

WORKED EXAMPLE – A walk through the main pages of the Ensembl browser, using the EPO (Erythropoietin precursor) gene as an example.

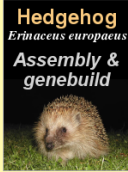
STEP 1:
Load Ensembl
www.ensembl.org

The screenshot shows the Ensembl genome browser homepage. The navigation column on the left includes sections like 'Your Ensembl', 'Healthchecks', 'Help & Documentation', 'Select a species', and 'What's new'. The main content area features a search bar, 'Ensembl tools', 'Ensembl headlines', 'About Ensembl', and 'Other Ensembl websites'. The 'Popular genomes' section lists various species, with 'Homo sapiens' highlighted by a yellow callout. The footer contains copyright information and a link to the code license.

STEP 3:
Type in 'EPO Gene'.
Click 'Go'.

Karyotype

- Your Ensembl
 - Show account · Log out
 - Bookmark this page
- Help & Documentation
 - Table of Contents
 - Helpdesk
 - What's New
 - About Ensembl
 - Downloading data
 - Displaying your own data
 - Ensembl software
- Select a species
 - Mammals
 - Other chordates
 - Other eukaryotes
- Ensembl Archive
 - View previous release of page in Archive!
 - Stable Archive: link for this page

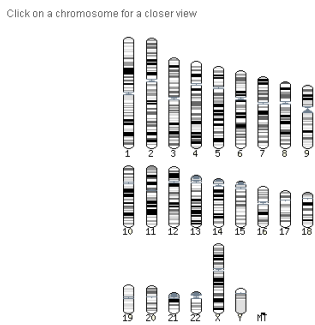


Search Ensembl *Homo sapiens*

Search:

e.g. chromosome X or 14:10000..20000 or BRCA2

Karyotype



Jump directly to sequence position

Chromosome: or region

From (bp):

To (bp):

What's New in Ensembl 43

- Homo sapiens News**
- cDNA Updates**
Ensembl Human and Mouse have received their regular cDNA updates
 - Updates to Human databases**
The Ensembl human gene set has been patched to remove some incorrect gene structures and to add a set of Immunoglobulin T-cell receptor gene segments, inferred from the alignment of segment sequences in the IMGT database.
[Read more...](#)
 - Human variation**
Ensembl Human has a new variation database that includes SNPs called from Celera reads, changed alleles/genotypes and updates to match the new patched gene set.
 - Xref updates**
Xrefs have been re-run for Human, Rat and Mouse.
 - Affy mapping**
Xrefs have been added for Affymetrix data mapped to the Cow, Yeast, Human and Zebrafish genomes.
- [More news...](#)

About the Human genome

Assembly

This release is based on the NCBI 36 assembly of the [human genome](#) (November 2005). The data consists of a reference assembly of the complete genome plus the Celera WGS and a number of alternative assemblies of individual haplotypic chromosomes or regions.
[Full list of assemblies](#)

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

- [Nature 431, 931 - 945 \(21 October 2004\)](#)
- [WT Sanger Institute Press Release](#)

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.

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

Source and version of assembly and genebuild

Statistics

Assembly:	NCBI 36, Oct 2005
Genebuild:	Ensembl, Aug 2006
Database version:	43,366
Known genes:	21,662
Novel genes:	1,064
Pseudogenes:	1,069
RNA genes:	3,994
Immunoglobulin T cell receptor gene segments:	388
Genscan gene predictions:	69,185
Gene exons:	270,239
Gene transcripts:	44,537
SNPs:	11,577,475
Base Pairs*:	3,253,037,807
Golden Path Length**:	3,093,120,360

* Total number of base pairs = sum of lengths of DNA table
** Reference assembly (Golden path) length = sum of non-redundant top level seq regions

A 'Vega' gene (a consortium external to Ensembl)

Ensembl Human Search View

Ensembl release 83 Feb 2007

Your Ensembl

- Show account Log out
- Bookmark this page
- Save DNS cookies
- Save configuration as...

Species

- Human sapiens (8)
- Mouse (6)
- Chimpanzee (6)
- Other (6)

Feature type

- Gene (4)
- Transcript (1)
- Gene (6)
- Transcript (6)
- Other (1)

Exalead Help

To exclude a category click on the minus (-) icon.

To restrict to a category click on the plus (+) icon.

To reset a category click on the 'R' icon.

To view a category click on the 'B' icon.

Ensembl Archive

View previous releases of pages as they change!

Stable Archived link for this page

sanger

Domestic Cat Felis catus 2x assembly now in Ensembl!

Ensembl text search

EPO Search

Your query matched 8 entries in the search database

Vega_external protein_coding Gene: OTTHM000000023044 **HGNC Symbol: VEGP** [\[Contig/View\]](#)

Vega_external protein_coding gene OTTHM000000023044 has 1 transcript: OTTHM000000059365, associated peptide: OTTHM00000024662 and 0 genes: enRytpo001n

The gene has the following external identifiers mapped to it

Ensembl Human Gene: ENSG00000130427

EnsemblGene: 2056

HGNC Symbol: **EPO**, **VU**, **EPO**, 3415

MM gene: 133170

RefSeq DNA: NM_000799.2, NM_000799

UniProt/Swiss-Prot: **EPO**, HUMAN, P01588

Vega gene: VEGP, OTTHM000000023044

Vega transcript: VU, **EPO**, OTTHM000000059365

Vega translation: OTTHM00000024662

Source: en43, Species: Homo sapiens, Gene, Feature type: Gene, Homo sapiens;

Vega_external processed_transcript Gene: OTTHM000000023047 **HGNC Symbol: SK-EPO** [\[Contig/View\]](#)

Vega_external processed_transcript gene OTTHM000000023047 has 1 transcript: OTTHM00000027332 and 0 genes: enRytpo001n

The gene has the following external identifiers mapped to it

Ensembl Human Gene: ENSG00000130427

EnsemblGene: 2056

HGNC Symbol: **EPO**, 3415, SK-**EPO**

MM gene: 133170

RefSeq DNA: NM_000799.2, NM_000799

UniProt/Swiss-Prot: **EPO**, HUMAN, P01588

Vega gene: VEGP, OTTHM000000023044

Vega transcript: VU, **EPO**, OTTHM000000059365

Vega translation: OTTHM00000027332, SK-**EPO**

Source: en43, Species: Homo sapiens, Gene, Feature type: Gene, Homo sapiens;

Ensembl protein_coding Gene: ENSG00000130427 **HGNC Symbol: EPO** [\[Contig/View\]](#)

Ensembl protein_coding gene ENSG00000130427 has 4 transcripts: ENST00000252723, associated peptide: ENSP00000252723 and 0 genes: enRytpo001n

ENSG00000130423, ENSG00000130431, ENSG00000144077

EnRytpo001n [\[Source: UniProt/Swiss-Prot, Acc: P01588\]](#)

The gene has the following external identifiers mapped to it

Affymetrix Focus: 201752_at

Affymetrix Microarray: HC0110_1023_at

Affymetrix Microarray: HUdenAF_L_201458_mat_at

Affymetrix Microarray: U133_201752_at, 217254_at

Affymetrix: U95_1023_at

Agilent: CGH_A_14_P13914

Agilent Probe: A_23_P145688_A_23_P145684

CCDB: CCDB9795, CCDB9795.1

EMBL: AF095555, AF095555.1, BC093928, AF202201, AF202213, H02157, AF202206, AF202214, AF202208, H02156, M1316, AF202212, AF202209, AF202210, AC008488, BC111937, AF202211

EnsemblGene: 2056, **EPO**, MOC138142, EP

OE: HealthCareAmerica: Codelink: VWA, OE19554

GO: GO:000515, GO:0001165, GO:0005128, GO:0005128, GO:0007287, GO:0030218, GO:0005178, GO:0001666, GO:0008015, GO:0007275, GO:0005578

HGNC Symbol: **EPO**, 3415

Illumina: V1_04_452518-40

Illumina V2: ILMN_6125

IP: IP0002726.3, IP0002726

MM gene: 133170

PDB: 1CN4, 1EER, 1E9V

Protein ID: A482271.1, CA436095, CA426884.1, AA452400.1, AA423121.1, AA423133.1, AA417572.1, AA417572.1, AA419308, AA417572.1, AA419308.1, AAC787891, AA423132, AA413864, CA426884, AA423257, AA452400, AA423134.1, AA423134.1, AA426895.1, AA438268.1, AA413864.1, AA423133, AA438268

RefSeq DNA: NM_000799.2, NM_000799

RefSeq peptide: NP_000799.2, NP_000799

UniGene: H4_2920

UniProt/Swiss-Prot: **EPO**, HUMAN, C64912, G91J23, G91J40, P01588, G91J25

UniProt/TrEMBL: G2M2L6, HUMAN, G2M2L6

Source: en43, Species: Homo sapiens, Gene, Feature type: Gene, Homo sapiens;

Ensembl protein family: ENSG0000007720

Ensembl protein family ENSG0000007720 | RYRHYTHOPOIETIN RECEPTOR PRECURSOR **EPRQ** has 4 members: ENSG00000107268, ENSP00000221239, P19235, Q2M205

Source: en43, Species: Homo sapiens, Family, Feature type: Family, Homo sapiens;

Ensembl protein_coding Gene: ENSG00000102205 **HGNC Symbol: TRMP1** [\[Contig/View\]](#)

Ensembl protein_coding gene ENSG00000102205 has 4 transcripts: ENST00000210368, ENST00000377017, ENST00000377018, associated peptides: ENSP00000368702, ENSP00000368703, ENSP00000368704, ENSP00000368705, ENSP00000368706, ENSP00000368707, ENSP00000368708, ENSP00000368709, ENSP00000368710, ENSP00000368711, ENSP00000368712, ENSP00000368713, ENSP00000368714, ENSP00000368715, ENSP00000368716, ENSP00000368717, ENSP00000368718, ENSP00000368719, ENSP00000368720, ENSP00000368721, ENSP00000368722, ENSP00000368723, ENSP00000368724, ENSP00000368725, ENSP00000368726, ENSP00000368727, ENSP00000368728, ENSP00000368729, ENSP00000368730, ENSP00000368731, ENSP00000368732, ENSP00000368733, ENSP00000368734, ENSP00000368735, ENSP00000368736, ENSP00000368737, ENSP00000368738, ENSP00000368739, ENSP00000368740, ENSP00000368741, ENSP00000368742, ENSP00000368743, ENSP00000368744, ENSP00000368745, ENSP00000368746, ENSP00000368747, ENSP00000368748, ENSP00000368749, ENSP00000368750, ENSP00000368751, 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The Gene View Page

Gene Model

Orthologues in other species

STEP 5:
Click on 'Transcript Information'

Matches in other databases

GO
(Gene Ontology)
terms

The screenshot displays the Ensembl Gene View page for the gene ENSG00000134127. The page is organized into several sections:

- Case:** Provides basic information about the gene, including its Ensembl Gene ID (ENSG00000134127) and its location on Chromosome 7.
- Description:** Offers a brief description of the gene's function, such as "Endoplasmic reticulum protein".
- Transcript Information:** This section is highlighted in yellow and contains a table of transcripts. A callout points to this section with the text "STEP 5: Click on 'Transcript Information'".
- Orthologues:** Lists orthologous genes in other species, such as "EPO_MOUSE" and "EPO_HUMAN".
- Matches in other databases:** Lists matches in various databases, including UniProt, RefSeq, and Ensembl.
- GO (Gene Ontology) terms:** Lists Gene Ontology terms associated with the gene, such as "GO:0005576" and "GO:0005577".
- Transcript Information:** Provides details about the transcript, including its length and sequence.

Result of Step 9: *Contigview*

Chromosome

1 Mb region

STEP 12:
Go back one page in the browser to return to the EPO gene. Select from the 'Features' drop-down menu 'SNPs, and 'Ensembl genes' (deselect other options) and close the menu

STEP 11:
Click and drag the mouse to draw a box around another gene (Trip6). Zoom into the gene in Detailed View.

1 kb – 1 Mb region

Gene models

Mapped proteins and cDNAs

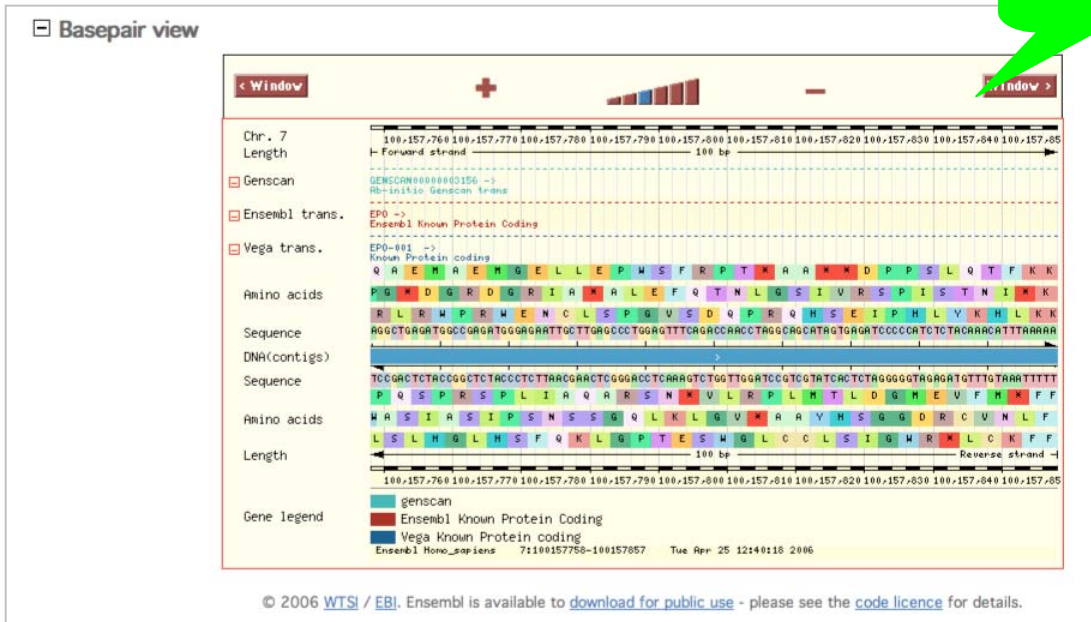
Assembly

STEP 10:
Click on the '+' in front of 'Basepair view' (collapse it afterwards)

Basepair view

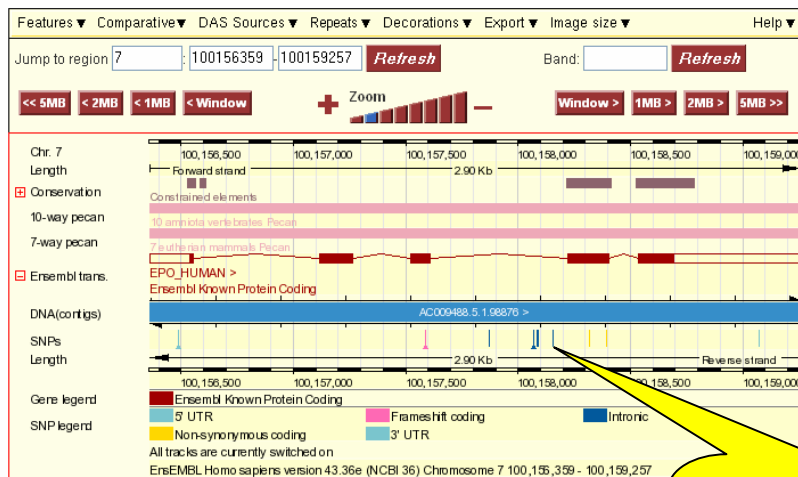
Result of STEP 10:

25 – 500 bp region



Result of STEP 12:

Detailed view



STEP 13:
Click on a SNP
(vertical line) and
subsequently on
'SNP properties'

Your Ensembl

- Login or Register
- About User Accounts

dbSNP: rs507392

- GeneSNP info
- rs507392 - SNP info
- rs507392 - LD info

Chromosome 7
100,157,872

- View of Chromosome 7
- 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

Ensembl Archive

- View previous release of page in Archive!
- Stable Archive! link for this page

dbSNP identifier

Alleles

dbSNP: rs507392 (dbSNP126)
HGVbase SNP000294357
G/A (ambiguity code: R) Ancestral allele: G
Proven by cluster, doublehit (SNP tested by additional method).
Validation status
Linkage disequilibrium data
Flanking sequence

SNP rs507392 is located in the following transcripts

Genomic location (strand)	Gene	Transcript relative SNP position	Translation relative SNP position	Type	GeneSNPView
7:100157872-100157872 (1)	ENSG00000130427	ENST00000252723: n/a	ENSP00000252723: n/a	INTRONIC	SNPs in gene context

Population genotypes and allele frequencies

Population	Alleles	Alleles	Description
	A	G	
ABI_Celera_Donors	unknown	unknown	5 human individuals' DNA from the following populations: European-American (two individuals)

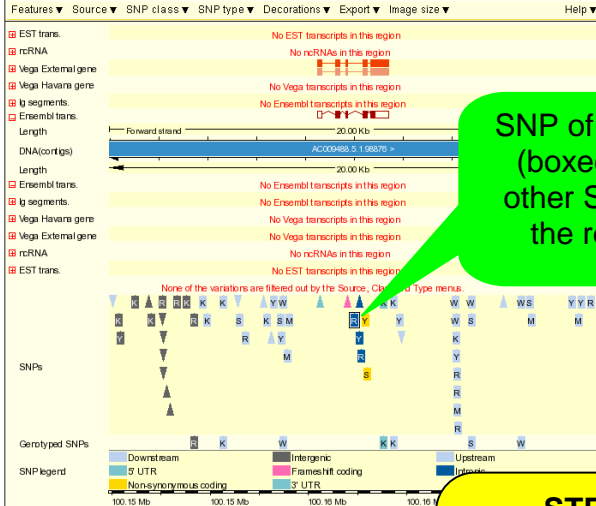
Allele and genotype frequencies

Bos taurus
Btau 3.1
Now in Ensembl



Individual genotypes for SNP rs507392

SNP Context - 7 100157872



Features: Source, SNP class, SNP type, Decorations, Export, Image size, Help

EST trans: No EST transcripts in this region

rcRNA: No rcRNAs in this region

Vega External gene: No Vega transcripts in this region

Vega Havana gene: No Vega transcripts in this region

Ig segments: No Ensembl transcripts in this region

Ensembl trans: No Ensembl transcripts in this region

SNPs: None of the variations are filtered out by the Sources, Chromosome, Type menus.

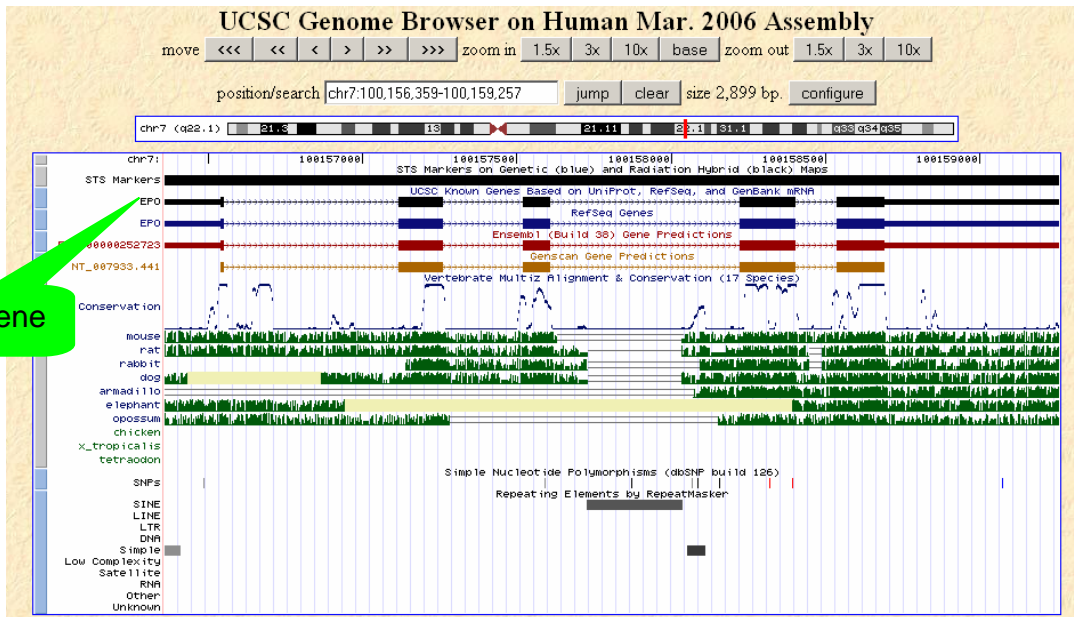
SNP legend: Downstream, 5' UTR, Intergenic, Frameshift coding, 3' UTR, Upstream, Ingenic

SNP of interest (boxed) and other SNPs in the region

STEP 14:
Go back to ContigView with the back button of the internet browser.

STEP 15:

To see the same chromosomal region in the UCSC genome browser, click on 'Show in UCSC browser' on the left of the page. A new window will open.



STEP 16:

Once you see the EPO gene and close this window. (You can turn on 'Ensembl genes' by changing 'hide' to 'full')

Click on 'Graphical Overview' on the left hand of the ContigView page to reach CytoView.

Ensembl Human genome browser

Ensembl release

Your Ensembl

Login or Register

About User

Chromosome 99,657,808 -

- View of Chromosomes
- Graphical view
- Graphical overview
- View alignment with
- View alongside
- View Syntenic regions ...
- View region at UCSC
- View region in NCBI browser

Export data

- 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

Ensembl Archive

- View previous release of page in Archive!
- Stable Archive! link for this page

Sanger EBI

Hedgehog *Eriaceus europaeus* Assembly & genebuild

STEP 18:
Click on 'View Syntenic regions ... with *Mus musculus*'

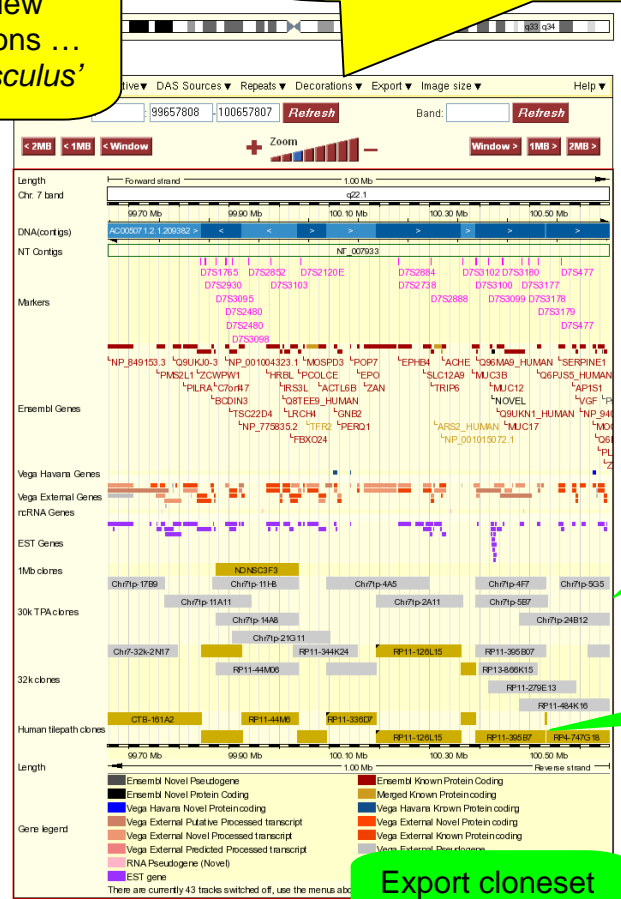
STEP 17:
Make sure '1Mb clones', '30k TPA clones', '32k clones' and 'Human tilepath clones' are selected under 'Decorations.' Zoom out 2 steps.

200 kb – 50 Mb region

BAC clones

Tiling path clones

Export cloneset information



Export data

Select Set of features to render: =select=

Output format: HTML

Select type to export: =select=

Export

Fields marked with * are required

Your Ensembl

- Login or Register
- About User Accounts

Chromosome 7

- View Chromosome 7
- View Chr 7 Synteny
- Map your data onto this chromosome

Ensembl Archive

- View previous release of page in Archive!
- Stable Archive! link for this page

Guinea Pig
Cavia porcellus

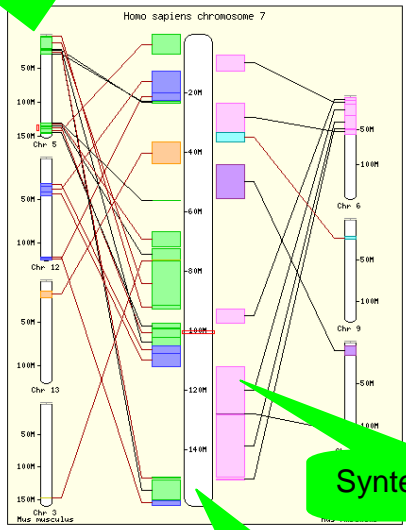


Assembly & genebuild

Mouse chromosomes

Human genes

Mouse homologues



Syntenic block

Human chromosome

Homo sapiens Genes	Mus musculus Homologues
EPO (0.10 Gb) [ContigView]	-> Epo (8: 137.71 Mb) [ContigView] [MultiContigView]
ZAN (0.10 Gb) [ContigView]	No homologues
EPHB4 (0.10 Gb) [ContigView]	No homologues
SLC12A9 (0.10 Gb) [ContigView]	-> Slc12a9 (5: 137.54 Mb) [ContigView] [MultiContigView]
	-> Slc12a2 (19: 58.80 Mb) [ContigView] [MultiContigView]
	-> Slc12a5 (2: 164.66 Mb) [ContigView] [MultiContigView]
	-> Slc12a6 (2: 112.07 Mb) [ContigView] [MultiContigView]
	-> Slc12a1 (2: 124.84 Mb) [ContigView] [MultiContigView]
	-> Slc12a4 (8: 108.83 Mb) [ContigView] [MultiContigView]
	-> Slc12a3 (8: 97.22 Mb) [ContigView] [MultiContigView]
	-> Slc12a7 (13: 74.20 Mb) [ContigView] [MultiContigView]
	-> Slc12a8 (18: 33.44 Mb) [ContigView] [MultiContigView]
P6 (0.10 Gb) [ContigView]	-> Trip6 (5: 137.54 Mb) [ContigView] [MultiContigView]
	-> Lpp (16: 24.31 Mb) [ContigView] [MultiContigView]
	-> Zyx (6: 42.28 Mb) [ContigView] [MultiContigView]
	-> Whip (7: 33.82 Mb) [ContigView] [MultiContigView]
	-> Jub (14: 53.52 Mb) [ContigView] [MultiContigView]
	-> Limd1 (9: 123.33 Mb) [ContigView] [MultiContigView]
	-> Fhlm1 (4: 140.85 Mb) [ContigView] [MultiContigView]
ARS2_HUMAN (0.10 Gb) [ContigView]	-> Ars2 (5: 137.53 Mb) [ContigView] [MultiContigView]
NP_001015072.1 (0.10 Gb) [ContigView]	-> 2700038N03Rik (5: 137.52 Mb) [ContigView] [MultiContigView]
	-> 1910047C23Rik (8: 47.47 Mb) [ContigView] [MultiContigView]
ACHE (0.10 Gb) [ContigView]	-> Ache (5: 137.52 Mb) [ContigView] [MultiContigView]
	-> Bche (3: 73.72 Mb) [ContigView] [MultiContigView]
	-> Mhm1 (3: 25.62 Mb) [ContigView] [MultiContigView]
	-> Cel (2: 28.38 Mb) [ContigView] [MultiContigView]
	-> Ces3 (8: 96.06 Mb) [ContigView] [MultiContigView]
	-> Es22 (8: 96.09 Mb)

STEP 19: Click on [MultiContigView]

Your Ensembl

- Login or Register
- About User Accounts

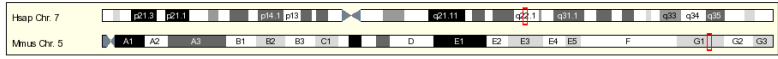
Chromosome 7
100,155,359 - 100,160,257

- View of Chromosome 7
- Graphical view of...
- Graphical overview
- View alignment with...
- View alongside...
- View Syntenic regions...
- View region at UCSC
- View region in NCBI browser

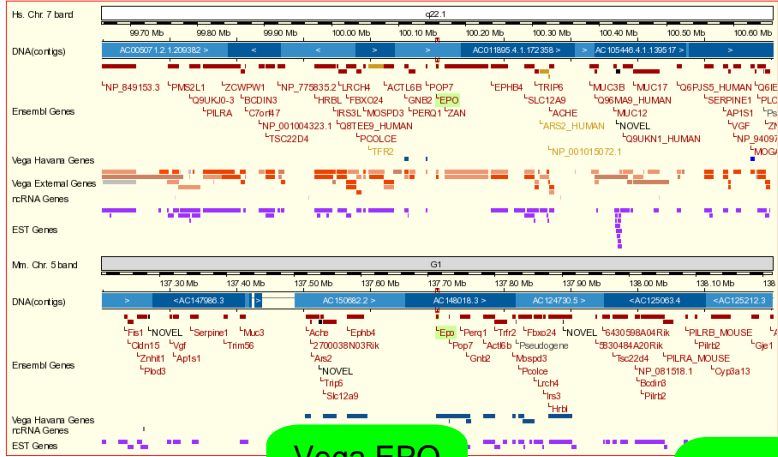
Export data

- Export information about region
- Export sequence as FASTA
- Export EMBL file
- Export gene info in region
- Export gene info in region
- Export gene info in region

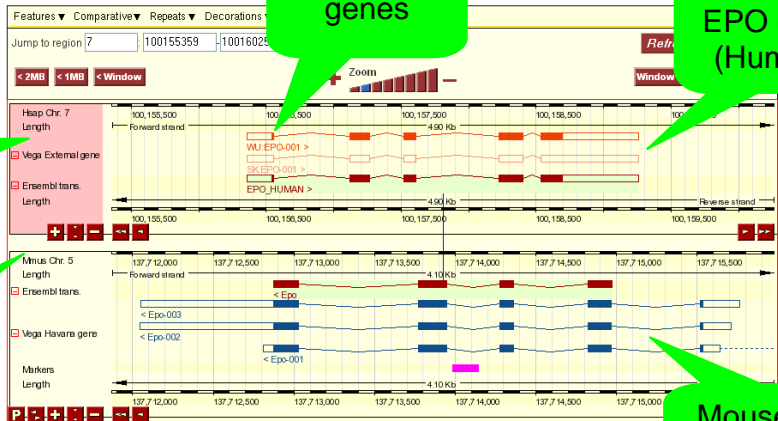
Top level



Navigational overview



Detailed View



STEP 20:
Click on 'Export sequence as FASTA'



Human

Mouse

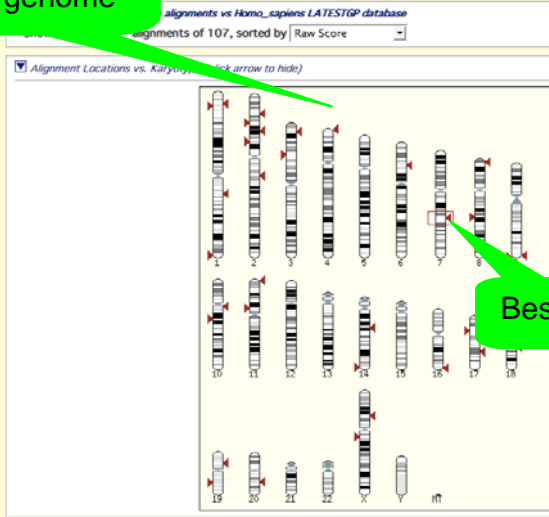
Vega EPO genes

Ensembl EPO gene (Human)

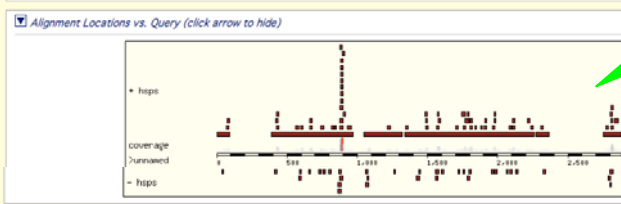
Mouse EPO homologue

- Use Ensembl
- Run a search
- Search for a gene
- 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
- Stommap
- Vega
- Pre-Ensembl
- View previous release of page in Archive!
- Stable Archival link for this page
- Archival sites
- Trace server

Location of hits on the genome



Best hit



Alignment of hits to query sequence

Alignment Summary (click arrow to hide)

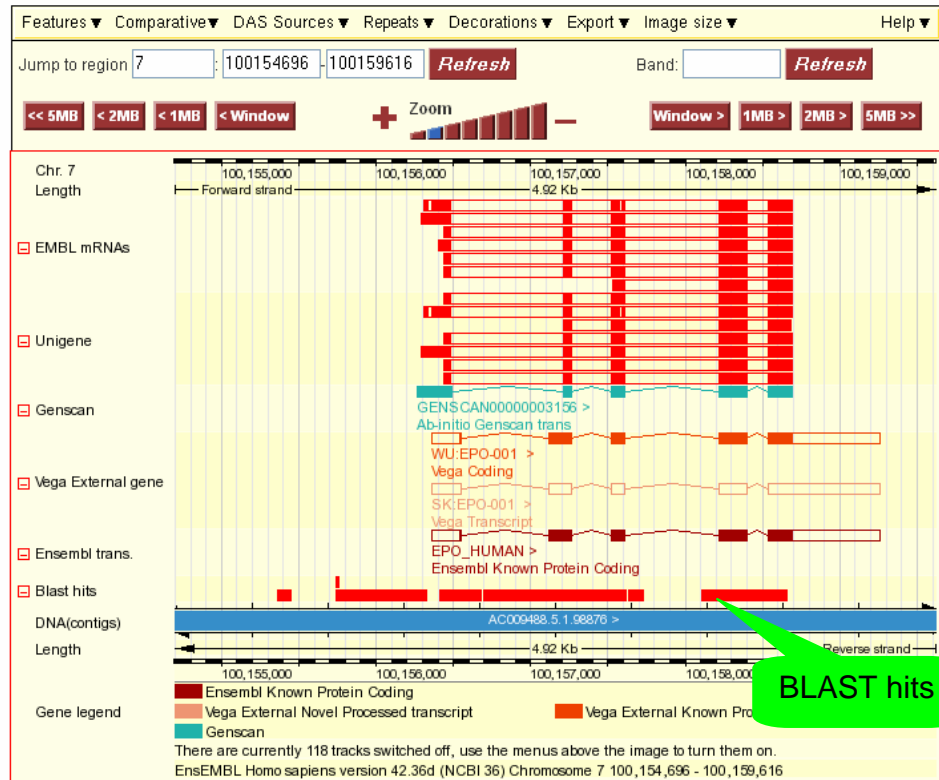
Select rows to include in table, and type of sort (Use the 'ctrl' key to select multiples)

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_ Name	>Chromosome						
Start	Start	Start	Start	Start	Start	Start	E-val	<Score						
Links	Query	Start	End	Chromosome	Start	End	Chromosome	Start	End	Stats	Score	E-val	XP	Length
[A] [S] [G] [C]	358	2258		Chr-7	100156696	100157616	Chr-7	100156696	100157616	921	0	100.00	921	
[A] [S] [G] [C]	397	2258		Chr-7	100155745	100156529	Chr-7	100155745	100156529	585	0	100.00	585	
[A] [S] [G] [C]	1051	1788		Chr-7	100156409	100156678	Chr-7	100156409	100156678	270	0	100.00	270	
[A] [S] [G] [C]	2758	2899		Chr-7	100158111	100158238	Chr-7	100158111	100158238	128	0	100.00	128	
[A] [S] [G] [C]	2274	2360		Chr-7	100157632	100157727	Chr-7	100157632	100157727	96	0	100.00	96	
[A] [S] [G] [C]	1	91		Chr-7	100155449	100155449	Chr-7	100155449	100155449	91	0	100.00	91	
[A] [S] [G] [C]	1571	1611		Chr-7	5074992	5074992	Chr-7	5074992	5074992	22	0.84	100.00	22	
[A] [S] [G] [C]	2852	2911		Chr-7	24002631	24002631	Chr-7	24002631	24002631	22	0.84	93.33	30	
[A] [S] [G] [C]	422	441		Chr-7	29054974	29054974	Chr-7	29054974	29054974	21	0.25	100.00	21	
[A] [S] [G] [C]	2355	2374		Chr-7	121454290	121454290	Chr-7	121454290	121454290	21	0.88	100.00	21	
[A] [S] [G] [C]	740	760		Chr-7	156849279	156849279	Chr-7	156849279	156849279	21	2.7	96.00	25	
[A] [S] [G] [C]	1212	1231		Chr-7	62162973	62162973	Chr-7	62162973	62162973	21	3.2	96.00	25	
[A] [S] [G] [C]	877	897		Chr-7	154988882	154988882	Chr-7	154988882	154988882	21	3.3	100.00	21	
[A] [S] [G] [C]	887	9		Chr-7	243694404	243694404	Chr-7	243694404	243694404	21	3.3	96.00	25	
[A] [S] [G] [C]	2814	2827		Chr-7	43166599	43166599	Chr-7	43166599	43166599	21	3.3	100.00	21	
[A] [S] [G] [C]	1454	1491		Chr-7	86415907	86415907	Chr-7	86415907	86415907	21	3.3	96.00	25	
[A] [S] [G] [C]	423	443		Chr-7	69322913	69322913	Chr-7	69322913	69322913	21	3.3	100.00	21	
[A] [S] [G] [C]	1906	1926		Chr-3	47263909	47263929	Chr-3	47263909	47263929	21	3.5	100.00	21	
[A] [S] [G] [C]	877	897		Chr-1	45147216	45147256	Chr-1	45147216	45147256	21	4.1	100.00	21	
[A] [S] [G] [C]	899	910		Chr-4	1010012	1010051	Chr-4	1010012	1010051	20	0.074	100.00	20	
[A] [S] [G] [C]	565	582		Chr-1	23045906	23045925	Chr-1	23045906	23045925	20	2.6	100.00	20	
[A] [S] [G] [C]	875	897		Chr-12	2245254	2245277	Chr-12	2245254	2245277	20	2.0	95.83	24	
[A] [S] [G] [C]	1072	1094		Chr-11	2404836	2404859	Chr-11	2404836	2404859	20	3.1	95.83	24	
[A] [S] [G] [C]	2235	2254		Chr-2	55009141	55009160	Chr-2	55009141	55009160	20	3.2	100.00	20	
[A] [S] [G] [C]	875	896		Chr-1	18119374	18119397	Chr-1	18119374	18119397	20	3.4	95.83	24	
[A] [S] [G] [C]	009	020		Chr-17	21163754	21163755	Chr-17	21163754	21163755	20	4.0	100.00	20	
[A] [S] [G] [C]	878	897		Chr-2	45261275	45261294	Chr-2	45261275	45261294	20	4.1	100.00	20	
[A] [S] [G] [C]	881	897		Chr-1	18608381	18608399	Chr-1	18608381	18608399	19	0.19	100.00	19	
[A] [S] [G] [C]	1768	1797		Chr-1	18656691	18656720	Chr-1	18656691	18656720	19	0.19	90.32	31	
[A] [S] [G] [C]	1741	1770		Chr-10	43140401	43140430	Chr-10	43140401	43140430	19	1.2	90.32	31	
[A] [S] [G] [C]	418	436		Chr-20	44598942	44598960	Chr-20	44598942	44598960	19	2.4	100.00	19	
[A] [S] [G] [C]	2209	2227		Chr-14	46044909	46044927	Chr-14	46044909	46044927	19	3.2	100.00	19	
[A] [S] [G] [C]	2804	2822		Chr-3	12983491	12983509	Chr-3	12983491	12983509	19	4.3	100.00	19	
[A] [S] [G] [C]	881	899		Chr-14	104884074	104884092	Chr-14	104884074	104884092	19	5.3	100.00	19	
[A] [S] [G] [C]	881	899		Chr-14	104884028	104884046	Chr-14	104884028	104884046	19	5.3	100.00	19	
[A] [S] [G] [C]	881	899		Chr-14	104883982	104884000	Chr-14	104883982	104884000	19	5.3	100.00	19	
[A] [S] [G] [C]	69	86		Chr-7	100155741	100155758	Chr-7	100155741	100155758	18	0	100.00	18	
[A] [S] [G] [C]	1905	1922		Chr-X	70306710	70306727	Chr-X	70306710	70306727	18	0.70	100.00	18	
[A] [S] [G] [C]	1700	1720		Chr-X	70306710	70306727	Chr-X	70306710	70306727	18	3.9	100.00	18	
[A] [S] [G] [C]	2306	2325		Chr-1	70247948	70247969	Chr-1	70247948	70247969	18	3.9	95.45	22	
[A] [S] [G] [C]	1801	1818		Chr-1	150284632	150284649	Chr-1	150284632	150284649	18	6.0	100.00	18	
[A] [S] [G] [C]	74	90		Chr-2	73022513	73022530	Chr-2	73022513	73022530	18	9.3	100.00	18	
[A] [S] [G] [C]	883	899		Chr-2	29024027	29024043	Chr-2	29024027	29024043	17	0.25	100.00	17	
[A] [S] [G] [C]	801	817		Chr-X	39611091	39611107	Chr-X	39611091	39611107	17	0.70	100.00	17	
[A] [S] [G] [C]	801	817		Chr-1	20541390	20541406	Chr-1	20541390	20541406	17	1.1	100.00	17	
[A] [S] [G] [C]	1798	1814		Chr-1	20511096	20511112	Chr-1	20511096	20511112	17	1.1	100.00	17	
[A] [S] [G] [C]	1407	1503		Chr-10	43031647	43031663	Chr-10	43031647	43031663	17	1.2	100.00	17	
[A] [S] [G] [C]	2100	2119		Chr-14	104633755	104633775	Chr-14	104633755	104633775	17	1.8	95.24	21	
[A] [S] [G] [C]	1564	1580		Chr-9	139178048	139178056	Chr-9	139178048	139178056	17	2.2	100.00	17	
[A] [S] [G] [C]	883	899		Chr-9	139163518	139163534	Chr-9	139163518	139163534	17	2.2	100.00	17	
[A] [S] [G] [C]	2805	2825		Chr-14	46020025	46020044	Chr-14	46020025	46020044	17	3.2	95.24	21	
[A] [S] [G] [C]	1577	1593		Chr-16	88233355	88233371	Chr-16	88233355	88233371	17	3.5	100.00	17	
[A] [S] [G] [C]	1613	1629		Chr-19	47367644	47367660	Chr-19	47367644	47367660	17	5.4	100.00	17	
[A] [S] [G] [C]	1805	1821		Chr-1	150273546	150273562	Chr-1	150273546	150273562	17	6.0	100.00	17	
[A] [S] [G] [C]	257	276		Chr-6	54166916	54166936	Chr-6	54166916	54166936	17	7.0	95.24	21	

STEP 28:
Click on [C] in front of best hit

Back in the contigview page...

☐ Detailed view



END of the
Worked Example