

BLAST ®

Basic Local Alignment Search Tool

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CGTA

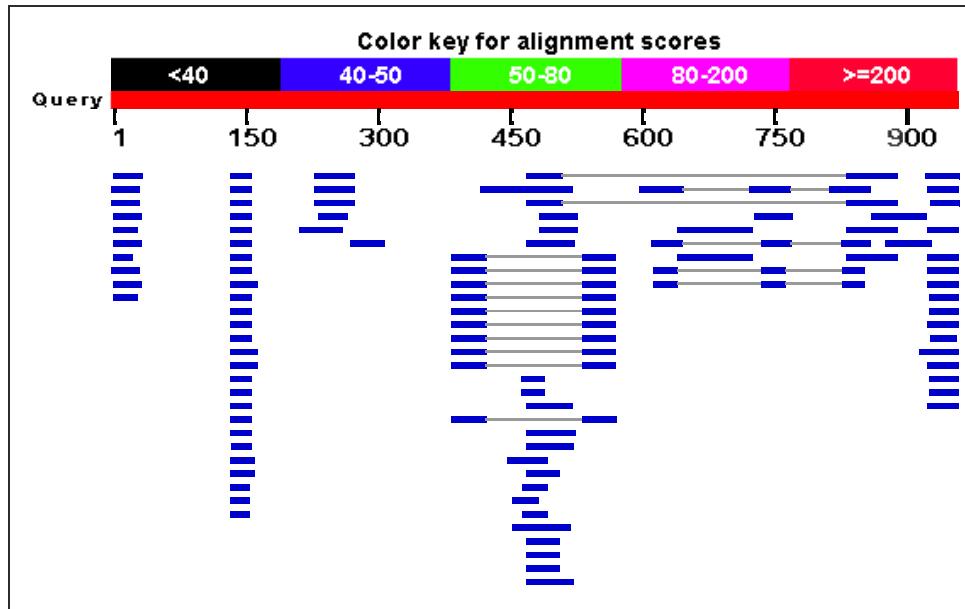
RID [Y0TP4DPH014](#) (Expires on 08-06 13:08 pm)

Query ID Icl|49555
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 122 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Strongylocentrotus purpuratus haplotype Endo16_P_11 Endo16 gene, promoter region	46.4	89.1	10%	0.62	87%	JQ408869.1
Candida parapsilosis strain CDC317 annotated contig 005806	46.4	137	14%	0.62	84%	HE605204.1
Oreochromis niloticus clone BAC T4-024BG04 RH2B opsin, RH2A alpha opsin, and RH2A beta opsin genes, complete cds	46.4	46.4	11%	0.62	72%	JF262086.1
Mus musculus chromosome 15, clone RP23-458G7, complete sequence	46.4	46.4	3%	0.62	89%	AC099594.6
Strongylocentrotus purpuratus clone A7 extracellular protein (endo16) gene, promoter region	46.4	89.1	10%	0.62	87%	DQ066837.1
Zebrafish DNA sequence from clone DKEY-29K15 in linkage group 14, complete sequence	46.4	46.4	2%	0.62	100%	BX005008.12
Zebrafish DNA sequence from clone CH73-47F2 in linkage group 5, complete sequence	44.6	44.6	2%	2.2	100%	CU571331.10
Zebrafish DNA sequence from clone CH1073-209I11 in linkage group 15, complete sequence	44.6	44.6	2%	2.2	100%	FO082022.4
Neospora caninum Liverpool complete genome, chromosome XI	44.6	44.6	6%	2.2	80%	FR823392.1
Zebrafish DNA sequence from clone CH73-289G7 in linkage group 1, complete sequence	44.6	44.6	2%	2.2	100%	CU915762.9
Zebrafish DNA sequence from clone CH1073-458H17 in linkage group 14, complete sequence	44.6	44.6	2%	2.2	100%	CU694755.7
Zebrafish DNA sequence from clone CH73-91H12 in linkage group 18, complete sequence	44.6	44.6	2%	2.2	100%	CU855784.7
Zebrafish DNA sequence from clone CH73-298E8 in linkage group 23, complete sequence	44.6	44.6	2%	2.2	100%	CU466286.6
Zebrafish DNA sequence from clone DKEY-264P8 in linkage group 11, complete sequence	44.6	44.6	2%	2.2	100%	CR931939.21
Zebrafish DNA sequence from clone DKEY-15I15 in linkage group 2, complete sequence	44.6	44.6	3%	2.2	94%	BX510342.7
Pan troglodytes BAC clone CH251-459A3 from chromosome unknown, complete sequence	44.6	44.6	3%	2.2	88%	AC159903.3
Zebrafish DNA sequence from clone DKEY-67F11 in linkage group 3, complete sequence	44.6	44.6	2%	2.2	100%	BX908755.10
Zebrafish DNA sequence from clone DKEYP-11A2 in linkage group 1, complete sequence	44.6	44.6	2%	2.2	100%	CR774194.4
Zebrafish DNA sequence from clone CH211-224B23 in linkage group 5, complete sequence	44.6	44.6	2%	2.2	100%	BX942837.5
Zebrafish DNA sequence from clone CH211-259A10 in linkage group 25, complete sequence	44.6	44.6	2%	2.2	100%	CR376764.13
Zebrafish DNA sequence from clone RP71-34B6 in linkage group 2, complete	44.6	44.6	3%	2.2	94%	BX537344.8

sequence						
Zebrafish DNA sequence from clone CH211-150K17 in linkage group 10, complete sequence	44.6	44.6	3%	2.2	94%	BX510911.10
Zebrafish DNA sequence from clone DKEY-28C2 in linkage group 20, complete sequence	44.6	44.6	2%	2.2	100%	BX950183.9
Rattus norvegicus vitamin A-deficient testicular protein 14-like mRNA, partial sequence	44.6	44.6	6%	2.2	80%	AY169302.1
Mouse DNA sequence from clone RP23-421L2 on chromosome 11, complete sequence	44.6	131	10%	2.2	91%	AL627348.12
Zebrafish DNA sequence from clone RP71-22K7 in linkage group 12, complete sequence	44.6	44.6	2%	2.2	100%	BX470069.10
Zebrafish DNA sequence from clone DKEY-53H9, complete sequence	44.6	44.6	2%	2.2	100%	AL929596.11
Zebrafish DNA sequence from clone CH211-277E21 in linkage group 12, complete sequence	44.6	44.6	2%	2.2	100%	BX248086.8
Zebrafish DNA sequence from clone CH211-199H23 in linkage group 12, complete sequence	44.6	44.6	2%	2.2	100%	AL935268.6
Homo sapiens genomic DNA, chromosome 11 clone:RP11-762B21, complete sequence	44.6	44.6	4%	2.2	84%	AP000926.6
Homo sapiens chromosome 5 clone CTB-17P2, complete sequence	44.6	44.6	3%	2.2	88%	AC008640.6
Homo sapiens gene for seven transmembrane helix receptor, complete cds, isolate:CBRC7TM_64	44.6	89.1	4%	2.2	82%	AB065501.1
Homo sapiens genomic DNA, chromosome 11q clone:RP11-116P9, complete sequences	44.6	89.1	4%	2.2	82%	AP002517.3
Solanum lycopersicum chromosome ch06, complete genome	42.8	42.8	5%	7.6	78%	HG975518.1
Solanum pennellii chromosome ch10, complete genome	42.8	42.8	5%	7.6	81%	HG975449.1
PREDICTED: Callorhinchus milii very low-density lipoprotein receptor-like (LOC103190431), transcript variant X3, misc_RNA	42.8	42.8	4%	7.6	81%	XR_489160.1
PREDICTED: Callorhinchus milii very low-density lipoprotein receptor-like (LOC103190431), transcript variant X2, mRNA	42.8	42.8	4%	7.6	81%	XM_007911212.1
PREDICTED: Callorhinchus milii very low-density lipoprotein receptor-like (LOC103190431), transcript variant X1, mRNA	42.8	42.8	4%	7.6	81%	XM_007911210.1
Zebrafish DNA sequence from clone DKEY-274K7 in linkage group 13, complete sequence	42.8	42.8	2%	7.6	100%	CR381612.6
PREDICTED: Bos mutus multiple PDZ domain protein (MPDZ), mRNA	42.8	85.5	7%	7.6	84%	XM_005910465.1
PREDICTED: Bos taurus multiple PDZ domain protein (MPDZ), transcript variant X8, mRNA	42.8	85.5	7%	7.6	84%	XM_005209941.1
PREDICTED: Bos taurus multiple PDZ domain protein (MPDZ), transcript variant X7, mRNA	42.8	85.5	7%	7.6	84%	XM_005209940.1
PREDICTED: Bos taurus multiple PDZ domain protein (MPDZ), transcript variant X6, mRNA	42.8	85.5	7%	7.6	84%	XM_005209939.1
PREDICTED: Bos taurus multiple PDZ domain protein (MPDZ), transcript variant X5, mRNA	42.8	85.5	7%	7.6	84%	XM_005209938.1
PREDICTED: Bos taurus multiple PDZ						

domain protein (MPDZ), transcript variant X4, mRNA	42.8	85.5	7%	7.6	84%	XM_005209937.1
PREDICTED: Bos taurus multiple PDZ domain protein (MPDZ), transcript variant X3, mRNA	42.8	85.5	7%	7.6	84%	XM_005209936.1
PREDICTED: Bos taurus multiple PDZ domain protein (MPDZ), transcript variant X2, mRNA	42.8	85.5	7%	7.6	84%	XM_005209935.1
PREDICTED: Bos taurus multiple PDZ domain protein (MPDZ), transcript variant X1, mRNA	42.8	85.5	7%	7.6	84%	XM_005209934.1
PREDICTED: Takifugu rubripes cleavage and polyadenylation specificity factor subunit 3-like (LOC101075419), mRNA	42.8	42.8	3%	7.6	89%	XM_003977462.1
Tetrapisispora blattae CBS 6284 chromosome 8, complete genome	42.8	42.8	5%	7.6	80%	HE806323.1
Strongylocentrotus purpuratus haplotype Endo16_P_6 Endo16 gene, promoter region	42.8	42.8	6%	7.6	78%	JQ408864.1
Eremothecium cymbalariae DBVPG#7215 hypothetical protein (Ecym_6231) mRNA, complete cds	42.8	42.8	2%	7.6	93%	XM_003647382.1
Eremothecium cymbalariae DBVPG#7215 chromosome 6, complete sequence	42.8	42.8	2%	7.6	93%	CP002502.1
Homo sapiens protein tyrosine phosphatase, non-receptor type 2 (PTPN2), RefSeqGene on chromosome 18	42.8	42.8	5%	7.6	81%	NG_029116.1
Bos taurus multiple PDZ domain protein (MPDZ), mRNA	42.8	85.5	7%	7.6	84%	NM_001192891.2
Callorhinchus milii BAC clone IMCB_Eshark-84H12 from chromosome unknown, complete sequence	42.8	42.8	3%	7.6	88%	AC242182.1
Zebrafish DNA sequence from clone CH73-81A7 in linkage group 17, complete sequence	42.8	42.8	2%	7.6	93%	CU655821.15
S_lycopersicum DNA sequence from clone SL_MboI-81L19, complete sequence	42.8	42.8	5%	7.6	78%	CU928680.5
Homo sapiens tyrosine-protein phosphatase non-receptor type 2 (PTN2) gene, complete cds, alternatively spliced	42.8	42.8	5%	7.6	81%	EF445017.1
Mouse DNA sequence from clone CH29-149F14 on chromosome 6, complete sequence	42.8	42.8	3%	7.6	88%	CU207392.14
Mouse DNA sequence from clone RP24-463G23 on chromosome 12, complete sequence	42.8	42.8	4%	7.6	84%	CU024890.15
Mouse DNA sequence from clone WI1-2581G20 on chromosome 4, complete sequence	42.8	128	8%	7.6	96%	CU207287.4
Oryza sativa Japonica Group Os02g0172800 (Os02g0172800) mRNA, complete cds	42.8	42.8	3%	7.6	86%	NM_001052569.1
Zebrafish DNA sequence from clone DKEYP-72A3 in linkage group 17, complete sequence	42.8	42.8	2%	7.6	93%	CR854889.15
Zebrafish DNA sequence from clone DKEY-89F23 in linkage group 17, complete sequence	42.8	42.8	2%	7.6	100%	CR352284.26
Mus musculus chromosome 5, clone RP24-57K14, complete sequence	42.8	42.8	3%	7.6	88%	AC120437.7
Mus musculus chromosome 8, clone RP24-485L5, complete sequence	42.8	42.8	2%	7.6	93%	AC110214.7
Mus musculus BAC clone RP23-129J20 from chromosome 6, complete sequence	42.8	42.8	3%	7.6	88%	AC165970.3

Mus musculus BAC clone RP23-448D23 from chromosome 12, complete sequence	42.8	42.8	9%	7.6	73%	AC162902.4
Mus musculus chromosome 3, clone RP23-288N9, complete sequence	42.8	42.8	3%	7.6	89%	AC107700.12
Mus musculus BAC clone RP23-105L19 from chromosome 6, complete sequence	42.8	42.8	3%	7.6	88%	AC147225.3
Mus musculus BAC RP24-83C9 (Roswell Park Cancer Institute (C57BL/6J Male) Mouse BAC Library) complete sequence	42.8	42.8	3%	7.6	88%	AC168278.2
Mus musculus BAC clone RP23-166K13 from chromosome 18, complete sequence	42.8	42.8	3%	7.6	88%	AC122848.3
Mus musculus BAC clone RP24-486E21 from chromosome 8, complete sequence	42.8	42.8	3%	7.6	88%	AC132569.3
Mus musculus BAC clone RP23-326N11 from chromosome 18, complete sequence	42.8	42.8	3%	7.6	88%	AC132427.4
Mus musculus BAC clone RP23-346N11 from chromosome 7, complete sequence	42.8	42.8	2%	7.6	93%	AC135963.3
Mus musculus BAC clone RP23-415J21 from chromosome 7, complete sequence	42.8	42.8	2%	7.6	93%	AC111008.6
Mus musculus BAC clone RP24-404N12 from chromosome 8, complete sequence	42.8	42.8	3%	7.6	88%	AC124380.4
Mus musculus BAC clone RP24-566O21 from chromosome 3, complete sequence	42.8	42.8	3%	7.6	89%	AC123553.4
Mus musculus BAC clone RP23-145J18 from 8, complete sequence	42.8	42.8	3%	7.6	93%	AC122866.4
Mus musculus chromosome 8, clone RP23-227D17, complete sequence	42.8	42.8	2%	7.6	93%	AC161188.5
Mus musculus chromosome 8, clone RP23-216D14, complete sequence	42.8	42.8	4%	7.6	84%	AC163014.5
Mus musculus BAC clone RP23-411F11 from chromosome 12, complete sequence	42.8	42.8	9%	7.6	73%	AC155312.2
Mus musculus BAC clone RP24-347B7 from chromosome 6, complete sequence	42.8	42.8	3%	7.6	88%	AC125145.3
Human DNA sequence from clone CTD-2280P12 on chromosome 13, complete sequence	42.8	42.8	6%	7.6	76%	AL929515.4
Homo sapiens chromosome 15, clone RP11-424E9, complete sequence	42.8	42.8	3%	7.6	91%	AC090259.5
Homo sapiens chromosome 15, clone RP11-466P9, complete sequence	42.8	42.8	3%	7.6	91%	AC105014.5
Homo sapiens BAC clone RP11-270I3 from 4, complete sequence	42.8	42.8	2%	7.6	100%	AC027625.5
Oryza sativa Japonica Group genomic DNA, chromosome 2, BAC clone:OSJNBa0073A21	42.8	42.8	3%	7.6	86%	AP005772.3
Oryza sativa Japonica Group genomic DNA, chromosome 2, PAC clone:P0030G02	42.8	42.8	3%	7.6	86%	AP004836.2
Oryza sativa Japonica Group cDNA clone:J033148H01, full insert sequence	42.8	42.8	3%	7.6	86%	AK103838.1
Mouse DNA sequence from clone RP23-426J14 on chromosome 4, complete sequence	42.8	42.8	4%	7.6	85%	AL691491.11
Ophiostoma minus isolate OM3 scyalone dehydratase (SD) gene, partial cds	42.8	42.8	2%	7.6	100%	AY098659.1

Mus musculus BAC clone RP23-408M14 from 6, complete sequence	42.8	42.8	3%	7.6	88%	AC123937.3
Mus musculus BAC clone RP24-247D2 from 6, complete sequence	42.8	42.8	3%	7.6	88%	AC147371.4
Mus musculus BAC clone RP23-336M12 from 8, complete sequence	42.8	42.8	3%	7.6	88%	AC141641.4
Homo sapiens genomic DNA, chromosome 18 clone:RP11-767P20, complete sequence	42.8	42.8	5%	7.6	81%	AP001077.6
Zebrafish DNA sequence from clone DKEY-12J12 in linkage group 14, complete sequence	42.8	42.8	2%	7.6	100%	BX000452.7
Mouse DNA sequence from clone RP23-18M2 on chromosome 4, complete sequence	42.8	128	8%	7.6	96%	AL606924.14
Mouse DNA sequence from clone RP23-56A14 on chromosome 7, complete sequence	42.8	42.8	2%	7.6	93%	AL603836.13

Alignments

Strongylocentrotus purpuratus haplotype Endo16_P_11 Endo16 gene, promoter region

Sequence ID: [gb|JQ408869.1](#) | Length: 1880 Number of Matches: 2

Range 1: 397 to 432

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	34/39(87%)	3/39(7%)	Plus/Minus	

Features:

Query	468	ACACACACATCCAGAGAGATATACTTCAGAGAGATATAG	506
Sbjct	432	ACACACACATAGAGAGAGATATA---CAGAGAGATATAG	397

Range 2: 397 to 444

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	45/58(78%)	10/58(17%)	Plus/Minus	

Features:

Query	828	ACACACACATCAACACATGAGTCACATCAGAGAGATATAGTACTACAGAGAGATATAG	885
Sbjct	444	ACACACACACCCACACA-----CACAT-AGAGAGAGATA---TACAGAGAGATATAG	397

Candida parapsilosis strain CDC317 annotated contig 005806

Sequence ID: [emb|HE605204.1](#) | Length: 1039767 Number of Matches: 3

Range 1: 906089 to 906137

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	41/49(84%)	2/49(4%)	Plus/Minus	

Features:

Query	808	AGAGATATAGTA-CTATGT-GTACACACACATCAACACATGAGTCACAT	854
Sbjct	906137	AGAGATATAGTATCAATATCGTACACACACATACACATTATTACAT	906089

Range 2: 906089 to 906137

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	41/49(84%)	2/49(4%)	Plus/Minus	

Features:

Query	595	AGAGATATAGTA-CTATGT-GTACACACACATCAACACATGAGTCACAT	641
Sbjct	906137	AGAGATATAGTATCAATATCGTACACACACATACACATTATTACAT	906089

Range 3: 906090 to 906137

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	40/48(83%)	2/48(4%)	Plus/Minus	

Features:

Query	718	AGAGATATAGTA-CTATGT-GTACACACACATCAACACATGAGTCACA	763
Sbjct	906137	AGAGATATAGTATCAATATCGTACACACACATACACACATTATTCACA	906090

Oreochromis niloticus clone BAC T4-024BG04 RH2B opsin, RH2A alpha opsin, and RH2A beta opsin genes, complete cds
Sequence ID: [gb|JF262086.1](#) Length: 177366 Number of Matches: 1

Sequence ID: [gb|EF232301](#) | Length: 117000 Number of Matches: 1
Range 1: 173058 to 173152

Range 1: 173058 to 173152

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	76/105(72%)	10/105(9%)	Plus/Minus	

Features:

Query	416	AGAGAGATATAGAACACATGAGTCACATCAGAGATATAGTACTATGTGTACACAC	475
Sbjct	173152	AGAGAGATATAGATATATA-GAG--AGAT-AGAGAGATATAGAGAGATATATAGAGAG	173097
Query	476	ATCCAGAGAGATATAGTTCAGAGAGATATAGTACTAAGAGATATA	520
Sbjct	173096	ATATAGAGAGATATA-TATAGAGAGATATAG-----AGATATA	173058

Mus musculus chromosome 15, clone RP23-458G7, complete sequence

Sequence ID: **gb|AC099594.6** | Length: 220242 Number of Matches: 1

Range 1: 106754 to 106789

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

Features:

Query	916	TACTATGTGTACACACACATCACTATGTGTACACACA	952
Sbjct	106754	TACTATATGACACACACATT-CTATGTGTACACACA	106789

Strongylocentrotus purpuratus clone A7 extracellular protein (endo16) gene, promoter region

Sequence ID: qb|DQ066837.1| Length: 838 Number of Matches: 2

Range 1: 397 to 432

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	34/39(87%)	3/39(7%)	Plus/Minus	

Features:

Query	468	ACACACACATCCAGAGAGATAATAGTTCAAGAGAGATATA	506
Sbjct	432	ACACACACATAGAGAGAGATATA--CAGAGAGATATA	397

Range 2: 397 to 444

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	45/58(78%)	10/58(17%)	Plus/Minus	

Features:

Query	828	ACACACACATCAACACATGAGTCACATCAGAGAGATATGTA	CTACAGAGAGATATAG	885
Sbjct	444	ACACACACACCCACACA-----CACAT-----AGAGAGATA-----TACAGAGAGATATAG		397

Zebrafish DNA sequence from clone DKEY-29K15 in linkage group 14, complete sequence

Sequence ID: embl:BX005008.12 | Length: 208014 Number of Matches: 1

Sequence ID: **embl|BX00**
Range 1: 46061 to 46085

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	25/25(100%)	0/25(0%)	Plus/Plus	

Features:

```

Query  134      CACTGACTGACTGACAGATCGACTG  158
Sbjct  46061      |||||      CACTGACTGACTGACAGATCGACTG  46085

```

Zebrafish DNA sequence from clone CH73-47F2 in linkage group 5, complete sequence

Sequence ID: **emb|CU571331.10|** Length: 112406 Number of Matches: 1

Range 1: 85548 to 85571

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	24/24(100%)	0/24(0%)	Plus/Plus	

Features:

Query 135 ACTGACTGACTGACAGATCGACTG 158
||||||| ||||| ||||| ||||| |||||
Sbjct 85548 ACTGACTGACTGACAGATCGACTG 85571

Zebrafish DNA sequence from clone CH1073-209I11 in linkage group 15, complete sequence

Sequence ID: **emb|FO082022.4|** Length: 29991 Number of Matches: 1

Range 1: 14690 to 14713

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	24/24(100%)	0/24(0%)	Plus/Minus	

Features:

Query 135 ACTGACTGACTGACAGATCGACTG 158
||||||| ||||| ||||| ||||| |||||
Sbjct 14713 ACTGACTGACTGACAGATCGACTG 14690

Neospora caninum Liverpool complete genome, chromosome XI

Sequence ID: **emb|FR823392.1|** Length: 6081843 Number of Matches: 1

Range 1: 429626 to 429677

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	48/60(80%)	8/60(13%)	Plus/Minus	

Features:

1165 bp at 5' side: CorA-like Mg2+ transporter domain-containing protein, rel...968 bp at 3' side: putative AT hook motif-containing protein

Query 856 AGAGAGATATAGTACTACAGAGAGATATAGTAACACATGAGTCACATCAGAGAGATATAG 915
||||||| ||||| ||||| ||||| |||||
Sbjct 429677 AGAGAGATATAG---ACAGAGAGATATAG--ACAGA-GAGACA-AGGAGAGAGATATAG 429626

Zebrafish DNA sequence from clone CH73-289G7 in linkage group 1, complete sequence

Sequence ID: **emb|CU915762.9|** Length: 63208 Number of Matches: 1

Range 1: 16692 to 16715

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	24/24(100%)	0/24(0%)	Plus/Minus	

Features:

Query 135 ACTGACTGACTGACAGATCGACTG 158
||||||| ||||| ||||| ||||| |||||
Sbjct 16715 ACTGACTGACTGACAGATCGACTG 16692

Zebrafish DNA sequence from clone CH1073-458H17 in linkage group 14, complete sequence

Sequence ID: **emb|CU694755.7|** Length: 35357 Number of Matches: 1

Range 1: 11336 to 11359

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	24/24(100%)	0/24(0%)	Plus/Minus	

Features:

Query 135 ACTGACTGACTGACAGATCGACTG 158
||||||| ||||| ||||| ||||| |||||
Sbjct 11359 ACTGACTGACTGACAGATCGACTG 11336

Zebrafish DNA sequence from clone CH73-91H12 in linkage group 18, complete sequence

Sequence ID: **emb|CU855784.7|** Length: 56005 Number of Matches: 1

Range 1: 21614 to 21637

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	24/24(100%)	0/24(0%)	Plus/Minus	

Features:

Query	135	ACTGACTGACTGACAGATCGACTG	158
Sbjct	21637	ACTGACTGACTGACAGATCGACTG	21614

Zebrafish DNA sequence from clone CH73-298E8 in linkage group 23, complete sequence

Sequence ID: **emb|CU466286.6|** Length: 42099 Number of Matches: 1

Range 1: 32869 to 32892

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	24/24(100%)	0/24(0%)	Plus/Plus	

Features:

Query	135	ACTGACTGACTGACAGATCGACTG	158
Sbjct	32869	ACTGACTGACTGACAGATCGACTG	32892

Zebrafish DNA sequence from clone DKEY-264P8 in linkage group 11, complete sequence

Sequence ID: **emb|CR931939.21|** Length: 132268 Number of Matches: 1

Range 1: 66017 to 66040

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	24/24(100%)	0/24(0%)	Plus/Minus	

Features:

Query	135	ACTGACTGACTGACAGATCGACTG	158
Sbjct	66040	ACTGACTGACTGACAGATCGACTG	66017

Zebrafish DNA sequence from clone DKEY-15I15 in linkage group 2, complete sequence

Sequence ID: **emb|BX510342.7|** Length: 186711 Number of Matches: 1

Range 1: 75220 to 75249

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	29/31(94%)	1/31(3%)	Plus/Minus	

Features:

Query	135	ACTGACTGACTGACAGATCGACTGCATCGAC	165
Sbjct	75249	ACTGACTGACTGACAGATTGACTG-ATCGAC	75220

Pan troglodytes BAC clone CH251-459A3 from chromosome unknown, complete sequence

Sequence ID: **gb|AC159903.3|** Length: 216963 Number of Matches: 1

Range 1: 124743 to 124776

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

Features:

Query	3	TGAGTATGTGTGTACACACACATCCATGAGTACT	36
Sbjct	124776	TGTGTGTGTGTGTACACACACATACTGAGAACT	124743

Zebrafish DNA sequence from clone DKEY-67F11 in linkage group 3, complete sequence

Sequence ID: **emb|BX908755.10|** Length: 160005 Number of Matches: 1

Range 1: 63507 to 63530

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	24/24(100%)	0/24(0%)	Plus/Minus	

Features:

Query	135	ACTGACTGACTGACAGATCGACTG	158
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Sbjct 63530 ACTGACTGACTGACAGATCGACTG 63507

Zebrafish DNA sequence from clone DKEYP-11A2 in linkage group 1, complete sequence

Sequence ID: **emb|CR774194.4|** Length: 160120 Number of Matches: 1

Range 1: 69580 to 69603

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	24/24(100%)	0/24(0%)	Plus/Minus	

Features:

Query 135 ACTGACTGACTGACAGATCGACTG 158
Sbjct 69603 ACTGACTGACTGACAGATCGACTG 69580

Zebrafish DNA sequence from clone CH211-224B23 in linkage group 5, complete sequence

Sequence ID: **emb|BX942837.5|** Length: 183605 Number of Matches: 1

Range 1: 153378 to 153401

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	24/24(100%)	0/24(0%)	Plus/Minus	

Features:

Query 135 ACTGACTGACTGACAGATCGACTG 158
Sbjct 153401 ACTGACTGACTGACAGATCGACTG 153378

Zebrafish DNA sequence from clone CH211-259A10 in linkage group 25, complete sequence

Sequence ID: **emb|CR376764.13|** Length: 123741 Number of Matches: 1

Range 1: 10651 to 10674

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	24/24(100%)	0/24(0%)	Plus/Plus	

Features:

Query 135 ACTGACTGACTGACAGATCGACTG 158
Sbjct 10651 ACTGACTGACTGACAGATCGACTG 10674

Zebrafish DNA sequence from clone RP71-34B6 in linkage group 2, complete sequence

Sequence ID: **emb|BX537344.8|** Length: 174019 Number of Matches: 1

Range 1: 73935 to 73964

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	29/31(94%)	1/31(3%)	Plus/Minus	

Features:

Query 135 ACTGACTGACTGACAGATCGACTGCATCGAC 165
Sbjct 73964 ACTGACTGACTGACAGATTGACTG-ATCGAC 73935

Zebrafish DNA sequence from clone CH211-150K17 in linkage group 10, complete sequence

Sequence ID: **emb|BX510911.10|** Length: 140584 Number of Matches: 1

Range 1: 23942 to 23971

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	29/31(94%)	1/31(3%)	Plus/Minus	

Features:

Query 135 ACTGACTGACTGACAGATCGACTGCATCGAC 165
Sbjct 23971 ACTGACTGACTGACTGATCGACTG-ATCGAC 23942

Zebrafish DNA sequence from clone DKEY-28C2 in linkage group 20, complete sequence

Sequence ID: **emb|BX950183.9|** Length: 200179 Number of Matches: 1

Range 1: 23694 to 23717

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	24/24(100%)	0/24(0%)	Plus/Plus	

Features:

Query 135 ACTGACTGACTGACAGATCGACTG 158
Sbjct 23694 ACTGACTGACTGACAGATCGACTG 23717

Rattus norvegicus vitamin A-deficient testicular protein 14-like mRNA, partial sequence

Sequence ID: **gb|AY169302.1|** Length: 301 Number of Matches: 1

Range 1: 161 to 219

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	48/60(80%)	3/60(5%)	Plus/Minus	

Features:

Query 828 ACACACACATCAACACATGAGTCACATCAGAGAGATATAG-TA-CTACAGAGAGATATAG 885
Sbjct 219 ACACACACACACACATATGTTAGAT-AGAGAGATATAGATAGAGAGATATAG 161

Mouse DNA sequence from clone RP23-421L2 on chromosome 11, complete sequence

Sequence ID: **emb|AL627348.12|** Length: 146061 Number of Matches: 3

Range 1: 21270 to 21303

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

Features:

Query 609 ATGTGTACACACACATCA-ACACATGAGTCACAT 641
Sbjct 21270 ATGTGAACACACACATCACACACATGATTTCACAT 21303

Range 2: 21270 to 21303

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

Features:

Query 822 ATGTGTACACACACATCA-ACACATGAGTCACAT 854
Sbjct 21270 ATGTGAACACACACATCACACACATGATTTCACAT 21303

Range 3: 21270 to 21302

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

Features:

Query 732 ATGTGTACACACACATCA-ACACATGAGTCACA 763
Sbjct 21270 ATGTGAACACACACATCACACACATGATTTCACA 21302

Zebrafish DNA sequence from clone RP71-22K7 in linkage group 12, complete sequence

Sequence ID: **emb|BX470069.10|** Length: 169641 Number of Matches: 1

Range 1: 164474 to 164497

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	24/24(100%)	0/24(0%)	Plus/Minus	

Features:

Query 135 ACTGACTGACTGACAGATCGACTG 158
Sbjct 164497 ACTGACTGACTGACAGATCGACTG 164474

Zebrafish DNA sequence from clone DKEY-53H9, complete sequence

Sequence ID: **emb|AL929596.11|** Length: 191874 Number of Matches: 1
Range 1: 133672 to 133695

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	24/24(100%)	0/24(0%)	Plus/Plus	

Features:

Query 135 ACTGACTGACTGACAGATCGACTG 158
Sbjct 133672 ACTGACTGACTGACAGATCGACTG 133695

Zebrafish DNA sequence from clone CH211-277E21 in linkage group 12, complete sequence

Sequence ID: **emb|BX248086.8|** Length: 173672 Number of Matches: 1
Range 1: 83539 to 83562

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	24/24(100%)	0/24(0%)	Plus/Minus	

Features:

Query 135 ACTGACTGACTGACAGATCGACTG 158
Sbjct 83562 ACTGACTGACTGACAGATCGACTG 83539

Zebrafish DNA sequence from clone CH211-199H23 in linkage group 12, complete sequence

Sequence ID: **emb|AL935268.6|** Length: 206438 Number of Matches: 1
Range 1: 187023 to 187046

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	24/24(100%)	0/24(0%)	Plus/Minus	

Features:

Query 135 ACTGACTGACTGACAGATCGACTG 158
Sbjct 187046 ACTGACTGACTGACAGATCGACTG 187023

Homo sapiens genomic DNA, chromosome 11 clone:RP11-762B21, complete sequence

Sequence ID: **dbj|AP000926.6|** Length: 196972 Number of Matches: 1
Range 1: 116281 to 116322

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

Features:

Query 724 ATAGTACTATGTGTACACACACATCAACACATGAGTCACAAGAGA 768
Sbjct 116322 ATATTCTATGTGTACACACAT--ACACATAAG-CACCAGAGA 116281

Homo sapiens chromosome 5 clone CTB-17P2, complete sequence

Sequence ID: **gb|AC008640.6|** Length: 153596 Number of Matches: 1
Range 1: 118647 to 118680

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

Features:

Query 919 TATGTGTACACACACATCACTATGTGTACACACA 952
Sbjct 118680 TATGTGTACACACACATCCATATGTACACTCA 118647

Homo sapiens gene for seven transmembrane helix receptor, complete cds, isolate:CBRC7TM_64

Sequence ID: **dbj|AB065501.1|** Length: 56423 Number of Matches: 2
Range 1: 1548 to 1591

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

Features:

Query 483 GAGATATAGTTCAGAGAGATATGACTAAGAGATATAGTACTA 526
 Sbjct 1591 GATATATAGTACTATGATATAGTACTATGATATAGTACTA 1548

Range 2: 1563 to 1606

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

Features:

Query 483 GAGATATAGTTCAGAGAGATATGACTAAGAGATATAGTACTA 526
 Sbjct 1606 GATATATAGTACTATGATATAGTACTATGATATAGTACTA 1563

Homo sapiens genomic DNA, chromosome 11q clone:RP11-116P9, complete sequences

Sequence ID: [dbJ|AP002517.3|](#) Length: 173251 Number of Matches: 2

Range 1: 125602 to 125645

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

Features:

Query 483 GAGATATAGTTCAGAGAGATATGACTAAGAGATATAGTACTA 526
 Sbjct 125602 GATATATAGTACTATGATATAGTACTATGATATAGTACTA 125645

Range 2: 125617 to 125660

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

Features:

Query 483 GAGATATAGTTCAGAGAGATATGACTAAGAGATATAGTACTA 526
 Sbjct 125617 GATATATAGTACTATGATATAGTACTATGATATAGTACTA 125660

Solanum lycopersicum chromosome ch06, complete genome

Sequence ID: [emb|HG975518.1|](#) Length: 46045610 Number of Matches: 1

Range 1: 11618426 to 11618480

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	45/58(78%)	6/58(10%)	Plus/Minus	

Features:

Query 467 TACACACACATCCAGAGAGATATGTTAGTCAGAGAGATATAGTACTA---AGAGATATAG 521
 Sbjct 11618480 TACAGAAAAATACAGAGAGATATA---CAGAGAGATATAGAAATACAGAGAGATAG 11618426

Solanum pennellii chromosome ch10, complete genome

Sequence ID: [emb|HG975449.1|](#) Length: 82529941 Number of Matches: 1

Range 1: 41882077 to 41882127

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	42/52(81%)	2/52(3%)	Plus/Plus	

Features:

Query 871 TACAGAGAGATATAGTAACAC-ATGAGTCACATCAGAGAGATATAGTACTAT 921
 Sbjct 41882077 TACAGAGAGATATAGAAATACAAGAGATATA-CAGAGAGATATAGAAATAT 41882127

PREDICTED: Callorhinchus milii very low-density lipoprotein receptor-like (LOC103190431), transcript variant X3, misc_RNA

Sequence ID: [ref|XR_489160.1|](#) Length: 2223 Number of Matches: 1

Range 1: 576 to 620

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	38/47(81%)	2/47(4%)	Plus/Minus	

Features:

Query	229	CTGGTCACAGTAGTCACTACAGTCAGCATACTATGTCAGTCAAACAGA	275
Sbjct	620	CTCGTCACTCTTGTCACTACAGTCGGCATAGTTGTCA--CAAACAGA	576

PREDICTED: Callorhinchus milii very low-density lipoprotein receptor-like (LOC103190431), transcript variant X2, mRNA
Sequence ID: [ref|XM_007911212.1|](#) Length: 3729 Number of Matches: 1
Range 1: 576 to 620

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	38/47(81%)	2/47(4%)	Plus/Minus	

Features:

Query	229	CTGGTCACAGTAGTCACTACAGTCAGCATACATGTCAGTCAAACAGA	275
Sbjct	620	CTCGTCACTCTTGTCACTACAGTCGGCATAGTTGTCA--CAAACAGA	576

PREDICTED: Callorhinchus milii very low-density lipoprotein receptor-like (LOC103190431), transcript variant X1, mRNA
Sequence ID: **refXM_007911210.1** | Length: 2157 Number of Matches: 1
Range 1: 578 to 622

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	38/47(81%)	2/47(4%)	Plus/Minus	

Features:

Query	229	CTGGTCACAGTAGTCACTACAGTCAGCATACATGTCAGTCAAACAGA	275
Sbjct	622	CTCGTCACTCTTGTCACTACAGTCGGCATAGTTGTCA--CAAACAGA	578

Zebrafish DNA sequence from clone DKEY-274K7 in linkage group 13, complete sequence

Sequence ID: **emb|CR381612.6|** Length: 41820 Number of Matches: 1
Range 1: 21863 to 21885

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

Features:

```

Query 136 CTGACTGACTGACAGATCGACTG 158
||| | | | | | | | | | | | | | | | |
Sbjct 21863 CTGACTGACTGACAGATCGACTG 21885

```

PREDICTED: Bos mutus multiple PDZ domain protein (MPDZ), mRNA

Sequence ID: **refXM_005910465.1** | Length: 2161 Number of Matches: 2
Range 1: 1446 to 1483

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

Features:

```

Query 530 GTCAAGCCAGAGATATACTAGTACTAGACGTCAGCCCCAGAGA 567
Sbjct 1483 GTCATCCTGAATACTACTATTGACGTCAGCCCCAGTGA 1446

```

Range 2: 1446 to 1483

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

Features:

Query	383	GTCAGGCCAGAGATAATAGTACTAGACGTCAGCCCCAGAGA	420
Sbjct	1483	GTCACTCTGAATATACTACTATTGACGTCAGCCCCAGTGA	1446

PREDICTED: Bos taurus multiple PDZ domain protein (MPDZ), transcript variant X8, mRNA
Sequence ID: [ref|XM_005209941.1|](#) Length: 10460 Number of Matches: 2
Range 1: 6036 to 6073

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

Features:

Query 530	GTCAGCCAGAGATATACTAGTACTAGACGTCAGCCCAGAGA	567
Sbjct 6073		
	GTCATCCTGAAATATACTACTTGACGTCAGCCCAGTGA	6036

Range 2: 6036 to 6073

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

Features:

Query 383	GTCAGCCAGAGATATACTAGTACTAGACGTCAGCCCAGAGA	420
Sbjct 6073		
	GTCATCCTGAAATATACTACTTGACGTCAGCCCAGTGA	6036

PREDICTED: Bos taurus multiple PDZ domain protein (MPDZ), transcript variant X7, mRNA

Sequence ID: [ref|XM_005209940.1|](#) Length: 10625 Number of Matches: 2

Range 1: 6201 to 6238

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

Features:

Query 530	GTCAGCCAGAGATATACTAGTACTAGACGTCAGCCCAGAGA	567
Sbjct 6238		
	GTCATCCTGAAATATACTACTTGACGTCAGCCCAGTGA	6201

Range 2: 6201 to 6238

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

Features:

Query 383	GTCAGCCAGAGATATACTAGTACTAGACGTCAGCCCAGAGA	420
Sbjct 6238		
	GTCATCCTGAAATATACTACTTGACGTCAGCCCAGTGA	6201

PREDICTED: Bos taurus multiple PDZ domain protein (MPDZ), transcript variant X6, mRNA

Sequence ID: [ref|XM_005209939.1|](#) Length: 10105 Number of Matches: 2

Range 1: 5681 to 5718

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

Features:

Query 530	GTCAGCCAGAGATATACTAGTACTAGACGTCAGCCCAGAGA	567
Sbjct 5718		
	GTCATCCTGAAATATACTACTTGACGTCAGCCCAGTGA	5681

Range 2: 5681 to 5718

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

Features:

Query 383	GTCAGCCAGAGATATACTAGTACTAGACGTCAGCCCAGAGA	420
Sbjct 5718		
	GTCATCCTGAAATATACTACTTGACGTCAGCCCAGTGA	5681

PREDICTED: Bos taurus multiple PDZ domain protein (MPDZ), transcript variant X5, mRNA

Sequence ID: [ref|XM_005209938.1|](#) Length: 10174 Number of Matches: 2

Range 1: 5750 to 5787

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

42.8 bits(46) 7.6() 32/38(84%) 0/38(0%) Plus/Minus

Features:

Query 530 GTCAGCCAGAGATATACTAGACTAGACGTCAGCCCAGAGA 567
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 5787 GTCATCCTGAAATATACTACTTGACGTCAGCCCAGTGA 5750

Range 2: 5750 to 5787

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

Features:

Query 383 GTCAGCCAGAGATATACTAGACTAGACGTCAGCCCAGAGA 420
||||| ||||| ||||| ||||| ||||| |||||
Sbjct 5787 GTCATCCTGAAATATACTACTTGACGTCAGCCCAGTGA 5750

PREDICTED: Bos taurus multiple PDZ domain protein (MPDZ), transcript variant X4, mRNA

Sequence ID: [ref|XM_005209937.1|](#) Length: 10177 Number of Matches: 2

Range 1: 5753 to 5790

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

Features:

Query 530 GTCAGCCAGAGATATACTAGACTAGACGTCAGCCCAGAGA 567
||||| ||||| ||||| ||||| |||||
Sbjct 5790 GTCATCCTGAAATATACTACTTGACGTCAGCCCAGTGA 5753

Range 2: 5753 to 5790

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

Features:

Query 383 GTCAGCCAGAGATATACTAGACTAGACGTCAGCCCAGAGA 420
||||| ||||| ||||| |||||
Sbjct 5790 GTCATCCTGAAATATACTACTTGACGTCAGCCCAGTGA 5753

PREDICTED: Bos taurus multiple PDZ domain protein (MPDZ), transcript variant X3, mRNA

Sequence ID: [ref|XM_005209936.1|](#) Length: 10288 Number of Matches: 2

Range 1: 5864 to 5901

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

Features:

Query 530 GTCAGCCAGAGATATACTAGACTAGACGTCAGCCCAGAGA 567
||||| ||||| ||||| |||||
Sbjct 5901 GTCATCCTGAAATATACTACTTGACGTCAGCCCAGTGA 5864

Range 2: 5864 to 5901

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

Features:

Query 383 GTCAGCCAGAGATATACTAGACTAGACGTCAGCCCAGAGA 420
||||| ||||| ||||| |||||
Sbjct 5901 GTCATCCTGAAATATACTACTTGACGTCAGCCCAGTGA 5864

PREDICTED: Bos taurus multiple PDZ domain protein (MPDZ), transcript variant X2, mRNA

Sequence ID: [ref|XM_005209935.1|](#) Length: 10387 Number of Matches: 2

Range 1: 5963 to 6000

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

Features:

Query 530 GTCAGCCAGAGATATACTAGTACTAGACGTCAGCCCAGAGA 567
 Sbjct 6000 GTCATCCTGAAATATACTACTTGACGTCAGCCCAGTGA 5963

Range 2: 5963 to 6000

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

Features:

Query 383 GTCAGCCAGAGATATACTAGTACTAGACGTCAGCCCAGAGA 420
 Sbjct 6000 GTCATCCTGAAATATACTACTTGACGTCAGCCCAGTGA 5963

PREDICTED: Bos taurus multiple PDZ domain protein (MPDZ), transcript variant X1, mRNA

Sequence ID: **ref|XM_005209934.1|** Length: 10441 Number of Matches: 2

Range 1: 6017 to 6054

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

Features:

Query 530 GTCAGCCAGAGATATACTAGTACTAGACGTCAGCCCAGAGA 567
 Sbjct 6054 GTCATCCTGAAATATACTACTTGACGTCAGCCCAGTGA 6017

Range 2: 6017 to 6054

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

Features:

Query 383 GTCAGCCAGAGATATACTAGTACTAGACGTCAGCCCAGAGA 420
 Sbjct 6054 GTCATCCTGAAATATACTACTTGACGTCAGCCCAGTGA 6017

PREDICTED: Takifugu rubripes cleavage and polyadenylation specificity factor subunit 3-like (LOC101075419), mRNA

Sequence ID: **ref|XM_003977462.1|** Length: 2091 Number of Matches: 1

Range 1: 1738 to 1771

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

Features:

Query 233 TCACAGTAGTCACTACAGTCAGCATACATGTCAGT 267
 Sbjct 1771 TCACCGTAGTGACTAC-GTCGGCATACATGTCAGT 1738

Tetrapisispora blattae CBS 6284 chromosome 8, complete genome

Sequence ID: **emb|HE806323.1|** Length: 956377 Number of Matches: 1

Range 1: 381327 to 381376

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	40/50(80%)	1/50(2%)	Plus/Minus	

Features:

Query 212 AACAAACACTGAGTTCTCTGGTCACAGTAGTCACTACAG-TCAGCATACA 260
 Sbjct 381376 AACAAACATGGAGTTCTCTGATTGTAGTTACTACAGAACATCATACA 381327

Strongylocentrotus purpuratus haplotype Endo16_P_6 Endo16 gene, promoter region

Sequence ID: **gb|JQ408864.1|** Length: 2037 Number of Matches: 1

Range 1: 562 to 609

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	45/58(78%)	10/58(17%)	Plus/Minus	

Features:

Query	828	ACACACACATCAACACATGAGTCACATCAGAGAGATATAGTACTACAGAGAGATATAG	885
Sbjct	609	ACACACACACCCACACA-----CACAT-AGAGACATATA---TACAGAGAGATATAG	562

Eremothecium cymbalariae DBVPG#7215 hypothetical protein (Ecym_6231) mRNA, complete cds
Sequence ID: **ref|XM_003647382.1|** Length: 1350 Number of Matches: 1
Range 1: 49 to 76

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

Features:

Query	461	TATGTGTACACACACATCCAGAGAGATA	488
Sbjct	76	TATGTGTACACATACATCCAGACAGATA	49

Eremothecium cymbalariae DBVPG#7215 chromosome 6, complete sequence
Sequence ID: **gb|CP002502.1|** Length: 959278 Number of Matches: 1
Range 1: 431645 to 431672

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

Features:

Query	461	TATGTGTACACACACATCCAGAGAGATA	488
Sbjct	431672	TATGTGTACACATACATCCAGACAGATA	431645

Homo sapiens protein tyrosine phosphatase, non-receptor type 2 (PTPN2), RefSeqGene on chromosome 18
Sequence ID: **ref|NG_029116.1|** Length: 105858 Number of Matches: 1
Range 1: 99467 to 99515

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	42/52(81%)	3/52(5%)	Plus/Plus	

Features:

Query	468	ACACACACATCCAGAGAGATATAGTTAGACAGAGATATAGTACTAAGAGATAT	519
Sbjct	99467	ACACACACATACAGAGAGATATA--TAAAATAGATATAAAATAA-AGATAT	99515

Bos taurus multiple PDZ domain protein (MPDZ), mRNA
Sequence ID: **ref|NM_001192891.2|** Length: 7507 Number of Matches: 2
Range 1: 5956 to 5993

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

Features:

Query	530	GTCAGCCAGAGATATAGTACTAGACGTCAGCCCCAGAGA	567
Sbjct	5993	GTCATCCTGAAATATACTACTTGACGTCAGCCCCAGTGA	5956

Range 2: 5956 to 5993

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

Features:

Query	383	GTCAGCCAGAGATATAGTACTAGACGTCAGCCCCAGAGA	420
Sbjct	5993	GTCATCCTGAAATATACTACTTGACGTCAGCCCCAGTGA	5956

Callorhinchus milii BAC clone IMCB_Eshark-84H12 from chromosome unknown, complete sequence
Sequence ID: **gb|AC242182.1|** Length: 182780 Number of Matches: 1
Range 1: 133817 to 133850

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	30/34(88%)	4/34(11%)	Plus/Minus	

Features:

```

Query 923 TGTACACACACA----TCACTATGTTGACACACA 952
Sbjct 133850 TGTACACACACAGTCCTACTATGTTGACACACA 133817

```

Zebrafish DNA sequence from clone CH73-81A7 in linkage group 17, complete sequence

Sequence ID: emb|CU655821.15| Length: 24456 Number of Matches: 1

Range 1: 20463 to 20490

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

Features:

Query	135	ACTGACTGACTGACAGATCGACTGCATC	162
Sbjct	20463	ACTGACTGACTGACCAGATCGACTGAATC	20490

S.lycopersicum DNA sequence from clone SL_MboI-81L19, complete sequence

Sequence ID: emb|CU928680.5| Length: 227938 Number of Matches: 1

Range 1: 191478 to 191532

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	45/58(78%)	6/58(10%)	Plus/Minus	

Features:

Query	467	TACACACACATCCAGAGAGATATAAGTTCAAGAGAGATATAGTACTA--AGAGATATAG	521
Sbjct	191532	TACAGAAAAATACAGAGAGATATA---CAGAGAGATAGAAATATACAGAGAGATAG	191478

Homo sapiens tyrosine-protein phosphatase non-receptor type 2 (PTN2) gene, complete cds, alternatively spliced
Sequence ID: **gb|EF445017.1** Length: 104850 Number of Matches: 1

Range 1: 7336 to 7384

42.8 bits(46) 7.6() 42/52(81%) 3/52(5%) Plus/Minus

Features.

Query 466 ACACACACATCCAGAGAGATATACTTACAGACACATATACATAC AACATATA 515
Sbjct 7384 ACACACACACATACAGAGAGATATA--TAAATAGATATAAAAATAA-AGATAT 7336

Mouse DNA sequence from clone CH29-149F14 on chromosome 6, complete sequence

Sequence ID: **emb|CU207392.14|** Length: 264250 Number of Matches: 1

Range 1: 87310 to 87339

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	30/34(88%)	4/34(11%)	Plus/Minus	

Features:

```

Query  919      TATGTGTACACACATCACTATGTGTACACACA  952
Sbjct  87339    TATGTGTACACACACA----TATGTGTACACACA  87310

```

Mouse DNA sequence from clone RP24-463G23 on chromosome 12, complete sequence

Sequence ID: emb|CU024890.15| Length: 145901 Number of Matches: 1

Range 1: 140547 to 140590

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

Features:

Query	447	GAGAGATATAG-TACTATGTGTACACACACATCCAGAGAGATA	490
Sbjct	140547	GAGAGATACAGATCAA-GTGTACACACACACAGAGACATATA	140590

Mouse DNA sequence from clone WI1-2581G20 on chromosome 4, complete sequence

Sequence ID: **emb|CU207287.4|** Length: 38661 Number of Matches: 3

Range 1: 26802 to 26827

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

Features:

Query 823 TGTGTACACACACATCAACACATGAG 848
Sbjct 26827 TGTGTTCACACACATCAACACATGAG 26802

Range 2: 26802 to 26827

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

Features:

Query 733 TGTGTACACACACATCAACACATGAG 758
Sbjct 26827 TGTGTTCACACACATCAACACATGAG 26802

Range 3: 26802 to 26827

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

Features:

Query 610 TGTGTACACACACATCAACACATGAG 635
Sbjct 26827 TGTGTTCACACACATCAACACATGAG 26802

Oryza sativa Japonica Group Os02g0172800 (Os02g0172800) mRNA, complete cds

Sequence ID: **ref|NM_001052569.1|** Length: 1508 Number of Matches: 1

Range 1: 172 to 207

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

Features:

Query 467 TACACACACATCCAGAGAGATATAAGTCAGAGAGAT 502
Sbjct 172 TACACACACATCTAGAGAGAGAAAGTAGAGAGAGAT 207

Zebrafish DNA sequence from clone DKEYP-72A3 in linkage group 17, complete sequence

Sequence ID: **emb|CR854889.15|** Length: 202336 Number of Matches: 1

Range 1: 63735 to 63762

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

Features:

Query 135 ACTGACTGACTGACAGATCGACTGCATC 162
Sbjct 63735 ACTGACTGACTGACCGATCGACTGAATC 63762

Zebrafish DNA sequence from clone DKEY-89F23 in linkage group 17, complete sequence

Sequence ID: **emb|CR352284.26|** Length: 181192 Number of Matches: 1

Range 1: 53347 to 53369

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

Features:

Query 135 ACTGACTGACTGACAGATCGACT 157

Sbjct 53369 ||||||| ACTGACTGACTGACAGAGATCGACT 53347

Mus musculus chromosome 5, clone RP24-571K14, complete sequence

Sequence ID: **gb|AC120437.7|** Length: 147493 Number of Matches: 1

Range 1: 140632 to 140662

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

Features:

Query 919 TATGTGTACACACACATCACTATGTGTACACACA 952
Sbjct 140662 TATGTGTACACACACAT---TATTGTACACACA 140632

Mus musculus chromosome 8, clone RP24-485L5, complete sequence

Sequence ID: **gb|AC110214.7|** Length: 213387 Number of Matches: 1

Range 1: 471 to 498

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

Features:

Query 463 TGTGTACACACACATCCAGAGAGATATA 490
Sbjct 498 TGTGTACACACACATAACAGAGATATATA 471

Mus musculus BAC clone RP23-129J20 from chromosome 6, complete sequence

Sequence ID: **gb|AC165970.3|** Length: 207303 Number of Matches: 1

Range 1: 21445 to 21474

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	30/34(88%)	4/34(11%)	Plus/Minus	

Features:

Query 919 TATGTGTACACACACATCACTATGTGTACACACA 952
Sbjct 21474 TATGTGTACACACACA---TATGTGTACACACA 21445

Mus musculus BAC clone RP23-448D23 from chromosome 12, complete sequence

Sequence ID: **gb|AC162902.4|** Length: 190357 Number of Matches: 1

Range 1: 80925 to 81015

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	66/91(73%)	4/91(4%)	Plus/Minus	

Features:

Query 636 TCACATCAGAGAGATATA-GTA---CTAACAGAGATATAGT-ACTAGACGTCAGCCAGAGAG 691
Sbjct 81015 TCACCTCAGAGAGATAACAGGTAAACCACAGAGAGATAGTAATTACAGGTCATCATGGGGAG 80956
Query 692 ATATAGTAACACATGAGTCACATCAGAGAGA 722
Sbjct 80955 ATACTGGAAGACACAAGTCACCTCAGGGAGA 80925

Mus musculus chromosome 3, clone RP23-288N9, complete sequence

Sequence ID: **gb|AC107700.12|** Length: 194390 Number of Matches: 1

Range 1: 27539 to 27573

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

Features:

Query 919 TATGTGTACACACACAT-CACTATGTGTACACACA 952
Sbjct 27573 TATGTGCACACACAGATACTACAGTGACACACA 27539

Mus musculus BAC clone RP23-105L19 from chromosome 6, complete sequence

Sequence ID: **gb|AC147225.3|** Length: 210239 Number of Matches: 1

Range 1: 188958 to 188990

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

Features:

Query 1 CATGAGTATGTGTACACACACATCCATGAGT 33
Sbjct 188958 CATGAGTATGTGTGCACACACATTATGTGT 188990

Mus musculus BAC RP24-83C9 (Roswell Park Cancer Institute (C57BL/6J Male) Mouse BAC Library) complete sequence

Sequence ID: **gb|AC168278.2|** Length: 247493 Number of Matches: 1

Range 1: 127818 to 127850

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

Features:

Query 1 CATGAGTATGTGTACACACACATCCATGAGT 33
Sbjct 127850 CATGAGTATGTGTGCACACACATTATGTGT 127818

Mus musculus BAC clone RP23-166K13 from chromosome 18, complete sequence

Sequence ID: **gb|AC122848.3|** Length: 204254 Number of Matches: 1

Range 1: 12748 to 12780

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

Features:

Query 920 ATGTGTACACACACATCACTATGTGTACACACA 952
Sbjct 12780 ATGTGTACACACACATATACTGTGTACACACA 12748

Mus musculus BAC clone RP24-486E21 from chromosome 8, complete sequence

Sequence ID: **gb|AC132569.3|** Length: 172340 Number of Matches: 1

Range 1: 2090 to 2122

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

Features:

Query 3 TGAGTATGTGTACACACACATCCATGAGTAC 35
Sbjct 2122 TGTGTGTGTGTACACACACATGCATGGGTAC 2090

Mus musculus BAC clone RP23-326N11 from chromosome 18, complete sequence

Sequence ID: **gb|AC132427.4|** Length: 192806 Number of Matches: 1

Range 1: 182507 to 182539

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

Features:

Query 920 ATGTGTACACACACATCACTATGTGTACACACA 952
Sbjct 182539 ATGTGTACACACACATATACTGTGTACACACA 182507

Mus musculus BAC clone RP23-346N11 from chromosome 7, complete sequence

Sequence ID: **gb|AC135963.3|** Length: 202404 Number of Matches: 1

Range 1: 104462 to 104489

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

42.8 bits(46) 7.6() 26/28(93%) 0/28(0%) Plus/Minus

Features:

Query 3 TGAGTATGTGTGTACACACACATCCATG 30
Sbjct 104489 TGACTATGTGTGTACACACACATGCATG 104462

Mus musculus BAC clone RP23-415J21 from chromosome 7, complete sequence

Sequence ID: **gb|AC111008.6|** Length: 193593 Number of Matches: 1

Range 1: 171687 to 171714

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

Features:

Query 453 TATAGTACTATGTGTACACACACATCCA 480
Sbjct 171714 TATATTACTATATGTACACACACATCCA 171687

Mus musculus BAC clone RP24-404N12 from chromosome 8, complete sequence

Sequence ID: **gb|AC124380.4|** Length: 149620 Number of Matches: 1

Range 1: 142256 to 142288

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

Features:

Query 3 TGAGTATGTGTGTACACACACATCCATGAGTAC 35
Sbjct 142256 TGTGTGTGTGTGTACACACACATGCATGGGTAC 142288

Mus musculus BAC clone RP24-566O21 from chromosome 3, complete sequence

Sequence ID: **gb|AC123553.4|** Length: 138553 Number of Matches: 1

Range 1: 92062 to 92096

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

Features:

Query 919 TATGTGTACACACACAT-CACTATGTGTACACACA 952
Sbjct 92096 TATGTGCAACACACAGATACTACACTACGTGTACACACA 92062

Mus musculus BAC clone RP23-145J18 from 8, complete sequence

Sequence ID: **gb|AC122866.4|** Length: 200136 Number of Matches: 1

Range 1: 92120 to 92149

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

Features:

Query 923 TGTACACACACACA-TCACTATGTGTACACAC 951
Sbjct 92149 TGTACACACACACTCACTGTGTACACAC 92120

Mus musculus chromosome 8, clone RP23-227D17, complete sequence

Sequence ID: **gb|AC161188.5|** Length: 143672 Number of Matches: 1

Range 1: 38453 to 38480

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

Features:

Query 463 TGTGTACACACACATCCAGAGAGATATA 490
Sbjct 38480 TGTGTACACACACATACAGAGATATA 38453

Mus musculus chromosome 8, clone RP23-216D14, complete sequence

Sequence ID: **gb|AC163014.5|** Length: 208407 Number of Matches: 1

Range 1: 145279 to 145320

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	36/43(84%)	1/43(2%)	Plus/Minus	

Features:

Query 910 ATATAGTACTATGTGTACACACACATCACTATGTGTACACACA 952
Sbjct 145320 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| 145279

Mus musculus BAC clone RP23-411F11 from chromosome 12, complete sequence

Sequence ID: **gb|AC155312.2|** Length: 197795 Number of Matches: 1

Range 1: 168490 to 168580

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	66/91(73%)	4/91(4%)	Plus/Minus	

Features:

Query 636 TCACATCAGAGAGATA-GTA---CTAAGAGATATAGT-ACTAGACGTCAGCCCAGAGAG 691
Sbjct 168580 TCACCTCAGAGAGATAACAGGTAAACCACAGAGAGATAGTAATTACAGGTATCATGGGGAG 168521
Query 692 ATATAGTAACACATGAGTCACATCAGAGAGA 722
Sbjct 168520 ATACTGGAAGACACAAGTCACCTCAGGGAGA 168490

Mus musculus BAC clone RP24-347B7 from chromosome 6, complete sequence

Sequence ID: **gb|AC125145.3|** Length: 186598 Number of Matches: 1

Range 1: 77265 to 77294

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	30/34(88%)	4/34(11%)	Plus/Minus	

Features:

Query 919 TATGTGTACACACACATCACTATGTGTACACACA 952
Sbjct 77294 TATGTGTACACACACA---TATGTGTACACACA 77265

Human DNA sequence from clone CTD-2280P12 on chromosome 13, complete sequence

Sequence ID: **emb|AL929515.4|** Length: 26561 Number of Matches: 1

Range 1: 18999 to 19063

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	52/68(76%)	6/68(8%)	Plus/Plus	

Features:

Query 452 ATATAGTACTATGTGTACACACACATCCAGAGAGATATAGTTAGAGAGATATA---GTA 508
Sbjct 18999 ATATATTA-TATGTGTACACACACA--GAGAGAGATAAAAAGACAGAGATAGAGGCAGTA 19055
Query 509 CTAAGAGA 516
Sbjct 19056 CAAAGAGA 19063

Homo sapiens chromosome 15, clone RP11-424E9, complete sequence

Sequence ID: **gb|AC090259.5|** Length: 143479 Number of Matches: 1

Range 1: 38832 to 38866

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

Features:

Query 920 ATGTGTACACACACAT-CAC-TATGTGTACACACA 952
Sbjct 38866 ATGTGTACACACACACCTGCACATATGTGTACACACA 38832

Homo sapiens chromosome 15, clone RP11-466P9, complete sequence

Sequence ID: **gb|AC105014.5|** Length: 189047 Number of Matches: 1

Range 1: 5501 to 5535

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

Features:

Query 920 ATGTGTACACACACAT-CAC-TATGTGTACACACA 952
Sbjct 5501 |||||||ATGTGTACACACACCTGCACATATGTGTACACACA 5535

Homo sapiens BAC clone RP11-270I3 from 4, complete sequence

Sequence ID: **gb|AC027625.5|** Length: 164856 Number of Matches: 1

Range 1: 129941 to 129963

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

Features:

Query 2 ATGAGTATGTGTGTACACACACA 24
Sbjct 129941 ATGAGTATGTGTGTACACACACA 129963

Oryza sativa Japonica Group genomic DNA, chromosome 2, BAC clone:OSJNBa0073A21

Sequence ID: **dbj|AP005772.3|** Length: 170051 Number of Matches: 1

Range 1: 18265 to 18300

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

Features:

Query 467 TACACACACATCCAGAGAGATATAAGTTTCAGAGAGAT 502
Sbjct 18265 TACACACACATCTAGAGAGAGAAAGTAGAGAGAGAT 18300

Oryza sativa Japonica Group genomic DNA, chromosome 2, PAC clone:P0030G02

Sequence ID: **dbj|AP004836.2|** Length: 187265 Number of Matches: 1

Range 1: 170070 to 170105

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

Features:

Query 467 TACACACACATCCAGAGAGATATAAGTTTCAGAGAGAT 502
Sbjct 170070 TACACACACATCTAGAGAGAGAAAGTAGAGAGAGAT 170105

Oryza sativa Japonica Group cDNA clone:J033148H01, full insert sequence

Sequence ID: **dbj|AK103838.1|** Length: 1509 Number of Matches: 1

Range 1: 173 to 208

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

Features:

Query 467 TACACACACATCCAGAGAGATATAAGTTTCAGAGAGAT 502
Sbjct 173 TACACACACATCTAGAGAGAGAAAGTAGAGAGAGAT 208

Mouse DNA sequence from clone RP23-426J14 on chromosome 4, complete sequence

Sequence ID: **emb|AL691491.11|** Length: 199017 Number of Matches: 1

Range 1: 8388 to 8427

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

Features:

Query	270	AACAGAGAGATATAGTTAGAGAGATATAGTA-CTATGTG	308
Sbjct	8427	AACAGAGAGCTAAATTAGAGAGATTAGTAGCTATCTG	8388

Ophistoma minus isolate OM3 scytalone dehydratase (SD) gene, partial cds

Sequence ID: **gb|AY098659.1|** Length: 428 Number of Matches: 1

Range 1: 117 to 139

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

Features:

Query	135	ACTGACTGACTGACAGATCGACT	157
Sbjct	117	ACTGACTGACTGACAGATCGACT	139

Mus musculus BAC clone RP23-408M14 from 6, complete sequence

Sequence ID: **gb|AC123937.3|** Length: 164294 Number of Matches: 1

Range 1: 144771 to 144803

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

Features:

Query	1	CATGAGTATGTGTGTACACACACATCCATGAGT	33
Sbjct	144771	CATGAGTATGTGTGTGCACACACATTTATGTGT	144803

Mus musculus BAC clone RP24-247D2 from 6, complete sequence

Sequence ID: **gb|AC147371.4|** Length: 178577 Number of Matches: 1

Range 1: 69245 to 69274

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	30/34(88%)	4/34(11%)	Plus/Minus	

Features:

Query	919	TATGTGTACACACACATCACTATGTGTACACACA	952
Sbjct	69274	TATGTGTACACACACA----TATGTGTACACACA	69245

Mus musculus BAC clone RP23-336M12 from 8, complete sequence

Sequence ID: **gb|AC141641.4|** Length: 184896 Number of Matches: 1

Range 1: 117158 to 117190

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

Features:

Query	3	TGAGTATGTGTGTACACACACATCCATGAGTAC	35
Sbjct	117190	TGAGTATGTGTGTACACACACATGCATGGGTAC	117158

Homo sapiens genomic DNA, chromosome 18 clone:RP11-767P20, complete sequence

Sequence ID: **dbj|AP001077.6|** Length: 199652 Number of Matches: 1

Range 1: 124387 to 124435

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	42/52(81%)	3/52(5%)	Plus/Minus	

Features:

Query	468	ACACACACATCCAGAGAGATATAGTTAGAGAGATATACTAAGAGATAT	519
Sbjct	124435	ACACACACATACAGAGAGATATA--TAAAATAGATATAAAAATAA-AGATAT	124387

Zebrafish DNA sequence from clone DKEY-12J12 in linkage group 14, complete sequence
Sequence ID: **emb|BX000452.7|** Length: 220420 Number of Matches: 1
Range 1: 96215 to 96237

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

Features:

Query	135	ACTGACTGACTGACAGATCGACT	157
Sbjct	96215	ACTGACTGACTGACAGATCGACT	96237

Mouse DNA sequence from clone RP23-18M2 on chromosome 4, complete sequence
Sequence ID: **emb|AL606924.14|** Length: 180444 Number of Matches: 3
Range 1: 107215 to 107240

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

Features:

Query	610	TGTGTACACACACATCAACACATGAG	635
Sbjct	107215	TGTGTTCACACACACATCAACACATGAG	107240

Range 2: 107215 to 107240

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

Features:

Query	733	TGTGTACACACACATCAACACATGAG	758
Sbjct	107215	TGTGTTCACACACACATCAACACATGAG	107240

Range 3: 107215 to 107240

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

Features:

Query	823	TGTGTACACACACATCAACACATGAG	848
Sbjct	107215	TGTGTTCACACACACATCAACACATGAG	107240

Mouse DNA sequence from clone RP23-56A14 on chromosome 7, complete sequence
Sequence ID: **emb|AL603836.13|** Length: 215366 Number of Matches: 1
Range 1: 28881 to 28908

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

Features:

Query	3	TGAGTATGTGTACACACACATCCATG	30
Sbjct	28908	TGACTATGTGTACACACACATGCATG	28881