

Basic Local Alignment Search Tool

NCBI/ [BLAST/ blastn suite/](#) Formatting Results - Y0UFFFF30015

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GTCA

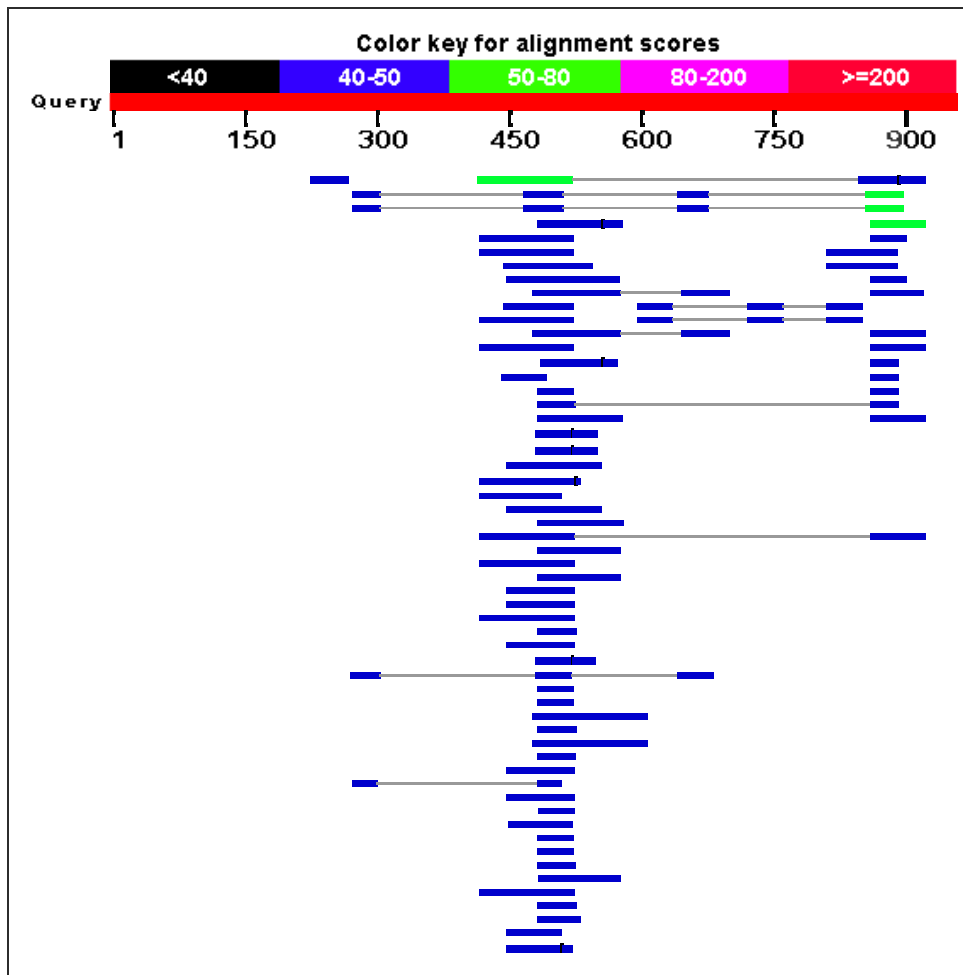
RID [Y0UFFFF30015](#) (Expires on 08-06 13:21 pm)

Query ID lc|22299
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 146 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Theileria orientalis strain Shintoku DNA, chromosome 4, complete genome	59.0	151	18%	1e-04	74%	AP011949.1
Mus musculus chromosome 6, clone RP24-548D19, complete sequence	51.8	190	15%	0.015	89%	AC120877.15
Mus musculus 6 BAC RP23-413D8 (Roswell Park Cancer Institute (C57BL/6J Female) Mouse BAC Library) complete sequence	51.8	190	15%	0.015	89%	AC159332.11
Pig DNA sequence from clone PigE-108A11 on chromosome 6, complete sequence	51.8	51.8	6%	0.015	81%	CR450381.1
Pig DNA sequence from clone CH242-86J23 on chromosome X, complete sequence	50.0	181	10%	0.051	80%	FP101971.13
Pan troglodytes BAC clone CH251-288H14 from chromosome 7, complete sequence	50.0	50.0	11%	0.051	74%	AC214786.5
Pan troglodytes BAC clone RP43-32E8 from chromosome 7, complete sequence	50.0	50.0	11%	0.051	74%	AC146225.2
Homo sapiens chromosome 8, clone RP11-466A10, complete sequence	50.0	50.0	10%	0.051	74%	AC106011.3
Homo sapiens BAC clone RP11-325I24 from 2, complete sequence	50.0	50.0	13%	0.051	72%	AC079256.5
Homo sapiens glypican 5 (GPC5), RefSeqGene on chromosome 13	48.2	92.7	16%	0.18	73%	NG_009370.1
Mus musculus chromosome 15, clone RP23-87G17, complete sequence	48.2	48.2	8%	0.18	75%	AC118038.15
Homo sapiens BAC clone RP11-719M18 from 4, complete sequence	48.2	48.2	11%	0.18	72%	AC019341.6
Human DNA sequence from clone RP11-93M14 on chromosome 13, complete sequence	48.2	92.7	16%	0.18	73%	AL157821.14
Homo sapiens 12 BAC RP11-291B21 (Roswell Park Cancer Institute Human BAC Library) complete sequence	48.2	48.2	11%	0.18	73%	AC068775.52
Mus musculus BAC clone RP23-50I19 from chromosome 13, complete sequence	48.2	135	9%	0.18	78%	AC162526.3
Mouse DNA sequence from clone RP24-260C8 on chromosome 11, complete sequence	48.2	48.2	5%	0.18	85%	BX000983.15
PREDICTED: Callithrix jacchus uncharacterized LOC100895454 (LOC100895454), mRNA	46.4	46.4	4%	0.62	86%	XM_003734947.1
Neospora caninum Liverpool complete genome, chromosome V	46.4	135	7%	0.62	88%	FR823386.1
Homo sapiens purinergic receptor P2Y, G-protein coupled, 8 (P2RY8), RefSeqGene on chromosome X and Y	46.4	46.4	10%	0.62	73%	NG_013252.1
Homo sapiens FOSMID clone ABC14-50188300J16 from chromosome 4, complete sequence	46.4	89.1	7%	0.62	77%	AC225697.1
Homo sapiens FOSMID clone ABC9-44049500F4 from chromosome 4, complete sequence	46.4	89.1	7%	0.62	77%	AC205795.3
Mouse DNA sequence from clone RP23-182F9 on chromosome 12, complete sequence	46.4	89.1	11%	0.62	72%	CR974423.21

Mus musculus chromosome 18, clone RP23-334D14, complete sequence	46.4	92.7	11%	0.62	72%	AC102588.7
Mus musculus chromosome 9 clone RP24-121D5, complete sequence	46.4	46.4	9%	0.62	73%	AC121870.2
Mus musculus chromosome 12, clone RP23-38N23, complete sequence	46.4	89.1	11%	0.62	72%	AC123618.26
Pan troglodytes BAC clone CH251-230I19 from Y, complete sequence	46.4	46.4	4%	0.62	88%	AC147147.2
Mus musculus BAC clone RP23-469P20 from chromosome 16, complete sequence	46.4	46.4	8%	0.62	75%	AC154534.2
Human DNA sequence from clone RP11-261P4 on chromosome X, complete sequence	46.4	46.4	10%	0.62	73%	AL683870.15
Human DNA sequence from clone RP11-450B15 on chromosome 1, complete sequence	46.4	89.1	17%	0.62	72%	AL359732.12
Homo sapiens chromosome 11, clone RP11-46P12, complete sequence	46.4	46.4	9%	0.62	73%	AC100770.2
Homo sapiens, clone RP11-13N12, complete sequence	46.4	46.4	11%	0.62	72%	AC011586.9
Human DNA sequence from clone RP11-49A12 on chromosome 6, complete sequence	46.4	46.4	9%	0.62	74%	AL596179.3
Mus musculus BAC clone RP24-302G10 from chromosome 16, complete sequence	46.4	46.4	8%	0.62	75%	AC154678.2
Pan troglodytes chromosome Y clone:PTB-548J12, complete sequences	46.4	46.4	4%	0.62	88%	BS000620.1
Homo sapiens chromosome 5 clone CTC-340I23, complete sequence	46.4	46.4	7%	0.62	74%	AC025434.6
Homo sapiens chromosome 5 clone CTB-83D3, complete sequence	46.4	46.4	7%	0.62	74%	AC011414.4
Homo sapiens chromosome 19 clone CTB-167G5, complete sequence	46.4	46.4	11%	0.62	72%	AC011487.5
Human chromosome 14 DNA sequence BAC R-62H20 of library RPCI-11 from chromosome 14 of Homo sapiens (Human), complete sequence	46.4	46.4	6%	0.62	80%	AL133299.4
Rattus norvegicus DNA, BAC clone: RNB1-342B21, strain: F344/Stm, complete sequence	44.6	44.6	4%	2.2	82%	AP012454.1
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Acat2:tm 1a(KOMP)Wtsi; transgenic	44.6	44.6	7%	2.2	75%	JN959926.1
Homo sapiens FOSMID clone COR2A-DD0002THMNU_K15 from chromosome 4, complete sequence	44.6	87.3	7%	2.2	77%	AC245844.1
Leptospira interrogans serovar Lai str. 56601 chromosome I, complete sequence	44.6	130	11%	2.2	85%	AE010300.2
Homo sapiens phosphatidylinositol-specific phospholipase C, X domain containing 1 (PLCXD1), RefSeqGene on chromosome X and Y	44.6	44.6	4%	2.2	85%	NG_016868.1
Homo sapiens phosphatidylinositol-specific phospholipase C, X domain containing 1 (PLCXD1), transcript variant 1, mRNA	44.6	44.6	4%	2.2	85%	NM_018390.3
Homo sapiens BAC clone RP11-458H19 from chromosome x, complete sequence	44.6	44.6	13%	2.2	69%	AC233725.3
Homo sapiens RAS p21 protein activator (GTPase activating protein) 1 (RASA1), RefSeqGene on chromosome 5	44.6	89.1	4%	2.2	82%	NG_011650.1
Homo sapiens BAC clone RP11-489H20						

from chromosome x, complete sequence	44.6	44.6	13%	2.2	69%	AC233291.3
Pig DNA sequence from clone CH242-240L11 on chromosome 13, complete sequence	44.6	89.1	4%	2.2	83%	CU468995.15
Pan troglodytes BAC clone CH251-376M16 from chromosome 19, complete sequence	44.6	44.6	7%	2.2	75%	AC197461.2
Zebrafish DNA sequence from clone DKEY-15B23 in linkage group 7, complete sequence	44.6	89.1	5%	2.2	96%	CR388156.7
Mus musculus chromosome 1, clone RP24-72P6, complete sequence	44.6	133	12%	2.2	88%	AC115968.10
Mus musculus strain C57BL/6J clone rp23-387d2 map 17, complete sequence	44.6	44.6	7%	2.2	75%	AC127172.13
Homo sapiens 3 BAC RP11-379K17 (Roswell Park Cancer Institute Human BAC Library) complete sequence	44.6	44.6	4%	2.2	88%	AC008040.7
Mus musculus 6 BAC RP24-339D12 (Roswell Park Cancer Institute (C57BL/6J Male) Mouse BAC Library) complete sequence	44.6	44.6	7%	2.2	76%	AC156951.7
Mus musculus chromosome 1, clone RP24-192L21, complete sequence	44.6	133	12%	2.2	88%	AC119212.15
Human DNA sequence from clone WI2-2074F5 on chromosome X, complete sequence	44.6	44.6	4%	2.2	85%	BX537334.4
Human DNA sequence from clone LL0XNC01-136G2 on chromosome X, complete sequence	44.6	44.6	4%	2.2	85%	BX000483.7
Human DNA sequence from clone RP13-455B8 on chromosome 1, complete sequence	44.6	44.6	4%	2.2	83%	AL929099.5
Homo sapiens chromosome 5 clone CTC-254B4, complete sequence	44.6	44.6	9%	2.2	72%	AC022103.5
Human DNA sequence from clone RP11-34D15 on chromosome 10, complete sequence	44.6	44.6	11%	2.2	71%	AL139819.8
Homo sapiens chromosome 5 clone CTD-2165G19, complete sequence	44.6	89.1	4%	2.2	82%	AC010410.8
Homo sapiens 12 BAC RP11-753B7 (Roswell Park Cancer Institute Human BAC Library) complete sequence	44.6	44.6	6%	2.2	79%	AC069262.24
Human DNA sequence from clone RP11-249P15 on chromosome 6, complete sequence	44.6	44.6	5%	2.2	81%	AL589646.4
Human DNA sequence from clone RP11-14H3 on chromosome 6, complete sequence	44.6	44.6	6%	2.2	78%	AL138824.19
Human DNA sequence from clone RP5-944H6 on chromosome 1p22.3-31.2, complete sequence	44.6	89.1	7%	2.2	77%	AL136324.6
Human DNA sequence from clone RP5-961O8 on chromosome Xq23-24, complete sequence	44.6	44.6	13%	2.2	69%	AL121879.14
Human DNA sequence from clone RP4-595K12 on chromosome 1p31.2-31.3, complete sequence	44.6	44.6	7%	2.2	73%	AL096829.17
Homo sapiens BAC clone RP11-11N6 from 4, complete sequence	44.6	87.3	7%	2.2	77%	AC093729.2
Homo sapiens BAC clone RP11-592A2 from 2, complete sequence	44.6	44.6	7%	2.2	74%	AC068288.6
Homo sapiens chromosome 5 clone CTD-2064K14, complete sequence	44.6	89.1	4%	2.2	82%	AC035142.4
Homo sapiens BAC clone RP11-45F23 from 4, complete sequence	44.6	221	13%	2.2	79%	AC020698.4
Homo sapiens Chromosome 22q11.2						

Cosmid Clone 79h12 In DGCR Region, complete sequence	44.6	44.6	7%	2.2	74%	AC004463.2
Mouse DNA sequence from clone RP23-351C7 on chromosome 17, complete sequence	44.6	44.6	7%	2.2	75%	AL589878.12
Homo sapiens clone DJ378P09, complete sequence	44.6	44.6	6%	2.2	78%	AC005002.2
Homo sapiens chromosome 17, clone hRPK.214_C_8, complete sequence	44.6	44.6	7%	2.2	75%	AC005803.1
Homo sapiens ceroid-lipofuscinosis, neuronal 6, late infantile, variant (CLN6), RefSeqGene on chromosome 15	42.8	42.8	10%	7.6	75%	NG_008764.2
PREDICTED: Leptonychotes weddellii LEM domain containing 3 (LEMD3), transcript variant X2, mRNA	42.8	85.5	6%	7.6	93%	XM_006731924.1
PREDICTED: Leptonychotes weddellii LEM domain containing 3 (LEMD3), transcript variant X1, mRNA	42.8	85.5	6%	7.6	93%	XM_006731923.1
Pandoravirus dulcis, complete genome	42.8	42.8	4%	7.6	84%	KC977570.1
PREDICTED: Odobenus rosmarus divergens LEM domain containing 3 (LEMD3), mRNA	42.8	85.5	6%	7.6	93%	XM_004415624.1
Mus musculus targeted non-conditional, lacZ-tagged mutant allele Magi1:tm1e(KOMP)Wtsi; transgenic	42.8	42.8	5%	7.6	77%	JN963555.1
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Magi1:tm1a(KOMP)Wtsi; transgenic	42.8	42.8	5%	7.6	77%	JN961060.1
Mus musculus targeted deletion, lacZ-tagged mutant allele C330006K01Rik:tm1(KOMP)Wtsi; transgenic	42.8	85.5	5%	7.6	93%	JN958234.1
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Mpp2:tm1a(KOMP)Wtsi; transgenic	42.8	42.8	6%	7.6	79%	JN947522.1
Rattus norvegicus Y Chr BAC RNECO-248P22 (Amplicon Express Rat SHR-Akr (EcoR1 Digest) BAC library) complete sequence	42.8	42.8	4%	7.6	84%	AC244840.5
Homo sapiens BAC clone CH17-129M10 from chromosome unknown, complete sequence	42.8	42.8	4%	7.6	86%	AC243569.3
Rattus norvegicus Y Chr BAC RNAEX-97M06 (Amplicon Express Rat SHR-Akr BAC library) complete sequence	42.8	42.8	4%	7.6	84%	AC243502.6
Homo sapiens BAC clone CH17-55D9 from chromosome 1, complete sequence	42.8	42.8	7%	7.6	75%	AC244033.1
Rattus norvegicus Y Chr BAC RNAEX-32P21 (Amplicon Express Rat SHR-Akr BAC library) complete sequence	42.8	42.8	4%	7.6	84%	AC241916.2
Homo sapiens FRAS1 related extracellular matrix 1 (FREM1), RefSeqGene on chromosome 9	42.8	42.8	11%	7.6	70%	NG_017005.2
Homo sapiens thyroglobulin (TG), RefSeqGene on chromosome 8	42.8	42.8	6%	7.6	76%	NG_015832.1
Homo sapiens nuclear receptor subfamily 3, group C, member 2 (NR3C2), RefSeqGene on chromosome 4	42.8	42.8	3%	7.6	90%	NG_013350.1
Homo sapiens FOSMID clone ABC8-2127640I11 from chromosome unknown, complete sequence	42.8	42.8	4%	7.6	81%	AC235001.2
Homo sapiens isolate NR3C2-VI-T mineralocorticoid (NR3C2) gene, complete cds, alternatively spliced	42.8	42.8	3%	7.6	90%	FJ515829.1
Homo sapiens nuclear receptor subfamily 3, group C, member 2						

(NR3C2) gene, complete cds, alternatively spliced	42.8	42.8	3%	7.6	90%	EU326312.1
Pongo abelii BAC clone CH276-161K21 from chromosome 21, complete sequence	42.8	42.8	7%	7.6	74%	AC200441.3
Rhesus Macaque BAC CH250-125J6 () complete sequence	42.8	42.8	7%	7.6	74%	AC198680.6
Macaca mulatta chromosome UNK clone CH250-87H12, complete sequence	42.8	42.8	4%	7.6	84%	AC188299.1
Pongo abelii chromosome UNK clone CH276-85H12, complete sequence	42.8	85.5	5%	7.6	96%	AC188114.1
Mouse DNA sequence from clone RP23-142L17 on chromosome 13, complete sequence	42.8	42.8	6%	7.6	77%	CT030176.18

Alignments

Theileria orientalis strain Shintoku DNA, chromosome 4, complete genome

Sequence ID: **dbj|AP011949.1** Length: 2019511 Number of Matches: 3

Range 1: 625919 to 626010

Score	Expect	Identities	Gaps	Strand	Frame
59.0 bits(64)	1e-04()	79/107(74%)	16/107(14%)	Plus/Plus	
Features:					
Query 415		GATATATACACATCAAGAGACTATCGAGACGATATATACACATCAGCACTCTCAGAGAGA			474
Sbjct 625919		GATATATACACATCAACAGA-TATATACA-GATATATACAGAT-----ACAAACATA			625968
Query 475		GACGGATATATACACATCCGATATATACACATCAGCA-ATATACACA			520
Sbjct 625969		GACAGATATATACA-----GATACATACACATCAACAGATATACACA			626010

Range 2: 625908 to 625949

Score	Expect	Identities	Gaps	Strand	Frame
50.0 bits(54)	0.051()	39/44(89%)	2/44(4%)	Plus/Plus	
Features:					
Query 842		AGACTATCGAGACGATATATACACATCAGCAGATATATACACAT			885
Sbjct 625908		AGAC-ATCCAGA-GATATATACACATCAACAGATATATACAGAT			625949

Range 3: 625907 to 625959

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	44/55(80%)	2/55(3%)	Plus/Plus	
Features:					
Query 861		TACACATCAGCAGATATATACACATCAAGAGACTATCGAGACGATATATACACAT			915
Sbjct 625907		TAGACATCCAGAGATATATACACATCAACAGA-TATATACA-GATATATACAGAT			625959

Mus musculus chromosome 6, clone RP24-548D19, complete sequence

Sequence ID: **gb|AC120877.15** Length: 228206 Number of Matches: 4

Range 1: 158800 to 158841

Score	Expect	Identities	Gaps	Strand	Frame
51.8 bits(56)	0.015()	39/44(89%)	4/44(9%)	Plus/Minus	
Features:					
Query 851		AGACG--ATATATACACATCAGCAGATATATACACATCAAGAGA			892
Sbjct 158841		AGACGGAATATATACACATCAG--GATATATACACATCAGGAGA			158800

Range 2: 158804 to 158848

Score	Expect	Identities	Gaps	Strand	Frame
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50.0 bits(54)	0.051()	41/46(89%)	3/46(6%)	Plus/Minus
Features:				
Query	466	TCAGAGAGAGACGGA-TATATACACATCCG-ATATATACACATCAG	509	
Sbjct	158848	TCAAAGA-AGACGGAATATATACACATCAGGATATATACACATCAG	158804	

Range 3: 158804 to 158841

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	34/38(89%)	3/38(7%)	Plus/Minus	
Features:					
Query	638	AGACG--ATATATACACATCAGCA-ATATACACATCAG	672		
Sbjct	158841	AGACGGAATATATACACATCAGGATATATACACATCAG	158804		

Range 4: 158804 to 158834

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	29/31(94%)	1/31(3%)	Plus/Minus	
Features:					
Query	273	ATATATACACATCCG-ATATATACACATCAG	302		
Sbjct	158834	ATATATACACATCAGGATATATACACATCAG	158804		

Mus musculus 6 BAC RP23-413D8 (Roswell Park Cancer Institute (C57BL/6J Female) Mouse BAC Library) complete sequence
Sequence ID: **gb|AC159332.11|** Length: 208808 Number of Matches: 4
Range 1: 205396 to 205437

Score	Expect	Identities	Gaps	Strand	Frame
51.8 bits(56)	0.015()	39/44(89%)	4/44(9%)	Plus/Plus	
Features:					
Query	851	AGACG--ATATATACACATCAGCAGATATATACACATCAAGAGA	892		
Sbjct	205396	AGACGGAATATATACACATCAG--GATATATACACATCAGGAGA	205437		

Range 2: 205389 to 205433

Score	Expect	Identities	Gaps	Strand	Frame
50.0 bits(54)	0.051()	41/46(89%)	3/46(6%)	Plus/Plus	
Features:					
Query	466	TCAGAGAGAGACGGA-TATATACACATCCG-ATATATACACATCAG	509		
Sbjct	205389	TCAAAGA-AGACGGAATATATACACATCAGGATATATACACATCAG	205433		

Range 3: 205396 to 205433

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	34/38(89%)	3/38(7%)	Plus/Plus	
Features:					
Query	638	AGACG--ATATATACACATCAGCA-ATATACACATCAG	672		
Sbjct	205396	AGACGGAATATATACACATCAGGATATATACACATCAG	205433		

Range 4: 205403 to 205433

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	29/31(94%)	1/31(3%)	Plus/Plus	
Features:					
Query	273	ATATATACACATCCG-ATATATACACATCAG	302		
Sbjct	205403	ATATATACACATCAGGATATATACACATCAG	205433		

Pig DNA sequence from clone PigE-108A11 on chromosome 6, complete sequence

Sequence ID: **emb|CR450381.1|** Length: 123687 Number of Matches: 1

Range 1: 117510 to 117570

Score	Expect	Identities	Gaps	Strand	Frame	
51.8 bits(56)	0.015()	50/62(81%)	2/62(3%)	Plus/Plus		
Features:						
Query	855	GATATATACACATCAGCAGATATATACACATCAAGAGACTATCGAGAC-GATATATACAC				913
Sbjct	117510	GATATATACACATATACAGATATATACACATATATAGA-TATACACCCAGATATATACAC				117568
Query	914	AT	915			
Sbjct	117569	AT	117570			

Pig DNA sequence from clone CH242-86J23 on chromosome X, complete sequence

Sequence ID: **emb|FP101971.13|** Length: 183346 Number of Matches: 4

Range 1: 67229 to 67295

Score	Expect	Identities	Gaps	Strand	Frame	
50.0 bits(54)	0.051()	59/74(80%)	7/74(9%)	Plus/Minus		
Features:						
Query	480	ATATATACACATCCGATATATACACATCAGCAATATACACATCAGCATAGTCGATGGATA				539
Sbjct	67295	ATATATACACATCACATATATATACATCATATATATATACA-CATCAT-GT--AT--ATA				67242
Query	540	TACACATCAGCATA	553			
Sbjct	67241	TACACATCA-CATA	67229			

Range 2: 67218 to 67263

Score	Expect	Identities	Gaps	Strand	Frame	
44.6 bits(48)	2.2()	38/46(83%)	2/46(4%)	Plus/Minus		
Features:						
Query	480	ATATATACACATCCG--ATATATACACATCAGCAATATACACATCA				523
Sbjct	67263	ATATATACACATCATGTATATATACACATCAGATATATATACATCA				67218

Range 3: 67267 to 67312

Score	Expect	Identities	Gaps	Strand	Frame	
44.6 bits(48)	2.2()	38/46(83%)	2/46(4%)	Plus/Minus		
Features:						
Query	480	ATATATACACATC--CGATATATACACATCAGCAATATACACATCA				523
Sbjct	67312	ATATATACACATCATATATATATACACATCAGATATATATACATCA				67267

Range 4: 67250 to 67344

Score	Expect	Identities	Gaps	Strand	Frame	
42.8 bits(46)	7.6()	74/102(73%)	12/102(11%)	Plus/Minus		
Features:						
Query	480	ATATATACACATCCGATATATACACATCAGCAATATACACATCAGCATAGTCGATGGATA				539
Sbjct	67344	ATATACACACATCATATATATATACATCATATATATATACA-CATCATAT---AT--ATA				67291
Query	540	TACACATCAGCATAG---TCGATGGGATATAT--ACACATCA				576
Sbjct	67290	TACACATCA-CATATATATACATCATATATATATACACATCA				67250