Mining Genomic Sequence Data

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Current Topics in Genome Analysis
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Accessing the public genome sequence data

UCSC's Genome Browser ("Golden Path")
http://genome.ucsc.edu

NCBI's Map Viewer
http://www.ncbi.nlm.nih.gov/mapview/

Ensembl
http://www.ensembl.org

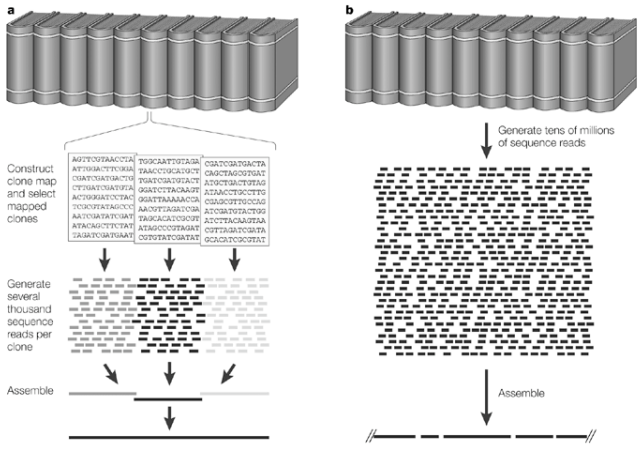
Types of data integrated in genome browsers

- Same starting material for all genome browsers: genomic sequence
- Annotations calculated independently by each genome browser
  - Genes
    - RefSeq mRNAs (non-redundant)
    - GenBank mRNAs (redundant)
    - ESTs
    - Gene predictions
  - SNPs
  - Homologous sequences from other organisms
  - STSs

Overview of genome sequencing strategies

Clone-by-clone shotgun sequencing

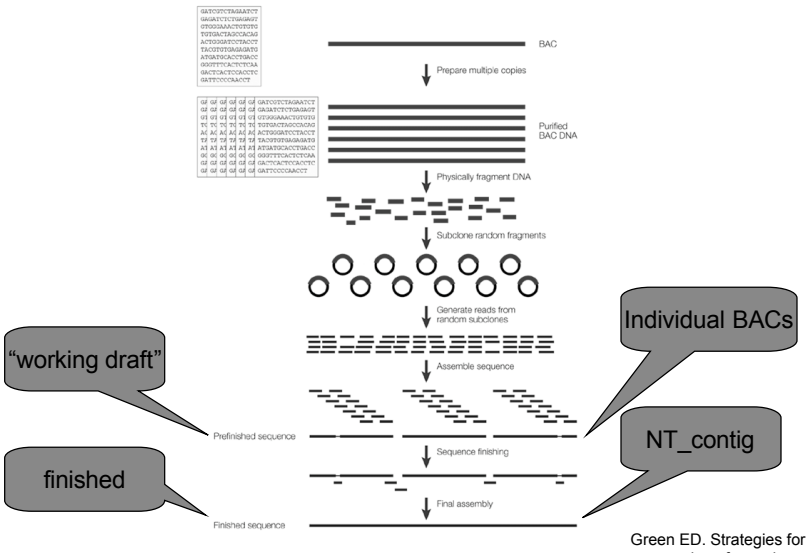
Whole-genome shotgun sequencing



Nature Reviews | Genetics

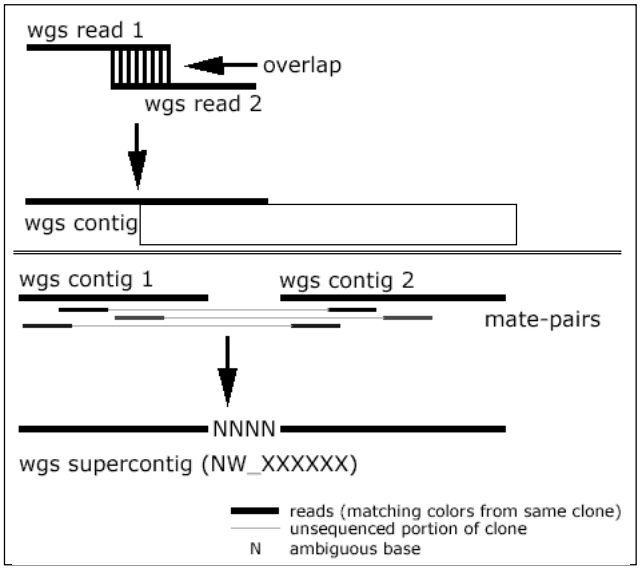
Green ED. Strategies for the systematic sequencing of complex genomes. Nat Rev Genet. 2001. 2:573-83.

Genome assembly: Clone-by-clone shotgun



Green ED. Strategies for the systematic sequencing of complex genomes. Nat Rev Genet. 2001. 2:573-83.

Genome assembly: Whole genome shotgun (WGS)



http://www.ncbi.nlm.nih.gov/genome/seq/NCBIContigInfo.html

Genome Sequence Assemblies

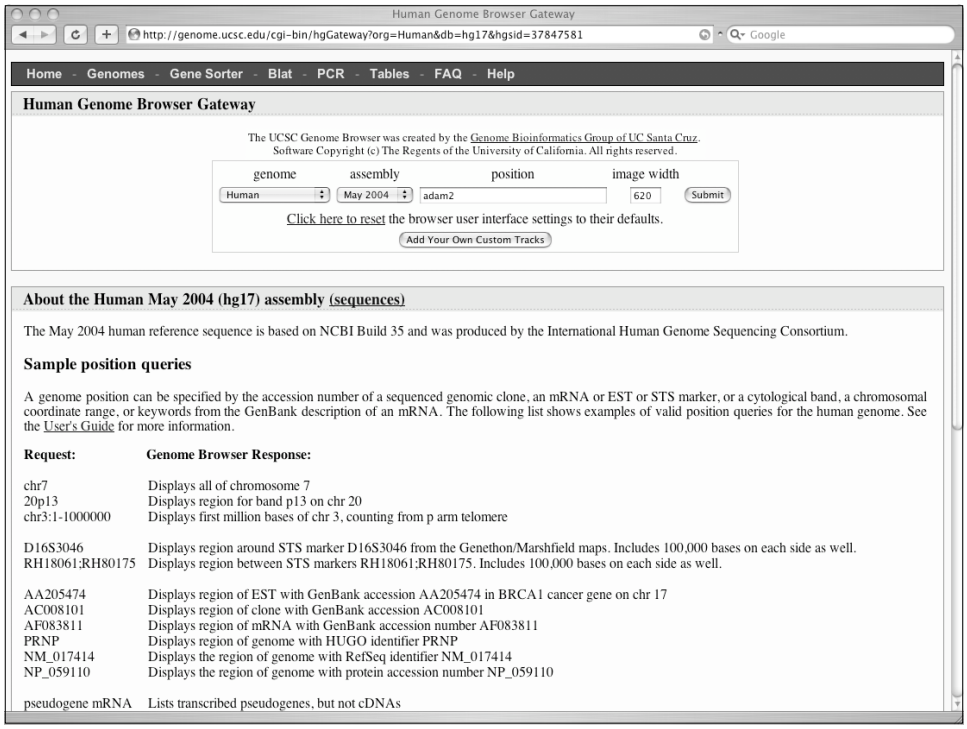
- Complex algorithms needed to incorporate all sequence data
- Assemblies updated periodically as new sequence becomes available
  - Mouse and human genomes assembled by NCBI
  - Other genomes assembled by sequencing centers or consortia
- UCSC is usually the first to display new assemblies, followed by NCBI and then Ensembl
  - "Pre-release" assemblies and annotations available at
    - UCSC: *http://genome-test.cse.ucsc.edu/*
    - pre!Ensembl: *http://pre.ensembl.org/*
  - UCSC provides access to older genome assemblies and annotations; NCBI and Ensembl do not
- IF YOU ARE COMPARING DATA FROM DIFFERENT GENOME BROWSERS, MAKE SURE YOU ARE LOOKING AT THE SAME VERSION OF THE ASSEMBLY

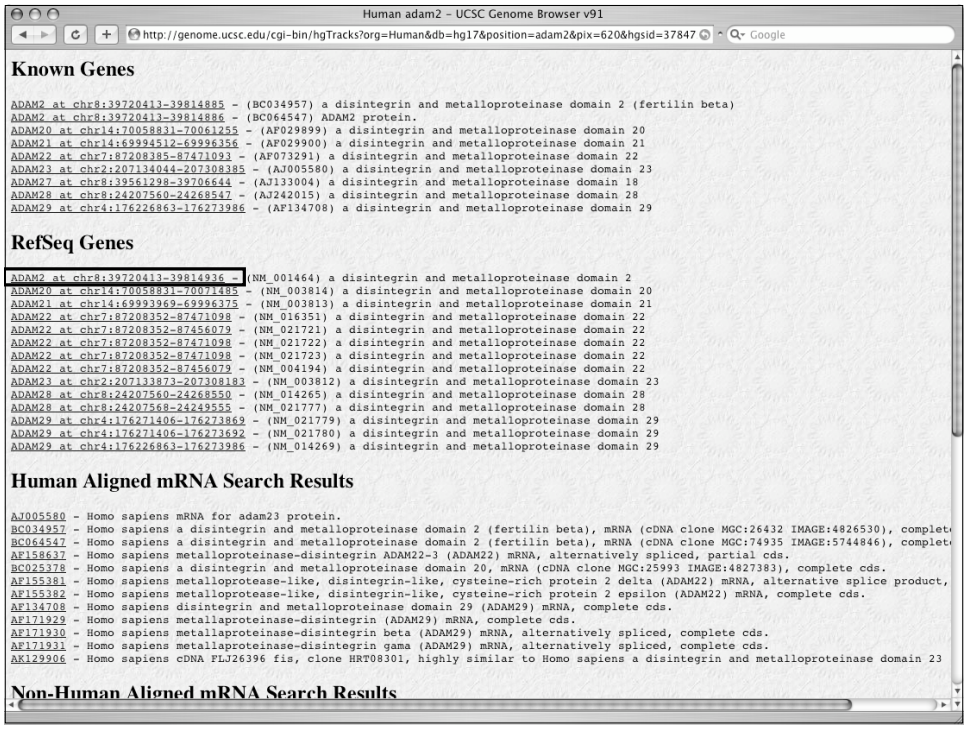
Genome Assembly Versions

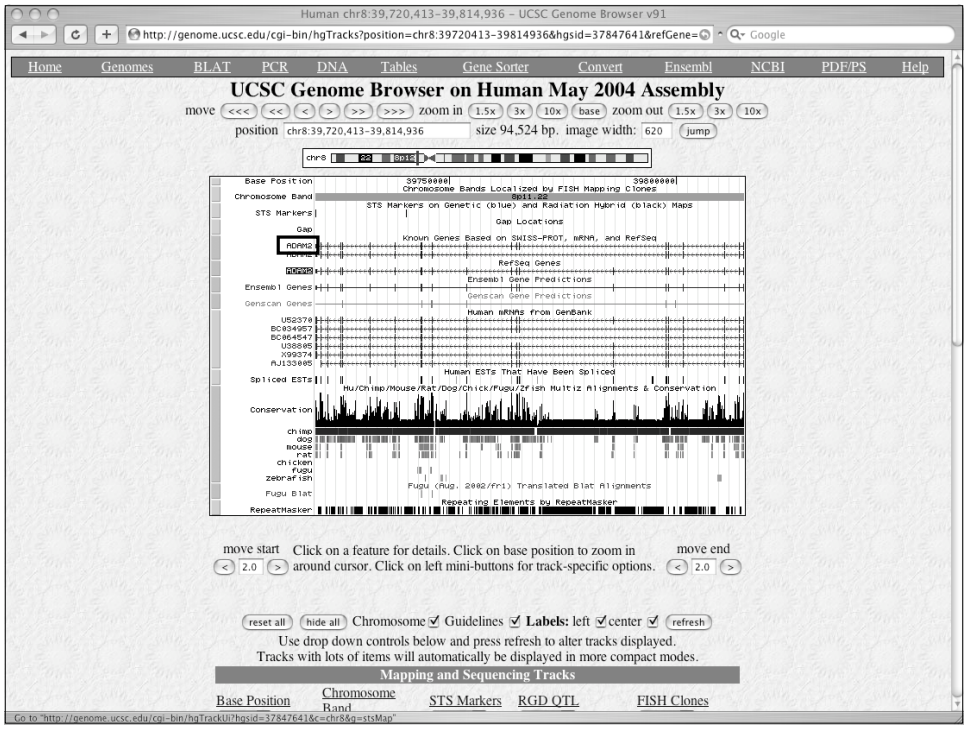
	Same assembly?	UCSC	NCBI	Ensembl
Human	Yes	May 2004/hg17/Build 35	Build 35.1	Build 35
Mouse	Yes	May 2004/mm5/Build 33	Build 33.1	Build 33
Rat	Yes	June 2003/rn3/RGSC 3.1	Build 2.1	RGSC 3.1 (RGSC 3.2 on pre!)
Chicken	Yes(?)	February 2004/galGal2	Build 1.1	WASHUC1
Chimp	Yes, but NCBI is using a different chromosome numbering system	November 2003/ panTro1/NCBI Build 1.1	Build 1.1	CHIMP1
Fugu	Yes	August 2002/ fr1/v3.0	-	Fugu v2.0

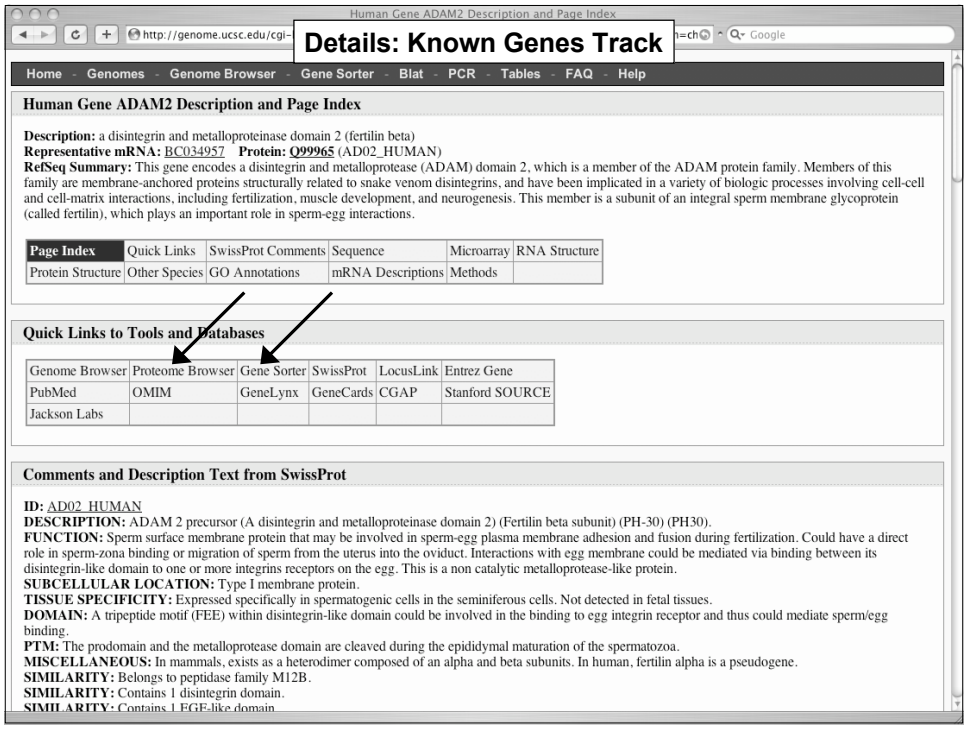
UCSC

View a region in the genome by querying with a gene symbol

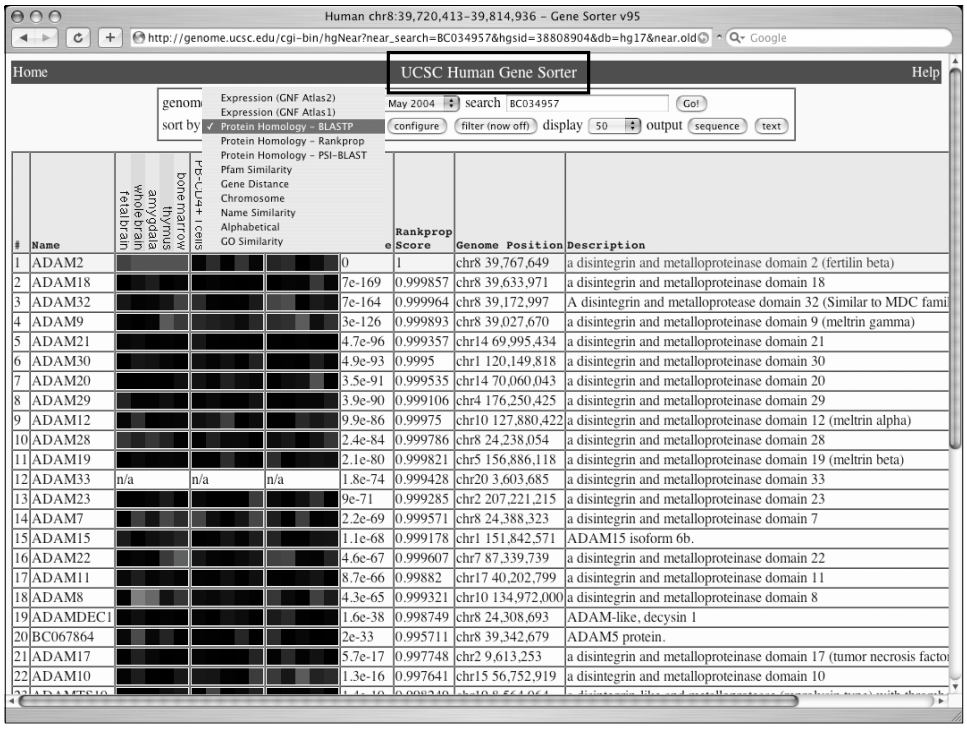


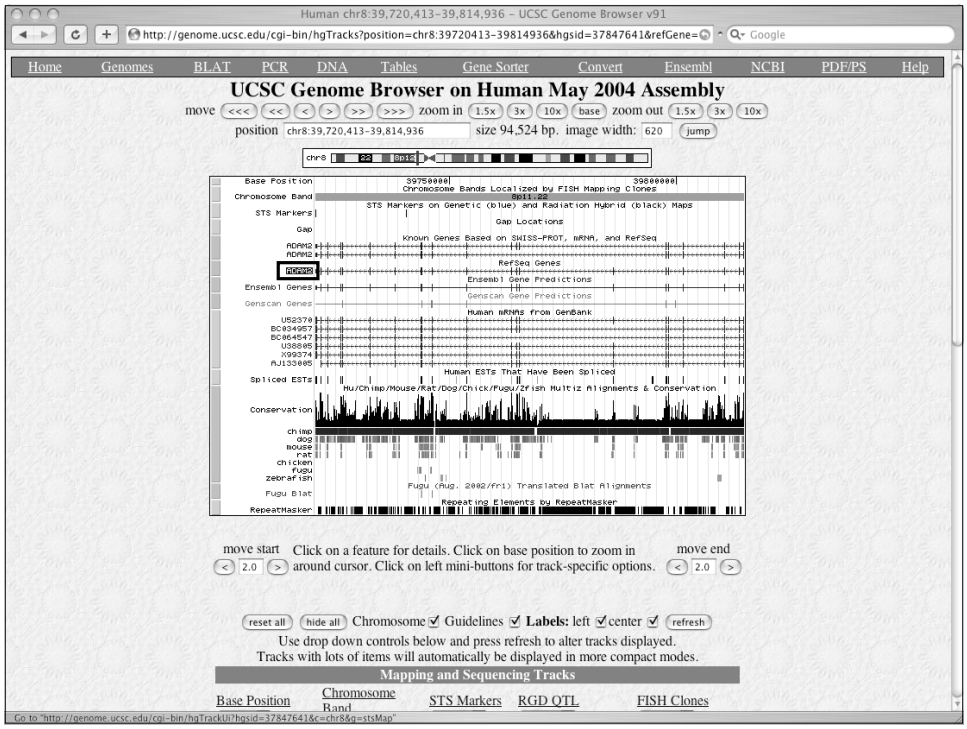

Human adam2 - UCSC Genome Browser v91
http://genome.ucsc.edu/cgi-bin/hgTracks?org=Human&db=hg17&position=adam2&pix=620&hgsid=37847
Known Genes
ADAM2 at chr8:39720413-39814885 - (BC034957) a disintegrin and metalloproteinase domain 2 (fertilin beta)
ADAM2 at chr8:39720413-39814886 - (BC064547) ADAM2 protein.
ADAM20 at chr14:70058831-70061255 - (AF029899) a disintegrin and metalloproteinase domain 20
ADAM21 at chr14:69994512-69996356 - (AF029900) a disintegrin and metalloproteinase domain 21
ADAM22 at chr7:87208385-87471093 - (AF073291) a disintegrin and metalloproteinase domain 22
ADAM23 at chr2:207134044-207308385 - (AJ005580) a disintegrin and metalloproteinase domain 23
ADAM27 at chr8:39561298-39706644 - (AJ133004) a disintegrin and metalloproteinase domain 18
ADAM28 at chr8:24207560-24268547 - (AJ242015) a disintegrin and metalloproteinase domain 28
ADAM29 at chr4:176226863-176273986 - (AF134708) a disintegrin and metalloproteinase domain 29
RefSeq Genes
ADAM2 at chr8:39720413-39814936 - (NM_001464) a disintegrin and metalloproteinase domain 2
ADAM20 at chr14:70058831-70071485 - (NM_003814) a disintegrin and metalloproteinase domain 20
ADAM21 at chr14:69993969-69996375 - (NM_003813) a disintegrin and metalloproteinase domain 21
ADAM22 at chr7:87208352-87471098 - (NM_016351) a disintegrin and metalloproteinase domain 22
ADAM22 at chr7:87208352-87456079 - (NM_021721) a disintegrin and metalloproteinase domain 22
ADAM22 at chr7:87208352-87471098 - (NM_021722) a disintegrin and metalloproteinase domain 22
ADAM22 at chr7:87208352-87471098 - (NM_021723) a disintegrin and metalloproteinase domain 22
ADAM22 at chr7:87208352-87456079 - (NM_004194) a disintegrin and metalloproteinase domain 22
ADAM23 at chr2:207133873-207308183 - (NM_003812) a disintegrin and metalloproteinase domain 23
ADAM28 at chr8:24207560-24268550 - (NM_014265) a disintegrin and metalloproteinase domain 28
ADAM28 at chr8:24207568-24249555 - (NM_021777) a disintegrin and metalloproteinase domain 28
ADAM29 at chr4:176271406-176273869 - (NM_021779) a disintegrin and metalloproteinase domain 29
ADAM29 at chr4:176271406-176273692 - (NM_021780) a disintegrin and metalloproteinase domain 29
ADAM29 at chr4:176226863-176273986 - (NM_014269) a disintegrin and metalloproteinase domain 29
Human Aligned mRNA Search Results
AJ005580 - Homo sapiens mRNA for adam23 protein.
BC034957 - Homo sapiens a disintegrin and metalloproteinase domain 2 (fertilin beta), mRNA (cDNA clone MGC:26432 IMAGE:4826530), complete
BC064547 - Homo sapiens a disintegrin and metalloproteinase domain 2 (fertilin beta), mRNA (cDNA clone MGC:74935 IMAGE:5744846), complete
AF158637 - Homo sapiens metalloproteinase-disintegrin ADAM22-3 (ADAM22) mRNA, alternatively spliced, partial cds.
BC025378 - Homo sapiens a disintegrin and metalloproteinase domain 20, mRNA (cDNA clone MGC:25993 IMAGE:4827383), complete cds.
AF155381 - Homo sapiens metalloprotease-like, disintegrin-like, cysteine-rich protein 2 delta (ADAM22) mRNA, alternative splice product,
AF155382 - Homo sapiens metalloprotease-like, disintegrin-like, cysteine-rich protein 2 epsilon (ADAM22) mRNA, complete cds.
AF134708 - Homo sapiens disintegrin and metalloproteinase domain 29 (ADAM29) mRNA, complete cds.
AF171929 - Homo sapiens metallaproteinase-disintegrin (ADAM29) mRNA, complete cds.
AF171930 - Homo sapiens metallaproteinase-disintegrin beta (ADAM29) mRNA, alternatively spliced, complete cds.
AF171931 - Homo sapiens metallaproteinase-disintegrin gama (ADAM29) mRNA, alternatively spliced, complete cds.
AK129906 - Homo sapiens cDNA FLJ26396 fis, clone HRT08301, highly similar to Homo sapiens a disintegrin and metalloproteinase domain 23
Non-Human Aligned mRNA Search Results

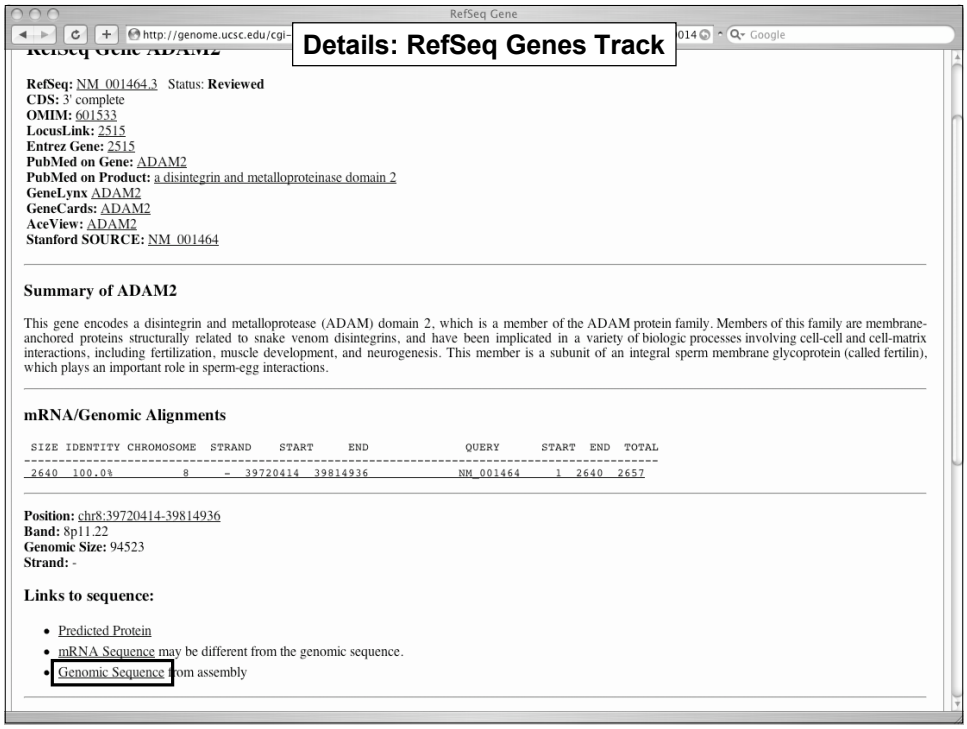

Human chr8:39,720,413-39,814,936 - UCSC Genome Browser v91
http://genome.ucsc.edu/cgi-bin/hgTracks?position=chr8:39720413-39814936&hgsid=37847641&refGene=
Home Genomes BLAT PCR DNA Tables Gene Sorter Convert Ensembl NCBI PDF/PS Help
UCSC Genome Browser on Human May 2004 Assembly
move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x
position chr8:39,720,413-39,814,936 size 94,524 bp. image width: 620 jump
Base Position
Chromosome Band
STS Markers
Gap
ADAM2
Known Genes Based on SWISS-PROT, mRNA, and RefSeq
RefSeq Genes
Ensembl Genes
Ensembl Gene Predictions
Genscan Genes
Genscan Gene Predictions
Human mRNAs from GenBank
Spliced ESTs
Human ESTs That Have Been Spliced
Conservation
Mu/Chimp/Mouse/Rat/Dog/Chick/Fugu/Zfish Multiz Alignments & Conservation
Fugu Blat
Fugu (fugu_2002/fr1) Translated Blat Alignments
RepeatMasker
Repeating Elements by RepeatMasker
move start Click on a feature for details. Click on base position to zoom in around cursor. Click on left mini-buttons for track-specific options. move end
reset all hide all Chromosome Guidelines Labels: left center refresh
Use drop down controls below and press refresh to alter tracks displayed.
Tracks with lots of items will automatically be displayed in more compact modes.
Mapping and Sequencing Tracks
Base Position Chromosome Band STS Markers RGD QTL FISH Clones

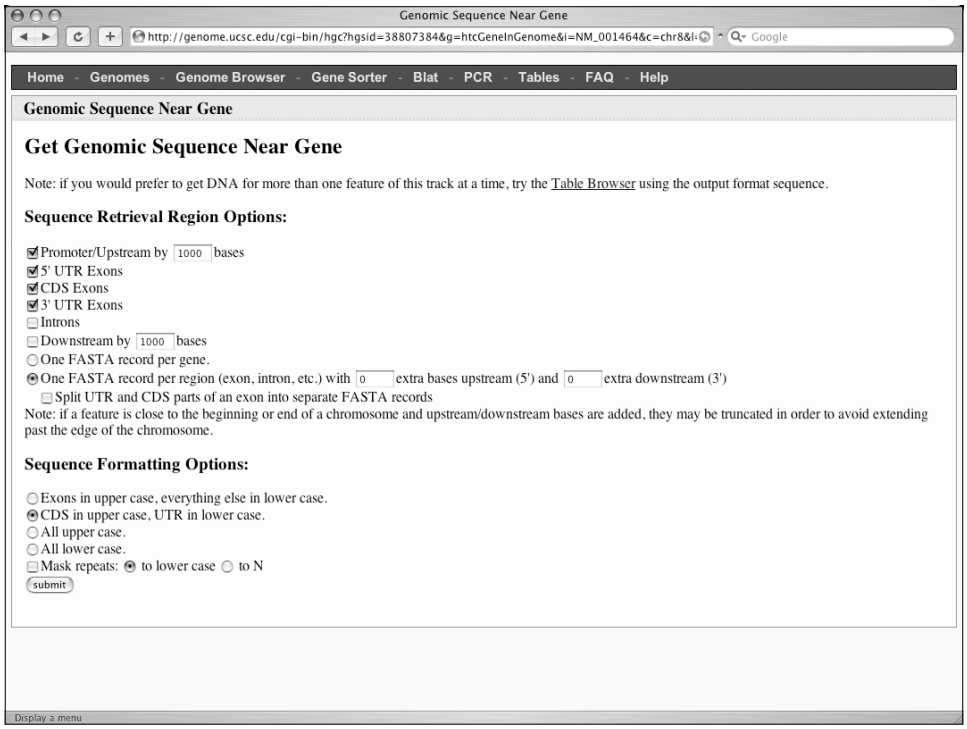

Human Gene ADAM2 Description and Page Index
Details: Known Genes Track
Home - Genomes - Genome Browser - Gene Sorter - Blat - PCR - Tables - FAQ - Help
Human Gene ADAM2 Description and Page Index
Description: a disintegrin and metalloproteinase domain 2 (fertilin beta)
Representative mRNA: BC034957 Protein: Q99965 (AD02_HUMAN)
RefSeq Summary: This gene encodes a disintegrin and metalloprotease (ADAM) domain 2, which is a member of the ADAM protein family. Members of this family are membrane-anchored proteins structurally related to snake venom disintegrins, and have been implicated in a variety of biologic processes involving cell-cell and cell-matrix interactions, including fertilization, muscle development, and neurogenesis. This member is a subunit of an integral sperm membrane glycoprotein (called fertilin), which plays an important role in sperm-egg interactions.
Page Index | Quick Links | SwissProt Comments | Sequence | Microarray | RNA Structure
Protein Structure | Other Species | GO Annotations | mRNA Descriptions | Methods
Quick Links to Tools and Databases
Genome Browser | Proteome Browser | Gene Sorter | SwissProt | LocusLink | Entrez Gene
PubMed | OMIM | GeneLynx | GeneCards | CGAP | Stanford SOURCE
Jackson Labs
Comments and Description Text from SwissProt
ID: AD02_HUMAN
DESCRIPTION: ADAM 2 precursor (A disintegrin and metalloproteinase domain 2) (Fertilin beta subunit) (PH-30) (PH30).
FUNCTION: Sperm surface membrane protein that may be involved in sperm-egg plasma membrane adhesion and fusion during fertilization. Could have a direct role in sperm-zona binding or migration of sperm from the uterus into the oviduct. Interactions with egg membrane could be mediated via binding between its disintegrin-like domain to one or more integrins receptors on the egg. This is a non catalytic metalloprotease-like protein.
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Expressed specifically in spermatogenic cells in the seminiferous cells. Not detected in fetal tissues.
DOMAIN: A tripeptide motif (FEE) within disintegrin-like domain could be involved in the binding to egg integrin receptor and thus could mediate sperm/egg binding.
PTM: The prodomain and the metalloprotease domain are cleaved during the epididymal maturation of the spermatozoa.
MISCELLANEOUS: In mammals, exists as a heterodimer composed of an alpha and beta subunits. In human, fertilin alpha is a pseudogene.
SIMILARITY: Belongs to peptidase family M12B.
SIMILARITY: Contains 1 disintegrin domain.
SIMILARITY: Contains 1 EGF-like domain


Human protein AD02_HUMAN - UCSC Proteome Browser
http://genome.ucsc.edu/cgi-bin/pbTracks?proteinID=AD02_HUMAN&hgsid=38806974&db=hg17
Home
UCSC Proteome Browser
PDF/PS
Help
Human protein: Q99965 (aka AD02_HUMAN) ADAM 2 precursor (A disintegrin and metalloproteinase domain 2) (Fertilin beta subunit) (PH-30) (PH30).
Move <<< << < > >> >>>
Current scale: FULL
Rescale to 1/6 1/2 FULL DNA
AA Scale
AA Sequence
Exons
Polarity
Hydrophobicity
Cysteines
Predicted Glycosylation
Superfamily/SCOP
AA Anomalies
Explanation of Protein Tracks
pI
Molecular Weight
Number of Exons
Amino Acid Frequencies
InterPro Domains
Hydrophobicity
Number of Cysteines
Amino Acid Anomalies
Display a menu


Human chr8:39,720,413-39,814,936 - Gene Sorter v95
http://genome.ucsc.edu/cgi-bin/hgNear?near_search=BC034957&hgsid=38808904&db=hg17&near.old
Home
UCSC Human Gene Sorter
Help
Expression (GNF Atlas2)
Expression (GNF Atlas1)
Protein Homology - BLASTP
Protein Homology - Rankprop
Protein Homology - PSI-BLAST
Pfam Similarity
Gene Distance
Chromosome
Name Similarity
Alphabetical
GO Similarity
May 2004
search
BC034957
Go!
sort by
configure
filter (now off)
display
50
output
sequence
text
fetalbrain
wholebrain
amygdala
thymus
bonemarrow
PBL-CD4+ Tcells
Name
Rankprop Score
Genome Position
Description
1 ADAM2 0 1 chr8 39,767,649 a disintegrin and metalloproteinase domain 2 (fertilin beta)
2 ADAM18 7e-169 0.999857 chr8 39,633,971 a disintegrin and metalloproteinase domain 18
3 ADAM32 7e-164 0.999964 chr8 39,172,997 A disintegrin and metalloprotease domain 32 (Similar to MDC fami
4 ADAM9 3e-126 0.999893 chr8 39,027,670 a disintegrin and metalloproteinase domain 9 (meltrin gamma)
5 ADAM21 4.7e-96 0.999357 chr14 69,995,434 a disintegrin and metalloproteinase domain 21
6 ADAM30 4.9e-93 0.9995 chr1 120,149,818 a disintegrin and metalloproteinase domain 30
7 ADAM20 3.5e-91 0.999535 chr14 70,060,043 a disintegrin and metalloproteinase domain 20
8 ADAM29 3.9e-90 0.999106 chr4 176,250,425 a disintegrin and metalloproteinase domain 29
9 ADAM12 9.9e-86 0.99975 chr10 127,880,422 a disintegrin and metalloproteinase domain 12 (meltrin alpha)
10 ADAM28 2.4e-84 0.999786 chr8 24,238,054 a disintegrin and metalloproteinase domain 28
11 ADAM19 2.1e-80 0.999821 chr5 156,886,118 a disintegrin and metalloproteinase domain 19 (meltrin beta)
12 ADAM33 n/a n/a n/a 1.8e-74 0.999428 chr20 3,603,685 a disintegrin and metalloproteinase domain 33
13 ADAM23 9e-71 0.999285 chr2 207,221,215 a disintegrin and metalloproteinase domain 23
14 ADAM7 2.2e-69 0.999571 chr8 24,388,323 a disintegrin and metalloproteinase domain 7
15 ADAM15 1.1e-68 0.999178 chr1 151,842,571 ADAM15 isoform 6b.
16 ADAM22 4.6e-67 0.999607 chr7 87,339,739 a disintegrin and metalloproteinase domain 22
17 ADAM11 8.7e-66 0.99882 chr17 40,202,799 a disintegrin and metalloproteinase domain 11
18 ADAM8 4.3e-65 0.999321 chr10 134,972,000 a disintegrin and metalloproteinase domain 8
19 ADAMDEC1 1.6e-38 0.998749 chr8 24,308,693 ADAM-like, decysin 1
20 BC067864 2e-33 0.995711 chr8 39,342,679 ADAM5 protein.
21 ADAM17 5.7e-17 0.997748 chr2 9,613,253 a disintegrin and metalloproteinase domain 17 (tumor necrosis facto
22 ADAM10 1.3e-16 0.997641 chr15 56,752,919 a disintegrin and metalloproteinase domain 10

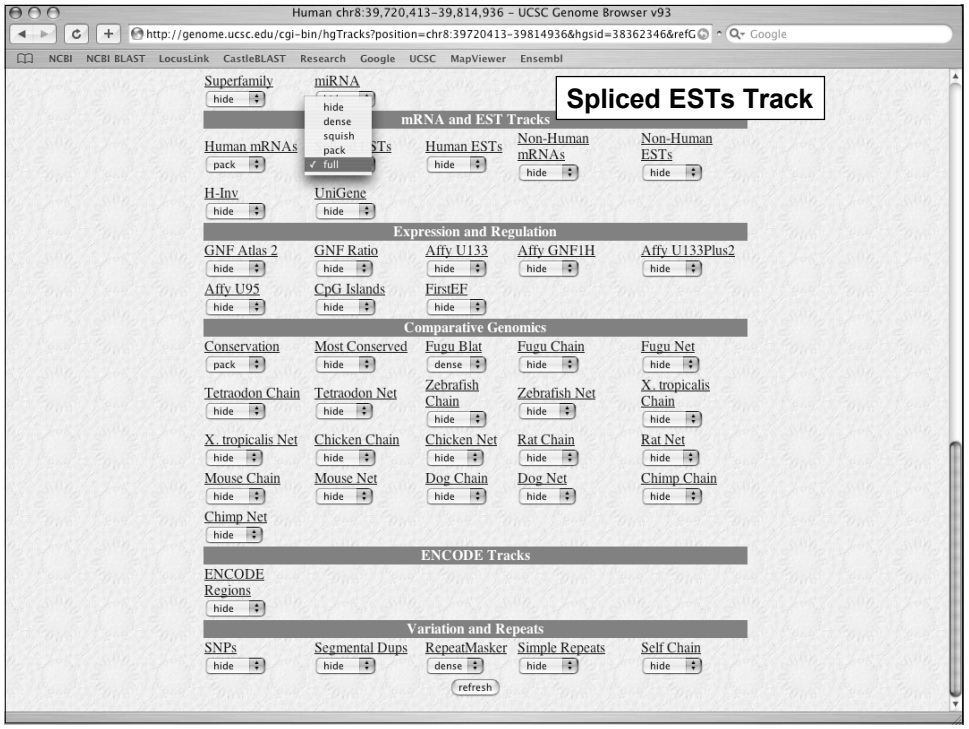

Human chr8:39,720,413-39,814,936 - UCSC Genome Browser v91
http://genome.ucsc.edu/cgi-bin/hgTracks?position=chr8:39720413-39814936&hgsid=37847641&refGene=
Home Genomes BLAT PCR DNA Tables Gene Sorter Convert Ensembl NCBI PDF/PS Help
UCSC Genome Browser on Human May 2004 Assembly
move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x
position chr8:39,720,413-39,814,936 size 94,524 bp. image width: 620 jump
Base Position
Chromosome Band
STS Markers
Gap
ADAM2
ADAM32
RefSeq Genes
Ensembl Genes
Ensembl Gene Predictions
Genscan Genes
Genscan Gene Predictions
Human mRNAs from GenBank
Spliced ESTs
Human ESTs That Have Been Spliced
Conservation
chimp
dog
mouse
rat
chicken
fugu
zebrafish
Fugu Blat
RepeatMasker
move start
move end
Click on a feature for details. Click on base position to zoom in around cursor. Click on left mini-buttons for track-specific options.
reset all hide all Chromosome Guidelines Labels: left center refresh
Use drop down controls below and press refresh to alter tracks displayed.
Tracks with lots of items will automatically be displayed in more compact modes.
Mapping and Sequencing Tracks
Base Position
Chromosome Band
STS Markers
RGD QTL
FISH Clones


RefSeq Gene
Details: RefSeq Genes Track
RefSeq: NM_001464.3 Status: Reviewed
CDS: 3' complete
OMIM: 601533
LocusLink: 2515
Entrez Gene: 2515
PubMed on Gene: ADAM2
PubMed on Product: a disintegrin and metalloproteinase domain 2
GeneLynx ADAM2
GeneCards: ADAM2
AceView: ADAM2
Stanford SOURCE: NM_001464
Summary of ADAM2
This gene encodes a disintegrin and metalloprotease (ADAM) domain 2, which is a member of the ADAM protein family. Members of this family are membrane-anchored proteins structurally related to snake venom disintegrins, and have been implicated in a variety of biologic processes involving cell-cell and cell-matrix interactions, including fertilization, muscle development, and neurogenesis. This member is a subunit of an integral sperm membrane glycoprotein (called fertilin), which plays an important role in sperm-egg interactions.
mRNA/Genomic Alignments
SIZE IDENTITY CHROMOSOME STRAND START END QUERY START END TOTAL
2640 100.0% 8 - 39720414 39814936 NM_001464 1 2640 2657
Position: chr8:39720414-39814936
Band: 8p11.22
Genomic Size: 94523
Strand: -
Links to sequence:
Predicted Protein
mRNA Sequence may be different from the genomic sequence.
Genomic Sequence from assembly


Genomic Sequence Near Gene
Home - Genomes - Genome Browser - Gene Sorter - Blat - PCR - Tables - FAQ - Help
Genomic Sequence Near Gene
Get Genomic Sequence Near Gene
Note: if you would prefer to get DNA for more than one feature of this track at a time, try the Table Browser using the output format sequence.
Sequence Retrieval Region Options:
Promoter/Upstream by 1000 bases
5' UTR Exons
CDS Exons
3' UTR Exons
Introns
Downstream by 1000 bases
One FASTA record per gene.
One FASTA record per region (exon, intron, etc.) with 0 extra bases upstream (5') and 0 extra downstream (3')
Split UTR and CDS parts of an exon into separate FASTA records
Note: if a feature is close to the beginning or end of a chromosome and upstream/downstream bases are added, they may be truncated in order to avoid extending past the edge of the chromosome.
Sequence Formatting Options:
Exons in upper case, everything else in lower case.
CDS in upper case, UTR in lower case.
All upper case.
All lower case.
Mask repeats: to lower case to N
submit
Display a menu

UCSC

Change the tracks displayed on the Genome Browser


Human chr8:39,720,413-39,814,936 - UCSC Genome Browser v93
http://genome.ucsc.edu/cgi-bin/hgTracks?position=chr8:39720413-39814936&hgsid=38362346&refG
NCBI NCBI BLAST LocusLink CastleBLAST Research Google UCSC MapViewer Ensembl
Spliced ESTs Track
Superfamily
miRNA
hide
dense
squish
pack
full
mRNA and EST Tracks
Human mRNAs
Human ESTs
Non-Human mRNAs
Non-Human ESTs
H-Inv
UniGene
Expression and Regulation
GNF Atlas 2
GNF Ratio
Affy U133
Affy GNF1H
Affy U133Plus2
Affy U95
CpG Islands
FirstEF
Comparative Genomics
Conservation
Most Conserved
Fugu Blat
Fugu Chain
Fugu Net
Tetraodon Chain
Tetraodon Net
Zebrafish Chain
Zebrafish Net
X. tropicalis Chain
X. tropicalis Net
Chicken Chain
Chicken Net
Rat Chain
Rat Net
Mouse Chain
Mouse Net
Dog Chain
Dog Net
Chimp Chain
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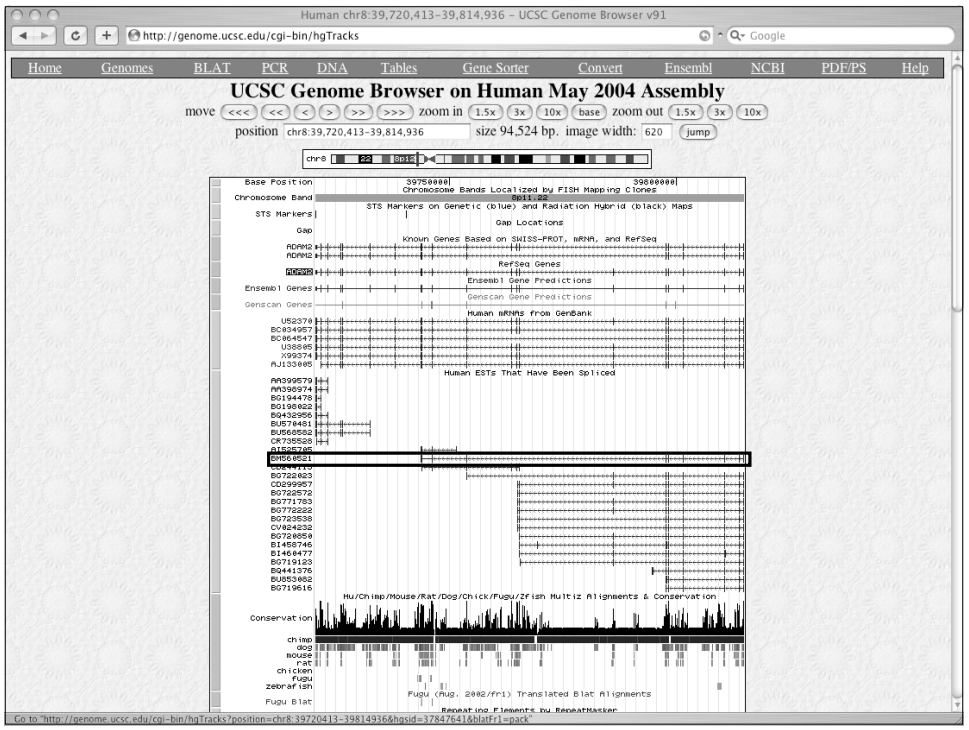
ENCODE Tracks
ENCODE Regions
Variation and Repeats
SNPs
Segmental Dups
RepeatMasker
Simple Repeats
Self Chain
refresh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UCSC Genome Browser on Human May 2004 Assembly
move zoom in zoom out
position chr8:39,720,413-39,814,936 size 94,524 bp. image width: 620 jump
Base Position
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STS Markers
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RefSeq Genes
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Ensembl Gene Predictions
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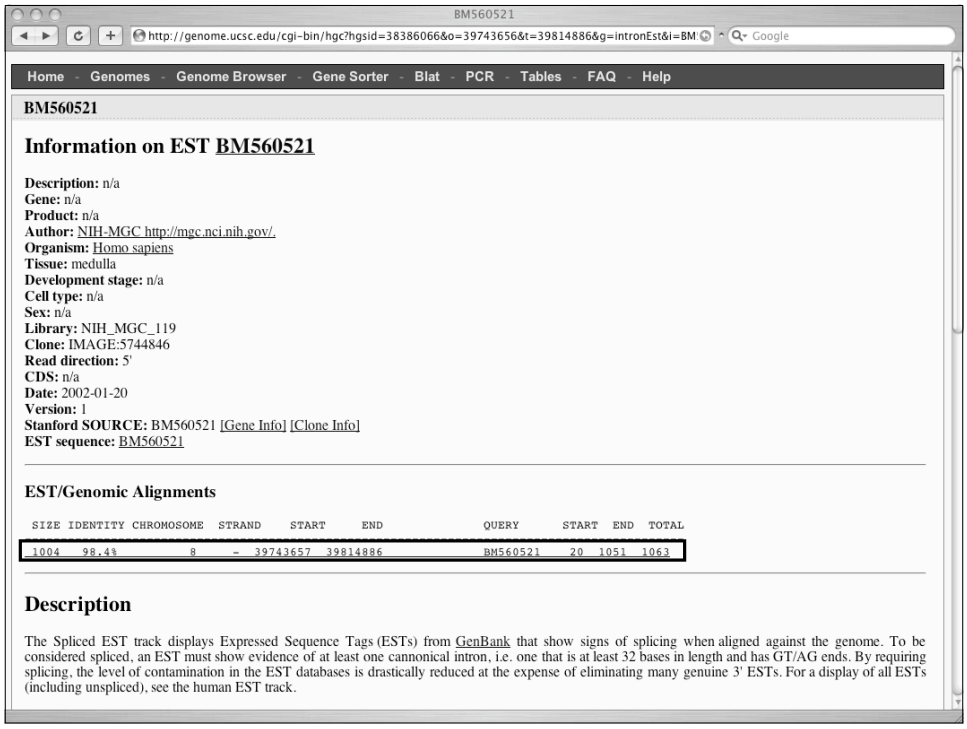
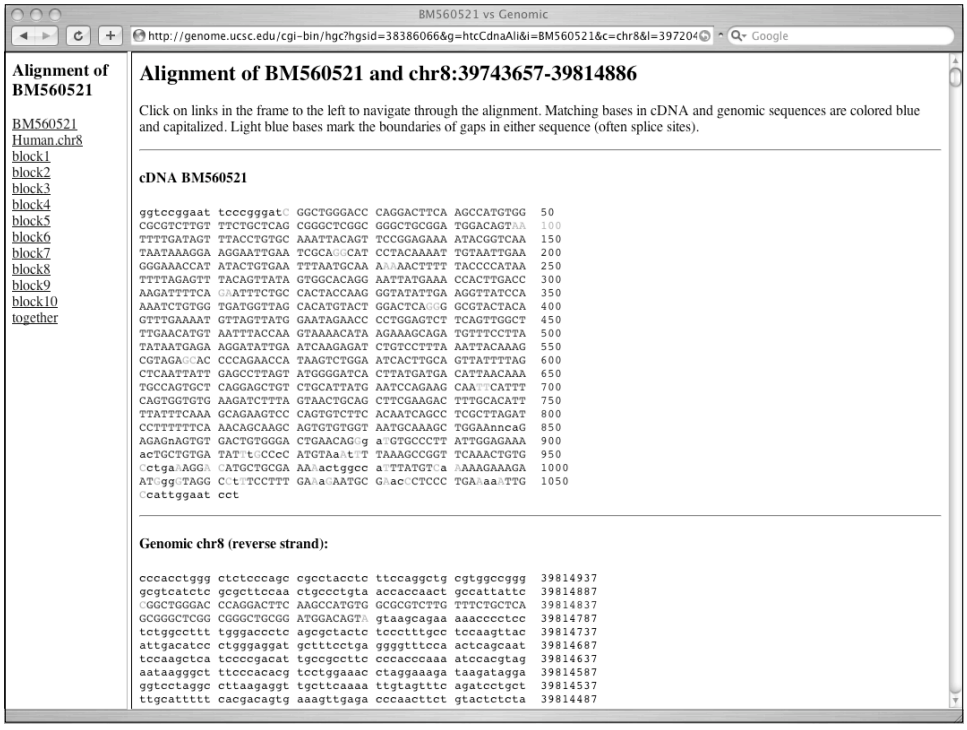
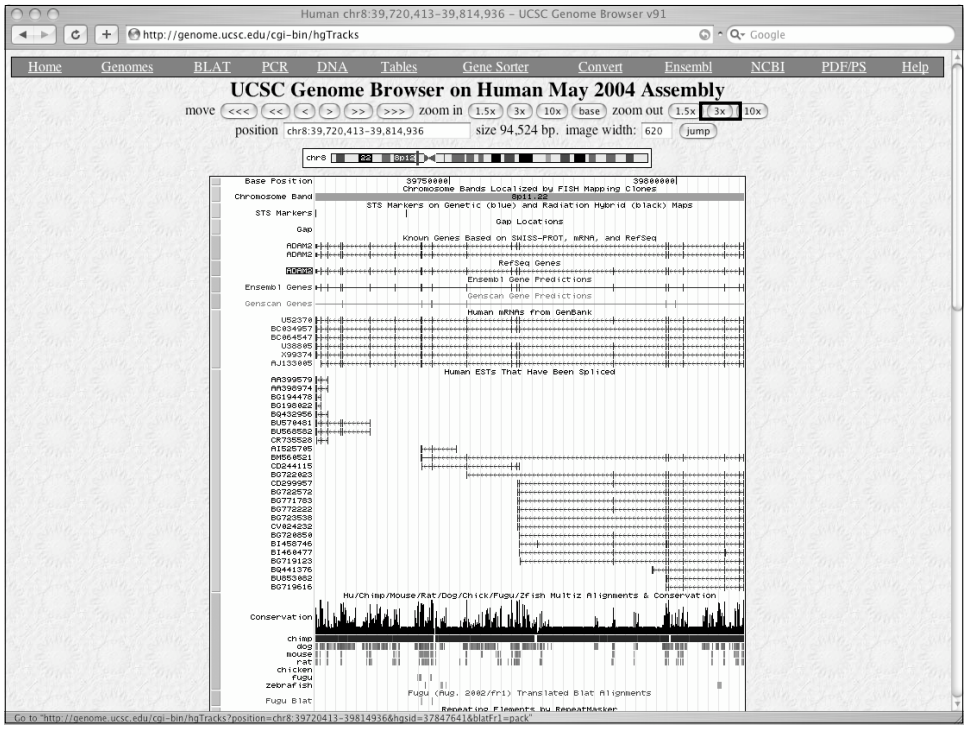
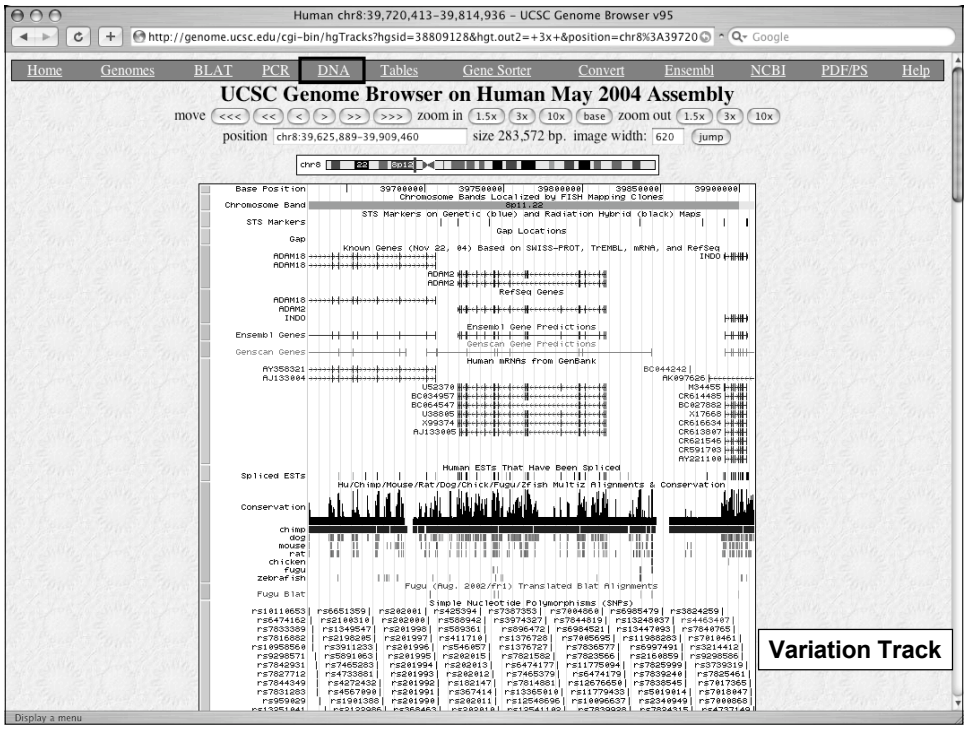
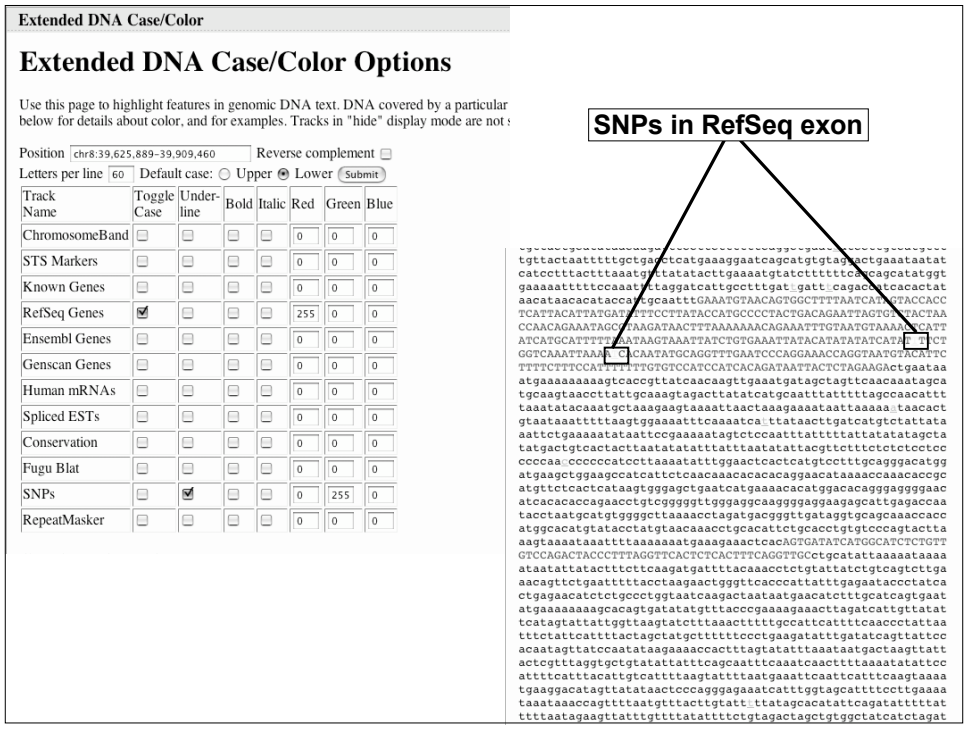
Human mRNAs from GenBank
Human ESTs That Have Been Spliced
Conservation
Mu/Chimp/Mouse/Rat/Dog/Chick/Fugu/Zfish Multiz Alignments & Conservation
chimp
dog
mouse
rat
chicken
fugu
zebrafish
Fugu Blat
Fugu (Fug. 2002/Fr1) Translated Blat Alignments
Repeating Elements by RepeatMasker


BM560521
http://genome.ucsc.edu/cgi-bin/hgc?hgsid=38386066&o=39743656&t=39814886&g=intronEst&i=BM
Google
Home - Genomes - Genome Browser - Gene Sorter - Blat - PCR - Tables - FAQ - Help
BM560521
Information on EST BM560521
Description: n/a
Gene: n/a
Product: n/a
Author: NIH-MGC http://mgc.nci.nih.gov/.
Organism: Homo sapiens
Tissue: medulla
Development stage: n/a
Cell type: n/a
Sex: n/a
Library: NIH_MGC_119
Clone: IMAGE:5744846
Read direction: 5'
CDS: n/a
Date: 2002-01-20
Version: 1
Stanford SOURCE: BM560521 [Gene Info] [Clone Info]
EST sequence: BM560521
EST/Genomic Alignments
SIZE IDENTITY CHROMOSOME STRAND START END QUERY START END TOTAL
1004 98.4% 8 - 39743657 39814886 BM560521 20 1051 1063
Description
The Spliced EST track displays Expressed Sequence Tags (ESTs) from GenBank that show signs of splicing when aligned against the genome. To be considered spliced, an EST must show evidence of at least one cannonical intron, i.e. one that is at least 32 bases in length and has GT/AG ends. By requiring splicing, the level of contamination in the EST databases is drastically reduced at the expense of eliminating many genuine 3' ESTs. For a display of all ESTs (including unspliced), see the human EST track.


BM560521 vs Genomic
http://genome.ucsc.edu/cgi-bin/hgc?hgsid=38386066&g=htcCdnaAli&i=BM560521&c=chr8&l=397204
Google
Alignment of BM560521
BM560521
Human.chr8
block1
block2
block3
block4
block5
block6
block7
block8
block9
block10
together
Alignment of BM560521 and chr8:39743657-39814886
Click on links in the frame to the left to navigate through the alignment. Matching bases in cDNA and genomic sequences are colored blue and capitalized. Light blue bases mark the boundaries of gaps in either sequence (often splice sites).
cDNA BM560521
ggtccggaat tcccgggatC GGCTGGGACC CAGGACTTCA AGCCATGTGG 50
CGCGTCTTGT TTCTGCTCAG CGGGCTCGGC GGGCTGCGGA TGGACAGTAA 100
TTTTGATAGT TTACCTGTGC AAATTACAGT TCCGGAGAAA ATACGGTCAA 150
TAATAAAGGA AGGAATTGAA TCGCAGGCAT CCTACAAAAT TGTAATTGAA 200
GGGAAACCAT ATACTGTGAA TTTAATGCAA AAAACTTTT TACCCCATAA 250
TTTTAGAGTT TACAGTTATA GTGGCACAGG AATTATGAAA CCACTTGACC 300
AAGATTTTCA GAATTTCTGC CACTACCAAG GGTATATTGA AGGTTATCCA 350
AAATCTGTGG TGATGGTTAG CACATGTACT GGACTCAGGG GCGTACTACA 400
GTTTGAAAAT GTTAGTTATG GAATAGAACC CCTGGAGTCT TCAGTTGGCT 450
TTGAACATGT AATTTACCAA GTAAAACATA AGAAAGCAGA TGTTTCCTTA 500
TATAATGAGA AGGATATTGA ATCAAGAGAT CTGTCCTTTA AATTACAAAG 550
CGTAGAGCAC CCCAGAACCA TAAGTCTGGA ATCACTTGCA GTTATTTTAG 600
CTCAATTATT GAGCCTTAGT ATGGGGATCA CTTATGATGA CATTAACAAA 650
TGCCAGTGCT CAGGAGCTGT CTGCATTATG AATCCAGAAG CAATCCATTT 700
CAGTGGTCTG AAGATCTTTA GTAACTGCAG CTTCGAAGAC TTTGCACATT 750
TTATTTCAAA GCAGAAGTCC CAGTGTCTTC ACAATCAGCC TCGCTTAGAT 800
CCTTTTTTCA AACAGCAAGC AGTGTGTGGT AATGCAAAGC TGGAAnncaG 850
AGAGnAGTGT GACTGTGGGA CTGAACAGGg aGGTGCCCTT ATTGGAGAAA 900
acTGCTGTGA TATTtGCCcC ATGTAaAtTT TAAAGCCGGT TCAAACTGTG 950
CctgaAAGGA CATGCTGCGA AAAactggcc aTTTATGTCa AAAAGAAAGA 1000
ATGggGTAGG CCtTTCCTTT GAAaGAATGC GAacCCTCCC TGAAaaATTG 1050
Ccattggaat cct
Genomic chr8 (reverse strand):
cccacctggg ctctcccagc cgcctacctc ttccaggctg cgtggccggg 39814937
gcgtcatctc gcgcttccaa ctgccctgta accaccaact gccattattc 39814887
CGGCTGGGAC CCAGGACTTC AAGCCATGTG GCGCGTCTTG TTTCTGCTCA 39814837
GCGGGCTCGG CGGGCTGCGG ATGGACAGTA gtaagcagaa aaacccctcc 39814787
tctggccttt tgggaccctc agcgctactc tccctttgcc tccaagttac 39814737
attgacatcc ctgggaggat gctttcctga ggggtttcca actcagcaat 39814687
tccaagctca tccccgacat tgccgccttc cccacccaaa atccacgtag 39814637
aataagggct ttcccacacg tcctggaaac ctaggaaaga taagatagga 39814587
ggtcctaggc cttaagaggt tgcttcaaaa ttgtagtttc agatcctgct 39814537
ttgcattttt cacgacagtg aaagttgaga cccaacttct gtactctcta 39814487

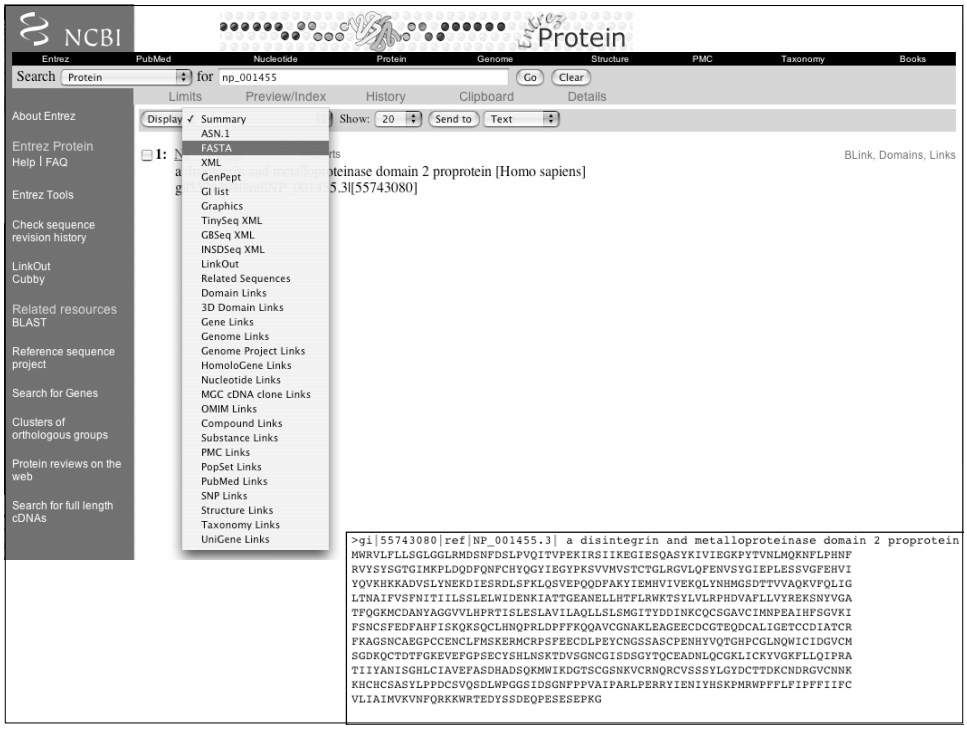

Human chr8:39,720,413-39,814,936 - UCSC Genome Browser v91
http://genome.ucsc.edu/cgi-bin/hgTracks
Home Genomes BLAT PCR DNA Tables Gene Sorter Convert Ensembl NCBI PDF/PS Help
UCSC Genome Browser on Human May 2004 Assembly
move zoom in zoom out
position chr8:39,720,413-39,814,936 size 94,524 bp. image width: 620 jump
Base Position
Chromosome Band
STS Markers
Gap
ADAM2
ADAM18
RefSeq Genes
Ensembl Genes
Ensembl Gene Predictions
Genscan Genes
Genscan Gene Predictions
Human mRNAs from GenBank
Human ESTs That Have Been Spliced
Mu/Chimp/Mouse/Rat/Dog/Chick/Fugu/Zfish Multiz Alignments & Conservation
Conservation
chimp
dog
mouse
rat
chicken
fugu
zebrafish
Fugu Blat
Fugu (Aug. 2002/fr1) Translated Blat Alignments

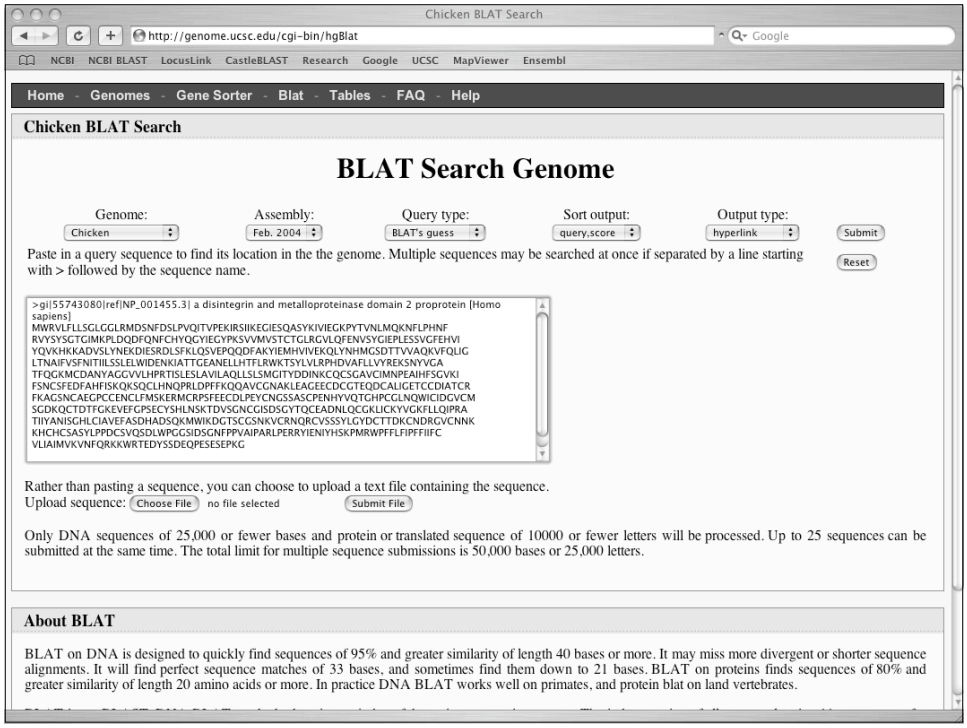

Human chr8:39,720,413-39,814,936 - UCSC Genome Browser v95
http://genome.ucsc.edu/cgi-bin/hgTracks?hgsid=38809128&hgt.out2=+3x+&position=chr8%3A39720
Home Genomes BLAT PCR DNA Tables Gene Sorter Convert Ensembl NCBI PDF/PS Help
UCSC Genome Browser on Human May 2004 Assembly
move zoom in zoom out
position chr8:39,625,889-39,909,460 size 283,572 bp. image width: 620 jump
Base Position
Chromosome Band
STS Markers
Gap
Known Genes (Nov 22, 04) Based on SWISS-PROT, TrEMBL, mRNA, and RefSeq
ADAM18
ADAM2
INDO
RefSeq Genes
Ensembl Genes
Ensembl Gene Predictions
Genscan Genes
Genscan Gene Predictions
Human mRNAs from GenBank
Human ESTs That Have Been Spliced
Spliced ESTs
Mu/Chimp/Mouse/Rat/Dog/Chick/Fugu/Zfish Multiz Alignments & Conservation
Conservation
chimp
dog
mouse
rat
chicken
fugu
zebrafish
Fugu Blat
Fugu (Aug. 2002/fr1) Translated Blat Alignments
Simple Nucleotide Polymorphisms (SNPs)
Variation Track
Display a menu

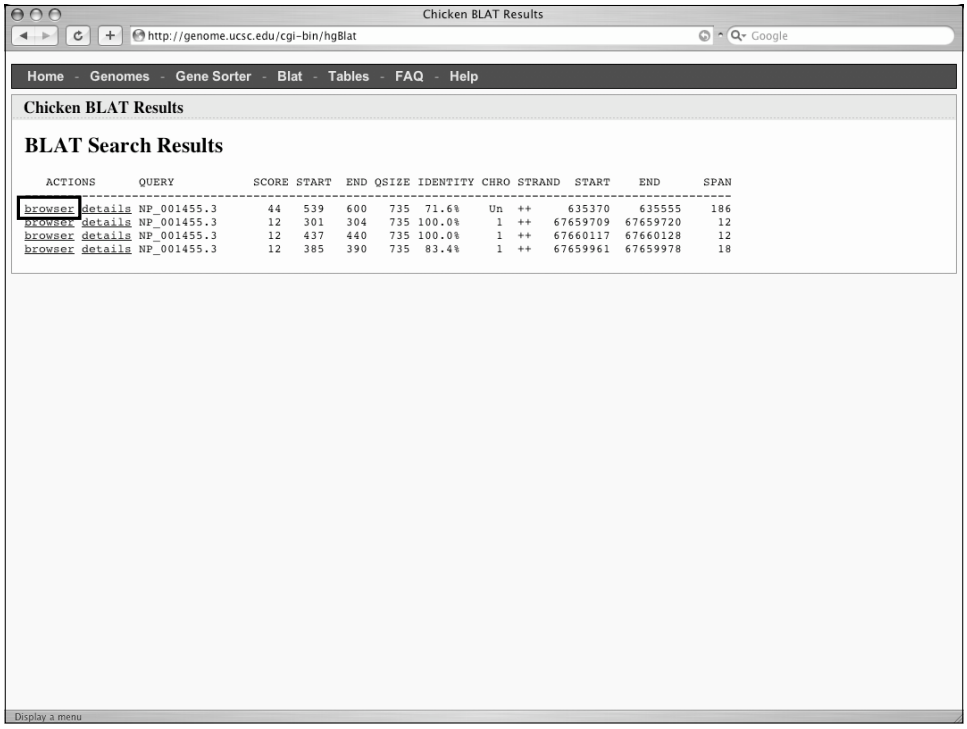


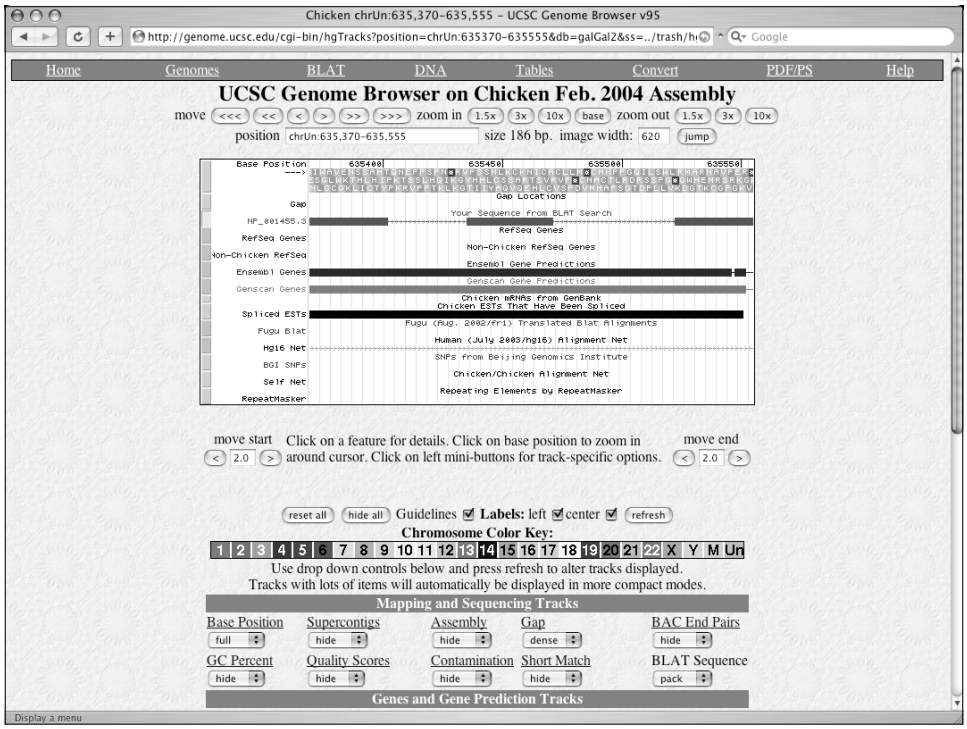
UCSC

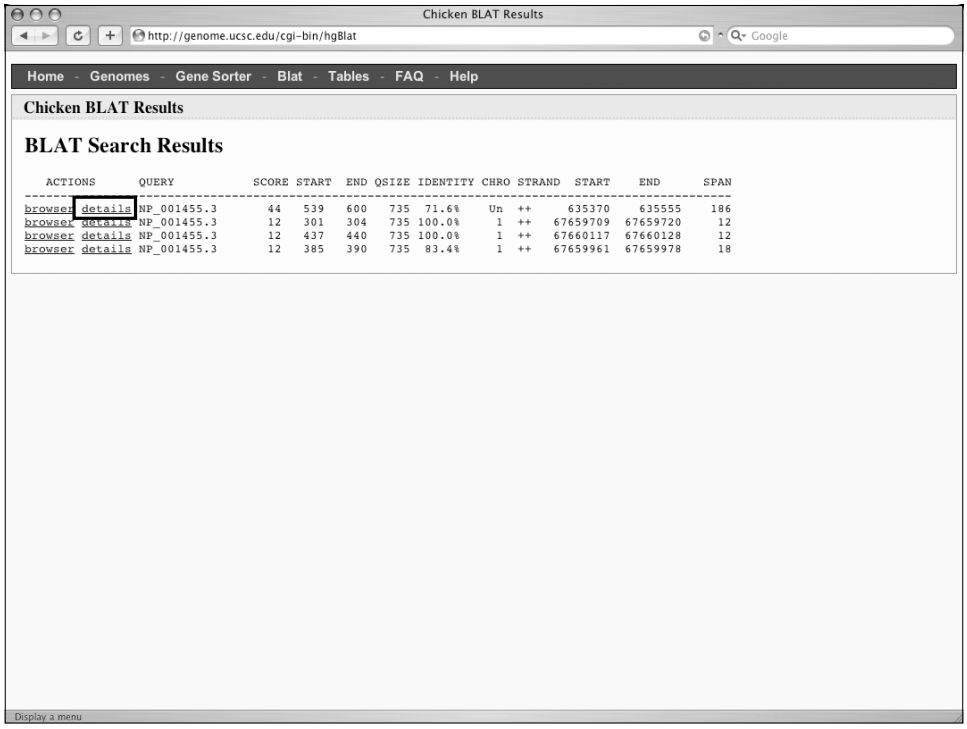
Find a chicken homolog of a human protein

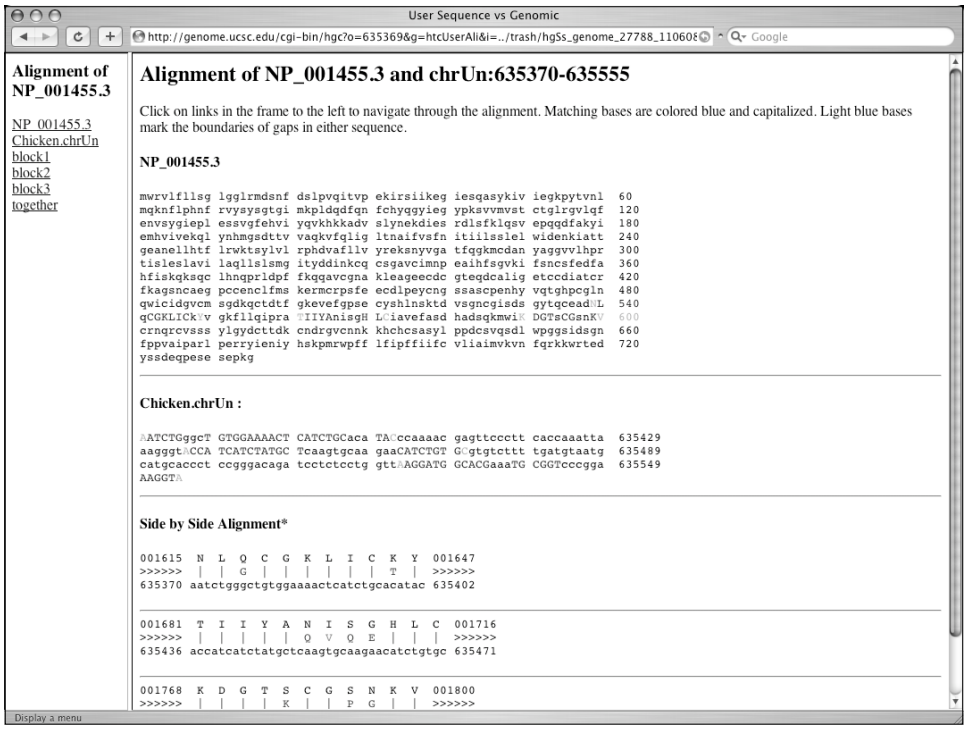

NCBI
Protein
Entrez PubMed Nucleotide Protein Genome Structure PMC Taxonomy Books
Search Protein for np_001455 Go Clear
Limits Preview/Index History Clipboard Details
About Entrez
Entrez Protein
Help | FAQ
Entrez Tools
Check sequence revision history
LinkOut
Cubby
Related resources
BLAST
Reference sequence project
Search for Genes
Clusters of orthologous groups
Protein reviews on the web
Search for full length cDNAs
Display Summary Show: 20 Send to Text
ASN.1
FASTA
XML
GenPept
GI list
Graphics
TinySeq XML
GBSeq XML
INSDSeq XML
LinkOut
Related Sequences
Domain Links
3D Domain Links
Gene Links
Genome Links
Genome Project Links
HomoloGene Links
Nucleotide Links
MGC cDNA clone Links
OMIM Links
Compound Links
Substance Links
PMC Links
PopSet Links
PubMed Links
SNP Links
Structure Links
Taxonomy Links
UniGene Links
BLink, Domains, Links
>gi|55743080|ref|NP_001455.3| a disintegrin and metalloproteinase domain 2 proprotein
MWRVLFLLSGLGGLRMDSNFDSLPVQITVPEKIRSIIKEGIESQASYKIVIEGKPYTVNLMQKNFLPHNF
RVYSYSGTGIMKPLDQDFQNFCHYQGYIEGYPKSVVMVSTCTGLRGVLQFENVSYGIEPLESSVGFEHVI
YQVKHKKADVSLYNEKDIESRDLSFKLQSVEPQQDFAKYIEMHVIVEKQLYNHMGSDTTVVAQKVFQLIG
LTNAIFVSFNITIILSSLELWIDENKIATTGEANELLHTFLRWKTSYLVLRPHDVAFLLVYREKSNYVGA
TFQGKMCDANYAGGVVLHPRTISLESLAVILAQLLSLSMGITYDDINKCQCSGAVCIMNPEAIHFSGVKI
FSNCSFEDFAHFISKQKSQCLHNQPRLDPFFKQQAVCGNAKLEAGEECDCGTEQDCALIGETCCDIATCR
FKAGSNCAEGPCCENCLFMSKERMCRPSFEECDLPEYCNGSSASCPENHYVQTGHPCGLNQWICIDGVCM
SGDKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNLQCGKLICKYVGKFLLQIPRA
TIIYANISGHLCIAVEFASDHADSQKMWIKDGTSCGSNKVCRNQRCVSSSYLGYDCTTDKCNDRGVCNNK
KHCHCSASYLPPDCSVQSDLWPGGSIDSGNFPPVAIPARLPERRYIENIYHSKPMRWPFFLFIPFFIIFC
VLIAIMVKVNFQRKKWRTEDYSSDEQPESESEPKG


Chicken BLAT Search
http://genome.ucsc.edu/cgi-bin/hgBlat
NCBI NCBI BLAST LocusLink CastleBLAST Research Google UCSC MapViewer Ensembl
Home - Genomes - Gene Sorter - Blat - Tables - FAQ - Help
Chicken BLAT Search
BLAT Search Genome
Genome: Chicken
Assembly: Feb. 2004
Query type: BLAT's guess
Sort output: query,score
Output type: hyperlink
Submit
Reset
Paste in a query sequence to find its location in the the genome. Multiple sequences may be searched at once if separated by a line starting with > followed by the sequence name.
>gi|55743080|ref|NP_001455.3| a disintegrin and metalloproteinase domain 2 proprotein [Homo sapiens]
MWRVLFLLSGLGGLRMDSNFDSLPVQITVPEKIRSIIKEGIESQASYKIVIEGKPYTVNLMQKNFLPHNF
RVYSYSGTGIMKPLDQDFQNFCHYQGYIEGYPKSVVMVSTCTGLRGVLQFENVSYGIEPLESSVGFEHVI
YQVKHKKADVSLYNEKDIESRDLSFKLQSVEPQQDFAKYIEMHVIVEKQLYNHMGSDTTVVAQKVFQLIG
LTNAIFVSFNITIILSSLELWIDENKIATTGEANELLHTFLRWKTSYLVLRPHDVAFLLVYREKSNYVGA
TFQGKMCDANYAGGVVLHPRTISLESLAVILAQLLSLSMGITYDDINKCQCSGAVCIMNPEAIHFSGVKI
FSNCSFEDFAHFISKQKSQCLHNQPRLDPFFKQQAVCGNAKLEAGEECDCGTEQDCALIGETCCDIATCR
FKAGSNCAEGPCCENCLFMSKERMCRPSFEECDLPEYCNGSSASCPENHYVQTGHPCGLNQWICIDGVCM
SGDKQCTDTFGKEVEFGPSECYSHLNSKTDVSGNCGISDSGYTQCEADNLQCGKLICKYVGKFLLQIPRA
TIIYANISGHLCIAVEFASDHADSQKMWIKDGTSCGSNKVCRNQRCVSSSYLGYDCTTDKCNDRGVCNNK
KHCHCSASYLPPDCSVQSDLWPGGSIDSGNFPPVAIPARLPERRYIENIYHSKPMRWPFFLFIPFFIIFC
VLIAIMVKVNFQRKKWRTEDYSSDEQPESESEPKG
Rather than pasting a sequence, you can choose to upload a text file containing the sequence.
Upload sequence: Choose File no file selected Submit File
Only DNA sequences of 25,000 or fewer bases and protein or translated sequence of 10000 or fewer letters will be processed. Up to 25 sequences can be submitted at the same time. The total limit for multiple sequence submissions is 50,000 bases or 25,000 letters.
About BLAT
BLAT on DNA is designed to quickly find sequences of 95% and greater similarity of length 40 bases or more. It may miss more divergent or shorter sequence alignments. It will find perfect sequence matches of 33 bases, and sometimes find them down to 21 bases. BLAT on proteins finds sequences of 80% and greater similarity of length 20 amino acids or more. In practice DNA BLAT works well on primates, and protein blat on land vertebrates.


Chicken BLAT Results
http://genome.ucsc.edu/cgi-bin/hgBlat
Home - Genomes - Gene Sorter - Blat - Tables - FAQ - Help
Chicken BLAT Results
BLAT Search Results
ACTIONS QUERY SCORE START END QSIZE IDENTITY CHRO STRAND START END SPAN
browser details NP_001455.3 44 539 600 735 71.6% Un ++ 635370 635555 186
browser details NP_001455.3 12 301 304 735 100.0% 1 ++ 67659709 67659720 12
browser details NP_001455.3 12 437 440 735 100.0% 1 ++ 67660117 67660128 12
browser details NP_001455.3 12 385 390 735 83.4% 1 ++ 67659961 67659978 18
Display a menu

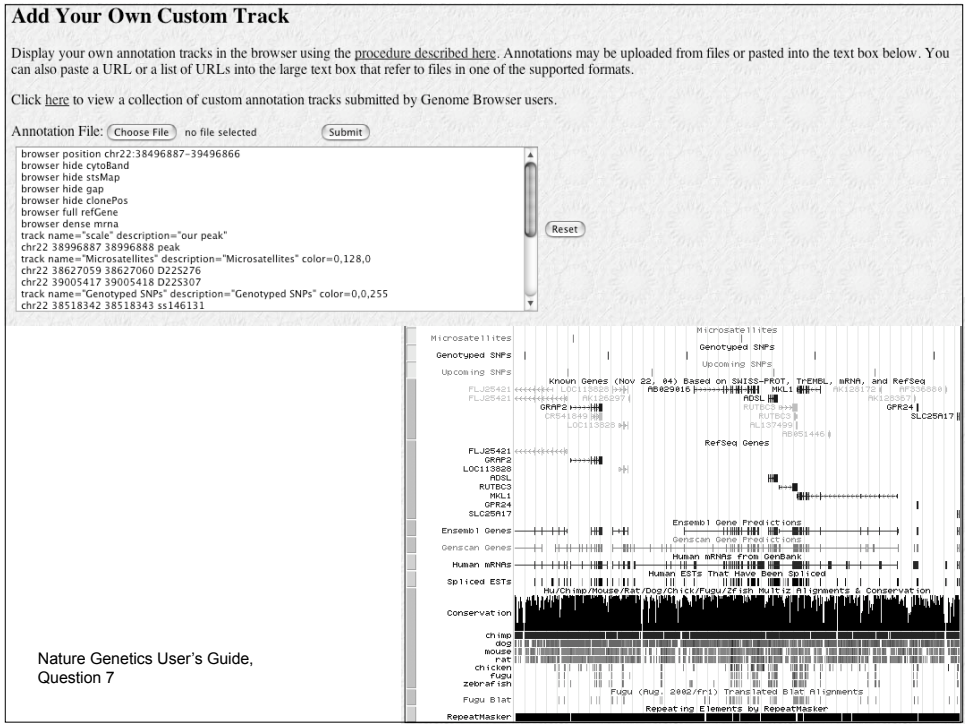

Chicken chrUn:635,370-635,555 - UCSC Genome Browser v95
Home Genomes BLAT DNA Tables Convert PDF/PS Help
UCSC Genome Browser on Chicken Feb. 2004 Assembly
move zoom in zoom out
position chrUn:635,370-635,555 size 186 bp. image width: 620 jump
Base Position
Gap
NP_001455.3
RefSeq Genes
Non-Chicken RefSeq
Ensembl Genes
Genscan Genes
Spliced ESTs
Fugu Blat
Hg16 Net
BGI SNPs
Self Net
RepeatMasker
Gap Locations
Your Sequence from BLAT Search
RefSeq Genes
Non-Chicken RefSeq Genes
Ensembl Gene Predictions
Genscan Gene Predictions
Chicken mRNAs from GenBank
Chicken ESTs That Have Been Spliced
Fugu (Aug. 2002/fr1) Translated Blat Alignments
Human (July 2003/hg16) Alignment Net
SNPs from Beijing Genomics Institute
Chicken/Chicken Alignment Net
Repeating Elements by RepeatMasker
move start Click on a feature for details. Click on base position to zoom in around cursor. Click on left mini-buttons for track-specific options. move end
reset all hide all Guidelines Labels: left center refresh
Chromosome Color Key:
Use drop down controls below and press refresh to alter tracks displayed.
Tracks with lots of items will automatically be displayed in more compact modes.
Mapping and Sequencing Tracks
Base Position Supercontigs Assembly Gap BAC End Pairs
GC Percent Quality Scores Contamination Short Match BLAT Sequence
Genes and Gene Prediction Tracks
Display a menu


Chicken BLAT Results
http://genome.ucsc.edu/cgi-bin/hgBlat
Google
Home - Genomes - Gene Sorter - Blat - Tables - FAQ - Help
Chicken BLAT Results
BLAT Search Results
ACTIONS QUERY SCORE START END QSIZE IDENTITY CHRO STRAND START END SPAN
browser details NP_001455.3 44 539 600 735 71.6% Un ++ 635370 635555 186
browser details NP_001455.3 12 301 304 735 100.0% 1 ++ 67659709 67659720 12
browser details NP_001455.3 12 437 440 735 100.0% 1 ++ 67660117 67660128 12
browser details NP_001455.3 12 385 390 735 83.4% 1 ++ 67659961 67659978 18
Display a menu


User Sequence vs Genomic
http://genome.ucsc.edu/cgi-bin/hgc?o=635369&g=htcUserAli&i=../trash/hgSs_genome_27788_11060
Google
Alignment of NP_001455.3
NP_001455.3
Chicken.chrUn
block1
block2
block3
together
Alignment of NP_001455.3 and chrUn:635370-635555
Click on links in the frame to the left to navigate through the alignment. Matching bases are colored blue and capitalized. Light blue bases mark the boundaries of gaps in either sequence.
NP_001455.3
mwrvlfllsg lgglrmdsnf dslpvqitvp ekirsiikeg iesqasykiv iegkpytvnl 60
mqknflphnf rvysysgtgi mkpldqdfqn fchyqgyieg ypksvvmvst ctglrgvlqf 120
envsygiepl essvgfehvi yqvkhkkadv slynekdies rdlsfklqsv epqqdfakyi 180
emhvivekql ynhmgsdttv vaqkvfglig ltnaifvsfn itiilsslel widenkiatt 240
geanellhtf lrwktsylvl rphdvafllv yreksnyvga tfqgkmcdan yagqvvlhpr 300
tisleslavi laqllslsmg ityddinkcq csgavcimnp eaihfsgvki fsncsfedfa 360
hfiskqksqc lhnqprldpf fkqqavcgna kleageecdc gteqdcalig etccdiatcr 420
fkaqsncaeg pccenclfms kermcrpsfe ecdlpeycng ssascpenhy vqtghpcgln 480
qwicidgvcm sgdkqctdtf gkevefgpse cyshlnsktd vsgncgisds gytqceadIL 540
qCGKLICkVv gkfllqipra TIIYAnisgH LCiavefasd hadsqkmwiK DGTsCGsnKV 600
crnqrcvsss ylgydcttdk cndrgvcnnk khchcsasyl ppdcsvqsdl wpggsidsgn 660
fppvaiparl perryieniy hskpmrwpff lfipffiifc vliaimvkvn fqrkkwrted 720
yssdeqpese sepkg
Chicken.chrUn :
AATCTGggcT GTGGAAAACT CATCTGCaca TACccaaaac gagttccctt caccaaatta 635429
aagggtACCA TCATCTATGC Tcaagtgcaa gaaCATCTGT GCgtgtcttt tgatgtaatg 635489
catgcaccct ccgggacaga tcctctcctg gttAAGGATG GCACGaaaTG CGGTcccgga 635549
AAGGTA
Side by Side Alignment*
001615 N L Q C G K L I C K Y 001647
>>>>>> | | G | | | | | | T | >>>>>>
635370 aatctgggctgtggaaaactcatctgcacatac 635402
001681 T I I Y A N I S G H L C 001716
>>>>>> | | | | | Q V Q E | | | >>>>>>
635436 accatcatctatgctcaagtgcaagaacatctgtgc 635471
001768 K D G T S C G S N K V 001800
>>>>>> | | | | K | | P G | | >>>>>>
Display a menu

UCSC

Add your own custom tracks



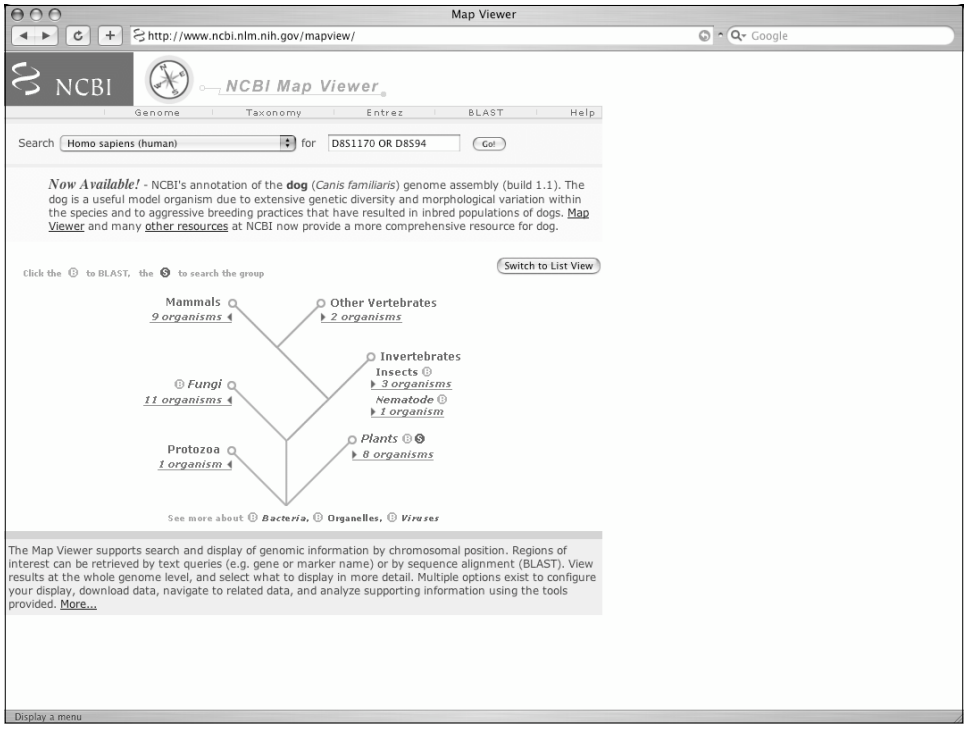
Nature Genetics User's Guide, Question 7

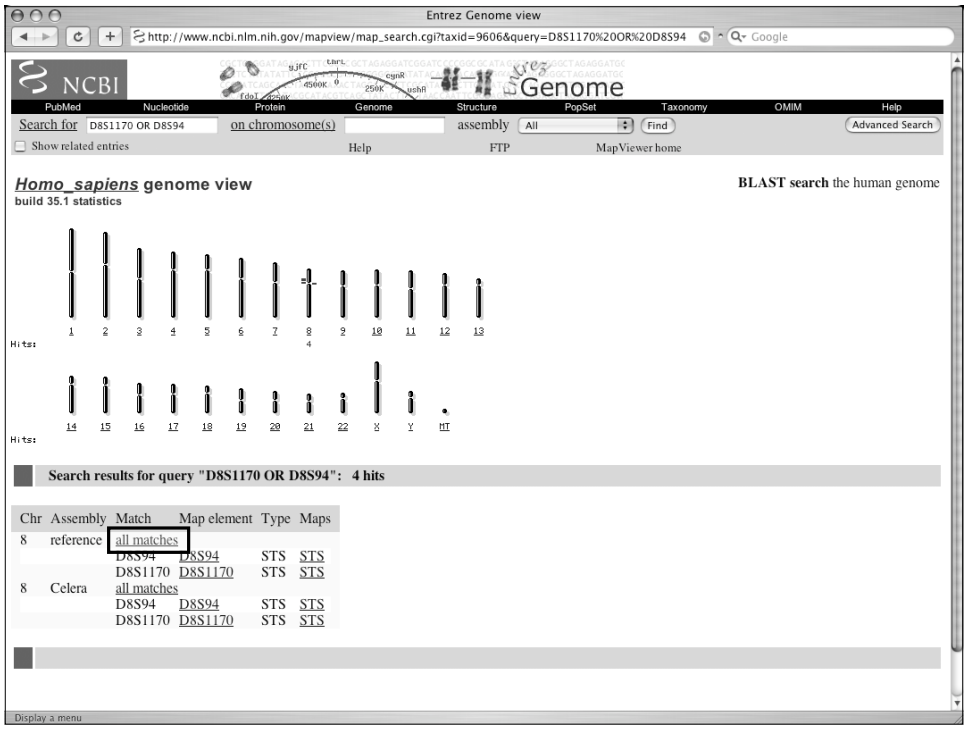
UCSC Table Browser

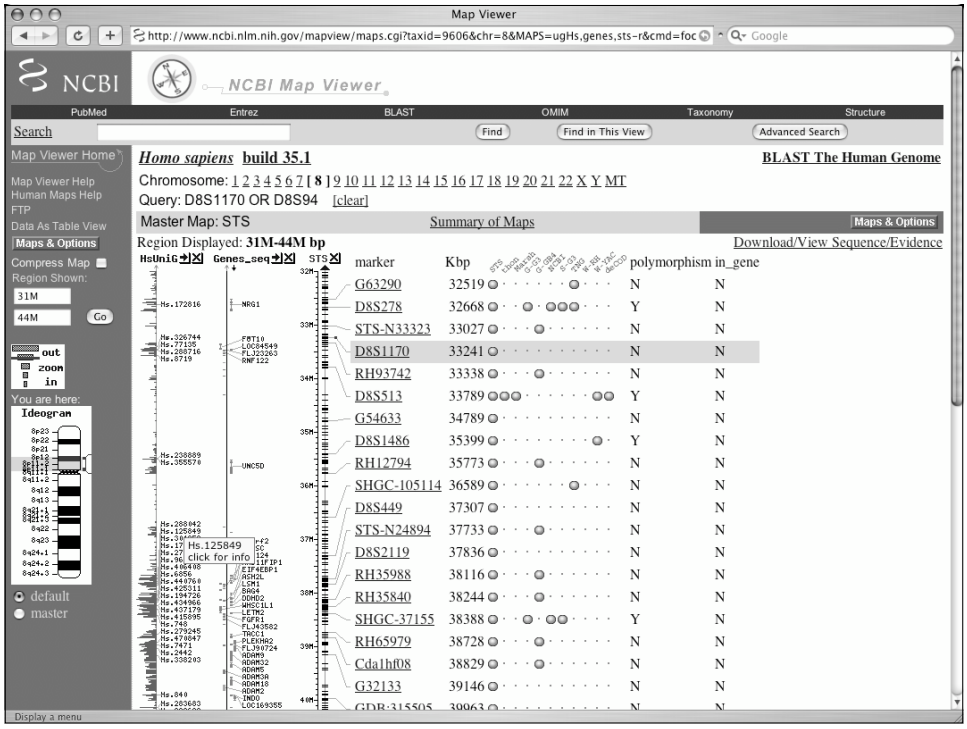
- Download track in text format
- Retrieve DNA sequence covered by a track
- Calculate intersections between tracks and view in the Genome Browser. For example:
  - Show all RefSeq genes that contain only one exon
  - Show all SNPs that are contained within a RefSeq coding region

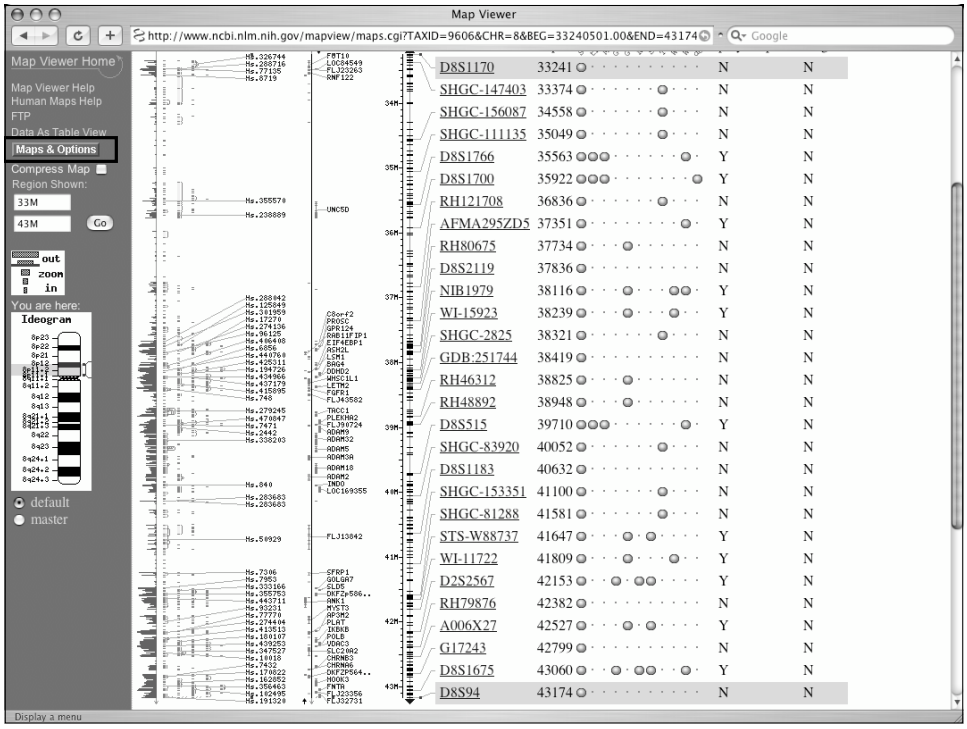
NCBI

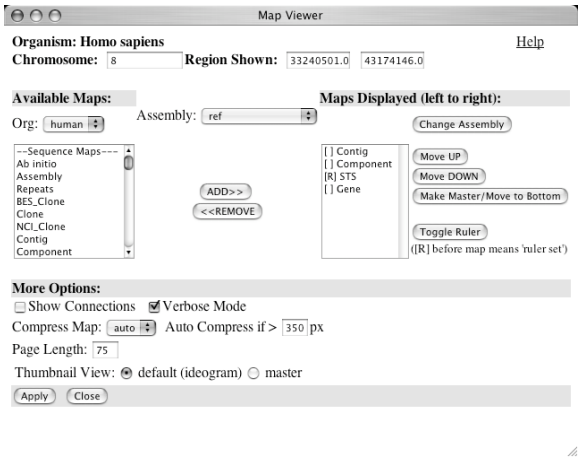
Identify all the genes between two STS markers

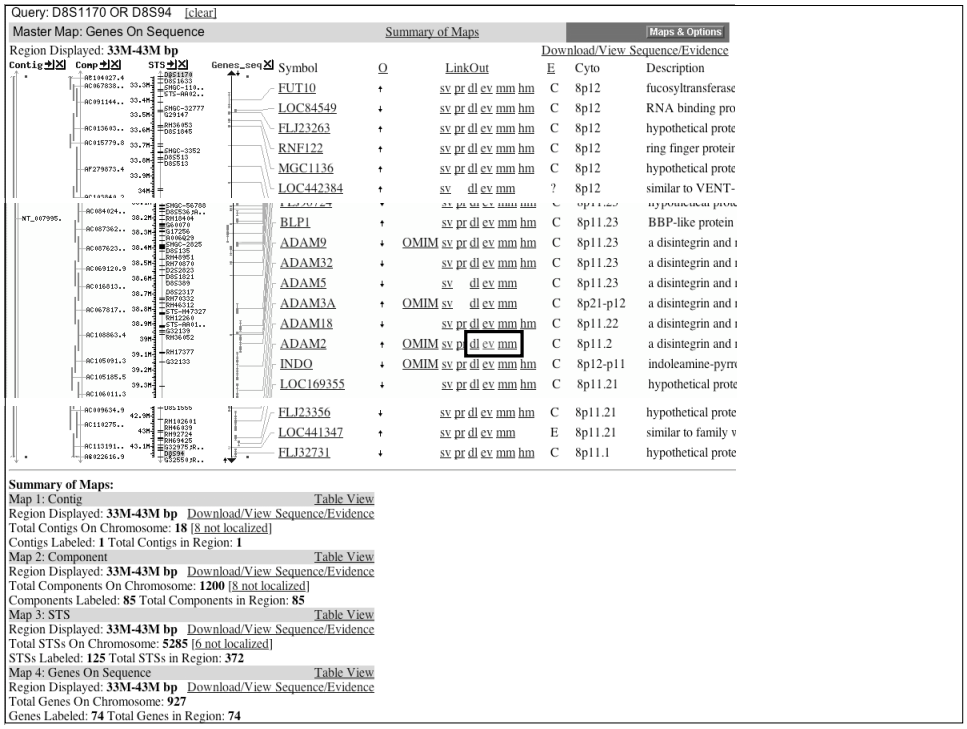

Map Viewer
http://www.ncbi.nlm.nih.gov/mapview/
NCBI
NCBI Map Viewer
Genome
Taxonomy
Entrez
BLAST
Help
Search
Homo sapiens (human)
for
D8S1170 OR D8S94
Go!
Now Available! - NCBI's annotation of the dog (Canis familiaris) genome assembly (build 1.1). The dog is a useful model organism due to extensive genetic diversity and morphological variation within the species and to aggressive breeding practices that have resulted in inbred populations of dogs. Map Viewer and many other resources at NCBI now provide a more comprehensive resource for dog.
Switch to List View
Mammals
9 organisms
Other Vertebrates
2 organisms
Invertebrates
Insects
3 organisms
Nematode
1 organism
Fungi
11 organisms
Protozoa
1 organism
Plants
8 organisms
The Map Viewer supports search and display of genomic information by chromosomal position. Regions of interest can be retrieved by text queries (e.g. gene or marker name) or by sequence alignment (BLAST). View results at the whole genome level, and select what to display in more detail. Multiple options exist to configure your display, download data, navigate to related data, and analyze supporting information using the tools provided. More...
Display a menu

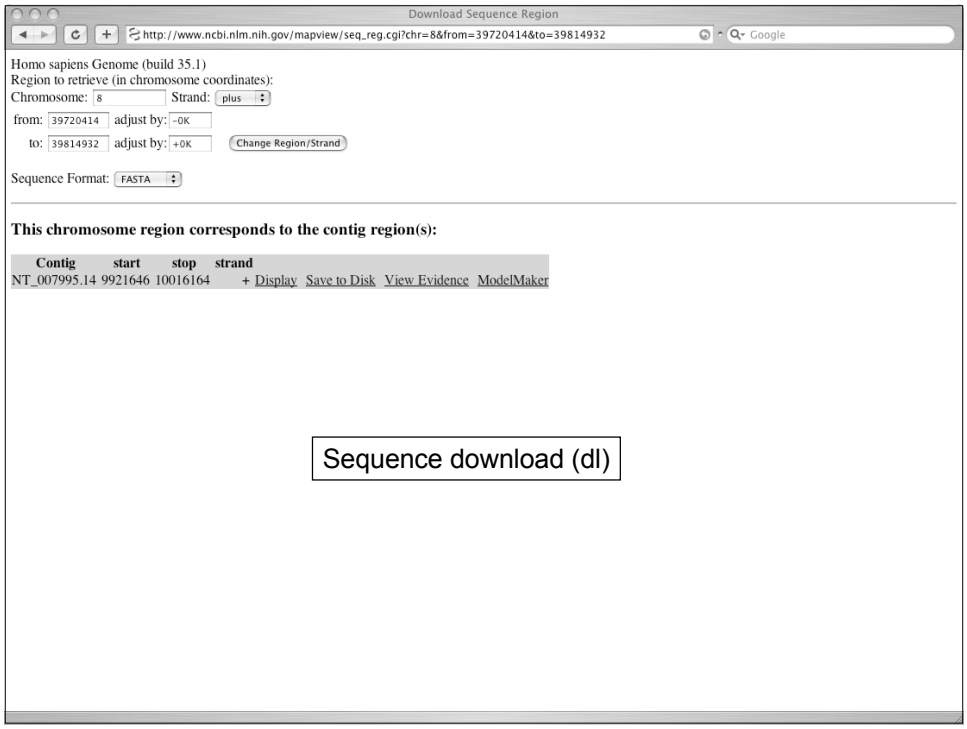

Entrez Genome view
http://www.ncbi.nlm.nih.gov/mapview/map_search.cgi?taxid=9606&query=D8S1170%20OR%20D8S94
NCBI
Genome
PubMed
Nucleotide
Protein
Genome
Structure
PopSet
Taxonomy
OMIM
Help
Search for
D8S1170 OR D8S94
on chromosome(s)
assembly
All
Find
Advanced Search
Show related entries
Help
FTP
MapViewer home
Homo_sapiens genome view
build 35.1 statistics
BLAST search the human genome
Hits:
Search results for query "D8S1170 OR D8S94": 4 hits
Chr Assembly Match Map element Type Maps
8 reference all matches
D8S94 D8S94 STS STS
D8S1170 D8S1170 STS STS
8 Celera all matches
D8S94 D8S94 STS STS
D8S1170 D8S1170 STS STS
Display a menu

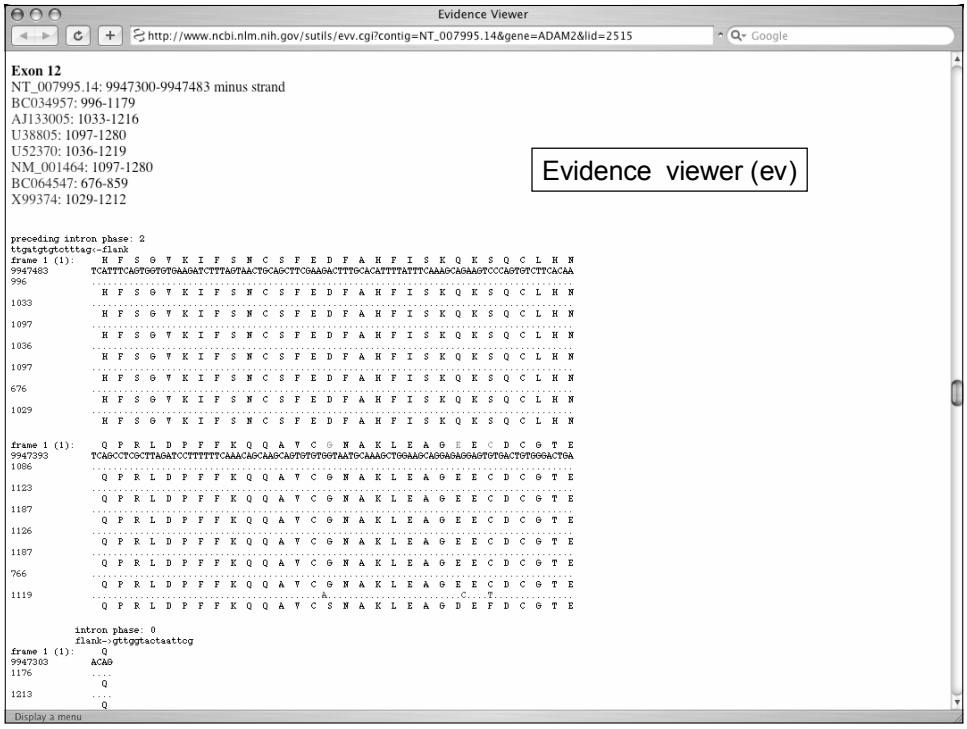

Map Viewer
http://www.ncbi.nlm.nih.gov/mapview/maps.cgi?taxid=9606&chr=8&MAPS=ugHs,genes,sts-r&cmd=foc
NCBI
NCBI Map Viewer
PubMed Entrez BLAST OMIM Taxonomy Structure
Search Find Find in This View Advanced Search
Map Viewer Home
Map Viewer Help
Human Maps Help
FTP
Data As Table View
Maps & Options
Compress Map
Region Shown:
31M
44M
Go
out
zoom
in
You are here:
Ideogram
default
master
Display a menu
Homo sapiens build 35.1
BLAST The Human Genome
Chromosome: 1 2 3 4 5 6 7 [8] 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y MT
Query: D8S1170 OR D8S94 [clear]
Master Map: STS
Summary of Maps
Maps & Options
Region Displayed: 31M-44M bp
Download/View Sequence/Evidence
HsUniG Genes_seq STS
marker Kbp polymorphism in_gene
G63290 32519 N N
D8S278 32668 Y N
STS-N33323 33027 N N
D8S1170 33241 N N
RH93742 33338 N N
D8S513 33789 Y N
G54633 34789 N N
D8S1486 35399 Y N
RH12794 35773 N N
SHGC-105114 36589 N N
D8S449 37307 N N
STS-N24894 37733 N N
D8S2119 37836 N N
RH35988 38116 N N
RH35840 38244 N N
SHGC-37155 38388 Y N
RH65979 38728 N N
Cda1hf08 38829 N N
G32133 39146 N N
GDB:315505 39963 N N
SHGC-85224 40501 N N
G59163 41007 N N
SHGC-81288 41581 N N
G19345 41707 N N
WI-15071 41906 Y N
GDB:185498 42171 N N
RH79839 42400 N N
D8S1209 42677 N N
RH28425 42923 N N
D8S94 43174 N N
Hs.125849 click for info
NRG1
UNC5D
D8S1170
D8S94
Summary of Maps:
Map 1: Human UniGene Clusters
Table View
Region Displayed: 31M-44M bp
Download/View Sequence/Evidence
Total EST/mRNA alignments On Chromosome: 147799 [384 not localized]
UniGene Clusters Labeled: 50 Total EST/mRNA alignments in Region: 11950
Histogram Data: Tick Width=16,645bp/pixel, Max Height=695 transcripts (logarithmic scale)
Map 2: Genes On Sequence
Table View
Region Displayed: 31M-44M bp
Download/View Sequence/Evidence
Total Genes On Chromosome: 927
Genes Labeled: 50 Total Genes in Region: 78
Map 3: STS
Table View
Region Displayed: 31M-44M bp
Download/View Sequence/Evidence
Total STSs On Chromosome: 5285 [6 not localized]
STSs Labeled: 30 Total STSs in Region: 421
Disclaimer | Write to the Help Desk
NCBI | NLM | NIH

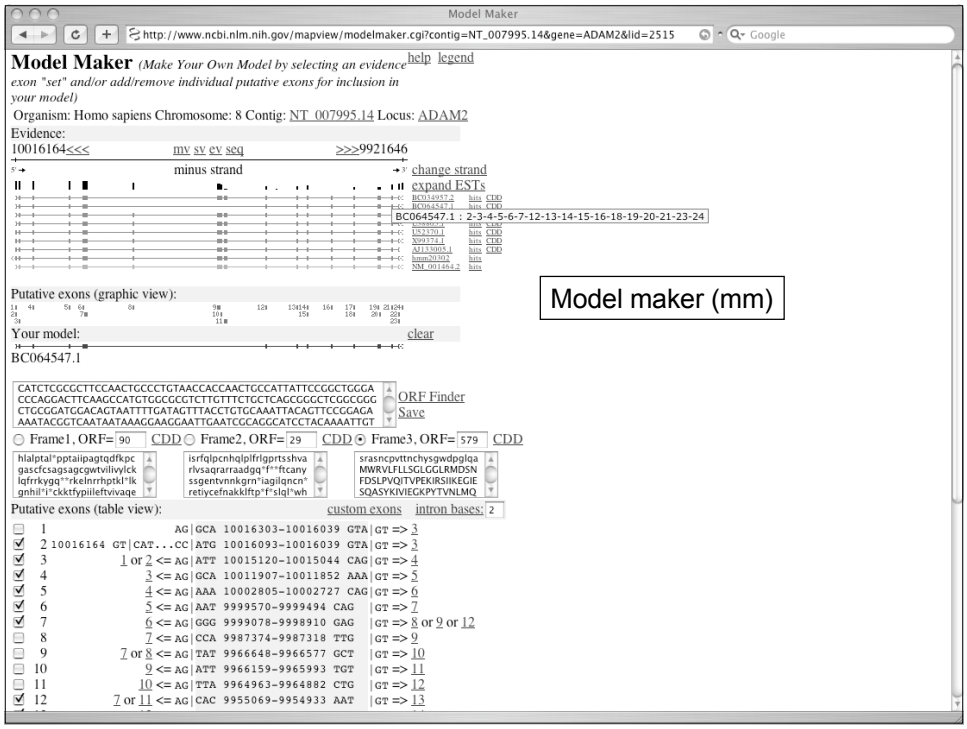

Map Viewer
http://www.ncbi.nlm.nih.gov/mapview/maps.cgi?TAXID=9606&CHR=8&BEG=33240501.00&END=43174
Google
Map Viewer Home
Map Viewer Help
Human Maps Help
FTP
Data As Table View
Maps & Options
Compress Map
Region Shown:
33M
43M
Go
out
zoom
in
You are here:
Ideogram
default
master
Display a menu
D8S1170 33241 N N
SHGC-147403 33374 N N
SHGC-156087 34558 N N
SHGC-111135 35049 N N
D8S1766 35563 Y N
D8S1700 35922 Y N
RH121708 36836 N N
AFMA295ZD5 37351 Y N
RH80675 37734 N N
D8S2119 37836 N N
NIB1979 38116 Y N
WI-15923 38239 Y N
SHGC-2825 38321 N N
GDB:251744 38419 N N
RH46312 38825 N N
RH48892 38948 N N
D8S515 39710 Y N
SHGC-83920 40052 N N
D8S1183 40632 N N
SHGC-153351 41100 N N
SHGC-81288 41581 N N
STS-W88737 41647 Y N
WI-11722 41809 Y N
D2S2567 42153 Y N
RH79876 42382 N N
A006X27 42527 Y N
G17243 42799 N N
D8S1675 43060 Y N
D8S94 43174 N N


Map Viewer
Organism: Homo sapiens
Help
Chromosome: 8
Region Shown: 33240501.0 43174146.0
Available Maps:
Maps Displayed (left to right):
Org: human
Assembly: ref
Change Assembly
--Sequence Maps---
Ab initio
Assembly
Repeats
BES_Clone
Clone
NCI_Clone
Contig
Component
ADD>>
<<REMOVE
[ ] Contig
[ ] Component
[R] STS
[ ] Gene
Move UP
Move DOWN
Make Master/Move to Bottom
Toggle Ruler
([R] before map means 'ruler set')
More Options:
Show Connections
Verbose Mode
Compress Map: auto
Auto Compress if > 350 px
Page Length: 75
Thumbnail View: default (ideogram) master
Apply
Close


Query: D8S1170 OR D8S94 [clear]
Master Map: Genes On Sequence
Summary of Maps
Maps & Options
Region Displayed: 33M-43M bp
Download/View Sequence/Evidence
Contig
Comp
STS
Genes_seq
Symbol O LinkOut E Cyto Description
FUT10 sv pr dl ev mm hm C 8p12 fucosyltransferase
LOC84549 sv pr dl ev mm hm C 8p12 RNA binding pro
FLJ23263 sv pr dl ev mm hm C 8p12 hypothetical prote
RNF122 sv pr dl ev mm hm C 8p12 ring finger protein
MGC1136 sv pr dl ev mm hm C 8p12 hypothetical prote
LOC442384 sv dl ev mm ? 8p12 similar to VENT-
BLP1 sv pr dl ev mm hm C 8p11.23 BBP-like protein
ADAM9 OMIM sv pr dl ev mm hm C 8p11.23 a disintegrin and
ADAM32 sv pr dl ev mm hm C 8p11.23 a disintegrin and
ADAM5 sv dl ev mm C 8p11.23 a disintegrin and
ADAM3A OMIM sv dl ev mm C 8p21-p12 a disintegrin and
ADAM18 sv pr dl ev mm hm C 8p11.22 a disintegrin and
ADAM2 OMIM sv pr dl ev mm C 8p11.2 a disintegrin and
INDO OMIM sv pr dl ev mm hm C 8p12-p11 indoleamine-pyrr
LOC169355 sv pr dl ev mm hm C 8p11.21 hypothetical prote
FLJ23356 sv pr dl ev mm hm C 8p11.21 hypothetical prote
LOC441347 sv pr dl ev mm E 8p11.21 similar to family
FLJ32731 sv pr dl ev mm hm C 8p11.1 hypothetical prote
Summary of Maps:
Map 1: Contig Table View
Region Displayed: 33M-43M bp Download/View Sequence/Evidence
Total Contigs On Chromosome: 18 [8 not localized]
Contigs Labeled: 1 Total Contigs in Region: 1
Map 2: Component Table View
Region Displayed: 33M-43M bp Download/View Sequence/Evidence
Total Components On Chromosome: 1200 [8 not localized]
Components Labeled: 85 Total Components in Region: 85
Map 3: STS Table View
Region Displayed: 33M-43M bp Download/View Sequence/Evidence
Total STSs On Chromosome: 5285 [6 not localized]
STSs Labeled: 125 Total STSs in Region: 372
Map 4: Genes On Sequence Table View
Region Displayed: 33M-43M bp Download/View Sequence/Evidence
Total Genes On Chromosome: 927
Genes Labeled: 74 Total Genes in Region: 74

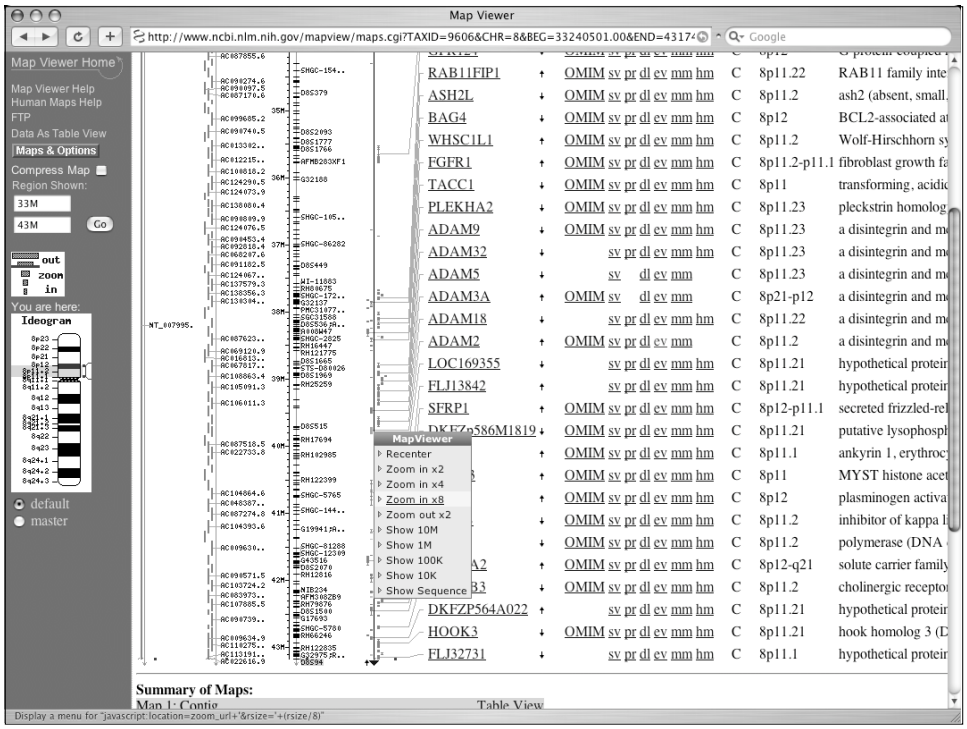

Download Sequence Region
http://www.ncbi.nlm.nih.gov/mapview/seq_reg.cgi?chr=8&from=39720414&to=39814932
Google
Homo sapiens Genome (build 35.1)
Region to retrieve (in chromosome coordinates):
Chromosome: 8 Strand: plus
from: 39720414 adjust by: -0K
to: 39814932 adjust by: +0K
Change Region/Strand
Sequence Format: FASTA
This chromosome region corresponds to the contig region(s):
Contig start stop strand
NT_007995.14 9921646 10016164 + Display Save to Disk View Evidence ModelMaker
Sequence download (dl)

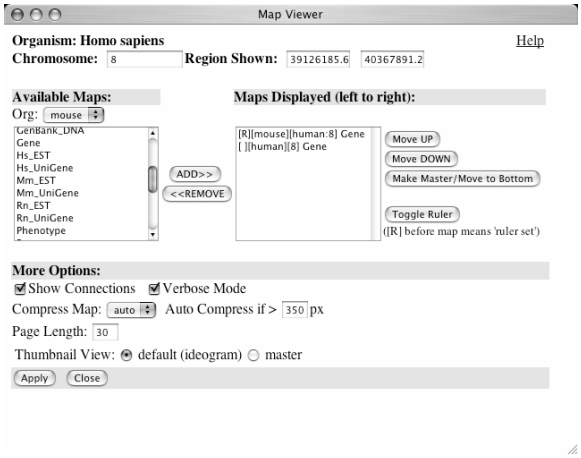

Evidence Viewer
http://www.ncbi.nlm.nih.gov/sutils/evv.cgi?contig=NT_007995.14&gene=ADAM2&lid=2515
Exon 12
NT_007995.14: 9947300-9947483 minus strand
BC034957: 996-1179
AJ133005: 1033-1216
U38805: 1097-1280
U52370: 1036-1219
NM_001464: 1097-1280
BC064547: 676-859
X99374: 1029-1212
Evidence viewer (ev)
Display a menu

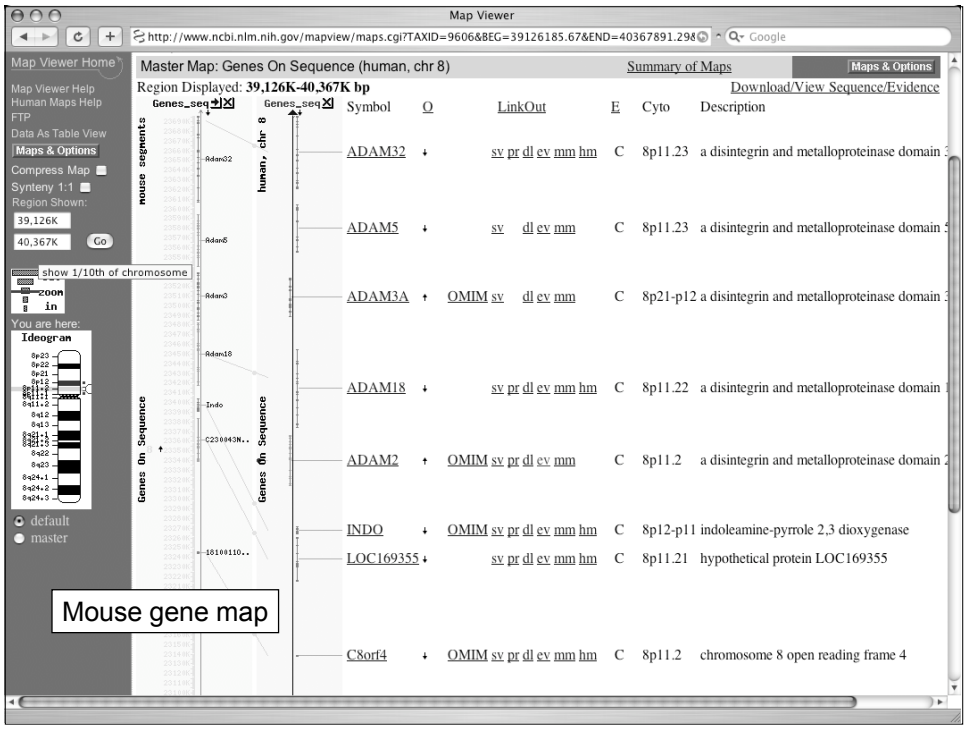

Model Maker
http://www.ncbi.nlm.nih.gov/mapview/modelmaker.cgi?contig=NT_007995.14&gene=ADAM2&lid=2515
Model Maker (Make Your Own Model by selecting an evidence exon "set" and/or add/remove individual putative exons for inclusion in your model)
help legend
Organism: Homo sapiens Chromosome: 8 Contig: NT_007995.14 Locus: ADAM2
Evidence:
10016164<<< mv sv ev seq >>>9921646
minus strand
change strand
expand ESTs
BC064547.1 : 2-3-4-5-6-7-12-13-14-15-16-18-19-20-21-23-24
Putative exons (graphic view):
Your model:
clear
BC064547.1
ORF Finder
Save
Frame1, ORF= 90 CDD Frame2, ORF= 29 CDD Frame3, ORF= 579 CDD
Putative exons (table view):
custom exons intron bases: 2
Model maker (mm)

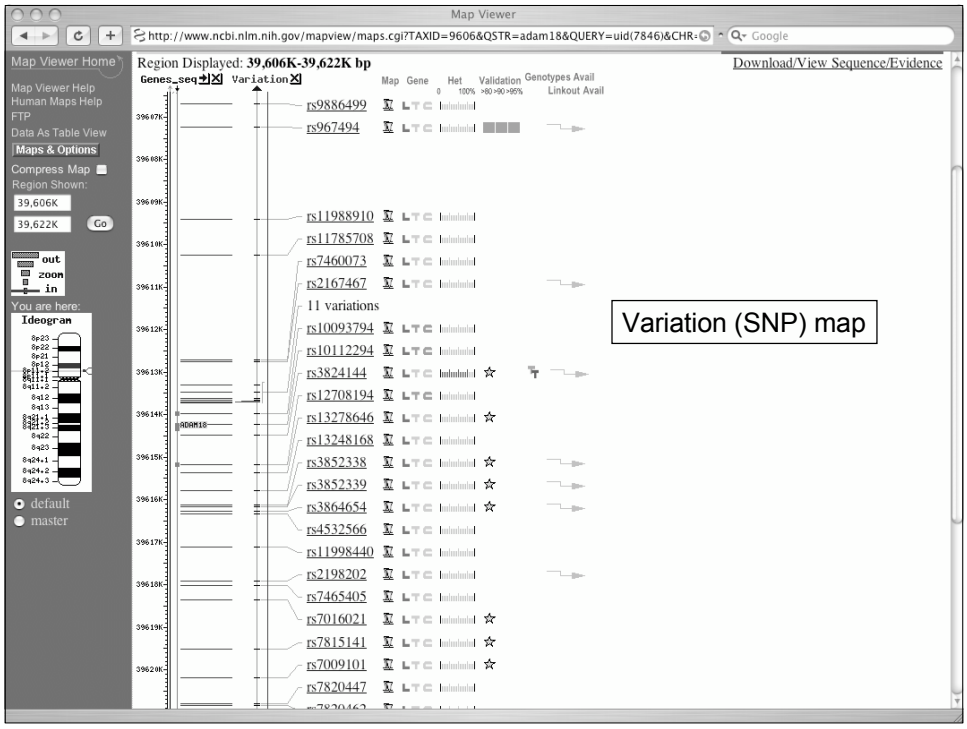
NCBI

Change the maps displayed on the Map Viewer



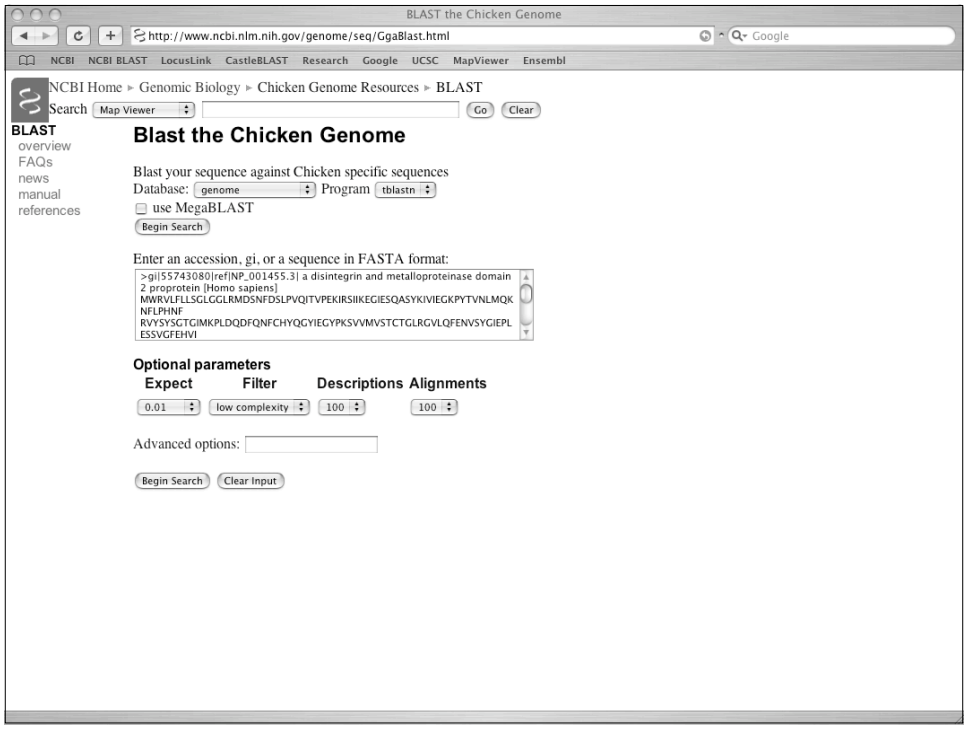

Map Viewer
Organism: Homo sapiens
Help
Chromosome: 8
Region Shown: 39126185.6 40367891.2
Available Maps:
Org: mouse
GenBank_DNA
Gene
Hs_EST
Hs_UniGene
Mm_EST
Mm_UniGene
Rn_EST
Rn_UniGene
Phenotype
ADD>>
<<REMOVE
Maps Displayed (left to right):
[R][mouse][human:8] Gene
[ ][human][8] Gene
Move UP
Move DOWN
Make Master/Move to Bottom
Toggle Ruler
([R] before map means 'ruler set')
More Options:
Show Connections
Verbose Mode
Compress Map: auto
Auto Compress if > 350 px
Page Length: 30
Thumbnail View: default (ideogram) master
Apply
Close

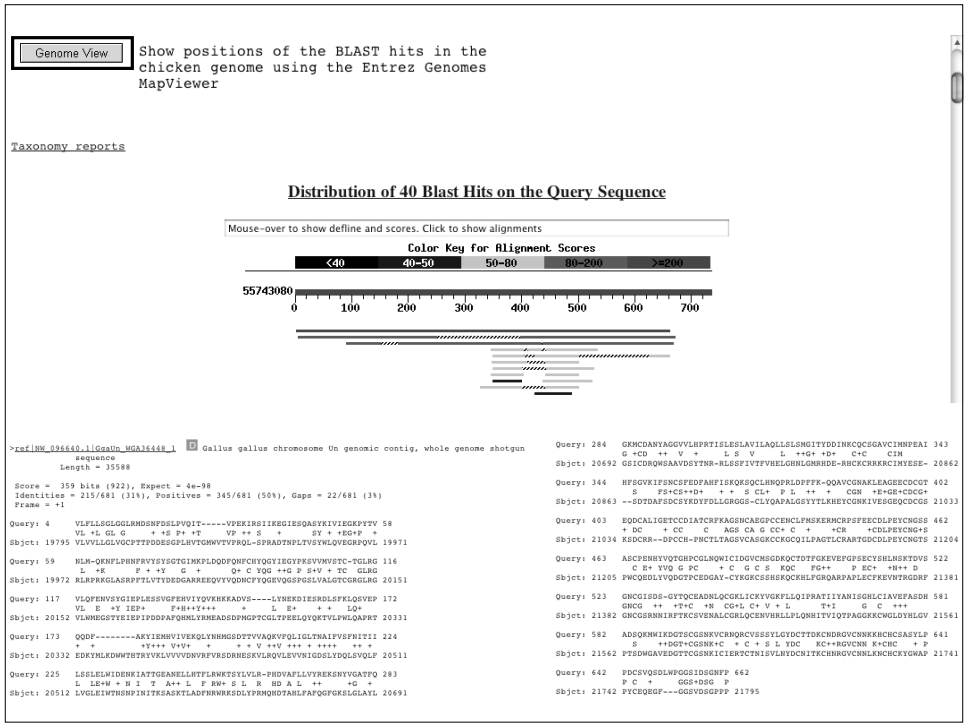

Map Viewer
http://www.ncbi.nlm.nih.gov/mapview/maps.cgi?TAXID=9606&BEG=39126185.67&END=40367891.298
Google
Map Viewer Home
Map Viewer Help
Human Maps Help
FTP
Data As Table View
Maps & Options
Compress Map
Synteny 1:1
Region Shown:
39,126K
40,367K
Go
show 1/10th of chromosome
zoom
in
You are here:
Ideogram
default
master
Mouse gene map
Master Map: Genes On Sequence (human, chr 8)
Summary of Maps
Maps & Options
Region Displayed: 39,126K-40,367K bp
Download/View Sequence/Evidence
Genes_seq
Genes_seq
mouse segments
human, chr 8
Genes On Sequence
Genes On Sequence
Symbol O LinkOut E Cyto Description
ADAM32 sv pr dl ev mm hm C 8p11.23 a disintegrin and metalloproteinase domain
ADAM5 sv dl ev mm C 8p11.23 a disintegrin and metalloproteinase domain
ADAM3A OMIM sv dl ev mm C 8p21-p12 a disintegrin and metalloproteinase domain
ADAM18 sv pr dl ev mm hm C 8p11.22 a disintegrin and metalloproteinase domain
ADAM2 OMIM sv pr dl ev mm C 8p11.2 a disintegrin and metalloproteinase domain
INDO OMIM sv pr dl ev mm hm C 8p12-p11 indoleamine-pyrrole 2,3 dioxygenase
LOC169355 sv pr dl ev mm hm C 8p11.21 hypothetical protein LOC169355
C8orf4 OMIM sv pr dl ev mm hm C 8p11.2 chromosome 8 open reading frame 4

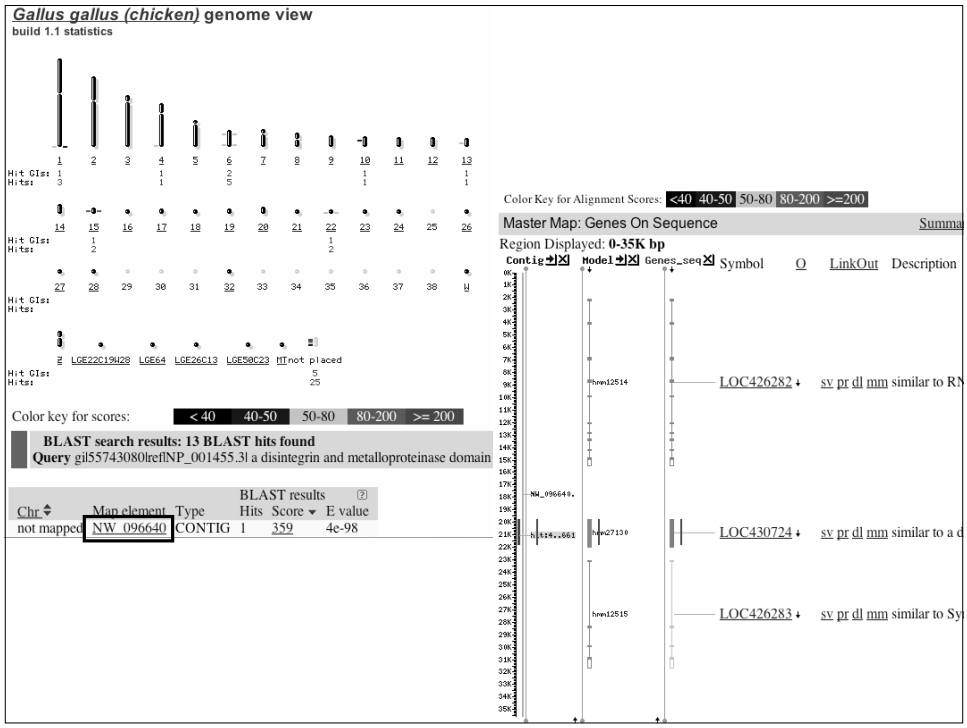


NCBI

Find a chicken homolog of a human protein

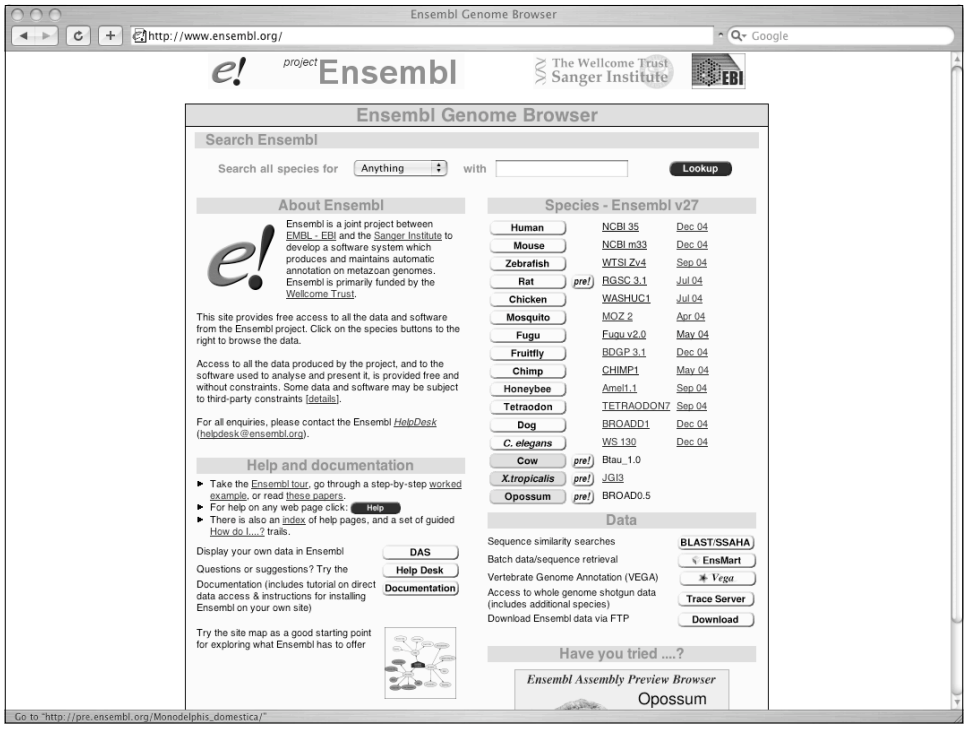

BLAST the Chicken Genome
http://www.ncbi.nlm.nih.gov/genome/seq/GgaBlast.html
NCBI Home ▸ Genomic Biology ▸ Chicken Genome Resources ▸ BLAST
Search Map Viewer
Go
Clear
BLAST
overview
FAQs
news
manual
references
Blast the Chicken Genome
Blast your sequence against Chicken specific sequences
Database: genome
Program tblastn
use MegaBLAST
Begin Search
Enter an accession, gi, or a sequence in FASTA format:
>gi|55743080|ref|NP_001455.3| a disintegrin and metalloproteinase domain 2 proprotein [Homo sapiens]
MWRVLFLLSGLGGLRMDSNFDSLPVQITVPEKIRSIIKEGIESQASYKIVIEGKPYTVNLMQK
NFLPHNF
RVYSYSGTGIMKPLDQDFQNFCHYQGYIEGYPKSVVMVSTCTGLRGVLQFENVSYGIEPL
ESSVGFEHVI
Optional parameters
Expect
Filter
Descriptions
Alignments
0.01
low complexity
100
100
Advanced options:
Begin Search
Clear Input


Genome View
Show positions of the BLAST hits in the chicken genome using the Entrez Genomes MapViewer
Taxonomy reports
Distribution of 40 Blast Hits on the Query Sequence
Mouse-over to show defline and scores. Click to show alignments
Color Key for Alignment Scores
<40
40-50
50-80
80-200
>=200
55743080
0
100
200
300
400
500
600
700
>ref|NW_036640.1|GgaUn_NGA36448_1 Gallus gallus chromosome Un genomic contig, whole genome shotgun sequence
Length = 35588
Score = 359 bits (922), Expect = 4e-98
Identities = 215/681 (31%), Positives = 345/681 (50%), Gaps = 22/681 (3%)
Frame = +1
Query: 4 VLFLLSGLGGLRMDSNFDSLPVQIT-----VPEKIRSIIKEGIESQASYKIVIEGKPYTV 58
VL +L GL G + +S P+ +T VP ++ S + SY + +EG+P +
Sbjct: 19795 VLVVLLGLVGCPTTPDDESGPLHVIGHWVTVPRQL-SPRADTNPLTYSYWLQVEGKRQVL 19971
Query: 59 NLM-QKNFLPHNFRVYSYSGTGIMKPLDQDFQNFCHYQGYIEGYPKSVVMVSTC-TGLRG 116
L +K F + +Y G + Q+ C YQG ++G P S+V + TC GLRG
Sbjct: 19972 RLRPRKGLASRPFTLVTYDEDGARREQVYVQDHCFYQGEVQGSPGSLVALGTCGRGLRG 20151
Query: 117 VLQFENVSYGIEPLESSVGFEHVIYQVKHKKADVS----LYNEKDIESRDLSFKLQSVEP 172
VL E +Y IEP+ F+H++Y+++ + L E+ + + LQ+
Sbjct: 20152 VLWMEGSTYEIEPIPDDPAFQHMLYRMEADSDPMGPTCGLTPEELQYQKTVLPWLQAPRT 20331
Query: 173 QQDF--------AKYIENHVIVEKQLYHHMGSDTTVVAQKVFQLIGLTNAIFVSFNITII 224
+ + +Y+++ V+V+ + + V ++V +++ + ++++ ++ +
Sbjct: 20332 EDKYMLKDWWTHTRYVKLVVVVDNVRFVRSDRNESKVLRQVLEVVNIGDSLYDQLSVQLF 20511
Query: 225 LSSLELWIDENKIATTGEANELLHTFLRWKTSYLVLR-PHDVAFLLVYREKSNYVGATFQ 283
L LE+W + N I T A++ L F RW+ S L R HD A L ++ +G +
Sbjct: 20512 LVGLEIWTNSNPIHITKSASKTLADFRRWRRSDLYPRNQHDTAHLFAFQGFGKSLGLAYL 20691
Query: 284 GKMCDANVAGGVVLHPRTISLESLAVILAQLLSLSNGITYDDINKCQCSGAVCINNPEAI 343
G +CD ++ V + L S V L +*G+ +D+ C+C CIM
Sbjct: 20692 GSICDRQWSAAVDSYTNR-RLSSFIVTFVHELGHNLGMRHDE-RHCKCRRKRCIMYESE- 20862
Query: 344 HFSGVKIFSNCSFEDFAHFISKQRSQCLHNQPRLDPFFK-QQAVCGNAKLEAGEECDCGT 402
S FS+CS++D+ + + S CL+ P L ++ + CGN +E+GE+CDCG+
Sbjct: 20863 --SDTDAFSDCSYKDYFDLLGRGGS-CLYQAPALGSYYTLKHEYCGNKIVESGEQCDCGS 21033
Query: 403 EQDCALIGETCCDIATCRFKAGSNCAEGPCCENCLFMSKERMCRPSFEECDLPEYCNGSS 462
+ DC + CC C AGS CA G CC+ C + +CR +CDLPEYCNG+S
Sbjct: 21034 KSDCRR--DPCCH-PNCTLTAGSVCASGKCCKGCQILPAGTLCRARTGDCDLPEYCNGTS 21204
Query: 463 ASCPENHVVQTGHPCGLNQWICIDGVCMSGDKQCTDTFGKEVEPGPSECYSHLNSKTDVS 522
C E+ YVQ G PC + C G C S KQC FG++ P EC+ +N++ D
Sbjct: 21205 PWCQEDLYVQDGTPCEDGAY-CYKGKCSSHSKQCKHLFGRQARPAPLECFKEVNTRGDRF 21381
Query: 523 GNCGISDS-GYTQCEADNLQCGKLICKYVGKPLLQIPRATIIYANISGHLCIAVEFASDH 581
GNCG ++ +T+C +N CG+L C+ V + L T+I G C +++
Sbjct: 21382 GNCGSRNNIRFTKCSVENALCGRLQCENVHRLLPLQNHITVIQTPAGGKKCWGLDYHLGV 21561
Query: 582 ADSQKMWIKDGTSCGSNKVCRNQRCVSSSYLGYDCTTDKCNDRGVCNNKKHCHCSASYLP 641
S ++DGT+CGSNK+C + C + S L YDC KC++RGVCNN K+CHC + P
Sbjct: 21562 PTSDWGAVEDGTTCGSNKICIERTCTNISVLNYDCNITKCHNRGVCNNLKNCHCKYGWAP 21741
Query: 642 PDCSVQSDLWPGGSIDSGNFP 662
P C + GGS+DSG P
Sbjct: 21742 PYCEQEGF---GGSVDSGFPP 21795



Ensembl

Identify genes and SNPs in a chromosomal band


Ensembl Genome Browser
http://www.ensembl.org/
project Ensembl
The Wellcome Trust Sanger Institute
EBI
Ensembl Genome Browser
Search Ensembl
Search all species for Anything with Lookup
About Ensembl
Ensembl is a joint project between EMBL - EBI and the Sanger Institute to develop a software system which produces and maintains automatic annotation on metazoan genomes. Ensembl is primarily funded by the Wellcome Trust.
This site provides free access to all the data and software from the Ensembl project. Click on the species buttons to the right to browse the data.
Access to all the data produced by the project, and to the software used to analyse and present it, is provided free and without constraints. Some data and software may be subject to third-party constraints [details].
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Help and documentation
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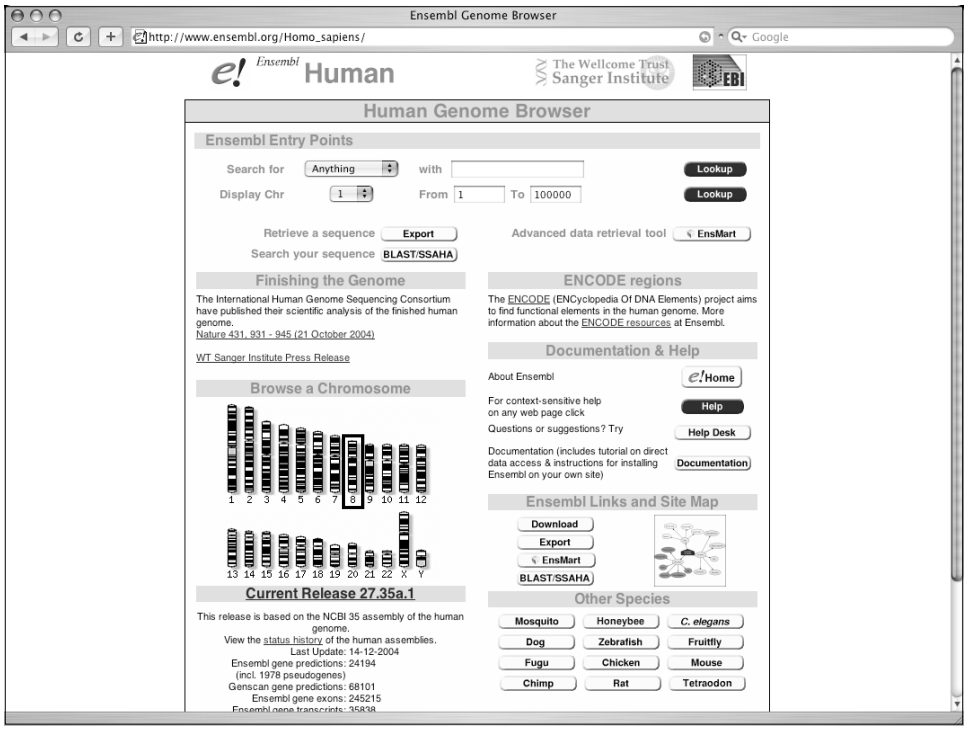
For help on any web page click: Help
There is also an index of help pages, and a set of guided How do I...? trails.
Display your own data in Ensembl DAS
Questions or suggestions? Try the Help Desk
Documentation (includes tutorial on direct data access & instructions for installing Ensembl on your own site) Documentation
Try the site map as a good starting point for exploring what Ensembl has to offer
Species - Ensembl v27
Human NCBI 35 Dec 04
Mouse NCBI m33 Dec 04
Zebrafish WTSI Zv4 Sep 04
Rat pre! RGSC 3.1 Jul 04
Chicken WASHUC1 Jul 04
Mosquito MOZ 2 Apr 04
Fugu Fugu v2.0 May 04
Fruitfly BDGP 3.1 Dec 04
Chimp CHIMP1 May 04
Honeybee Amel1.1 Sep 04
Tetraodon TETRAODON7 Sep 04
Dog BROADD1 Dec 04
C. elegans WS 130 Dec 04
Cow pre! Btau_1.0
X.tropicalis pre! JGI3
Opossum pre! BROAD0.5
Data
Sequence similarity searches BLAST/SSAHA
Batch data/sequence retrieval EnsMart
Vertebrate Genome Annotation (VEGA) Vega
Access to whole genome shotgun data (includes additional species) Trace Server
Download Ensembl data via FTP Download
Have you tried ....?
Ensembl Assembly Preview Browser
Opossum
Go to "http://pre.ensembl.org/Monodelphis_domestica/"


Ensembl Genome Browser
http://www.ensembl.org/Homo_sapiens/
Ensembl Human
The Wellcome Trust Sanger Institute
EBI
Human Genome Browser
Ensembl Entry Points
Search for Anything with Lookup
Display Chr 1 From 1 To 100000 Lookup
Retrieve a sequence Export
Search your sequence BLAST/SSAHA
Advanced data retrieval tool EnsMart
Finishing the Genome
The International Human Genome Sequencing Consortium have published their scientific analysis of the finished human genome.
Nature 431, 931 - 945 (21 October 2004)
WT Sanger Institute Press Release
Browse a Chromosome
1 2 3 4 5 6 7 8 9 10 11 12
13 14 15 16 17 18 19 20 21 22 X Y
Current Release 27.35a.1
This release is based on the NCBI 35 assembly of the human genome.
View the status history of the human assemblies.
Last Update: 14-12-2004
Ensembl gene predictions: 24194
(incl. 1978 pseudogenes)
Genscan gene predictions: 68101
Ensembl gene exons: 245215
ENCODE regions
The ENCODE (ENCyclopedia Of DNA Elements) project aims to find functional elements in the human genome. More information about the ENCODE resources at Ensembl.
Documentation & Help
About Ensembl e! Home
For context-sensitive help on any web page click Help
Questions or suggestions? Try Help Desk
Documentation (includes tutorial on direct data access & instructions for installing Ensembl on your own site) Documentation
Ensembl Links and Site Map
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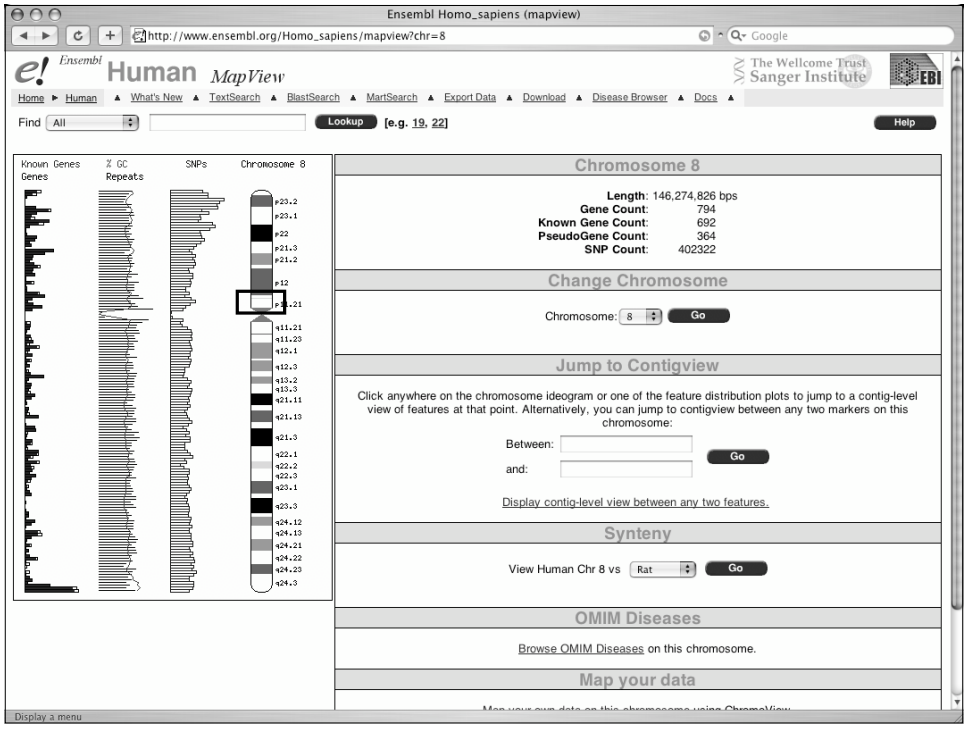
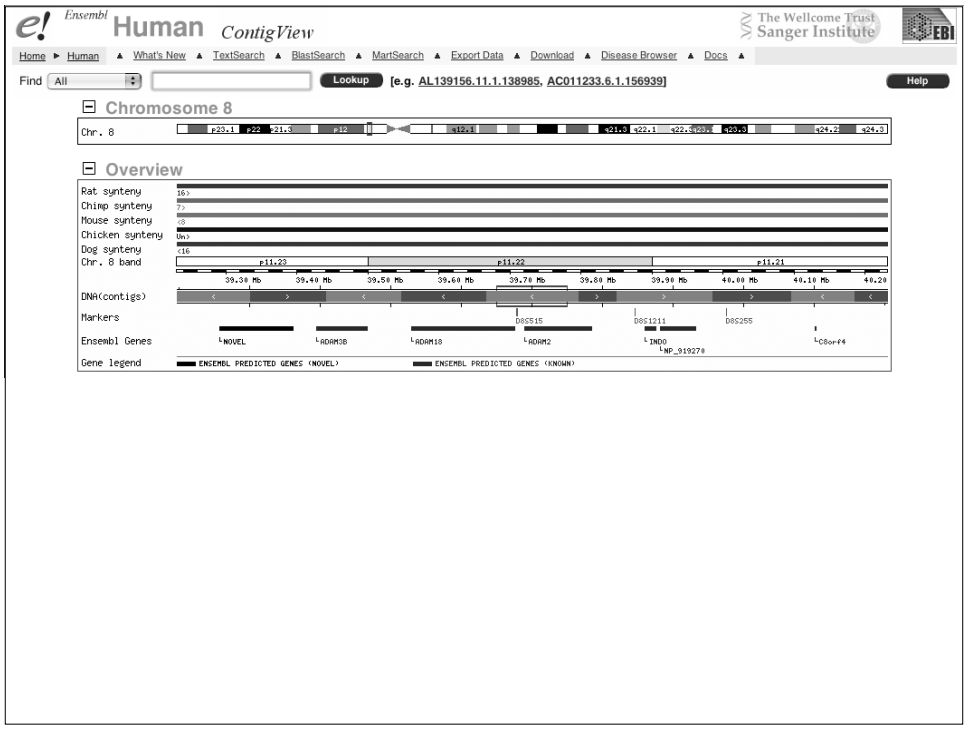
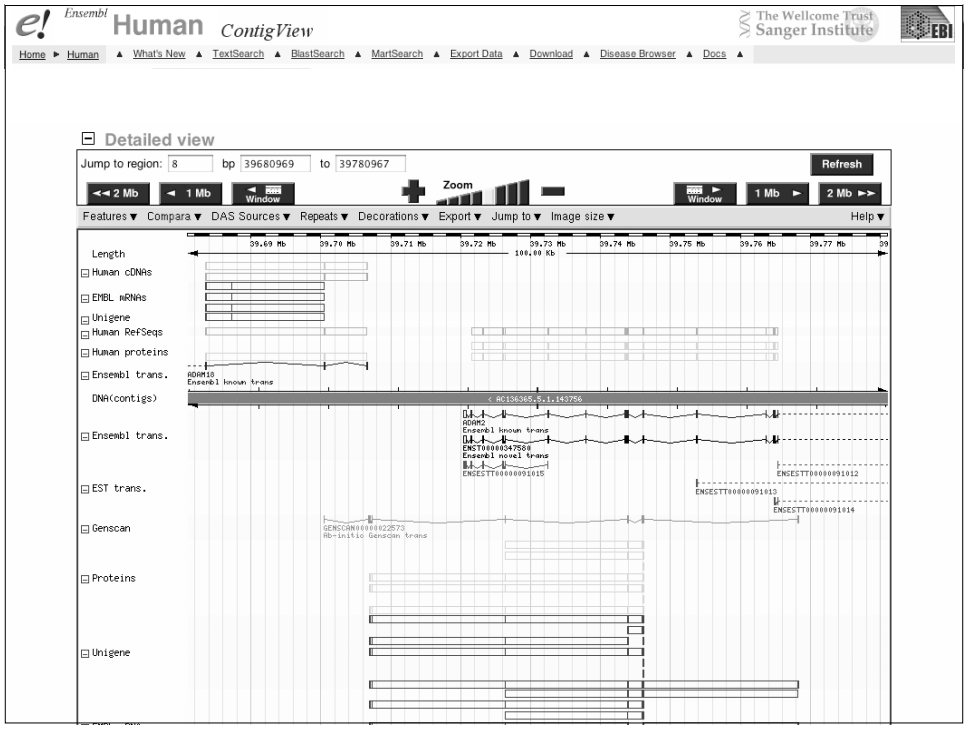
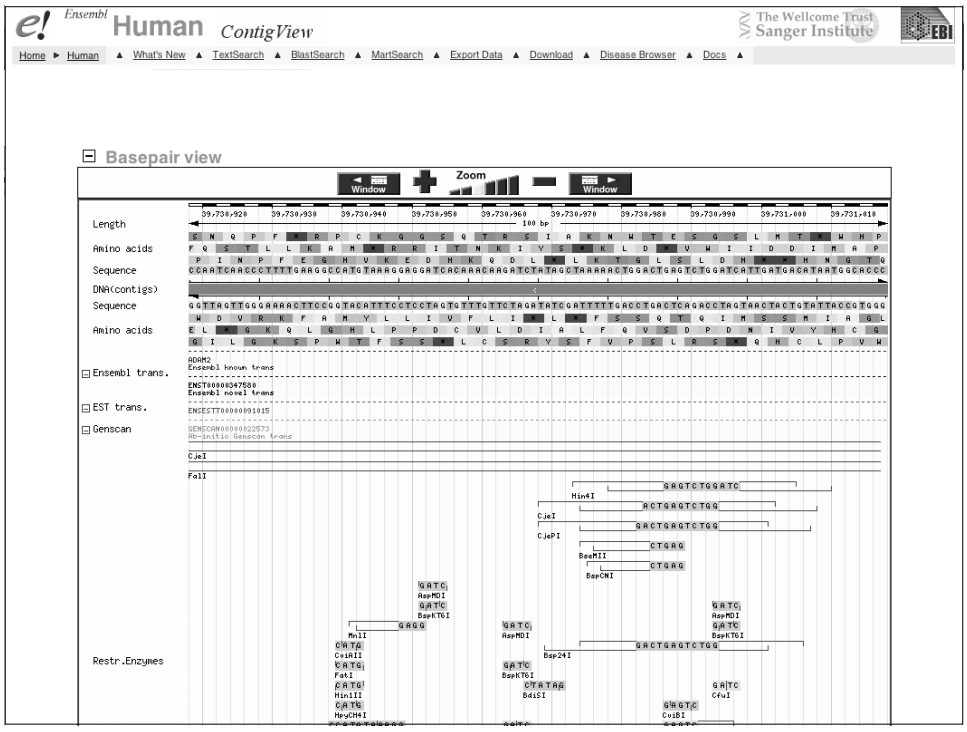
EnsMart
BLAST/SSAHA
Other Species
Mosquito Honeybee C. elegans
Dog Zebrafish Fruitfly
Fugu Chicken Mouse
Chimp Rat Tetraodon


Ensembl Homo_sapiens (mapview)
http://www.ensembl.org/Homo_sapiens/mapview?chr=8
Ensembl Human MapView
The Wellcome Trust Sanger Institute
Home ▶ Human ▲ What's New ▲ TextSearch ▲ BlastSearch ▲ MartSearch ▲ Export Data ▲ Download ▲ Disease Browser ▲ Docs ▲
Find All Lookup [e.g. 19, 22] Help
Known Genes
Genes
% GC
Repeats
SNPs
Chromosome 8
Chromosome 8
Length: 146,274,826 bps
Gene Count: 794
Known Gene Count: 692
PseudoGene Count: 364
SNP Count: 402322
Change Chromosome
Chromosome: 8 Go
Jump to Contigview
Click anywhere on the chromosome ideogram or one of the feature distribution plots to jump to a contig-level view of features at that point. Alternatively, you can jump to contigview between any two markers on this chromosome:
Between:
and:
Go
Display contig-level view between any two features.
Synteny
View Human Chr 8 vs Rat Go
OMIM Diseases
Browse OMIM Diseases on this chromosome.
Map your data
Display a menu

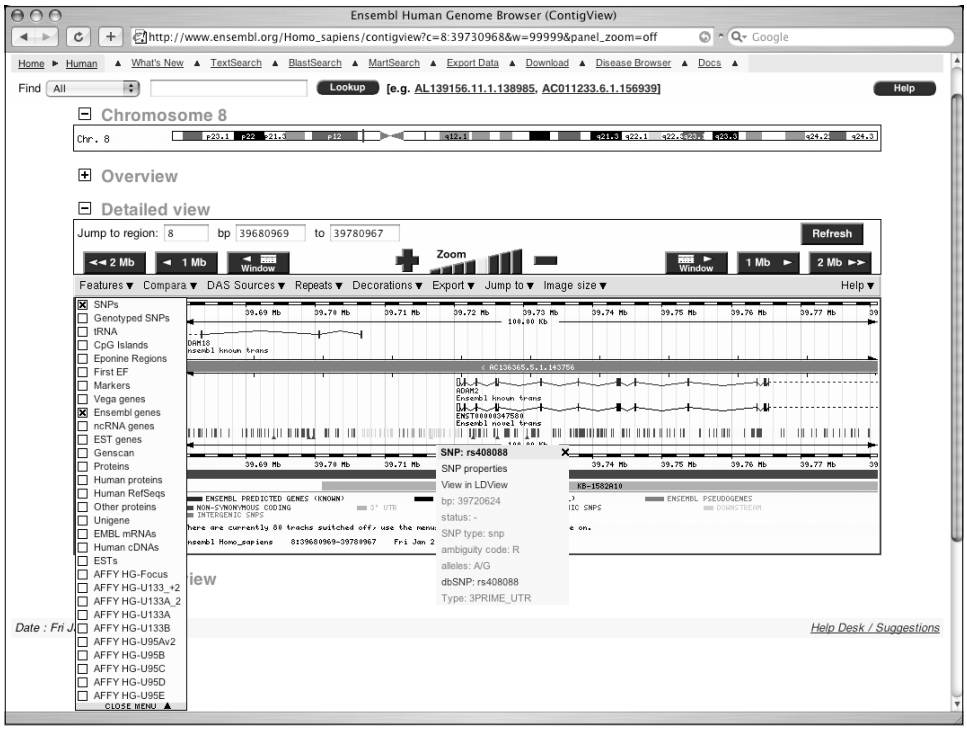

Ensembl Human ContigView
The Wellcome Trust Sanger Institute
Home ▶ Human ▲ What's New ▲ TextSearch ▲ BlastSearch ▲ MartSearch ▲ Export Data ▲ Download ▲ Disease Browser ▲ Docs ▲
Find All Lookup [e.g. AL139156.11.1.138985, AC011233.6.1.156939] Help
Chromosome 8
Chr. 8
Overview
Rat synteny
Chimp synteny
Mouse synteny
Chicken synteny
Dog synteny
Chr. 8 band
DNA(contigs)
Markers
Ensembl Genes
Gene legend
ENSEMBL PREDICTED GENES (NOVEL)
ENSEMBL PREDICTED GENES (KNOWN)

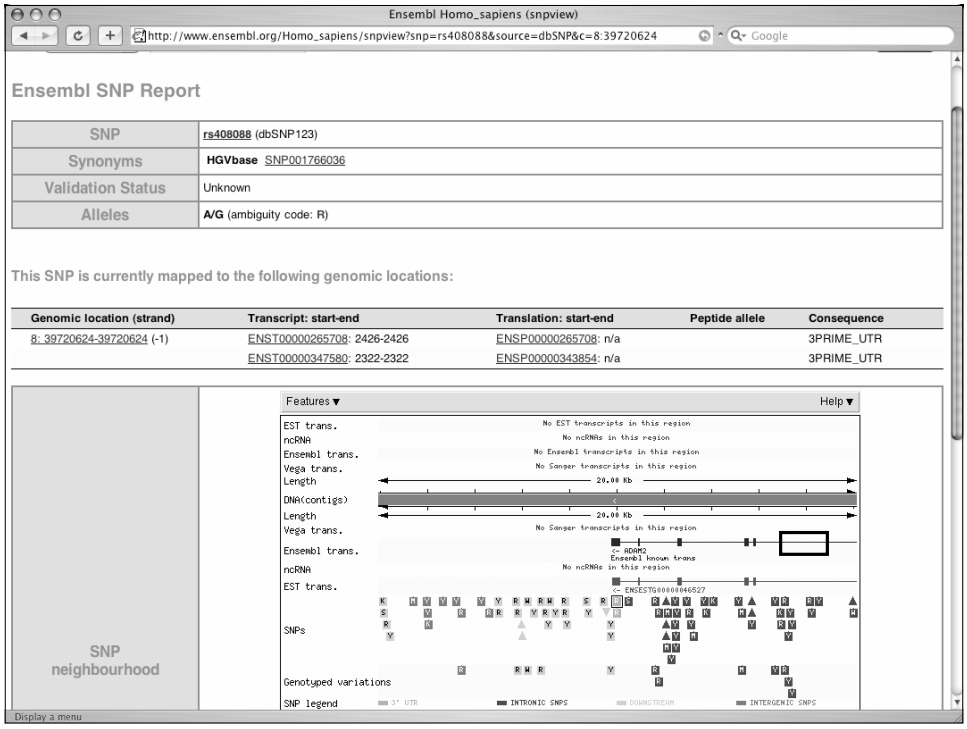

Ensembl Human ContigView
The Wellcome Trust Sanger Institute
EBI
Home ▶ Human ▲ What's New ▲ TextSearch ▲ BlastSearch ▲ MartSearch ▲ Export Data ▲ Download ▲ Disease Browser ▲ Docs ▲
Detailed view
Jump to region: 8 bp 39680969 to 39780967
Refresh
◄◄ 2 Mb ◄ 1 Mb Window Zoom Window 1 Mb ► 2 Mb ►►
Features ▼ Compara ▼ DAS Sources ▼ Repeats ▼ Decorations ▼ Export ▼ Jump to ▼ Image size ▼ Help ▼
Length
Human cDNAs
EMBL mRNAs
Unigene
Human RefSeqs
Human proteins
Ensembl trans.
DNA(contigs)
Ensembl trans.
EST trans.
Genscan
Proteins
Unigene

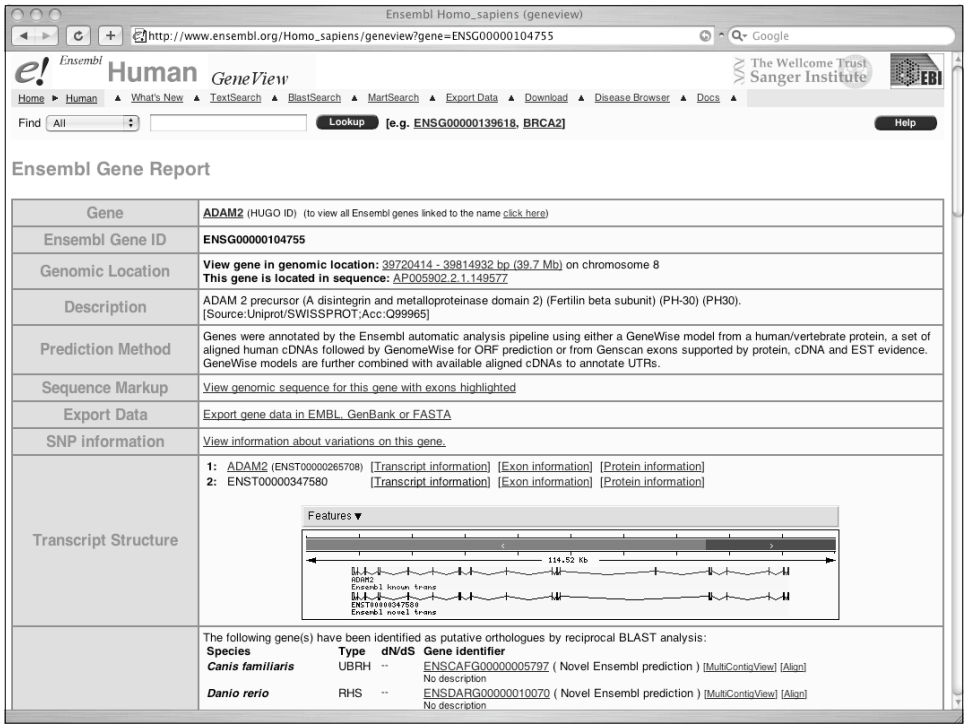

Ensembl Human ContigView
The Wellcome Trust Sanger Institute
EBI
Home ▶ Human ▲ What's New ▲ TextSearch ▲ BlastSearch ▲ MartSearch ▲ Export Data ▲ Download ▲ Disease Browser ▲ Docs ▲
Basepair view
Window Zoom Window
Length
Amino acids
Sequence
DNA(contigs)
Sequence
Amino acids
Ensembl trans.
EST trans.
Genscan
Restr.Enzymes

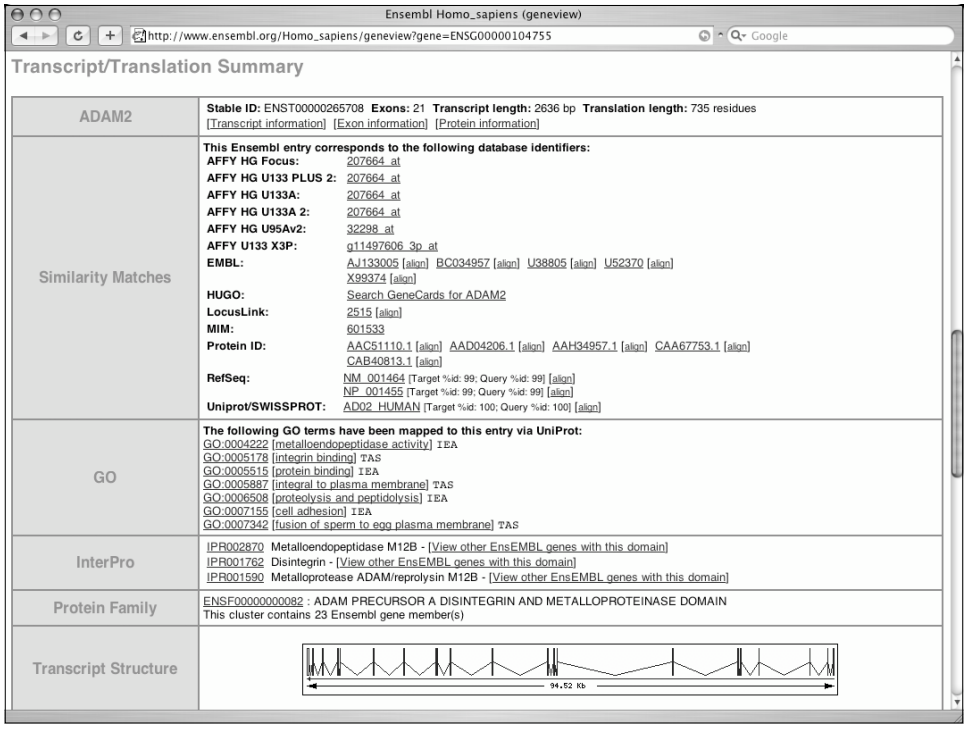
Ensembl

Change the tracks displayed on the ContigView



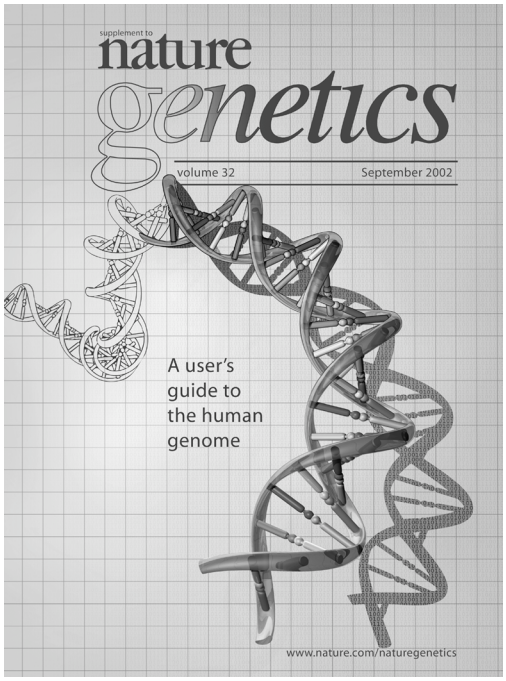

Ensembl Homo_sapiens (snpview)
http://www.ensembl.org/Homo_sapiens/snpview?snp=rs408088&source=dbSNP&c=8:39720624
Google
Ensembl SNP Report
SNP
rs408088 (dbSNP123)
Synonyms
HGVbase SNP001766036
Validation Status
Unknown
Alleles
A/G (ambiguity code: R)
This SNP is currently mapped to the following genomic locations:
Genomic location (strand)
Transcript: start-end
Translation: start-end
Peptide allele
Consequence
8: 39720624-39720624 (-1)
ENST00000265708: 2426-2426
ENSP00000265708: n/a
3PRIME_UTR
ENST00000347580: 2322-2322
ENSP00000343854: n/a
3PRIME_UTR
SNP neighbourhood
Features
Help
EST trans.
ncRNA
Ensembl trans.
Vega trans.
Length
DNA(contigs)
SNPs
Genotyped variations
SNP legend
INTRONIC SNPS
INTERGENIC SNPS
Display a menu


Ensembl Homo_sapiens (geneview)
http://www.ensembl.org/Homo_sapiens/geneview?gene=ENSG00000104755
Google
Ensembl Human GeneView
The Wellcome Trust Sanger Institute
EBI
Home
Human
What's New
TextSearch
BlastSearch
MartSearch
Export Data
Download
Disease Browser
Docs
Find
All
Lookup
[e.g. ENSG00000139618, BRCA2]
Help
Ensembl Gene Report
Gene
ADAM2 (HUGO ID) (to view all Ensembl genes linked to the name click here)
Ensembl Gene ID
ENSG00000104755
Genomic Location
View gene in genomic location: 39720414 - 39814932 bp (39.7 Mb) on chromosome 8
This gene is located in sequence: AP005902.2.1.149577
Description
ADAM 2 precursor (A disintegrin and metalloproteinase domain 2) (Fertilin beta subunit) (PH-30) (PH30).
[Source:Uniprot/SWISSPROT;Acc:Q99965]
Prediction Method
Genes were annotated by the Ensembl automatic analysis pipeline using either a GeneWise model from a human/vertebrate protein, a set of aligned human cDNAs followed by GenomeWise for ORF prediction or from Genscan exons supported by protein, cDNA and EST evidence. GeneWise models are further combined with available aligned cDNAs to annotate UTRs.
Sequence Markup
View genomic sequence for this gene with exons highlighted
Export Data
Export gene data in EMBL, GenBank or FASTA
SNP information
View information about variations on this gene.
Transcript Structure
1: ADAM2 (ENST00000265708) [Transcript information] [Exon information] [Protein information]
2: ENST00000347580 [Transcript information] [Exon information] [Protein information]
Features
114.52 Kb
ADAM2
Ensembl known trans
ENST00000347580
Ensembl novel trans
The following gene(s) have been identified as putative orthologues by reciprocal BLAST analysis:
Species
Type
dN/dS
Gene identifier
Canis familiaris
UBRH
ENSCAFG00000005797 (Novel Ensembl prediction) [MultiContigView] [Align]
No description
Danio rerio
RHS
ENSDARG00000010070 (Novel Ensembl prediction) [MultiContigView] [Align]
No description



Online resources

- UCSC Human Genome Browser User Guide
  http://genome.ucsc.edu/goldenPath/help/hgTracksHelp.html
- NCBI Genomic Biology
  http://www.ncbi.nih.gov/Genomes/
- NCBI MapViewer Help
  http://www.ncbi.nlm.nih.gov/mapview/static/MapViewerHelp.html
- Ensembl Tour
  http://www.ensembl.org/Docs/enstour/
- The NCBI Handbook
  http://www.ncbi.nlm.nih.gov/books/bv.fcgi?call=bv.View..ShowSection&rid=handbook



http://www.nature.com/genomics/

References

- Current Protocols in Bioinformatics
  UNIT 1.4: The UCSC Genome Browser
  UNIT 1.5: Using the NCBI Map Viewer to Browse Genomic Sequence Data
  Access through *http://nihlibrary.nih.gov/ResearchTools/OnlineJournals.htm*

- UCSC
  Hsu F *et al*. The UCSC Proteome Browser. Nucleic Acids Res. 2005. 33:D454-8.
  Karolchik D *et al*. The UCSC Table Browser data retrieval tool. Nucleic Acids Res. 2004. 32:D493-6.
  Karolchik D *et al*. The UCSC Genome Browser Database. Nucleic Acids Res. 2003. 31:51-4.

- NCBI
  Wheeler DL *et al*. Database resources of the National Center for Biotechnology Information. Nucleic Acids Res. 2005:D39-45.

- Ensembl
  Hubbard T *et al*. Ensembl 2005. Nucleic Acids Res. 2005. 33:D447-53.
  Hammond MP, and Birney E. Genome information resources - developments at Ensembl. 2004. Trends Genet. 20:268-72.
  Birney E *et al*. An overview of Ensembl. 2004. Genome Res. 14:925-8.