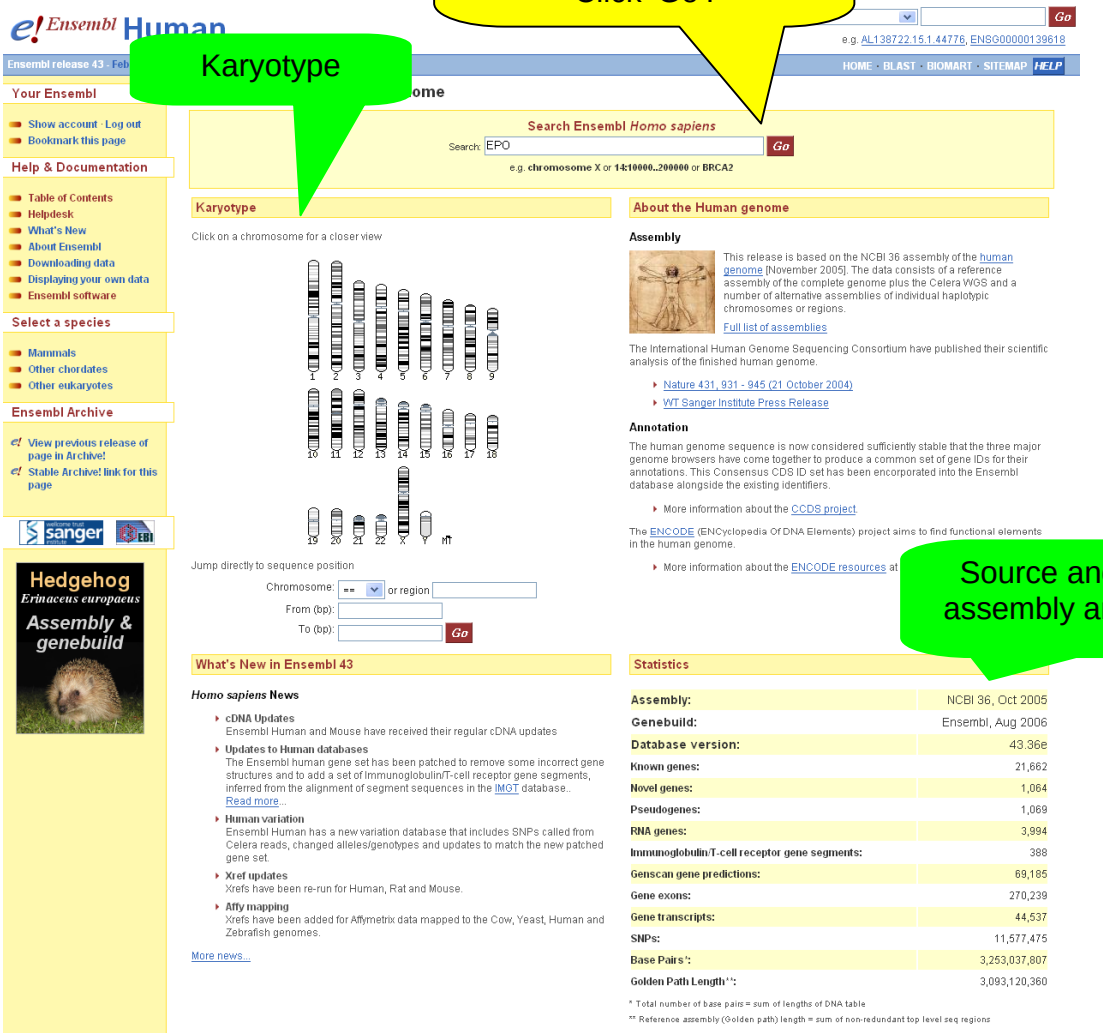
WORKED EXAMPLE – A walk through the main pages of the Ensembl browser, using the EPO (Erythropoietin precursor) gene as an example.

STEP 1:
Load Ensembl
www.ensembl.org

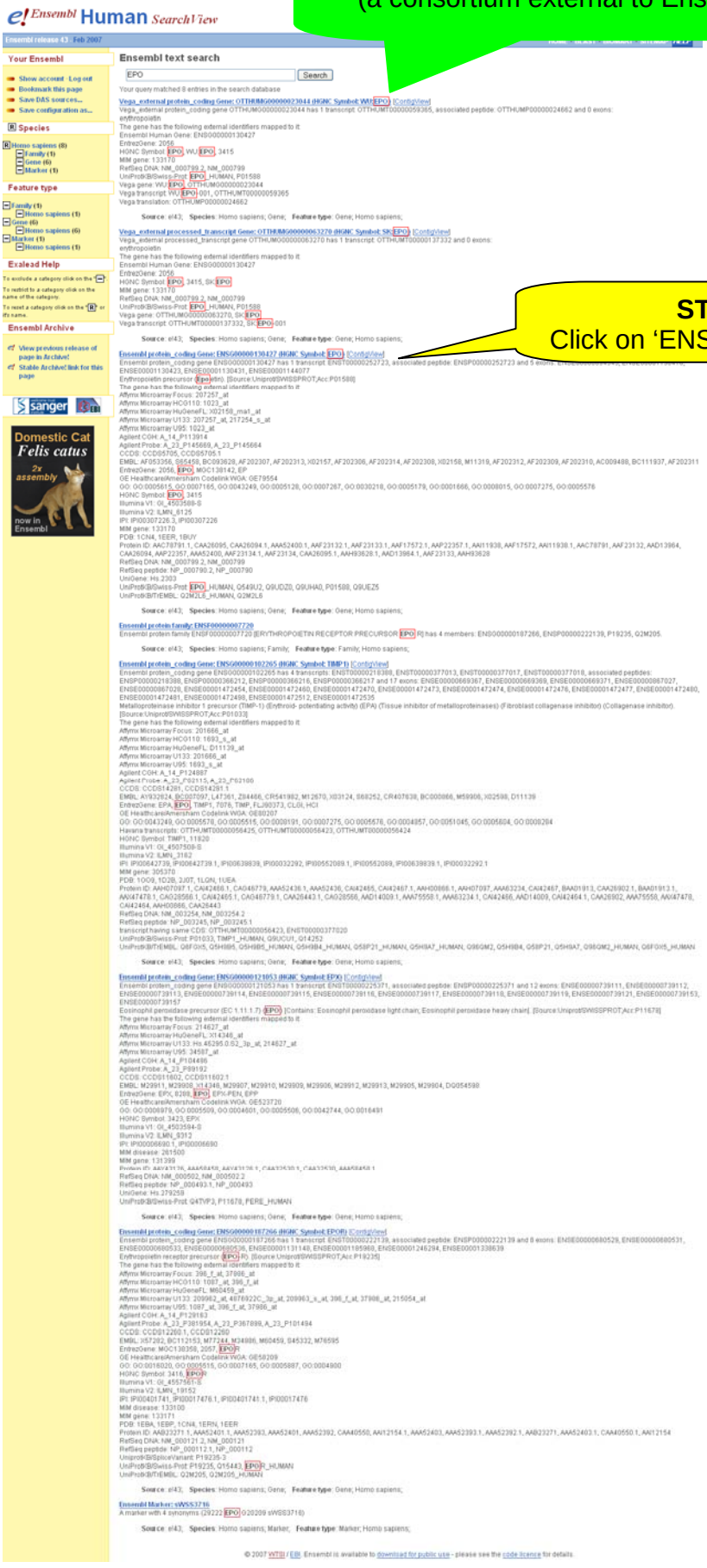
STEP 3:
Type in ‘EPO Gene’.
Click ‘Go’.

Karyotype

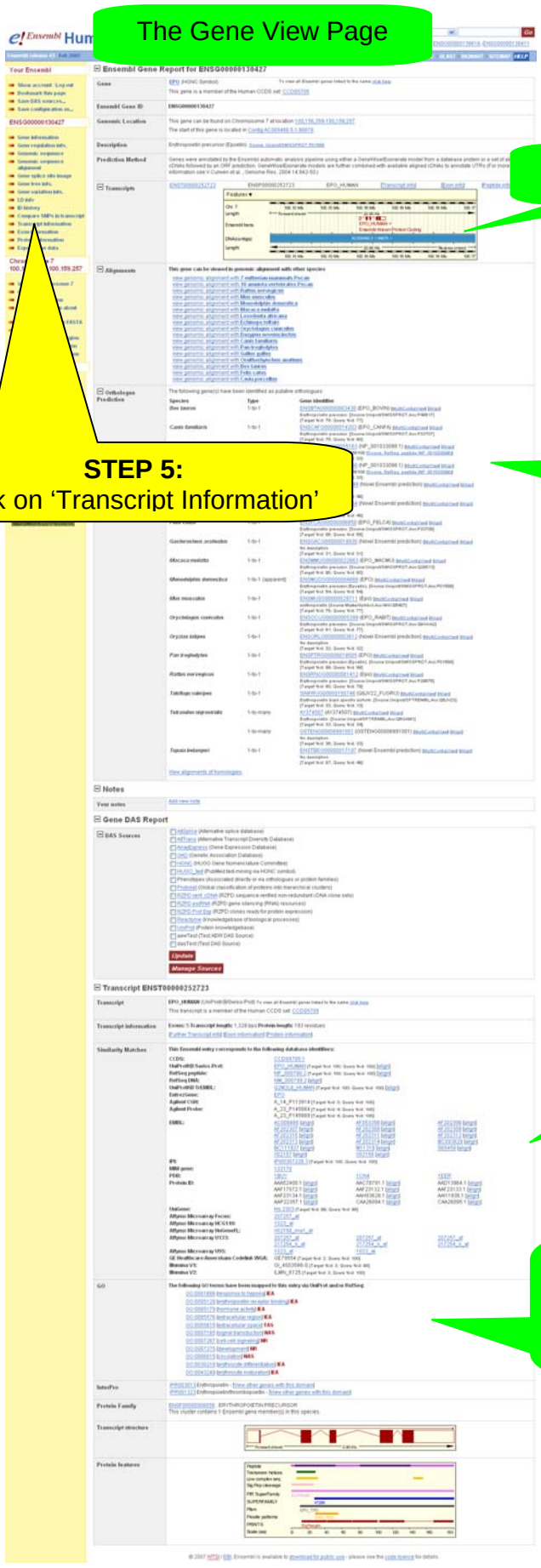
Source and version of assembly and genebuild

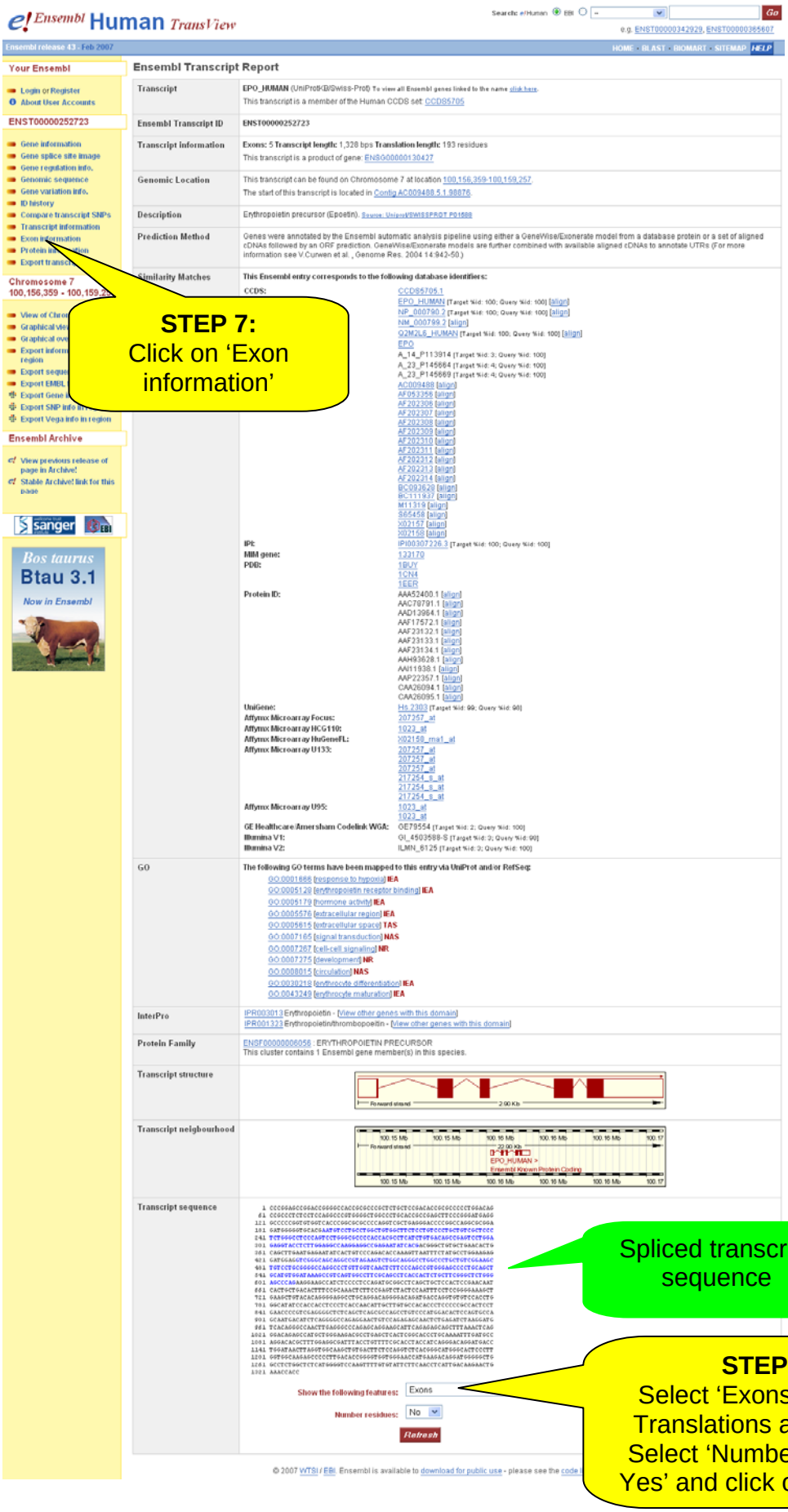


A ‘Vega’ gene
(a consortium external to Ensembl)

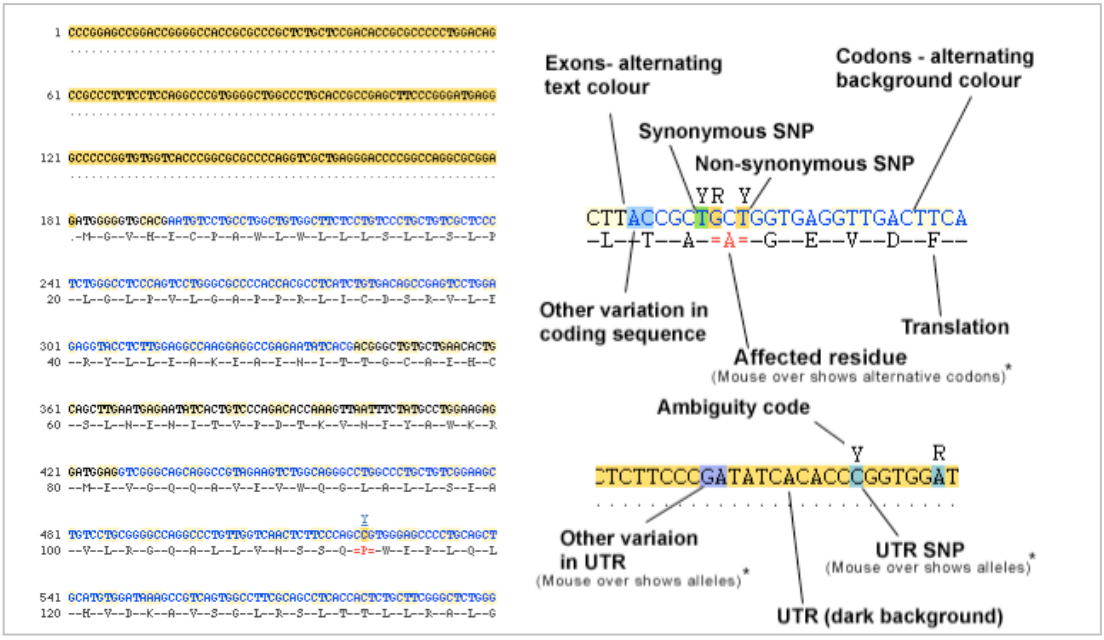


STEP 4:
Click on ‘ENSG00000130427’


The Gene View Page
Gene Model
Orthologues in other species
STEP 5:
Click on 'Transcript Information'
Matches in other databases
GO (Gene Ontology) terms

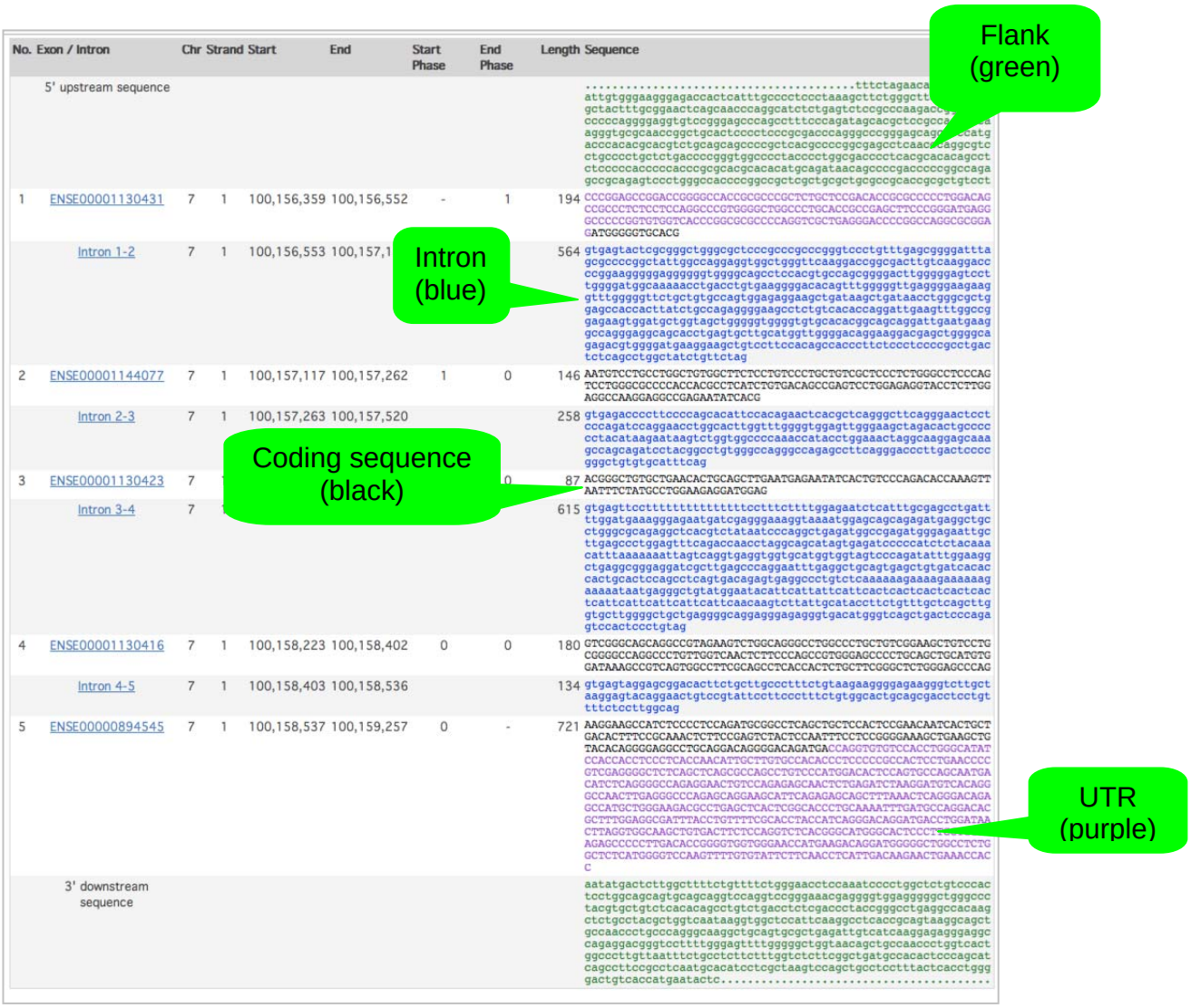

Ensembl Human TransView
Ensembl release 43 - Feb 2007
HOME · BLAST · BIOMART · SITEMAP · HELP
Your Ensembl
Login or Register
About User Accounts
ENST00000252723
Gene information
Gene splice site image
Gene regulation info.
Genomic sequence
Gene variation info.
ID history
Compare transcript SNPs
Transcript information
Exon information
Protein information
Export transcript data
Chromosome 7
100,156,359 - 100,159,257
View of Chromosome
Graphical view
Graphical overview
Export information for region
Export sequence
Export EMBL
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
Bos taurus
Btau 3.1
Now in Ensembl
Ensembl Transcript Report
Transcript
EPO_HUMAN (UniProtKB/Swiss-Prot) To view all Ensembl genes linked to the name click here.
This transcript is a member of the Human CCDS set: CCDS6705
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.
Description
Erythropoietin precursor (Epoetin). Source: UniJoin/SWISSPROT P01588
Prediction Method
Genes were annotated by the Ensembl automatic analysis 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 UTRs (For more information see V.Curwen et al. , Genome Res. 2004 14:942-50.)
Similarity Matches
This Ensembl entry corresponds to the following database identifiers:
CCDS:
CCDS6705.1
EPO_HUMAN [Target %id: 100; Query %id: 100] [align]
NP_000790.2 [Target %id: 100; Query %id: 100] [align]
NM_000799.2 [align]
Q2M2L8_HUMAN [Target %id: 100; Query %id: 100] [align]
EPO
A_14_P113914 [Target %id: 3; Query %id: 100]
A_23_P145664 [Target %id: 4; Query %id: 100]
A_23_P145669 [Target %id: 4; Query %id: 100]
AC009488 [align]
AF053356 [align]
AF202308 [align]
AF202307 [align]
AF202308 [align]
AF202309 [align]
AF202310 [align]
AF202311 [align]
AF202312 [align]
AF202313 [align]
AF202314 [align]
BC093628 [align]
BC111937 [align]
M11319 [align]
S65458 [align]
X02157 [align]
X02158 [align]
IPI:
IPI00307226.3 [Target %id: 100; Query %id: 100]
MIM gene:
133170
PDB:
1BUY
1CN4
1EER
Protein ID:
AAA52400.1 [align]
AAC78791.1 [align]
AAD13964.1 [align]
AAF17572.1 [align]
AAF23132.1 [align]
AAF23133.1 [align]
AAF23134.1 [align]
AAH93628.1 [align]
AAI11938.1 [align]
AAP22357.1 [align]
CAA26094.1 [align]
CAA26095.1 [align]
UniGene:
Hs.2303 [Target %id: 99; Query %id: 98]
Affymetrix Microarray Focus:
207257_at
Affymetrix Microarray HCG110:
1023_at
Affymetrix Microarray HuGeneFL:
X02158_rna1_at
Affymetrix Microarray U133:
207257_at
207257_at
207257_at
217254_s_at
217254_s_at
217254_s_at
Affymetrix Microarray U95:
1023_at
1023_at
GE Healthcare/Amersham Codelink WGA:
GE79554 [Target %id: 2; Query %id: 100]
Illumina V1:
GI_4503588-S [Target %id: 0; Query %id: 99]
Illumina V2:
ILMN_6125 [Target %id: 0; Query %id: 100]
GO
The following GO terms have been mapped to this entry via UniProt and/or RefSeq:
GO:0001666 [response to hypoxia] IEA
GO:0005128 [erythropoietin receptor binding] IEA
GO:0005179 [hormone activity] IEA
GO:0005576 [extracellular region] IEA
GO:0005615 [extracellular space] TAS
GO:0007165 [signal transduction] NAS
GO:0007267 [cell-cell signaling] NR
GO:0007275 [development] NR
GO:0008015 [circulation] NAS
GO:0030218 [erythrocyte differentiation] IEA
GO:0043249 [erythrocyte maturation] IEA
InterPro
IPR003013 Erythropoietin - [View other genes with this domain]
IPR001323 Erythropoietin/thrombopoietin - [View other genes with this domain]
Protein Family
ENSF00000006056 : ERYTHROPOIETIN PRECURSOR
This cluster contains 1 Ensembl gene member(s) in this species.
Transcript structure
Forward strand
2.90 Kb
Transcript neighbourhood
Forward strand
22.90 Kb
EPO_HUMAN >
Ensembl Known Protein Coding
Transcript sequence
Show the following features:
Exons
Number residues:
No
Refresh
© 2007 WTSI / EBI. Ensembl is available to download for public use - please see the code
STEP 7:
Click on 'Exon information'
Spliced transcript sequence
STEP 6:
Select 'Exons, Codons, Translations and SNPs'.
Select 'Number residues: Yes' and click on [Refresh]

Result of STEP 6:



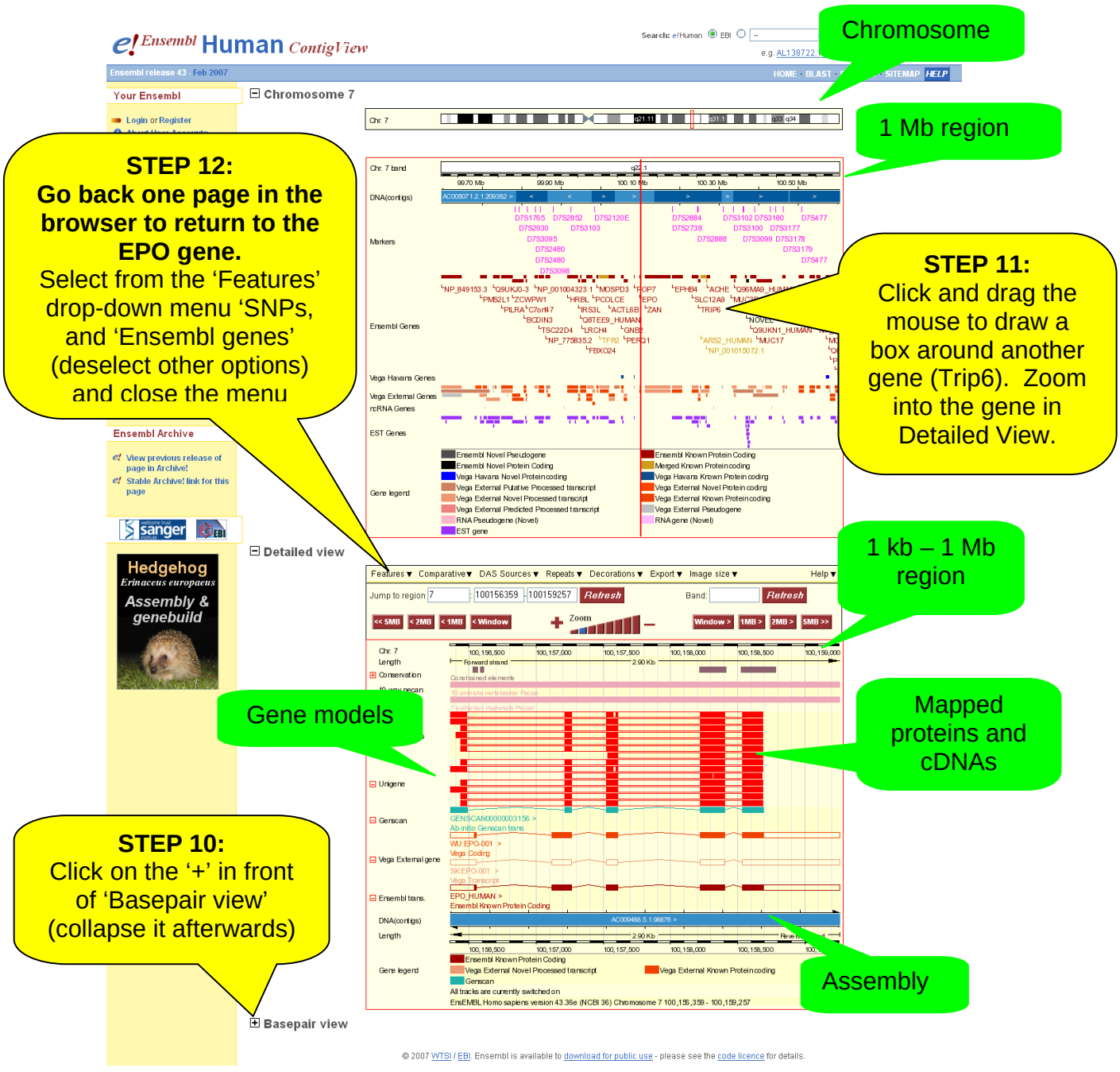
Result of STEP 7:

Result of STEP 8:

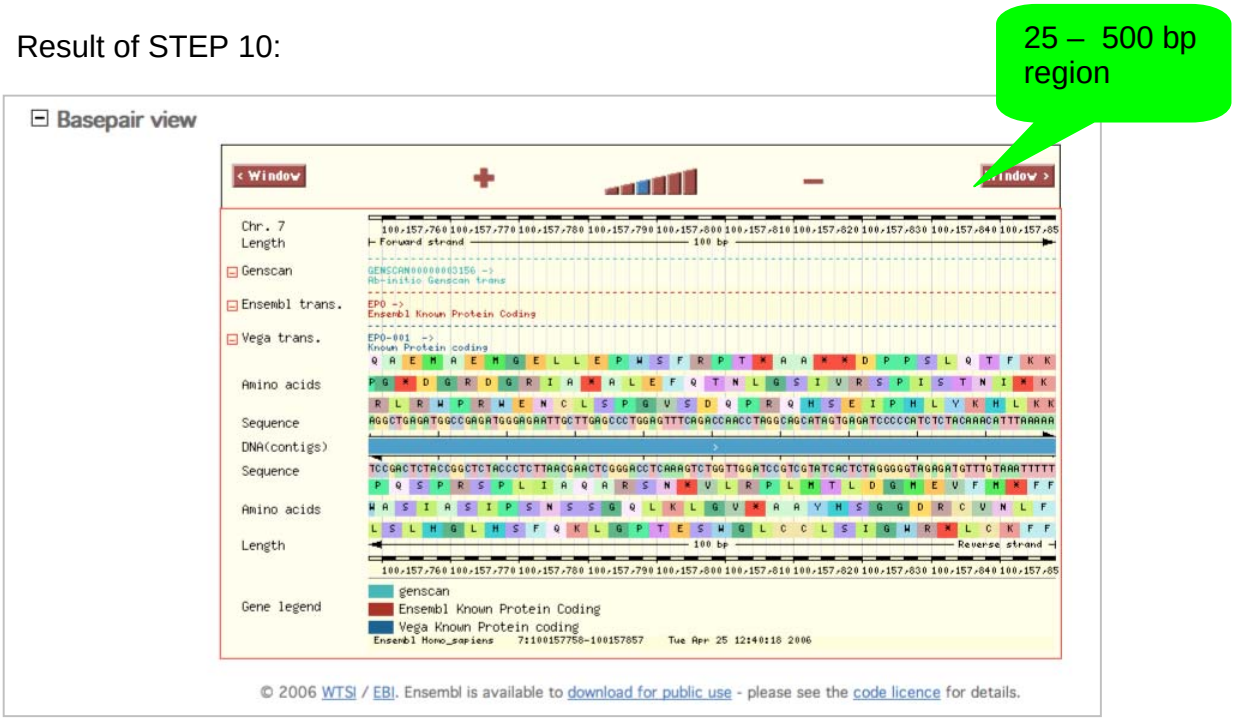


No.	Exon / Intron	Chr	Strand	Start	End	Start Phase	End Phase	Length	Sequence
	5' upstream sequence								.....tttctagaaca attgtgggaagggagaccactcatttgcccctccctaaagcttctgggctt gctactttgcggaactcagcaacccaggcatctctgagtctccgcccaagacc ccccagggggaggtgtccgggagcccagcctttcccagatagcacgctccgcca agggtgcgcaaccggctgcactccctcccgcgacccagggcccgggagcagg acccacacgcacgtctgcagcagccccgctcacgccccggcgagcctcaac ctgcccctgctctgacccccgggtggccctaccctggcgacccctcacgcacacagcct ctccccacccccacccgcgcacgcacacatgcagataacagcccgacccccggccaga gccgcagagtccctgggccacccccggccgctcgctgcgctgcgccgcaccgcgctgtcct
1	ENSE00001130431	7	1	100,156,359	100,156,552	-	1	194	CCCGGAGCCGGACCGGGGCCACCGCCGCCCGCTCTGCTCCGACACCGCGCCCCCCTGGACAG CCGCCCTCTCCTCCAGGCCCGTGGGGCTGGCCCTGCACCGCCGAGCTTCCCGGGATGAGG GCCCCCGGTGTGGTCACCCGGCGCCGCCCCAGGTCGCTGAGGGACCCCGGCCAGGCGCGGA GATGGGGGTGCACG
	Intron 1-2	7	1	100,156,553	100,157,1			564	gtgagtactcgcgggctgggcgctcccgcccgcccgggtccctgtttgagcggggattta gcgccccggctattggccaggaggtggctgggttcaaggaccggcgacttgtcaaggacc ccggaagggggaggggggtggggcagcctccacgtgccagcggggacttgggggagtcct tggggatggcaaaaacctgacctgtgaaggggacacagtttgggggttgagggaagaag gtttgggggttctgctgtgccagtggagaggaagctgataagctgataacctgggcgctg gagccaccacttatctgccagaggggaagcctctgtcacaccaggattgaagtttggccg gagaagtggatgctggtagctgggggtgggtgtgcacacggcagcaggattgaatgaag gccagggaggcagcacctgagtgcttgcatggttggggacaggaaggacgagctgggca gagacgtgggagtgaaggaagctgtccttccacagccacccttctccctccccgcctgac tctcagcctggctatctgttctag
2	ENSE00001144077	7	1	100,157,117	100,157,262	1	0	146	AATGTCCTGCCTGGCTGTGGCTTCTCCTGTCCCTGCTGTCGCTCCCTCTGGGCCTCCCAG TCCTGGGCGCCCCCACCACGCCTCATCTGTGACAGCCGAGTCCTGGAGAGGTACCTCTTGG AGGCCAAGGAGGCCGAGAATATCACG
	Intron 2-3	7	1	100,157,263	100,157,520			258	gtgagaccccttccccagcacattccacagaactcacgctcagggcttcagggaactcct cccagatccaggaacctggcacttggtttggggtggagttgggaagctagacactgcccc cctacataagaataagtctggtggccccaaaccatacctggaaactaggcaaggagcaaa gccagcagatcctacggcctgtgggccagggccagagcctcagggaccctgactcccc gggctgtgtgcatttcag
3	ENSE00001130423	7					0	87	ACGGGCTGTGCTGAACACTGCAGCTTGAATGAGAATATCACTGTCCCAGACACCAAAGTT AATTTCTATGCCTGGAAGAGGATGGAG
	Intron 3-4	7						615	gtgagttcctttttttttttttttccttttcttttggagaatctcatttgcgagcctgatt ttggatgaaagggagaatgatcgagggaaaggtaaaatggagcagcagagatgaggctgc ctgggcgcagaggctcacgtctataatcccaggctgagatggccgagatgggagaattgc ttgagccctggagtttcagaccaacctaggcagcatagtgagatccccccatctctacaaa catttaaaaaaattagtcaggtgaggtggtgcatggtggtagtcccagatatttggaagg ctgaggcgggaggatcgcttgagcccaggaatttgaggctgcagtgagctgtgatcacac cactgcactccagcctcagtgacagagtgaggccctgtctcaaaaaagaaaagaaaaaag aaaaatatgagggctgtatggaatacattcattattcattcactcactcactcactcac tcattcattcattcattcaacaagtcttattgcatacctttctgtttgctcagcttg gtgcttggggctgctgaggggcaggagggagagggtgacatggtcagctgactcccaga gtccactccctgtag
4	ENSE00001130416	7	1	100,158,223	100,158,402	0	0	180	GTCGGGCAGCAGGCCGTAGAAGTCTGGCAGGGCCTGGCCCTGCTGTCGGAAGCTGTCCTG CGGGGCCAGGCCCTGTTGGTCAACTCTTCCCAGCCGTGGGAGCCCCTGCAGCTGCATGTG GATAAAGCCGTCAGTGGCCTTCGCAGCCTCACCACTCTGCTTCGGGCTCTGGGAGCCCAG
	Intron 4-5	7	1	100,158,403	100,158,536			134	gtgagtaggagcggacacttctgcttgcccttctgtaagaagggagaagggtcttgct aaggagtacaggaactgtccgtattccttcccttttctgtggcactgcagcgacctcctgt tttctccttggcag
5	ENSE00000894545	7	1	100,158,537	100,159,257	0	-	721	AAGGAAGCCATCTCCCCTCCAGATGCGGCCTCAGCTGCTCCACTCCGAACAATCACTGCT GACACTTTCCGCAAACTCTTCCGAGTCTACTCCAATTTCCTCCGGGGAAAGCTGAAGCTG TACACAGGGAGGCCTCCAGCACAGGGGACAGATGACCAGGTGTGTCCACCTGGGCATAT CCACCACCTCCCTCACCAACATTGCTTGTGCCACACCCTCCCCCGCCACTCCTGAACCCC GTCGAGGGGCTCTCAGCTCAGCGCCAGCCTGTCCCATGGACACTCCAGTGCCAGCAATGA CATCTCAGGGGCCAGAGGAACTGTCCAGAGAGCAACTCTGAGATCTAAGGATGTCACAGG GCCAACTTGAGGGCCCAGAGCAGGAAGCATTCAGAGAGCAGCTTTAAACTCAGGGACAGA GCCATGCTGGGAAGACGCCTGAGCTCACTCGGCACCCTGCAAAATTTGATGCCAGGACAC GCTTTGGAGGCGATTTACCTGTTTTCGCACCTACCATCAGGGACAGGATGACCTGGATAA CTTAGGTGGCAAGCTGTGACTTCTCCAGGTCTCACGGGCATGGGCACTCCCTTTTTTTTT AGAGCCCCCTTGACACCGGGGTGGTGGGAACCATGAAGACAGGATGGGGGCTGGCCTCTG GCTCTCATGGGGTCCAAGTTTTGTGTATTCTTCAACCTCATTGACAAGAACTGAAACCAC C
	3' downstream sequence								aatatgactcttggcttttctgttttctgggaacctccaaatccgctggctctgtcccac tcctggcagcagtgcagcaggtccaggtccgggaaacgagggtggaggggctgggccc tacgtgctgtctcacacagcctgtctgacctctcgacctaccgggcctgaggccacaag ctctgcctacgctggtcaataaggtggctccattcaaggcctcaccgcagtaaggcagct gccaaccctgcccagggcaaggctgcagtgcgctgagattgtcatcaaggagaggaggc cagaggacgggtcctttgggagttttgggggctggtaacagctgccaaccctggtcact ggccctgttaatttctgcctcttctttggtctcttcggctgatgccacactcccagcat cagccttccgcctcaatgcacatcctcgctaagtccagctgcctccttactcacctggg gactgtcaccatgaatactc.....

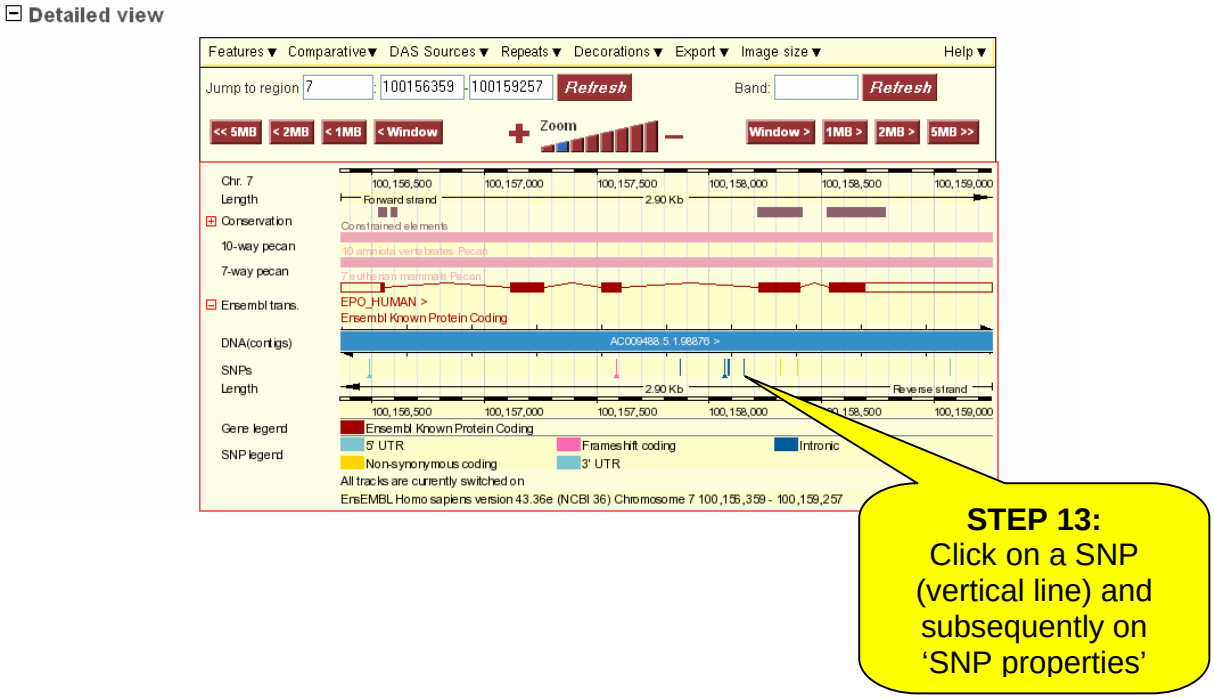
Result of Step 9: *Contigview*



Result of STEP 10:



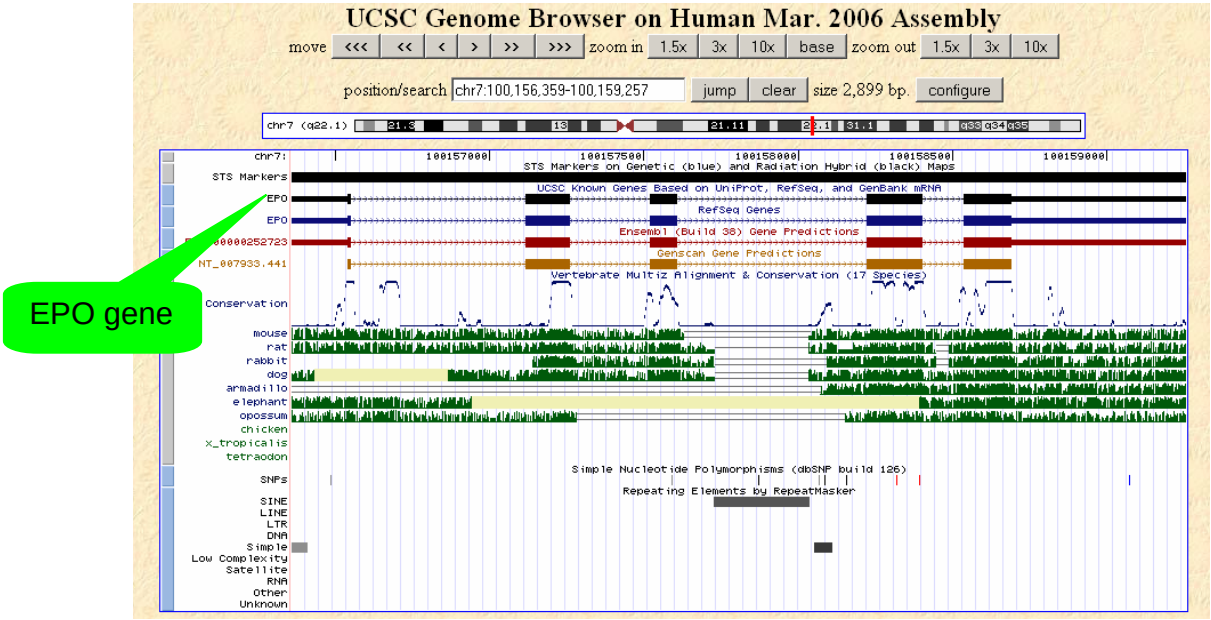
Result of STEP 12:



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

Ensembl Human SNPView
Search: e!Human EBI Go
e.g. rs10264683, rs11571658
Ensembl release 43 : Feb 2007
HOME · BLAST · BIOMART · SITEMAP HELP
dbSNP identifier
rs507392 (dbSNP126)
HGVbase SNP000294357
Alleles
G/A (ambiguity code: R)
Ancestral allele: G
Validation status
Proven by cluster, doublehit (SNP tested
Linkage disequilibrium data
No linkage data for this SNP
Flanking sequence
(SNP highlighted)
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
Allele and genotype frequencies
Population
Alleles A
Alleles G
Description
ABI:Celera_Donors
unknown
unknown
Individual genotypes for SNP rs507392
SNP Context - 7 100157872
Features
Source
SNP class
SNP type
Decorations
Export
Image size
Help
EST trans.
ncRNA
Vega External gene
Vega Havana gene
Ig segments.
Ensembl trans.
No EST transcripts in this region
No ncRNAs in this region
No Vega transcripts in this region
No Ensembl transcripts in this region
Length
Forward strand
20.00 Kb
DNA(contigs)
SNPs
Genotyped SNPs
SNP legend
Downstream
Intergenic
Upstream
5' UTR
Frameshift coding
3' UTR
Non-synonymous coding
100.15 Mb
100.16 Mb
SNP of interest (boxed) and other SNPs in the region
© 2007 WTSI / EBI. Ensembl is available to download for public use - please see t
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.

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

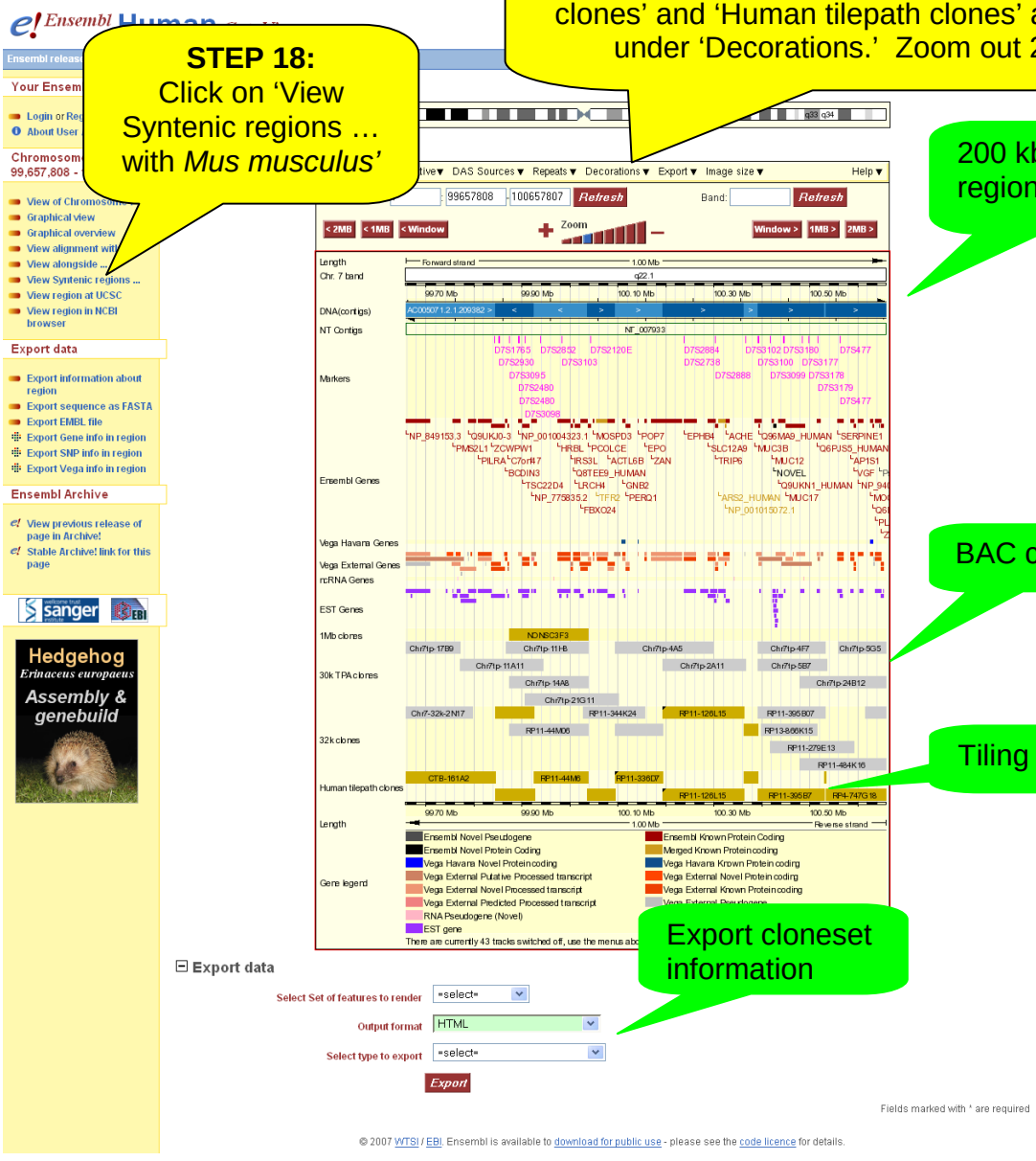
STEP 18:
Click on ‘View Syntenic regions … with *Mus musculus*’

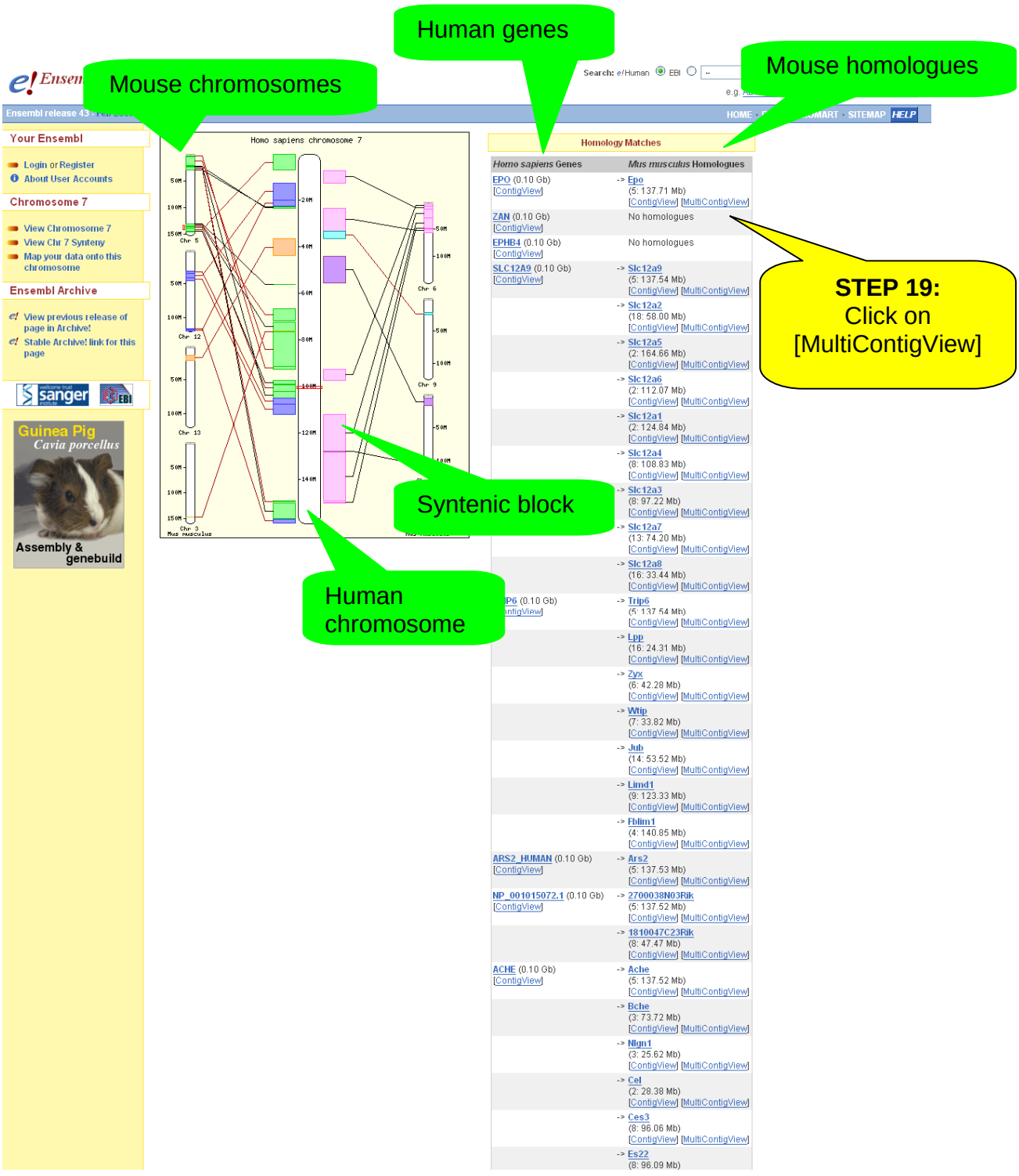
200 kb – 50 Mb region

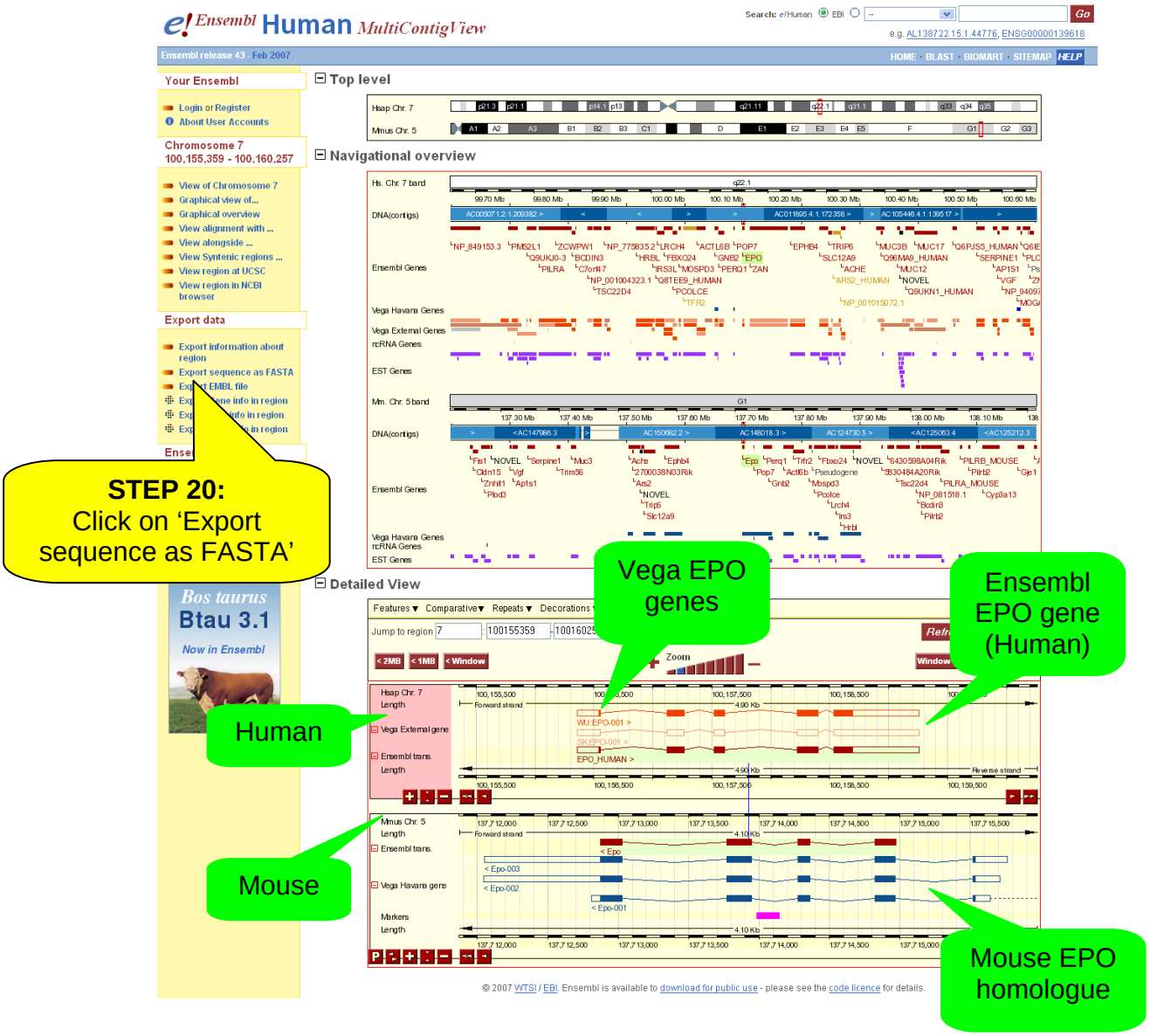
BAC clones

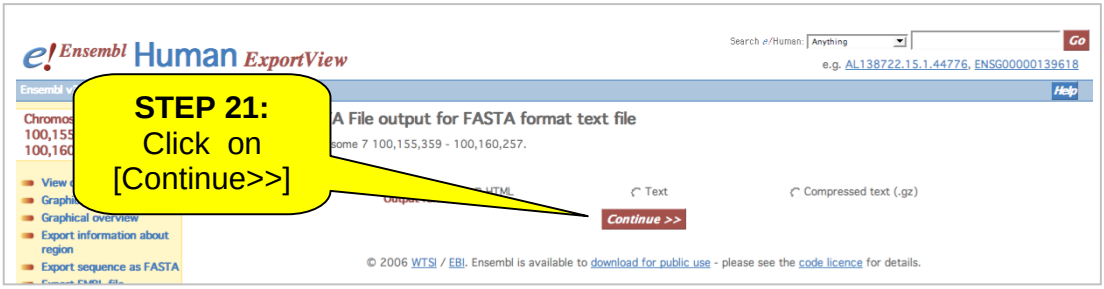
Tiling path clones

Export cloneset information




Human genes
Mouse homologues
Mouse chromosomes
Syntenic block
Human chromosome
Homology Matches
Homo sapiens Genes
Mus musculus Homologues
Homo sapiens chromosome 7
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
EPO (0.10 Gb) [ContigView] -> Epo (5: 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 (18: 58.00 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 (16: 33.44 Mb) [ContigView] [MultiContigView]
-> Trip6 (5: 137.54 Mb) [ContigView] [MultiContigView]
-> Lpp (16: 24.31 Mb) [ContigView] [MultiContigView]
-> Zyx (6: 42.28 Mb) [ContigView] [MultiContigView]
-> Wtip (7: 33.82 Mb) [ContigView] [MultiContigView]
-> Jub (14: 53.52 Mb) [ContigView] [MultiContigView]
-> Limd1 (9: 123.33 Mb) [ContigView] [MultiContigView]
-> Fblim1 (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]
-> 1810047C23Rik (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]
-> Nlgn1 (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]


Ensembl Human MultiContigView
Ensembl release 43 - Feb 2007
HOME · BLAST · BIOMART · SITEMAP HELP
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
Top level
Navigational overview
Detailed View
Bos taurus
Btau 3.1
Now in Ensembl
STEP 20:
Click on 'Export sequence as FASTA'
Vega EPO genes
Ensembl EPO gene (Human)
Human
Mouse
Mouse EPO homologue
© 2007 WTSI / EBI. Ensembl is available to download for public use - please see the code licence for details.


Ensembl Human ExportView
Search e!/Human: Anything Go
e.g. AL138722.15.1.44776, ENSG00000139618
Help
A File output for FASTA format text file
some 7 100,155,359 - 100,160,257.
Text
Compressed text (.gz)
Continue >>
Graphical overview
Export information about region
Export sequence as FASTA
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STEP 21:
Click on [Continue>>]

Ensembl Human ExportView
Search e!/Human: Go
e.g. AL138722.15.1.44776, ENSG00000196160
HOME · BLAST · BIOMART · SITEMAP HELP
STEP 22:
Select and copy a part of the sequence
STEP 23:
Click on 'BLAST'
Your Ensembl
Show account · Log
Save bookmark
Save configuration as...
Chromosome 7
100,155,359 - 100,160,257
View of Chromosome 7
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
Healthchecks
Health checks
Old Health checks
Ensembl Archive
View previous release of page in Archive!
Stable Archive! link for this page
Saccharomyces cerevisiae
Yeast
Revised assembly
You are using the web team's integration server. More →
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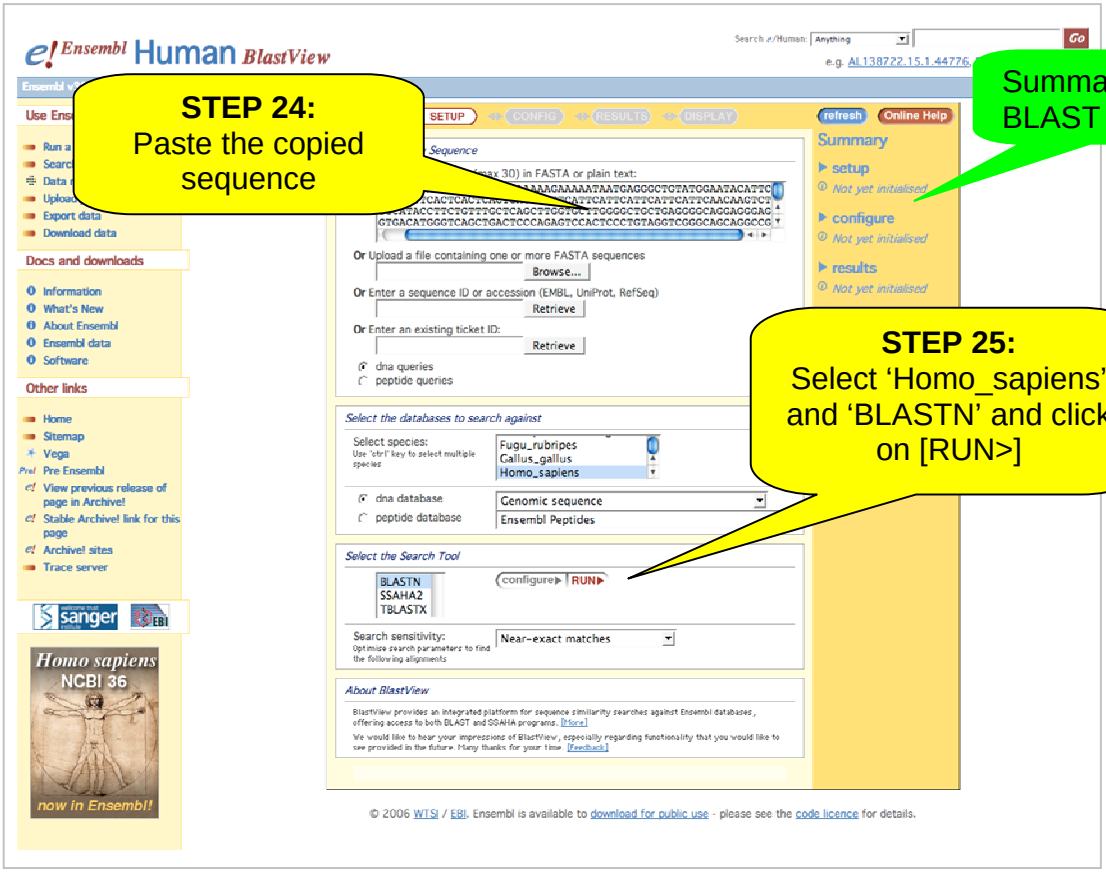
Ensembl Human BlastView
STEP 24:
Paste the copied sequence
Summary of BLAST search
STEP 25:
Select 'Homo_sapiens' and 'BLASTN' and click on [RUN>]
SETUP
CONFIG
RESULTS
DISPLAY
refresh
Online Help
Summary
setup
configure
results
Or Upload a file containing one or more FASTA sequences
Browse...
Or Enter a sequence ID or accession (EMBL, UniProt, RefSeq)
Retrieve
Or Enter an existing ticket ID:
dna queries
peptide queries
Select the databases to search against
Select species:
Fugu_rubripes
Gallus_gallus
Homo_sapiens
dna database
Genomic sequence
peptide database
Ensembl Peptides
Select the Search Tool
BLASTN
SSAHA2
TBLASTX
configure
RUN
Search sensitivity:
Near-exact matches
About BlastView
Use Ensembl to...
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
Homo sapiens
NCBI 36
now in Ensembl!
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STEP 26:
Click on [Retrieve] to check for results
STEP 27:
Click on [VIEW]
CONFIG
RESULTS
DISPLAY
refresh
Online Help
Summary
setup
Homo_sapiens
Genomic sequence
BLASTN
Low sensitivity
configure
-E: 10
-B: 100
-filter: dust
-RepeatMasker
-W: 15
display
Retrieve result for ID:
BLA_SJJPkRIMNU
Retrieve
Alignment Display Options:
Locations vs. Karyotype
Locations vs. Query
Summary Table
1: unnamed (2880 letters) Vs. LATESTGP
Homo_sapiens
107 alignments, 40 hits
[RawResult]
view
Use Ensembl to...
Docs and downloads
Other links
now in Pre!
Danio rerio
New assembly
WTSI Zv6
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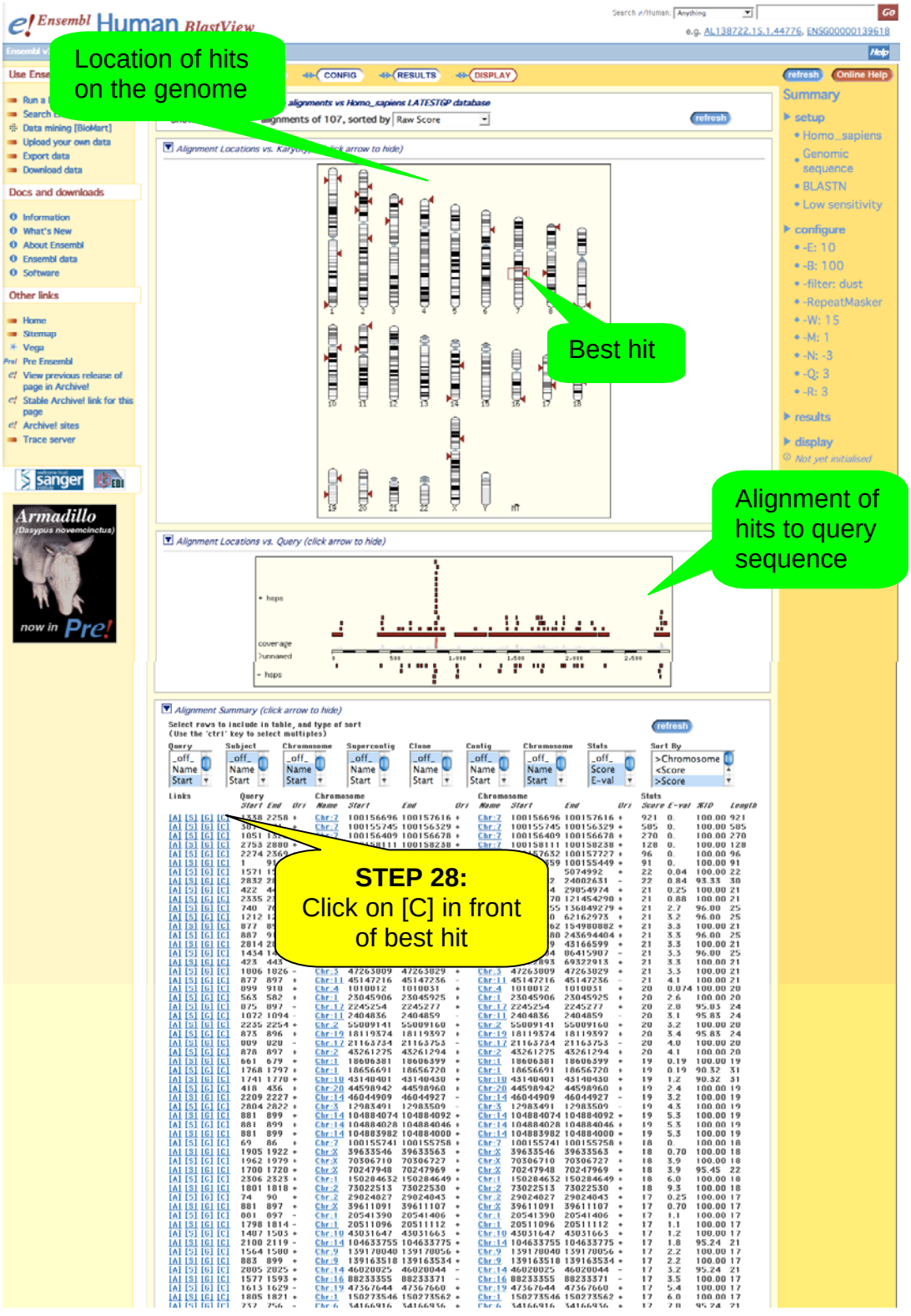
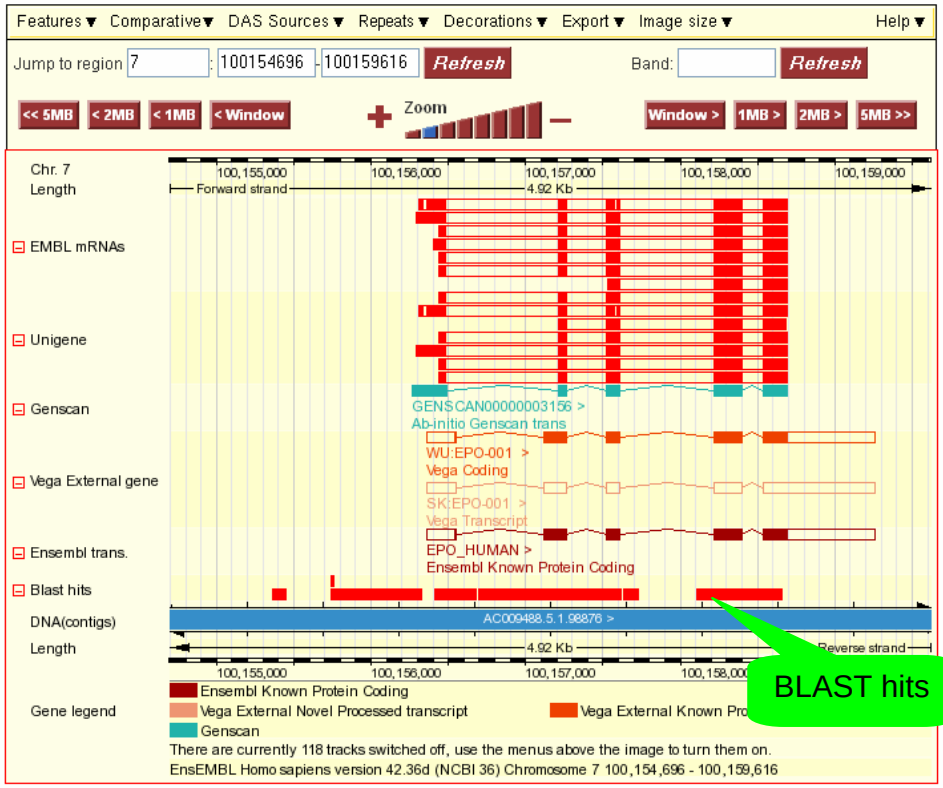

Location of hits on the genome
Best hit
Alignment of hits to query sequence
STEP 28:
Click on [C] in front of best hit

Back in the contigview page…

⊟ **Detailed view**



BLAST hits

END of the Worked Example