

Ensembl worked example

STEP 1

Go to
<http://www.ensembl.org>

Multi-species text searching

Search all Ensembl:

Ensembl v32 - May 2005 [Help](#)

Use Ensembl to...

- Run a BLAST search
- Search Ensembl
- Data mining [BioMart]
- Upload your own data
- Download data

Docs and downloads

- Information
- About Ensembl
- Ensembl data
- Software

Other links

- Home
- Sitemap
- What's New
- Archive/ sites
- Stable Archive/ link for this page

browse a genome

Mammals

- Homo sapiens** [NCBI 35]
[browse](#) | [what's new](#) | [Vega](#)
- Pan troglodytes** [CHIMP1]
[browse](#) | [what's new](#)
- Mus musculus** [NCBI m34]
[browse](#) | [what's new](#) | [Vega](#)
- Rattus norvegicus** [ROSC 3.4]
[browse](#) | [what's new](#)
- Canis familiaris** [CanFam1.0]
[browse](#) | [what's new](#) | [Vega](#)
- Bos taurus** [Btau 1.0] - **NEW!**
[browse](#) | [what's new](#)
- Monodelphis domestica** [MonDom2]
[browse](#) | [what's new](#)

Other chordates

- Gallus gallus** [WASHUC1]
[browse](#) | [what's new](#)
- Xenopus tropicalis** [XJOI 3]
[browse](#) | [what's new](#)
- Danio rerio** [WTSI Zv5]
[browse](#) | [what's new](#) | [Vega](#)
- Takifugu rubripes** [Fugu 2.0]
[browse](#) | [what's new](#)
- Tetraodon lineare** [TETRAODON 7]
[browse](#) | [what's new](#)
- Ciona intestinalis** [XJOI 1.95]
[browse](#) | [what's new](#)

Other eukaryotes

- Drosophila melanogaster** [BGDP 4]
[browse](#) | [what's new](#)
- Anopheles gambiae** [MOZ 2]
[browse](#) | [what's new](#)
- Apis mellifera** [Amel 2.0]
[browse](#) | [what's new](#)
- Caenorhabditis elegans** [WGS140]
[browse](#) | [what's new](#)
- Saccharomyces cerevisiae** [SGO]
[browse](#) | [what's new](#)

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 selected eukaryotic 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 a species name 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](#).

For all enquiries, please contact the Ensembl [HelpDesk](#) (helpdesk@ensembl.org).

What's New in Ensembl 32

- [New Bos taurus genebuild](#)
- [New Zebrafish assembly \(Zv5\) and genebuild](#)
- [Import of FlyBase annotations](#)
- [New Mouse assembly NCBI 34](#)
- [New look'n'feel for the Ensembl website](#)

[More news...](#)

Have you tried...?

Ciona intestinalis

See [squirt assembly](#) now available at Ensembl

[Click for more information](#)

© 2005 [WTSI](#) / [EBI](#). Ensembl is available to [download for public use](#) - please see the [code licence](#) for details.

STEP 2

Choose human

Help!

STEP 3
Pick chromosome X

Ensembl v32 - May 2005

Use Ensembl to...

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- Search Ensembl
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- Upload your own data
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Docs and downloads

- Information
- About Ensembl
- Ensembl data
- Software

Select a species

- Mammals
- Other chordates
- Other eukaryotes

Other links

- Home
- Sitemap
- What's New
- Archived sites
- Stable Archive/ link for this page



Explore the Human genome

What's New in Ensembl 32

Homo sapiens news

- Vega
New Ensembl-Vega database for Homo sapiens
- cDNA
Monthly update of the human cDNA database
- Gene annotation
New non-coding gene annotation based on RFAM domains

Ensembl news

- New look/feel for the Ensembl website
www.ensembl.org has had a major redesign, both on the surface and 'under the bonnet'. Most of the dynamic pages (e.g. ContigView, GeneView) have only minor cosmetic changes - in addition to the new template and stylesheets, some links have been moved from the body of the view to the new side-bar.
[Read more...](#)
- New variation databases
All species have new variation databases owing to schema changes.

More news...

About the Human genome

Assembly

This release is based on [version 2 of the NCBI 35 assembly](#) of the human genome (November 2003).

- [Status history](#) of the human assemblies.

The International Human Genome Sequencing Consortium have published their scientific analysis of the finished human genome.

- [Nature 421, 931 - 945 \(21 October 2004\)](#)
- [WT Sanger Institute Press Release](#)

Annotation

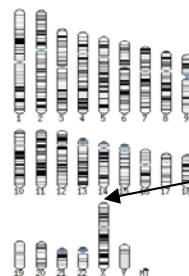
The human genome sequence is now considered sufficiently stable that the three major genome browsers have come together to produce a common set of gene IDs for their annotations. This Consensus CDS ID set has been incorporated into the Ensembl database alongside the existing identifiers.

- More information about the [CCDS project](#)

The [ENCODE](#) (ENCyclopedia Of DNA Elements) project aims to find functional elements in the human genome.

Karyotype

Click on a chromosome for a closer view



Statistics

| | |
|--|--|
| Assembly: | NCBI 35, July 2004 |
| Genebuild: | Ensembl, July 2005 |
| Database version: | 32.35e |
| Ensembl gene predictions (incl. 1976 pseudogenes): | 24,194 |
| GenScan gene predictions: | 68,101 |
| Ensembl gene exons: | 245,231 |
| Ensembl gene transcripts: | 35,845 |
| Base Pairs: | 3,272,187,692 |
| Golden Path Length: | 2,883,476,365 |
| Most common InterPro domains: | Top 40 Top 500 |

Ensembl v32 - May 2005

Chromosome X

- View Chromosome X
- View Chr X Synteny
- Map your data onto this chromosome
- Browse OMIM diseases

Use Ensembl to...

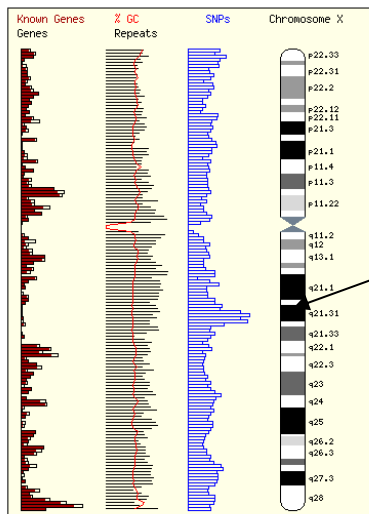
- Run a BLAST search
- Search Ensembl
- Data mining [BioMart]
- Upload your own data
- Download data
- Export data

Docs and downloads

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Other links

- Home
- Sitemap
- What's New
- Stable (archive) link for this page



Click on the image above to zoom into that point

Chromosome X

Length: 154,824,264 bps
Gene Count: 931
Known Gene Count: 766
PseudoGene Count: 380
SNP Count: 320,997

Change Chromosome

Chromosome

Fields marked with * are required

Jump to ContigView

Choose two features from this chromosome as anchor points and display the region between them. Both features must be mapped to the current Ensembl golden tiling path. If you select "None" for the second feature, the display will be based around the first feature.

Please note that if you select widely spaced features there may be an significant delay while Ensembl builds the DNA display.

Region

From (type):

To (type):

Context

Bp Downstream

Bp upstream

Click to display a region

Display a region between any two features (markers, cytogenetic bands...)

STEP 4

Display the region between markers DXS7096 and DXS7094

Ensembl is available to [download for public use](#) - please see the [code licence](#) for details.

The screenshot displays the Ensembl Human ContigView interface. The top section shows the 'Overview' view of Chromosome X, with a yellow bar indicating the selected region (138,229,875 - 138,686,223). The 'Detailed view' below shows various tracks including Genes, Transcripts, and Variants. A yellow bar at the bottom of the detailed view allows for customizing the view. The interface includes a sidebar on the left with navigation shortcuts and a top menu bar with options like 'View of Chromosome X', 'Graphical overview', and 'Export sequence as FASTA'.

Entire chromosome

‘Overview’ displays chromosomal region

The ‘sidebar’ includes shortcuts to easy navigation providing access to different views

Chromosome X
138,229,875 - 138,686,223

- View of Chromosome X
- Graphical view
- Graphical overview
- Export sequence as FASTA
- Export EMBL file
- Export Gene info in region
- Export SNP info in region
- Export Vega info in region
- View alongside ...
- View Syntenic regions ...
- View region in NCBI browser
- View region in UCSC browser

Use Ensembl to...

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‘Detailed view’ use menus on yellow bar to customise view

STEP 5

Click on location in overview panel to center on the F9 gene

And then zoom in using the ‘+’ button

STEP 6

Click on a marker

Link to BLAST, data mining, ftp downloads, export data.

Documentation about Ensembl

STEP 7

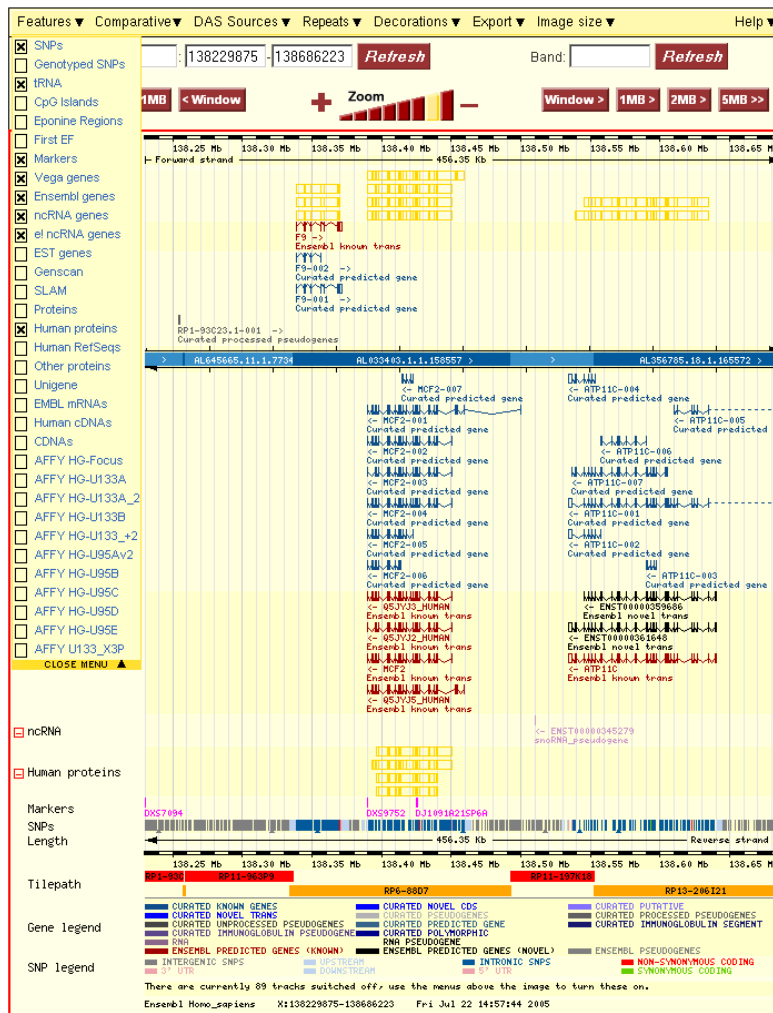
**Back to
ContigView**

Chromosome Map Marker DXS9752

| | | |
|-----------------|---|--|
| Marker Source | 82913 (database: unists) | |
| Marker Location | Basepairs 138389786 - 138390044 on chromosome X [Export data] | |
| Marker Synonyms | <p>Gdb: GDB:737728 GDB:738733</p> <p>Genbank: G13636</p> <p>Other: SHGC-11927 DXS9752 RH8108</p> | |
| Marker Primers | <p>Expected Product Size</p> <p>Left Primer 259 TTTTCAGGTTAATGGACACGC</p> <p>Right Primer CCATTTTGCAGCCGTAATTT</p> | |

Marker DXS9752 map locations

| Map Name | Synonym | Chromosome | Position | LOD Score |
|----------|---------|------------|----------|-----------|
| gm99g3 | RH8108 | X | 4259 | 3.5 |



STEP 8

**Customise the
'Detailed view'
panel of
ContigView with
the 'Features'
menu.**

- ☒ SNPs
 - ☐ Genotyped SNPs
 - ☒ tRNA
 - ☐ CpG Islands
 - ☐ Eponine Regions
 - ☐ First EF
 - ☒ Markers
 - ☒ Vega genes
 - ☒ Ensembl genes
 - ☒ ncRNA genes
 - ☒ el ncRNA genes
 - ☐ EST genes
 - ☐ Genscan
 - ☐ SLAM
 - ☐ Proteins
 - ☒ Human proteins
 - ☐ Human RefSeqs
 - ☐ Other proteins
 - ☐ Unigene
 - ☐ EMBL mRNAs
 - ☐ Human cDNAs
 - ☐ CDNAs
 - ☐ AFFY HG-Focus
 - ☐ AFFY HG-U133A
 - ☐ AFFY HG-U133A_2
 - ☐ AFFY HG-U133B
 - ☐ AFFY HG-U133_+2
 - ☐ AFFY HG-U95Av2
 - ☐ AFFY HG-U95B
 - ☐ AFFY HG-U95C
 - ☐ AFFY HG-U95D
 - ☐ AFFY HG-U95E
 - ☐ AFFY U133_X3P
- CLOSE MENU ▲**

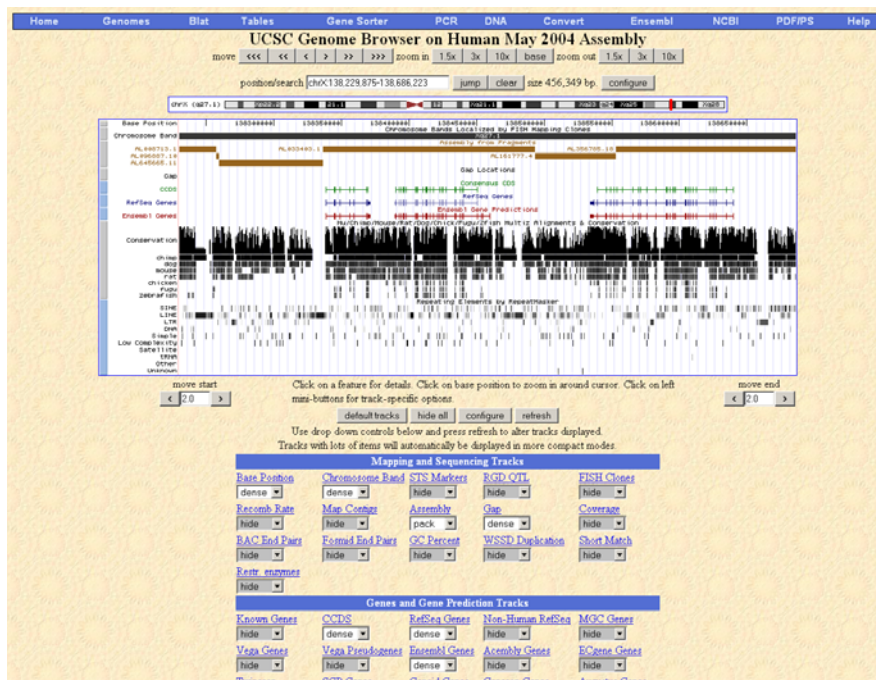
See this region in UCSC

 [View region in UCSC browser](#)

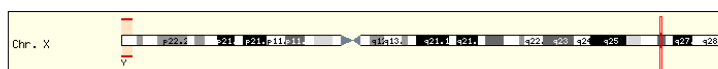
STEP 10

Back to ContigView
go to CytoView

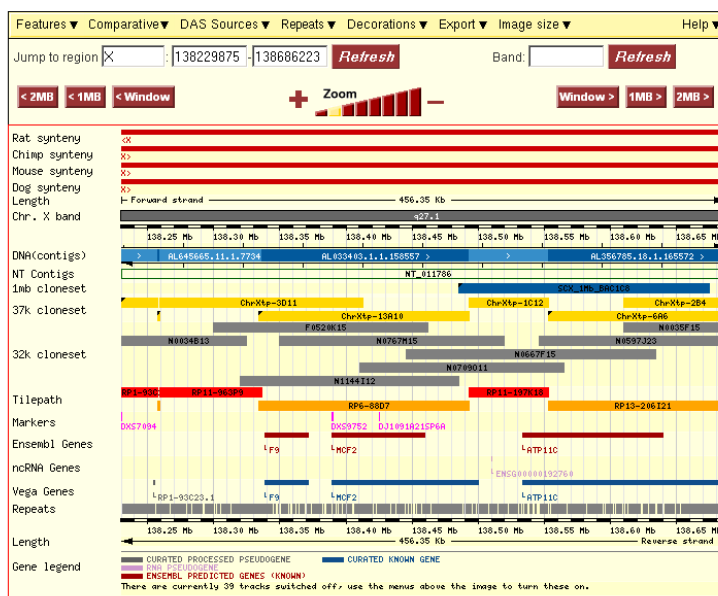
- Graphical overview



[- Chromosome X



 Detailed view



 Export data

Select Set of features to render Tile path clones

Output format HTML

Select type to export: **Features on this chromosome**

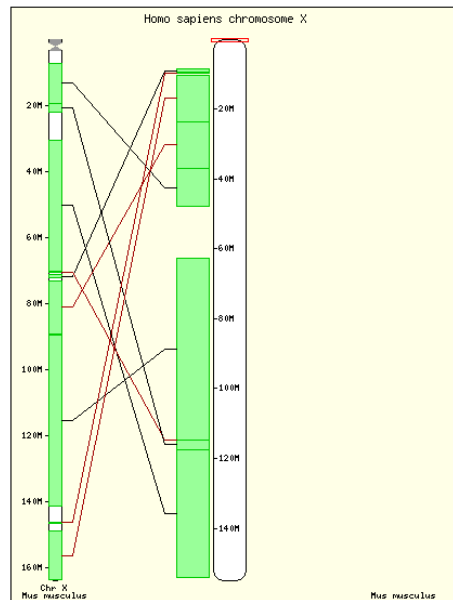
Export

STEP 11

Using the sidebar jump to SyntenyView

Chromosome X
138,229,875 - 138,686,223

- View of Chromosome X
- Graphical view
- Graphical overview
- Export information about region
- Export sequence as FASTA
- Export EMBL file
- Export Gene info in region
- Export SNP info in region
- Export Vega info in region
- View alongside ...
- View Synteny regions
- ... with *Canis familiaris*
- View r... brows
- ... with *Gallus gallus*
- View r... brows
- ... with *Mus musculus*
- Graphi... brows
- ... with *Pan troglodytes*
- ... with *Rattus norvegicus*



Homology Matches

| Homo sapiens Genes | | Mus musculus Homologues |
|---|----|--|
| MCF2 (138.39 Mb) [ContigView] | -> | Mcf2 [ContigView] [MultiContigView] |
| ATP11C (138.53 Mb) [ContigView] | -> | Atp11c [ContigView] [MultiContigView] |
| XP_372255.1 (138.90 Mb) [ContigView] | -> | XP_205232.2 [ContigView] [MultiContigView] |
| SOX3 (139.31 Mb) [ContigView] | -> | Sox3 [ContigView] [MultiContigView] |
| LDOC1 (140.00 Mb) [ContigView] | -> | Ldoc1 [ContigView] [MultiContigView] |

Navigate Homology

[Upstream](#) (<138.39 Mb) [Downstream](#) (>140.51 Mb)

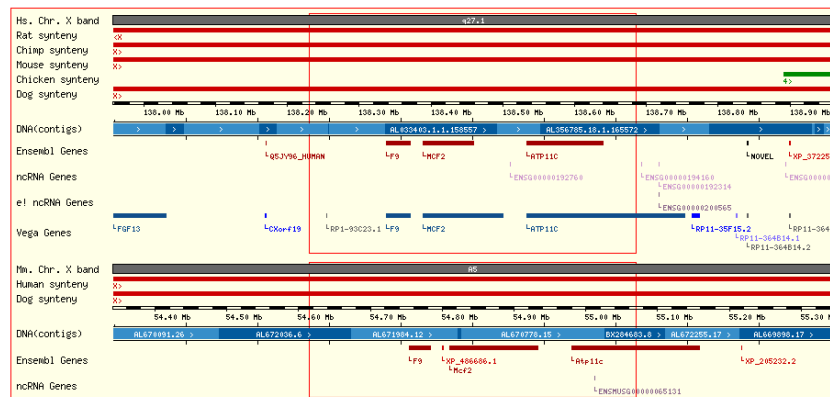
Change Chromosome

Chromosome

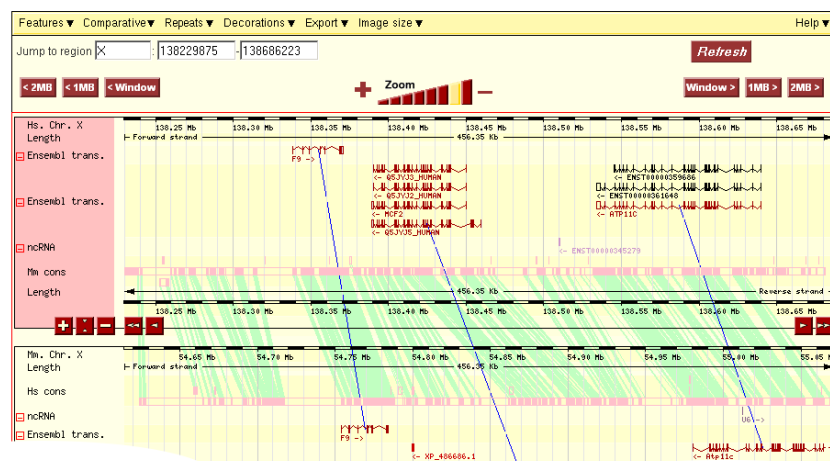
Fields marked with * are required

STEP 12

Using the sidebar jump to MultiContigView



Detailed View



Chromosome X
138,229,875 - 138,686,223

- View of Chromosome X
- Graphical view
- Graphical overview
- Export sequence as FASTA
- Export EMBL file
- Export Gene info in region
- Export SNP info in region
- Export Vega info in region
- View alongside ...
- View Synteny regions
- ... with *Bos taurus*
- View r... brows
- ... with *Canis familiaris*
- View r... brows
- ... with *Ciona intestinalis*
- View r... brows
- ... with *Danio rerio*
- Use Ensembl
- ... with *Fugu rubripes*
- ... with *Gallus gallus*
- Run a ...
- ... with *Mus musculus*
- Search ...
- ... with *Pan troglodytes*
- Data n...
- ... with *Rattus norvegicus*
- Upload...
- ... with *Tetraodon nigriviridis*
- Downl...
- ... with *Xenopus tropicalis*
- Export...

Back in ContigView, click the F9 gene model and follow the link to GeneView

Customise 'Transcript structure' to display SNPs

Homologies with other species

Go to TransView

GO annotation

Protein structure

Features ▼

- ☒ SNPs
- ☐ Vega genes
- ☒ Ensembl genes
- ☐ ncRNA genes
- ☐ el ncRNA genes
- ☐ EST genes
- ☐ Genscan
- ☐ SLAM

138,33 Mb 138,34 Mb 138,35 Mb 138,36 Mb 138,37 Mb 138

Forward strand

52.72 Kb

F9 -> Ensembl known trans

Reverse strand

138,33 Mb 138,34 Mb 138,35 Mb 138,36 Mb 138,37 Mb 138

CLOSE MENU ▲

STEP 18

Export sequence in FASTA format

Ensembl Exon Report

| | |
|------------------------|---|
| Transcript | F9 (HUGO ID) (to view all Ensembl genes linked to the name click here) This transcript is a member of the human CCDS set: CCDS14666 |
| Ensembl Transcript ID | ENST00000218099 |
| Transcript information | Exons: 8 Transcript length: 2,802 bps Translation length: 461 residues This transcript is a product of gene: ENSG00000101981 |
| Genomic Location | This transcript can be found on Chromosome X at location: 138,338,415-138,371,137 This start of this transcript is located in Contig AL033403.1.1.158557 . |
| Description | Coagulation factor IX precursor (EC 3.4.21.22) (Christmas factor) (Plasma thromboplastin component) (PTC). Source: Uniprot/SwissProt P00740 |

Export sequence as FASTA

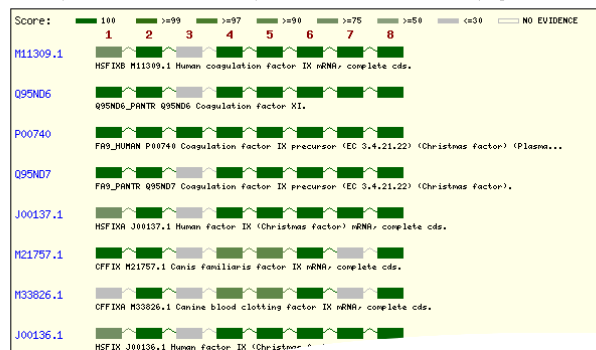
Exon Information

| No. | Exon / Intron | Chr | Strand | Start | End | Length | Sequence |
|----------------------|---------------------------------|-----|--------|-------------|-------------|----------|---|
| 5' upstream sequence | | | | | | |ccagaagtaaatcacagctcagcttctgactttgtcacaactaatcgacott |
| 1 | ENSE00000677288 | X | 1 | 138,338,415 | 138,338,531 | 117 bp | ACCACCTTTCACAATCTGCTAGCAAGGTTATGCGAGCGGTGAACATGATCTGGCAGAAT CACCAGGCGCTCATCACCATTCTGCCTTTAGGATATCTACTCACTGCTGAATGTACAG |
| Intron 1-2 | | | | | | | gtttgtttcccttttttaaatatcat.....aaagaattattcttttaccattccag |
| 2 | ENSE00000677287 | X | 1 | 138,344,689 | 138,344,852 | 164 bp | TTTTTCTTGATCATGAAACGCCAACAAATCTGTAATGGCCAAAGAGGTATAATTCAG GTAAATTGGAAAGATTGTTCAGGGGAACCTTGAGAGAGAAATGTATGGAAAGAAAGTTGA GTTTGAAGAGCAGCAGAAAGTTTGTGAAACACTGAAAGAAACA |
| Intron 2-3 | | | | | | | gtgagtatttccacataataccott.....attgtgtctctttattcttttatag |
| 3 | ENSE00001173335 | X | 1 | 138,345,041 | 138,345,065 | 25 bp | ACTGAATTTTGAAGCAGTATGTTG |
| Intron 3-4 | | | | | | | gtaagcaattcttttctctctag.....ttcaattctttaaactatctcaaaag |
| 4 | ENSE00001173327 | X | 1 | 138,348,755 | 138,348,868 | 114 bp | ATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAAGTTGCAAGATGACATTA ATTCTTATGAATGTTGGTGCCTTTTGGATTGGAAGGAAAGCACTGGAATTAG |
| Intron 4-5 | | | | | | | gtaagtaactatttttgaatactc.....ttactgtctattttgtctcttttag |
| 5 | ENSE00001173320 | X | 1 | 138,356,042 | 138,356,170 | 129 bp | ATGTAACATGTAACATTAAAGATGGCAGATGCGAGCAGTTTGTGAAAAATAGTGTGATGA ACAAGGTGGTTTGTCTCTGTAAGGGATATCGACTTGCAGAAACACAGAACTCTGTG AACCAGCAG |
| Intron 5-6 | | | | | | | gtcataactctgtaataagatttttta.....actaatttttctctctattttt |
| 6 | ENSE00001173315 | X | 1 | 138,358,741 | 138,358,943 | 203 bp | TGCCATTTCATCTGGAGAGCTTTCTGTTTCCAACTCTTAAGCTCACCGCTGCT CTGTTTTCTGATGTGGACTATGTAAATTTCTACTGAAGCTGAACACTTTTGGAT TCACTCAAGACCCCAATCATTTAATGACTTCACTCGGTTGTTGGTGGAGAGAT AACAGGTCAATTCTCCTGGCAG |
| Intron 6-7 | | | | | | | gtactttatactgatggtgtgtcga.....aagagcttataattttgttttcacag |
| 7 | ENSE00001173311 | X | 1 | 138,368,420 | 138,368,534 | 115 bp | GTGTTTGAATGGTAAGTTGATGCAATCTGTGGAGGCTCTATCTGTTAAATGAAATGG ATTGTAACTGCTGCCCACTGTGTTGAAGCTGTTGTTAAATTTACAGTTGTGCGAG |
| Intron 7-8 | | | | | | | gtaaatcacacagaagaataaata.....ttaaaatgaattatttttaaatag |
| 8 | ENSE00001029145 | X | 1 | 138,369,203 | 138,371,137 | 1,935 bp | GTGAACATAATTATGGAGGACAGACATACAGACAAAAGCGAAATGTGATTCGAATTA TTCTCCACCACTACATGAGTCAAGTATTAATAGTCAACCATGATTCGCTCTTGG AAGTGGAGCAACCTTAGTGTAAACAGCTACGTTACACCTATTGCAATGCTGCAAGG AATACAGCAACTCTTCTCAAAATTTGGATCTGCTATGTAAGTGGCTGGGGAAGTCTT TCCACAAAGGAGATCAGCTTTAGTTCTTCAGTACCTTAGAGTTCCACTGTGTGACCGAG CCACATGTCTTGCATCTCAAAAGTCCACCATCTATACCAACATGTCTGTGCTGGCTTCC ATGAAGGAGGTAGAGATTCAATGTCAAGGAGATAGTGGGGGACCCCATGTACTGAAGTGG AAGGGACAGTTCTTAACTGGAATTATTAGTGGGTGAAGAGTGTGCAATGAAGAGCA AATATGGAATATATACCAAGGTATCCGGTATGTCAACTGGATTGAAGGAAAAACAAAGC TCACCTTAATGAAAGATGGATTCCAAAGGTTAATTCATTGGAATTGAAATTAACAGGGCC TCTCACTAACTAATCACTTTCCCATCTTTGTGAGATTGGAATATACATTCTATGATC ATTGCTTTTCTCTTTACAGGGGGAATTCATATTTTACCTGAGCAAAATGATTAGAAA ATTGGAACACTAGAGGAATATAATGTGTAGGAAATTACAGTCAATTTCTAAGGGCCAGC CTTGACAAAATTGTGAAGTTAAATTTCCACTCTGTCATCAGATACTATGTTCTTCCA CTATGGCACTAAGTCACTCAATTTTCCCTCTTAGCAGCATTCCTCTCCCATCTCTTC TTTCTCTCTCAACCAAAACATCAATGTGTTAATGTTCTGTATACAGTACAGGATCTTGT GTCTACTCTATCAGAGGCGAGTACCACACTCATGTAAGAAAGAACACAGGAGTACGTGAG AGGCTAAACCTCATCAAAACACTACTCTTTTCTCTACCTATCCCTCACTCTTTTAC CTTTTCCAAATCCCAATCCCAATCAGTTTCTCTTCTTACTCCCTCTCTCCCTTTT ACCTCTCAATGGTCTTAAAGGAGAGATGGGGAGCATCACTTGTATACTTCTGTACACA GTATACATGTCTATCAAAACGAGCTTCTCTGCTGATGGAGACTTGTCTTTCAGAACCA TAGGGATGAAGTAAGGTGCTGAAAAAGTTTGGGGGAAAGTTTCTTTCAGAGAGTTAAGT TATTTTATATATAATATATATAAATATATAATATACAATATAATATATATATGTGTG TGTGTATGCTGTGTGTAGACACACACGATACACACATATAATGGAGCAATAAGGCAT TCTAAGAGCTTGTATGTTGTATGGAGTCTGACTAGGCAATGATTTCAGAGGCGAAGATTG GCATATCAATTGTAACATAAAAGCTGACATTGACCAGACATATTGTACTCTTCTTCTT ATAATAATAATAAGTCAACAGAAAGAGAGAACCGTCTGTTTGAATCTACAGCT GAGACTTTGAGGAAGAAATCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAAGCAA TTGAAGTTGCTAGACAGAGGACATAAGTATCATGTCTCTTAACTAGCATACC AGTGGAGAGGCTGACAGGCTCAAGGCAATAGTCAATTCATCAGCAAGCAACTAA TCTTTTCTGTTGCTGTGTACCATGGCAATTTGATTATAGTAACTCTCTA GAATCTCTAGAGAGTGTGACCAACTGAGTGTGTTCCCTTTGTGAATTAAATG GGTGTCTGTTTCACT |

Exon/intron
sequenceEvidence used
to build gene

Support Evidence

The supporting evidence below consists of the sequence matches on which the exon predictions were based and are sorted by alignment score.



Configuring FASTA File output for FASTA format text file

You are exporting Chromosome X 138,333,415 - 138,376,137.

FASTA format options

Output format

☒ HTML

☐ Text

☐ Compressed text (.gz)

[Continue >>](#)

e!Ensembl Human Export view

e.g. [AL390997.10.1.112328](#), [RH9632](#), [ENS000000139618](#)

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[Help](#)

Chromosome X
138,333,415 - 138,376,137

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Other links

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- Stable (archive) link for this page



Results

```

X   dna:chromosome:chromosome.MCB125.X.138333415..138376137..1
ACTGGCAATTGGATAAAGAGTCAAGACCCATCACTGTGCTGTATTGAGGAACTCATCT
CACATGCGAGAGACACATAGGCTCAAAATAAGGGGATGGAGGAAGATCTCAAGCAAA
TGGAAAAACAAAAGGACAGGGTTTGAATCTCTGATATATCAAGAGACTTTAAACAAA
CAAAGATCAAAAGAGACAAAGAGGCCATTACATATGOTAAAGGGATCAATTCACCAAG
AAGAGCTAATCTCTAAATATATATGCAACCCAAATACAGGAGCACCCAGATTATAAAGC
AAGTCTTTAGAGACCTACAAAGAGACTTACACTCCACACAAATATATATGGAGACTTTA
ACACATCTCTGCAATATAGCAGAGTCAAGAGAGACAAAGATTAAAGAGATATCCAGG
AATTCAGTCTGATTCTGCAACAGAGGACTATAGCATCTACAGAACTCTCCACCCCA
ANTCAGAGATATACATTTCTTCTCAGGACTACACCACTCTTCCAAATTTGATCACA
TAGTTGAAAGTAAAGCACTCTCAGCAATGTAAAAGAACAGAAATATACCAAACTATC
TCTCAGAGCACAGTGCATCAAACTAGAACTCAGGATTAAAGAACTCACTCAAAACCACT
CGACTACATGGAACTGAACAACTGCTCTCTGATGACTACTGGGTACATAAAGAAATGA
AGGAGGAATAAAGATGTTCTTTGAAACCAACAGAACAAAGAGCAGCAATACCAAGATC
TCTGGGCACTCTCAAGAGATGTATAGAGAGCAATTTATAGCATATATATGGCACAAAG
GAAAGCAGGAGGATCTAAATGGATACCTTACATCAATCAATTAAGAACTAGAGAGG
AAGAGCAACACACTTCAAAAGCTAGCAGAGGCAAGAAATAACTAAGATCAGAGCAGAAC
TGAAGGAATAGAGACACAAAAAATCTTTCAAAATCAATGAACCCAGGAGCTGGTTTT
TTGAAAGATCAACAAAAACGATAGACCACTAGCAAGACTAATAAGAGAAAAAGAGAGA
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TACAACCTACATCAGAGAACTACTATAAACACCTCTATACAAATAACTAGAAAACTAG
AAGAAATGGATTAATTTCTCGACACATACACCTCTCCAAAGCTAAACCGGAGAGATTTG
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CCAAAAAATCCAGGAGGAGATGGATTCAAGGCCAATTTCTCCAGAGGCTACAGGAGG
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TGGCAACCAAAATCCAGGAGCACATCAAAAGGCTTGTCCACCATANTCAAGTGGGCTCA
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ACAGACATACAGCAAAACAGCATGATTACTCAATAGATGCAAAAGAGGCTTTGACAA
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CAGAGTGACAGGCACTAAAGAAATGGGAGAAAAATTTGCAATCTACTCATCTGTCCA
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CCCATCAACAGTGGGTGAAGGATATGACAGACACTCTCAAAAGAGACATTTATGCA
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ATTATGACAGTGTATTATTGGCAGAGGATTAATACATAGGCAAAAGATAGATAG
AGAACTGGAGTAGACCCAAACAAATATGTTAATCTGACTACGAAAAATTTAGAGAG
```

STEP 19

Copy part of the sequence

new SETUP CONFIG RESULTS DISPLAY refresh Online Help

Enter the Query Sequence

Either Paste sequences (max 30) in FASTA or plain text:

```
>X dna:chromosome chromosome:NCBI35:X:138333415:138376137
ACTGGCAAATTGGATAAAAGAGTCAAGACCCATCAGTGTGCTGTATTCAGGAAACTCA
CACATGCAGAGACACACATAGGCTCAAAATAAAGGATGGAGGAAGATCTACCAAGC.
TGGAAAACAAAAGGCAGGGTTTGCATCTCTAGTCTCTGATAAAACAGACTTTAAAC
```

Or Upload a file containing one or more FASTA sequences

Or Enter a sequence ID or accession (EMBL, UniProt, RefSeq)

Or Enter an existing ticket ID:

☒ dna queries
☐ peptide queries

Select the databases to search against

Select species:
Use 'ctrl' key to select multiple species

Fugu_rubripes
Gallus_gallus
Homo_sapiens

☒ dna database
☐ peptide database

Genomic sequence
Consensus CDS Peptides (CCDS peptides)

Select the Search Tool

BLASTN
SSAHA
TBLASTX

configure RUN

Search sensitivity:
Optimise search parameters to find the following alignments

Near-exact matches

About BlastView

BlastView provides an integrated platform for sequence similarity searches against offering access to both BLAST and SSAHA programs. [\[More\]](#)

We would like to hear your impressions of BlastView, especially regarding function see provided in the future. Many thanks for your time. [\[Feedback Form\]](#)

STEP 20

Follow the 'Run a BLAST Search' link and paste the sequence in the box. Select '*Homo sapiens*' and BLASTN against 'Ensembl cDNAs'.

STEP 21

Click to retrieve results – repeat till see that query is completed – then click 'view'

new SETUP CONFIG RESULTS DISPLAY refresh Online Help

Summary

Retrieve result for ID:

BLA_CIHGmnSd Retrieve

Retrieving Results

'Job pending' results can be retrieved by clicking on the button above. Alternatively, this page can be bookmarked for later, or the ID noted and entered on the BLAST page.

Results are retained for 7 days. After this, they must be re-submitted.

1: X (4129 letters) Vs. LATESTGP

Homo_sapiens Job Queued

Summary

setup

- Homo_sapiens
- Genomic sequence
- BLASTN
- Low sensitivity

configure

- E: 10
- B: 100
- filter: dust
- RepeatMasker
- W: 15
- M: 1
- N: -3
- Q: 3
- R: 3

results

display

new SETUP CONFIG RESULTS DISPLAY

refresh Online Help

Summary

Displaying X sequence alignments vs Homo_sapiens LATESTGP database

Showing top 100 alignments of 265, sorted by Raw Score

Alignment Locations vs. Karyotype (click arrow to hide)

Key (%ID): 0 - 20 20 - 40 40 - 60 60 - 80 80 - 100

Alignment Locations vs. Query (click arrow to view)

Alignment Summary (click arrow to hide)

Select rows to include in table, and type of sort (Use the 'ctrl' key to select multiples)

| Query | Subject | Chromosome | Supercontig | Clone | | | |
|-----------------|---------|------------|-------------|-------|------------|-------------|-------|
| off | off | off | off | off | | | |
| Name | Name | Name | Name | Name | | | |
| Start | Start | Start | Start | Start | | | |
| Links | Query | Start | End | Chr | Chromosome | Supercontig | Clone |
| [A] [S] [G] [C] | 4719 | 5411 | + | ChrX | 138338133 | | |
| [A] [S] [G] [C] | 5465 | 6196 | + | ChrX | 138338880 | | |
| [A] [S] [G] [C] | 6140 | 6744 | + | ChrX | 138339554 | | |
| [A] [S] [G] [C] | 7962 | 8511 | + | ChrX | 138341376 | | |
| [A] [S] [G] [C] | 7089 | 7521 | + | ChrX | 138340503 | | |
| [A] [S] [G] [C] | 9058 | 9333 | + | ChrX | 138342472 | | |

Features Comparative DAS Sources Repeats Decorations Export Image size Help

Jump to region 138294760 - 138394759 Refresh Band: Refresh

<< 5MB < 2MB < 1MB < Window Zoom Window > 1MB > 2MB > 5MB >>

Chr. X Length 138,30 Mb 138,31 Mb 138,32 Mb 138,33 Mb 138,34 Mb 138,35 Mb 138,36 Mb 138,37 Mb 138,38 Mb 138,39 Mb

Human proteins

Ensembl trans.

Vega trans.

Blast hits

DNA(contigs)

Vega trans.

Ensembl trans.

Human proteins

Markers

SNPs

Length

Tilepath

Gene legend

SNP legend

STEP 22

Click [C] to view the hit in context in ContigView.

[G]- shows the hit in the context of the annotated genome sequence.

[S]- displays the query sequence with the bases of all hit alignments marked.

[A]- displays the alignment for the relevant HSP