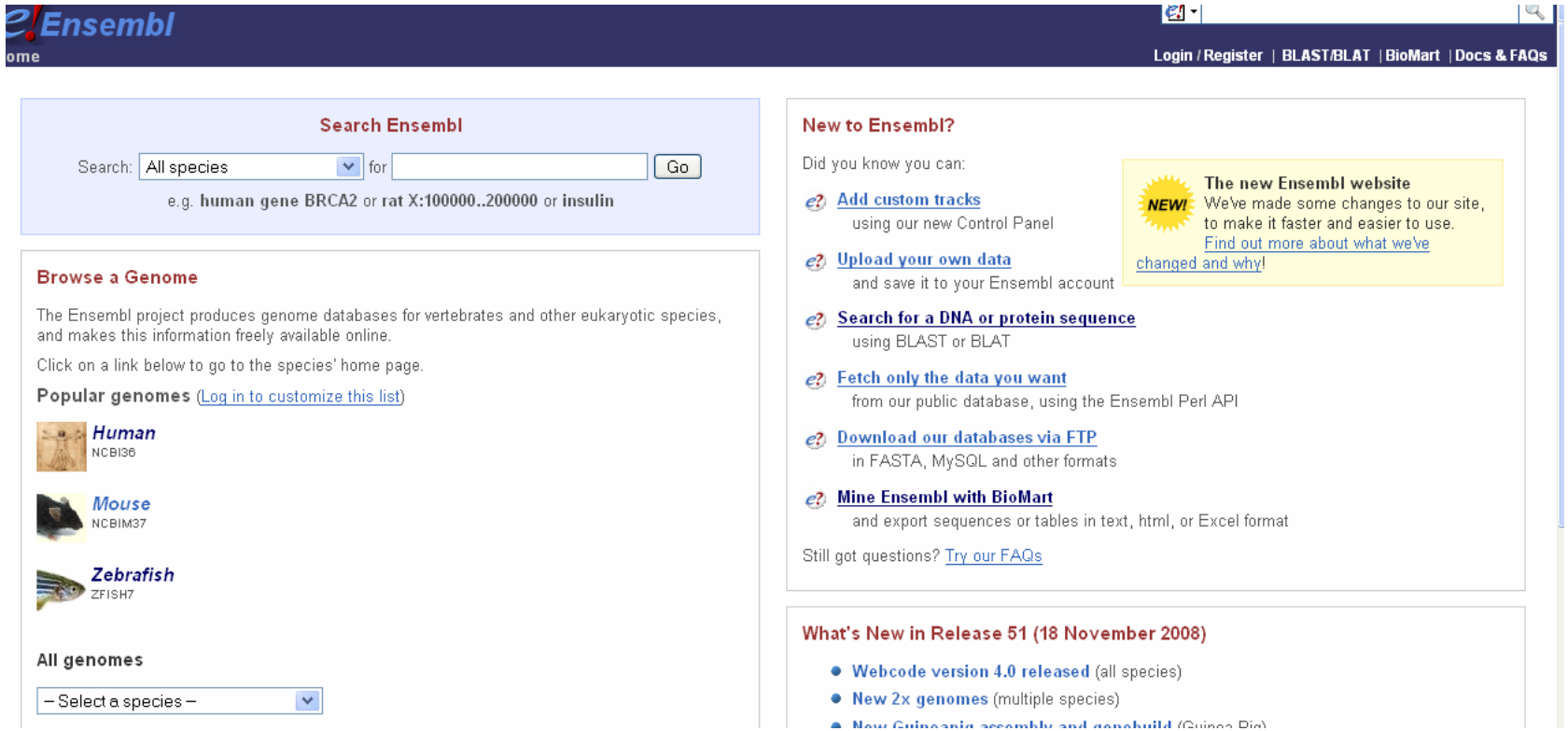
Genomes with Ensembl



Subjects

An introduction to genome browsers.

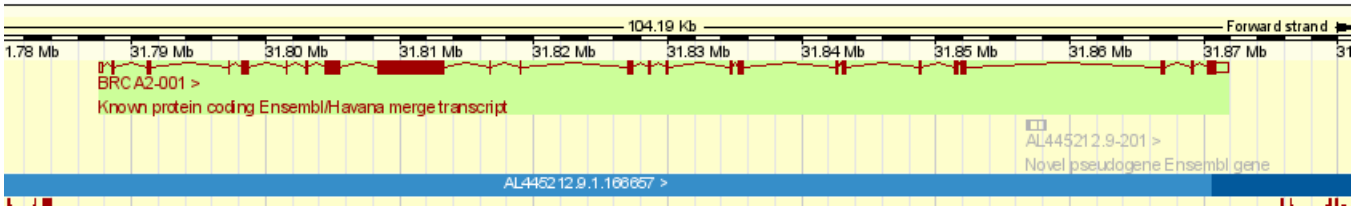
What is an Ensembl gene?

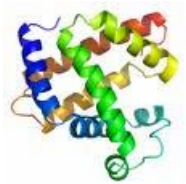
How can we extract data from Ensembl?

Genome Browsers

- Ensembl Genome browser
  http://www.ensembl.org
- NCBI Map Viewer
  http://www.ncbi.nlm.nih.gov/mapview/
- UCSC Genome Browser
  http://genome.ucsc.edu

Ensembl Genome Browser





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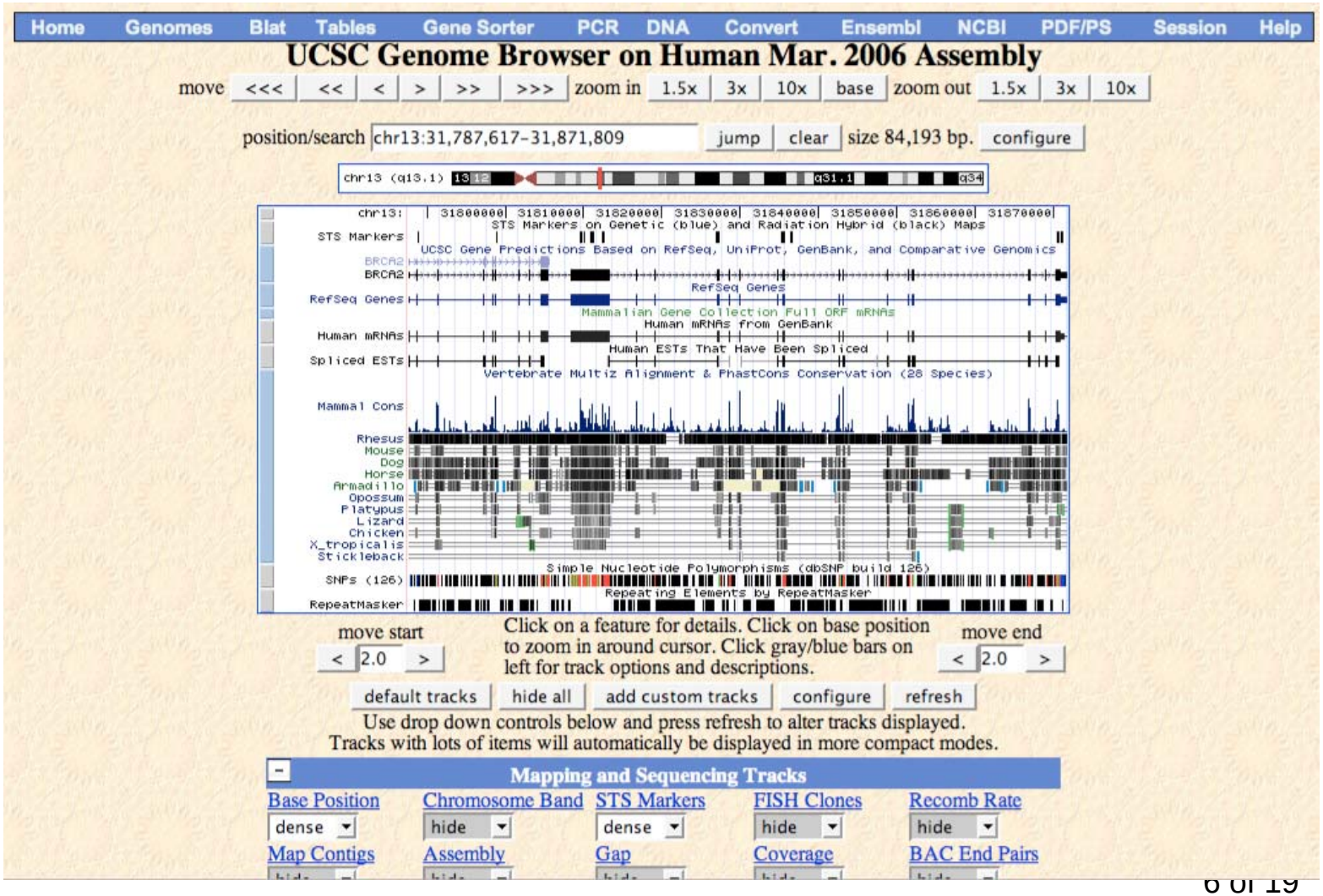
→ **Ensembl Genes**

Protein/ mRNA Sequence Assembly

NCBI Map Viewer

UCSC Genome Browser



To meet a challenge…

Ensembl's AIM: To provide annotation for the biological community that is freely available and of high quality

- **Started in 2000**
- **Joint project between EBI and Sanger**
- **Funded primarily by the Wellcome Trust, additional funding by EMBL, NIH-NIAID, EU, BBSRC and MRC**

What Distinguishes Ensembl from the UCSC and NCBI Browsers?

- The gene set. Automatic annotation based on mRNA and protein information.
- Programmatic access via the Perl API (open source)
- BioMart
- Integration with other databases (DAS)
- Comparative analysis (gene trees)

Ensembl Genes – biological basis

All Ensembl transcripts are based on proteins and mRNAs in:

- **UniProt/Swiss-Prot (*manually curated*)**
- **UniProt/TrEMBL**

www.uniprot.org

- **NCBI RefSeq (*manually curated*)**

www.ncbi.nlm.nih.gov/RefSeq

Ensembl and VEGA/Havana

- **Automatic annotation pipeline: Gene building all at once (whole genome)**

  Ensembl

- **Manual curation: case-by-case basis**

  VEGA: Vertebrate Genome Annotation

  Havana

Genes and Transcripts in Ensembl

- **Ensembl** known **transcripts**
- **Ensembl** novel **transcripts**
- **Ensembl** merged **transcripts (Havana)**

- **EST clusters**

- **More manual curation (SGD, WormBase, FlyBase)**

What annotation is available?

- Gene/transcript/peptide models (coding and noncoding (ncRNAs))
- IDs in other databases
- Mapped cDNAs, peptides, micro array probes, BAC clones etc.
- Other features of the genome:

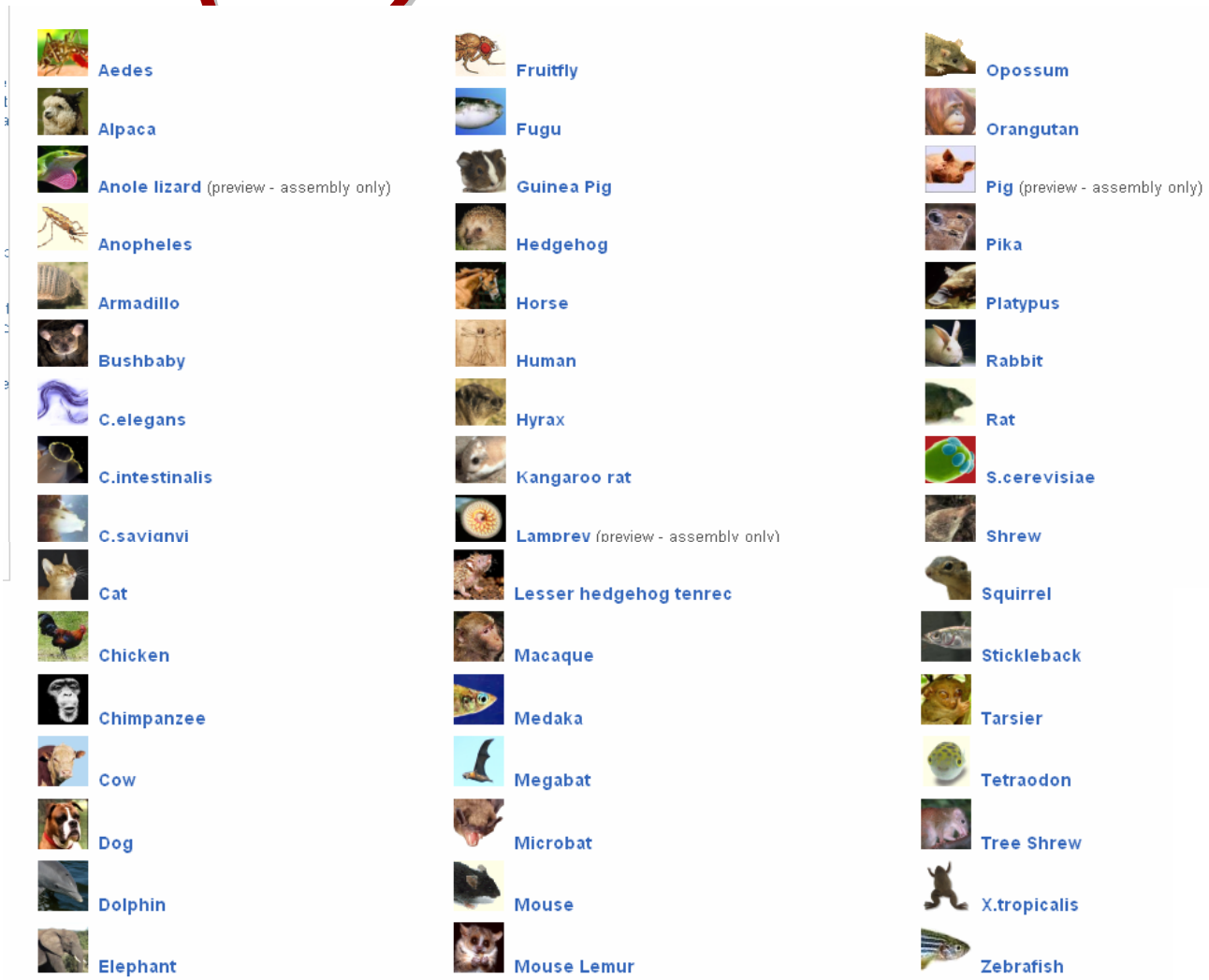
  cytogenetic bands, markers, repeats etc.
- Comparative data:

  orthologues and paralogues, protein families, whole genome alignments, syntenic regions
- Variation data:

  SNPs
- Regulatory data:

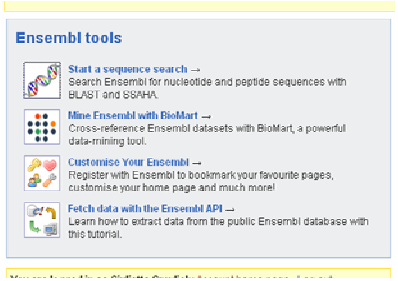
  “best guess” set of regulatory elements from ENCODE
- Data from external sources (DAS)

What species are available (v52)? Chordate focus.



How is this information organised?

- **Ensembl Views (Website)**



- **Ensembl Database (open source)**

- **BioMart 'DataMining tool'**

Names in Ensembl

- **ENSG###** — **Ensembl Gene ID**
- **ENST###** — **Ensembl Transcript ID**
- **ENSP###** — **Ensembl Peptide ID**
- **ENSE###** — **Ensembl Exon ID**

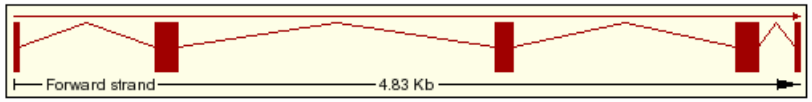
- **For other species than human a suffix is added:**

MUS (*Mus musculus*) for mouse: ENSMUSG###

DAR (*Danio rerio*) for zebrafish: ENSDARG###, etc.

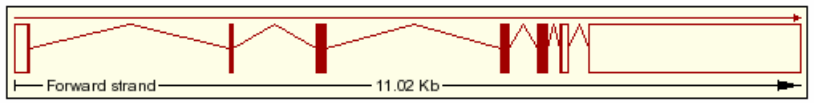
Gene Structure in Ensembl

No UTRs



Calmodulin Chicken

UTRs annotated



Calmodulin Human

Help and Information

- Comments and questions?
  helpdesk@ensembl.org
- View our help videos
- Mailing lists:
  ensembl-dev@ebi.ac.uk
  ensembl-announce@ebi.ac.uk
- Come visit our blog! *http://ensembl.blogspot.com/*

Cambridge

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