Question 1

How does one find a gene of interest and determine that gene's structure? Once the gene has been located on the map, how does one easily examine other genes in that same region?

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This question serves as a basic introduction to the three major genome viewers. One gene, *ADAM23*, will be examined using all three sites so that the reader can gain an appreciation of the subtle differences in information presented at each of these sites.

National Center for Biotechnology Information Map Viewer

The NCBI Map Viewer can be accessed from the NCBI's home page, at http://www.ncbi.nlm.nih.gov. Follow the hyperlink in the right-hand column labeled *Map Viewer* to go to the Map Viewer home page. NCBI provides Map Viewers for 17 organisms, including mammals, other vertebrates, plants, protozoa, fungi, and invertebrates. Select an organism from the pull-down menu, enter a search term in the text box, and press *Go!* The search term can be any element mapped in that genome, which in human includes gene symbol, GenBank accession number, marker name or disease name. For this example, change the Organism to human, and enter 'ADAM23'.

The notation at the top of the resulting page (Figure 1.1) indicates that this is Build 31, or the NCBI's 31st assembly of the human genome. Build 31 is based on sequence data from 15 November 2002. The previous genome assembly, Build 30, was based on sequence data from 28 June 2002. This overview page shows a schematic of all of the human chromosomes, pinpointing the position of *ADAM23* to the q arm of chromosome 2 (Fig. 1.1). The hit on chromosome 8 is to ADAM28, which was at one time called ADAM23. The search results section shows that ADAM23 exists on two NCBI maps, Genes_cyto and Genes_seq. Genes_cyto refers to the cytogenetic map, whereas Genes_seq refers to the sequence map. Clicking on either of those two links opens a view of just that map.

Detailed descriptions of these and other NCBI human maps are available at http://www.ncbi.nlm.nih.gov/mapview/static/humansearch.html. To get the most general overview of the genomic context of *ADAM23*, including all available maps, click on the item in the *Map element* column (in this case, *ADAM23*). This view shows *ADAM23* and a bit of flanking sequence on chromosome 2q33. By default, the maps are shown compressed. To display the maps in a wider format, remove the check mark next to *Compress Map* in the left blue sidebar (Fig. 1.2). Three maps are displayed in this view, each of which will be discussed below. Additional maps, discussed in other examples in this guide, can be added to this view using the *Maps & Options* link.

The rightmost map is the master map, the map providing the most detail. The master map in this case is the Genes_seq map, which depicts the intron/exon organization of *ADAM23* and is created by aligning the ADAM23 mRNA to the genome. The gene appears to have 27 exons. The vertical arrow next to the *ADAM23* gene symbol (within the pink box) shows the direction in which the gene is transcribed. The gene symbol itself is linked to LocusLink, an NCBI resource that provides comprehensive information about the gene, including aliases, nucleotide and protein sequences, and links to other resources[10] (see Question 10). The links to the right of the gene symbol point to additional information about the gene.

- *sv*, or sequence view, shows the position of the gene in the context of the genomic contig, including the nucleotide and encoded protein sequences.
- *ev* brings the user to the evidence viewer, a view that displays the biological evidence supporting a particular gene model. This view shows all RefSeq models, GenBank mRNAs, transcripts (whether annotated, known or potential) and expressed sequence tags (ESTs) aligning to this genomic contig. More information on the evidence viewer can be found on the NCBI Web site by clicking *Evidence Viewer Help* on any ev report page.
- *hm* is a link to the NCBI's Human–Mouse Homology Map, showing genome sequences with predicted orthology between mouse and human (Fig. 12.2).
- *seq* allows the user to retrieve the genomic sequence of the region in text format. The region of sequence displayed can easily be changed.
- *mm* is a link to the Model Maker, which shows the exons that result when GenBank mRNAs, ESTs and gene predictions are aligned to the genomic sequence. The user can then select individual exons to create a customized model of the gene. More information on the Model Maker can be found on the NCBI web site by clicking *help* on any mm report page.

The UniG_Hs map shows human UniGene clusters that have been aligned to the genome. The gray histogram depicts the number of aligning ESTs and the blue lines show the mapping of UniGene clusters to the genome. The thick blue bars are regions of alignment (that is, exons) and the thin blue lines indicate potential introns. In this example, the mapping of UniGene cluster Hs.7164 to the genome follows that of *ADAM23*, and all the exons align.

The Genes_cyto map shows genes that have been mapped cytogenetically; the orange bar shows the position of the gene. Many genes have been broadly mapped to this regoin of chromosome 2.

Clicking on the zoom control in the blue sidebar allows the user to zoom out to view a larger region of chromosome 2. Zooming out one level shows 1/100th of the chromosome. There are 22 genes in the region, but only 20 are labeled (displayed) in this view (Fig. 1.3). The region of *ADAM23* is highlighted in red on all maps. On the basis of the Genes_seq map, *ADAM23* is located between *KIAA1571* and *LOC151405*.

University of California, Santa Cruz Genome Browser

The home page for the UCSC Genome Browser is http://genome.ucsc.edu/. UCSC provides browsers not only for the most recent version of the rat, mouse, and human genome data, but also for several earlier assemblies. To use the Genome Browser, select the appropriate organism from the pull-down menu at the top of the blue sidebar (*Human*, in this case) and then click the link labeled *Browser*. On the resulting page, select the version of the human assembly to view. The *Dec. 2001* browser displays annotations based on NCBI's build 28 of the human genome, the *Apr. 2002* browser displays annotations on NCBI's build 29, the *June 2002* browser displays annotations of NCBI's build 30, and the *Nov. 2002* browser displays annotations on NCBI's build 31. Select *Human Nov. 2002* from the pull-down menu to access the assembly from that date (Fig. 1.4).

Supported types of queries are listed below the text input boxes. Enter 'ADAM23' in the box labeled *position* and then click *Submit*. The results of this search are presented in two categories, *RefSeq Genes* and *mRNA Associated Search Results* (Fig. 1.5). The section marked *RefSeq Genes* shows the mapping of the NCBI Reference mRNA sequences to the genome. The *mRNA Associated Search Results* represent the mapping of other GenBank mRNA sequences to the genome. Click on the *RefSeq Genes* link for *ADAM23* (arrow, Fig. 1.5) to see the genomic context of the *ADAM23* mRNA Reference Sequence (NM_003812).

The resulting zoomed-in view shows a region of chromosome 2 from base pair 206032982 to 206207297, located within 2q33.3 (Fig. 1.6). The blue track entitled *Known Genes based on SWISS-PROT, TrEMBL, mRNA, and RefSeq* shows the intron–exon structure of known genes. The vertical boxes indicate exons and the horizontal lines introns. The *ADAM23* gene seems to have 26 exons. The direction of transcription is indicated by the arrowheads on the introns. The tracks labeled Ensembl Genes, Acembly Genes, Twinscan, SGP Genes, and Genscan Genes are the results of gene predictions (see Question 7). Alignments of other database nucleotide sequences are shown in the Human mRNAs from GenBank, Spliced EST, and Nonhuman mRNAs from GenBank tracks. Translated alignments of *Fugu rubripes* genomic sequence are in the Fugu BLAT tracks. The Mouse Cons and Best Mouse tracks shows conservation between the human and mouse genomes. Tracks displaying single-nucleotide polymorphisms (SNPs) and repetitive elements are shown at the bottom. Additional details about each track are available by selecting the track name in the Track Controls at the bottom.

To view the genomic context of *ADAM23*, zoom out 3x by clicking on the *zoom out 3x* box in the upper right corner. *ADAM23* is located between *AF338192* and *BC033509* (Fig. 1.7).

Ensembl

The Ensembl[7] project, http://www.ensembl.org/, provides genome browsers for nine species: human, mouse, rat, zebrafish, fugu, mosquito, fruitflly, *C. elegans*, and *C. briggsea*. Click on *Human* to view the main entry point for the human genome. The current version of human Ensembl is version 11.31.1, based on the NCBI's 31st build of the genome. To perform a text search, enter 'ADAM23' in the text box, and limit the search by selecting *Gene* from the pull-down search. Click on the upper button labeled *Lookup*. As at NCBI, two results are returned, the first with a link to the ADAM28 gene, and the second with a link to the ADAM23 gene (Fig. 1.8).

Click on either of the *ADAM23* links (Ensembl Gene ENSG00000114948) to retrieve the GeneView window. The returned page contains two sections of data. The Ensembl Gene Report (Fig. 1.9) is an overview of *ADAM23*, including a link to the genomic location of the gene, a schematic of the intron/exon structure, and links to homologous genes from other organisms. Some of these fields will be described in more detail in later examples. The Transcripts/Translation Summary provides information on the gene transcript (Fig. 1.10). This section of the GeneView shows links to ADAM23 in other databases, as well as protein domain information. If more than one transcript is predicted for the gene, each is allocated its own summary section.

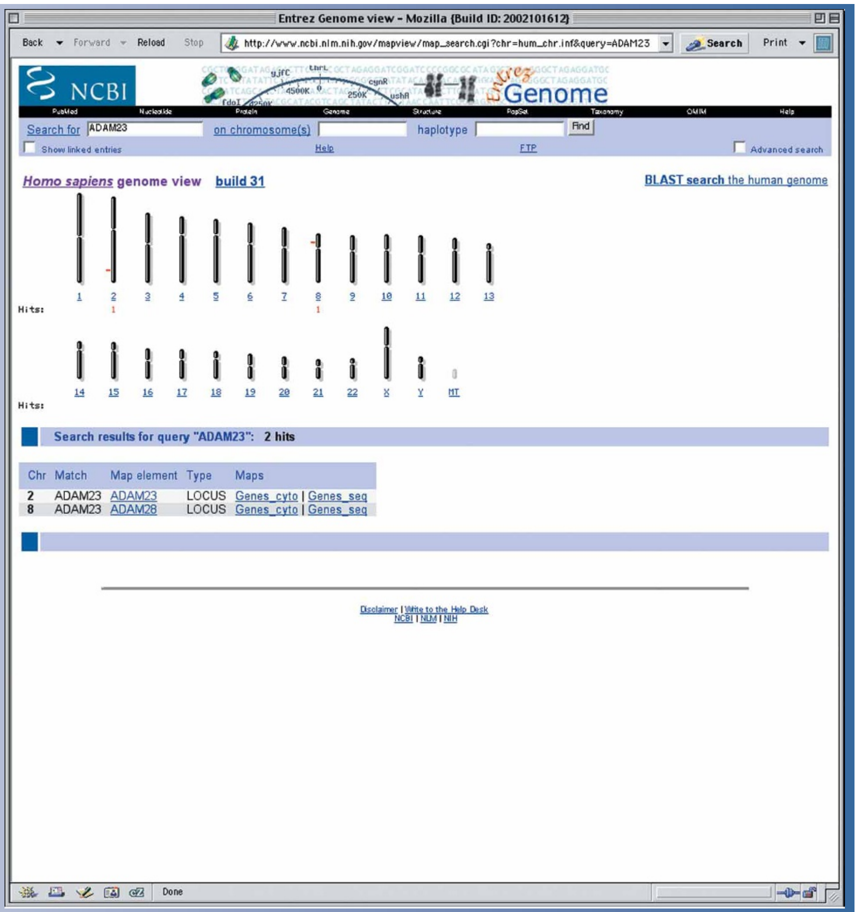
The complete genomic context of *ADAM23* is viewed by returning to the first section of the GeneView (Fig. 1.9) and clicking on one of the two links within the *Genomic Location* box. The top portion of the resulting ContigView (Fig. 1.11) depicts the chromosome, with the region of interest outlined in red. The Overview shows the genomic context of the gene, including the chromosome bands, contigs, markers and genes that map to near 2q33.3. Clicking on any of these items recenters the display around that item. The section of interest is boxed in red on the DNA(contigs) map. The known genes annotated by Ensembl as being around *ADAM23* are Q9BZ60 and *NM_014929*.

The middle panel of the ContigView, the Detailed View (Fig. 1.12), shows a zoomed-in view of the boxed region, highlighting all features that have been mapped to this region of the human genome. The navigator buttons between the Overview and the Detailed View move the display to the left and right and zoom in and out. The features to be displayed can be changed by selecting the *Features* pull-down menu and then checking which features to view.

The Features shown in Fig. 1.12 are the defaults. The DNA (contigs) map separates items on the forward strand (above) from those on the reverse (below). The forward strand shows seven types of features. Starting at the bottom, the *ADAM23* transcript is shown in red, indicating that it is a known transcript corresponding to a near-full-length cDNA sequence, protein sequence or both already available in the public sequence database. Black transcripts are predicted based on EST or protein sequence similarity. *EST Transcr.* links to individual aligning ESTs, whereas the *UniGene* track near the top displays UniGene clusters. The *Genscan* model on the forward strand contains many exons found in the known transcript and was predicted by the GENSCAN gene prediction program[11] (see Question 7). The *Proteins* and *Human proteins* boxes indicate protein sequences that align to this version of the genome, whereas *Human cDNAs* shows mRNA sequences in the EMBL nucleotide sequence database and NCBI RefSeqs. Positioning the computer mouse over any feature brings up the feature's name and links to more detailed information. The only features on the reverse strand in this view are portions of an EST transcript and a Genscan transcript. The Basepair view, at the bottom of the ContigView (Figure 1.13) shows a very fine view of a 101 nucleotide region of ADAM23, showing the actual nucleotide and protein sequence, as well as restriction enzyme sites.

The NCBI, UCSC and Ensembl sometimes use different symbols for the same genes, so it can be difficult to compare the views obtained by the different browsers. Furthermore, the three sites maintain independent annotation pipelines and do not all attempt to align the same mRNA sequences to the genome. All three sites are currently displaying annotations based on NCBI's build 31. However, it takes significant time to update an annotation based on a new genome assembly, so shortly after the release of a new assembly, the sites may display different versions. At present, UCSC is the only site to maintain browsers based on older assemblies. Nevertheless, it is fairly easy to navigate among the three sites. The NCBI, for example, links to Ensembl and UCSC through the black boxes at the top of LocusLink entries for human genes, and Ensembl directs users to NCBI and UCSC through the "Jump to" link in its ContigView. Some versions of UCSC's Genome Browser have links to Ensembl and NCBI's Map Viewer in the blue bar at the top of each browser page.

Figure 1.1



Entrez Genome view - Mozilla {Build ID: 2002101612}

http://www.ncbi.nlm.nih.gov/mapview/map_search.cgi?chr=hum_chr.inf&query=ADAM23

Search for: ADAM23 on chromosome(s) haplotype Find

□ Show linked entries Help FTP □ Advanced search

Homo sapiens genome view build 31 BLAST search the human genome

Hits: 2: 1, 8: 1

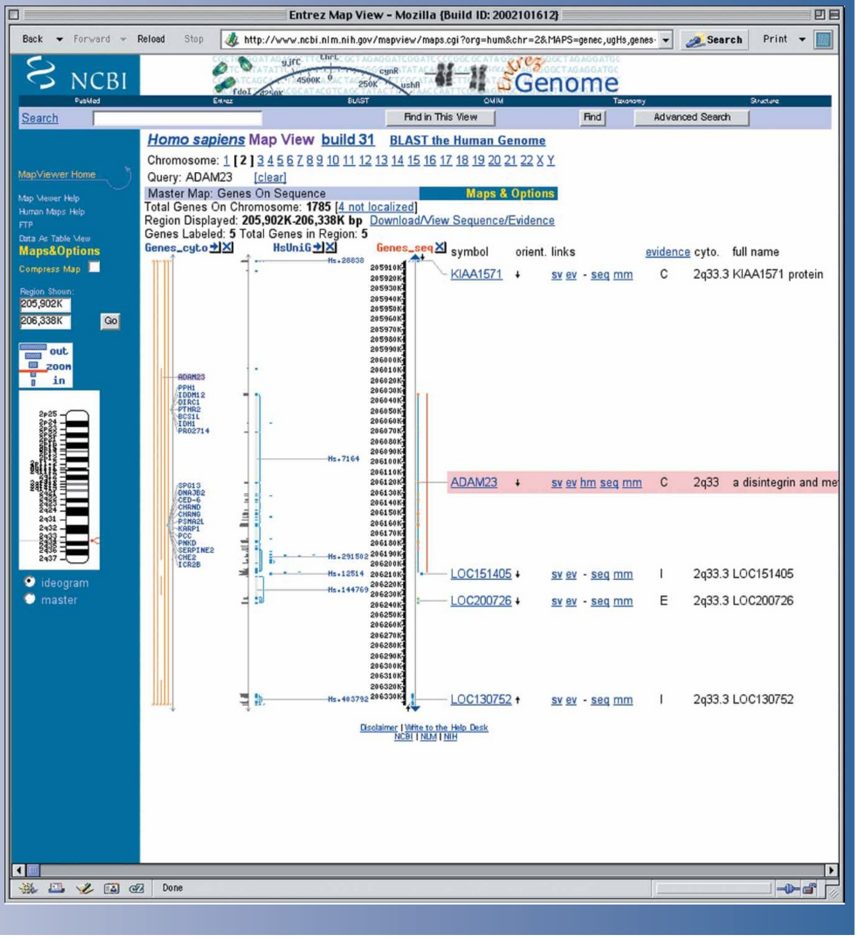
Search results for query "ADAM23": 2 hits

Chr	Match	Map element	Type	Maps
2	ADAM23	ADAM23	LOCUS	Genes_cyto | Genes_seq
8	ADAM23	ADAM28	LOCUS	Genes_cyto | Genes_seq

Disclaimer | Write to the Help Desk
NCBI | NLM | NIH

Done

Figure 1.2



Entrez Map View - Mozilla {Build ID: 2002101612}

http://www.ncbi.nlm.nih.gov/mapview/maps.cgi?org=hum&chr=2&MAPS=genec,ugHs,genes-

Homo sapiens Map View build 31 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

Query: ADAM23 [clear]

Master Map: Genes On Sequence Maps & Options

Total Genes On Chromosome: **1785** [4 not localized]

Region Displayed: **205,902K-206,338K bp** Download/View Sequence/Evidence

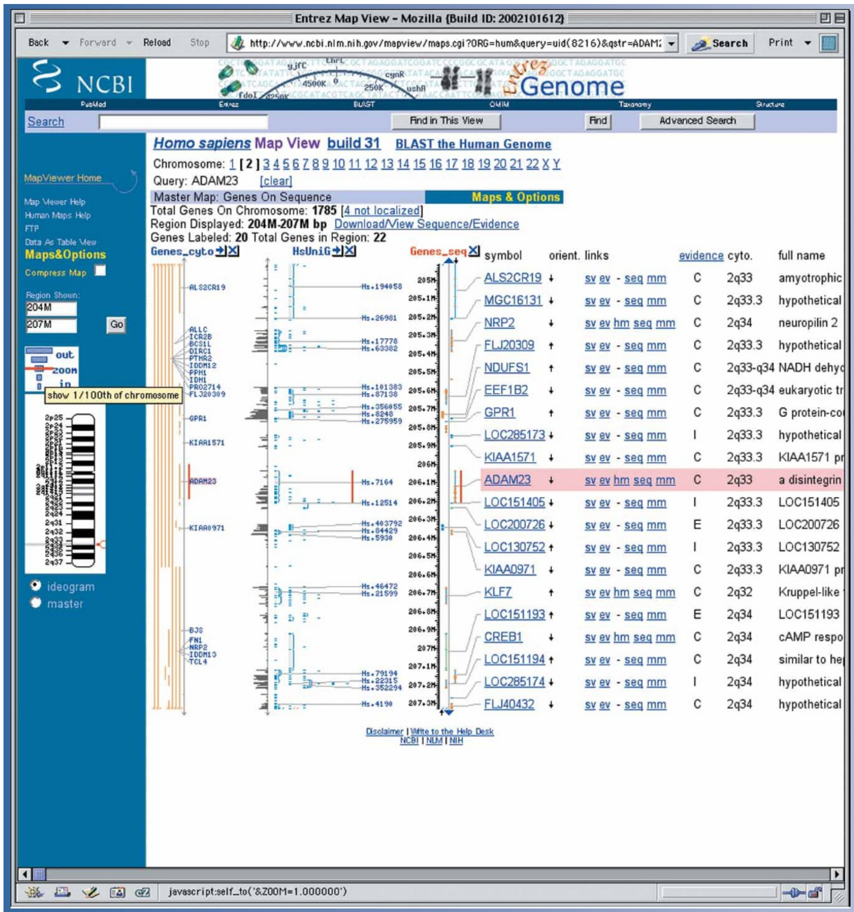
Genes Labeled: **5** Total Genes in Region: **5**

Region Shown: 205,902K 206,338K Go

symbol	orient.	links	evidence	cyto.	full name
KIAA1571	↓	sv ev - seq mm	C	2q33.3	KIAA1571 protein
ADAM23	↓	sv ev hm seq mm	C	2q33	a disintegrin and me
LOC151405	↓	sv ev - seq mm	I	2q33.3	LOC151405
LOC200726	↓	sv ev - seq mm	E	2q33.3	LOC200726
LOC130752	↑	sv ev - seq mm	I	2q33.3	LOC130752

Disclaimer | Write to the Help Desk
NCBI | NLM | NIH

Done



http://www.ncbi.nlm.nih.gov/mapview/maps.cgi?ORG=hum&query=uid(8216)&qstr=ADAM2

Homo sapiens Map View build 31 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

Query: ADAM23 [clear]

Master Map: Genes On Sequence — Maps & Options

Total Genes On Chromosome: **1785** [4 not localized]

Region Displayed: **204M-207M bp** Download/View Sequence/Evidence

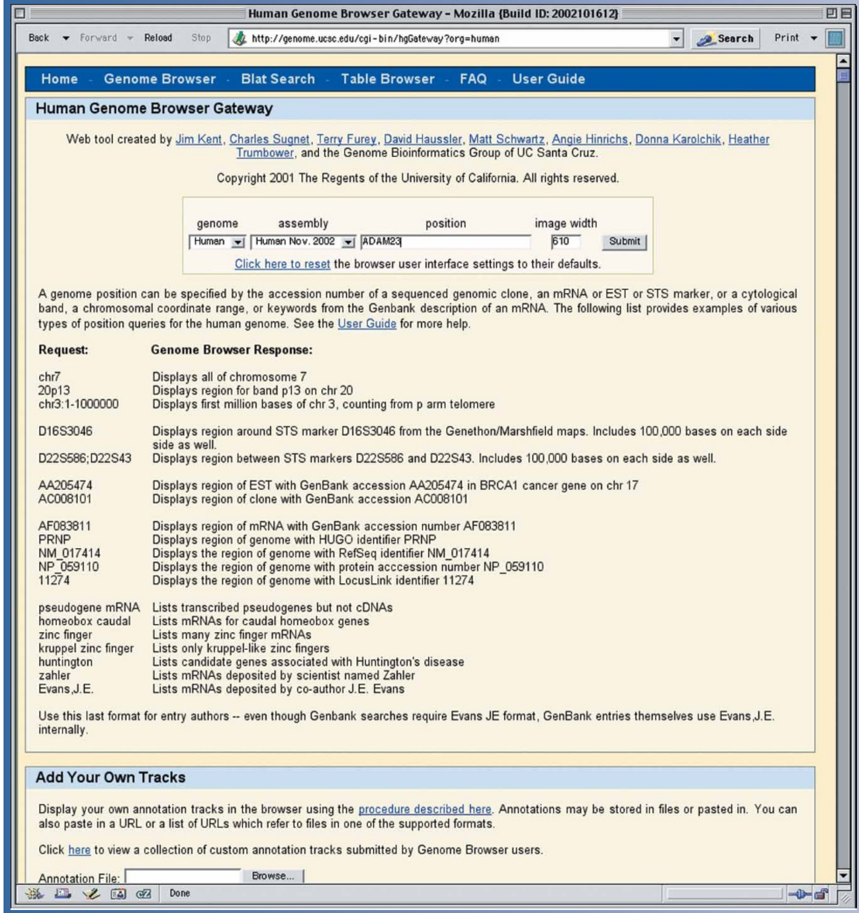
Genes Labeled: **20** Total Genes in Region: **22**

Region Shown: 204M – 207M

symbol	orient.	links	evidence	cyto.	full name
ALS2CR19	↓	sv ev - seq mm	C	2q33	amyotrophic
MGC16131	↓	sv ev - seq mm	C	2q33.3	hypothetical
NRP2	↓	sv ev hm seq mm	C	2q34	neuropilin 2
FLJ20309	↑	sv ev - seq mm	C	2q33.3	hypothetical
NDUFS1	↑	sv ev - seq mm	C	2q33-q34	NADH dehyd
EEF1B2	↓	sv ev - seq mm	C	2q33-q34	eukaryotic tr
GPR1	↑	sv ev - seq mm	C	2q33.3	G protein-co
LOC285173	↓	sv ev - seq mm	I	2q33.3	hypothetical
KIAA1571	↓	sv ev - seq mm	C	2q33.3	KIAA1571 pr
ADAM23	↓	sv ev hm seq mm	C	2q33	a disintegrin
LOC151405	↓	sv ev - seq mm	I	2q33.3	LOC151405
LOC200726	↓	sv ev - seq mm	E	2q33.3	LOC200726
LOC130752	↑	sv ev - seq mm	I	2q33.3	LOC130752
KIAA0971	↓	sv ev - seq mm	C	2q33.3	KIAA0971 pr
KLF7	↑	sv ev hm seq mm	C	2q32	Kruppel-like
LOC151193	↑	sv ev - seq mm	E	2q34	LOC151193
CREB1	↓	sv ev hm seq mm	C	2q34	cAMP respo
LOC151194	↑	sv ev - seq mm	C	2q34	similar to he
LOC285174	↓	sv ev - seq mm	I	2q34	hypothetical
FLJ40432	↓	sv ev - seq mm	C	2q34	hypothetical

javascript:self_to('&ZOOM=1.000000')

Figure 1.3



http://genome.ucsc.edu/cgi-bin/hgGateway?org=human

Human Genome Browser Gateway

Web tool created by Jim Kent, Charles Sugnet, Terry Furey, David Haussler, Matt Schwartz, Angie Hinrichs, Donna Karolchik, Heather Trumbower, and the Genome Bioinformatics Group of UC Santa Cruz.

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genome	assembly	position	image width
Human	Human Nov. 2002	ADAM23	610

Click here to reset the browser user interface settings to their defaults.

A genome position can be specified by the accession number of a sequenced genomic clone, an mRNA or EST or STS marker, or a cytological band, a chromosomal coordinate range, or keywords from the Genbank description of an mRNA. The following list provides examples of various types of position queries for the human genome. See the User Guide for more help.

Request:	Genome Browser Response:
chr7	Displays all of chromosome 7
20p13	Displays region for band p13 on chr 20
chr3:1-1000000	Displays first million bases of chr 3, counting from p arm telomere
D16S3046	Displays region around STS marker D16S3046 from the Genethon/Marshfield maps. Includes 100,000 bases on each side side as well.
D22S586;D22S43	Displays region between STS markers D22S586 and D22S43. Includes 100,000 bases on each side as well.
AA205474	Displays region of EST with GenBank accession AA205474 in BRCA1 cancer gene on chr 17
AC008101	Displays region of clone with GenBank accession AC008101
AF083811	Displays region of mRNA with GenBank accession number AF083811
PRNP	Displays region of genome with HUGO identifier PRNP
NM_017414	Displays the region of genome with RefSeq identifier NM_017414
NP_059110	Displays the region of genome with protein acccession number NP_059110
11274	Displays the region of genome with LocusLink identifier 11274
pseudogene mRNA	Lists transcribed pseudogenes but not cDNAs
homeobox caudal	Lists mRNAs for caudal homeobox genes
zinc finger	Lists many zinc finger mRNAs
kruppel zinc finger	Lists only kruppel-like zinc fingers
huntington	Lists candidate genes associated with Huntington's disease
zahler	Lists mRNAs deposited by scientist named Zahler
Evans,J.E.	Lists mRNAs deposited by co-author J.E. Evans

Use this last format for entry authors -- even though Genbank searches require Evans JE format, GenBank entries themselves use Evans,J.E. internally.

Add Your Own Tracks

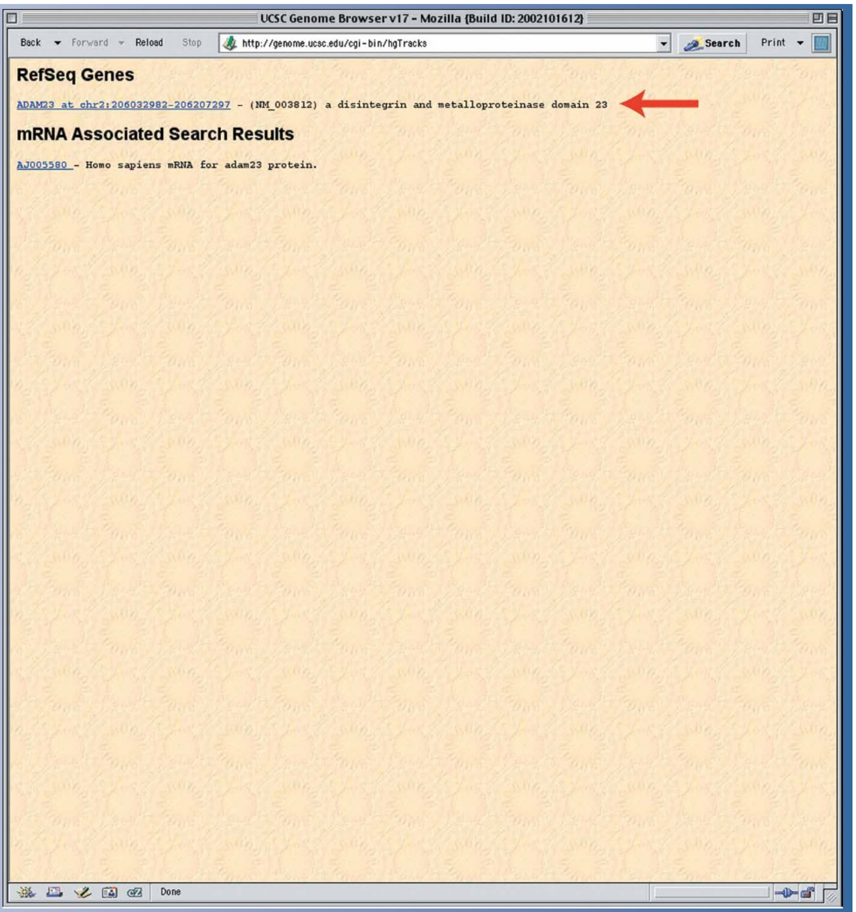
Display your own annotation tracks in the browser using the procedure described here. Annotations may be stored in files or pasted in. You can also paste in a URL or a list of URLs which refer to files in one of the supported formats.

Click here to view a collection of custom annotation tracks submitted by Genome Browser users.

Annotation File:

Figure 1.4

Figure 1.5



UCSC Genome Browser v17 - Mozilla {Build ID: 2002101612}
Back
Forward
Reload
Stop
http://genome.ucsc.edu/cgi-bin/hgTracks
Search
Print
Done

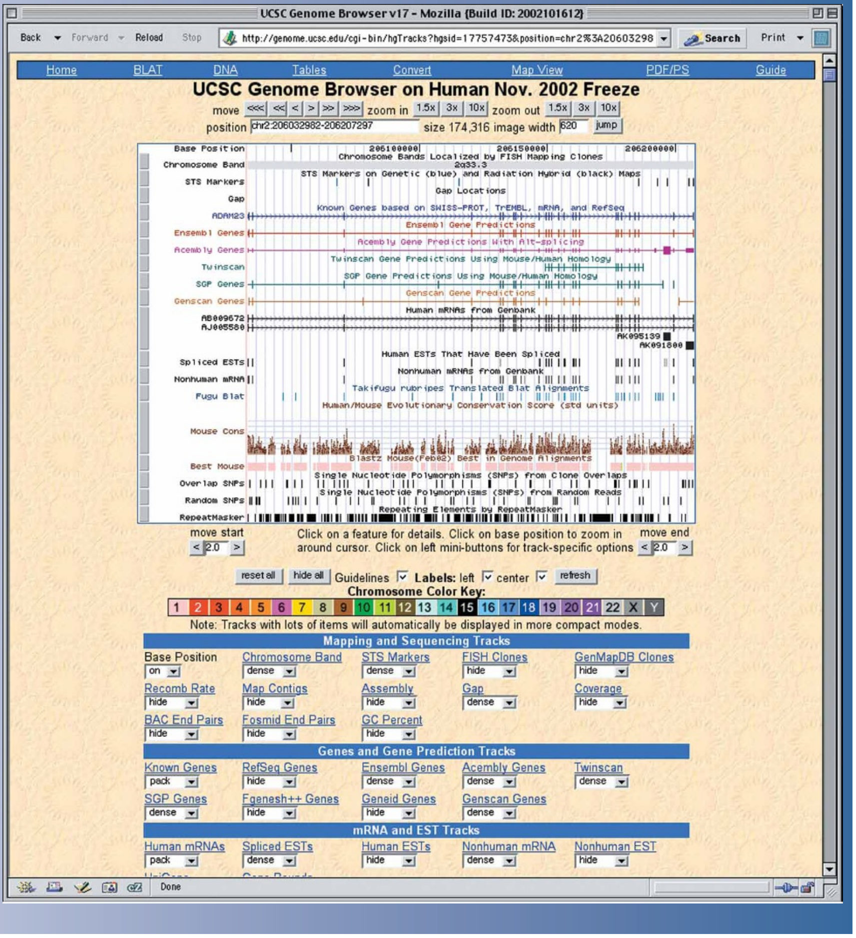
RefSeq Genes

ADAM23 at chr2:206032982-206207297 - (NM_003812) a disintegrin and metalloproteinase domain 23

mRNA Associated Search Results

AJ005580 - Homo sapiens mRNA for adam23 protein.

Figure 1.6



UCSC Genome Browser v17 - Mozilla {Build ID: 2002101612}
Back
Forward
Reload
Stop
http://genome.ucsc.edu/cgi-bin/hgTracks?hgsid=17757473&position=chr2%3A20603298
Search
Print
Home
BLAT
DNA
Tables
Convert
Map View
PDF/PS
Guide
Base Position
206100000
206150000
206200000
Chromosome Bands Localized by FISH Mapping Clones
Chromosome Band
2q33.3
STS Markers on Genetic (blue) and Radiation Hybrid (black) Maps
STS Markers
Gap Locations
Gap
Known Genes based on SWISS-PROT, TrEMBL, mRNA, and RefSeq
ADAM23
Ensembl Gene Predictions
Ensembl Genes
Acembly Gene Predictions With Alt-splicing
Acembly Genes
Twinscan Gene Predictions Using Mouse/Human Homology
Twinscan
SGP Gene Predictions Using Mouse/Human Homology
SGP Genes
Genscan Gene Predictions
Genscan Genes
Human mRNAs from Genbank
AB009672
AJ005580
AK095139
AK091800
Human ESTs That Have Been Spliced
Spliced ESTs
Nonhuman mRNAs from Genbank
Nonhuman mRNA
Takifugu rubripes Translated Blat Alignments
Fugu Blat
Human/Mouse Evolutionary Conservation Score (std units)
Mouse Cons
Blastz Mouse(Feb02) Best in Genome Alignments
Best Mouse
Single Nucleotide Polymorphisms (SNPs) from Clone Overlaps
Overlap SNPs
Single Nucleotide Polymorphisms (SNPs) from Random Reads
Random SNPs
Repeating Elements by RepeatMasker
RepeatMasker
reset all
hide all
refresh
Done

UCSC Genome Browser on Human Nov. 2002 Freeze

move <<< << < > >> >>> zoom in 1.5x 3x 10x zoom out 1.5x 3x 10x

position chr2:206032982-206207297 size 174,316 image width 620 jump

move start < 2.0 >

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 < 2.0 >

Guidelines ☑ **Labels:** left ☑ center ☑

Chromosome Color Key:

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y

Note: Tracks with lots of items will automatically be displayed in more compact modes.

Mapping and Sequencing Tracks

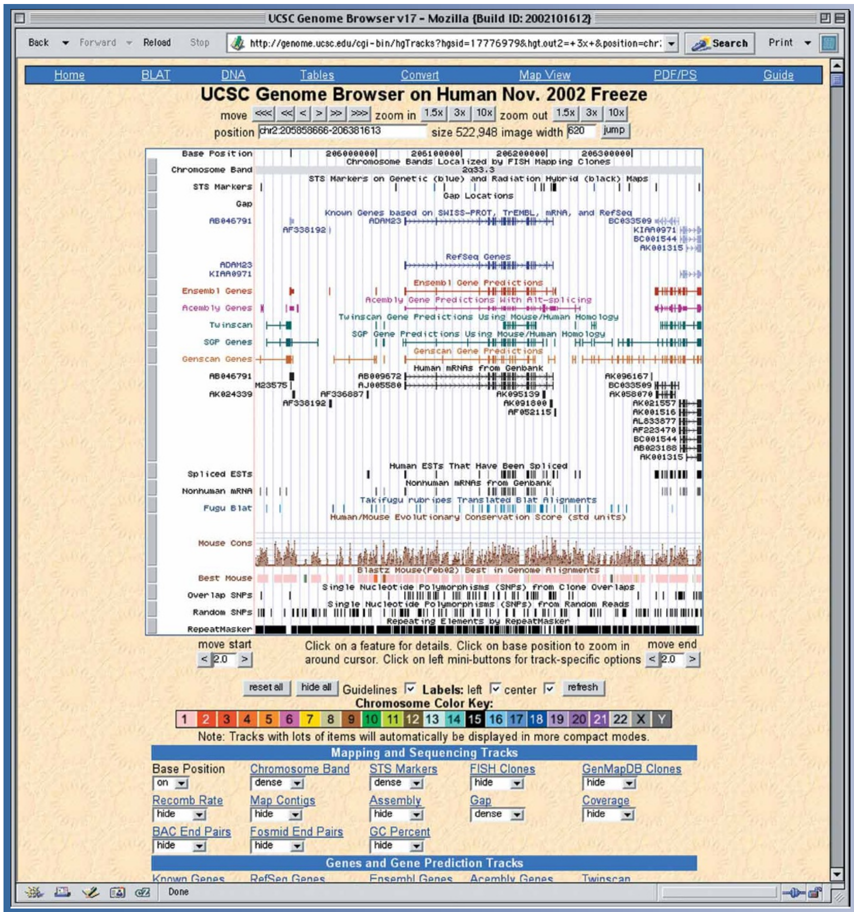
Base Position on	Chromosome Band dense	STS Markers dense	FISH Clones hide	GenMapDB Clones hide
Recomb Rate hide	Map Contigs hide	Assembly hide	Gap dense	Coverage hide
BAC End Pairs hide	Fosmid End Pairs hide	GC Percent hide		

Genes and Gene Prediction Tracks

Known Genes pack	RefSeq Genes hide	Ensembl Genes dense	Acembly Genes dense	Twinscan dense
SGP Genes dense	Fgenesh++ Genes hide	Geneid Genes hide	Genscan Genes dense	

mRNA and EST Tracks

Human mRNAs pack	Spliced ESTs dense	Human ESTs hide	Nonhuman mRNA dense	Nonhuman EST hide



UCSC Genome Browser v17 - Mozilla {Build ID: 2002101612}

Back Forward Reload Stop http://genome.ucsc.edu/cgi-bin/hgTracks?hgsid=17776979&hgt.out2=+3x+&position=chr: Search Print

Home BLAT DNA Tables Convert Map View PDF/PS Guide

UCSC Genome Browser on Human Nov. 2002 Freeze

move <<< << < > >> >>> zoom in 1.5x 3x 10x zoom out 1.5x 3x 10x

position chr2:205858666-206381613 size 522,948 image width 620 jump

Base Position
206000000
206100000
206200000
206300000
Chromosome Bands Localized by FISH Mapping Clones
Chromosome Band
2q33.3
STS Markers on Genetic (blue) and Radiation Hybrid (black) Maps
STS Markers
Gap Locations
Gap
Known Genes based on SWISS-PROT, TrEMBL, mRNA, and RefSeq
AB046791
ADAM23
BC033509
AF338192
KIAA0971
BC001544
AK001315
RefSeq Genes
ADAM23
KIAA0971
Ensembl Gene Predictions
Ensembl Genes
Acembly Gene Predictions With Alt-splicing
Acembly Genes
Twinscan Gene Predictions Using Mouse/Human Homology
Twinscan
SGP Gene Predictions Using Mouse/Human Homology
SGP Genes
Genscan Gene Predictions
Genscan Genes
Human mRNAs from Genbank
AB046791
AB009672
AK096167
M23575
AJ005580
BC033509
AK024339
AF336887
AK095139
AK058070
AF338192
AK091800
AK021557
AF052115
AK001516
AL833877
AF223470
BC001544
AB023188
AK001315
Human ESTs That Have Been Spliced
Spliced ESTs
Nonhuman mRNAs from Genbank
Nonhuman mRNA
Takifugu rubripes Translated Blat Alignments
Fugu Blat
Human/Mouse Evolutionary Conservation Score (std units)
Mouse Cons
Blastz Mouse(Feb02) Best in Genome Alignments
Best Mouse
Single Nucleotide Polymorphisms (SNPs) from Clone Overlaps
Overlap SNPs
Single Nucleotide Polymorphisms (SNPs) from Random Reads
Random SNPs
Repeating Elements by RepeatMasker
RepeatMasker

move start < 2.0 >

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 < 2.0 >

reset all hide all Guidelines ☑ **Labels:** left ☑ center ☑ refresh

Chromosome Color Key:

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y

Note: Tracks with lots of items will automatically be displayed in more compact modes.

Mapping and Sequencing Tracks

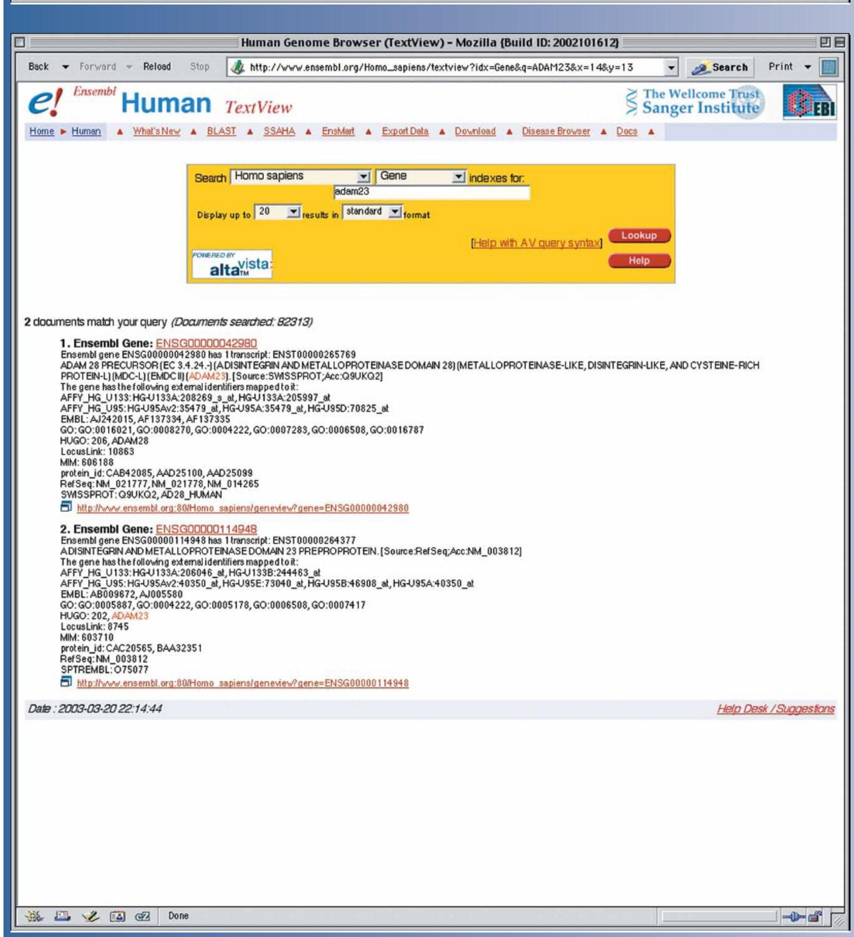
Base Position	Chromosome Band	STS Markers	FISH Clones	GenMapDB Clones
on	dense	dense	hide	hide
Recomb Rate	Map Contigs	Assembly	Gap	Coverage
hide	hide	hide	dense	hide
BAC End Pairs	Fosmid End Pairs	GC Percent		
hide	hide	hide		

Genes and Gene Prediction Tracks

Known Genes RefSeq Genes Ensembl Genes Acembly Genes Twinscan

Done

Figure 1.7



Human Genome Browser (TextView) - Mozilla {Build ID: 2002101612}

Back Forward Reload Stop http://www.ensembl.org/Homo_sapiens/textview?idx=Gene&q=ADAM23&x=14&y=13 Search Print

e! Ensembl Human TextView
The Wellcome Trust Sanger Institute
EBI

Home ▶ Human ▲ What's New ▲ BLAST ▲ SSAHA ▲ EnsMart ▲ Export Data ▲ Download ▲ Disease Browser ▲ Docs ▲

Search Homo sapiens Gene indexes for: adam23

Display up to 20 results in standard format

[Help with AV query syntax] Lookup Help

2 documents match your query *(Documents searched: 82313)*

1. Ensembl Gene: ENSG00000042980
Ensembl gene ENSG00000042980 has 1 transcript: ENST00000265769
ADAM 28 PRECURSOR (EC 3.4.24.-) (A DISINTEGRIN AND METALLOPROTEINASE DOMAIN 28) (METALLOPROTEINASE-LIKE, DISINTEGRIN-LIKE, AND CYSTEINE-RICH PROTEIN-L) (MDC-L) (EMDC II) (ADAM23). [Source:SWISSPROT;Acc:Q9UKQ2]
The gene has the following external identifiers mapped to it:
AFFY_HG_U133: HG-U133A:208269_s_at, HG-U133A:205997_at
AFFY_HG_U95: HG-U95Av2:35479_at, HG-U95A:35479_at, HG-U95D:70825_at
EMBL: AJ242015, AF137334, AF137335
GO: GO:0016021, GO:0008270, GO:0004222, GO:0007283, GO:0006508, GO:0016787
HUGO: 206, ADAM28
LocusLink: 10863
MIM: 606188
protein_id: CAB42085, AAD25100, AAD25099
RefSeq: NM_021777, NM_021778, NM_014265
SWISSPROT: Q9UKQ2, AD28_HUMAN
http://www.ensembl.org:80/Homo_sapiens/geneview?gene=ENSG00000042980

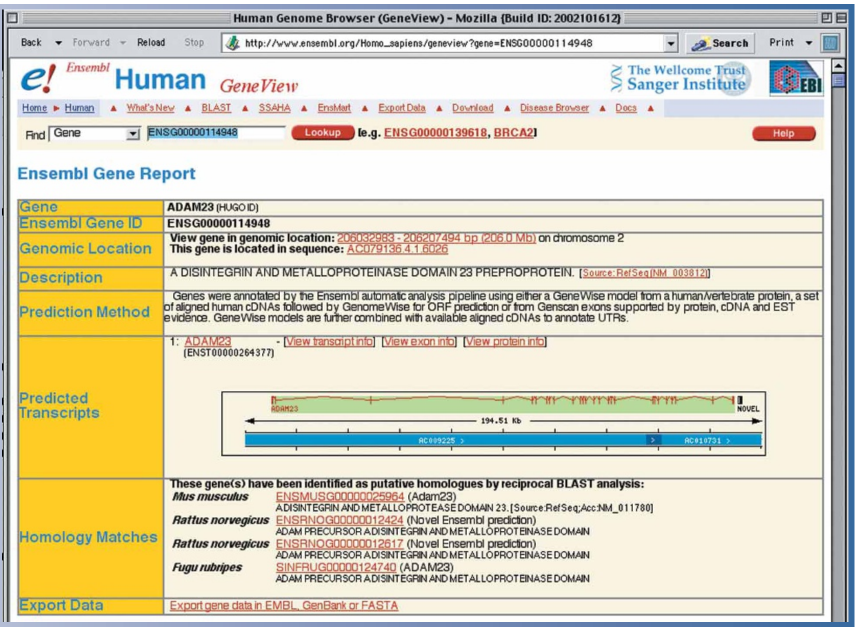
2. Ensembl Gene: ENSG00000114948
Ensembl gene ENSG00000114948 has 1 transcript: ENST00000264377
A DISINTEGRIN AND METALLOPROTEINASE DOMAIN 23 PREPROPROTEIN. [Source:RefSeq;Acc:NM_003812]
The gene has the following external identifiers mapped to it:
AFFY_HG_U133: HG-U133A:206046_at, HG-U133B:244463_at
AFFY_HG_U95: HG-U95Av2:40350_at, HG-U95E:73040_at, HG-U95B:46908_at, HG-U95A:40350_at
EMBL: AB009672, AJ005580
GO: GO:0005887, GO:0004222, GO:0005178, GO:0006508, GO:0007417
HUGO: 202, ADAM23
LocusLink: 8745
MIM: 603710
protein_id: CAC20565, BAA32351
RefSeq: NM_003812
SPTREMBL: O75077
http://www.ensembl.org:80/Homo_sapiens/geneview?gene=ENSG00000114948

Date : 2003-03-20 22:14:44 *Help Desk / Suggestions*

Done

Figure 1.8

Figure 1.9

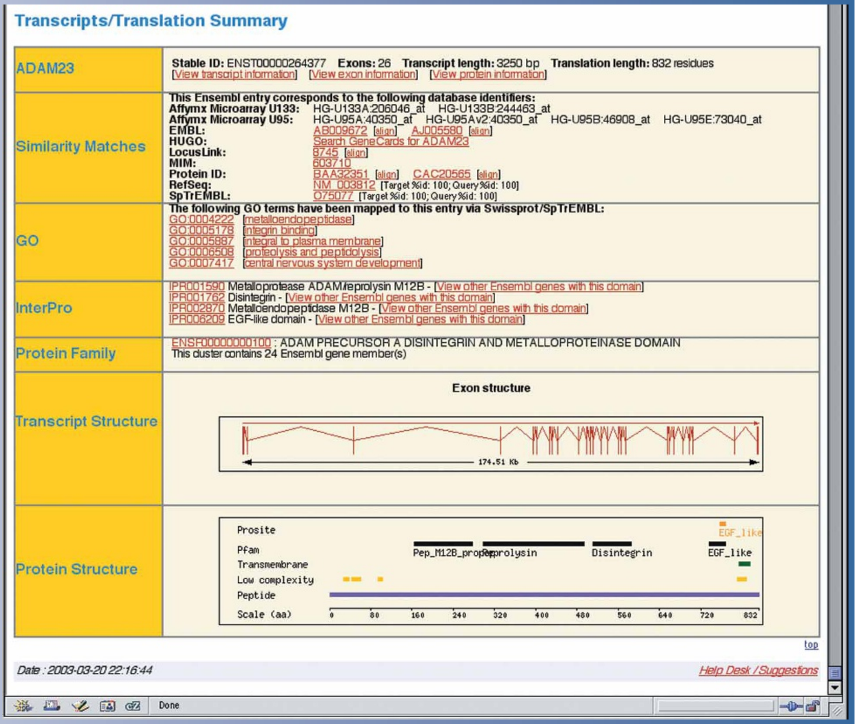

Human Genome Browser (GeneView) - Mozilla {Build ID: 2002101612}
Back
Forward
Reload
Stop
http://www.ensembl.org/Homo_sapiens/geneview?gene=ENSG00000114948
Search
Print
e! Ensembl Human GeneView
The Wellcome Trust Sanger Institute
EBI
Home ▸ Human ▲ What's New ▲ BLAST ▲ SSAHA ▲ EnsMart ▲ Export Data ▲ Download ▲ Disease Browser ▲ Docs ▲
Find
Gene
Lookup
Help
ADAM23
NOVEL
194.51 Kb
AC009225 >
AC010731 >

Find Gene ENSG00000114948 Lookup [e.g. ENSG00000139618, BRCA2]

Ensembl Gene Report

Gene	ADAM23 (HUGO ID)
Ensembl Gene ID	ENSG00000114948
Genomic Location	**View gene in genomic location:** 206032983 - 206207494 bp (206.0 Mb) on chromosome 2 **This gene is located in sequence:** AC079136.4.1.6026
Description	A DISINTEGRIN AND METALLOPROTEINASE DOMAIN 23 PREPROPROTEIN. [Source:RefSeq(NM_003812)]
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.
Predicted Transcripts	1: ADAM23 (ENST00000264377) - [View transcript info] [View exon info] [View protein info]
Homology Matches	**These gene(s) have been identified as putative homologues by reciprocal BLAST analysis:** ***Mus musculus*** ENSMUSG00000025964 (Adam23) ADISINTEGRIN AND METALLOPROTEASE DOMAIN 23. [Source:RefSeq;Acc:NM_011780] ***Rattus norvegicus*** ENSRNOG00000012424 (Novel Ensembl prediction) ADAM PRECURSOR ADISINTEGRIN AND METALLOPROTEINASE DOMAIN ***Rattus norvegicus*** ENSRNOG00000012617 (Novel Ensembl prediction) ADAM PRECURSOR ADISINTEGRIN AND METALLOPROTEINASE DOMAIN ***Fugu rubripes*** SINFRUG00000124740 (ADAM23) ADAM PRECURSOR ADISINTEGRIN AND METALLOPROTEINASE DOMAIN
Export Data	Export gene data in EMBL, GenBank or FASTA

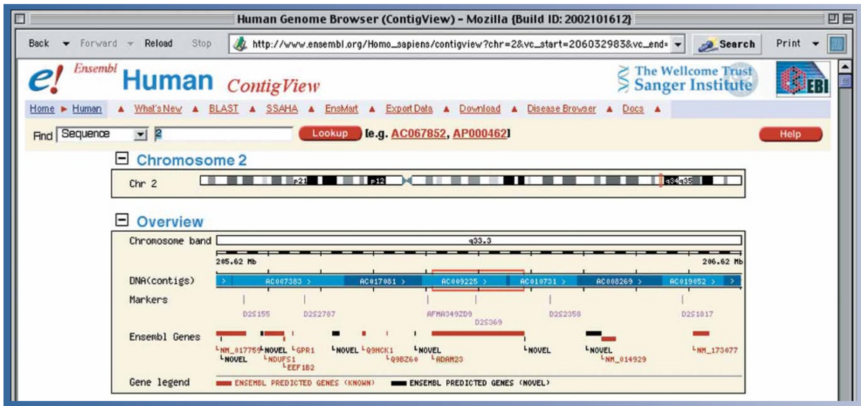
Figure 1.10



Transcripts/Translation Summary

ADAM23	**Stable ID:** ENST00000264377 **Exons:** 26 **Transcript length:** 3250 bp **Translation length:** 832 residues [View transcript information] [View exon information] [View protein information]
Similarity Matches	**This Ensembl entry corresponds to the following database identifiers:** **Affymx Microarray U133:** HG-U133A:206046_at HG-U133B:244463_at **Affymx Microarray U95:** HG-U95A:40350_at HG-U95Av2:40350_at HG-U95B:46908_at HG-U95E:73040_at **EMBL:** AB009672 [align] AJ005580 [align] **HUGO:** Search GeneCards for ADAM23 **LocusLink:** 8745 [align] **MIM:** 603710 **Protein ID:** BAA32351 [align] CAC20565 [align] **RefSeq:** NM_003812 [Target %id: 100; Query %id: 100] **SpTrEMBL:** O75077 [Target %id: 100; Query %id: 100]
GO	**The following GO terms have been mapped to this entry via Swissprot/SpTrEMBL:** GO:0004222 [metalloendopeptidase] GO:0005178 [integrin binding] GO:0005887 [integral to plasma membrane] GO:0006508 [proteolysis and peptidolysis] GO:0007417 [central nervous system development]
InterPro	IPR001590 Metalloprotease ADAM/reprolysin M12B - [View other Ensembl genes with this domain] IPR001762 Disintegrin - [View other Ensembl genes with this domain] IPR002870 Metalloendopeptidase M12B - [View other Ensembl genes with this domain] IPR006209 EGF-like domain - [View other Ensembl genes with this domain]
Protein Family	ENSF00000000100 : ADAM PRECURSOR A DISINTEGRIN AND METALLOPROTEINASE DOMAIN This cluster contains 24 Ensembl gene member(s)
Transcript Structure	**Exon structure**
Protein Structure	

Date : 2003-03-20 22:16:44 *Help Desk / Suggestions*

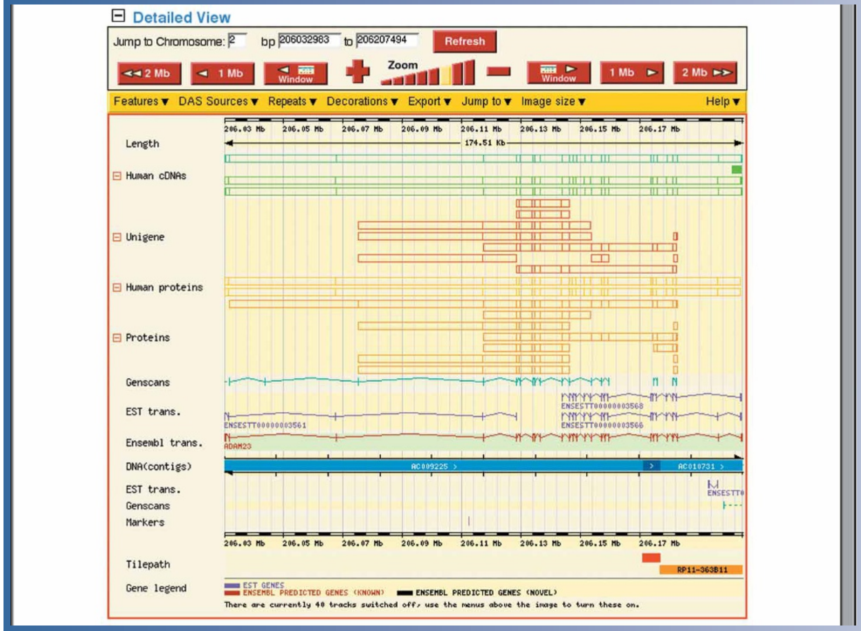


Human Genome Browser (ContigView) - Mozilla {Build ID: 2002101612}

http://www.ensembl.org/Homo_sapiens/contigview?chr=2&vc_start=206032983&vc_end=

Find Sequence 2 Lookup [e.g. AC067852, AP000462]

Figure 1.11

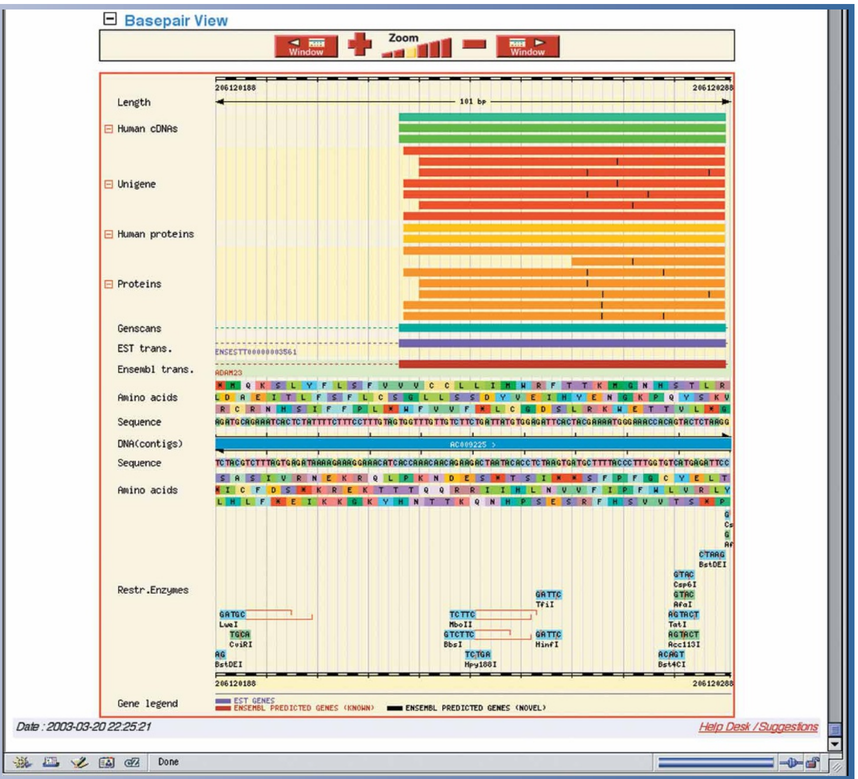


Jump to Chromosome: 2 bp 206032983 to 206207494 Refresh

There are currently 40 tracks switched off, use the menus above the image to turn these on.

Figure 1.12

Figure 1.13


Basepair View
Window
Zoom
Window
206120188
206120288
Length
101 bp
Human cDNAs
Unigene
Human proteins
Proteins
Genscans
EST trans.
ENSESTT00000003561
Ensembl trans.
ADAM23
Amino acids
Sequence
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AC009225 >
Sequence
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Amino acids
Restr.Enzymes
CTAAG
BstDEI
GTAC
Csp6I
GTAC
AfaI
GATTC
TfiI
GATGC
LweI
TGCA
CviRI
AG
BstDEI
TCTTC
MboII
GTCTTC
BbsI
TCTGA
Hpy188I
GATTC
HinfI
AGTACT
TatI
AGTACT
Acc113I
ACAGT
Bst4CI
206120188
206120288
Gene legend
EST GENES
ENSEMBL PREDICTED GENES (KNOWN)
ENSEMBL PREDICTED GENES (NOVEL)
Date : 2003-03-20 22:25:21
Help Desk / Suggestions
Done