

## WORKED EXAMPLE

**STEP 1:**  
Load Ensembl  
[www.ensembl.org](http://www.ensembl.org)

**Navigation**

The screenshot shows the Ensembl homepage for release 40. On the left, there's a navigation sidebar with sections like 'Use Ensembl to...', 'Docs and downloads', and 'Other links'. A large green speech bubble labeled 'Navigation' points to this sidebar.

**Documents and downloads**

A green speech bubble labeled 'Documents and downloads' points to the 'About Ensembl' section of the page, which contains information about the project's history and partners.

**STEP 2:**  
Click on “Homo sapiens”

**Search**

A green speech bubble labeled 'Search' points to the search bar at the top right. Another green speech bubble labeled 'Help' points to the 'Help' link in the top right corner. The main content area shows a list of species with their names, status (e.g., 'UPDATED!', 'NEW!'), and version numbers. A large green speech bubble labeled 'What's new' points to the 'What's new' section, which highlights recent assembly and genebuilds for species like *Homo sapiens*, *Pan troglodytes*, and *Macaca mulatta*.

## Ensembl Human

Karyotype

STEP 3:  
Select 'Gene', fill in  
'EPO' and click on [Go]

Source and version of assembly and genebuild

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

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 [CDS project](#).

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

More information about the [ENCODE resources](#) at Ensembl.

Jump directly to sequence position

Chromosome:  or region

From (bp):

To (bp):  Go

What's New in Ensembl

Homo sapiens News

- Updates for Ensembl Human
- New ncRNA gene sets
- cDNA Update
- OMIM (disease) data
- Human variation database

More news...

NCBI 36, Oct 2005  
Ensembl, Mar 2006  
39.36a

Known genes:	21,561
Novel genes:	2,149
Pseudogenes:	731
RNA genes:	4,019
Genscan gene predictions:	69,185
Gene exons:	164,357
Gene transcripts:	25,078
Base Pairs:	3,433,077,231
Golden Path Length:	2,878,791,990
Most common InterPro domains:	<a href="#">Top 40</a> <a href="#">Top 500</a>

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# Ensembl Human Search View

Search eHuman: Anything  Go  
e.g. AL138722.15.1.44776, ENSG00000139618

Help

Ensembl release 40 - Jun 2006

**Feature type**

- Family (1)
- Homo sapiens (1)
- Gene (5)
- Homo sapiens (5)
- Marker (1)
- Homo sapiens (1)

**Species**

Homo sapiens (7)

- Family (1)
- Gene (5)
- Marker (1)

**Exalead Help**

To exclude a category click on the  or  
To restrict to a category click on the  name of the category.  
To reset a category click on the  or its name.

**Use Ensembl to...**

- Run a BLAST search
- Search Ensembl
- Data mining [BioMart]
- Upload and view data on chromosome
- Export data
- Download data

**Docs and downloads**

- Information
- What's New
- About Ensembl
- Ensembl data
- Software

**Other links**

- Home
- Sitemap
- Vega
- Pre Ensembl**
- View previous release of page in Archive!
- Stable Archive! link for this page
- Archive! sites
- Trace server



**Mus musculus**  
NCBI m36  
*now in Ensembl!*

## Ensembl text search

epo

Your query matched 7 entries in the search database

**Ensembl Gene: ENSG00000130427**

Ensembl gene ENSG00000130427 has 1 transcript: ENST00000253029. Erythropoietin precursor [EPO]. [Source: UniProtKB/Swiss-Prot; Acc: P11235] The gene has the following external identifiers mapped:  
Affymetrix Microarray Focus: 207257\_at  
Affymetrix Microarray HG0110\_1023\_at  
Affymetrix Microarray HuGeneFL\_X02158\_mat\_at  
Affymetrix Microarray U95\_1023\_at  
Affymetrix Microarray U133\_207257\_at,g4503588\_3p\_at,  
Affymetrix Microarray U95\_14\_P113914\_at  
Agilent COH\_A\_14\_P113914\_at  
Agilent Probe\_A\_23\_P145689\_A\_23\_P145664  
CCDS: CCD57056, CCD857051  
EMBL: AF052356, B65458, BC093628, AF202307, AF202313, X02157, AF202306, AF202314, AF202308, X02158, M11319, AF202312, AF202309, AF202310, AC009488, BC111937, AF202311 EntrezGene: 2056  
GO: GO:0005615, GO:0007165, GO:0005128, GO:0043249, GO:0006950, GO:0007267, GO:0001666, GO:0005179, GO:0008015, GO:0007275, GO:0005576

HGNC Symbol:  3415

IPI: IPI0307226, IPI0307226.3

MIM gene: 133170

PDB: 1CNA, 1BUY, 1EER

Protein ID: AAC78791.1, CAA26095, AAA52400.1, CAA26094.1, AAC23131.1, AAC23132.1, AAF17572.1, AAP22357.1, AAU11938, AAF17572, AAU11938.1, AAC78791, AAF23132, AAD13964, CA26094, AAP22357, AA52400, AAC23134, AAC23134, CAA26095.1, AAC13964.1, AAH93628.1, AAH93628, AAF23133

RefSeq DNA: NM\_000799.2, NM\_000799

RefSeq peptide: NP\_000790, NP\_000790.2

UniGene: Hs.2303

UniprotKB/Swiss-Prot:  HUMAN, Q9UDZ0, Q549U2, Q9UHA0, P01588, Q9UEZ5

UniprotKB/EMBL: Q2M2LC\_HUMAN, Q2M2L6

**Feature type:** Gene; Homo sapiens; **Species:** Homo sapiens; **Gene:**

**Ensembl protein family: ENSF00000007051**

Ensembl protein family ENSF00000007051 [ERYTHROPOIETIN RECEPTOR PRECURSOR]  R has 4 members: ENSG00000187266, ENSP00000222139, P19235, Q2M25.

**Feature type:** Family; Homo sapiens; **Species:** Homo sapiens; **Family:**

**Ensembl Gene: ENSG00000102265**

Ensembl gene ENSG00000102265 has 5 transcripts: ENST00000219388, ENST00000377013, ENST00000377017, ENST00000377018, ENST00000377020 and associated peptides: ENSP00000218388, ENSP00000368212, ENSP00000366217, ENSP00000366219 Metalloproteinase inhibitor 1 precursor (TIMP-1) (Endothelial potentiating activity) (EPA) (Tissue inhibitor of metalloproteinases) (Fibroblast collagenase inhibitor) (Collagenase inhibitor). [Source: UniprotKB/SWISSPROT; Acc: P1033]

Protein ID: AAC78791.1, CAA26095, AAC23131, AAC23132, AAF17572.1, AAP22357.1, AAU11938, AAF17572, AAU11938.1, AAC78791, AAF23132, AAD13964, CA26094, AAP22357, AA52400, AAC23134, AAC23134, CAA26095.1, AAC13964.1, AAH93628.1, AAH93628, AAF23133

RefSeq DNA: NM\_000799.2, NM\_000799

RefSeq peptide: NP\_000790, NP\_000790.2

UniGene: Hs.2303

UniprotKB/Swiss-Prot:  HUMAN, Q9UDZ0, Q549U2, Q9UHA0, P01588, Q9UEZ5

UniprotKB/EMBL: Q2M2LC\_HUMAN, Q2M2L6

**Feature type:** Gene; Homo sapiens; **Species:** Homo sapiens; **Gene:**

**Ensembl Gene: ENSG00000121053**

Ensembl gene ENSG00000121053 has 1 transcript: ENST00000225371 and associated peptide: ENSP00000225371

Eosinophil peroxidase precursor (EC 1.11.1.7)  R [Contains: Eosinophil peroxidase light chain, Eosinophil peroxidase heavy chain]. [Source: UniprotKB/SWISSPROT; Acc: P11678]

The gene has the following external identifiers mapped to it:

Affymetrix Microarray Focus: 201666\_at

Affymetrix Microarray HG0110\_1693\_s\_at

Affymetrix Microarray U95\_1693\_s\_at

Affymetrix Microarray U95\_1693\_s\_at

Agilent COH\_A\_14\_P12083

Agilent Probe\_A\_23\_P62115\_A\_23\_P62106

CCDS: CLGI, CCD514281,  TIMP, CCDS14281.1

EMBL: AY932824, BC007097,  L47361, CR51496, Z84646, M12670, TIMP, CR07638, S86225, X03124, BC000866, CLGI, M59908, A10416, D11139, K02598

EntrezGene: CLGI,  TIMP1,  L47361

GO: GO:0005615,  GO\_00043249, TIMP, GO\_0005578, CLGI, GO\_0005515, GO\_0008191, GO\_0007275, GO\_0005576, GO\_0004857, GO\_0051045, GO\_0005604, GO\_0008284

Havana transcripts: CTD:000000056425, OTTHUMT00000056423, OTTHUMT00000056424

HGNC Symbol: TIMP1, 11920

Illumina: GL\_450750

IPI: CLGI, IP00642739,  IP00642739, IP00639839, IP00032292, TIMP, IP0052089, IP0052089.1, IP00639839.1, IP00032292.1

MIM gene: CLGI, 305370,  TIMP

PDB: 1009\_CLGI,  1D2B, 1LQV, 1UEA, TIMP

RefSeq DNA: NM\_003254, NM\_003254.2

RefSeq peptide: NP\_003245, CLGI,  NP\_003245.1, TIMP

UniprotKB/Swiss-Prot: CLGI,  P01033, TIMP1\_HUMAN, Q9UCU1, TIMP, Q14252

UniprotKB/EMBL: Q6FOX5,  Q6FOX5, Q6H9B6\_HUMAN, Q6H9B4\_HUMAN, Q6H9A7\_HUMAN, Q58P21\_HUMAN, Q98QM2, TIMP, Q5H9B4, Q58P21, CLGI, Q6H9A7, Q98QM2\_HUMAN, Q6FGX5\_HUMAN

**Feature type:** Gene; Homo sapiens; **Species:** Homo sapiens; **Gene:**

**Ensembl Gene: ENSG00000121056**

Ensembl gene ENSG00000121056 has 1 transcript: ENST00000225371 and associated peptide: ENSP00000225371

Eosinophil peroxidase precursor (EC 1.11.1.7)  R [Contains: Eosinophil peroxidase light chain, Eosinophil peroxidase heavy chain]. [Source: UniprotKB/SWISSPROT; Acc: P11678]

The gene has the following external identifiers mapped to it:

Affymetrix Microarray Focus: 214627\_at

Affymetrix Microarray HuGeneFL\_X14348\_at

Affymetrix Microarray U95\_1693\_s\_3p\_at, 214627\_at

Affymetrix Microarray U95\_34587\_at

Agilent COH\_A\_23\_P89192

Agilent Probe\_A\_23\_P89192

CCDS: CCD511602,  EPX-PEN, CCDS11602.1, EPP

EMBL: M29911, M29908, X14346,  M29910, M29907, M29909, M29912, M29906, M29905, EPX-PEN, M29904, DQ054598, EPP

EntrezGene: 8288,  EPX-PEN, EPP

GO: GO:0005615,  GO\_0005506, GO\_0006979, GO\_0006509, GO\_0004601, EPX-PEN, GO\_0042744, GO\_0016491, EPP

HGNC Symbol: 3423, EPX

Illumina: GL\_450750

IP: EPX-PEN, IP00066990, IP00066900, EPX-PEN, 26160\_EPP

MIM gene:  131300,  EPX-PEN, EPP

Protein ID: AAY43126.1,  AAY43126, AAA58458, EPX-PEN, CAA3250.1, CAA3250, AAA58458.1, EPP

RefSeq DNA: NM\_000502, NM\_000502.2

RefSeq peptide: NP\_000493.1,  EPX-PEN, NP\_000493, EPP

UniGene: Hs.279259

UniprotKB/Swiss-Prot:  Q4TPV3, EPX-PEN, P11678, EPP, PERE\_HUMAN

**Feature type:** Gene; Homo sapiens; **Species:** Homo sapiens; **Gene:**

**Ensembl Gene: ENSG00000187266**

Ensembl gene ENSG00000187266 has 1 transcript: ENST00000222139 and associated peptide: ENSP00000222139

Erythropoietin receptor precursor [ EPO\_R]. [Source: UniprotKB/SWISSPROT; Acc: P11235]

The gene has the following external identifiers mapped to it:

Affymetrix Microarray Focus: 37988\_at, 396\_f\_at

Affymetrix Microarray HG0110\_1087\_at, 396\_f\_at

Affymetrix Microarray HuGeneFL\_1087\_at, 396\_f\_at

Affymetrix Microarray U95\_1087\_at, 396\_f\_at

Affymetrix Microarray U95\_209963\_at, 37986\_at, 396\_f\_at, X97671cds\_3p\_s\_at, 396\_3p\_f\_at, g182200\_3p\_x\_at, 215054\_at

Affymetrix Microarray U95\_1087\_at, 39788\_at, 396\_f\_at

Agilent COH\_A\_14\_P129163

Agilent Probe\_A\_23\_P381954\_A\_23\_P101494\_A\_23\_P367899

CCDS: CCD512260.1, CCD512260

EMBL: M27282, M27282, M77244, M34986, M60459, M76595, S45332

EntrezGene: 2057

GO: GO:0016020, GO:0005987, GO:0005515, GO:0007165, GO:0004900, GO:0016021

HGNC Symbol: 2416,  EPO\_R

Illumina: GL\_455761

IP: IP00401741, IP00401741, IP00017476.1, IP00017476

MIM disease: 131300

MIM gene: 1313171

PDB: 1EBP, 1EBA, 1CNA, 1EER

Protein ID: AA823271.1, AA852401.1, AA52393, AA52401, AA12154.1, CAA40550, AAA52392, AAA52403, AA52393.1, AA52392.1, AAB23271, CAA40550.1, AA52403.1, AAI12154

RefSeq DNA: NM\_000121, NM\_000121

RefSeq peptide: NP\_000121, NP\_000121

UniprotKB/SpliceVariants: P19235

UniprotKB/Protein: P19235, Q15443,  EPO\_R\_HUMAN

UniprotKB/EMBL: Q2M205, Q2M205\_HUMAN

**Feature type:** Gene; Homo sapiens; **Species:** Homo sapiens; **Gene:**

**Vega Gene: OTTHUMG000000023044**

Vega gene OTTHUMG000000023044 has 1 transcript: OTTHUMT00000059365 and associated peptide: OTTHUMP00000244662

Erythropoietin

The gene has the following external identifiers mapped to it:

CCDS: CCD55705, CCD85705.1

EntrezGene: 2056,  EPO\_R

HGNC Symbol:  3415

RefSeq DNA: NM\_000798

UniprotKB/Swiss-Prot: P01598

Vega gene:  EPO\_R

Vega transcript:  EPO\_R\_HUMAN

Vega translation: OTTHUMP00000244662

**Feature type:** Gene; Homo sapiens; **Species:** Homo sapiens; **Gene:**

**Ensembl Marker: swSS3716**

A marker with 4 synonyms (29222  EPO\_R G20209 sWS3716)

**STEP 4:**  
Click on 'ENSG00000130427'

This screenshot shows the Ensembl Human Gene View interface. The main content area displays the gene report for ENSG00000130427, which encodes the Erythropoietin precursor (EPO). The page includes sections for Gene Information, Genomic Location, Description, Prediction Method, and Transcript information. A yellow callout box labeled 'STEP 5: Click on "Transcript information"' points to the transcript section. A green callout box labeled 'Gene model' highlights the genomic track showing forward and reverse strands with exons and introns. Another green callout box labeled 'Orthologue other species' points to the 'View alignments of homologues' section. A third green callout box labeled 'Matches database' points to the 'Similarity Matches' section. A large green callout box labeled 'GO terms' points to the 'GO terms mapped to this entry' section at the bottom.

**STEP 7:** Click on 'Exon information'

The following GO terms have been mapped to this entry via UniProt and/or RefSeq:

- GO:0005128 [erythropoietin receptor binding] ITA
- GO:0005179 [hormone activity] ITA
- GO:0005615 [extracellular space] ITA
- GO:0006950 [response to stress] ITA
- GO:0007165 [signal transduction] ITA
- GO:0007267 [cell-cell signaling] ITA
- GO:0007275 [development] ITA
- GO:0008015 [circulation] ITA
- GO:0043249 [erythrocyte maturation] ITA

**STEP 6:** Select 'Exons, Codons, Translations and SNPs', select 'Number residues: Yes' and click on [Refresh]

Ensembl Transcript Report

Transcript EPO (HNC Symbol ID) . To view all Ensembl genes linked to the name [click here](#).  
This transcript is a member of the human CCDS set: [CCDS5705](#)

Ensembl Transcript ID ENST00000252723

Transcript information Exons: 5 Transcript length: 1,328 bps Translation length: 193 residues  
This transcript is a product of gene: [ENSG00000130427](#)

Genomic Location This transcript can be found on Chromosome 7 at location [100,156,359-100,159,257](#).  
The start of this transcript is located in [Contig AC009488.5.1.98876](#).

Protein (Epoetin). [Source](#) [Uniprot/SwissProt P01588](#)

Annotations were generated by the Ensembl automatic annotation pipeline using either a GeneWise/Exonerate model from a database protein or a set of aligned cDNAs followed by an ORF prediction. GeneWise/Exonerate models are further combined with available aligned cDNAs to annotate the transcript. For more information see V.Curwen et al., Genome Res. 2004 14:942-50.)

This corresponds to the following database identifiers:

UniProtKB/Swiss-Prot:	EPO_HUMAN [Target #id: 100; Query #id: 100] [align] NP_000790.2 [Target #id: 100; Query #id: 100] [align] NM_000799.2 [Target #id: 99; Query #id: 99] [align] Q2M2L6_HUMAN [Target #id: 100; Query #id: 100] [align]
UniProtKB/Trembl:	2056
EntrezGene:	A_14_P113914 [Target #id: 2; Query #id: 100] A_23_P145669 [Target #id: 4; Query #id: 100] A_23_P145669 [Target #id: 4; Query #id: 100]
Agilent CGT:	AC09488 [align]
Agilent Probe:	AF053356 [align]
EMBL:	AF202306 [align] AF202310 [align] AF202311 [align] AF202313 [align] BC093628 [align]
IPI:	IP00307226.3 [Target #id: 100; Query #id: 100]
MIM:	133170
PDB:	1BYU
Protein ID:	1CN4
UniGene:	1FEER
Affymetrix Microarray Focus:	Hs.2303 [Target #id: 99; Query #id: 98] 207257_at
Affymetrix Microarray HGU110:	1023_at
Affymetrix Microarray HuGeneFL:	X02158_rna1_at
Affymetrix Microarray U133:	207257_at 217254_s_at
Affymetrix Microarray U95:	207257_at 217254_s_at Hs.2303.S1_3p_a_at g4503588_3p_at

GO

InterPro IPR003013 Erythropoietin - [View other genes with this domain]  
IPR001323 Erythropoietin/thrombopoietin - [View other genes with this domain]

Protein Family ENSF00000004758 : ERYTHROPOIETIN PRECURSOR  
This cluster contains 1 Ensembl gene member(s) in this species.

Transcript structure

Transcript neighbourhood

Spliced transcript sequence

Transcript sequence

Show the following features: Exons  
Number residues: No  
Refresh

## Result of STEP 6:

The diagram illustrates the classification of sequence variations:

- Exons - alternating text colour**: Variations in exon regions.
- Codons - alternating background colour**: Variations in codon positions.
- Synonymous SNP**: Variation at a synonymous site.
- Non-synonymous SNP**: Variation at a non-synonymous site.
- Other variation in coding sequence**: Variations that do not fall into the above categories.
- Translation**: The process of reading the codon sequence.
- Ambiguity code**: A table showing the correspondence between codons and amino acids, including Y (Tyr) and R (Arg).
- Affected residue**: A mouse-over label indicating alternative codons for a specific residue.
- UTR SNP**: Variations in the Untranslated Region, shown with a dark background.
- Other variation in UTR**: Variations in the UTR region, shown with a light background.

## Result of STEP 7:

**STEP 9:** Click on 'Graphical view'

**STEP 8:** Choose ' Flanking sequence at either end of transcript – 500', tick 'Show full intronic sequence' and click on [Go]

Flank

Intron

Exon

Coding sequence

UTR

Supporting evidence

## Result of STEP 8:

## Result of STEP 9:

**STEP 11:**  
Select from the 'Features' drop-down menu 'SNPs', 'Markers', and 'Ensembl genes' and close the menu

Ensembl Human ContigView

Search e/Human: Anything e.g. AL13872.15.1.44776, A...

Chr. 7 band

Rat synteny

Mouse synteny

Dog synteny

DNA(contigs)

Markers

Ensembl Genes

ncRNA Genes

e1 ncRNA Genes

Vega Genes

Gene legend

Features ▾ Comparative ▾ DAS Sources ▾ Repeats ▾ Decorations ▾ Export ▾ Image size ▾ Help ▾

Jump to region 7 : 100156359-100159257 Refresh Band: Refresh

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

Chr. 7

EMBL mRNAs

Gene models

Assembly

Mapped proteins and cDNAs

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**STEP 10:**  
Click on the '+' in front of 'Basepair view'

## Result of STEP 10:

25 – 500 bp region

Basepair view

Chr. 7  
Length  
Genscan  
Ensembl trans.  
Vega trans.  
Amino acids  
Sequence  
DNA(contigs)  
Sequence  
Amino acids  
Length  
Gene legend

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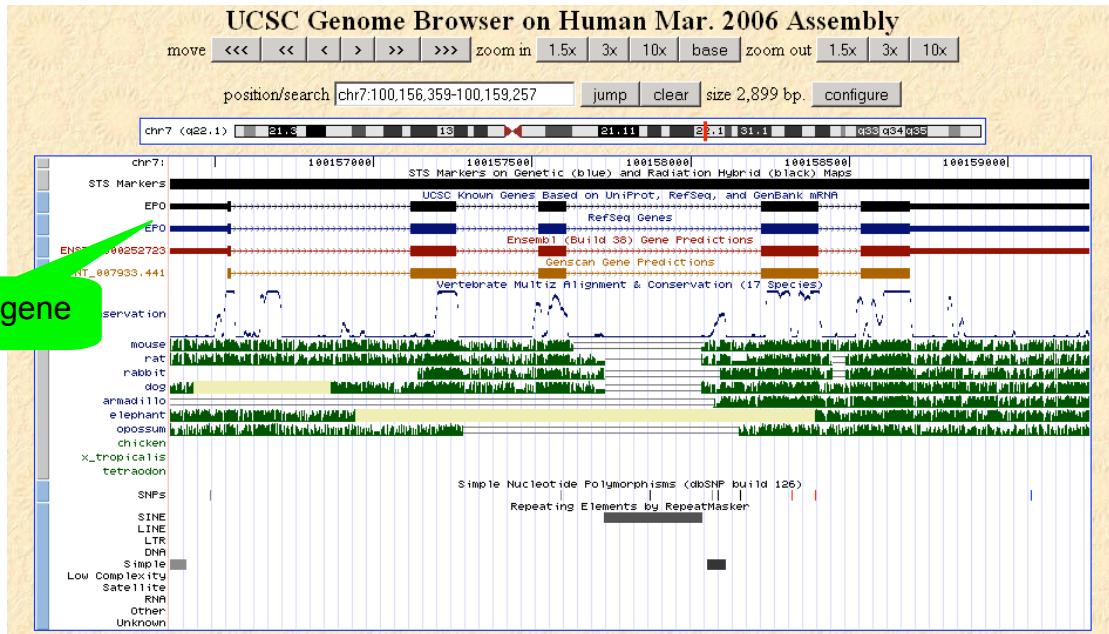
## Result of STEP 11:

STEP 12:  
Click on a SNP and subsequently on  
'SNP properties'

Detailed view

Features ▼ Comparative ▼ DAS Sources ▼ Repeats ▼ Decorations ▼ Export ▼ Image size ▼ Help ▼  
Jump to region 7 : 100156359-100159257 Refresh  
<< 5MB < 2MB < 1MB < Window 1MB > 2MB > 5MB >>  
Chr. 7 Length 100,156,500 100,157,000 100,157,500 100,158,000 100,158,500 100,159,000  
Ensembl trans. EPO → Ensembl Known Protein Coding  
DNA(contigs)  
SNPs Length 2.00 kb  
Gene legend Ensembl Known Protein Coding  
SNP legend Intron Non-synonymous coding SNP 3' UTR  
There are currently 85 tracks switched off, use the menus above the image to turn these on.  
Ensembl Homo\_sapiens 7:100156359-100159257 Tue Apr 25 12:14:13 2006

**STEP 13:**  
Go back to ContigView with the back button of the internet browser and click on 'Show in UCSC browser' in the navigation column



EPO gene

**STEP 14:**  
Close the UCSC  
browser window and  
click on

'Graphical overview'  
in the sidemenu

In the Detailed View  
Panel: make sure that in  
the 'Decorations' menu  
the options '1Mb clones',  
'30k TPA clones', '32k  
clones' and 'Human  
tilepath clones' are  
selected. Zoom out 2  
steps

**e! Ensembl Human CytoView**

Ensembl v38  
Chromosome 99,657,808

**STEP 15:**  
Click on 'View Syntenic regions ... with *Mus musculus*'

Search e/Human: Anything e.g. AC016942.13.1.152014, ALT3

200 kb – 50 Mb region

BAC clones

Tiling path clones

Export cloneset information

Length Chr. 7 band 1,44 Mb 922.1

DNA(contigs) RC#4571.0.1.249582 < > RC#11895.4.1.17235 >

NT Contigs NT\_097933

Markers

Ensembl Genes ncRNA Genes e1 ncRNA Genes Vega Genes 1Mb clones

30k TPA clones

32k clones

Human tilingpath clones CTB-161R2 RP11-758P17 RP11-44M6 RP11-396A7 RP11-124L15 RP11-395E7 994-747610

Repeats

Length 99.70 Mb 99.81 Mb 99.99 Mb 100.00 Mb 100.10 Mb 100.20 Mb 100.30 Mb 100.40 Mb 100.50 Mb 100.60 Mb

Novel Protein coding Known Protein coding Known Processed transcript RNA gene RNA Pseudogene Ensembl Novel Pseudogene Ensembl Novel Protein Coding

Gene legend There are currently 23 tracks switched off, use the menus to switch them back on.

Export data

Select Set of features to render =select=

Output format HTML

Select type to export =select=

Export

Fields marked with \* are required

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**MartView**  
Advanced query and export  
Data mining across Ensembl species and/or feature types  
powered by bioMart

Human genes

Mouse homologs

**STEP 16:**  
Click on  
[MultiContigView]

Make sure that  
from the  
'Comparative'  
menu the option  
'Conserved' is  
selected

**Human genes**

**Mouse homologs**

**Mouse chromosome**

**Human chromosomes**

**Syntenic block**

**Homology Matches**

Homo sapiens Genes	Mus musculus Homologues
EPO (0.10 Gb) [ContigView]	-> Epo (136.40 Mb) [ContigView] [MultiContigView]
ZAN (0.10 Gb) [ContigView]	-> Zan (136.32 Mb) [ContigView] [MultiContigView]
EPHB4 (0.10 Gb) [ContigView]	-> Ephb4 (136.27 Mb) [ContigView] [MultiContigView]
SLC12A9 (0.10 Gb) [ContigView]	-> Scl2a9 (136.23 Mb) [ContigView] [MultiContigView]
TRIP6 (0.10 Gb) [ContigView]	-> Trip6 (136.23 Mb) [ContigView] [MultiContigView]
ARS2_HUMAN (0.10 Gb) [ContigView]	-> Ars2 (136.21 Mb) [ContigView] [MultiContigView]
NP_001015072_1 (0.10 Gb) [ContigView]	-> 2700038N03Rik (136.21 Mb) [ContigView] [MultiContigView]
ACHE (0.10 Gb) [ContigView]	-> Ache (136.21 Mb) [ContigView] [MultiContigView]
MUC3B (0.10 Gb) [ContigView]	No homologues
ENSG00000205277 (0.10 Gb) [ContigView]	No homologues
Q6PJS_HUMAN (0.10 Gb) [ContigView]	No homologues
Q6PJS_HUMAN (0.10 Gb) [ContigView]	-> Muc3 (136.11 Mb) [ContigView] [MultiContigView]
Q6PJS_HUMAN (0.10 Gb) [ContigView]	-> Muc3 (136.11 Mb) [ContigView] [MultiContigView]
O6PJS_HUMAN (0.10 Gb) [ContigView]	-> Trim56 (136.08 Mb) [ContigView] [MultiContigView]

**Navigate Homology**

**Upstream** (<0.10 Gb)   **Downstream** (>0.10 Gb)

**Change Chromosome**

Chromosome: 7

Fields marked with \* are required

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**STEP 17:** Click on 'Export sequence as FASTA'

Ensembl Human MultiContigView

Search e/Human: Anything Go  
e.g. AL138722.15.1.44776, ENSG00000139618 Help

Chromosome 100,153,100,160

View sequence as FASTA  
Graphical overviews  
Export information region  
Export sequence as FASTA  
Export EMBL file  
Export Gene info in region  
Export SNP info in region  
Export Vega info in region  
View alignment with ...  
View alongside ...  
View Syntenic regions ...  
View region in NCBI browser  
View region in UCSC browser

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

Docs and downloads  
Information  
What's New  
About Ensembl  
Ensembl data  
Software

Other links  
Home  
Sitemap  
Vega  
Pre Ensembl  
View previous page in Archive  
Stable Archive link for this page  
Archive sites  
Trace server

Sanger EBI

Human

Mus musculus NCBI now in Ensembl!

Ensembl Genes ncRNA Genes e! ncRNA Genes Vega Genes

Hs. Chr. 7 band Rat synteny Mouse synteny Dog synteny

DNA (contigs)

Ensembl Genes ncRNA Genes e! ncRNA Genes Vega Genes

Mm. Chr. 5 band Human synteny Dog synteny

DNA (contigs)

Ensembl Genes

Human EPO gene

Conserved sequences

Mouse EPO homologue

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The screenshot shows the Ensembl Human ExportView interface. A large yellow callout bubble points to the 'Continue >>' button. The main content area displays a file output for a FASTA format text file, containing the sequence from position 7,100,155,359 to 100,160,257. Below the sequence are download options: HTML, Text, and Compressed text (.gz). At the bottom, a footer notes the copyright to 2006 WTSI / EBI and provides a link to the code licence.

Ensembl Human ExportView

Search e!Human: Anything

e.g. AL138722.15.1.44776, ENSG00000139618

Go

Ensembl view

Chromosome 100,155,359 - 100,160,257

View details  
Graphical view  
Graphical overview  
Export information about region  
Export sequence as FASTA

**STEP 18:**  
Click on  
[Continue>>]

A File output for FASTA format text file

some 7 100,155,359 - 100,160,257.

Output type:  HTML  Text  Compressed text (.gz)

**Continue >>**

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**STEP 21:**  
Paste the copied sequence

Ensembl v36 Human BlastView

Sequence  
(max 30) in FASTA or plain text:  
TCACTCACTACATTTT...  
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**

Select the Search Tool  
BLASTN  
SSAHA2  
TBLASTX

Search sensitivity: Near-exact matches

About BlastView

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**STEP 22:**  
Select 'Homo\_sapiens'  
and 'BLASTN' and click  
on [RUN>]

**Summary of BLAST search**

**STEP 23:**  
Click on [Retrieve]  
to check for results

**STEP 24:**  
Click on [VIEW>]

Ensembl v36 Human BlastView

Sequence  
e.g. AL138722.15.1.44776, ENSG00000139618

SEARCH

RESULTS

Alignment Display Options:  
Locations vs. Karyotype  
Summary Table

1: unnamed (2880 letters) Vs. LATESTGP  
Homo\_sapiens 107 alignments, 40 hits [RawResult](#) [view](#)

Summary  
setup  
Homo\_sapiens  
Genomic sequence  
BLASTN  
Low sensitivity

configure  
-E: 10  
-B: 100  
-filter: dust  
-RepeatMasker  
-W: 15

display  
Not yet initialised

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**Location of hits on the genome**

**Best hit**

**Alignment of hits to query sequence**

**STEP 25:**  
Click on [C] in front of best hit

Ensembl Human BlastView

Search e/Human: Anything

e.g. AL138722.15.1.44776, ENSG00000139618

Help

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
  - Not yet initialised

refresh Online Help

CONFIG RESULTS DISPLAY

Alignments vs Homo\_sapiens LATESTGP database

Alignments of 107, sorted by Raw Score

refresh

Alignment Locations vs. Karyogram (click arrow to hide)

Alignment Locations vs. Query (click arrow to hide)

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	Contig	Chromosome	Stats	Sort By
Off_ Name	Off_ Name	Off_ Name	Off_ Name	Off_ Name	Off_ Name	Off_ Name	Off_ Score	>Chromosome
Start	Start	Start	Start	Start	Start	Start	E-val	<Score
[A] [S] [G] [C]	384... 824... +	Chr:7 100155745	100156329 +	Chr:7 100155743	100156329 +	Chr:7 100155744	585 0.	100.00 585
[A] [S] [G] [C]	1051 1... +	Chr:7 100156409	100156678 +	Chr:7 100156401	100156678 +	Chr:7 100156402	270 0.	100.00 270
[A] [S] [G] [C]	2753 4... 8600 +	Chr:7 100158111	100158238 +	Chr:7 100158111	100158238 +	Chr:7 100158111	5128 0.	100.00 128
[A] [S] [G] [C]	2744 2569 +	Chr:1 91		Chr:1 91		Chr:1 91	94 0.	100.00 96
[A] [S] [G] [C]	1571 15	Chr:1 1571		Chr:1 1571		Chr:1 1571	559 0.	100.00 91
[A] [S] [G] [C]	2832 26	Chr:1 1571		Chr:1 1571		Chr:1 1571	5074992 0.	100.00 22
[A] [S] [G] [C]	60 70	Chr:1 1571		Chr:1 1571		Chr:1 1571	2 2406267 0.	93.33 30
[A] [S] [G] [C]	2335 22	Chr:1 1571		Chr:1 1571		Chr:1 1571	40 2685774 0.	0.25 11
[A] [S] [G] [C]	740 76	Chr:1 1571		Chr:1 1571		Chr:1 1571	70 121454290 0.	0.05 21
[A] [S] [G] [C]	423 443	Chr:5 423		Chr:5 423		Chr:5 423	55 136849279 0.	2.7 96.00 25
[A] [S] [G] [C]	1803 826 -	Chr:5 472638009	472638299 +	Chr:5 472638009	472638299 +	Chr:5 472638009	921 0.	100.00 921
[A] [S] [G] [C]	877 85	Chr:11 45147216	45147236 +	Chr:11 45147216	45147236 +	Chr:11 45147216	62 1547630 0.	100.00 21
[A] [S] [G] [C]	804 91	Chr:11 45147216	45147236 +	Chr:11 45147216	45147236 +	Chr:11 45147216	60 35694404 0.	3.3 35
[A] [S] [G] [C]	2814 26	Chr:11 45147216	45147236 +	Chr:11 45147216	45147236 +	Chr:11 45147216	9 43166599 0.	100.00 21
[A] [S] [G] [C]	1434 14	Chr:11 45147216	45147236 +	Chr:11 45147216	45147236 +	Chr:11 45147216	4 86415907 0.	2.7 96.00 25
[A] [S] [G] [C]	1803 826 -	Chr:5 472638009	472638299 +	Chr:5 472638009	472638299 +	Chr:5 472638009	21 3.2 96.00 25	
[A] [S] [G] [C]	875 897 -	Chr:17 2245254	2245277 +	Chr:17 2245254	2245277 +	Chr:17 2245254	20 2.8 95.83 24	
[A] [S] [G] [C]	872 1094 -	Chr:11 2404636	2500160 +	Chr:11 2404636	2500160 +	Chr:11 2404636	20 3.1 95.83 24	
[A] [S] [G] [C]	2209 2202 +	Chr:14 104864074	104864092 +	Chr:14 104864074	104864092 +	Chr:14 104864074	20 3.2 95.83 20	
[A] [S] [G] [C]	803 899 +	Chr:14 104864074	104864092 +	Chr:14 104864074	104864092 +	Chr:14 104864074	20 3.1 95.83 24	
[A] [S] [G] [C]	881 899 +	Chr:14 104864028	104864046 +	Chr:14 104864028	104864046 +	Chr:14 104864028	19 5.3 100.00 19	
[A] [S] [G] [C]	881 899 +	Chr:14 104863998	104864000 +	Chr:14 104863998	104864000 +	Chr:14 104863998	19 5.3 100.00 19	
[A] [S] [G] [C]	69 80 +	Chr:7 100155741	100155758 +	Chr:7 100155741	100155758 +	Chr:7 100155741	18 0. 100.00 18	
[A] [S] [G] [C]	1962 1979 +	Chr:X 3986710	70306727 +	Chr:X 3986710	70306727 +	Chr:X 3986710	18 0.70 100.00 18	
[A] [S] [G] [C]	1700 1720 +	Chr:X 70247940	70247969 +	Chr:X 70247940	70247969 +	Chr:X 70247940	18 3.9 100.00 18	
[A] [S] [G] [C]	418 436 +	Chr:20 44598942	44598960 +	Chr:20 44598942	44598960 +	Chr:20 44598942	19 2.4 100.00 19	
[A] [S] [G] [C]	2209 2227 +	Chr:14 46044909	46044927 -	Chr:14 46044909	46044927 -	Chr:14 46044909	19 3.2 100.00 19	
[A] [S] [G] [C]	2804 2802 +	Chr:3 1203832	1203832 +	Chr:3 1203832	1203832 +	Chr:3 1203832	19 4.3 100.00 19	
[A] [S] [G] [C]	803 899 +	Chr:14 104864074	104864092 +	Chr:14 104864074	104864092 +	Chr:14 104864074	19 4.3 100.00 19	
[A] [S] [G] [C]	881 899 +	Chr:14 104864028	104864046 +	Chr:14 104864028	104864046 +	Chr:14 104864028	19 5.3 100.00 19	
[A] [S] [G] [C]	881 899 +	Chr:14 104863998	104864000 +	Chr:14 104863998	104864000 +	Chr:14 104863998	19 5.3 100.00 19	
[A] [S] [G] [C]	69 80 +	Chr:7 100155741	100155758 +	Chr:7 100155741	100155758 +	Chr:7 100155741	18 0. 100.00 18	
[A] [S] [G] [C]	1962 1979 +	Chr:X 3986710	70306727 +	Chr:X 3986710	70306727 +	Chr:X 3986710	18 0.70 100.00 18	
[A] [S] [G] [C]	1700 1720 +	Chr:X 70247940	70247969 +	Chr:X 70247940	70247969 +	Chr:X 70247940	18 3.9 100.00 18	
[A] [S] [G] [C]	2306 2323 +	Chr:1 150284632	150284649 -	Chr:1 150284632	150284649 -	Chr:1 150284632	18 6. 100.00 18	
[A] [S] [G] [C]	1801 1818 +	Chr:2 73022513	73022500 +	Chr:2 73022513	73022500 +	Chr:2 73022513	18 9.3 100.00 18	
[A] [S] [G] [C]	7 8 +	Chr:2 29968484	29968484 +	Chr:2 29968484	29968484 +	Chr:2 29968484	18 0.25 100.00 17	
[A] [S] [G] [C]	881 897 +	Chr:1 59611091	59611107 +	Chr:1 59611091	59611107 +	Chr:1 59611091	18 0.70 100.00 17	
[A] [S] [G] [C]	881 897 -	Chr:1 20541390	20541406 +	Chr:1 20541390	20541406 +	Chr:1 20541390	17 1. 100.00 17	
[A] [S] [G] [C]	1798 1814 -	Chr:1 20511090	20511112 +	Chr:1 20511090	20511112 +	Chr:1 20511090	17 1. 100.00 17	
[A] [S] [G] [C]	1798 1814 -	Chr:10 43031647	43031647 +	Chr:10 43031647	43031647 +	Chr:10 43031647	17 1.2 100.00 17	
[A] [S] [G] [C]	2100 2119 +	Chr:14 104863998	104864000 +	Chr:14 104863998	104864000 +	Chr:14 104863998	17 1.8 100.00 17	
[A] [S] [G] [C]	1564 1580 +	Chr:9 139178040	139178056 +	Chr:9 139178040	139178056 +	Chr:9 139178040	17 2.2 100.00 17	
[A] [S] [G] [C]	883 899 +	Chr:9 139163518	139163534 +	Chr:9 139163518	139163534 +	Chr:9 139163518	17 2.2 100.00 17	
[A] [S] [G] [C]	2805 2825 +	Chr:14 46020025	46020044 -	Chr:14 46020025	46020044 -	Chr:14 46020025	17 3.2 95.24 21	
[A] [S] [G] [C]	1571 1583 +	Chr:16 47367660	47367660 +	Chr:16 47367660	47367660 +	Chr:16 47367660	17 3.5 100.00 17	
[A] [S] [G] [C]	1519 1622 +	Chr:16 47367664	47367664 +	Chr:16 47367664	47367664 +	Chr:16 47367664	17 3.4 100.00 17	
[A] [S] [G] [C]	1805 1821 +	Chr:1 150273546	150273562 +	Chr:1 150273546	150273562 +	Chr:1 150273546	17 6.0 100.00 17	
[A] [S] [G] [C]	1805 1821 +	Chr:6 34166916	34166936 +	Chr:6 34166916	34166936 +	Chr:6 34166916	17 7.0 95.24 21	

## Detailed view

