|** Length: 369 Number of Matches: 1

Range 1: 305 to 342

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	35/40(88%)	2/40(5%)	Plus/Minus	

Features:

Query	482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGAT	521
Sbjct	342	ATATAGAGATAACATATATAGAGATAAC—ATATAGAGAT	305

Apis mellifera apamin protein (Apamin), mRNA

Sequence ID: **ref|NM\_001011612.1|** Length: 304 Number of Matches: 1

▶ See 1 more title(s)

Range 1: 240 to 277

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	35/40(88%)	2/40(5%)	Plus/Minus	

Features:

Query	482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGAT	521
Sbjct	277	ATATAGAGATAACATATATAGAGATAAC—ATATAGAGAT	240

Human DNA sequence from clone DAMC-108L3 on chromosome 6, complete sequence

Sequence ID: **emb|CR933878.7|** Length: 102907 Number of Matches: 1

Range 1: 42571 to 42637

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	54/70(77%)	3/70(4%)	Plus/Plus	

Features:

Query	415	CATATATAGAGATGAACACAGTATGCACAGCATATATAGAGATGACGAGTGTGACACACA	474
Sbjct	42571	CATATATATACGAACACAGCA—CACAGCATATATGGTATTGTGACAGA—ACACTCA	42627
Query	475	CAGCCATATA	484
Sbjct	42628	CAGCCATATA	42637

Human DNA sequence from clone DAAP-218M18 on chromosome 6, complete sequence

Sequence ID: **emb|CR812478.6|** Length: 75620 Number of Matches: 1

Range 1: 39742 to 39808

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	54/70(77%)	3/70(4%)	Plus/Plus	

Features:

Query	415	CATATATAGAGATGAACACAGTATGCACAGCATATATAGAGATGACGAGTGTGACACACA	474
Sbjct	39742	CATATATATACGAACACAGCA—CACAGCATATATGGTATTGTGACAGA—ACACTCA	39798
Query	475	CAGCCATATA	484
Sbjct	39799	CAGCCATATA	39808

Human DNA sequence from clone DAMA-358M23 on chromosome 6, complete sequence

Sequence ID: **emb|BX927239.5|** Length: 102588 Number of Matches: 1

Range 1: 32404 to 32470

Score	Expect	Identities	Gaps	Strand	Frame
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48.2 bits(52)      0.18()      54/70(77%)      3/70(4%)      Plus/Plus

#### Features:

Query	415	CATATATAGAGATGAACACAGTATGCACAGCATATATAGAGATGACGAGTGTGACACACA	474
Sbjct	32404	CATATATATACGAACACAGCA--CACAGCATATGGTGATTGTGACAGA-ACACTCA	32460
Query	475	CAGCCATATA 484	
Sbjct	32461	CAGCCATATA 32470	

Botryotinia fuckeliana T4 SupSuperContig\_8\_105\_1 genomic supercontig

Sequence ID: emb|FQ790346.1| Length: 720179 Number of Matches: 2

Range 1: 355559 to 355595

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

## Features:

Query	615	ACACACACAGCAA-CACAGTATGCACAGCATATATA	650
Sbjct	355559	ACACACACAGCATGCACAGTATGCACAGCATGCATAG	355595

Range 2: 355559 to 355595

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

#### Features:

```

Query 828      ACACACACAGCAA-CACAGTATGCACAGCATATATA 863
Sbjct 355559   ACACACACAGCATGGCACAGTATGCACAGCATGATAG 3555595

```

*Plasmodium falciparum* 3D7 conserved Plasmodium protein, unknown function (MAL4P1-163) mRNA, complete cds

Sequence ID: refXM\_002808612\_1 | Length: 20310 Number of Matches: 1

Sequence ID: telXm\_  
Range 1: 7096 to 7160

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	51/65(78%)	6/65(9%)	Plus/Plus	

#### Features:

Query	859	TATAGAGATGACGACATATATAGAGATGAACACA-GTATGCAC---AGCATA--TATAGA	912
Sbjct	7096	TATAGAGATGAAAATATTATAGAGATGAACATTTATGGACATGAACATATTTATAGA	7155
Query	913	GATGA 917	
Sbjct	7156	GATGA 7160	

## *Plasmodium falciparum* 3D7 chromosome 4

Sequence ID: [emb|AI 844503.1](#) | Length: 1204112 Number of Matches: 1

Sequence ID: **emBL8443**  
Range 1: 770370 to 770434

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	51/65(78%)	6/65(9%)	Plus/Plus	

#### Features:

Query	859	TATAGAGATGACGACATATATAGAGATGAACACA-GTATGCAC---AGCATA--TATAGA	912
Sbjct	770370	TATAGAGATAAAATTTATAGAGATGAACATATTATGGACATGAACATATTATAGA	770429
Query	913	GATGA 917	
Sbjct	770430	GATGA 770434	

Zebrafish DNA sequence from clone DKEY-30.19 in linkage group 25, complete sequence

Sequence ID: [emb|CB933757.8](#) | Length: 60542 Number of Matches: 1

Sequence ID: **embCR**  
Range 1: 4670 to 4702

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(50)	0.62()	30/32(91%)	0/23(0%)	Plus/Plus	

Features:

Query	772	ATGACGATACTGCATCCAACACAGTATGCACAG	804
Sbjct	4670	ATGACAATACTGTATCCATCACAGTATGCACAG	4702

Homo sapiens cosmid D66B10, chromosome 21 5' of IFNAR1

Sequence ID: **gb|AF039904.1|** Length: 25076 Number of Matches: 17  
Range 1: 24233 to 24269

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/41(88%)	4/41(9%)	Plus/Plus	

Features:

Query	482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG	522
Sbjct	24233	ATATAGAGATGG--AATATAGAGATG--GAATATAGAGATG	24269

Range 2: 24259 to 24295

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/41(88%)	4/41(9%)	Plus/Plus	

Features:

Query	482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG	522
Sbjct	24259	ATATAGAGATGG--AATATAGAGATG--GAATATAGAGATG	24295

Range 3: 24285 to 24321

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/41(88%)	4/41(9%)	Plus/Plus	

Features:

Query	482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG	522
Sbjct	24285	ATATAGAGATGG--AATATAGAGATG--GAATATAGAGATG	24321

Range 4: 24311 to 24347

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/41(88%)	4/41(9%)	Plus/Plus	

Features:

Query	482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG	522
Sbjct	24311	ATATAGAGATGG--AATATAGAGATG--GAATATAGAGATG	24347

Range 5: 24409 to 24445

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/41(88%)	4/41(9%)	Plus/Plus	

Features:

Query	482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG	522
Sbjct	24409	ATATAGAGATGG--AATATAGAGATG--GAATATAGAGATG	24445

Range 6: 24735 to 24771

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/41(88%)	4/41(9%)	Plus/Plus	

Features:

Query	482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG	522
Sbjct	24735	ATATAGAGATGG--GATATAGAGATG--GAATATAGAGATG	24771

Range 7: 24761 to 24797

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/41(88%)	4/41(9%)	Plus/Plus	

Features:

Query 482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG	522
Sbjct 24761	ATATAGAGATGG--GATATAGAGATG--GAATATAGAGATG	24797

Range 8: 24826 to 24862

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/41(88%)	4/41(9%)	Plus/Plus	

Features:

Query 482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG	522
Sbjct 24826	ATATAGAGATGGAATATAT--AGATG--GAATATAGAGATG	24862

Range 9: 24155 to 24191

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/41(85%)	4/41(9%)	Plus/Plus	

Features:

Query 482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG	522
Sbjct 24155	ATATAGAGATGGAATATAT--ATATG--GAATATAGAGATG	24191

Range 10: 24181 to 24217

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/41(85%)	4/41(9%)	Plus/Plus	

Features:

Query 482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG	522
Sbjct 24181	ATATAGAGATGGAATATAT--ATATG--GAATATAGAGATG	24217

Range 11: 24207 to 24243

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/41(85%)	4/41(9%)	Plus/Plus	

Features:

Query 482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG	522
Sbjct 24207	ATATAGAGATGGAATATAT--ATATG--GAATATAGAGATG	24243

Range 12: 24520 to 24556

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/41(85%)	4/41(9%)	Plus/Plus	

Features:

Query 482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG	522
Sbjct 24520	ATATAGAGATGG--AATATAGAGATG--GGATATAGAGATG	24556

Range 13: 24546 to 24582

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/41(85%)	4/41(9%)	Plus/Plus	

Features:

Query 482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG	522
Sbjct 24546	ATATAGAGATGG--GATATAGAGATG--GGATATAGAGATG	24582

Range 14: 24572 to 24608

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/41(85%)	4/41(9%)	Plus/Plus	

42.8 bits(46) 7.6() 35/41(85%) 4/41(9%) Plus/Plus

Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522  
Sbjct 24572 ATATAGAGATGG--GATATAGAGATG--GGATATAGAGATG 24608

Range 15: 24598 to 24634

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/41(85%)	4/41(9%)	Plus/Plus	

Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522  
Sbjct 24598 ATATAGAGATGG--GATATAGTGTGATG--GAATATAGAGATG 24634

Range 16: 24709 to 24745

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/41(85%)	4/41(9%)	Plus/Plus	

Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522  
Sbjct 24709 ATATAGAGATGG--AATATAGAGATG--GGATATAGAGATG 24745

Range 17: 24787 to 24823

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/41(85%)	4/41(9%)	Plus/Plus	

Features:

Query 482 ATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522  
Sbjct 24787 ATATAGAGATGG--GATATAGAGATG--GAATATAGTGTGATG 24823

Human DNA sequence from clone CH502-105D18 on chromosome 6, complete sequence

Sequence ID: [emb|AL662828.5|](#) Length: 138992 Number of Matches: 1

Range 1: 133303 to 133369

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	56/73(77%)	9/73(12%)	Plus/Plus	

Features:

Query 415 CATATATAGAGATGAAACACAGTATGCACAGCATATATAGAGA---TGACGAGTGTGACAC 471  
Sbjct 133303 CATATATATATACGAACACAGCA--CACAGCATATATGGTACTGTGAC-AGA---ACAC 133356  
Query 472 ACACAGCCATATA 484  
Sbjct 133357 TCACAGCCATATA 133369

Human DNA sequence from clone RP3-418A9 on chromosome 6q21, complete sequence

Sequence ID: [emb|Z84480.1|](#) Length: 121424 Number of Matches: 2

Range 1: 113439 to 113481

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/43(84%)	0/43(0%)	Plus/Plus	

Features:

Query 480 ATATATAGAGATGGCATATATAGAGATGACGAATATAGAGATG 522  
Sbjct 113439 ATATATACAGATGGCATATATAGATGGTATATATAGATG 113481

Range 2: 113439 to 113466

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

Features:

Query	273	ATATATAGAGATGGCATATATAGAGATG	300
Sbjct	113439	ATATATACAGATGGCATATATAGATG	113466

Oryza sativa Japonica Group genomic DNA, chromosome 9, PAC clone:P0668D04  
Sequence ID: **dbj|AP005426.3|** Length: 148848 Number of Matches: 1  
Range 1: 68111 to 68138

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

Features:

Query	861	TAGAGATGACGACATATATAGAGATGAA	888
Sbjct	68138	TAGAGATGACGACATATATAGATGAA	68111

Oryza sativa Japonica Group genomic DNA, chromosome 9, PAC clone:P0701F11  
Sequence ID: **dbj|AP005429.3|** Length: 154950 Number of Matches: 1  
Range 1: 145914 to 145941

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

Features:

Query	861	TAGAGATGACGACATATATAGAGATGAA	888
Sbjct	145941	TAGAGATGACGACATATATAGATGAA	145914

Plasmodium yoelii yoelii str. 17XNL hypothetical protein (PY05377) partial mRNA  
Sequence ID: **ref|XM\_720735.1|** Length: 8085 Number of Matches: 1  
Range 1: 1862 to 1906

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	37/45(82%)	0/45(0%)	Plus/Plus	

Features:

Query	484	ATAGAGATGGCATATATAGAGATGACGAATATAGAGATGACGATA	528
Sbjct	1862	ATAGAGATGACAATAATAGAGATGAAGATAACAGAGATGACGATA	1906

Akistrodon contortrix clone E33DIFJ02JN0T4 microsatellite sequence  
Sequence ID: **gb|GQ194915.1|** Length: 243 Number of Matches: 1  
Range 1: 88 to 151

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	52/67(78%)	4/67(5%)	Plus/Plus	

Features:

Query	846	TATGCACAGCATATATAGAGATGACGACA-TATATAGAGATGAACACAGTATGCACAGCA	904
Sbjct	88	TATGTACAGCATATATAGAG-TGTATACAGTATATATAT--ATACAGTATATACAGTA	144
Query	905	TATATAG 911	
Sbjct	145	TATACAG 151	

Pan troglodytes BAC clone CH251-607M18 from chromosome 6, complete sequence  
Sequence ID: **gb|AC190421.3|** Length: 223525 Number of Matches: 1  
Range 1: 30525 to 30591

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	53/70(76%)	3/70(4%)	Plus/Minus	

Features:

Query	415	CATATATAGAGATGAACACAGTATGCACAGCATATATAGAGATGACGAGTGTGACACACA	474
Sbjct	30591	CATATACATATACGAACACAGCA--CACAGCATATATGGTATTGTGACAGA-ACACTCA	30535
Query	475	CAGCCATATA 484	

Sbjct 30534 CAGCCATATA 30525

Rattus norvegicus strain Brown Norway chromosome 6 clone RP31-263K14, complete sequence  
Sequence ID: **gb|AC079389.2|** Length: 151836 Number of Matches: 1  
Range 1: 63982 to 64032

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	42/51(82%)	2/51(3%)	Plus/Plus	

Features:

Query 232 TGCACATGATGCAC-GACATGCAT-CAGACAGTGCATGCAAACATATATAG 280  
Sbjct 63982 TGCACATGATGCACAGACATGCATACAGACAAACATTACAGATAGAG 64032

Homo sapiens chromosome 16 clone CTD-2535I10, complete sequence  
Sequence ID: **gb|AC093515.4|** Length: 184182 Number of Matches: 4  
Range 1: 18560 to 18601

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

Features:

Query 874 ATATATAGAGATGAACACAGTATGCACAGCATATATAGAGAT 915  
Sbjct 18601 ATATATAGATATATACAGTATATAGAGCATATATAGAGAT 18560

Range 2: 18560 to 18601

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

Features:

Query 686 ATATATAGAGATGAACACAGTATGCACAGCATATATAGAGAT 727  
Sbjct 18601 ATATATAGATATATACAGTATATAGAGCATATATAGAGAT 18560

Range 3: 18560 to 18601

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

Features:

Query 563 ATATATAGAGATGAACACAGTATGCACAGCATATATAGAGAT 604  
Sbjct 18601 ATATATAGATATATACAGTATATAGAGCATATATAGAGAT 18560

Range 4: 18560 to 18601

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

Features:

Query 416 ATATATAGAGATGAACACAGTATGCACAGCATATATAGAGAT 457  
Sbjct 18601 ATATATAGATATATACAGTATATAGAGCATATATAGAGAT 18560

Plasmodium yoelii yoelii str. 17XNL hypothetical protein (PY07183) partial mRNA

Sequence ID: **ref|XM\_722897.1|** Length: 3036 Number of Matches: 1  
Range 1: 1311 to 1391

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	63/83(76%)	13/83(15%)	Plus/Plus	

Features:

Query 480 ATATATAGA-GATGG-CATATA--TAGAGATGACGA-----ATATAGAGATGACGATAC 529  
Sbjct 1311 ATATATAGATGATGGTCATGTAAGTATAGATGATGATATTATATAGATGACGATAC 1370  
Query 530 TGCATCCATATAGA-GATGACGA 551

Sbjct 1371 TGCA--AGTATAGATGATGATGA 1391

Mouse DNA sequence from clone RP23-479D16 on chromosome X, complete sequence

Sequence ID: **emb|AL807398.8|** Length: 106217 Number of Matches: 1

Range 1: 73176 to 73237

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	49/63(78%)	2/63(3%)	Plus/Minus	

Features:

Query 468	ACACACACAGCCATATATAGAGAT-GGCATATATAGAGATGACGAATATAGAGATGACGA	526
Sbjct 73237	ACACACACAC-CCATATATAGAGATATACTAGATATAGATGATATAGATACAGATATAGA	73179
Query 527	TAC 529	
Sbjct 73178	TAC 73176	

PREDICTED: Microtus ochrogaster anaphase promoting complex subunit 1 (Anapc1), mRNA

Sequence ID: **ref|XM\_005365655.1|** Length: 9010 Number of Matches: 3

Range 1: 6489 to 6524

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

Features:

Query 810	ATAGAGATGACGAGTGTGACACACACAGCAACACAG	845
Sbjct 6524	ATAGAGAAAGACGAGTGTGACACAGAAAGACAACACAG	6489

Range 2: 6489 to 6524

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

Features:

Query 720	ATAGAGATGACGAGTGTGACACACACAGCAACACAG	755
Sbjct 6524	ATAGAGAAAGACGAGTGTGACACAGAAAGACAACACAG	6489

Range 3: 6489 to 6524

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

Features:

Query 597	ATAGAGATGACGAGTGTGACACACACAGCAACACAG	632
Sbjct 6524	ATAGAGAAAGACGAGTGTGACACAGAAAGACAACACAG	6489

Neospora caninum Liverpool complete genome, chromosome IX

Sequence ID: **emb|FR823385.1|** Length: 5490906 Number of Matches: 1

Range 1: 509422 to 509458

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

Features:

**3243 bp at 5' side: hypothetical protein1038 bp at 3' side: conserved hypothetical protein**

Query 261	GTGCATGAAACATATATAGAGATGGCATATATAGAGA	298
Sbjct 509458	GTGGATGTACATATATAGAGA-GGCATATATAGAGA	509422

Pongo abelii BAC clone CH276-51D13 from chromosome unknown, complete sequence

Sequence ID: **gb|AC226682.2|** Length: 202763 Number of Matches: 1

Range 1: 176791 to 176831

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

Features:

Query	480	ATATATAGAGATGGCATATATAGAGATGACGAATATAGAGA	520
Sbjct	176831		176791
		ATATATAGAGAGGAATATAGAGAGAGGAATATAGA	

Plasmodium falciparum 3D7 conserved Plasmodium protein, unknown function (PF13\_0148) mRNA, complete cds

Sequence ID: **refXM\_002808990.1** Length: 14343 Number of Matches: 1

Range 1: 6228 to 6277

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	43/52(83%)	3/52(5%)	Plus/Plus	

Features:

Query	478	CCATATATAGAGATGGC-ATATATAGAGATGACGAATATAGAGATGACGATA	528
Sbjct	6228		6277
		CCATA-ATAAAGATGACCATA-ATAAAGATGACGATAATAAAGATGACGATA	

Mus musculus predicted gene 8728 (Gm8728) pseudogene on chromosome 7

Sequence ID: **ref|NG\_019220.1** Length: 19691 Number of Matches: 1

Range 1: 18228 to 18265

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

Features:

Query	761	ACAATATAGAGATGACGATACTGCAT-CCAACACAGTA	797
Sbjct	18265		18228
		ACAATATAGAGAGGAGGAGACTGCATACAAACACAGTA	

Mus musculus predicted gene 8685 (Gm8685) pseudogene on chromosome 7

Sequence ID: **ref|NG\_019213.1** Length: 19700 Number of Matches: 1

Range 1: 18237 to 18274

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

Features:

Query	761	ACAATATAGAGATGACGATACTGCATCCAA-CACAGTA	797
Sbjct	18274		18237
		ACAATATAGAGAGGAGGAGACTGCATACAAGCACAGTA	

Mus musculus predicted gene 8486 (Gm8486) pseudogene on chromosome 7

Sequence ID: **ref|NG\_019185.1** Length: 19698 Number of Matches: 1

Range 1: 18235 to 18272

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

Features:

Query	761	ACAATATAGAGATGACGATACTGCATCCAA-CACAGTA	797
Sbjct	18272		18235
		ACAATATAGAGAGGAGGAGACTGCATACAAGCACAGTA	

Plasmodium falciparum 3D7 chromosome 13

Sequence ID: **emb|AL844509.2** Length: 2895605 Number of Matches: 1

Range 1: 1114303 to 1114352

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	43/52(83%)	3/52(5%)	Plus/Plus	

Features:

Query	478	CCATATATAGAGATGGC-ATATATAGAGATGACGAATATAGAGATGACGATA	528
Sbjct	1114303		1114352
		CCATA-ATAAAGATGACCATA-ATAAAGATGACGATAATAAAGATGACGATA	

Pan troglodytes BAC clone CH251-623J17 from chromosome x, complete sequence  
Sequence ID: **gb|AC193009.2|** Length: 187001 Number of Matches: 1  
Range 1: 109687 to 109730

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

Features:

Query	480	ATATATAGAGATGGCATATATAGAGATGACGA-ATATAGAGATGA	523
Sbjct	109687	ATATATAGAGAGAGGATATAGAGA-GAGGATATATAGAGAGGA	109730

Sus scrofa clone KVL2978 microsatellite sequence

Sequence ID: **gb|EF132836.1|** Length: 692 Number of Matches: 1  
Range 1: 397 to 472

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	62/81(77%)	5/81(6%)	Plus/Minus	

Features:

Query	440	CACAGCATATATAGAGATGACGAGTGTGACACACAGCCATATATAGAGATGGCATATA	499
Sbjct	472	CACA-CACATATAGAGA-GA-GTGTGTG-ATATATATACATATATAGAGAGAGAAATATA	417
Query	500	TAGAGATGACGAATATAGAGA	520
Sbjct	416	TAGATA-GATGTATATAGAGA	397

Mus musculus chromosome 7, clone RP23-287I20, complete sequence

Sequence ID: **gb|AC101716.6|** Length: 182151 Number of Matches: 1  
Range 1: 52160 to 52185

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

Features:

Query	258	ACAGTGCATGCAAACATATATAGAGA	283
Sbjct	52185	ACAGTGCATGCAAAATATATAGAGA	52160

Apis cerana cerana mast cell degranulating peptide precursor, mRNA, complete cds

Sequence ID: **gb|AY327447.1|** Length: 341 Number of Matches: 1  
Range 1: 278 to 315

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	34/40(85%)	2/40(5%)	Plus/Minus	

Features:

Query	482	ATATAGAGATGGCATATATAGAGATGACGAATATAGAGAT	521
Sbjct	315	ATATAGAGATAACATATATAGAGAT--AGCATATAGAGAT	278

Mus musculus BAC clone RP23-362F11 from chromosome 7, complete sequence

Sequence ID: **gb|AC151988.3|** Length: 196173 Number of Matches: 1  
Range 1: 55084 to 55121

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

Features:

Query	761	ACAATATAGAGATGACGATACTGCATCCAA-CACAGTA	797
Sbjct	55121	ACAATATAGAGAGGGAGACTGCATACAAGCACAGTA	55084

Mus musculus BAC clone RP23-82H2 from chromosome 7, complete sequence

Sequence ID: **gb|AC133951.3|** Length: 176364 Number of Matches: 1

Range 1: 144394 to 144431

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

Features:

Query 761 ACAATATAGAGATGACGATACTGCATCCAA-CACAGTA 797  
Sbjct 144431 ACAATATAGAGAGGAGACTGCATACAAGCACAGTA 144394

Mus musculus chromosome 1, clone RP24-228M19, complete sequence

Sequence ID: **gb|AC161221.7|** Length: 164548 Number of Matches: 1

Range 1: 70846 to 70878

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

Features:

Query 734 TGTGACACACACAGCAACACAGTATGCACAATA 766  
Sbjct 70878 TGTGACACACACATCAACACACAAAGCACAATA 70846

Mus musculus chromosome 7, clone RP23-332G12, complete sequence

Sequence ID: **gb|AC164001.4|** Length: 190345 Number of Matches: 1

Range 1: 157288 to 157313

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

Features:

Query 258 ACAGTGCATGCAAACATATATAGAGA 283  
Sbjct 157288 ACAGTGCATGCAAAAATATATAGAGA 157313

Mus musculus BAC clone RP23-6N4 from chromosome 7, complete sequence

Sequence ID: **gb|AC161002.2|** Length: 182230 Number of Matches: 1

Range 1: 105337 to 105374

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

Features:

Query 761 ACAATATAGAGATGACGATACTGCAT-CCAACACAGTA 797  
Sbjct 105374 ACAATATAGAGAGGAGACTGCATACAAACACAGTA 105337

Mus musculus BAC clone RP23-145O23 from chromosome 7, complete sequence

Sequence ID: **gb|AC150900.5|** Length: 211722 Number of Matches: 1

Range 1: 27296 to 27333

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

Features:

Query 761 ACAATATAGAGATGACGATACTGCAT-CCAACACAGTA 797  
Sbjct 27333 ACAATATAGAGAGGAGACTGCATACAAACACAGTA 27296

Homo sapiens chromosome 3 clone RP11-523D22, complete sequence

Sequence ID: **gb|AC104305.2|** Length: 149858 Number of Matches: 2

Range 1: 21757 to 21840

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

42.8 bits(46)      7.6()      65/89(73%)      8/89(8%)      Plus/Plus

#### Features:

Range 2: 21818 to 21848

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	31/34(91%)	3/34(8%)	Plus/Plus	

## Features:

```

Query 468 ACACACACAGCCATATATAAGAGATGGCATATATA 501
Sbjct 21818 ACACACACA--CCATATATAAGAGAT--CATATATA 21848

```

## Zebrafish DNA sequence from clone CH211-280H1 in linkage group 17, complete sequence

Sequence ID: **emb|BX469900.4** | Length: 84299 Number of Matches: 2

Range 1: 15671 to 15704

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	30/34(88%)	3/34(8%)	Plus/Plus	

## Features:

Query	497	ATATAGAGATG--ACGAATATAGAGATGACGAT	527
Sbjct	15671	ATATAGAGATGGCCACGAATATAGAGATGATGAT	15704

Range 2: 15671 to 15704

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	30/34(88%)	3/34(8%)	Plus/Plus	

#### Features:

Query	645	ATATAGAGATG--ACGAATATAGAGATGACGAT	675
Sbjct	15671	ATATAGAGATGCCACGAATATAGAGATGTATGAT	15704

Mus musculus BAC clone RP23-248K5 from chromosome 7, complete sequence

Sequence ID: qb|AC168909.4 | Length: 181751 Number of Matches: 1

Sequence ID: gBJACT003  
Range 1: 32944 to 32981

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

#### Features:

```

Query 761 ACAATATAGAGATGACGTACTGCAT-CCAACACAGTA 797
Sbjct 32944 ACAATATAGAGAGGGAGACTGCATAACAAACAGTA 32981

```

Mus musculus BAC clone RP24-101E7 from chromosome 7, complete sequence

Sequence ID: qb|AC171682.2| Length: 228837 Number of Matches: 1

Sequence ID: gsp1011  
Range 1: 7120 to 7157

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

#### Features:

```

Query 761 ACAATATAGAGATGACGATACTGCATCCAA-CACAGTA 797
      ||||| | | | | | | | | | | | | | | | | | | | | |
Sbjct 7157 ACAATATAGAGAGGGAGACTGCATAACAGCACAGTA 7120

```

Mus musculus BAC clone RP24-163J14 from chromosome 7, complete sequence.

Sequence ID: qbJAC171240.3 | Length: 180133 Number of Matches: 1

Range 1: 58974 to 59011

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

Features:

Query	761	ACAATATAGAGATGACGATACTGCAT-CCAACACAGTA	797
Sbjct	58974	ACAATATAGAGAGGGAGACTGCATACAAACACAGTA	59011

Mus musculus BAC clone RP23-170J16 from chromosome 7, complete sequence

Sequence ID: **gb|AC168854.4|** Length: 226303 Number of Matches: 1

Range 1: 94649 to 94686

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

Features:

Query	761	ACAATATAGAGATGACGATACTGCAT-CCAACACAGTA	797
Sbjct	94686	ACAATATAGAGAGGGAGACTGCATACAAACACAGTA	94649

Mus musculus BAC clone RP23-182D23 from chromosome 7, complete sequence

Sequence ID: **gb|AC171196.1|** Length: 228024 Number of Matches: 1

Range 1: 58301 to 58338

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

Features:

Query	761	ACAATATAGAGATGACGATACTGCATCCAA-CACAGTA	797
Sbjct	58301	ACAATATAGAGAGGGAGACTGCATACAAGCACAGTA	58338

Mus musculus BAC clone RP23-88M21 from chromosome 7, complete sequence

Sequence ID: **gb|AC164312.3|** Length: 223232 Number of Matches: 1

Range 1: 147698 to 147735

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

Features:

Query	761	ACAATATAGAGATGACGATACTGCAT-CCAACACAGTA	797
Sbjct	147698	ACAATATAGAGAGGGAGACTGCATACAAACACAGTA	147735

Zebrafish DNA sequence from clone CH211-195M7, complete sequence

Sequence ID: **emb|AL805945.5|** Length: 212604 Number of Matches: 2

Range 1: 153129 to 153162

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	30/34(88%)	3/34(8%)	Plus/Minus	

Features:

Query	645	ATATAGAGATG---ACGAATATAGAGATGACGAT	675
Sbjct	153162	ATATAGAGATGGCCACGAATATAGAGATGATGAT	153129

Range 2: 153129 to 153162

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	30/34(88%)	3/34(8%)	Plus/Minus	

Features:

Query	497	ATATAGAGATG---ACGAATATAGAGATGACGAT	527
Sbjct	153162	ATATAGAGATGGCCACGAATATAGAGATGATGAT	153129

