

Basic Local Alignment Search Tool

NCBI/ [BLAST](#)/ [blastn suite](#)/ [Formatting Results - Y0U8E7CU014](#)

► [Formatting options](#)

► [Download](#)

[Blast report description](#)

GCTA

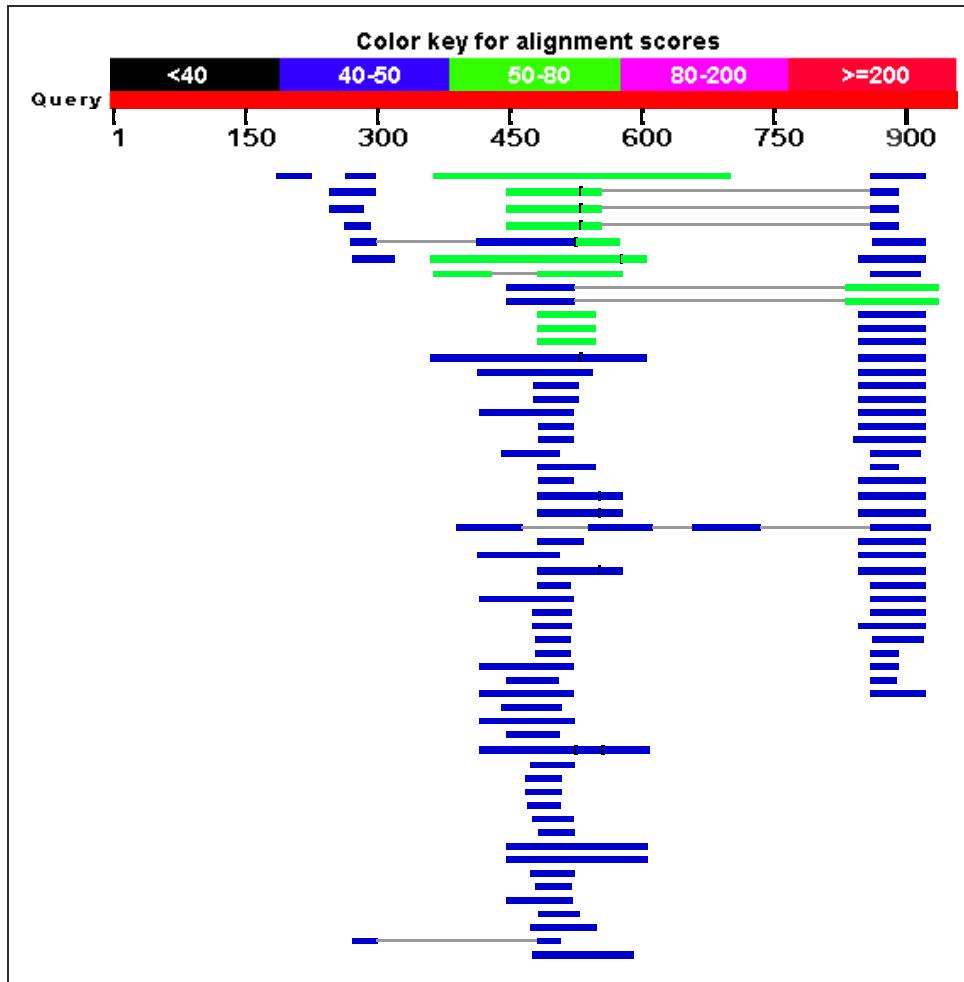
RID [Y0U8E7CU014](#) (Expires on 08-06 13:18 pm)

Query ID Icl|44283
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 167 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Mus musculus BAC clone RP23-83G6 from chromosome 12, complete sequence	66.2	153	35%	7e-07	66%	AC160138.2
Mus musculus targeted non-conditional, lacZ-tagged mutant allele Ctnbp2:tm1e(KOMP)Wtsi; transgenic	62.6	316	14%	8e-06	77%	JN963729.1
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Ctnbp2:tm1a(KOMP)Wtsi; transgenic	62.6	316	14%	8e-06	77%	JN945565.1
Mus musculus strain C57BL/6J chromosome 6 clone RP23-219K14, complete sequence	62.6	316	14%	8e-06	77%	AC027654.3
Mus musculus 13 days embryo heart cDNA, RIKEN full-length enriched library, clone:D330002H21 product:unclassifiable, full insert sequence	60.8	149	19%	3e-05	75%	AK084464.1
Homo sapiens BAC clone CH17-449C21 from chromosome 1, complete sequence	57.2	721	25%	3e-04	68%	AC241952.2
Mus musculus chromosome 12, clone RP23-456E21, complete sequence	55.4	107	17%	0.001	75%	AC102626.9
Rattus norvegicus CH230-6E20 (Children's Hospital Oakland Research Institute Rat (BN/SsNHsd/MCW) BAC library) complete sequence	51.8	94.5	19%	0.015	74%	AC131965.5
Rattus norvegicus CH230-333G12 (Children's Hospital Oakland Research Institute Rat (BN/SsNHsd/MCW) BAC library) complete sequence	51.8	94.5	19%	0.015	74%	AC128103.4
Mus musculus 10 BAC RP24-324P5 (Roswell Park Cancer Institute (C57BL/6J Male) Mouse BAC Library) complete sequence	51.8	51.8	7%	0.015	81%	AC164624.3
Mus musculus 10 BAC RP23-475H6 (Roswell Park Cancer Institute (C57BL/6J Female) Mouse BAC Library) complete sequence	51.8	51.8	7%	0.015	81%	AC158642.8
Mus musculus BAC clone RP24-444D19 from 10, complete sequence	51.8	51.8	7%	0.015	81%	AC131789.4
Homo sapiens chromosome 1 clone WI2-2264119, complete sequence	50.0	187	25%	0.051	68%	AC196529.1
Mus musculus BAC clone RP23-286N12 from chromosome 16, complete sequence	50.0	50.0	13%	0.051	73%	AC164302.2
Mus musculus BAC clone RP23-270P19 from chromosome 3, complete sequence	50.0	50.0	6%	0.051	80%	AC123876.5
Human DNA sequence from clone RP11-541I19 on chromosome 10 Contains the 3' end of the gene for a novel protein similar to mannose receptor C type 1 (MRC1), complete sequence	50.0	94.5	5%	0.051	84%	BX255924.4
Homo sapiens chromosome 10 clone RP11-457D2, complete sequence	50.0	94.5	5%	0.051	84%	AC069023.5
PREDICTED: Callithrix jacchus uncharacterized LOC100894812 (LOC100894812), mRNA	48.2	48.2	11%	0.18	72%	XM_003735540.1
Mus musculus targeted deletion, lacZ-tagged mutant allele	48.2	48.2	4%	0.18	87%	JN958386.1

Bri3:tm1(KOMP)Ucd; transgenic						
Mus musculus chromosome 5, clone RP24-182D2, complete sequence	48.2	48.2	4%	0.18	87%	AC139636.12
Human DNA sequence from clone RP11-57G10 on chromosome 10, complete sequence	48.2	48.2	6%	0.18	81%	AL133551.13
Mus musculus 10 BAC RP24-339G14 (Roswell Park Cancer Institute (C57BL/6J Male) Mouse BAC Library) complete sequence	48.2	48.2	6%	0.18	80%	AC157089.5
Mus musculus MHC class I related protein 1 isoform B (MR1B) pseudogene mRNA, complete sequence	48.2	48.2	7%	0.18	80%	AF010449.1
Mus musculus BAC clone RP24-82B23 from 5, complete sequence	48.2	48.2	4%	0.18	87%	AC121845.3
Human DNA sequence from clone RP11-759G12 on chromosome 22, complete sequence	46.4	139	7%	0.62	74%	FO681547.3
Mus musculus targeted non-conditional, lacZ-tagged mutant allele Dhx8:tm1e(EUCOMM)Wtsi; transgenic	46.4	89.1	10%	0.62	79%	JN961110.1
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Fabp5:tm1a(EUCOMM)Wtsi; transgenic	46.4	46.4	5%	0.62	80%	JN960738.1
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Dhx8:tm1a(EUCOMM)Wtsi; transgenic	46.4	89.1	10%	0.62	79%	JN949282.1
Homo sapiens FOSMID clone COR2A-DD0002RCQNU_A23 from chromosome 22, complete sequence	46.4	92.7	7%	0.62	74%	AC240169.3
Homo sapiens FOSMID clone ABC16-2235N21 from chromosome 22, complete sequence	46.4	89.1	7%	0.62	74%	AC238718.3
Homo sapiens FOSMID clone ABC24-1739C22 from chromosome 22, complete sequence	46.4	92.7	7%	0.62	74%	AC237679.2
Homo sapiens FOSMID clone ABC8-648022D8 from chromosome unknown, complete sequence	46.4	46.4	7%	0.62	74%	AC235038.3
Homo sapiens FOSMID clone ABC14-1050114M3 from chromosome unknown, complete sequence	46.4	46.4	7%	0.62	74%	AC236044.3
Homo sapiens FOSMID clone ABC11-47241400B7 from chromosome unknown, complete sequence	46.4	89.1	7%	0.62	74%	AC234926.3
Homo sapiens FOSMID clone ABC10-44686500B23 from chromosome unknown, complete sequence	46.4	92.7	7%	0.62	74%	AC235016.2
Homo sapiens FOSMID clone ABC11-47139300P5 from chromosome unknown, complete sequence	46.4	46.4	7%	0.62	74%	AC234920.3
Homo sapiens FOSMID clone ABC7-42392500M17 from chromosome unknown, complete sequence	46.4	92.7	7%	0.62	74%	AC235558.3
Zebrafish DNA sequence from clone CH1073-416D2 in linkage group 17, complete sequence	46.4	90.9	8%	0.62	73%	CU657975.12
Mus musculus chromosome 3, clone RP23-20F10, complete sequence	46.4	46.4	5%	0.62	80%	AC157379.7
Mus musculus BAC clone RP24-372O13 from 12, complete sequence	46.4	176	30%	0.62	78%	AC122023.3
Mus musculus BAC clone RP24-194J17 from chromosome 9, complete sequence	46.4	46.4	3%	0.62	93%	AC157996.2
Homo sapiens chromosome 22 clone WI2-3379H11, complete sequence	46.4	46.4	7%	0.62	74%	AC158336.1
Homo sapiens glutathione S-transferase						

theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds	46.4	135	7%	0.62	74%	AF240786.1
Mouse DNA sequence from clone RP23-356F21 on chromosome 13, complete sequence	46.4	46.4	5%	0.62	77%	CT025557.11
Mouse DNA sequence from clone RP23-226L18 on chromosome 2, complete sequence	46.4	89.1	9%	0.62	77%	AL929164.12
Mouse DNA sequence from clone RP23-382C19 on chromosome 11, complete sequence	46.4	89.1	10%	0.62	79%	AL590994.13
Homo sapiens genomic DNA, chromosome 22q11.2, clone KB226F1	46.4	135	7%	0.62	74%	AP000351.3
Homo sapiens genomic DNA, chromosome 22q11.2, clone KB1561E1	46.4	92.7	7%	0.62	74%	AP000352.2
Human DNA sequence from clone CTA-322B1 on chromosome 22q11-12, complete sequence	46.4	46.4	7%	0.62	74%	Z84718.2
Homo sapiens genomic DNA, chromosome 22q11.2, clone KB1125A3	46.4	46.4	7%	0.62	74%	AP000350.1
Homo sapiens chromosome 17, clone hRPK.60_A_24, complete sequence	46.4	46.4	4%	0.62	87%	AC005325.1
Homo sapiens BAC clone CH17-277L15 from chromosome 8, complete sequence	44.6	44.6	11%	2.2	71%	AC245121.2
Mus musculus targeted non-conditional, lacZ-tagged mutant allele Aldh1a3:tm1e(KOMP)Wtsi; transgenic	44.6	44.6	4%	2.2	83%	JN957473.1
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Aldh1a3:tm1a(KOMP)Wtsi; transgenic	44.6	44.6	4%	2.2	83%	JN957472.1
Mus musculus targeted non-conditional, lacZ-tagged mutant allele Nfatc2:tm1e(EUCOMM)Wtsi; transgenic	44.6	44.6	4%	2.2	84%	JN948916.1
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Nfatc2:tm1a(EUCOMM)Wtsi; transgenic	44.6	44.6	4%	2.2	84%	JN948915.1
Schistosoma mansoni strain Puerto Rico chromosome 2, complete genome	44.6	44.6	4%	2.2	85%	HE601625.1
Homo sapiens FOSMID clone ABC9-43973000L3 from chromosome 8, complete sequence	44.6	44.6	11%	2.2	71%	AC243065.3
Pig DNA sequence from clone CH242-169K14 on chromosome X, complete sequence	44.6	44.6	6%	2.2	77%	CU856563.5
Homo sapiens FOSMID clone ABC13-49766800L3 from chromosome 8, complete sequence	44.6	44.6	11%	2.2	71%	AC217626.3
Pan troglodytes BAC clone CH251-284B16 from chromosome 10, complete sequence	44.6	44.6	6%	2.2	79%	AC191768.3
Homo sapiens chromosome 8, clone RP11-715M14, complete sequence	44.6	44.6	11%	2.2	71%	AC022257.20
Rhesus macaque BAC clone CH250-65H12 from chromosome unknown, complete sequence	44.6	44.6	6%	2.2	76%	AC187497.2
Pan troglodytes BAC clone CH251-631F3 from chromosome 8, complete sequence	44.6	217	20%	2.2	73%	AC184709.2
Mus musculus BAC clone RP23-264M10 from chromosome 16, complete sequence	44.6	44.6	5%	2.2	82%	AC161376.2
Mus musculus chromosome 7, clone RP23-24N16, complete sequence	44.6	44.6	6%	2.2	79%	AC110520.12

Mus musculus 10 BAC RP23-3P24 (Roswell Park Cancer Institute (C57BL/6J Female) Mouse BAC Library) complete sequence	44.6	44.6	4%	2.2	85%	AC167221.9
Mus musculus 10 BAC RP23-150M2 (Roswell Park Cancer Institute (C57BL/6J Female) Mouse BAC Library) complete sequence	44.6	44.6	4%	2.2	85%	AC166082.11
Mus musculus chromosome 1, clone RP23-22I7, complete sequence	44.6	44.6	3%	2.2	89%	AC158925.4
Mus musculus chromosome 7, clone RP23-7G1, complete sequence	44.6	44.6	4%	2.2	83%	AC091324.10
Mus musculus BAC clone RP24-401P10 from 6, complete sequence	44.6	44.6	3%	2.2	89%	AC122031.2
Mus musculus 12 days embryo embryonic body between diaphragm region and neck cDNA, RIKEN full-length enriched library, clone:9430010I07 product:hyaluronan and proteoglycan link protein 3, full insert sequence	44.6	44.6	6%	2.2	79%	AK136956.1
Mus musculus BAC clone RP24-496G24 from chromosome 17, complete sequence	44.6	44.6	5%	2.2	81%	AC155242.2
Homo sapiens chromosome 18, clone RP11-104H13, complete sequence	44.6	44.6	4%	2.2	88%	AC110015.5
Mus musculus 10 BAC RP24-347J14 (Roswell Park Cancer Institute (C57BL/6J Male) Mouse BAC Library) complete sequence	44.6	44.6	16%	2.2	71%	AC156949.9
Mus musculus 6 BAC RP24-204J8 (Roswell Park Cancer Institute (C57BL/6J Male) Mouse BAC Library) complete sequence	44.6	44.6	6%	2.2	79%	AC155722.9
Mus musculus 10 BAC RP23-53D13 (Roswell Park Cancer Institute (C57BL/6J Female) Mouse BAC Library) complete sequence	44.6	44.6	16%	2.2	71%	AC153824.9
Mus musculus BAC clone RP24-401O6 from 16, complete sequence	44.6	44.6	5%	2.2	82%	AC125371.4
Mouse DNA sequence from clone RP23-156F1 on chromosome 2, complete sequence	44.6	44.6	4%	2.2	84%	AL844575.4
Homo sapiens BAC clone CH17-476P10 from chromosome 22, complete sequence	42.8	85.5	7%	7.6	73%	AC253536.1
PREDICTED: Callithrix jacchus uncharacterized LOC100895454 (LOC100895454), mRNA	42.8	42.8	7%	7.6	75%	XM_003734947.1
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Slc12a1:tm1a(EUCOMM)Hmg; transgenic	42.8	42.8	4%	7.6	85%	JN960771.1
Homo sapiens FOSMID clone ABC16-2279J16 from chromosome x, complete sequence	42.8	42.8	4%	7.6	85%	AC238719.3
Zebrafish DNA sequence from clone CH73-352P18 in linkage group 22, complete sequence	42.8	42.8	7%	7.6	78%	FP067424.7
Tupaia belangeri BAC clone CH275-65H12 from chromosome unknown, complete sequence	42.8	85.5	5%	7.6	96%	AC236278.1
Homo sapiens keratin 18 (KRT18), RefSeqGene on chromosome 12	42.8	42.8	5%	7.6	79%	NG_008351.1
Rattus norvegicus BAC CH230-34B22 (Children's Hospital Oakland Research Institute Rat (BN/SsNHsd/MCW) BAC library) complete sequence	42.8	42.8	3%	7.6	90%	AC128786.3
Mouse DNA sequence from clone RP23-25G2 on chromosome 13, complete sequence	42.8	42.8	11%	7.6	70%	CU025215.12

Zebrafish DNA sequence from clone DKEY-160M3 in linkage group 6, complete sequence	42.8	42.8	3%	7.6	93%	CT573376.5
Mus musculus BAC clone RP23-110D19 from chromosome 1, complete sequence	42.8	42.8	3%	7.6	90%	AC153019.8
Zebrafish DNA sequence from clone DKEYP-29C12 in linkage group 11, complete sequence	42.8	42.8	4%	7.6	83%	CR931977.8
Mus musculus chromosome 7, clone RP24-63H14, complete sequence	42.8	42.8	4%	7.6	84%	AC118621.6
Mus musculus chromosome 3, clone RP23-277L18, complete sequence	42.8	42.8	4%	7.6	83%	AC152400.9
Mus musculus chromosome 8, clone RP23-80D9, complete sequence	42.8	42.8	6%	7.6	75%	AC161217.7
Mus musculus 6 BAC RP24-483K3 (Roswell Park Cancer Institute (C57BL/6J Male) Mouse BAC Library) complete sequence	42.8	42.8	4%	7.6	82%	AC155946.7
Mouse DNA sequence from clone RP24-274P18 on chromosome 17, complete sequence	42.8	42.8	4%	7.6	81%	CT025573.9
Mus musculus chromosome 16, clone RP23-73P19, complete sequence	42.8	42.8	5%	7.6	79%	AC116118.16
Mus musculus chromosome 1, clone RP23-311K2, complete sequence	42.8	42.8	3%	7.6	93%	AC107746.9
Mus musculus BAC clone RP24-87K15 from 9, complete sequence	42.8	42.8	6%	7.6	77%	AC110091.4
Dasyurus novemcinctus clone VMRC5-356N21, complete sequence	42.8	42.8	4%	7.6	81%	AC145363.4

Alignments

Mus musculus BAC clone RP23-83G6 from chromosome 12, complete sequence

Sequence ID: [gb|AC160138.2|](#) Length: 223906 Number of Matches: 3

Range 1: 118824 to 119149

Score	Expect	Identities	Gaps	Strand	Frame
66.2 bits(72)	7e-07()	241/366(66%)	71/366(19%)	Plus/Minus	
Features:					
Query 365		ACACATATACTAGTACAGCTGACGGACACATATACTAGTACAGCTGACGGGACACACATA			424
Sbjct 119149		ACATATATACTAGTACA---CACACACACATACACTAGTATA---GAC-ACACACACATA			119097
Query 425		TACTA-----AGAGAT-CACTGAGATGACACACATATACTAGTA-TCTC-TAGAGAG			473
Sbjct 119096		CACTAGTATACACACACATACACT-AGTACACACACATACACTAGTACACACATACACTA			119038
Query 474		AGATGGACACACATATACTTG----ACACACATATACTAGTA-----ACACATAT			519
Sbjct 119037		GTATACACACACATACACTAGTACACACACACATACACTAGTATAGACACACACACATAC			118978
Query 520		ACTAGTACAGCTGACGGACACATATACTAGTACAGCTGACGGGACACACATATACTAAGA			579
Sbjct 118977		ACTAGTA-----TACACACACATACACTAGTATA---GAC---ACACACATACACTAATA			118929
Query 580		GATCACTGAGATGACACACATATACTAGTATCTCTAGAGAGAGATGAAGAGATCACTGAG			639
Sbjct 118928		TA-CAC-----ACACACATACACTAGTA---TAGACACACACACATA---CACTAGT			118884
Query 640		AT-GACACACATATACTAGTA-----ACACATATACTAGTACAGCTGACGGGACACACAT			693
Sbjct 118883		ATACACACACATACACTAGTATACACACACATACACTAGTATA---CAC---ACACACAT			118830
Query 694		ATACTA 699			
Sbjct 118829		ACACTA 118824			

Range 2: 119089 to 119163

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	58/79(73%)	11/79(13%)	Plus/Minus	
Features:					
Query 480		ACACACATATACTGACACACATATACTAGTA-----ACACATATACTAGTACAGCTG			532

```

Sbjct 119163 |||||||ACACACACACAC---ACACATATACTACTAGTACACACACACACATACTAGTATAG-AC 119108
Query 533 ACGGACACATATACTACTAGTA 551
Sbjct 119107 ACACACACATACACTAGTA 119089

```

Range 3: 119049 to 119151

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	79/113(70%)	15/113(13%)	Plus/Minus	

Features:

```

Query 446 ACACACATATACTACTAGTATCTCTAGAGAGAGATGGACACACATATACTTGACACACATATA 505
Sbjct 119151 |||||||ACACATATACTACTAGTA-CAC-ACACACACATACACTAGTATAGAC-ACACACACATACA 119095
Query 506 CTAGTA----ACACATATACTACTAGTACAGCTGACGGACACATATACTAGTACA 553
Sbjct 119094 CTAGTATACACACACATACACTAGTACA-----CACACATACACTAGTACA 119049

```

Mus musculus targeted non-conditional, lacZ-tagged mutant allele Ctnbp2:tm1e(KOMP)Wtsi; transgenic

Sequence ID: [gb|JN963729.1](#) | Length: 39486 Number of Matches: 6

Range 1: 1544 to 1630

Score	Expect	Identities	Gaps	Strand	Frame
62.6 bits(68)	8e-06()	67/87(77%)	4/87(4%)	Plus/Minus	

Features:

```

Query 446 ACACACATATACTACTAGTATCTCTAGAGAGAGATGGACACACATATACTTG-ACACACATAT 504
Sbjct 1630 |||||||ACACACATATACATGTACACACATACATACATGTACACACATATACTGTACACACATAT 1571
Query 505 ACTAGTA---ACACATATACTACTAGTACA 528
Sbjct 1570 ACATGTACACACACATATACTGTACA 1544

```

Range 2: 1474 to 1580

Score	Expect	Identities	Gaps	Strand	Frame
55.4 bits(60)	0.001()	81/114(71%)	13/114(11%)	Plus/Minus	

Features:

```

Query 446 ACACACATATACTACTAGTATCTCTAGAGAGAGATGGACACACATATACTTG---ACACACAT 502
Sbjct 1580 |||||||ACACACATATACATGTACACACACATACATGTACACACATATACTGTACACACACAT 1521
Query 503 ATACTAGTA---ACACATATACTACTAGTACAGCTGACGGACACATATACTAGTACA 553
Sbjct 1520 ATACATGTACACACACATATACTGTACA-----CACACATATACTGTACA 1474

```

Range 3: 1262 to 1338

Score	Expect	Identities	Gaps	Strand	Frame
51.8 bits(56)	0.015()	62/84(74%)	13/84(15%)	Plus/Minus	

Features:

```

Query 476 ATGGACACACATATACTTG---ACACACATATACTACTAGTA---ACACATATACTAGTACAG 529
Sbjct 1338 |||||||ATGTACACACATATACTGTACACACACATATACTGTACCGCACACATATACTGT---- 1283
Query 530 CTGACGGACACATATACTACTAGTACA 553
Sbjct 1282 ---ACGCACACATATACTGTACA 1262

```

Range 4: 1393 to 1474

Score	Expect	Identities	Gaps	Strand	Frame
50.0 bits(54)	0.051()	61/82(74%)	6/82(7%)	Plus/Minus	

Features:

```

Query 446 ACACACATATACTACTAGTATCTCTAGAGAGAGATGGACACACATATACTTG---ACACACAT 502
Sbjct 1474 |||||||ACACACATATACTGTACACACACATACATGTACACACATATACTGTACACACACAT 1415
Query 503 ATACTAGTA---ACACATATAC 521
Sbjct 1414 ATACGTGTACACACACATAC 1393

```

Range 5: 1578 to 1666

Score	Expect	Identities	Gaps	Strand	Frame
50.0 bits(54)	0.051()	66/89(74%)	6/89(6%)	Plus/Minus	

Features:

Query 446	ACACACATATACTAGTATCTCTAGAGAGAGATG--GACACACATATACTTG---ACACAC	500
Sbjct 1666	ACACACATATAACAAGTACACACACATATACTGTACACACACATATACTGTACACATAC	1607
Query 501	ATATACTAGTA-ACACATATACTAGTACA	528
Sbjct 1606	ATATACATGTACACACACATATACTGTACA	1578

Range 6: 1637 to 1666

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	28/30(93%)	0/30(0%)	Plus/Minus	

Features:

Query 856	ACACACATATACTAGTAGACACACATATACT	885
Sbjct 1666	ACACACATATAACAAGTACACACACATATACT	1637

Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Ctnnb2:tm1a(KOMP)Wtsi; transgenic
Sequence ID: [gb|JN945565.1|](#) Length: 39537 Number of Matches: 6
Range 1: 1544 to 1630

Score	Expect	Identities	Gaps	Strand	Frame
62.6 bits(68)	8e-06()	67/87(77%)	4/87(4%)	Plus/Minus	

Features:

Query 446	ACACACATATACTAGTATCTCTAGAGAGAGATGGACACACATATACTTG-ACACACATAT	504
Sbjct 1630	ACACACATATACTGTACACACACATATACTGTACACACACATATACTGTACACACATAT	1571
Query 505	ACTAGTA---ACACATATACTAGTACA	528
Sbjct 1570	ACATGTACACACACATATACTGTACA	1544

Range 2: 1474 to 1580

Score	Expect	Identities	Gaps	Strand	Frame
55.4 bits(60)	0.001()	81/114(71%)	13/114(11%)	Plus/Minus	

Features:

Query 446	ACACACATATACTAGTATCTCTAGAGAGAGATGGACACACATATACTTG---ACACACAT	502
Sbjct 1580	ACACACATATACTGTACACACACATATACTGTACACACACATATACTGTACACACACAT	1521
Query 503	ATACTAGTA---ACACATATACTAGTACAGCTGACGGACACATATACTAGTACA	553
Sbjct 1520	ATACATGTACACACACATATACTGTACA-----CACACATATACTGTACA	1474

Range 3: 1262 to 1338

Score	Expect	Identities	Gaps	Strand	Frame
51.8 bits(56)	0.015()	62/84(74%)	13/84(15%)	Plus/Minus	

Features:

Query 476	ATGGACACACATATACTTG---ACACACATATACTAGTA---ACACATATACTAGTACAG	529
Sbjct 1338	ATGTACACACACATATACTGTACACACACATATACTGTACCGCACACATATACTGT---	1283
Query 530	CTGACGGACACATATACTAGTACA	553
Sbjct 1282	---ACGCACACACATATACTGTACA	1262

Range 4: 1393 to 1474

Score	Expect	Identities	Gaps	Strand	Frame
50.0 bits(54)	0.051()	61/82(74%)	6/82(7%)	Plus/Minus	

Features:

Query	446	ACACACATATACTAGTATCTCTAGAGAGAGATGGACACACATATACTTG---ACACACAT	502
Sbjct	1474	ACACACATATACTACATGTACACACACATATACTACATGTACACACACATATACTGTACACACACAT	1415
Query	503	ATACTAGTA---ACACATATAAC	521
Sbjct	1414	ATACGTGTACACACACATATAAC	1393

Range 5: 1578 to 1666

Score	Expect	Identities	Gaps	Strand	Frame
50.0 bits(54)	0.051()	66/89(74%)	6/89(6%)	Plus/Minus	

Features:

Query	446	ACACACATATACTAGTATCTCTAGAGAGAGATG--GACACACATATACTTG---ACACAC	500
Sbjct	1666	ACACACATATAACAAGTACACACACATATACTACATGTACACACACATATACTGTACACATAC	1607
Query	501	ATATACTAGTA-ACACATATACTAGTACA	528
Sbjct	1606	ATATACATGTACACACACATATACTGTACA	1578

Range 6: 1637 to 1666

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	28/30(93%)	0/30(0%)	Plus/Minus	

Features:

Query	856	ACACACATATACTAGTAGACACACATATAAC	885
Sbjct	1666	ACACACATATAACAAGTACACACACATATAAC	1637

Mus musculus strain C57BL6/J chromosome 6 clone RP23-219K14, complete sequence

Sequence ID: **gb|AC027654.3|** Length: 223678 Number of Matches: 6

Range 1: 105805 to 105891

Score	Expect	Identities	Gaps	Strand	Frame
62.6 bits(68)	8e-06()	67/87(77%)	4/87(4%)	Plus/Plus	

Features:

Query	446	ACACACATATACTAGTATCTCTAGAGAGAGATGGACACACATATACTTG-ACACACATAT	504
Sbjct	105805	ACACACATATACTACATGTACACACATATACTACATGTACACACATATACTGTGTACACACATAT	105864
Query	505	ACTAGTA---ACACATATACTAGTACA	528
Sbjct	105865	ACATGTACACACACATATACTGTACA	105891

Range 2: 105855 to 105961

Score	Expect	Identities	Gaps	Strand	Frame
55.4 bits(60)	0.001()	81/114(71%)	13/114(11%)	Plus/Plus	

Features:

Query	446	ACACACATATACTAGTATCTCTAGAGAGAGATGGACACACATATACTTG---ACACACAT	502
Sbjct	105855	ACACACATATACTACATGTACACACACATATACTACATGTACACACATATACTGTACACACAT	105914
Query	503	ATACTAGTA---ACACATATACTAGTACAGCTGACGGACACATATACTAGTACA	553
Sbjct	105915	ATACATGTACACACACATATACTGTACA-----CACACATATACTGTACA	105961

Range 3: 106097 to 106173

Score	Expect	Identities	Gaps	Strand	Frame
51.8 bits(56)	0.015()	62/84(74%)	13/84(15%)	Plus/Plus	

Features:

Query	476	ATGGACACACATATACTTG---ACACACATATACTAGTA---ACACATATACTAGTACAG	529
Sbjct	106097	ATGTACACACATATACTACATGTACACACACATATACTACATGTACGCACACATATACTGT----	106152
Query	530	CTGACGGACACATATACTAGTACA	553
Sbjct	106153	---ACGCACACATATACTGTACA	106173

Range 4: 105769 to 105857

Score	Expect	Identities	Gaps	Strand	Frame
50.0 bits(54)	0.051()	66/89(74%)	6/89(6%)	Plus/Plus	
Features:					
Query 446	ACACACATATACTAGTATCTAGAGAGAGATG--GACACACATATACTTG---ACACAC				500
Sbjct 105769	ACACACATATAACAAGTACACACACATATACTGTACACACACATATACTGTACACACATAC				105828
Query 501	ATATACTAGTA-ACACATATACTAGTACA	528			
Sbjct 105829	ATATACATGTACACACATATACTGTACA	105857			

Range 5: 105961 to 106042

Score	Expect	Identities	Gaps	Strand	Frame
50.0 bits(54)	0.051()	61/82(74%)	6/82(7%)	Plus/Plus	
Features:					
Query 446	ACACACATATACTAGTATCTAGAGAGATGGACACACATATACTTG---ACACACAT				502
Sbjct 105961	ACACACATATACTGTACACACACATATACTGTACACACACATATACTGTACACACATAC				106020
Query 503	ATACTAGTA---ACACATATAAC	521			
Sbjct 106021	ATACGTGTACACACACATATAAC	106042			

Range 6: 105769 to 105798

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	28/30(93%)	0/30(0%)	Plus/Plus	
Features:					
Query 856	ACACACATATACTAGTAGACACACATATAAC	885			
Sbjct 105769	ACACACATATAACAAGTACACACACATATAAC	105798			

Mus musculus 13 days embryo heart cDNA, RIKEN full-length enriched library, clone:D330002H21 product:unclassifiable, full insert sequence

Sequence ID: **dbj|AK084464.1|** Length: 2447 Number of Matches: 3

Range 1: 461 to 550

Score	Expect	Identities	Gaps	Strand	Frame
60.8 bits(66)	3e-05()	73/97(75%)	7/97(7%)	Plus/Minus	
Features:					
Query 478	GGCACACATATACTTGACACACATATACTAGTAACACATATACTAGTACAGCTGACGGA				537
Sbjct 550	GGCACACATATAACGACACACATATAACGATACACATATAACACATATAACGAC--A				493
Query 538	CACATATACTAGTACAGCTGACGGGACACACATATAAC	574			
Sbjct 492	CACATATAAC---ACATAT-ACACGACACACATATAAC	461			

Range 2: 446 to 551

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	79/110(72%)	5/110(4%)	Plus/Minus	
Features:					
Query 413	GGGACACACATATACTAAGAGAT-CACTGAGATGACACACATATACTAGTATCTAGAG				471
Sbjct 551	GGGACACACATATAAC-ACGACACACATATAACGATACACATATAACACATATA-CACGAC				494
Query 472	AGAGATGGACACACATATACTTGACACACATATACTAGTAACACATATAAC	521			
Sbjct 493	ACACAT--ATACACATATAACGACACACATATAACACAATACACATATAAC	446			

Range 3: 522 to 549

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	26/28(93%)	0/28(0%)	Plus/Minus	
Features:					
Query 272	GACACACATATACTTGACACACATATAAC	299			
Sbjct 549	GACACACATATAACGACACACATATAAC	522			

Homo sapiens BAC clone CH17-449C21 from chromosome 1, complete sequence

Sequence ID: **gb|AC241952.2|** Length: 210815 Number of Matches: 14

Range 1: 107536 to 107713

Score	Expect	Identities	Gaps	Strand	Frame
57.2 bits(62)	3e-04()	129/190(68%)	17/190(8%)	Plus/Plus	

Features:

Query 390	ACACATATACTAGTACAGCTGACGGGACACACATATACTAAGAGATCACTGAGATG-ACA	448
Sbjct 107536	ACACATATACTATGTACATATATATGTACACACATATACATGTACATATAT---ATGTACA	107592
Query 449	CACATATACTAGTATCTCTAGAGAGAGATGGACACACATATACTTGACACACATATACTA	508
Sbjct 107593	CACATATACTATGTACATATATA---TGTACACACATATACTATGT---ACATATATAT	107643
Query 509	GTA-ACACATATACTAGTACAGCTGACGG---ACACATATACTAGTACAGCTGACGGGAC	564
Sbjct 107644	GTACACACATATACATGTACATATGTATGTACACACATATACATGTACATATGTATGTAC	107703
Query 565	ACACATATAAC 574	
Sbjct 107704	ACACATATAAC 107713	

Range 2: 107419 to 107629

Score	Expect	Identities	Gaps	Strand	Frame
55.4 bits(60)	0.001()	151/223(68%)	20/223(8%)	Plus/Plus	

Features:

Query 360	CATGTACACATATACTAGTACAGCT-GACG---GACACATATACTAGTACAGCTGACGGGA	416
Sbjct 107419	CATGTACACATATACTATGTACATATATATGTACACACATATACATGTACATATATATGTAA	107478
Query 417	CACACATATACTAAAGAGATCACTGAGATG-ACACACATATACTAGTATCTCTAGAGAGAG	475
Sbjct 107479	CACACATATAC---ATGTACATATATATGTACACACATATAC---ATGTACATATATATGTAA	107529
Query 476	ATGGACACACATATACTTGACACACATATACTAGTA-ACACATATACTAGTACAGCT-GA	533
Sbjct 107530	ATGTACACACATATACATG---TACATATATATGTACACACATATACATGTACATATATA	107586
Query 534	CG---GACACATATACTAGTACAGCTGACGGGACACACATATAC 574	
Sbjct 107587	TGTACACACATATACATGTACATATATGTACACACATATAC 107629	

Range 3: 107676 to 107881

Score	Expect	Identities	Gaps	Strand	Frame
55.4 bits(60)	0.001()	148/218(68%)	20/218(9%)	Plus/Plus	

Features:

Query 365	ACACATATACTAGTACAGCTGACGG---ACACATATACTAGTACAGCTGACGGGACACAC	421
Sbjct 107676	ACACATATACTATGTACATATGTATGTACACACATATACATGTACATATGTATGTACACAC	107735
Query 422	ATATACTAAAGAGATCACTGAGATG-ACACACATATACTAGTATCTCTAGAGAGAGATGGA	480
Sbjct 107736	ATATACATGTACAT---ATG-TATGTACACACATATAC---ATGTACATATGTATGTAA	107786
Query 481	CACACATATACTTGACACACATATACTAGTA-ACACATATACTAGTACAGCTG-ACG--G	536
Sbjct 107787	CACACATATACTATG---TACATATGTATGTACACACATATACATGTACATATGTATGTAC	107843
Query 537	ACACATATACTAGTACAGCTGACGGGACACACATATAC 574	
Sbjct 107844	ACACATATACTATGTACATATGTATGTACACACATATAC 107881	

Range 4: 107732 to 107937

Score	Expect	Identities	Gaps	Strand	Frame
55.4 bits(60)	0.001()	148/218(68%)	20/218(9%)	Plus/Plus	

Features:

Query 365	ACACATATACTAGTACAGCTGACGG---ACACATATACTAGTACAGCTGACGGGACACAC	421
Sbjct 107732	ACACATATACTATGTACATATGTATGTACACACATATACATGTACATATGTATGTACACAC	107791
Query 422	ATATACTAAAGAGATCACTGAGATG-ACACACATATACTAGTATCTCTAGAGAGAGATGGA	480
Sbjct 107792	ATATACATGTACAT---ATG-TATGTACACACATATAC---ATGTACATATGTATGTAA	107842
Query 481	CACACATATACTTGACACACATATACTAGTA-ACACATATACTAGTACAGCTG-ACG--G	536
Sbjct 107843	CACACATATACTATG---TACATATGTATGTACACACATATACATGTACATATGTATGTAC	107899

Query	537	ACACATATACTAGTACAGCTGACGGGACACACATATAAC	574
Sbjct	107900	ACACATATACTAGTACATATGTATGTACACACATATAAC	107937

Range 5: 107788 to 107993

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

55.4 bits(60) 0.001() 148/218(68%) 20/218(9%) Plus/Plus

Features:

Query	365	ACACATATACTAGTACAGCTGACGG---ACACATATACTAGTACAGCTGACGGGACACAC	421
Sbjct	107788	ACACATATACTAGTACATATGTATGTACACACATATACTAGTACATATGTATGTACACAC	107847
Query	422	ATATACTAAGAGATCACTGAGATG-ACACACATATACTAGTATCTCTAGAGAGAGATGGA	480
Sbjct	107848	ATATACTAGTACAT---ATG-TATGTACACACATATACTAC-----ATGTACATATGTATGTAA	107898
Query	481	CACACATATACTTGACACACATATACTAGTA-ACACATATACTAGTACAGCTG-ACG--G	536
Sbjct	107899	CACACATATACTAGTACACACATATACTAGTACATGTACATATGTATGTAC	107955
Query	537	ACACATATACTAGTACAGCTGACGGGACACACATATAAC	574
Sbjct	107956	ACACATATACTAGTACATATGTATGTACACACATATAAC	107993

Range 6: 107844 to 108081

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

53.6 bits(58) 0.004() 168/250(67%) 23/250(9%) Plus/Plus

Features:

Query	365	ACACATATACTAGTACAGCTGACGG---ACACATATACTAGTACAGCTGACGGGACACAC	421
Sbjct	107844	ACACATATACTAGTACATATGTATGTACACACATATACTAGTACATATGTATGTACACAC	107903
Query	422	ATATACTAAGAGATCACTGAGATG-ACACACATATACTAGTATCTCTAGAGAGAGATGGA	480
Sbjct	107904	ATATACTAGTACAT---ATG-TATGTACACACATATACTAC-----ATGTACATATGTATGTAA	107954
Query	481	CACACATATACTTGACACACATATACTAGTA-ACACATATACTAGTACAGCTG-ACG--G	536
Sbjct	107955	CACACATATACTAGTACACACATATACTAGTACACACATATACTAGTACATATGTATGTAC	108011
Query	537	ACACATATACTAGTACAGCTGACGGGACACACATATAAC---TAAGAGATCACTGAGATG-A	593
Sbjct	108012	ACACATATACTAGTACATATATGTACACACATATACTAGTACATATATGTACATGTAA	108071
Query	594	CACACATATA 603	
Sbjct	108072	CACACATATA 108081	

Range 7: 107508 to 107685

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

51.8 bits(56) 0.015() 128/190(67%) 17/190(8%) Plus/Plus

Features:

Query	390	ACACATATACTAGTACAGCTGACGGGACACACATATACTAAGAGATCACTGAGATG-ACA	448
Sbjct	107508	ACACATATACTAGTACATATATATGTACACACATATACTAGTACATATAT---ATGTACA	107564
Query	449	CACATATACTAGTATCTCTAGAGAGAGATGGACACACATATACTTGACACACATATACTA	508
Sbjct	107565	CACATATACTAGTACATATATA-----TGTACACACATATACTAGT---ACATATATAT	107615
Query	509	GTA-ACACATATACTAGTACAGCTGACGG---ACACATATACTAGTACAGCTGACGGGAC	564
Sbjct	107616	GTACACACATATACTAGTACATATATGTACACACATATACTAGTACATATGTATGTAC	107675
Query	565	ACACATATAAC 574	
Sbjct	107676	ACACATATAAC 107685	

Range 8: 107564 to 107741

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

51.8 bits(56) 0.015() 128/190(67%) 17/190(8%) Plus/Plus

Features:

Query	390	ACACATATACTAGTACAGCTGACGGGACACACATATACTAAGAGATCACTGAGATG-ACA	448
Sbjct	107564	ACACATATACTAGTACATATATATGTACACACATATACTAGTACATATAT---ATGTACA	107620
Query	449	CACATATACTAGTATCTCTAGAGAGAGATGGACACACATATACTTGACACACATATACTA	508
Sbjct	107621	CACATATACTAGTACATATATA-----TGTACACACATATACTAGT---ACATATGTAT	107671

Query	509	GTA-ACACATATACTAGTACAGCTGACGG--ACACATATACTAGTACAGCTGACGGGAC	564
Sbjct	107672	GTACACACATATACTAGTACATATGTATGTACACACATATACTAGTACATATGTATGTAC	107731
Query	565	ACACATATAAC 574	
Sbjct	107732	ACACATATAAC 107741	

Range 9: 107648 to 107825

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

51.8 bits(56) 0.015() 130/190(68%) 17/190(8%) Plus/Plus

Features:

Query	390	ACACATATACTAGTACAGCTGACGGGACACACATATACTAAGAGATCACTGAGATG-ACA	448
Sbjct	107648	ACACATATACTAGTACATATGTATGTACACACATATACTAGTACAT-ATG-TATGTACA	107704
Query	449	CACATATACTAGTATCTCTAGAGAGAGATGGACACACATATACTTGACACACATATACTA	508
Sbjct	107705	CACATATAC-----ATGTACATATGTATGTACACACATATACTAG---TACATATGTAT	107755
Query	509	GTA-ACACATATACTAGTACAGCTG-ACG--GACACATATACTAGTACAGCTGACGGGAC	564
Sbjct	107756	GTACACACATATACTAGTACATATGTATGTACACACATATACTAGTACATATGTATGTAC	107815
Query	565	ACACATATAAC 574	
Sbjct	107816	ACACATATAAC 107825	

Range 10: 107620 to 107797

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

48.2 bits(52) 0.18() 129/190(68%) 17/190(8%) Plus/Plus

Features:

Query	390	ACACATATACTAGTACAGCTGACGGGACACACATATACTAAGAGATCACTGAGATG-ACA	448
Sbjct	107620	ACACATATACTAGTACATATATATGTACACACATATACTAGTACAT-ATG-TATGTACA	107676
Query	449	CACATATACTAGTATCTCTAGAGAGAGATGGACACACATATACTTGACACACATATACTA	508
Sbjct	107677	CACATATAC-----ATGTACATATGTATGTACACACATATACTAG---TACATATGTAT	107727
Query	509	GTA-ACACATATACTAGTACAGCTG-ACG--GACACATATACTAGTACAGCTGACGGGAC	564
Sbjct	107728	GTACACACATATACTAGTACATATGTATGTACACACATATACTAGTACATATGTATGTAC	107787
Query	565	ACACATATAAC 574	
Sbjct	107788	ACACATATAAC 107797	

Range 11: 107956 to 108111

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

48.2 bits(52) 0.18() 111/161(69%) 10/161(6%) Plus/Plus

Features:

Query	365	ACACATATACTAGTACAGCTGACGG--ACACATATACTAGTACAGCTGACGGGACACAC	421
Sbjct	107956	ACACATATACTAGTACATATGTATGTACACACATATACTAGTACATATGTATGTACACAC	108015
Query	422	ATATACTAAGAGATCACTGAGATG-ACACACATATACTAGTATCTCTAGAGAGAGATGGA	480
Sbjct	108016	ATATAC---ATGTACATATATATGTACACACATATACTAGTACATATATA-TGACATGTA	108071
Query	481	CACACATATA-CTTGACACACATATACTAGTAACACATATA 520	
Sbjct	108072	CACACATATATACACATATA-TATAAAATATATATA 108111	

Range 12: 107406 to 107601

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

46.4 bits(50) 0.62() 144/219(66%) 28/219(12%) Plus/Plus

Features:

Query	361	ATGTACACATATACTAGTACAGCTGACGGACACATATACTAGTACAGCTGACGGGACACA	420
Sbjct	107406	ATGTACACATATACTAGTACATATGTATGTACACACATATACTAGTACATATGTACACA	107454
Query	421	CATATACTAAGAGATCACTGAGATG-ACACACATATACTAGTATCTCTAGAGAGAGATGG	479
Sbjct	107455	CATATAC---ATGTACATATATATGTACACACATATACTAGTACATATATA-TGACATGTA	107505
Query	480	ACACACATATACTTGACACACATATACTAGTA-ACACATATACTAGTACAGCT-GACG--	535
Sbjct	107506	ACACACATATACTAG---TACATATATATGTACACACATATACTAGTACATATATA-TGTA	107562

Query 536 GACACATATACTAGTACAGCTGACGGGACACACATATAC 574
 Sbjct 107563 CACACATATACTAGTACATATATGTACACACATATAC 107601

Range 13: 107900 to 108056

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	115/169(68%)	17/169(10%)	Plus/Plus	

Features:

Query 365 ACACATATACTAGTACAGCTGACGG---ACACATATACTAGTACAGCTGACGGGACACAC 421
 Sbjct 107900 ACACATATACTAGTACATATGTATGTACACACATATACATGTACATATGTATGTACACAC 107959
 Query 422 ATATACTAAGAGATCACTGAGATG-ACACACATATACTAGTATCTCTAGAGAGATGGA 480
 Sbjct 107960 ATATACATGTACAT---ATG-TATGTACACACATATAC-----ATGTACATATGTATGTA 108010
 Query 481 CACACATATACTTGACACACATATACTAGTA-ACACATATACTAGTACA 528
 Sbjct 108011 CACACATATACTG---TACATATATATGTACACACATATACATGTACA 108056

Range 14: 107446 to 107545

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	73/103(71%)	7/103(6%)	Plus/Plus	

Features:

Query 476 ATGGACACACATATACTTGACACACATATACTAGTA-ACACATATACTAGTACAGCTGAC 534
 Sbjct 107446 ATGTACACACATATACTAGT---ACATATATATGTACACACATATACATGTACATATATA 107502
 Query 535 GG---ACACATATACTAGTACAGCTGACGGGACACACATATAC 574
 Sbjct 107503 TGTACACACATATACTAGTACATATATATGTACACACATATAC 107545

Mus musculus chromosome 12, clone RP23-456E21, complete sequence

Sequence ID: **gb|AC102626.9|** Length: 222905 Number of Matches: 2

Range 1: 152038 to 152123

Score	Expect	Identities	Gaps	Strand	Frame
55.4 bits(60)	0.001()	73/97(75%)	11/97(11%)	Plus/Plus	

Features:

Query 480 ACACACATATACTTGACACACATATACTAGTAACACATATACTAGTACAGCTGACGGACA 539
 Sbjct 152038 ACACACAGACAC---ACACACACATACAT---ACACACATACTAGTACAAATG-CGCACA 152090
 Query 540 CATATACTAGTACAGCTGACGGGACACACATATACTA 576
 Sbjct 152091 CACATACTAGTACAAATG-CG---CACACACATACTA 152123

Range 2: 152063 to 152123

Score	Expect	Identities	Gaps	Strand	Frame
51.8 bits(56)	0.015()	53/66(80%)	5/66(7%)	Plus/Plus	

Features:

Query 364 TACACATATACTAGTACAGCTGACGGACACATATACTAGTACAGCTGACGGGACACACAT 423
 Sbjct 152063 TACACACATACTAGTACAAATG-CGCACACACATACATAGTACAAATG-CG---CACACAC 152117
 Query 424 ATACTA 429
 Sbjct 152118 ATACTA 152123

Rattus norvegicus CH230-6E20 (Children's Hospital Oakland Research Institute Rat (BN/SsNHsd/MCW) BAC library) complete sequence

Sequence ID: **gb|AC131965.5|** Length: 237757 Number of Matches: 2

Range 1: 49692 to 49797

Score	Expect	Identities	Gaps	Strand	Frame
51.8 bits(56)	0.015()	80/108(74%)	5/108(4%)	Plus/Minus	

Features:

Query 828 AGAGAGAGATGAAGAGATCACTGAGATGACACACATATACTAGTAGACACACATATACTA 887
 Sbjct 49797 AGAGAGAGAGGAGATA-CACAGAGAT-ACACACATATACAAACAGAGACAGACACTC 49740

Query 888 AGAGA-TCACTGAGA-TGACACACATATAAC-TAGTATCTCTAGAGAGA 932
 Sbjct 49739 AGAGACGAACAGAGACACAAACATATAACAAAGTATAACAAAGAGAGA 49692

Range 2: 46038 to 46109

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	57/76(75%)	4/76(5%)	Plus/Minus	

Features:

Query 446 ACACACATATACTAGTATCTCTAGAGAGAGATGGACACACATATACTTGACACACATATA 505
 Sbjct 46109 ACACACATATACATATATAACATACACATACATACATACACATATA-TACACACACATATA 46051
 Query 506 CTAGTAACACATATAAC 521
 Sbjct 46050 -TA--CACACATATAAC 46038

Rattus norvegicus CH230-333G12 (Children's Hospital Oakland Research Institute Rat (BN/SsNHsd/MCW) BAC library) complete sequence

Sequence ID: **gb|AC128103.4|** Length: 204491 Number of Matches: 2

Range 1: 89622 to 89727

Score	Expect	Identities	Gaps	Strand	Frame
51.8 bits(56)	0.015()	80/108(74%)	5/108(4%)	Plus/Minus	

Features:

Query 828 AGAGAGAGATGAAGAGATCACTGAGATGACACACATATACTAGTAGACACACATATACTA 887
 Sbjct 89727 AGAGAGAGAGGCAGATA-CACAGAGAT-ACACACATATAACAAACAGAGACAGACACTC 89670
 Query 888 AGAGA-TCACTGAGA-TGACACACATATAAC-TAGTATCTCTAGAGAGA 932
 Sbjct 89669 AGAGACGAACAGAGACACAAACATATAACAAAGTATAACAAAGAGAGA 89622

Range 2: 85968 to 86039

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	57/76(75%)	4/76(5%)	Plus/Minus	

Features:

Query 446 ACACACATATACTAGTATCTCTAGAGAGAGATGGACACACATATACTTGACACACATATA 505
 Sbjct 86039 ACACACATATACATATATAACATACACATACATACACATATA-TACACACACATATA 85981
 Query 506 CTAGTAACACATATAAC 521
 Sbjct 85980 -TA--CACACATATAAC 85968

Mus musculus 10 BAC RP24-324P5 (Roswell Park Cancer Institute (C57BL/6J Male) Mouse BAC Library) complete sequence

Sequence ID: **gb|AC164624.3|** Length: 199853 Number of Matches: 1

Range 1: 3471 to 3534

Score	Expect	Identities	Gaps	Strand	Frame
51.8 bits(56)	0.015()	55/68(81%)	5/68(7%)	Plus/Plus	

Features:

Query 480 ACACACATATACTTGACACACATATACTAGTA-ACACATATACTAGTACAGCTGACGGAC 538
 Sbjct 3471 ACACACATACA-TTGACACACATATACTGTACACATATA--AGCACAGGTG-CACAC 3526
 Query 539 ACATATAAC 546
 Sbjct 3527 ACATAGAC 3534

Mus musculus 10 BAC RP23-475H6 (Roswell Park Cancer Institute (C57BL/6J Female) Mouse BAC Library) complete sequence

Sequence ID: **gb|AC158642.8|** Length: 183526 Number of Matches: 1

Range 1: 124642 to 124705

Score	Expect	Identities	Gaps	Strand	Frame
51.8 bits(56)	0.015()	55/68(81%)	5/68(7%)	Plus/Minus	

Features:

Query 480 ACACACATATACTTGACACACATATACTAGTA-ACACATATACTAGTACAGCTGACGGAC 538

Sbjct	124705	ACACACATACA-TTGACACACATATACTGTACACATATA--AGCACAGGTG-CACAC	124650
Query	539	ACATATAC 546	
Sbjct	124649	ACATAGAC 124642	

Mus musculus BAC clone RP24-444D19 from 10, complete sequence

Sequence ID: **gb|AC131789.4|** Length: 178210 Number of Matches: 1
Range 1: 150000 to 150063

Score	Expect	Identities	Gaps	Strand	Frame
51.8 bits(56)	0.015()	55/68(81%)	5/68(7%)	Plus/Plus	

Features:

Query	480	ACACACATATACTTGACACACATATACTGTACAGCTGACGGAC	538
Sbjct	150000	ACACACATACA-TTGACACACATATACTGTACACATATA--AGCACAGGTG-CACAC	150055
Query	539	ACATATAC 546	
Sbjct	150056	ACATAGAC 150063	

Homo sapiens chromosome 1 clone WI2-2264I19, complete sequence

Sequence ID: **gb|AC196529.1|** Length: 43786 Number of Matches: 4
Range 1: 41339 to 41500

Score	Expect	Identities	Gaps	Strand	Frame
50.0 bits(54)	0.051()	119/174(68%)	17/174(9%)	Plus/Minus	

Features:

Query	360	CATGTACACATATACTAGTACAGCT-GACG--GACACATATACTAGTACAGCTGACGGGA	416
Sbjct	41500	CATGTACACATATACTATGTACATATACTGTACACACATATACTGTACATATACTGTAA	41441
Query	417	CACACATATACTAAGAGATCACTGAGATG-ACACACATATACTAGTACAGCTAGAGAGAG	475
Sbjct	41440	CACACATATAAC---ATGTACATATAATGTACACACATATAAC-----ATGTACATATA	41390
Query	476	ATGGACACACATATACTTGACACACATATACTAGTA-ACACATATACTAGTACA 528	
Sbjct	41389	ATGTACACACATATACTATG---TACATATATATGTACACACATATACTGTACA 41339	

Range 2: 41374 to 41473

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	75/103(73%)	7/103(6%)	Plus/Minus	

Features:

Query	476	ATGGACACACATATACTTGACACACATATACTAGTA-ACACATATACTAGTACAGCT-GA	533
Sbjct	41473	ATGTACACACATATACTATG---TACATATATGTACACACATATACTGTACATATA	41417
Query	534	CG--GACACATATACTAGTACAGCTGACGGGACACACATATAAC 574	
Sbjct	41416	TGTACACACATATACTGTACATATACTGTACACACATATAAC 41374	

Range 3: 41314 to 41469

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	112/165(68%)	16/165(9%)	Plus/Minus	

Features:

Query	446	ACACACATATACTAGTATCTCTAGAGAGAGATGGACACACATATACTTGACACACATATA	505
Sbjct	41469	ACACACATATACTATGTACATATAACACACATATACTGTACACACATATAACATATA	41419
Query	506	CTAGTA-ACACATATACTAGTACAGCTGACGG--ACACATATACTAGTACAGCTGACGG	561
Sbjct	41418	TATGTACACACATATACTGTACATATACTGTACACACATATACTGTACATATAATG	41359
Query	562	GACACACATATAAC--TAAGAGATCACTGAGATG-ACACACATATA 603	
Sbjct	41358	TACACACATATACTGTACATATACTGTACACACATATAAC 41314	

Range 4: 41402 to 41481

Score	Expect	Identities	Gaps	Strand	Frame

42.8 bits(46) 7.6() 65/92(71%) 13/92(14%) Plus/Minus

Features:

Query 484	ACATATACTTG-ACACACATATACTAGTAACACATATACTAGTACAGCTGACGGACACAT	542
Sbjct 41481	ACATATACATGTACACACATATACTATGTA---CATATACATGTACA-----CACAT	41434
Query 543	ATACTAGTACAGCTGACGGGACACACATATACT	574
Sbjct 41433	ATACATGTACATATATATGTACACACATATACT	41402

Mus musculus BAC clone RP23-286N12 from chromosome 16, complete sequence

Sequence ID: **gb|AC164302.2|** Length: 192765 Number of Matches: 1

Range 1: 67890 to 68009

Score	Expect	Identities	Gaps	Strand	Frame
50.0 bits(54)	0.051()	96/132(73%)	15/132(11%)	Plus/Minus	

Features:

Query 415	GACACACATATACTAAGAGAT-CACTGAGATG-ACACACATATACTAGTATCTCTAGAGA	472
Sbjct 68009	GACACACATATACTTACAGATACATACACATGCACACACAGACACACATA-CTCT-TACA	67952
Query 473	GAGATGGACACACATATACTTGACACACATATACT-TAGTAACACATATACTAGTACAGCT	531
Sbjct 67951	GACAT--ACACATATATAC---ACAGACATATACATAGGCACACGTATACT--TACA---	67902
Query 532	GACGGACACATA 543	
Sbjct 67901	GACACACACATA 67890	

Mus musculus BAC clone RP23-270P19 from chromosome 3, complete sequence

Sequence ID: **gb|AC123876.5|** Length: 203639 Number of Matches: 1

Range 1: 156224 to 156283

Score	Expect	Identities	Gaps	Strand	Frame
50.0 bits(54)	0.051()	49/61(80%)	2/61(3%)	Plus/Minus	

Features:

Query 856	ACACACATATACTAGTAGACACACATATACTAAGAGATCACTGAGATG-ACACACATATA	914
Sbjct 156283	ACACACATATACACATACACACATATACACAG-GAACACACACATGCACACACATATA	156225
Query 915	C 915	
Sbjct 156224	C 156224	

Human DNA sequence from clone RP11-541I19 on chromosome 10 Contains the 3' end of the gene for a novel protein similar to mannose receptor C type 1 (MRC1), complete sequence

Sequence ID: **emb|BX255924.4|** Length: 33404 Number of Matches: 2

Range 1: 15161 to 15208

Score	Expect	Identities	Gaps	Strand	Frame
50.0 bits(54)	0.051()	41/49(84%)	1/49(2%)	Plus/Minus	

Features:

Query 480	ACACACATATACTTGACACACATATACTAGTAACACATATACTAGTACA	528
Sbjct 15208	ACACATATATACTGTACACACATATACTACACATATATACT-GTACA	15161

Range 2: 15146 to 15196

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	45/54(83%)	5/54(9%)	Plus/Minus	

Features:

Query 477	TGGACACACATATACTTGACACACATATACTAGTAACACAT--ATACTAGTACA	528
Sbjct 15196	TGTACACACATATACTACACATATATACT-GT-ACACATCCATACT-GTACA	15146

Homo sapiens chromosome 10 clone RP11-457D2, complete sequence

Sequence ID: **gb|AC069023.5|** Length: 131345 Number of Matches: 2

Range 1: 49539 to 49586

Score	Expect	Identities	Gaps	Strand	Frame
50.0 bits(54)	0.051()	41/49(84%)	1/49(2%)	Plus/Plus	

Features:

Query 480	ACACACATATACTTACACACATATACTAGTAACACATATACTAGTACA	528
Sbjct 49539	ACACATATATACTGTACACACATATACTACACATATACT-GTACA	49586

Range 2: 49551 to 49601

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	45/54(83%)	5/54(9%)	Plus/Plus	

Features:

Query 477	TGGACACACATATACTTACACACATATACTAGTAACACAT--ATACTAGTACA	528
Sbjct 49551	TGTACACACATATACTACACATATACT-GT-ACACATCCATACT-GTACA	49601

PREDICTED: Callithrix jacchus uncharacterized LOC100894812 (LOC100894812), mRNA

Sequence ID: **ref|XM_003735540.1|** Length: 1845 Number of Matches: 1

Range 1: 636 to 735

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

Features:

Query 416	ACACACATATACTAAGAGAT-CACTGAGATGACACACATATACTAGTATCTCTAGAGAGA	474
Sbjct 735	ACACACATATACATATATACACATATAT-ACACACATATACATATATACACACATA	677
Query 475	GATGGACACACATATACTTACACACATATACTAGTAACACATATAC	521
Sbjct 676	TATACACACACATATA-TATACACATATATAC---ACACATATAC	636

Mus musculus targeted deletion, lacZ-tagged mutant allele Bri3:tm1(KOMP)Ucd; transgenic

Sequence ID: **gb|JN958386.1|** Length: 37222 Number of Matches: 1

Range 1: 3011 to 3049

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	34/39(87%)	0/39(0%)	Plus/Minus	

Features:

Query 483	CACATATACTTACACACATATACTAGTAACACATATAC	521
Sbjct 3049	CACATATACTACACACATATACTCACAAACACATATAC	3011

Mus musculus chromosome 5, clone RP24-182D2, complete sequence

Sequence ID: **gb|AC139636.12|** Length: 172097 Number of Matches: 1

Range 1: 122007 to 122045

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	34/39(87%)	0/39(0%)	Plus/Plus	

Features:

Query 483	CACATATACTTACACACATATACTAGTAACACATATAC	521
Sbjct 122007	CACATATACTACACACATATACTCACAAACACATATAC	122045

Human DNA sequence from clone RP11-57G10 on chromosome 10, complete sequence

Sequence ID: **emb|AL133551.13|** Length: 175940 Number of Matches: 1

Range 1: 76121 to 76184

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	54/67(81%)	4/67(5%)	Plus/Minus	

Features:

Query 441	AGATGACACACATATA-CTAGTATCTCTAGAGAGAGATGGACACACATATACTTGACACA	499
Sbjct 76184	AGAT-ACACACATATCTA-TATATAGAGAGATACACACACATATA-TATACACA	76128

Query 500 CATATAC 506
Sbjct 76127 ||||| CACATAC 76121

Mus musculus 10 BAC RP24-339G14 (Roswell Park Cancer Institute (C57BL/6J Male) Mouse BAC Library) complete sequence
Sequence ID: **gb|AC157089.5|** Length: 160723 Number of Matches: 1
Range 1: 43062 to 43116

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	47/59(80%)	4/59(6%)	Plus/Plus	

Features:

Query 857 CACACATATACTAGTAGACACACATATACTAAGAGATCACTGAGATGACACACATATA 915
Sbjct 43062 CAGACATACACAAGTACACACACATATACACAGA---CACAGAGAT-ACACACACATAC 43116

Mus musculus MHC class I related protein 1 isoform B (MR1B) pseudogene mRNA, complete sequence
Sequence ID: **gb|AF010449.1|AF010449** Length: 2122 Number of Matches: 1
Range 1: 2001 to 2066

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	55/69(80%)	5/69(7%)	Plus/Plus	

Features:

Query 480 ACACACATATACTTGACACACATATACTAGTA-ACACATATACTAGTACAGCTG-ACGGA 537
Sbjct 2001 ACACACATACA-TTGACACACATATACTACATGTACACATATA--AGCACAGGTGCACACA 2057
Query 538 CACATATAAC 546
Sbjct 2058 CTCACACATAC 2066

Mus musculus BAC clone RP24-82B23 from 5, complete sequence
Sequence ID: **gb|AC121845.3|** Length: 217530 Number of Matches: 1
Range 1: 16232 to 16270

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	34/39(87%)	0/39(0%)	Plus/Plus	

Features:

Query 483 CACATATACTTGACACACATATACTAGTAACACATATAAC 521
Sbjct 16232 CACATATACTACACACACATATACTCACAAACACATATAAC 16270

Human DNA sequence from clone RP11-759G12 on chromosome 22, complete sequence
Sequence ID: **emb|FO681547.3|** Length: 177121 Number of Matches: 3
Range 1: 27901 to 27966

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	55/74(74%)	8/74(10%)	Plus/Plus	

Features:

Query 842 AGATCACTGAGATGACACACATATACTAGTAGACACACATATACTAAGAGATCACTGAGA 901
Sbjct 27901 AGTTCACTCACATCACACACATATAAC-----ACCCACATACAC--ACAGTTCACTCACA 27952
Query 902 TGACACACATATAAC 915
Sbjct 27953 TCACACACACATATAAC 27966

Range 2: 59668 to 59733

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	55/74(74%)	8/74(10%)	Plus/Minus	

Features:

Query 842 AGATCACTGAGATGACACACATATACTAGTAGACACACATATACTAAGAGATCACTGAGA 901
Sbjct 59733 AGTTCACTCACATCACACACATATAAC-----ACCCACATACAC--ACAGTTCACTCACA 59682
Query 902 TGACACACATATAAC 915

Sbjct 59681 |TCACACACATATACT 59668

Range 3: 59708 to 59773

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	55/74(74%)	8/74(10%)	Plus/Minus	

Features:

Query 842 AGATCACTGAGATGACACACATATACTAGTAGACACACATATACTAAGAGATCACTGAGA 901
Sbjct 59773 AGTTCACTCACATCACACACATATACTAC----ACCCACATACAC--ACAGTTCACTCACA 59722
Query 902 TGACACACATATACT 915
Sbjct 59721 TCACACACATATACT 59708

Mus musculus targeted non-conditional, lacZ-tagged mutant allele Dhx8:tm1e(EUCOMM)Wtsi; transgenic

Sequence ID: **gb|JN961110.1|** Length: 36509 Number of Matches: 2

Range 1: 28448 to 28513

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	55/70(79%)	5/70(7%)	Plus/Plus	

Features:

Query 480 ACACACATATACTTGANACACACATATACTA-GTAACACATATACTAGTAGCTGACGGAC 538
Sbjct 28448 ACACACATATACT--ATACACATATACTACACACCACATATACTA-CACATAT-ACACAC 28503
Query 539 ACATATACTA 548
Sbjct 28504 ACATACACTA 28513

Range 2: 28399 to 28490

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	72/95(76%)	7/95(7%)	Plus/Plus	

Features:

Query 486 ATATACTTG-ACACACATATACTAGTAACA-CATATACTAGTAGCTGACGGACACATA 543
Sbjct 28399 ATACACATGTACACACATATACTACACACACACATA-TAGTACA-CATACACACACATA 28456
Query 544 TACTAGTACAGCT-GACGGGACA-CACATATACTA 576
Sbjct 28457 TACTA-TACACATATACTACACACCACATATACTA 28490

Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Fabp5:tm1a(EUCOMM)Wtsi; transgenic

Sequence ID: **gb|JN960738.1|** Length: 38472 Number of Matches: 1

Range 1: 29497 to 29546

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	44/55(80%)	5/55(9%)	Plus/Plus	

Features:

Query 856 ACACACATATACTAGTAGACACACATATACTAAGAGATCACTGAGATGACACACA 910
Sbjct 29497 ACACACATATACTA--TAGACACACATATACAAAGA---CACACACATCACACACA 29546

Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Dhx8:tm1a(EUCOMM)Wtsi; transgenic

Sequence ID: **gb|JN949282.1|** Length: 36487 Number of Matches: 2

Range 1: 28426 to 28491

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	55/70(79%)	5/70(7%)	Plus/Plus	

Features:

Query 480 ACACACATATACTTGANACACACATATACTA-GTAACACATATACTAGTAGCTGACGGAC 538
Sbjct 28426 ACACACATATACT--ATACACATATACTACACACCACATATACTA-CACATAT-ACACAC 28481
Query 539 ACATATACTA 548
Sbjct 28482 ACATACACTA 28491

Range 2: 28377 to 28468

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	72/95(76%)	7/95(7%)	Plus/Plus	
Features:					
Query 486	ATATACTTG-ACACACATATACTAGTAACA-CATATACTAGTACAGCTGACGGACACATA				543
Sbjct 28377	ATACACATGTACACACATATACTACACACACCACATA-TAGTACA-CATACACACACATA				28434
Query 544	TACTAGTACAGCT-GACGGGACA-CACATATACTA				576
Sbjct 28435	TACTA-TACACATATACTACACACACCACATATACTA				28468

Homo sapiens FOSMID clone COR2A-DD0002RCQNU_A23 from chromosome 22, complete sequence

Sequence ID: **gb|AC240169.3|** Length: 37888 Number of Matches: 2

Range 1: 16461 to 16526

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	55/74(74%)	8/74(10%)	Plus/Minus	
Features:					
Query 842	AGATCACTGAGATGACACACATATACTAGTAGACACACATATACTAAGAGATCACTGAGA				901
Sbjct 16526	AGTTCACTCACATCACACACATATAC-----ACCCACATACAC--ACAGTTCACTCACA				16475
Query 902	TGACACACATATAC	915			
Sbjct 16474	TCACACACATATAC	16461			

Range 2: 16501 to 16566

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	55/74(74%)	8/74(10%)	Plus/Minus	
Features:					
Query 842	AGATCACTGAGATGACACACATATACTAGTAGACACACATATACTAAGAGATCACTGAGA				901
Sbjct 16566	AGTTCACTCACATCACACACATATAC-----ACCCACATACAC--ACAGTTCACTCACA				16515
Query 902	TGACACACATATAC	915			
Sbjct 16514	TCACACACATATAC	16501			

Homo sapiens FOSMID clone ABC16-2235N21 from chromosome 22, complete sequence

Sequence ID: **gb|AC238718.3|** Length: 39288 Number of Matches: 2

Range 1: 11844 to 11909

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	55/74(74%)	8/74(10%)	Plus/Minus	
Features:					
Query 842	AGATCACTGAGATGACACACATATACTAGTAGACACACATATACTAAGAGATCACTGAGA				901
Sbjct 11909	AGTTCACTCACACACACATATAC-----ACCCACATACAC--ACAGTTCACTCACA				11858
Query 902	TGACACACATATAC	915			
Sbjct 11857	TCACACACATATAC	11844			

Range 2: 11884 to 11949

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	54/74(73%)	8/74(10%)	Plus/Minus	
Features:					
Query 842	AGATCACTGAGATGACACACATATACTAGTAGACACACATATACTAAGAGATCACTGAGA				901
Sbjct 11949	AGTTCACTCACACACACATATAC-----ACCCACATACAC--ACAGTTCACTCACA				11898
Query 902	TGACACACATATAC	915			
Sbjct 11897	TCACACACATATAC	11884			

Homo sapiens FOSMID clone ABC24-1739C22 from chromosome 22, complete sequence

Sequence ID: **gb|AC237679.2|** Length: 40435 Number of Matches: 2

Range 1: 12076 to 12141

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	55/74(74%)	8/74(10%)	Plus/Minus	
Features:					
Query 842	AGATCACTGAGATGACACACATATACTAGTAGACACACATATACTAAGAGATCACTGAGA				901
Sbjct 12141	AGTTCACTCACATCACACACATATAC-----ACCCACATACAC--ACAGTTCACTCACA				12090
Query 902	TGACACACATATAC 915				
Sbjct 12089	TCACACACATATAC 12076				

Range 2: 12116 to 12181

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	55/74(74%)	8/74(10%)	Plus/Minus	
Features:					
Query 842	AGATCACTGAGATGACACACATATACTAGTAGACACACATATACTAAGAGATCACTGAGA				901
Sbjct 12181	AGTTCACTCACATCACACACATATAC-----ACCCACATACAC--ACAGTTCACTCACA				12130
Query 902	TGACACACATATAC 915				
Sbjct 12129	TCACACACATATAC 12116				

Homo sapiens FOSMID clone ABC8-648022D8 from chromosome unknown, complete sequence

Sequence ID: **gb|AC235038.3|** Length: 34078 Number of Matches: 1

Range 1: 7168 to 7233

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	55/74(74%)	8/74(10%)	Plus/Plus	
Features:					
Query 842	AGATCACTGAGATGACACACATATACTAGTAGACACACATATACTAAGAGATCACTGAGA				901
Sbjct 7168	AGTTCACTCACATCACACACATATAC-----ACCCACATACAC--ACAGTTCACTCACA				7219
Query 902	TGACACACATATAC 915				
Sbjct 7220	TCACACACATATAC 7233				

Homo sapiens FOSMID clone ABC14-1050114M3 from chromosome unknown, complete sequence

Sequence ID: **gb|AC236044.3|** Length: 40948 Number of Matches: 1

Range 1: 13734 to 13799

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	55/74(74%)	8/74(10%)	Plus/Plus	
Features:					
Query 842	AGATCACTGAGATGACACACATATACTAGTAGACACACATATACTAAGAGATCACTGAGA				901
Sbjct 13734	AGTTCACTCACATCACACACATATAC-----ACCCACATACAC--ACAGTTCACTCACA				13785
Query 902	TGACACACATATAC 915				
Sbjct 13786	TCACACACATATAC 13799				

Homo sapiens FOSMID clone ABC11-47241400B7 from chromosome unknown, complete sequence

Sequence ID: **gb|AC234926.3|** Length: 41952 Number of Matches: 2

Range 1: 24412 to 24477

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	55/74(74%)	8/74(10%)	Plus/Plus	
Features:					
Query 842	AGATCACTGAGATGACACACATATACTAGTAGACACACATATACTAAGAGATCACTGAGA				901
Sbjct 24412	AGTTCACTCACATCACACACATATAC-----ACCCACATACAC--ACAGTTCACTCACA				24463
Query 902	TGACACACATATAC 915				

Sbjct 24464 TCACACACATATAAC 24477

Range 2: 24372 to 24437

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	54/74(73%)	8/74(10%)	Plus/Plus	
Features:					
Query 842	AGATCACTGAGATGACACACATATACTAGTAGACACACATATACTAAGAGATCACTGAGA	901			
Sbjct 24372	AGTTCACTCACACCACACATATAAC-----ACCCACATACAC--ACAGTTCACTCACA	24423			
Query 902	TGACACACATATAAC 915				
Sbjct 24424	TCACACACATATAAC 24437				

Homo sapiens FOSMID clone ABC10-44686500B23 from chromosome unknown, complete sequence

Sequence ID: **gb|AC235016.2|** Length: 40743 Number of Matches: 2

Range 1: 11185 to 11250

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	55/74(74%)	8/74(10%)	Plus/Plus	
Features:					
Query 842	AGATCACTGAGATGACACACATATACTAGTAGACACACATATACTAAGAGATCACTGAGA	901			
Sbjct 11185	AGTTCACTCACATCACACACATATAAC-----ACCCACATACAC--ACAGTTCACTCACA	11236			
Query 902	TGACACACATATAAC 915				
Sbjct 11237	TCACACACATATAAC 11250				

Range 2: 11225 to 11290

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	55/74(74%)	8/74(10%)	Plus/Plus	
Features:					
Query 842	AGATCACTGAGATGACACACATATACTAGTAGACACACATATACTAAGAGATCACTGAGA	901			
Sbjct 11225	AGTTCACTCACATCACACACATATAAC-----ACCCACATACAC--ACAGTTCACTCACA	11276			
Query 902	TGACACACATATAAC 915				
Sbjct 11277	TCACACACATATAAC 11290				

Homo sapiens FOSMID clone ABC11-47139300P5 from chromosome unknown, complete sequence

Sequence ID: **gb|AC234920.3|** Length: 39347 Number of Matches: 1

Range 1: 20279 to 20344

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	55/74(74%)	8/74(10%)	Plus/Minus	
Features:					
Query 842	AGATCACTGAGATGACACACATATACTAGTAGACACACATATACTAAGAGATCACTGAGA	901			
Sbjct 20344	AGTTCACTCACATCACACACATATAAC-----ACCCACATACAC--ACAGTTCACTCACA	20293			
Query 902	TGACACACATATAAC 915				
Sbjct 20292	TCACACACATATAAC 20279				

Homo sapiens FOSMID clone ABC7-42392500M17 from chromosome unknown, complete sequence

Sequence ID: **gb|AC235558.3|** Length: 34834 Number of Matches: 2

Range 1: 33725 to 33790

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	55/74(74%)	8/74(10%)	Plus/Plus	
Features:					
Query 842	AGATCACTGAGATGACACACATATACTAGTAGACACACATATACTAAGAGATCACTGAGA	901			
Sbjct 33725	AGTTCACTCACATCACACACATATAAC-----ACCCACATACAC--ACAGTTCACTCACA	33776			

Query 902 TGACACACATATACT 915
 Sbjct 33777 TCACACACATATACT 33790

Range 2: 33765 to 33830

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	55/74(74%)	8/74(10%)	Plus/Plus	

Features:

Query 842 AGATCACTGAGATGACACACATATACTAGTAGACACACATATACTAAGAGATCACTGAGA 901
 Sbjct 33765 AGTTCACTCACATCACACACATATACT----ACCCACATACAC--ACAGTTCACTCACA 33816
 Query 902 TGACACACATATACT 915
 Sbjct 33817 TCACACACATATACT 33830

Zebrafish DNA sequence from clone CH1073-416D2 in linkage group 17, complete sequence

Sequence ID: **emb|CU657975.12|** Length: 34271 Number of Matches: 2

Range 1: 22446 to 22528

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	61/83(73%)	4/83(4%)	Plus/Plus	

Features:

Query 837 TGAAGAGATCACTGAGATGACACACATATACTAGTAGACACAC---CATATACTA-AGAGA 892
 Sbjct 22446 TGCAGAGATCACGGTAATGACACACACACACACACAGAACACACTGCAGAGA 22505
 Query 893 TCACTGAGATGACACACATATACT 915
 Sbjct 22506 TCACGGTAATGACACACATACAC 22528

Range 2: 21914 to 21992

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	61/83(73%)	8/83(9%)	Plus/Plus	

Features:

Query 837 TGAAGAGATCACTGAGATGACACACATATACTAGTAGACACAC---CATATACTA-AGAGA 892
 Sbjct 21914 TGCAGAGATCACGGTAATGACACACACACACACAGAACACACTGCAGAGA 21969
 Query 893 TCACTGAGATGACACACATATACT 915
 Sbjct 21970 TCACGGTAATGACACACATACAC 21992

Mus musculus chromosome 3, clone RP23-20F10, complete sequence

Sequence ID: **gb|AC157379.7|** Length: 183455 Number of Matches: 1

Range 1: 57776 to 57825

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	44/55(80%)	5/55(9%)	Plus/Minus	

Features:

Query 856 ACACACATATACTAGTAGACACACATATACTAAGAGATCACTGAGATGACACACACA 910
 Sbjct 57825 ACACACATATACTA---TAGACACACATATACAAAGA---CACACACATCACACACA 57776

Mus musculus BAC clone RP24-372O13 from 12, complete sequence

Sequence ID: **gb|AC122023.3|** Length: 179947 Number of Matches: 4

Range 1: 107958 to 108023

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

Features:

Query 856 ACACACATATACTAGTAGACACACATATACT-AAGAGATCACTGAGATGACACACATA 914
 Sbjct 108023 ACACACATATACTAAGTGCACACACATACTCAAGTGCACAAGTAAATG-CACACATAC 107965
 Query 915 CTAGTAT 921
 Sbjct 107964 CAAGTAT 107958

Range 2: 108090 to 108164

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	60/80(75%)	8/80(10%)	Plus/Minus	

Features:

Query 656 AGTA-ACACATATACTAGTACAGC--TGACGGGACACACATATACTAAGAGATCACTGAG 712
Sbjct 108164 ||||| AGTACACACATACACAAGTACAGAAGTGAC---ACACACATACACAAACACACAAGTGAG 108108
Query 713 ATGACACACATATACTAGTA 732
Sbjct 108107 C--ACACACATATACAAGTA 108090

Range 3: 108090 to 108159

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	56/75(75%)	7/75(9%)	Plus/Minus	

Features:

Query 537 ACACATATACTAGTACAGC--TGACGGGACACACATATACTAAGAGATCACTGAGATGAC 594
Sbjct 108159 ||||| ACACATACACAAGTACAGAAGTGAC---ACACACATACACAAACACACAAGTGAGC--AC 108105
Query 595 ACACATATACTAGTA 609
Sbjct 108104 ACACATATACAAGTA 108090

Range 4: 108090 to 108159

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	56/75(75%)	7/75(9%)	Plus/Minus	

Features:

Query 390 ACACATATACTAGTACAGC--TGACGGGACACACATATACTAAGAGATCACTGAGATGAC 447
Sbjct 108159 ||||| ACACATACACAAGTACAGAAGTGAC---ACACACATACACAAACACACAAGTGAGC--AC 108105
Query 448 ACACATATACTAGTA 462
Sbjct 108104 ACACATATACAAGTA 108090

Mus musculus BAC clone RP24-194J17 from chromosome 9, complete sequence

Sequence ID: **gb|AC157996.2|** Length: 158268 Number of Matches: 1

Range 1: 57071 to 57100

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	28/30(93%)	0/30(0%)	Plus/Plus	

Features:

Query 856 ACACACATATACTAGTAGACACACATATAC 885
Sbjct 57071 ||||| ACACACATATACAAGTATACACACATATAC 57100

Homo sapiens chromosome 22 clone WI2-3379H11, complete sequence

Sequence ID: **gb|AC158336.1|** Length: 37861 Number of Matches: 1

Range 1: 11686 to 11751

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	55/74(74%)	8/74(10%)	Plus/Plus	

Features:

Query 842 AGATCACTGAGATGACACACATATACTAGTAGACACACATATACTAAGAGATCACTGAGA 901
Sbjct 11686 ||||| AGTTCACTCACATCACACACATATAC-----ACCCACATACAC--ACAGTTCACTCACA 11737
Query 902 TGACACACATATAC 915
Sbjct 11738 TCACACACATATAC 11751

Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds

Sequence ID: **gb|AF240786.1|AF240786** Length: 118999 Number of Matches: 3

Range 1: 5972 to 6037

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	55/74(74%)	8/74(10%)	Plus/Plus	
Features:					
Query 842	AGATCACTGAGATGACACACATATACTAGTAGACACACATATACTAAGAGATCACTGAGA				901
Sbjct 5972	AGTTCACTCACATCACACACATATAC	-----	ACCCACATACAC	--ACAGTTCACTCACA	6023
Query 902	TGACACACATATAAC	915			
Sbjct 6024	TCACACACATATAAC	6037			

Range 2: 37742 to 37807

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	55/74(74%)	8/74(10%)	Plus/Minus	
Features:					
Query 842	AGATCACTGAGATGACACACATATACTAGTAGACACACATATACTAAGAGATCACTGAGA				901
Sbjct 37807	AGTTCACTCACATCACACACATATAC	-----	ACCCACATACAC	--ACAGTTCACTCACA	37756
Query 902	TGACACACATATAAC	915			
Sbjct 37755	TCACACACATATAAC	37742			

Range 3: 37782 to 37847

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	54/74(73%)	8/74(10%)	Plus/Minus	
Features:					
Query 842	AGATCACTGAGATGACACACATATACTAGTAGACACACATATACTAAGAGATCACTGAGA				901
Sbjct 37847	AGTTCACTCACACCACACATATAC	-----	ACCCACATACAC	--ACAGTTCACTCACA	37796
Query 902	TGACACACATATAAC	915			
Sbjct 37795	TCACACACATATAAC	37782			

Mouse DNA sequence from clone RP23-356F21 on chromosome 13, complete sequence

Sequence ID: **emb|CT025557.11|** Length: 186496 Number of Matches: 1

Range 1: 60523 to 60582

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	46/60(77%)	6/60(10%)	Plus/Plus	
Features:					
Query 480	ACACACATATACTTGACACACATATACTAGTA	-----	ACACATATACTAGTACAGCTGA		533
Sbjct 60523	ACACACATATACATGTCAACACATATACGTGTACATATCACACATATAACAATAACAACTGA			--	60582

Mouse DNA sequence from clone RP23-226L18 on chromosome 2, complete sequence

Sequence ID: **emb|AL929164.12|** Length: 170293 Number of Matches: 2

Range 1: 118988 to 119048

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	48/62(77%)	1/62(1%)	Plus/Plus	
Features:					
Query 445	GACACACATATACTAGTATCTCTAGAGAGAGATGGACACACATATACTTGACACACATAT				504
Sbjct 118988	GACACACATATAACCACATATACTAGACACACATATACCCACATATA	-----	TAGACACACATAT	-	119046
Query 505	AC 506				
Sbjct 119047	AC 119048				

Range 2: 118988 to 119072

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	66/92(72%)	7/92(7%)	Plus/Plus	

Features:

```
Query 415      GACACACATATACTAAGAGATCACTGAGATGACACACATATACTAGTATCTCTAGAGAGA 474
Sbjct 118988    |||||||-----ATA-GACACACATATACCCACATATAGACACA 119041
Query 475      GATGGACACACATATACTTGACACACATATAC 506
Sbjct 119042    CATATACACATATACAC-AGACACACATATAC 119072
```

Mouse DNA sequence from clone RP23-382C19 on chromosome 11, complete sequence

Sequence ID: **emb|AL590994.13|** Length: 207814 Number of Matches: 2

Range 1: 190356 to 190421

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	55/70(79%)	5/70(7%)	Plus/Plus	

Features:

```
Query 480      ACACACATATACTTGACACACATATACTA-GTAACACATATACTAGTACAGCTGACGGAC 538
Sbjct 190356    |||||||-----ATACACATATACTACACACCACATATACTA-CACATAT-ACACAC 190411
Query 539      ACATATACTA 548
Sbjct 190412    ACATACACTA 190421
```

Range 2: 190307 to 190398

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	72/95(76%)	7/95(7%)	Plus/Plus	

Features:

```
Query 486      ATATACTTG-ACACACATATACTAGTAACA-CATATACTAGTACAGCTGACGGACACATA 543
Sbjct 190307    |||||||-----ATACACATGTACACACATATACTACACACACCACATA-TAGTACA-CATAACACACACATA 190364
Query 544      TACTAGTACAGCT-GACGGGACA-CACATATACTA 576
Sbjct 190365    |||||||-----TACTA-TACACATATACTACACACCACATATACTA 190398
```

Homo sapiens genomic DNA, chromosome 22q11.2, clone KB226F1

Sequence ID: **dbj|AP000351.3|** Length: 118999 Number of Matches: 3

Range 1: 5972 to 6037

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	55/74(74%)	8/74(10%)	Plus/Plus	

Features:

```
Query 842      AGATCACTGAGATGACACACATATACTAGTAGACACACATATACTAAGAGATCACTGAGA 901
Sbjct 5972     AGTTCACTCACATCACACACATATACTACACACATACAC--ACAGTTCACTCACA 6023
Query 902      TGACACACATATAAC 915
Sbjct 6024     TCACACACATATAAC 6037
```

Range 2: 37742 to 37807

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	55/74(74%)	8/74(10%)	Plus/Minus	

Features:

```
Query 842      AGATCACTGAGATGACACACATATACTAGTAGACACACATATACTAAGAGATCACTGAGA 901
Sbjct 37807    AGTTCACTCACATCACACACATATACTACACACATACAC--ACAGTTCACTCACA 37756
Query 902      TGACACACATATAAC 915
Sbjct 37755    TCACACACATATAAC 37742
```

Range 3: 37782 to 37847

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	54/74(73%)	8/74(10%)	Plus/Minus	

Features:

```
Query 842      AGATCACTGAGATGACACACATATACTAGTAGACACACATATACTAAGAGATCACTGAGA 901
```

Sbjct	37847	AGTTCACTCACACACACACATATAAC-----ACCCACATACAC--ACAGTTCACTCACA	37796
Query	902	TGACACACATATAAC	915
Sbjct	37795	TCACACACATATAAC	37782

Homo sapiens genomic DNA, chromosome 22q11.2, clone KB1561E1

Sequence ID: **dbj|AP000352.2|** Length: 152244 Number of Matches: 2
Range 1: 13457 to 13522

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	55/74(74%)	8/74(10%)	Plus/Minus	

Features:

Query	842	AGATCACTGAGATGACACACATATACTACTAGTAGACACACATATACTAAGAGATCACTGAGA	901
Sbjct	13522	AGTTCACTCACACACACATATAAC-----ACCCACATACAC--ACAGTTCACTCACA	13471
Query	902	TGACACACATATAAC	915
Sbjct	13470	TCACACACATATAAC	13457

Range 2: 13497 to 13562

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	55/74(74%)	8/74(10%)	Plus/Minus	

Features:

Query	842	AGATCACTGAGATGACACACATATACTACTAGTAGACACACATATACTAAGAGATCACTGAGA	901
Sbjct	13562	AGTTCACTCACACACACATATAAC-----ACCCACATACAC--ACAGTTCACTCACA	13511
Query	902	TGACACACATATAAC	915
Sbjct	13510	TCACACACATATAAC	13497

Human DNA sequence from clone CTA-322B1 on chromosome 22q11-12, complete sequence

Sequence ID: **emb|Z84718.2|** Length: 76798 Number of Matches: 1
Range 1: 63270 to 63335

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	55/74(74%)	8/74(10%)	Plus/Plus	

Features:

Query	842	AGATCACTGAGATGACACACATATACTACTAGTAGACACACATATACTAAGAGATCACTGAGA	901
Sbjct	63270	AGTTCACTCACACACACATATAAC-----ACCCACATACAC--ACAGTTCACTCACA	63321
Query	902	TGACACACATATAAC	915
Sbjct	63322	TCACACACATATAAC	63335

Homo sapiens genomic DNA, chromosome 22q11.2, clone KB1125A3

Sequence ID: **dbj|AP000350.1|** Length: 162328 Number of Matches: 1
Range 1: 148790 to 148855

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	55/74(74%)	8/74(10%)	Plus/Plus	

Features:

Query	842	AGATCACTGAGATGACACACATATACTACTAGTAGACACACATATACTAAGAGATCACTGAGA	901
Sbjct	148790	AGTTCACTCACACACACATATAAC-----ACCCACATACAC--ACAGTTCACTCACA	148841
Query	902	TGACACACATATAAC	915
Sbjct	148842	TCACACACATATAAC	148855

Homo sapiens chromosome 17, clone hRPK.60_A_24, complete sequence

Sequence ID: **gb|AC005325.1|AC005325** Length: 165228 Number of Matches: 1
Range 1: 131610 to 131646

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	55/74(74%)	8/74(10%)	Plus/Plus	

46.4 bits(50) 0.62() 34/39(87%) 2/39(5%) Plus/Minus

Features:

Query 480 ACACACATATACTTGACACACATATACTAGTAACACATA 518
Sbjct 131646 ACACACATACACCTGACACACATACACT--TAACACATA 131610

Homo sapiens BAC clone CH17-277L15 from chromosome 8, complete sequence

Sequence ID: **gb|AC245121.2|** Length: 201829 Number of Matches: 1

Range 1: 16904 to 16997

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	76/107(71%)	14/107(13%)	Plus/Plus	

Features:

Query 416 ACACACATATACTAAGAGATCACTGAGATG-ACACACATATACTAGTATCTCTAGAGAGA 474
Sbjct 16904 ACACACATATACTATA----CACACATATGCATACACATATA---TATACATACACATA 16955
Query 475 GATGGACACACATATACTTGACACACATATACTAGTAACACATATAAC 521
Sbjct 16956 TAT--ACACACAAATAC---ACACACATATACTATACACACATATAAC 16997

Mus musculus targeted non-conditional, lacZ-tagged mutant allele Aldh1a3:tm1e(KOMP)Wtsi; transgenic

Sequence ID: **gb|JN957473.1|** Length: 37842 Number of Matches: 1

Range 1: 3881 to 3921

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	38/46(83%)	6/46(13%)	Plus/Plus	

Features:

Query 476 ATGGACACACATATAAC-TTGACACACATATACTAGTAACACATATA 520
Sbjct 3881 ATGGACACACATATACATGGACACACACATAC----ACACATATA 3921

Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Aldh1a3:tm1a(KOMP)Wtsi; transgenic

Sequence ID: **gb|JN957472.1|** Length: 37902 Number of Matches: 1

Range 1: 3881 to 3921

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	38/46(83%)	6/46(13%)	Plus/Plus	

Features:

Query 476 ATGGACACACATATAAC-TTGACACACATATACTAGTAACACATATA 520
Sbjct 3881 ATGGACACACATATACATGGACACACACATAC----ACACATATA 3921

Mus musculus targeted non-conditional, lacZ-tagged mutant allele Nfatc2:tm1e(EUCOMM)Wtsi; transgenic

Sequence ID: **gb|JN948916.1|** Length: 38942 Number of Matches: 1

Range 1: 26451 to 26493

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	36/43(84%)	2/43(4%)	Plus/Minus	

Features:

Query 478 GGACACACATATACTTG--ACACACATATACTAGTAACACATA 518
Sbjct 26493 GGACACACATATACTGGAACACACATATAACCACACATA 26451

Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Nfatc2:tm1a(EUCOMM)Wtsi; transgenic

Sequence ID: **gb|JN948915.1|** Length: 38970 Number of Matches: 1

Range 1: 26479 to 26521

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	36/43(84%)	2/43(4%)	Plus/Minus	

Features:

Query 478 GGACACACATATACTTG--ACACACATATACTAGTAACACATA 518

Sbjct 26521 GGACACACATATACTGGAACACACATATAACCATACCACATA 26479

Schistosoma mansoni strain Puerto Rico chromosome 2, complete genome

Sequence ID: **emb|HE601625.1|** Length: 34464480 Number of Matches: 1

Range 1: 3080444 to 3080484

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

Features:
hypothetical protein

Query 187 CACATATACTAGTACAGCTGACGGTAAGAAGAGTC-ACTTT 226
Sbjct 3080484 CAAATACCCCTGGTACAGCTGAGGGTAAGAAGAGTCACATT 3080444

Homo sapiens FOSMID clone ABC9-43973000L3 from chromosome 8, complete sequence

Sequence ID: **gb|AC243065.3|** Length: 39149 Number of Matches: 1

Range 1: 24195 to 24288

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	76/107(71%)	14/107(13%)	Plus/Minus	

Features:

Query 416 ACACACATATACTAAGAGATCACTGAGATG-ACACACATATACTAGTATCTCTAGAGAGA 474
Sbjct 24288 ACACACATATACTATA---CACACATATGCATACACATATA---TATACATACACATA 24237
Query 475 GATGGACACACATATACTTGACACACATATACTAGTAACACATATAC 521
Sbjct 24236 TAT--ACACACAAATAC---ACACACATATACTATACACACATATAC 24195

Pig DNA sequence from clone CH242-169K14 on chromosome X, complete sequence

Sequence ID: **emb|CU856563.5|** Length: 131431 Number of Matches: 1

Range 1: 38637 to 38693

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	46/60(77%)	3/60(5%)	Plus/Minus	

Features:

Query 446 ACACACATATACTAGTATCTCTAGAGAGAGATGGACACACATATACTTGACACACATATA 505
Sbjct 38693 ACACACATATATATGTATATATATATACACACATATAC---ACACACATATA 38637

Homo sapiens FOSMID clone ABC13-49766800L3 from chromosome 8, complete sequence

Sequence ID: **gb|AC217626.3|** Length: 34122 Number of Matches: 1

Range 1: 1988 to 2081

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	76/107(71%)	14/107(13%)	Plus/Plus	

Features:

Query 416 ACACACATATACTAAGAGATCACTGAGATG-ACACACATATACTAGTATCTCTAGAGAGA 474
Sbjct 1988 ACACACATATACTATA---CACACATATGCATACACATATA---TATACATACACATA 2039
Query 475 GATGGACACACATATACTTGACACACATATACTAGTAACACATATAC 521
Sbjct 2040 TAT--ACACACAAATAC---ACACACATATACTATACACACATATAC 2081

Pan troglodytes BAC clone CH251-284B16 from chromosome 10, complete sequence

Sequence ID: **gb|AC191768.3|** Length: 158711 Number of Matches: 1

Range 1: 140660 to 140723

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	53/67(79%)	4/67(5%)	Plus/Plus	

Features:

Query 441 AGATGACACACATATA-CTAGTATCTCTAGAGAGAGATGGACACACATATACTTGACACA 499
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct	140660	AGAT-ACACACATATCTA-TATAGAGAGAGATAACACACATATA-TATACACA	140716
Query	500	CATATAC	506
Sbjct	140717	CACATAC	140723

Homo sapiens chromosome 8, clone RP11-715M14, complete sequence

Sequence ID: [gb|AC022257.20|](#) Length: 174628 Number of Matches: 1

Range 1: 118576 to 118669

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	76/107(71%)	14/107(13%)	Plus/Minus	
Features:					
Query	416	ACACACATATACTAAGAGATCACTGAGATG-ACACACATATACTAGTATCTCTAGAGAGA	474		
Sbjct	118669	ACACACATATACTATA---CACACATATGCATACACATATA---TATACATACACATA			118618
Query	475	GATGGACACACATATACTTGACACACATATACTAGTAACACATATAAC	521		
Sbjct	118617	TAT--ACACACAAATAC---ACACACATATACTATACACACATATAAC			118576

Rhesus macaque BAC clone CH250-65H12 from chromosome unknown, complete sequence

Sequence ID: [gb|AC187497.2|](#) Length: 227787 Number of Matches: 1

Range 1: 31553 to 31615

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	48/63(76%)	3/63(4%)	Plus/Plus	
Features:					
Query	446	ACACACATATACTAGTATCTCTAGAGAGAGATGGACACACATATA---CTTGACACACAT	502		
Sbjct	31553	ACACACACATCCATGTATCTGTAGATAGATATAAACACACATATACATACACACAT			31612
Query	503	ATA 505			
Sbjct	31613	ATA 31615			

Pan troglodytes BAC clone CH251-631F3 from chromosome 8, complete sequence

Sequence ID: [gb|AC184709.2|](#) Length: 178242 Number of Matches: 5

Range 1: 135002 to 135095

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	78/107(73%)	14/107(13%)	Plus/Plus	
Features:					
Query	416	ACACACATATACTAAGAGATCACTGAGATG-ACACACATATACTAGTATCTCTAGAGAGA	474		
Sbjct	135002	ACACACATATACT-ATACAT-AC---ATATGCATACACATATA---TATACATACACATA			135053
Query	475	GATGGACACACATATACTTGACACACATATACTAGTAACACATATAAC	521		
Sbjct	135054	TAT--ACACACAAATAC---ACACACATATACTATACACACATATAAC			135095

Range 2: 135069 to 135141

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	57/75(76%)	3/75(4%)	Plus/Plus	
Features:					
Query	480	ACACACATATACTTGACACACATATACTAGTAACACATATACTAGTACA-GCTGACGGAC	538		
Sbjct	135069	ACACACATATACTATAACACATATAAC-ATACACATATACACATACATGCATACACAC			135127
Query	539	ACATATACTAGTACA 553			
Sbjct	135128	ATACATACTA-TACA 135141			

Range 3: 134711 to 134832

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	91/129(71%)	9/129(6%)	Plus/Plus	
Features:					
Query	480	ACACACATATACTTGACACACATATACTAGTAACACATATACTAGTACA--GCTGACGGGA	537		

Sbjct	134711		ACACACACATACTATACACACATACACAC--ACATATATACACATACAATGCATAACACA	134767
Query	538		CACATATACTAGTACAGCTGACGGGACACACATACTAAGAGATCACTGAGATGACACA	597
Sbjct	134768		CACATACACTA-TACA-CACACTATACACACATATACACATACATGCAT-ACACA	134823
Query	598		CATATACTA 606	
Sbjct	134824		CATATACTA 134832	

Range 4: 134819 to 134861

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

Features:

Query	480		ACACACATATACTTGACACACATATAC-TAGTAACACATATAC 521
Sbjct	134819		ACACACATATACTATACACACATATACACATACATACATATAC 134861

Range 5: 135330 to 135368

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/42(83%)	3/42(7%)	Plus/Plus	

Features:

Query	480		ACACACATATACTTGACACACATATAC-TAGTAACACATATAC 521
Sbjct	135330		ACACACAAATAC---ACACACATATACTATACACACATATAC 135368

Mus musculus BAC clone RP23-264M10 from chromosome 16, complete sequence

Sequence ID: **gb|AC161376.2|** Length: 199086 Number of Matches: 1

Range 1: 172390 to 172438

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	40/49(82%)	1/49(2%)	Plus/Plus	

Features:

Query	474		AGATGGACACACATATACTTGACACACATATACTAGTA-ACACATATAC 521
Sbjct	172390		AGATAACACACATATAATCACACACATATACACACATACATATAC 172438

Mus musculus chromosome 7, clone RP23-24N16, complete sequence

Sequence ID: **gb|AC110520.12|** Length: 248540 Number of Matches: 1

Range 1: 88919 to 88977

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	48/61(79%)	2/61(3%)	Plus/Plus	

Features:

Query	855		GACACACATATACTAGTAGACACACATATACTAAGAGATCACTGAGATGACACACATATA 914		
Sbjct	88919		GACACACATACACAAAGAGACACACATATACACATACACAT-ACAGAGA-CACATACATATA 88976		
Query	915	C 915			
Sbjct	88977	C 88977			

Mus musculus 10 BAC RP23-3P24 (Roswell Park Cancer Institute (C57BL/6J Female) Mouse BAC Library) complete sequence

Sequence ID: **gb|AC167221.9|** Length: 204841 Number of Matches: 1

Range 1: 113764 to 113802

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

Features:

Query	468		AGAGAGAGATGGACACACATATACTTGACACACATATAC 506
Sbjct	113802		AGAGACACATGCACACACATATACCACACACATATAC 113764

Mus musculus 10 BAC RP23-150M2 (Roswell Park Cancer Institute (C57BL/6J Female) Mouse BAC Library) complete sequence
Sequence ID: **gb|AC166082.11|** Length: 170819 Number of Matches: 1
Range 1: 126422 to 126460

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

Features:

Query 468	AGAGAGAGATGGACACACATATACTTGACACACATATA	506
Sbjct 126460		
	AGAGACACATGCACACACATATAACCACACACATATA	126422

Mus musculus chromosome 1, clone RP23-22I7, complete sequence
Sequence ID: **gb|AC158925.4|** Length: 181897 Number of Matches: 1
Range 1: 69693 to 69727

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

Features:

Query 470	AGAGAGATGGACACACATATACTTGACACACATATA	505
Sbjct 69693		
	AGATAGATAGACACACATATA-TTGACAGACATATA	69727

Mus musculus chromosome 7, clone RP23-7G1, complete sequence
Sequence ID: **gb|AC091324.10|** Length: 225556 Number of Matches: 1
Range 1: 83394 to 83434

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	38/46(83%)	6/46(13%)	Plus/Plus	

Features:

Query 476	ATGGACACACATATACT-TTGACACACATATACTAGTAACACATATA	520
Sbjct 83394		
	ATGGACACACATATACTGGACACACACATAC---ACACATATA	83434

Mus musculus BAC clone RP24-401P10 from 6, complete sequence
Sequence ID: **gb|AC122031.2|** Length: 157782 Number of Matches: 1
Range 1: 53683 to 53714

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	31/35(89%)	3/35(8%)	Plus/Plus	

Features:

Query 265	ACTGAAAGACACACATATACTTGACACACATATA	299
Sbjct 53683		
	ACTGAAAGACACACATATACTT---ACACATACAC	53714

Mus musculus 12 days embryo embryonic body between diaphragm region and neck cDNA, RIKEN full-length enriched library, clone:9430010I07 product:hyaluronan and proteoglycan link protein 3, full insert sequence
Sequence ID: **dbj|AK136956.1|** Length: 3311 Number of Matches: 1
Range 1: 2270 to 2328

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	48/61(79%)	2/61(3%)	Plus/Minus	

Features:

Query 855	GACACACATATACTAGTAGACACACATATACTAAGAGATCACTGAGATGACACACATATA	914
Sbjct 2328		
	GACACACATACACAAAGAGACACACATACATACACAT-ACAGAGA-CACATACATATA	2271
Query 915	C 915	
Sbjct 2270	C 2270	

Mus musculus BAC clone RP24-496G24 from chromosome 17, complete sequence

Sequence ID: **gb|AC155242.2|** Length: 132408 Number of Matches: 1
Range 1: 102170 to 102221

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	43/53(81%)	2/53(3%)	Plus/Plus	

Features:

Query 247 AGACTGAC-GATAGATCTGACTGAAAGACACACATATACTTGACACACATATA 298
Sbjct 102170 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 102221
AGACAGACAGACAGA-CAGACAGAAAGACACACACACTGCACACACATATA

Homo sapiens chromosome 18, clone RP11-104H13, complete sequence

Sequence ID: **gb|AC110015.5|** Length: 168389 Number of Matches: 1
Range 1: 119410 to 119449

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	36/41(88%)	2/41(4%)	Plus/Minus	

Features:

Query 483 CACATATACTTGACA-CACATATACTAGTAACACATATACT 522
Sbjct 119449 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| 119410
CACATATACTT-ACATCACATATACTTATATCACATATACT

Mus musculus 10 BAC RP24-347J14 (Roswell Park Cancer Institute (C57BL/6J Male) Mouse BAC Library) complete sequence

Sequence ID: **gb|AC156949.9|** Length: 149183 Number of Matches: 1
Range 1: 50312 to 50470

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	116/164(71%)	10/164(6%)	Plus/Plus	

Features:

Query 446 ACACACATATACTAGTATCTCTAGAGAGAGATGGACACACATATACT-TTGACACACATAT 504
Sbjct 50312 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 50371
ACACACATATACACATATATATACACACATACACACACATATAACACATACACATAT
Query 505 ACTAGTA-AC-ACATATACTAGTACAGCTGACGGACACATATACTAGTACAGCTGACGGG 562
Sbjct 50372 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 50426
ACACATACACAACATATA-TA-CACA-CATACATACACATATAACACATACATCT-AC-AT
Query 563 ACACACATATACTAAGAGAT-CACTGAGAT-GACACACATATACT 604
Sbjct 50427 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| 50470
ACACACATACACACATATAACACATACATACACACACATAC

Mus musculus 6 BAC RP24-204J8 (Roswell Park Cancer Institute (C57BL/6J Male) Mouse BAC Library) complete sequence

Sequence ID: **gb|AC155722.9|** Length: 198481 Number of Matches: 1
Range 1: 88161 to 88219

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	49/62(79%)	4/62(6%)	Plus/Plus	

Features:

Query 855 GACACACATATACTAGTACAGACACACATATACTAACAGAGATCACTGAGATG-ACACACATAT 913
Sbjct 88161 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 88217
GACACACATGTACTCATAGACACACATGTACTCATAGA-CAC--ACATGCACAGACACAT
Query 914 AC 915
Sbjct 88218 ||| AC 88219

Mus musculus 10 BAC RP23-53D13 (Roswell Park Cancer Institute (C57BL/6J Female) Mouse BAC Library) complete sequence

Sequence ID: **gb|AC153824.9|** Length: 233119 Number of Matches: 1
Range 1: 166659 to 166817

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	116/164(71%)	10/164(6%)	Plus/Plus	

Features:

Query 446 ACACACATATACTAGTATCTCTAGAGAGAGATGGACACACATATACT-TTGACACACATAT 504
Sbjct 166659 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| 166718
ACACACATATACACATATATATACACACATACACACACATATAACACATACACACATAT
Query 505 ACTAGTA-AC-ACATATACTAGTACAGCTGACGGACACATATACTAGTACAGCTGACGGG 562
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct	166719	ACACATACACAACATATA-TA-CACA-CATACATACACATATAACATACATCT-AC-AT	166773
Query	563	ACACACATATACTAAAGAGAT-CACTGAGAT-GACACACATATAAC	604
Sbjct	166774	ACACACATACACACATATAACATACATATAACACACATATAAC	166817

Mus musculus BAC clone RP24-401O6 from 16, complete sequence

Sequence ID: **gb|AC125371.4|** Length: 194685 Number of Matches: 1
Range 1: 76008 to 76056

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	40/49(82%)	1/49(2%)	Plus/Plus	

Features:

Query	474	AGATGGCACACATATACTTGACACACATATACTAGTA-ACACATATAAC	521
Sbjct	76008	AGATACACACACATATAAAATCACACACATATAACACATACACACATATAAC	76056

Mouse DNA sequence from clone RP23-156F1 on chromosome 2, complete sequence

Sequence ID: **emb|AL844575.4|** Length: 190718 Number of Matches: 1
Range 1: 66640 to 66682

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	36/43(84%)	2/43(4%)	Plus/Plus	

Features:

Query	478	GGACACACATATACTTG--ACACACATATACTAGTAACACATA	518
Sbjct	66640	GGACACACATATACTGGAACACACATATAACCATACACCACATA	66682

Homo sapiens BAC clone CH17-476P10 from chromosome 22, complete sequence

Sequence ID: **gb|AC253536.1|** Length: 228396 Number of Matches: 2
Range 1: 30480 to 30545

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	54/74(73%)	8/74(10%)	Plus/Minus	

Features:

Query	842	AGATCACTGAGATGACACACATATACTAGTAGACACACATATACTAAGAGATCACTGAGA	901
Sbjct	30545	AGTTCACTCACATCACACACATATAAC-----ACCCACATACAC--ACAGTTCACACACA	30494
Query	902	TGACACACATATAAC	915
Sbjct	30493	TCACACACATATAAC	30480

Range 2: 30520 to 30585

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	54/74(73%)	8/74(10%)	Plus/Minus	

Features:

Query	842	AGATCACTGAGATGACACACATATACTAGTAGACACACATATACTAAGAGATCACTGAGA	901
Sbjct	30585	AGTTCACTCACACACACACATATAAC-----ACCCACATACAC--ACAGTTCACTCACA	30534
Query	902	TGACACACATATAAC	915
Sbjct	30533	TCACACACATATAAC	30520

PREDICTED: Callithrix jacchus uncharacterized LOC100895454 (LOC100895454), mRNA

Sequence ID: **ref|XM_003734947.1|** Length: 1017 Number of Matches: 1
Range 1: 216 to 288

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	56/75(75%)	2/75(2%)	Plus/Minus	

Features:

Query	446	ACACACATATACTAGTATCTCTAGAGAGAGATGGACACACATATACTTGACACACATATA	505
Sbjct	288	ACACACATATACTATATACACACATATAACACACATATA-TACACACACATATA	230

Query	506	CTAGTAACACATATA	520
Sbjct	229	-TACACACACATATA	216

Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Slc12a1:tm1a(EUCOMM)Hmgu; transgenic
Sequence ID: **gb|JN960771.1|** Length: 38021 Number of Matches: 1
Range 1: 34778 to 34816

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

Features:

Query	247	AGACTGACGATAGATCTGACTGAAAGACACACATATACTT	286
Sbjct	34816	AGACTGAAAATAGAT-TGAATGTAAGACCCACATATACTT	34778

Homo sapiens FOSMID clone ABC16-2279J16 from chromosome x, complete sequence
Sequence ID: **gb|AC238719.3|** Length: 41625 Number of Matches: 1
Range 1: 41077 to 41120

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	40/47(85%)	3/47(6%)	Plus/Plus	

Features:

Query	482	ACACATATACTTGACACACATATACTAGTAACACATATACTAGTACA	528
Sbjct	41077	ACATATATAGTACACACATATA-TAGT-ACACATATA-TAGTACA	41120

Zebrafish DNA sequence from clone CH73-352P18 in linkage group 22, complete sequence
Sequence ID: **emb|FP067424.7|** Length: 87896 Number of Matches: 1
Range 1: 54212 to 54281

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	59/76(78%)	9/76(11%)	Plus/Minus	

Features:

Query	474	AGATGGACACACATATACTTG---ACACACATATACTAGTAACACATATACTAGTACAGC	530
Sbjct	54281	AGATGTACACACATATACACGCACACACGCATATAC-AGACACACACATA-TA-TACA--	54227
Query	531	TGACGGACACATATAAC	546
Sbjct	54226	TG-CAGACACATATAAC	54212

Tupaia belangeri BAC clone CH275-65H12 from chromosome unknown, complete sequence
Sequence ID: **gb|AC236278.1|** Length: 156968 Number of Matches: 2
Range 1: 144050 to 144075

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

Features:

Query	480	ACACACATATACTTGACACACATATA	505
Sbjct	144075	ACACACATATACTTGACAAACATATA	144050

Range 2: 144050 to 144075

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

Features:

Query	273	ACACACATATACTTGACACACATATA	298
Sbjct	144075	ACACACATATACTTGACAAACATATA	144050

Homo sapiens keratin 18 (KRT18), RefSeqGene on chromosome 12

Sequence ID: **ref|NG_008351.1|** Length: 11031 Number of Matches: 1
Range 1: 10954 to 11008

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

Features:

```
Query 858      ACACATATACTAGTAGACACACATATACTAAGAGATCACTGAGATGACACACATATA  914
Sbjct 11008     ACACATATACTCATATACACATATACTCATATAT-ACATATAT-ACACACATATA  10954
```

Rattus norvegicus BAC CH230-34B22 (Children's Hospital Oakland Research Institute Rat (BN/SsNHsd/MCW) BAC library) complete sequence

Sequence ID: **gb|AC128786.3|** Length: 220895 Number of Matches: 1
Range 1: 125096 to 125126

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

Features:

```
Query 856      ACACACATATACTAGTAGACACACATATACT  886
Sbjct 125096   ACACACATATACATGTACACACACATATACT  125126
```

Mouse DNA sequence from clone RP23-25G2 on chromosome 13, complete sequence

Sequence ID: **emb|CU025215.12|** Length: 72405 Number of Matches: 1
Range 1: 25648 to 25761

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	84/120(70%)	12/120(10%)	Plus/Plus	

Features:

```
Query 476      ATGGACACACATATACTTG-----ACACACATATACTAGTAACACATATACTAGTACAGC  530
Sbjct 25648    ATGTACACACATATACATGCAAATACATACATATAACACATACACATATACT-CACAAA  25705
Query 531      TG-ACGGACACATATACTAGTACAGCTGACGGGACACACATATACTAAAGAGATCACTGAG  589
Sbjct 25706    TGCACGCACACACATACATGTACA-CACAC---ACACATACACACTGAGAGAAGTCTGAG  25761
```

Zebrafish DNA sequence from clone DKEY-160M3 in linkage group 6, complete sequence

Sequence ID: **emb|CT573376.5|** Length: 94397 Number of Matches: 1
Range 1: 59310 to 59338

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

Features:

```
Query 856      ACACACATATACTAGTAGACACACATATAC  885
Sbjct 59338    ACACACATATAC-AGTACACACACATATAC  59310
```

Mus musculus BAC clone RP23-110D19 from chromosome 1, complete sequence

Sequence ID: **gb|AC153019.8|** Length: 213842 Number of Matches: 1
Range 1: 153090 to 153120

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

Features:

```
Query 264      GACTGAAAGACACACATATACTTGACACACA  294
Sbjct 153120   GACAGAAAGACACACATATAACACACACA  153090
```

Zebrafish DNA sequence from clone DKEYP-29C12 in linkage group 11, complete sequence

Sequence ID: **emb|CR931977.8|** Length: 83211 Number of Matches: 1
Range 1: 44715 to 44759

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	39/47(83%)	2/47(4%)	Plus/Plus	

Features:

Query 462 ATCTCTAGAGAGAGATGGACACACATATACTTGACACACATATACTA 508
Sbjct 44715 ATCTCTGG-GAGAGATCCACACACACACA-TTCACACACATATACTA 44759

Mus musculus chromosome 7, clone RP24-63H14, complete sequence

Sequence ID: **gb|AC118621.6|** Length: 230898 Number of Matches: 1

Range 1: 178335 to 178377

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

Features:

Query 460 GTATCTCTAGAGAGAGATGGACACACATATACTTGACACACACA 501
Sbjct 178335 GTATCTATAGATAGACACACACACATATACTTGACACACACA 178377

Mus musculus chromosome 3, clone RP23-277L18, complete sequence

Sequence ID: **gb|AC152400.9|** Length: 190913 Number of Matches: 1

Range 1: 56263 to 56309

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	39/47(83%)	2/47(4%)	Plus/Plus	

Features:

Query 476 ATGGACACACATATACTTG-ACACACATATACTAGTA-ACACATATA 520
Sbjct 56263 ATGTACACACATATACATGTACACACATATACACGTACATGCATA 56309

Mus musculus chromosome 8, clone RP23-80D9, complete sequence

Sequence ID: **gb|AC161217.7|** Length: 234127 Number of Matches: 1

Range 1: 35879 to 35938

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	48/64(75%)	4/64(6%)	Plus/Minus	

Features:

Query 443 ATGACACACATATACTACTAGTATCTCTAGAGAGAGATGGACACACAT 502
Sbjct 35938 ATCACACACACACATA----ATGTGTATACATACATGCACACACATACATCACACAC 35883
Query 503 ATAC 506
Sbjct 35882 ATAC 35879

Mus musculus 6 BAC RP24-483K3 (Roswell Park Cancer Institute (C57BL/6J Male) Mouse BAC Library) complete sequence

Sequence ID: **gb|AC155946.7|** Length: 178502 Number of Matches: 1

Range 1: 9460 to 9500

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	36/44(82%)	3/44(6%)	Plus/Minus	

Features:

Query 480 ACACACATATACTTGACACACATATACTACTAGTAACACATATACTA 523
Sbjct 9500 ACACACATATACTACACACATGTACCACACACATATACTA 9460

Mouse DNA sequence from clone RP24-274P18 on chromosome 17, complete sequence

Sequence ID: **emb|CT025573.9|** Length: 210893 Number of Matches: 1

Range 1: 103982 to 104024

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

Features:

Query 479 GACACACATATACTTGACACACATATACTAGTAACACATATAC 521
Sbjct 103982 GACACACATATACATAACACATATAACACACAACATATAC 104024

Mus musculus chromosome 16, clone RP23-73P19, complete sequence

Sequence ID: **gb|AC116118.16|** Length: 128851 Number of Matches: 1

Range 1: 73513 to 73565

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	44/56(79%)	5/56(8%)	Plus/Plus	

Features:

Query 468 AGAGAGAGATGGACACACATATACTTGACACA--CATATACTAGTAACACATATAC 521
Sbjct 73513 AGAGAGACAAGGACACACATATAAC--ACACATGCACATACACGTACCACATGTAC 73565

Mus musculus chromosome 1, clone RP23-311K2, complete sequence

Sequence ID: **gb|AC107746.9|** Length: 202822 Number of Matches: 1

Range 1: 114523 to 114552

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

Features:

Query 856 ACACACATATACT-AGTAGACACACATATA 884
Sbjct 114552 ACACACATATACACAGTAGACACACATATA 114523

Mus musculus BAC clone RP24-87K15 from 9, complete sequence

Sequence ID: **gb|AC110091.4|** Length: 222792 Number of Matches: 1

Range 1: 188344 to 188404

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

Features:

Query 855 GACACACATATACTAGTAGACACACATATACTAAGAGATCACTGAGATG-ACACACATAT 913
Sbjct 188344 GACACACATATACATGTACACACATATATGTATACA-CACTAACATGAACATAAATAT 188402
Query 914 AC 915
Sbjct 188403 AC 188404

Dasyurus novemcinctus clone VMRC5-356N21, complete sequence

Sequence ID: **gb|AC145363.4|** Length: 108046 Number of Matches: 1

Range 1: 71288 to 71331

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	38/47(81%)	3/47(6%)	Plus/Plus	

Features:

Query 273 ACACACATATACTTGACACACATATACTAGTATCTCTAGAGAGAGAT 319
Sbjct 71288 ACACACATATACAT---ACACATATACATATATCGTAGAGAGAGAT 71331