

Genomes

Genome Browser

Tools

Mirrors

Downloads

My Data

About Us

Help

Human BLAT Search

BLAT Search Genome

Genome:

Human

 Assembly:

May 2004 (NCBI35/hg17)

Output:

Output type:

hyperlink

Blat

Table Browser

Variant Annotation Integrator

Gene Sorter

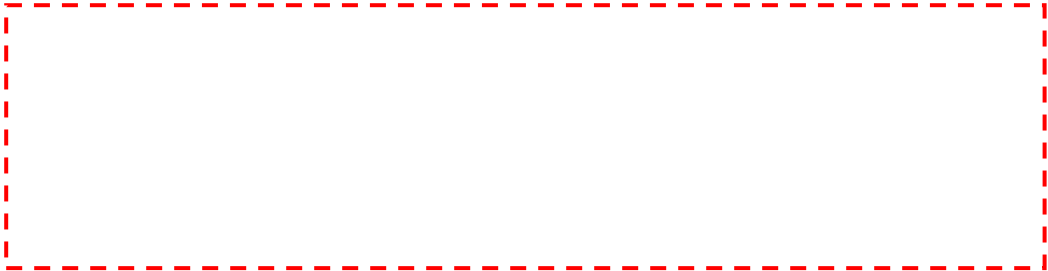
Genome Graphs

In-Silico PCR

LiftOver

VisiGene

Other Utilities



BLAT Search Results

ACTIONS	QUERY	SCORE	START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
browser details	hg17_dna	533	1	873	873	94.8%	10	+	81315688	81316242	555
browser details	hg17_dna	287	300	604	873	97.1%	5	-	101791646	101791950	305
browser details	hg17_dna	286	282	594	873	96.5%	15	+	83651541	83651862	322
browser details	hg17_dna	281	302	600	873	97.0%	7	-	132943638	132943936	299
browser details	hg17_dna	281	299	602	873	96.4%	4	-	42153003	42153307	305
browser details	hg17_dna	279	289	602	873	95.2%	6	+	49946897	49947210	314
browser details	hg17_dna	277	284	602	873	93.7%	9	+	125798716	125799038	323
browser details	hg17_dna	277	303	598	873	97.0%	5	+	155209819	155210131	313

v.

Genome: Chimp Assembly: Feb. 2011 (CSAC 2.1.4/panTro4) Query type: BLAT's guess Sort output: query,score Output type: hyperlink

>hg17_dna range=chr10:83728344-83729216 5'pad=0 3'pad=0 strand=+
repeatMasking=none
AAGAAACAAATAATAGGAAGATAAAGTTAGGTATTGTCATCAGAGCATTAA
ACACAGTGATCTTATTTTCGTAAACTCTTAATATCATATATATATATT
TGCATCTTTCTTTTCTTTCTTTTGTGTTTATAGAGATAGGGTCTTGCTGT
GTTGCCCTAGGTTTGTCTCAAAGTCTGGCCTCAAAGTATCCTCTTGCCCTC
AGTCTCCAAAAACATTGGGATTATAGGTATGAGCCACCATGCTGGCCCA
GCATCTTATGTTTGTAGCATCTAGCCATAATGTATTTTTAAAAATTTCC
TGGCCGGGCGTGGTGGCTCATGCCTGTAATCCAGCACCTTGGGAGGCCG
AGGTGGGCGGATCACAAGGTCAAGAGATCAAGACCATCCTGGCCAAACATG
ATGAAACCCCGTCTCTATTAAAAAGTACAAAAATTAGCTGGGCGTAGTGGC
GCACGCCCTGTAGTCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTT
GAACCTGGGAGGCAGAGGTTGCACTGAGCCGGGATTGTGCCACTGCACCT
CAGCCTGGCGCAGAGGCGGGACTCCGCTCTCAAAAAAATTTTTAAAAA

submit I'm feeling lucky clear

vi.

vii.

Alignment of hg17_dna

Alignment of hg17_dna and chr10:81315688-81316242

[hg17_dna](#)
[Chimp: chr10](#)
[Block1](#)
[together](#)

Click on links in the frame to the left to navigate through the alignment. Matching bases in cDNA

cDNA hg17_dna

AAGAAACAAA	TAATAGGAAG	ATAAAGTTAG	GTATTGTCAT	CAGAGCATTAA	50
ACACAGTGAT	CTTATTTTCG	TAAACTCTTA	ATATCATATA	TATATATATT	100
TGCATCTTTC	TTTTTCTTTT	CTTTCTTTT	TAGAGATAGG	GTCTTGCTGT	150
GTGCGCTAGG	TTTGTCTCAA	ACTGCTGGCC	TCAAGTGATC	CTCTTGCCCTC	200
AGTCTCCAAA	AACATTGGGA	TTATAGGTAT	GAGCCACCAT	GCGTGGCCCA	250
GCATCTTATG	TTTTGTAGCA	TCTAGCCATA	ATGTATTTTT	AAAAATTTTC	300
TGGCGGGGGG	TGGTGGCTCA	TGCCTGTAAT	CCAGCACCTT	TGGGAGGCCG	350
AGGTGGGCGG	ATCACAAGGT	CAAGAGATCA	AGACCATCCT	GGCCAAACATG	400
ATGAAACCCG	GTCTCTATT	AAAAAGTAC	AAAAATTAG	CTGGGCGTAG	450
GCACGCCCTG	TAGTCCAGCT	ACTTGGGAGG	CTGAGGCAGG	AGAATCGCTT	500
GAACCTGGGA	GCAGGTTTGC	AGTCTGAGCC	GGGATTGTGC	CAGTGCACCT	550
CAGCCTGGCG	CAGAGGTTGC	AGTCTGAGCC	GGGATTGTGC	CAGTGCACCT	600
AAAAATTTTC	TTTTGTAGCA	TCTAGCCATA	ATGTATTTTT	AAAAATTTTC	650
ATGTTATCTC	TGATTTCTCT	CACAGAGTCT	CTATGGGAAA	TATTTGTAGG	700
GTTATGGCTT	CCACCTTAAC	AATAATATAA	CATAAAAAGA	AATTCTAATA	750
TCTTGCTCAT	ATCTAATGGG	AGCATTTTTG	GGAGGCATTG	TGCACACATT	800
GCTAGAGAGC	TATGAAGGAA	CTGTTTCAAA	TGAAGAGAAA	TGCAAGGCTA	850
GACAGTATGA	AATGTATCTT	GGT			

viii.

ix.

>Human cacagctctgacgttgggggactgggacccctcttccagctgccgtgttttggcaggaactctgagaatgcttgaactaaaaactggcattttggatctTTACGTAGTGGTATTTCOAAGTAAGAGGAATAGAGCATACTTTATTTAACAACTTTG.
>Chimp cacagctctgacgttgggggactgggacccctcttccagctgccgtgttttggcaggaactctgagaatgcttgaactaaaaactggcattttggatctTTATGTAGTGGTATTTCOAAGTAAGAGGAATAGAGCATACTTTATTTAACAACTTTG.
>Gorilla cacagctctgacgttgggggactgggacccctcttccagctgccgtgttttggcaggaactctgagaatgcttgaactaaaaactggcattttggatctTTATGTAGTGGTATTTCOAAGTAAGAGGAATAGAGCATACTTTATTTAACAACTTTG.
>Orangutan cacagctctgacgttgggggactgggacccctcttccagctgccgtgttttggcaggaactctgagaatgcttgaactaaaaactggcattttggatctTTATGTAGTGGTATTTCOAAGTAAGAGGAATAGAGCATACTTTATTTAACAACTTTG.
>Gibbon cacagctctgacgttgggggactgggacccctcttccagctgccgtgttttggcaggaactctgagaatgcttgaactaaaaactggcattttggatctTTATGTAGTGGTATTTCOAAGTAAGAGGAATAGAGCATACTTTATTTAACAACTTTG.
>Rhesus gctctgacgtctgggagactgggacccctcttccagctgccgtgttttggcaggaactctgagaatgcttgaactaaaaactggcattttggatctTTATGTAGTGGTATTTCOAAGTAAGAGGAATAGAGCATACTTTATTTAACAACTTTGATG

Figure S2. Retrieve similar DNA sequence using BLAT.

Basic Options

or

Sequence:

Search Engine: ☒ abblast ☐ rmbblast ☐ hmmer ☐ cross_match

Speed/Sensitivity: ☐ rush ☐ quick ☐ default ☒ slow

DNA source: Human

Return Format: ☒ html ☐ tar file

Return Method: ☒ html ☐ email Your email address

Results

Right-click and select "Save As" to save results to your computer or click on the link to view the file in the browser.

Annotation File: [EM2icqpload5_1372728873.out.html](#) (NEW XHTML Format)

[EM2icqpload5_1372728873.out.txt](#) (Text File Format)

Masked File: [EM2icqpload5_1372728873.masked](#)

Alignment File: [EM2icqpload5_1372728873.aln](#)

SW	perc	perc	perc	query	position	in	query	matching	repeat	position	in	repeat	
score	div.	del.	ins.	sequence	begin	end	(left)	repeat	class/family	begin	end	(left)	ID
551	26.1	8.1	3.2	Chimp	17	226	(844)	+	MER115	DNA/hAT-Tip100	450	669	(24) 1
17	18.5	0.0	0.0	Chimp	802	832	(238)	+	A-rich	Low_complexity	1	31	(0) 2
17	12.1	2.4	7.0	Chimp	959	1000	(70)	+	GA-rich	Low_complexity	1	43	(0) 3
575	26.1	9.7	1.3	Gibbon	32	248	(821)	+	MER115	DNA/hAT-Tip100	459	693	(0) 4
17	18.5	0.0	0.0	Gibbon	801	831	(238)	+	A-rich	Low_complexity	1	31	(0) 5
17	12.1	2.4	7.0	Gibbon	958	999	(70)	+	GA-rich	Low_complexity	1	43	(0) 6
564	27.5	8.2	2.9	Gorila	17	248	(822)	+	MER115	DNA/hAT-Tip100	450	693	(0) 7
17	18.5	0.0	0.0	Gorila	802	832	(238)	+	A-rich	Low_complexity	1	31	(0) 8
15	12.8	2.5	7.3	Gorila	959	998	(72)	+	GA-rich	Low_complexity	1	41	(0) 9
542	28.4	8.2	2.9	Human	17	248	(822)	+	MER115	DNA/hAT-Tip100	450	693	(0) 10
17	18.5	0.0	0.0	Human	802	832	(238)	+	A-rich	Low_complexity	1	31	(0) 11
15	12.8	2.5	7.3	Human	959	998	(72)	+	GA-rich	Low_complexity	1	41	(0) 12
597	27.8	7.8	2.5	Orangutan	17	248	(814)	+	MER115	DNA/hAT-Tip100	450	693	(0) 13
17	14.6	2.3	6.7	Orangutan	951	994	(68)	+	GA-rich	Low_complexity	1	45	(0) 14
609	24.2	10.2	1.4	Rhesus	28	232	(898)	+	MER115	DNA/hAT-Tip100	459	681	(12) 15

Figure S3. TE identification using RepeatMasker.

Sequence source:

Force translated search: ☐

Search for identity: ☐

Report simple repeats: ☐

Mask pseudogenes: ☐

Enter query file name:
(Up to 2MB; IC-Stanford, FASTA, GENBANK, EMBL formats are supported)

OR

Paste query sequences here:
(Up to 2MB; IC-Stanford, FASTA, GENBANK, EMBL formats are supported)

```

cacagctctgacgttgggggactgggcacccctctccagctgccgtgttttggcaggaactctgag
aatgcttgaacttaaaactggcattttggatctTTAtGTAGTGGTATTTCCAAGTAAAGAGGAATAGA
GCATACTTTATTTAAACAACCTTTGATGTCCTGACTTACTACTTTTAAACACTAAGATTTATGTGGGCT
TCCATTGTTACTCTTACCTCAGGCCACAGAtGTCATAGAAGAGCTTGGAAAAAGTTAAATTCTTGGG
GAGAATAGAATAGAATCTAAAAGAGGGTGATTTTGGACTCCAGCATCTCTCAGGTTTCTGTTTACCCA
CCTGCACCTTCTCTTCTGGTTCTGAGaCAGGTGCTTATCTCTTTGGAGATGTGCTGAGGCAGAATCA

```



Figure S4. TE identification using Censor