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?

doi:10.1038/ng966

This question serves as a basic introduction to the three major genome viewers. One gene, *ADAM2*, 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 Human 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 *Human map viewer* to go to the Map Viewer home page. The notation at the top of the page indicates that this is Build 29, or the NCBI's 29th assembly of the human genome. Build 29 is based on sequence data from 5 April 2002. The previous genome assembly, Build 28, was based on sequence data from 24 December 2001. To search for any mapped element, such as a gene symbol, GenBank accession number, marker name or disease name, enter that term in the *Search for* box and then press *Find*. For this example, enter 'ADAM2' and then press *Find*. The *on chromosome(s)* box may be left blank for text-based searches such as this one.

The resulting overview page shows a schematic of all of the human chromosomes, pinpointing the position of *ADAM2* to the p arm of chromosome 8 (Fig. 1.1). The search results section shows that the gene 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 maps are available at http://www.ncbi.nlm.nih.gov/PMGifs/Genomes/humansearch.html. To get the most general overview of the genomic context of *ADAM2*, including all available maps, click on the item in the *Map element* column (in this case, *ADAM2*). This view shows *ADAM2* and a bit of flanking sequence on chromosome 8p11.2 (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 *ADAM2* and is created by aligning the ADAM2 mRNA to the genome. The gene appears to have 14 exons. The vertical arrow next to the *ADAM2* 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.177959 to the genome follows that of *ADAM2*, 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. Although *ADAM2* has been finely mapped and is represented by a short line, other genes, such as the group below it on a longer line, have been cytogenetically mapped to broader regions of chromosome 8.

Clicking on the zoom control in the blue sidebar allows the user to zoom out to view a larger region of chromosome 8. Zooming out one level shows 1/100th of the chromosome. There are 20 genes in the region, and all 20 are labeled (displayed) in this view (Fig. 1.3). The region of *ADAM2* is highlighted in red on all maps. On the basis of the Genes_seq map, *ADAM2* is located between *ADAM18* and LOC206849.

University of California, Santa Cruz Genome Browser

The home page for the UCSC Genome Browser is http://genome.ucsc.edu/. At present, UCSC provides browsers not only for the most recent version of the 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 genome browser from August 2001 is based on an assembly of the human genome done by UCSC using sequence data available on that date. The *Dec. 2001* browser displays annotations based on NCBI's build 28 of the human genome, and the Apr. 2002 browser displays annotations on NCBI's build 29. As the annotations presented in this most recent human assembly are not yet as comprehensive as those from the December 2001 assembly, the examples in this text are based on the earlier assembly. Select *Dec. 2001* 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 'ADAM2' in the box labeled *position* and then click *Submit*. The results of this search are presented in two categories, *Known Genes* and *mRNA Associated Search Results* (Fig. 1.5). The section marked *Known 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 *Known Genes* link for *ADAM2* (arrow, Fig. 1.5) to see the genomic context of the *ADAM2* mRNA Reference Sequence (NM_001464).

The resulting zoomed-in view shows a region of chromosome 8 from base pair 36234934 to 36280132, located within 8p12 (Fig. 1.6). The blue track entitled *Known Genes (from RefSeq)* shows the intron–exon structure of known genes. The vertical boxes indicate exons and the horizontal lines introns. The *ADAM2* gene seems to have 14 exons. The direction of transcription is indicated by the arrowheads on the introns. The tracks labeled Acembly Gene Predictions, Ensembl Gene Predictions and Fgenesh++ Gene Predictions 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, UniGene and Nonhuman mRNAs from GenBank tracks. Translated alignments of mouse and *Tetraodon* genomic sequence are in the mouse and fish BLAT tracks. Tracks displaying single-nucleotide polymorphisms (SNPs), repetitive elements and microarray data 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 *ADAM2*, zoom out 10× by clicking on the *zoom out 10×* box in the upper right corner. *ADAM2* is located between *TEM*5 and *ADAM18* (Fig. 1.7).

Ensembl

The Ensembl[7] project, http://www.ensembl.org/, provides genome browsers for four species: human, mouse, zebrafish and mosquito. Click on *Human* to view the main entry point for the human genome. The current version of human Ensembl is version 6.28.1, based on the NCBI's 28th build of the genome. To perform a text search, enter 'ADAM2' in the text box, and limit the search by selecting *Gene* from the pull-down search. Click on the upper button labeled *Lookup*. A single result is returned with a link to the *ADAM2* gene (Fig. 1.8).

Click on either of the *ADAM2* links to retrieve the GeneView window. The returned page contains four sections of data. The first section (Fig. 1.9) is an overview of *ADAM2*, including links to accession numbers and protein domains and families. Links to the Ensembl view of highly similar mouse sequences are presented in the *Homology Matches* section. Some of these fields will be described in more detail in later examples. The second section of the GeneView window provides information on the gene transcript (Fig. 1.10). The sequence of the cDNA is shown, as is a graphic of its intron–exon structure. A limited amount of the genomic context around the gene is shown schematically as well. Exon sequences are shown in the third section of the GeneView (Fig. 1.11) and splice sites in the fourth (Fig. 1.12). If more than one transcript is predicted for the gene, each is allocated its own transcript, exon and splice-site sections.

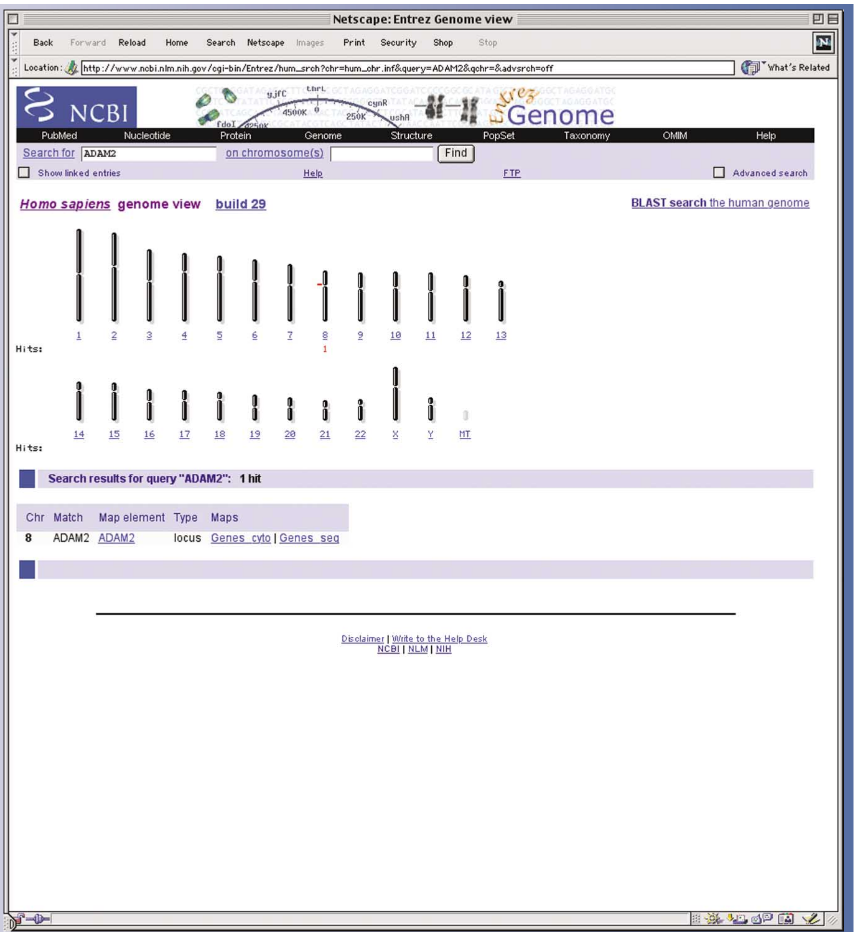
The complete genomic context of *ADAM2* is viewed by returning to the first section of the GeneView (Fig. 1.9) and clicking on one of the two links within the *Genomic Location* box. The top portion of the resulting ContigView (Fig. 1.13) depicts the chromosome, with the region of interest outlined in red. The Overview shows the genomic context of the gene, including the chromosome bands, contigs, markers and genes that map to near 8p12. 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 genes annotated by Ensembl as being around *ADAM2* are Q96KB2 and *ADAM18*.

The bottom panel of the ContigView, the Detailed View (Fig. 1.14), 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. 1.14 are the defaults. The DNA (contigs) map separates items on the forward strand (above) from those on the reverse (below). The only feature on the reverse strand in this view is a single Genscan transcript, predicted by the GENSCAN gene prediction program[11] (see Question 7). The forward strand shows five types of features. Starting at the bottom, the *ADAM2* 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. The *Proteins* and *Human proteins* boxes indicate protein sequences that align to this version of the genome, whereas *NCBI Transcr.* links to the NCBI Map Viewer. Positioning the computer mouse over any feature brings up the feature's name and links to more detailed information.

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. The NCBI is currently displaying build 29, Ensembl shows build 28, and UCSC offers both builds 28 (December 2001) and 29 (April 2002), although all examples from UCSC in this guide will be illustrated using the better-annotated build 28. Because of the differences between the two assemblies, there are subtle discrepancies between what is shown at the NCBI and what is available at UCSC and Ensembl. However, 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



Netscape: Entrez Genome view

Location: http://www.ncbi.nlm.nih.gov/cgi-bin/Entrez/hum_srch?chr=hum_chr.inf&query=ADAM2&qchr=&advsrch=off

Search for ADAM2 on chromosome(s) Find

□ Show linked entries Help FTP □ Advanced search

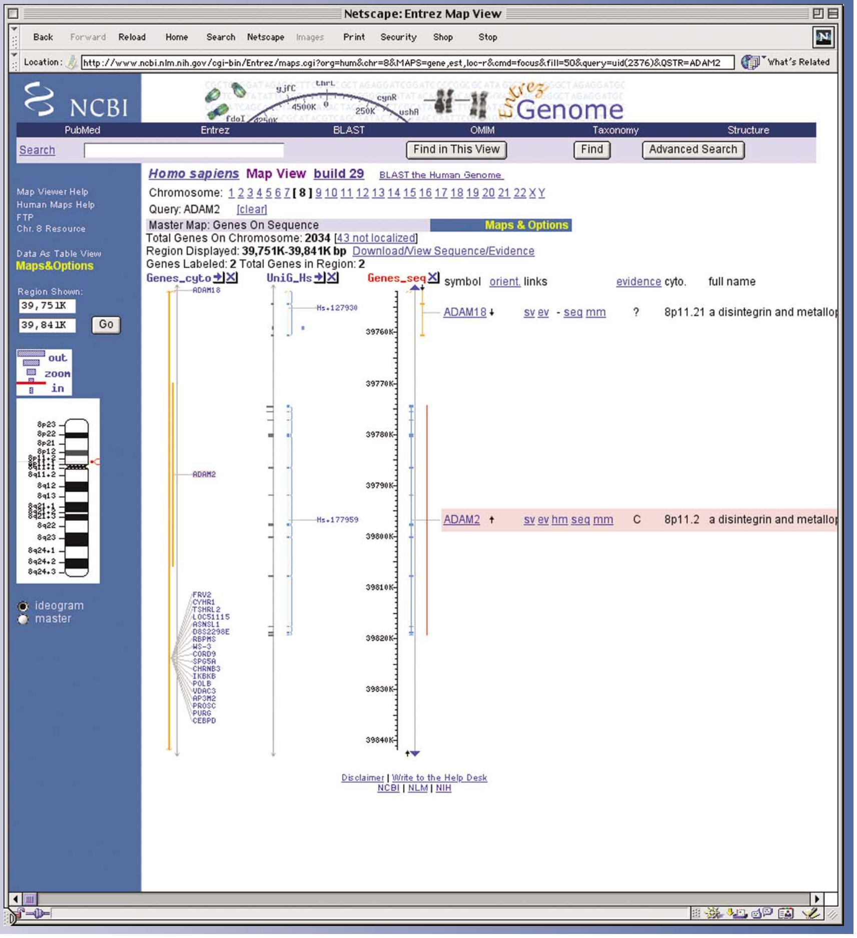
Homo sapiens genome view build 29 BLAST search the human genome

Search results for query "ADAM2": 1 hit

Chr	Match	Map element	Type	Maps
8	ADAM2	ADAM2	locus	Genes_cyto | Genes_seq

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

Figure 1.2



Netscape: Entrez Map View

Location: http://www.ncbi.nlm.nih.gov/cgi-bin/Entrez/maps.cgi?org=hum&chr=8&MAPS=gene,est,loc-r&cmd=focus&fill=50&query=uid(2376)&QSTR=ADAM2

Homo sapiens Map View build 29 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: ADAM2 [clear]

Master Map: Genes On Sequence Maps & Options

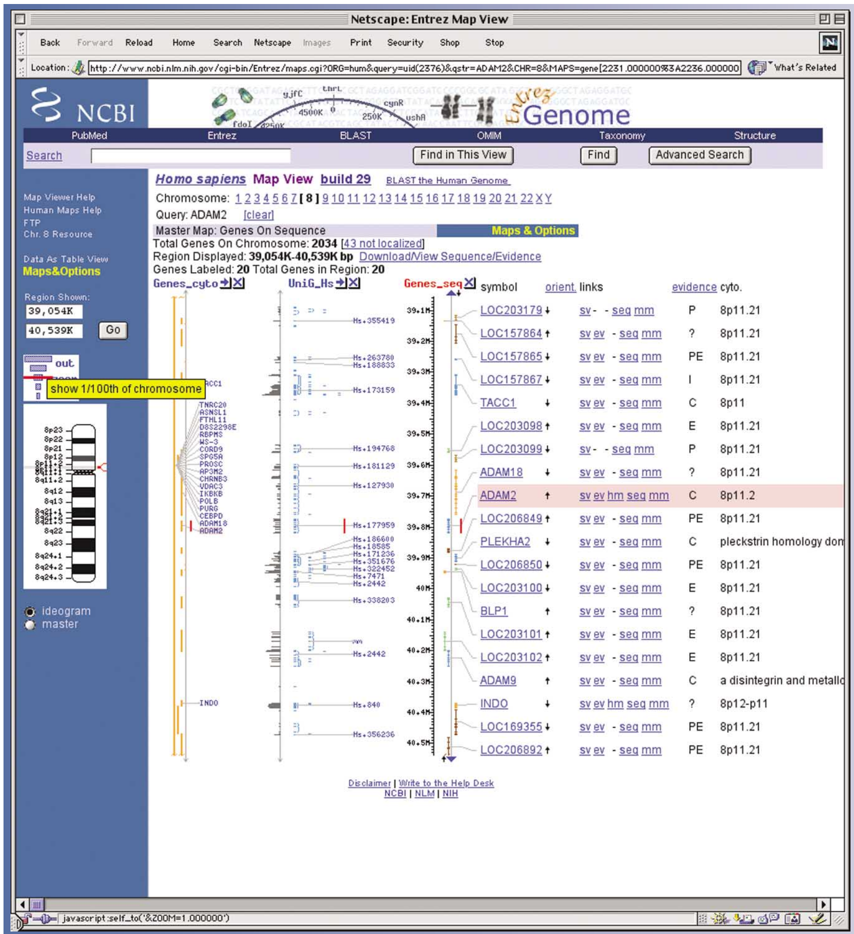
Total Genes On Chromosome: **2034** [43 not localized]

Region Displayed: **39,751K-39,841K bp** Download/View Sequence/Evidence

Genes Labeled: **2** Total Genes in Region: **2**

symbol	orient.	links	evidence	cyto.	full name
ADAM18	↓	sv ev - seq mm	?	8p11.21	a disintegrin and metallo
ADAM2	↑	sv ev hm seq mm	C	8p11.2	a disintegrin and metallo

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



Location: http://www.ncbi.nlm.nih.gov/cgi-bin/Entrez/maps.cgi?ORG=hum&query=uid(2376)&qstr=ADAM2&CHR=8&MAPS=gene[2231.000000%3A2236.000000

Homo sapiens Map View build 29 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: ADAM2 [clear]

Master Map: Genes On Sequence — Maps & Options

Total Genes On Chromosome: **2034** [43 not localized]

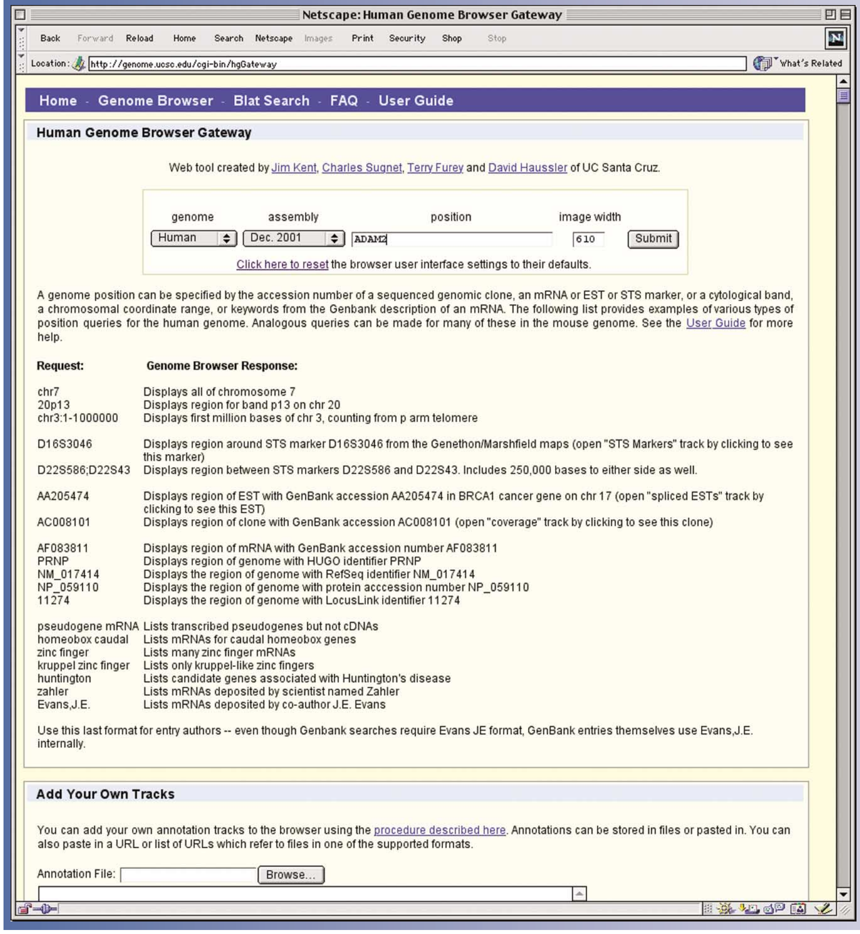
Region Displayed: **39,054K-40,539K bp** Download/View Sequence/Evidence

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

symbol	orient.	links	evidence	cyto.
LOC203179	↓	sv - - seq mm	P	8p11.21
LOC157864	↑	sv ev - seq mm	?	8p11.21
LOC157865	↓	sv ev - seq mm	PE	8p11.21
LOC157867	↓	sv ev - seq mm	I	8p11.21
TACC1	↓	sv ev - seq mm	C	8p11
LOC203098	↑	sv ev - seq mm	E	8p11.21
LOC203099	↓	sv - - seq mm	P	8p11.21
ADAM18	↓	sv ev - seq mm	?	8p11.21
ADAM2	↑	sv ev hm seq mm	C	8p11.2
LOC206849	↑	sv ev - seq mm	PE	8p11.21
PLEKHA2	↓	sv ev - seq mm	C	pleckstrin homology dom
LOC206850	↓	sv ev - seq mm	PE	8p11.21
LOC203100	↓	sv ev - seq mm	E	8p11.21
BLP1	↑	sv ev - seq mm	?	8p11.21
LOC203101	↑	sv ev - seq mm	E	8p11.21
LOC203102	↑	sv ev - seq mm	E	8p11.21
ADAM9	↑	sv ev - seq mm	C	a disintegrin and metallo
INDO	↓	sv ev hm seq mm	?	8p12-p11
LOC169355	↓	sv ev - seq mm	PE	8p11.21
LOC206892	↑	sv ev - seq mm	PE	8p11.21

javascript:self_to('&ZOOM=1.000000')

Figure 1.3


Netscape: Human Genome Browser Gateway
Back Forward Reload Home Search Netscape Images Print Security Shop Stop
What's Related
Home - Genome Browser - Blat Search - FAQ - User Guide
Submit
Browse...

Location: http://genome.ucsc.edu/cgi-bin/hgGateway

Human Genome Browser Gateway

Web tool created by Jim Kent, Charles Sugnet, Terry Furey and David Haussler of UC Santa Cruz.

genome: Human; assembly: Dec. 2001; position: ADAM2; image width: 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. Analogous queries can be made for many of these in the mouse 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 (open "STS Markers" track by clicking to see this marker)
D22S586;D22S43	Displays region between STS markers D22S586 and D22S43. Includes 250,000 bases to either side as well.
AA205474	Displays region of EST with GenBank accession AA205474 in BRCA1 cancer gene on chr 17 (open "spliced ESTs" track by clicking to see this EST)
AC008101	Displays region of clone with GenBank accession AC008101 (open "coverage" track by clicking to see this clone)
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.

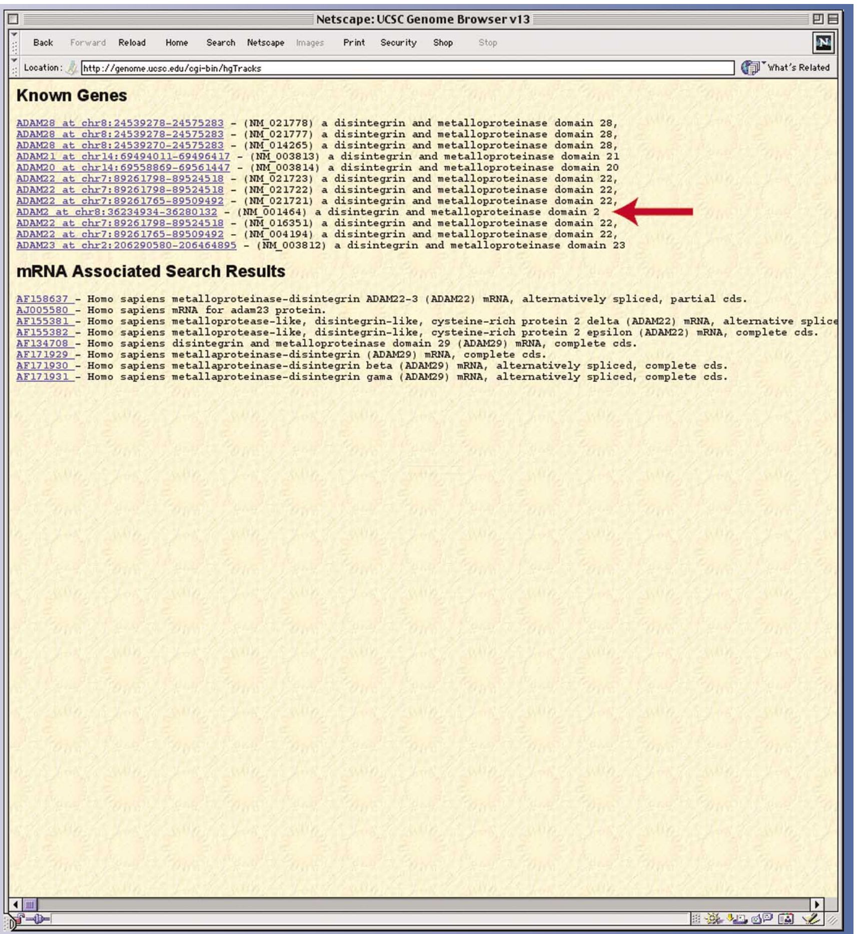
Add Your Own Tracks

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

Annotation File:

Figure 1.4

Figure 1.5



http://genome.ucsc.edu/cgi-bin/hgTracks

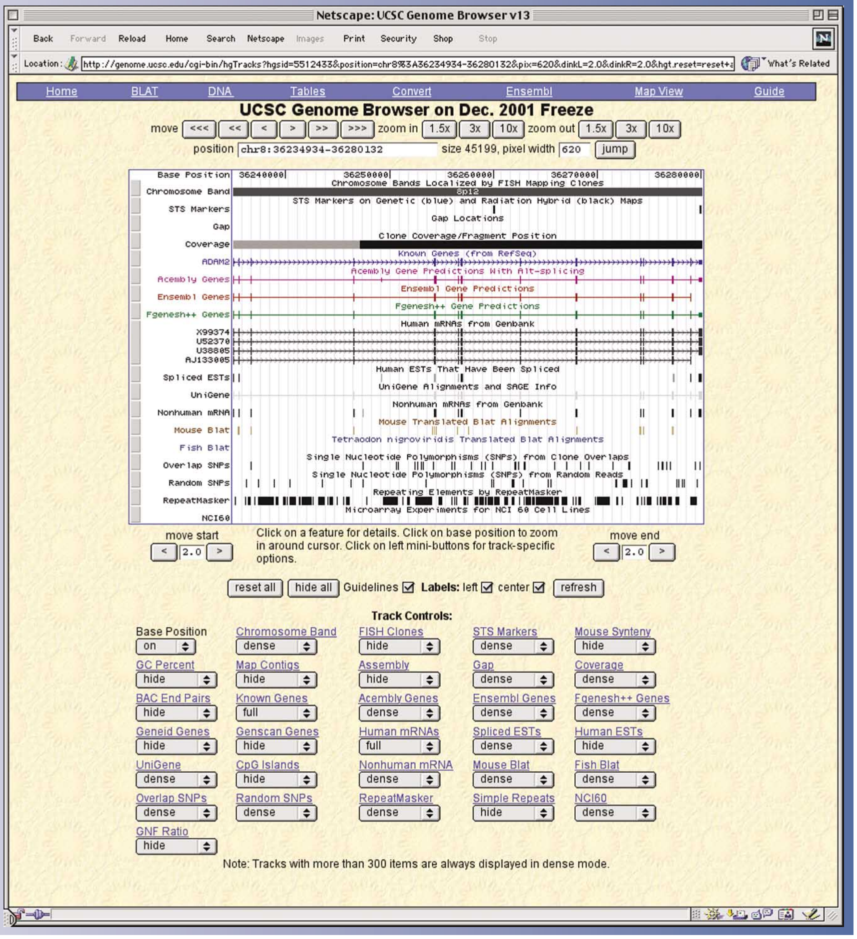
Known Genes

```
ADAM28 at chr8:24539278-24575283 - (NM_021778) a disintegrin and metalloproteinase domain 28,
ADAM28 at chr8:24539278-24575283 - (NM_021777) a disintegrin and metalloproteinase domain 28,
ADAM28 at chr8:24539270-24575283 - (NM_014265) a disintegrin and metalloproteinase domain 28,
ADAM21 at chr14:69494011-69496417 - (NM_003813) a disintegrin and metalloproteinase domain 21
ADAM20 at chr14:69558869-69561447 - (NM_003814) a disintegrin and metalloproteinase domain 20
ADAM22 at chr7:89261798-89524518 - (NM_021723) a disintegrin and metalloproteinase domain 22,
ADAM22 at chr7:89261798-89524518 - (NM_021722) a disintegrin and metalloproteinase domain 22,
ADAM22 at chr7:89261765-89509492 - (NM_021721) a disintegrin and metalloproteinase domain 22,
ADAM2 at chr8:36234934-36280132 - (NM_001464) a disintegrin and metalloproteinase domain 2
ADAM22 at chr7:89261798-89524518 - (NM_016351) a disintegrin and metalloproteinase domain 22,
ADAM22 at chr7:89261765-89509492 - (NM_004194) a disintegrin and metalloproteinase domain 22,
ADAM23 at chr2:206290580-206464895 - (NM_003812) a disintegrin and metalloproteinase domain 23
```

mRNA Associated Search Results

```
AF158637 - Homo sapiens metalloproteinase-disintegrin ADAM22-3 (ADAM22) mRNA, alternatively spliced, partial cds.
AJ005580 - Homo sapiens mRNA for adam23 protein.
AF155381 - Homo sapiens metalloprotease-like, disintegrin-like, cysteine-rich protein 2 delta (ADAM22) mRNA, alternative splice
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.
```

Figure 1.6


Netscape: UCSC Genome Browser v13
Back
Forward
Reload
Home
Search
Netscape
Images
Print
Security
Shop
Stop
Location:
What's Related
Home
BLAT
DNA
Tables
Convert
Ensembl
Map View
Guide
move
<<<
<<
<
>
>>
>>>
zoom in
1.5x
3x
10x
zoom out
1.5x
3x
10x
jump
Base Position
36240000
36250000
36260000
36270000
36280000
Chromosome Bands Localized by FISH Mapping Clones
Chromosome Band
8p12
STS Markers on Genetic (blue) and Radiation Hybrid (black) Maps
STS Markers
Gap Locations
Gap
Clone Coverage/Fragment Position
Coverage
Known Genes (from RefSeq)
ADAM2
Acembly Gene Predictions With Alt-splicing
Acembly Genes
Ensembl Gene Predictions
Ensembl Genes
Fgenesh++ Gene Predictions
Fgenesh++ Genes
Human mRNAs from Genbank
X99374
U52370
U38805
AJ133005
Human ESTs That Have Been Spliced
Spliced ESTs
UniGene Alignments and SAGE Info
UniGene
Nonhuman mRNAs from Genbank
Nonhuman mRNA
Mouse Translated Blat Alignments
Mouse Blat
Tetraodon nigroviridis Translated Blat Alignments
Fish Blat
Single Nucleotide Polymorphisms (SNPs) from Clone Overlaps
Overlap SNPs
Single Nucleotide Polymorphisms (SNPs) from Random Reads
Random SNPs
Repeating Elements by RepeatMasker
RepeatMasker
Microarray Experiments for NCI 60 Cell Lines
NCI60
move start
<
>
move end
<
>
reset all
hide all
refresh

http://genome.ucsc.edu/cgi-bin/hgTracks?hgsid=5512433&position=chr8%3A36234934-36280132&pix=620&dinkL=2.0&dinkR=2.0&hgt.reset=reset+a

UCSC Genome Browser on Dec. 2001 Freeze

position chr8:36234934-36280132 size 45199, pixel width 620

move start 2.0 move end 2.0

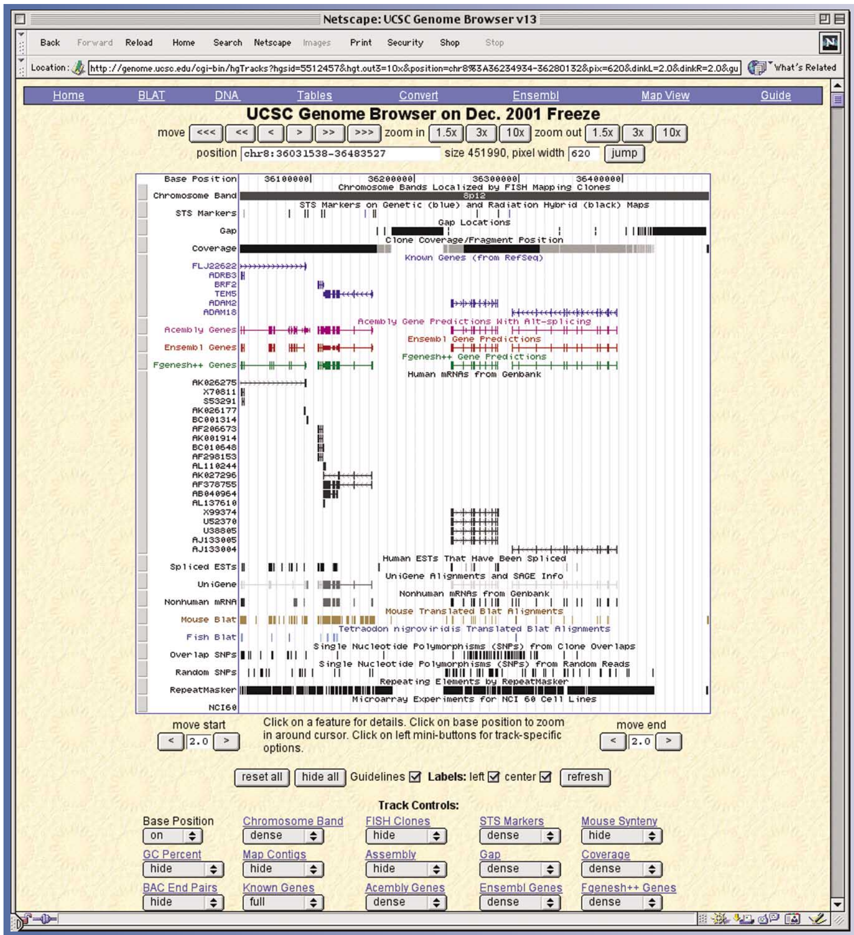
Click on a feature for details. Click on base position to zoom in around cursor. Click on left mini-buttons for track-specific options.

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

Track Controls:

Base Position on	Chromosome Band dense	FISH Clones hide	STS Markers dense	Mouse Synteny hide
GC Percent hide	Map Contigs hide	Assembly hide	Gap dense	Coverage dense
BAC End Pairs hide	Known Genes full	Acembly Genes dense	Ensembl Genes dense	Fgenesh++ Genes dense
Geneid Genes hide	Genscan Genes hide	Human mRNAs full	Spliced ESTs dense	Human ESTs hide
UniGene dense	CpG Islands hide	Nonhuman mRNA dense	Mouse Blat dense	Fish Blat dense
Overlap SNPs dense	Random SNPs dense	RepeatMasker dense	Simple Repeats hide	NCI60 dense
GNF Ratio hide				

Note: Tracks with more than 300 items are always displayed in dense mode.



Location: http://genome.ucsc.edu/cgi-bin/hgTracks?hgsid=5512457&hgt.out3=10x&position=chr8%3A36234934-36280132&pix=620&dinkL=2.0&dinkR=2.0&gu

UCSC Genome Browser on Dec. 2001 Freeze

position chr8:36031538-36483527 size 451990, pixel width 620

move start 2.0 | move end 2.0

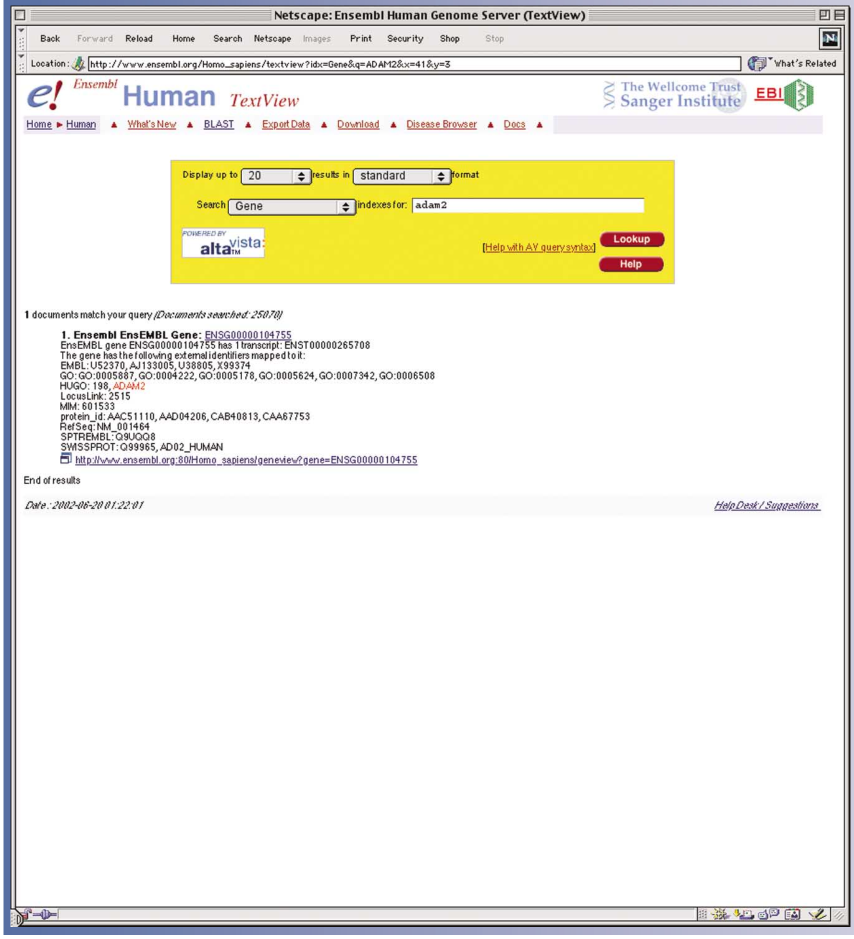
Click on a feature for details. Click on base position to zoom in around cursor. Click on left mini-buttons for track-specific options.

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

Track Controls:

Base Position: on
Chromosome Band: dense
FISH Clones: hide
STS Markers: dense
Mouse Synteny: hide
GC Percent: hide
Map Contigs: hide
Assembly: hide
Gap: dense
Coverage: dense
BAC End Pairs: hide
Known Genes: full
Acembly Genes: dense
Ensembl Genes: dense
Fgenesh++ Genes: dense

Figure 1.7



Location: http://www.ensembl.org/Homo_sapiens/textview?idx=Gene&q=ADAM2&x=41&y=3

Display up to 20 results in standard format

Search Gene indexes for: adam2

1 documents match your query *(Documents searched: 25070)*

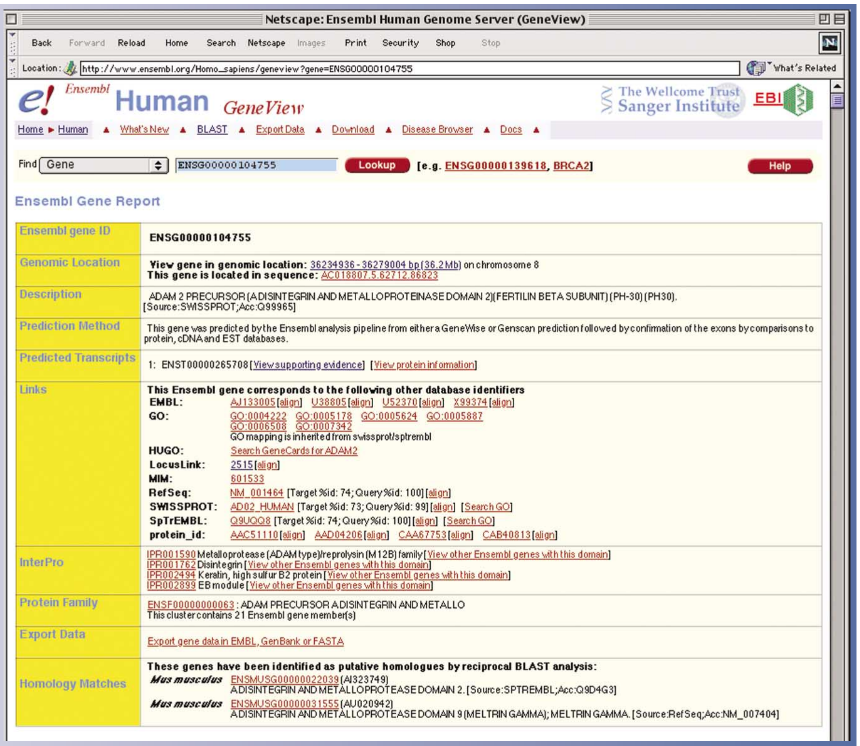
1. Ensembl EnsEMBL Gene: ENSG00000104755
EnsEMBL gene ENSG00000104755 has 1 transcript: ENST00000265708
The gene has the following external identifiers mapped to it:
EMBL: U52370, AJ133005, U38805, X99374
GO: GO:0005887, GO:0004222, GO:0005178, GO:0005624, GO:0007342, GO:0006508
HUGO: 198, ADAM2
LocusLink: 2515
MIM: 601533
protein_id: AAC51110, AAD04206, CAB40813, CAA67753
RefSeq: NM_001464
SPTREMBL: Q9UQQ8
SWISSPROT: Q99965, AD02_HUMAN
http://www.ensembl.org:80/Homo_sapiens/geneview?gene=ENSG00000104755

End of results

Date : 2002-06-20 01:22:01

Figure 1.8

Figure 1.9


Netscape: Ensembl Human Genome Server (GeneView)
Back
Forward
Reload
Home
Search
Netscape
Images
Print
Security
Shop
Stop
Location:
What's Related
Ensembl
e!
Human
GeneView
The Wellcome Trust Sanger Institute
EBI
Home ▶ Human ▲ What's New ▲ BLAST ▲ Export Data ▲ Download ▲ Disease Browser ▲ Docs ▲
Find
Gene
Lookup
Help

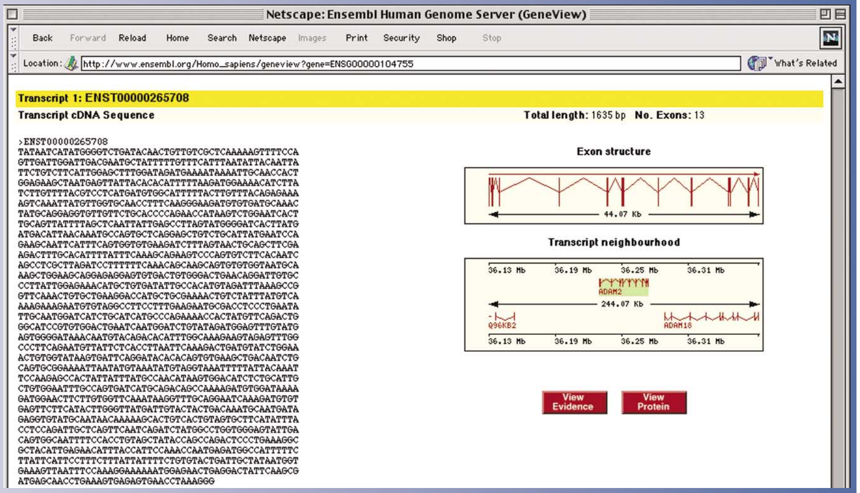
http://www.ensembl.org/Homo_sapiens/geneview?gene=ENSG00000104755

Find Gene ENSG00000104755 [e.g. ENSG00000139618, BRCA2]

Ensembl Gene Report

Ensembl gene ID	ENSG00000104755
Genomic Location	**View gene in genomic location:** 36234936 - 36279004 bp (36.2 Mb) on chromosome 8 **This gene is located in sequence:** AC018807.5.62712.86823
Description	ADAM 2 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE DOMAIN 2)(FERTILIN BETA SUBUNIT) (PH-30) (PH30). [Source:SWISSPROT;Acc:Q99965]
Prediction Method	This gene was predicted by the Ensembl analysis pipeline from either a GeneWise or Genscan prediction followed by confimation of the exons by comparisons to protein, cDNA and EST databases.
Predicted Transcripts	1: ENST00000265708 [View supporting evidence] [View protein information]
Links	**This Ensembl gene corresponds to the following other database identifiers** **EMBL:** AJ133005 [align] U38805 [align] U52370 [align] X99374 [align] **GO:** GO:0004222 GO:0005178 GO:0005624 GO:0005887 GO:0006508 GO:0007342 GO mapping is inherited from swissprot/sptrembl **HUGO:** Search GeneCards for ADAM2 **LocusLink:** 2515 [align] **MIM:** 601533 **RefSeq:** NM_001464 [Target %id: 74; Query %id: 100] [align] **SWISSPROT:** AD02_HUMAN [Target %id: 73; Query %id: 99] [align] [Search GO] **SpTrEMBL:** Q9UQQ8 [Target %id: 74; Query %id: 100] [align] [Search GO] **protein_id:** AAC51110 [align] AAD04206 [align] CAA67753 [align] CAB40813 [align]
InterPro	IPR001590 Metalloprotease (ADAM type)/reprolysin (M12B) family [View other Ensembl genes with this domain] IPR001762 Disintegrin [View other Ensembl genes with this domain] IPR002494 Keratin, high sulfur B2 protein [View other Ensembl genes with this domain] IPR002899 EB module [View other Ensembl genes with this domain]
Protein Family	ENSF00000000063 : ADAM PRECURSOR A DISINTEGRIN AND METALLO This cluster contains 21 Ensembl gene member(s)
Export Data	Export gene data in EMBL, GenBank or FASTA
Homology Matches	**These genes have been identified as putative homologues by reciprocal BLAST analysis:** ***Mus musculus*** ENSMUSG00000022039 (AI323749) A DISINTEGRIN AND METALLOPROTEASE DOMAIN 2. [Source:SPTREMBL;Acc:Q9D4G3] ***Mus musculus*** ENSMUSG00000031555 (AU020942) A DISINTEGRIN AND METALLOPROTEASE DOMAIN 9 (MELTRIN GAMMA); MELTRIN GAMMA. [Source:RefSeq;Acc:NM_007404]

Figure 1.10

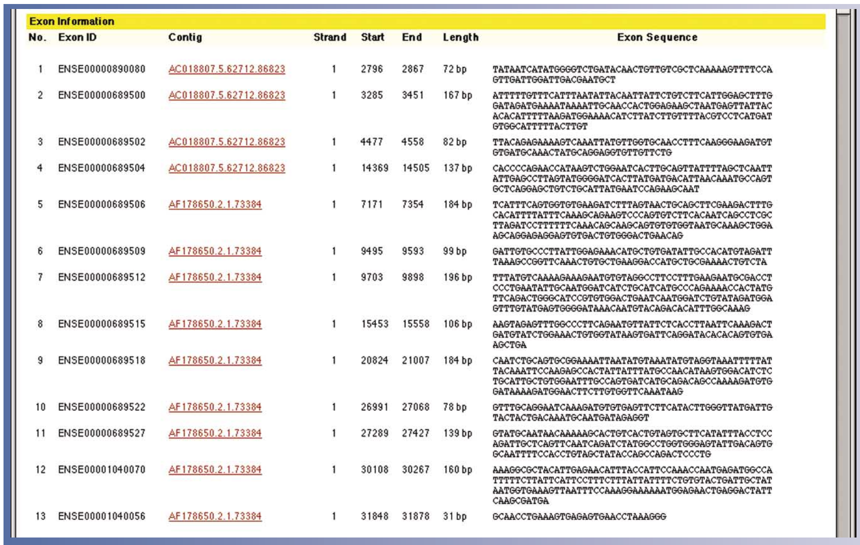


http://www.ensembl.org/Homo_sapiens/geneview?gene=ENSG00000104755

Transcript 1: ENST00000265708

Transcript cDNA Sequence **Total length:** 1635 bp **No. Exons:** 13

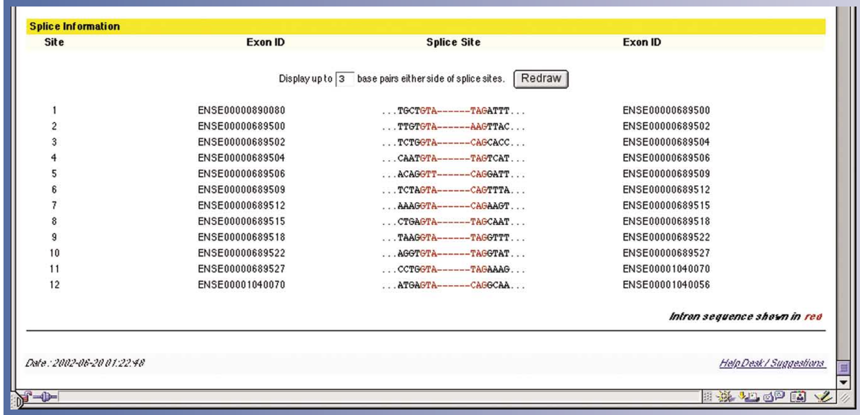
```
>ENST00000265708
TATAATCATATGGGGTCTGATACAACTGTTGTCGCTCAAAAAGTTTTCCA
GTTGATTGGATTGACGAATGCTATTTTTGTTTCATTTAATATTACAATTA
TTCTGTCTTCATTGGAGCTTTGGATAGATGAAAATAAAATTGCAACCACT
GGAGAAGCTAATGAGTTATTACACACATTTTTAAGATGGAAAACATCTTA
TCTTGTTTTACGTCCTCATGATGTGGCATTTTTACTTGTTTACAGAGAAA
AGTCAAATTATGTTGGTGCAACCTTTCAAGGGAAGATGTGTGATGCAAAC
TATGCAGGAGGTGTTGTTCTGCACCCCAGAACCATAAGTCTGGAATCACT
TGCAGTTATTTTAGCTCAATTATTGAGCCTTAGTATGGGGATCACTTATG
ATGACATTAACAAATGCCAGTGCTCAGGAGCTGTCTGCATTATGAATCCA
GAAGCAATTCATTTCAGTGGTGTGAAGATCTTTAGTAACTGCAGCTTCGA
AGACTTTGCACATTTTATTTCAAAGCAGAAGTCCCAGTGTCTTCACAATC
AGCCTCGCTTAGATCCTTTTTTCAAACAGCAAGCAGTGTGTGGTAATGCA
AAGCTGGAAGCAGGAGAGGAGTGTGACTGTGGGACTGAACAGGATTGTGC
CCTTATTGGAGAAACATGCTGTGATATTGCCACATGTAGATTTAAAGCCG
GTTCAAACTGTGCTGAAGGACCATGCTGCGAAAACTGTCTATTTATGTCA
AAAGAAAGAATGTGTAGGCCTTCCTTTGAAGAATGCGACCTCCCTGAATA
TTGCAATGGATCATCTGCATCATGCCCAGAAAACCACTATGTTCAGACTG
GGCATCCGTGTGGACTGAATCAATGGATCTGTATAGATGGAGTTTGTATG
AGTGGGGATAAACAATGTACAGACACATTTGGCAAAGAAGTAGAGTTTGG
CCCTTCAGAATGTTATTCTCACCTTAATTCAAAGACTGATGTATCTGGAA
ACTGTGGTATAAGTGATTCAGGATACACACAGTGTGAAGCTGACAATCTG
CAGTGCGGAAAATTAATATGTAAATATGTAGGTAAATTTTTATTACAAAT
TCCAAGAGCCACTATTATTTATGCCAACATAAGTGGACATCTCTGCATTG
CTGTGGAATTTGCCAGTGATCATGCAGACAGCCAAAAGATGTGGATAAAA
GATGGAACTTCTTGTGGTTCAAATAAGGTTTGCAGGAATCAAAGATGTGT
GAGTTCTTCATACTTGGGTTATGATTGTACTACTGACAAATGCAATGATA
GAGGTGTATGCAATAACAAAAAGCACTGTCACTGTAGTGCTTCATATTTA
CCTCCAGATTGCTCAGTTCAATCAGATCTATGGCCTGGTGGGAGTATTGA
CAGTGGCAATTTTCCACCTGTAGCTATACCAGCCAGACTCCCTGAAAGGC
GCTACATTGAGAACATTTACCATTCCAAACCAATGAGATGGCCATTTTTC
TTATTCATTCCTTTCTTTATTATTTTCTGTGTACTGATTGCTATAATGGT
GAAAGTTAATTTCCAAAGGAAAAAATGGAGAACTGAGGACTATTCAAGCG
ATGAGCAACCTGAAAGTGAGAGTGAACCTAAAGGG
```



Exon Information

No.	Exon ID	Contig	Strand	Start	End	Length	Exon Sequence
1	ENSE00000890080	AC018807.5.62712.86823	1	2796	2867	72 bp	TATAATCATATGGGGTCTGATACAACTGTTGTCGCTCAAAAAGTTTTCCAGTTGATTGGATTGACGAATGCT
2	ENSE00000689500	AC018807.5.62712.86823	1	3285	3451	167 bp	ATTTTTGTTTCATTTAATATTACAATTATTCTGTCTTCATTGGAGCTTTGGATAGATGAAAATAAAATTGCAACCACTGGAGAAGCTAATGAGTTATTACACACATTTTTAAGATGGAAAACATCTTATCTTGTTTTACGTCCTCATGATGTGGCATTTTTACTTGT
3	ENSE00000689502	AC018807.5.62712.86823	1	4477	4558	82 bp	TTACAGAGAAAAGTCAAATTATGTTGGTGCAACCTTTCAAGGGAAGATGTGTGATGCAAACTATGCAGGAGGTGTTGTTCTG
4	ENSE00000689504	AC018807.5.62712.86823	1	14369	14505	137 bp	CACCCCAGAACCATAAGTCTGGAATCACTTGCAGTTATTTTAGCTCAATTATTGAGCCTTAGTATGGGGATCACTTATGATGACATTAACAAATGCCAGTGCTCAGGAGCTGTCTGCATTATGAATCCAGAAGCAAT
5	ENSE00000689506	AF178650.2.1.73384	1	7171	7354	184 bp	TCATTTCAGTGGTGTGAAGATCTTTAGTAACTGCAGCTTCGAAGACTTTGCACATTTTATTTCAAAGCAGAAGTCCCAGTGTCTTCACAATCAGCCTCGCTTAGATCCTTTTTTCAAACAGCAAGCAGTGTGTGGTAATGCAAAGCTGGAAGCAGGAGAGGAGTGTGACTGTGGGACTGAACAG
6	ENSE00000689509	AF178650.2.1.73384	1	9495	9593	99 bp	GATTGTGCCCTTATTGGAGAAACATGCTGTGATATTGCCACATGTAGATTTAAAGCCGGTTCAAACTGTGCTGAAGGACCATGCTGCGAAAACTGTCTA
7	ENSE00000689512	AF178650.2.1.73384	1	9703	9898	196 bp	TTTATGTCAAAAGAAAGAATGTGTAGGCCTTCCTTTGAAGAATGCGACCTCCCTGAATATTGCAATGGATCATCTGCATCATGCCCAGAAAACCACTATGTTCAGACTGGGCATCCGTGTGGACTGAATCAATGGATCTGTATAGATGGAGTTTGTATGAGTGGGGATAAACAATGTACAGACACATTTGGCAAAG
8	ENSE00000689515	AF178650.2.1.73384	1	15453	15558	106 bp	AAGTAGAGTTTGGCCCTTCAGAATGTTATTCTCACCTTAATTCAAAGACTGATGTATCTGGAAACTGTGGTATAAGTGATTCAGGATACACACAGTGTGAAGCTGA
9	ENSE00000689518	AF178650.2.1.73384	1	20824	21007	184 bp	CAATCTGCAGTGCGGAAAATTAATATGTAAATATGTAGGTAAATTTTTATTACAAATTCCAAGAGCCACTATTATTTATGCCAACATAAGTGGACATCTCTGCATTGCTGTGGAATTTGCCAGTGATCATGCAGACAGCCAAAAGATGTGGATAAAAGATGGAACTTCTTGTGGTTCAAATAAG
10	ENSE00000689522	AF178650.2.1.73384	1	26991	27068	78 bp	GTTTGCAGGAATCAAAGATGTGTGAGTTCTTCATACTTGGGTTATGATTGTACTACTGACAAATGCAATGATAGAGGT
11	ENSE00000689527	AF178650.2.1.73384	1	27289	27427	139 bp	GTATGCAATAACAAAAAGCACTGTCACTGTAGTGCTTCATATTTACCTCCAGATTGCTCAGTTCAATCAGATCTATGGCCTGGTGGGAGTATTGACAGTGGCAATTTTCCACCTGTAGCTATACCAGCCAGACTCCCTG
12	ENSE00001040070	AF178650.2.1.73384	1	30108	30267	160 bp	AAAGGCGCTACATTGAGAACATTTACCATTCCAAACCAATGAGATGGCCATTTTTCTTATTCATTCCTTTCTTTATTATTTTCTGTGTACTGATTGCTATAATGGTGAAAGTTAATTTCCAAAGGAAAAAATGGAGAACTGAGGACTATTCAAGCGATGA
13	ENSE00001040056	AF178650.2.1.73384	1	31848	31878	31 bp	GCAACCTGAAAGTGAGAGTGAACCTAAAGGG

Figure 1.11



Splice Information

Display up to 3 base pairs either side of splice sites. Redraw

Site	Exon ID	Splice Site	Exon ID
1	ENSE00000890080	...TGCTGTA------TAGATTT...	ENSE00000689500
2	ENSE00000689500	...TTGTGTA------AAGTTAC...	ENSE00000689502
3	ENSE00000689502	...TCTGGTA------CAGCACC...	ENSE00000689504
4	ENSE00000689504	...CAATGTA------TAGTCAT...	ENSE00000689506
5	ENSE00000689506	...ACAGGTT------CAGGATT...	ENSE00000689509
6	ENSE00000689509	...TCTAGTA------CAGTTTA...	ENSE00000689512
7	ENSE00000689512	...AAAGGTA------CAGAAGT...	ENSE00000689515
8	ENSE00000689515	...CTGAGTA------TAGCAAT...	ENSE00000689518
9	ENSE00000689518	...TAAGGTA------TAGGTTT...	ENSE00000689522
10	ENSE00000689522	...AGGTGTA------TAGGTAT...	ENSE00000689527
11	ENSE00000689527	...CCTGGTA------TAGAAAG...	ENSE00001040070
12	ENSE00001040070	...ATGAGTA------CAGGCAA...	ENSE00001040056

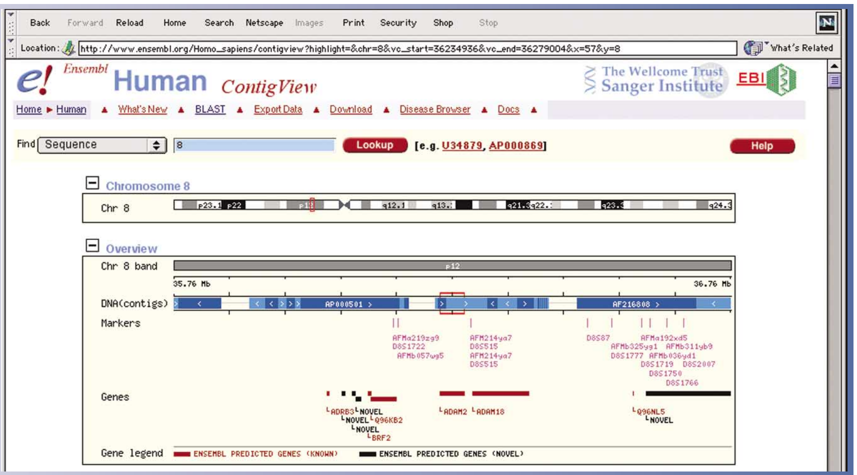
Intron sequence shown in red

Date : 2002-06-20 01:22:48

Help Desk / Suggestions

Figure 1.12

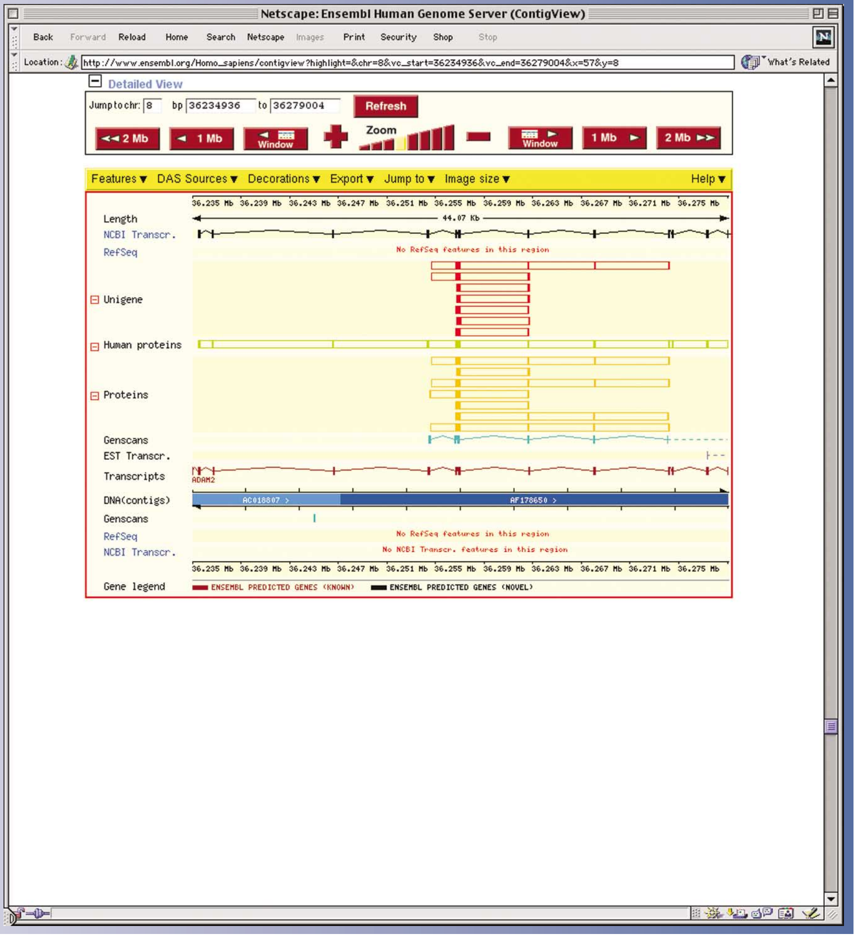
Figure 1.13



Location: http://www.ensembl.org/Homo_sapiens/contigview?highlight=&chr=8&vc_start=36234936&vc_end=36279004&x=57&y=8

Find Sequence 8 Lookup [e.g. U34879, AP000869]

Figure 1.14



Netscape: Ensembl Human Genome Server (ContigView)

Location: http://www.ensembl.org/Homo_sapiens/contigview?highlight=&chr=8&vc_start=36234936&vc_end=36279004&x=57&y=8

Jump to chr: 8 bp 36234936 to 36279004 Refresh