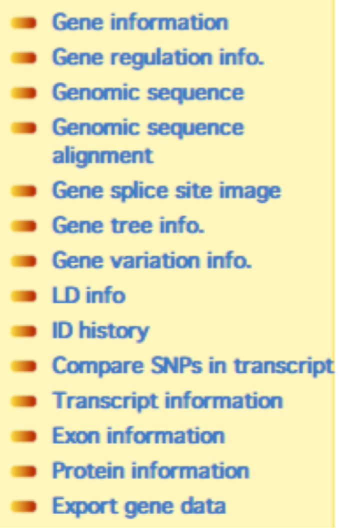
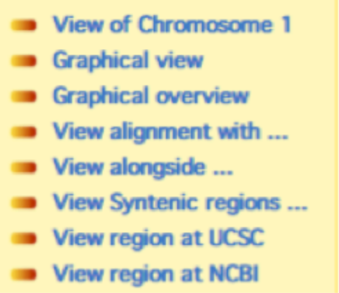
Side menu



Gene information	GeneView
Gene regulation info.	GeneRegulationView
Genomic sequence	GeneSeqView
Genomic sequence alignment	GeneSeqAlignView
Gene splice site image	GeneSpliceView
Gene tree info.	GeneTreeView
Gene variation info.	GeneSNPView
LD info	LDView
ID history	IDHistoryView
Compare SNPs in transcript	TranscriptSNPView
Transcript information	TransView
Exon information	ExonView
Protein information	ProtView
Export gene data	ExportView



View of Chromosome 1	MapView
Graphical view	ContigView
Graphical overview	CytoView
View alignment with ...	AlignSliceView
View alongside ...	MultiContigView
View Syntenic regions ...	SyntenyView
View region at UCSC	UCSC Genome Browser
View region at NCBI	NCBI Map Viewer

Export information about region	ExportView
Export sequence as FASTA	ExportView
Export EMBL file	ExportView
Export Gene info in region	BioMart
Export SNP info in region	BioMart
Export Vega info in region	BioMart

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

Ensembl Views

AlignSliceView: pairwise or multiple genomic alignment for a genomic region
AlignView: alignment for a set of nucleotide or protein sequences
BLASTView: do a BLAST or SSAHA sequence similarity search
ContigView: genome annotation for a 1 bp – 1 Mb region
CytoView: genome annotation for a 200 kb – 50 Mb region
DASConfView: upload your data to the Ensembl DAS server or add your own DAS server
DotterView: dot plot for a conserved block
DomainView: Ensembl genes containing a given InterPro domain
ExonView: exon, intron and flanking sequence and supporting evidence for a transcript
ExportView: export sequence and/or annotation for a feature or region
FamilyView: information for a protein family
FastaView: sequence and associated details for feature external to the Ensembl core databases
FeatureView: locations to which a given feature (e.g. microarray probeset, mRNA, protein) has been mapped
GeneRegulationView: regulatory factors for a gene
GeneSeqAlignView: pairwise or multiple alignment of genomic sequence for a gene
GeneSeqView: genomic sequence for a gene
GeneSNPView: SNPs for a gene
GeneSpliceView: alternative splicing for a gene
GeneTreeView: gene tree with orthologues and paralogues for a gene
GeneView: information for a gene
GOView: information for a GO term, including hierarchy
HelpView: help information for an Ensembl view
HistoryView: retrieve the history for a batch of Ensembl stable IDs
IDHistoryView: history for an Ensembl stable ID
KaryoView: annotate a chromosome or karyotype with your own data
LDTableView: LD values between SNPs in table format
LDView: LD values between SNPs, including the possibility of dumping for upload into Haploview software
MapView: explore a chromosome
MarkerView: information for a marker
MartView: data mine with BioMart
MultiContigView: simultaneous display of genome annotation for multiple species
ProtView: information for a protein, including protein sequence
SearchView: search in Ensembl
SequenceAlignView: alignment of sequences of different individuals / strains
SNPView: information for a SNP
SyntenyView: syntenic regions between species pairs
TranscriptSNPView: comparison of SNPs in individuals / strains / populations for a transcript
TransView: information for a transcript, including spliced transcript sequence

Questions or Problems?

Contact helpdesk@ensembl.org

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Glossary of Terms

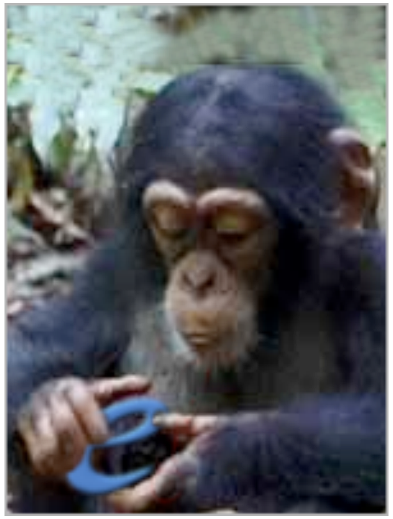
Assembly: the whole of sequenced pieces of DNA of an organism put back together to create a representation of the original chromosomes from which the DNA originated
BLAST: Basic Local Alignment Search Tool, a program that finds sequence similarity
CDS: coding sequence
Contig: a contiguous stretch of DNA sequence without gaps that has been assembled based on direct sequencing information
DAS: Distributed Annotation System, a communication protocol used to exchange biological annotations
EST: expressed sequence tag
Genebuild: the process according to which Ensembl gene predictions are created and annotated
GENSCAN: *ab initio* gene prediction program
GO term: Gene Ontology term; the Gene Ontology Consortium produces an organised hierarchy of terms, used to describe biological processes, cellular components, and molecular functions (see also ‘Databases & Websites)
Havana: Human And Vertebrate Analysis and Annotation; the Havana team is part of the Vega consortium (see ‘Databases and websites’)
Manual annotation: annotation of nucleotide or protein sequences by a human being
NCBI: National Center for Biotechnology Information
SNP: single nucleotide polymorphism
SSAHA: Sequence Search and Alignment by Hashing Algorithm, a program that finds sequence similarity
UCSC: University of California Santa Cruz
UTR: untranslated region

Databases & Websites

CCDS: Consensus CDS database (http://www.ncbi.nlm.nih.gov/CCDS/)
dbSNP: SNP repository at the NCBI (http://www.ncbi.nlm.nih.gov/projects/SNP/)
DAS registration server: registry of available DAS sources (http://www.dasregistry.org)
EMBL-Bank/GenBank/DDBJ: nucleotide sequence repositories (http://www.ebi.ac.uk/embl/)
GO: Gene Ontology database (http://www.ebi.ac.uk/GO/)
HapMap: multi-country effort to identify and catalog genetic similarities and differences in human beings (http://www.hapmap.org/)
InterPro: database of protein families, domains and functional sites (http://www.ebi.ac.uk/interpro/)
NCBI Map Viewer: genome browser of the NCBI (http://www.ncbi.nlm.nih.gov/mapview/)
RefSeq: partially manually curated protein and nucleotide sequence database at the NCBI (http://www.ncbi.nlm.nih.gov/RefSeq/)
UCSC Genome Browser: genome browser of the UCSC (http://genome.ucsc.edu/)
UniProt/Swiss-Prot: manually curated protein sequence database (http://www.ebi.ac.uk/swissprot/)
UniProt/TrEMBL: computer-annotated protein sequence database (http://www.ebi.ac.uk/trembl/)
Vega: Vertebrate Genome Annotation database, containing manually annotated vertebrate genome sequence (http://vega.sanger.ac.uk/)

Quick Reference Guide to the

Ensembl Genome Browser



version 3, August 2007