

Basic Local Alignment Search Tool

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CGAT

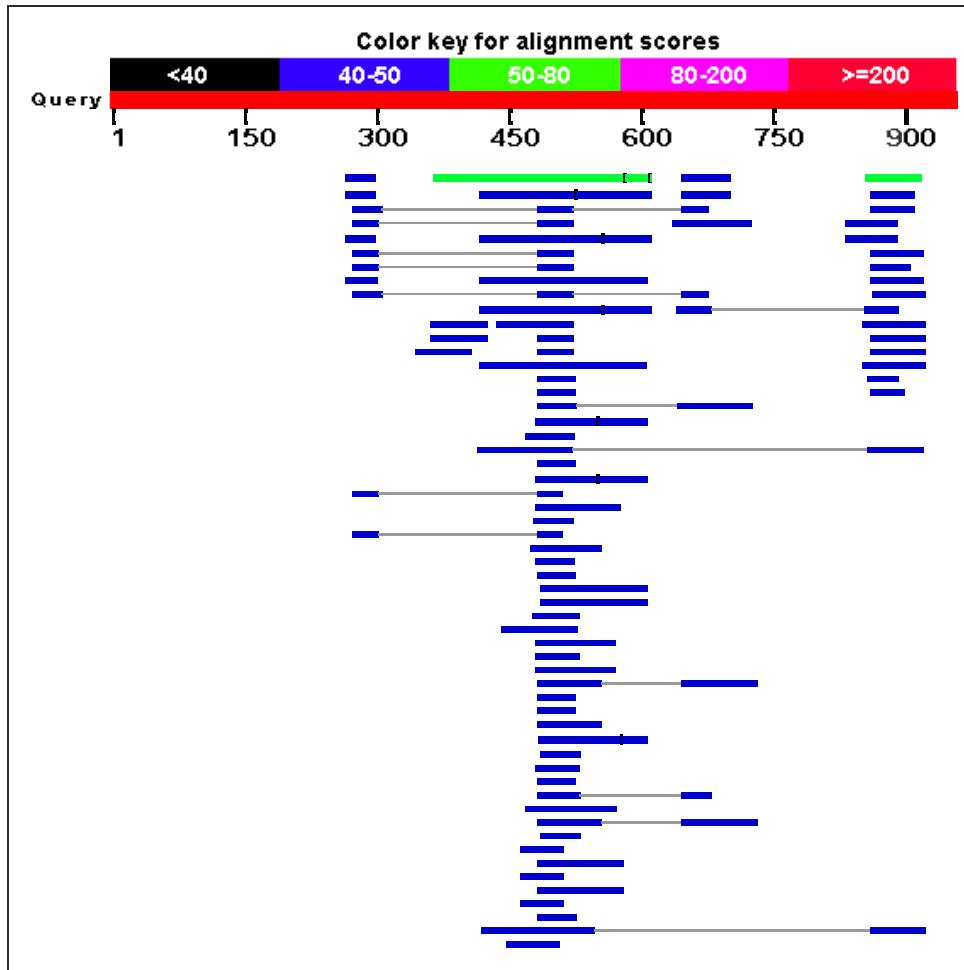
RID [Y0TJW46H01R](#) (Expires on 08-06 13:06 pm)

Query ID Icl|132423
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 169 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Rattus norvegicus CH230-55H2 (Children's Hospital Oakland Research Institute Rat (BN/SsNHsd/MCW) BAC library) complete sequence	69.8	462	25%	5e-08	69%	AC111287.5
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Ntn4:tm1a(KOMP)Wtsi; transgenic	51.8	198	20%	0.015	79%	JN947524.1
Mus musculus BAC clone RP23-377M11 from chromosome 8, complete sequence	51.8	51.8	6%	0.015	83%	AC137157.3
Mus musculus strain 129S6/SvEvTac clone rp21-493n6 map 11a2, complete sequence	50.0	140	11%	0.051	94%	AC005528.43
Mus musculus BAC clone RP23-69N8 from chromosome 10, complete sequence	50.0	94.5	7%	0.051	86%	AC122896.4
Mus musculus BAC clone RP23-130P17 from chromosome 10, complete sequence	50.0	96.3	20%	0.051	72%	AC124585.3
Mus musculus BAC clone RP23-116L23 from chromosome 10, complete sequence	50.0	94.5	7%	0.051	86%	AC133207.3
Mus Musculus Strain C57BL6/J Chromosome 10 BAC, RP23-337L15, Complete Sequence, complete sequence	50.0	94.5	7%	0.051	86%	AC087889.15
Rattus norvegicus chromosome 5 BAC CH230-510H6, complete sequence	50.0	146	20%	0.051	71%	CR937047.1
Mouse DNA sequence from clone RP23-338J18 on chromosome 11, complete sequence	50.0	140	11%	0.051	94%	AL645845.14
Mus musculus BAC clone RP24-446O20 from 10, complete sequence	50.0	96.3	20%	0.051	72%	AC151976.3
Mouse DNA sequence from clone RP23-425K3 on chromosome 4, complete sequence	50.0	50.0	9%	0.051	75%	AL805912.5
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Pla2g10:tm1a(EUCOMM)Hmg; transgenic	48.2	48.2	4%	0.18	89%	JN961285.1
Mus musculus targeted non-conditional, lacZ-tagged mutant allele Pla2g10:tm1e(EUCOMM)Hmg; transgenic	48.2	48.2	4%	0.18	89%	JN949423.1
Homo sapiens contig freeze2_3604 genomic sequence	48.2	48.2	19%	0.18	68%	GU268116.1
Rattus norvegicus CH230-38F9 (Children's Hospital Oakland Research Institute Rat (BN/SsNHsd/MCW) BAC library) complete sequence	48.2	94.5	4%	0.18	84%	AC098114.7
Pan troglodytes BAC clone CH251-1137N7 from chromosome 7, complete sequence	48.2	48.2	5%	0.18	86%	AC230049.3
Rattus norvegicus BAC CH230-277M9 (Children's Hospital Oakland Research Institute Rat (BN/SsNHsd/MCW) BAC library) complete sequence	48.2	94.5	4%	0.18	84%	AC120721.5
Pan troglodytes BAC clone CH251-656I16 from chromosome 7, complete sequence	48.2	48.2	5%	0.18	86%	AC187752.3

Mus musculus BAC clone RP24-247B20 from chromosome 9, complete sequence	48.2	90.9	13%	0.18	84%	AC151968.3
Mus musculus chromosome 1, clone RP23-39C19, complete sequence	48.2	48.2	6%	0.18	81%	AC138232.10
Mus musculus chromosome 14, clone RP24-218I13, complete sequence	48.2	137	6%	0.18	80%	AC119886.7
Mus musculus chromosome 10, clone RP23-139F20, complete sequence	48.2	94.5	13%	0.18	77%	AC102114.9
Mus musculus BAC clone RP24-235G7 from chromosome 12, complete sequence	48.2	48.2	3%	0.18	91%	AC160391.2
Mus musculus chromosome 1, clone RP23-293I7, complete sequence	48.2	48.2	5%	0.18	82%	AC144905.10
Homo sapiens chromosome 5 clone CTD-2281M20, complete sequence	48.2	652	17%	0.18	75%	AC114279.2
Mus musculus BAC clone RP23-283B12 from chromosome 14, complete sequence	48.2	137	6%	0.18	80%	AC154646.2
Mus musculus BAC clone RP23-331D17 from chromosome 16, complete sequence	48.2	48.2	4%	0.18	89%	AC154607.2
Mus musculus 10 BAC RP23-402A24 (Roswell Park Cancer Institute (C57BL/6J Female) Mouse BAC Library) complete sequence	48.2	94.5	13%	0.18	77%	AC158636.5
Mouse DNA sequence from clone RP23-118D1 on chromosome 4, complete sequence	48.2	96.3	6%	0.18	97%	AL732624.6
Mus musculus BAC clone RP23-446B6 from chromosome 14, complete sequence	48.2	48.2	10%	0.18	72%	AC164977.2
Mus musculus chromosome 1, clone RP24-537H9, complete sequence	48.2	48.2	6%	0.18	81%	AC105168.8
Mouse DNA sequence from clone RP23-193M23 on chromosome 4, complete sequence	48.2	48.2	4%	0.18	87%	AL929433.10
Mouse DNA sequence from clone RP23-441A11 on chromosome 4, complete sequence	48.2	96.3	6%	0.18	97%	AL611923.19
Mouse DNA sequence from clone RP23-95I4 on chromosome 3, complete sequence	48.2	48.2	8%	0.18	75%	AL691419.10
PREDICTED: Homo sapiens NADH-ubiquinone oxidoreductase chain 5-like (LOC101930318), mRNA	46.4	89.1	4%	0.62	88%	XM_005275980.1
Human DNA sequence from clone RP11-375H17 on chromosome 22, complete sequence	46.4	46.4	4%	0.62	86%	AL121885.23
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Fam151b:tm1a(EUCOMM)Hmg; transgenic	46.4	89.1	12%	0.62	71%	JN958061.1
Mus musculus targeted non-conditional, lacZ-tagged mutant allele Fam151b:tm1e(EUCOMM)Hmg; transgenic	46.4	89.1	12%	0.62	71%	JN947737.1
Homo sapiens FOSMID clone ABC10-44455000E13 from chromosome 1, complete sequence	46.4	46.4	6%	0.62	80%	AC203660.3
Rattus norvegicus BAC CH230-126O18 (Children's Hospital Oakland Research Institute Rat (BN/SsNHsd/MCW) BAC library) complete sequence	46.4	46.4	5%	0.62	81%	AC105598.5
Zebrafish DNA sequence from clone CH211-62D7, complete sequence	46.4	46.4	9%	0.62	76%	CR855268.9
Mus musculus chromosome 10, clone RP24-175N4, complete sequence	46.4	90.9	4%	0.62	89%	AC125276.18
Mus musculus BAC clone RP23-325H1						

from chromosome 15, complete sequence	46.4	46.4	9%	0.62	77%	AC153010.3
Mus musculus BAC clone RP23-65G17 from chromosome 16, complete sequence	46.4	46.4	5%	0.62	80%	AC164635.5
Mus musculus BAC clone RP24-362N7 from chromosome 15, complete sequence	46.4	46.4	9%	0.62	77%	AC142474.4
Mus musculus BAC clone RP23-380J24 from chromosome 2, complete sequence	46.4	90.9	16%	0.62	76%	AC117228.2
Mus musculus BAC clone RP23-224I23 from 8, complete sequence	46.4	89.1	4%	0.62	85%	AC122830.4
Mus musculus BAC clone RP23-37M7 from 8, complete sequence	46.4	89.1	4%	0.62	85%	AC117185.2
Mus musculus chromosome 8, clone RP24-372D19, complete sequence	46.4	46.4	7%	0.62	76%	AC116693.23
Mus musculus BAC clone RP23-154K12 from chromosome 13, complete sequence	46.4	219	12%	0.62	71%	AC154363.2
Human DNA sequence from clone RP1-111J24 on chromosome 22, complete sequence	46.4	46.4	4%	0.62	82%	Z83836.2
Mus musculus chromosome 16 clone RP23-239I17, complete sequence	46.4	46.4	5%	0.62	80%	AC122281.2
Homo sapiens chromosome 1 clone RP11-397A15, complete sequence	46.4	46.4	6%	0.62	80%	AC113174.3
Homo sapiens Chromosome 22q11.2 BAC Clone b437g10 In BCRL2-GGT Region, complete sequence	46.4	46.4	4%	0.62	86%	AC004032.7
Mus musculus chromosome 8, clone RP23-365O13, complete sequence	46.4	89.1	8%	0.62	80%	AC114589.30
Mus musculus BAC clone RP23-406A5 from chromosome 13, complete sequence	46.4	46.4	6%	0.62	79%	AC157656.3
Mus musculus chromosome 7, clone RP23-227K15, complete sequence	46.4	46.4	10%	0.62	74%	AC110192.14
Zebrafish DNA sequence from clone CH211-167H2 in linkage group 16, complete sequence	46.4	89.1	8%	0.62	86%	BX005277.11
Mouse DNA sequence from clone RP23-89M14 on chromosome 2, complete sequence	46.4	90.9	16%	0.62	76%	AL928793.13
H.sapiens repetitive DNA (ancient bone DNA; clone N696)	46.4	46.4	4%	0.62	82%	Z82048.1
Mus musculus targeted deletion, lacZ-tagged mutant allele Gpaa1:tm1(KOMP)Wtsi; transgenic	44.6	44.6	4%	2.2	83%	JN961052.1
Mus musculus targeted non-conditional, lacZ-tagged mutant allele Dock4:tm1e(EUCOMM)Hmg; transgenic	44.6	44.6	10%	2.2	73%	JN952723.1
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Exosc4:tm1a(KOMP)Ucd; transgenic	44.6	44.6	4%	2.2	83%	JN950206.1
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Dock4:tm1a(EUCOMM)Hmg; transgenic	44.6	44.6	10%	2.2	73%	JN948497.1
Mus musculus targeted non-conditional, lacZ-tagged mutant allele Exosc4:tm1e(KOMP)Ucd; transgenic	44.6	44.6	4%	2.2	83%	JN947740.1
Rattus norvegicus Y Chr BAC RNECO-258K04 (Amplicon Express Rat SHR-Akr (EcoR1 Digest) BAC library) complete sequence	44.6	44.6	3%	2.2	89%	AC243008.4
Rattus norvegicus Y Chr BAC RNECO-69P24 (Amplicon Express Rat SHR-Akr						

(EcoR1 Digest) BAC library) complete sequence	44.6	44.6	3%	2.2	89%	AC242892.3
Rattus norvegicus CH230-365N4 (Children's Hospital Oakland Research Institute Rat (BN/SsNHsd/MCW) BAC library) complete sequence	44.6	44.6	4%	2.2	85%	AC127006.5
Pan troglodytes BAC clone CH251-167J5 from chromosome 7, complete sequence	44.6	89.1	19%	2.2	69%	AC215812.4
Felis catus FLA distal class I region genomic sequence	44.6	44.6	6%	2.2	77%	EU153402.1
Pan troglodytes BAC clone CH251-50H23 from chromosome 10, complete sequence	44.6	44.6	11%	2.2	71%	AC196787.2
Mus musculus BAC clone RP24-326K24 from chromosome 17, complete sequence	44.6	44.6	5%	2.2	80%	AC191933.3
Mouse DNA sequence from clone RP23-163K5 on chromosome 16, complete sequence	44.6	44.6	5%	2.2	81%	CT573086.9
Mouse DNA sequence from clone CH29-511O15 on chromosome 17, complete sequence	44.6	44.6	3%	2.2	89%	CT009662.23
Mus musculus BAC clone RP24-108C24 from chromosome 17, complete sequence	44.6	44.6	5%	2.2	80%	AC154493.2
Mus musculus BAC clone RP24-430M9 from chromosome 17, complete sequence	44.6	44.6	5%	2.2	80%	AC165948.2
Mus musculus chromosome 15, clone RP24-274M4, complete sequence	44.6	89.1	4%	2.2	83%	AC102914.9
Mus musculus chromosome 5 clone RP24-340B11, complete sequence	44.6	44.6	7%	2.2	76%	AC122005.3
Mus musculus chromosome 5, clone RP24-258B22, complete sequence	44.6	44.6	6%	2.2	78%	AC103624.9
Mus musculus BAC clone RP23-378M19 from chromosome 16, complete sequence	44.6	87.3	11%	2.2	73%	AC165961.2
Rattus norvegicus 7 BAC CH230-33J22 (Children's Hospital Oakland Research Institute) complete sequence	44.6	44.6	4%	2.2	86%	AC102999.7
Mus musculus chromosome 14, clone RP24-550E9, complete sequence	44.6	89.1	4%	2.2	83%	AC137961.5
Mus musculus chromosome 1, clone RP24-285E3, complete sequence	44.6	44.6	7%	2.2	75%	AC120554.12
Mus musculus BAC clone RP23-77O10 from chromosome 16, complete sequence	44.6	87.3	11%	2.2	73%	AC168220.1
Mus musculus chromosome 5, clone RP24-242C19, complete sequence	44.6	44.6	6%	2.2	78%	AC163995.4
Mus musculus chromosome 15, clone RP24-127H11, complete sequence	44.6	44.6	4%	2.2	83%	AC155074.12
Mus musculus BAC clone RP23-409N21 from chromosome 12, complete sequence	44.6	44.6	10%	2.2	73%	AC159271.4
Mus musculus BAC clone RP24-572L22 from chromosome 5, complete sequence	44.6	44.6	7%	2.2	76%	AC137154.2
Mus musculus BAC clone RP23-250N10 from chromosome 19, complete sequence	44.6	44.6	3%	2.2	88%	AC125381.4
Mus musculus BAC clone RP23-345K19 from chromosome 15, complete sequence	44.6	178	19%	2.2	81%	AC123858.4
Human DNA sequence from clone ICI-21CG7 on chromosome 10, complete sequence	44.6	87.3	11%	2.2	71%	AL683826.14
Mus musculus chromosome 1, clone	44.6	44.6	7%	2.2	76%	AC099696.12

RP23-453N3, complete sequence						
Mus musculus BAC clone RP23-192O14 from 12, complete sequence	44.6	44.6	10%	2.2	73%	AC134599.4
Mus musculus chromosome 3, clone RP23-223N19, complete sequence	44.6	44.6	19%	2.2	70%	AC116720.16
Mus musculus BAC clone RP23-112C14 from 3, complete sequence	44.6	44.6	9%	2.2	75%	AC144631.3
Mus musculus BAC clone RP24-386B19 from 7, complete sequence	44.6	44.6	3%	2.2	86%	AC134536.5
Mus musculus BAC clone RP24-279A17 from 16, complete sequence	44.6	44.6	4%	2.2	85%	AC135673.5
Mus musculus genomic DNA, chromosome 16q clone:RP21-567F3, complete sequences	44.6	44.6	5%	2.2	81%	AP003155.1
Mouse DNA sequence from clone RP23-99K18 on chromosome X, complete sequence	44.6	44.6	6%	2.2	77%	AL807250.9

Alignments

Rattus norvegicus CH230-55H2 (Children's Hospital Oakland Research Institute Rat (BN/SsNHsd/MCW) BAC library) complete sequence
Sequence ID: **gb|AC111287.5|** Length: 246163 Number of Matches: 8
Range 1: 238931 to 239121

Score	Expect	Identities	Gaps	Strand	Frame
69.8 bits(76)	5e-08()	150/216(69%)	29/216(13%)	Plus/Plus	
Features:					
Query 365	TGTGTATATGATC-ATGTCGACTGCCTGTATATGATC-ATGTCGACTGCCCTGTGTGT				422
Sbjct 238931	TGTGTATATGATGTATATGTACTGTGTGTATATGATGTATATGTACTG---TGTGTGT				238987
Query 423	ATATGATTCTCTAGTGACTCTACTGTGTGTATATGATCATAGAGATCTCTCTAC-CTG				481
Sbjct 238988	ATATGAT-----GTATATGTACTGTGTATAT-AT-----GATGTATATGTACTGTG				239034
Query 482	TGTGTATATGAACGTGTGTATATGATCATTGTGTATATGAT-CATGTCGACTGCCGTGT				540
Sbjct 239035	TATGTATATGA---TGTATATATACTGTATATGATATGATGTATATGTACTGTGTGT				239090
Query 541	TATATGATCATGTCGACTGCCCTGTGTGTATATGAT	576			
Sbjct 239091	TATATGTATATGT---ACT---ATGTGTGTATATGAT				239121

Range 2: 238957 to 239196

Score	Expect	Identities	Gaps	Strand	Frame
68.0 bits(74)	2e-07()	180/259(69%)	36/259(13%)	Plus/Plus	
Features:					
Query 365	TGTGTATATGATC-ATGTCGACTGCCTGTATATGATC-ATGTCGACTGCCCTGTGTGT				422
Sbjct 238957	TGTGTATATGATGTATATGTACTGTGTGTATATGATGTATATGTACTG---TGTGTAT				239013
Query 423	ATATGATTCTCTAGTGACTCTACTGTGTGTATATGATCATAGAGAT-CTCTCTACACC				479
Sbjct 239014	ATATGATG-TATA-----TGTACTGTGTATGTATATGATG-TATATATACTGTATATGTA				239066
Query 480	TGTG-TGTATATGAACGTGTGTGTATATGATC-AT-TGTGTATATGATC-ATG				527
Sbjct 239067	TATGATGTATATGTACTGTGTGTATATGATACTATGTGTATATGATGTATA				239126
Query 528	TCGACTGCCTGTGTATATGATCATGTCGACTGCCCTGTGTGTATATGATTCTCTAGTGAC				587
Sbjct 239127	TGTACTGTGTGTATATGATATGT---ACTA---TGTGTGTATATGATG-TATATGTAC				239180
Query 588	TCTACTGTGTGTATATGAT	606			
Sbjct 239181	TAT---GTGTGTATATGAT				239196

Range 3: 239159 to 239347

Score	Expect	Identities	Gaps	Strand	Frame
68.0 bits(74)	2e-07()	150/217(69%)	35/217(16%)	Plus/Plus	

Features:

Query	365	TGTGTATATGATC-ATGTCGACTGCCTGTATATGATC-ATGTCGACTGCCCTGTGTGT	422
Sbjct	239159	TGTGTATATGATGTATATGTACTATGTGTATATGATGTATATCTACCG---TGTGTGT	239215
Query	423	ATATGATTCTCTAGTGACTCTAC---TGTGTATATGAT-CATAGAGATCTCTCTAC	479
Sbjct	239216	ATATGAT-----GTATATGTACCGTGTGTATATGATGCATA-----TGTACC	239259
Query	480	-TGTGTATATGAACGTGTGTATATGATCATTGTGTATATGAT-CATGTCGACTGCCT	537
Sbjct	239260	ATGTGTATATGA---TGTATATGTACTGTGTGTATATGATGTATATGTACTGTGT	239315
Query	538	GTGTATATGATCATGTCGACTGCCCTGTGTGTATATG	574
Sbjct	239316	GTGTATATGTATATGT---ACTG---TGTGTATATG	239347

Range 4: 239087 to 239300

Score	Expect	Identities	Gaps	Strand	Frame
62.6 bits(68)	8e-06()	170/246(69%)	36/246(14%)	Plus/Plus	

Features:

Query	365	TGTGTATATGATCATGTCGACTGCCTGTATATGATC-ATGTCGACTGCCCTGTGTGT	423		
Sbjct	239087	TGTGTATATGTATATGT---ACTATGTGTATATGATGTATATGTACTG---TGTGTGT	239141		
Query	424	TATGATTCTCTAGTGACTCTACTGTGTATATGATCATAGAGATCTCTCTACCTGTG	483		
Sbjct	239142	TATGTATATGTA-----CTA-TGTGTGTATATGATGT-----ATATGTA-CTA--TGTG	239186		
Query	484	TGTATATGAACTGTGTATATGATCAT-TGTGTATATGATC-ATGTCGACTGCCCTGTG	541		
Sbjct	239187	TGTATATGA---TGTATATCT-ACCGTGTGTATATGATGTATATGTACCGTGTGTG	239241		
Query	542	ATATGAT-CATGTCGACTGCCCTGTGTATATGATTCTCTAGTGACTCTACTGTGTG	600		
Sbjct	239242	ATATGATGCATATGTAC---CATGTGTGTATATGA-TGTATATGTACT---GTGTGTG	239294		
Query	601	TATGAT 606			
Sbjct	239295	TATGAT 239300			

Range 5: 239037 to 239253

Score	Expect	Identities	Gaps	Strand	Frame
55.4 bits(60)	0.001()	171/253(68%)	45/253(17%)	Plus/Plus	

Features:

Query	367	TGTATATGATC-ATGTCGACTGCCTGTGTATATGATC-ATGTCGACTGCCCTGTGTAT	424		
Sbjct	239037	TGTATATGATGTATATATACTGTATATGTATATGATGTATATGTACTG---TGTGTGT	239093		
Query	425	ATGATTCTCTAGTGACTCTACTGTGTATATGATCATAGAGATCTCTCTACCT-G	483		
Sbjct	239094	ATGTATATGTA-----CTA-TGTGTGTATATGATG-----TATATGTA-CTG	239137		
Query	484	TGTATATGAACTGTGTGTA-TATGATCATTGTGTATATGATC-ATGTCGACTGCCCTGTG	541		
Sbjct	239138	TGTATATGTA---TATGTA-CTG---TGTGTATATGATGTATATGTA-CTATGTGTG	239189		
Query	542	ATATGATC-ATGTCGACTGCCCTGTGTATATGATTCTCTAGTGACTCTAC---TGTG	598		
Sbjct	239190	ATATGATGTATATCTACCG---TGTGTGTATATGAT-----GTATATGTACCGTGTG	239240		
Query	599	TATATGAT-CATA 610			
Sbjct	239241	TATATGATGCATA 239253			

Range 6: 239211 to 239344

Score	Expect	Identities	Gaps	Strand	Frame
51.8 bits(56)	0.015()	101/144(70%)	13/144(9%)	Plus/Plus	

Features:

Query	365	TGTGTATATGATC-ATGTCGACTGCCTGTGTATATGAT-CATGTCGACTGCCCTGTGTG	422		
Sbjct	239211	TGTGTATATGATGTATATGTACCGTGTGTATATGATGCATATGTAC---CATGTGTG	239267		
Query	423	ATATGATTCTCTAGTGACTCTACTGTGTATATGATCATAGAGATCT-CTCTCTACCTG	481		
Sbjct	239268	ATATGAT-----GTATATGTACTGTGTGTAT-ATGATGTATATGTA-CTGTGTGTG	239320		
Query	482	TGTGTATATGAACTGTGTGATAT 505			
Sbjct	239321	TATGTATATGTACTGTGTGTAT 239344			

Range 7: 238929 to 239121

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	141/208(68%)	32/208(15%)	Plus/Plus	

Features:

Query 416	TGTGTGTATATGATTCTCTAGTGAECTACTGTGTATATGATCATAGAGAT-CTCTCT	474
Sbjct 238929	TGTGTGTATATGATG-TATATGTACTGT---GTGTGTATATGATG-TATATGTACTGTGT	238983
Query 475	CTACCTGTG-TGTATATGAACGTGTG-TATATGAT-CAT-----TGTGTATAT	520
Sbjct 238984	GTGTATATGATGTATATGTACTGTGTATATGATGTATATGTACTGTGTATATGATAT	239043
Query 521	GAT-CATGTCGACTGCCGTGTATATGAT-CATGTCGACTGCCGTGTGTATATGATTC	578
Sbjct 239044	GATGTATATATACTGTATATGTATATGATGTATATGTACTG---TGTGTATATGTATA	239100
Query 579	TCTAGTGACTCTACTGTGTGTATATGAT	606
Sbjct 239101	TGTA-----CTA-TGTGTGTATATGAT	239121

Range 8: 238914 to 239015

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	85/125(68%)	26/125(20%)	Plus/Plus	

Features:

Query 482	TGTGTATATGAAC--GTGTGTATATGATCATTGTGTATATGATCATGTCGACTGCCGT	539
Sbjct 238914	TGTATGTATGTACTATGTGTGTATATGA-----TGTATATG-----TACTGTGTGT	238959
Query 540	GTATATGAT-CATGTCGACTGCCGTGTGTATATGATTCTCTAGTGAECTACTGTGTG	598
Sbjct 238960	GTATATGATGTATATGTACTG---TGTGTGTATATGAT-----GTATATGACTGTGTG	239010
Query 599	TATAT 603	
Sbjct 239011	TATAT 239015	

Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Ntn4:tm1a(KOMP)Wtsi; transgenic

Sequence ID: [gb|JN947524.1|](#) Length: 38067 Number of Matches: 4

Range 1: 28954 to 29028

Score	Expect	Identities	Gaps	Strand	Frame
51.8 bits(56)	0.015()	60/76(79%)	5/76(6%)	Plus/Plus	

Features:

Query 482	TGTGTATATGAA-CTGTGTGTATATGATCATTGTGTATATGATCATGT-CGACTGCCGT	539
Sbjct 28954	TGTGTATATGAATGTGTGTATATGA-GTGTGTGTATATGAGCATGTGTATGAGTGT	29012
Query 540	G---TATATGATCATGT 553	
Sbjct 29013	GTATATATGAGCATGT 29028	

Range 2: 28876 to 28998

Score	Expect	Identities	Gaps	Strand	Frame
50.0 bits(54)	0.051()	95/132(72%)	11/132(8%)	Plus/Plus	

Features:

Query 480	TGTGTGTATATGAACCTGTGTATATGATCATTGTGTATATGATCATGTCGACTGCCGT	539
Sbjct 28876	TGTGTGTATATGAAC-ATGTGTGTATGA-GTGTGTGTATATGAACATGT---ATGAGTGT	28930
Query 540	GTATATGATCATGTCGA-CTGCCGTGTGTATATGATTCTCTAGTGAECTACTGTGT	597
Sbjct 28931	GTGTATGAGTGTGTGTATATG---AATGTGTATATGAATGTGT-GTGTATATGAGTGTGT	28986
Query 598	GTATATGATCAT 609	
Sbjct 28987	GTATATGAGCAT 28998	

Range 3: 28876 to 28980

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	81/110(74%)	8/110(7%)	Plus/Plus	

Features:

Query 416	TGTGTGTATATGATTCTCTAGTGAECTACTGTGTATATGATCATAGA-GA-TCTCTC	473
Sbjct 28876	TGTGTGTATATGAACATGT-GTGTATG-AGTGTGTGTATATGAACATGTATGAGTGTGT	28933
Query 474	TCTACCTGTGTGTATATGAACGTGTGTATATG-ATCATTGTGTATATGA 522	
Sbjct 28934	TATGAGTGTGTGTATATGAA---TGTGTATATGAATGTGTGTATATGA 28980	

Range 4: 28968 to 29008

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	38/43(88%)	2/43(4%)	Plus/Plus	

Features:

Query 480 TGTGTGTATATGAACGTGTGTATATGATCATTGTGTATATGA 522
Sbjct 28968 TGTGTGTATATGAG-TGTGTGTATATGAGCA-TGTGTGTATGA 29008

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

Sequence ID: **gb|AC137157.3|** Length: 187666 Number of Matches: 1

Range 1: 104837 to 104897

Score	Expect	Identities	Gaps	Strand	Frame
51.8 bits(56)	0.015()	53/64(83%)	4/64(6%)	Plus/Plus	

Features:

Query 850 CTCTACTGTGTGTAT-ATGATCATCTGTGTGTATATGATTCTCTAGTGACTCTACTGTGT 908
Sbjct 104837 CTCT-CTGTGTGTATTATGAATATCTGTGTATATGAATGTCT-GTGTGTGT-CTGTGT 104893

Query 909 GTAT 912
Sbjct 104894 GTAT 104897

Mus musculus strain 129S6/SvEvTac clone rp21-493n6 map 11a2, complete sequence

Sequence ID: **gb|AC005528.43|** Length: 199326 Number of Matches: 3

Range 1: 39192 to 39225

Score	Expect	Identities	Gaps	Strand	Frame
50.0 bits(54)	0.051()	32/34(94%)	1/34(2%)	Plus/Minus	

Features:

Query 273 TGTGTGTATATGAAC-TGTGTGTATATGATCATA 305
Sbjct 39225 TGTGTGTATATGAACATGTGTATATGAACATA 39192

Range 2: 39183 to 39225

Score	Expect	Identities	Gaps	Strand	Frame
48.2 bits(52)	0.18()	38/43(88%)	2/43(4%)	Plus/Minus	

Features:

Query 480 TGTGTGTATATGAAC-TGTGTGTATATGATCAT-TGTGTATAT 520
Sbjct 39225 TGTGTGTATATGAACATGTGTATATGAACATATATGTACAT 39183

Range 3: 39193 to 39225

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

Features:

Query 643 TGTGTGTATATGATCAT-TGTGTATATGATCAT 674
Sbjct 39225 TGTGTGTATATGAACATGTGTATATGAACAT 39193

Mus musculus BAC clone RP23-69N8 from chromosome 10, complete sequence

Sequence ID: **gb|AC122896.4|** Length: 232473 Number of Matches: 2

Range 1: 180114 to 180155

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

Features:

Query 480 TGTGTGTATATGAACGTGTGTATATGATCATTGTGTATATG 521
Sbjct 180114 TGTGTGTATATGATATGTGTATATGATATGTGTATGTG 180155

Range 2: 180114 to 180142

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

Features:

Query 273 TGTGTGTATATGAACGTGTGTATATGAT 301
Sbjct 180114 TGTGTGTATATGATATGTGTATATGAT 180142