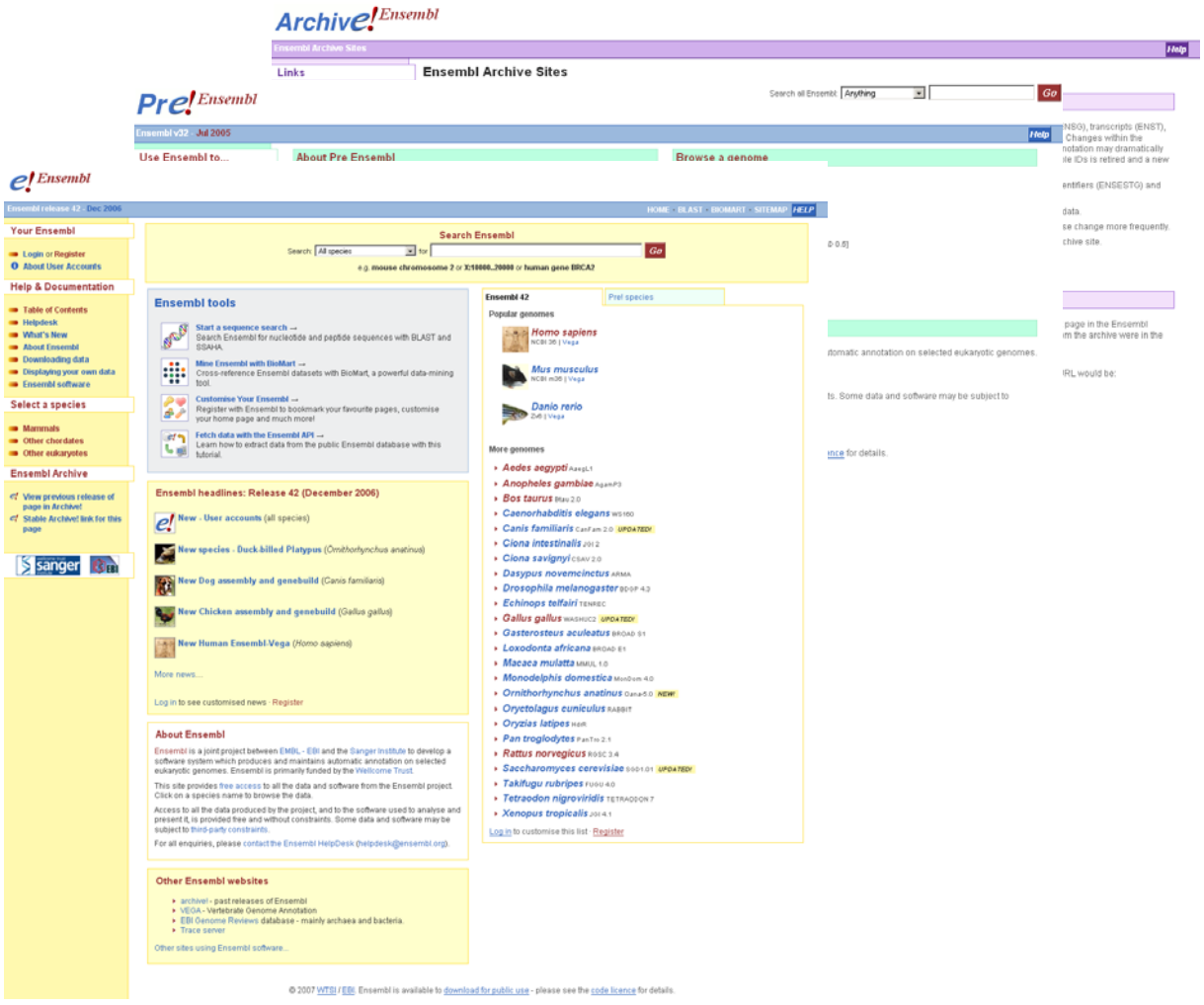
Browsing Genomes with Ensembl



Ensembl - Project

- **Joint project**
  - EMBL – European Bioinformatics Institute (EBI)
  - Wellcome Trust Sanger Institute
- **Produce accurate, automatic genome annotation**
- **Focused on selected eukaryotic genomes**
- **Integrate external (distributed) biological data**
- **Presentation of the analysis to all via the Web at**

  http://www.ensembl.org
- **Open distribution of the analysis the community**
- **Development of open, collaborative software (databases and APIs)**

Beyond classical *ab initio* gene prediction

- Ensembl automatic gene prediction relies on homology 'supporting evidence' to avoid overprediction.
- Classical *ab initio* gene prediction (*eg* *GENSCAN*) relies partly on global statistics of protein coding potentials, not used in the cell
- Genes are just a series of short signals
  - Transcription start site
  - Translation start site
  - 5' & 3' Intron splicing signals
  - Termination signals
- Short signal sequences difficult to recognise over background noise in large genomes

EMBL-EBI

wellcome trust sanger institute

Ensembl

Ensembl 42 | Pre! species

Popular genomes

Rattus norvegicus RGSC 3.4

More genomes

- *Aedes aegypti* AaegL1
- *Anopheles gambiae* AgamP3
- *Bos taurus* Btau 2.0
- *Caenorhabditis elegans* WS160
- *Canis familiaris* CanFam 2.0 *UPDATED!*
- *Ciona intestinalis* JGI 2
- *Ciona savignyi* CSAV 2.0
- *Danio rerio* Zv6
- *Dasypus novemcinctus* ARMA
- *Drosophila melanogaster* BDGP 4.3
- *Echinops telfairi* TENREC
- *Gallus gallus* WASHUC2 *UPDATED!*
- *Gasterosteus aculeatus* BROAD S1
- *Homo sapiens* NCBI 36
- *Loxodonta africana* BROAD E1
- *Macaca mulatta* MMUL 1.0
- *Monodelphis domestica* MonDom 4.0
- *Mus musculus* NCBI m36
- *Ornithorhynchus anatinus* Oana-5.0 *NEW!*
- *Oryctolagus cuniculus* RABBIT
- *Oryzias latipes* HdrR
- *Pan troglodytes* PanTro 2.1
- *Saccharomyces cerevisiae* SGD1.01 *UPDATED!*
- *Takifugu rubripes* FUGU 4.0
- *Tetraodon nigroviridis* TETRAODON 7
- *Xenopus tropicalis* JGI 4.1

Pre! species

Cavia porcellus
cavPor1 *NEW!*

Erinaceus europaeus
eriEur1

Felis catus
CAT

Myotis lucifugus
MICROBAT 1

Otolemur garnettii
BUSHBABY 1

Sorex araneus
sorAra1

Spermophilus tridecemlineatus
speTri1 *NEW!*

Sus scrofa
[clone map]

Tupaia belangeri
tupBel1 *NEW!*

DAS Registry

http://www.dasregistry.org

[home | list services | validate | register new | statistics | help] search

AVAILABLE DAS SERVICES

available DAS services

organism:	authority:	type:	capability:	label:	
any	any	any	any	ENSEMBL	display

id	clients nickname	status	capabilities	coordinateSystem	description
DS_109	uniprot		sequence features	UniProt,Protein Sequence	The UniProt DAS Reference Server serves both sequence and feature data from UniProt/Swiss-Prot and UniProt/TrEMBL. In addition to this, feature links to InterPro for all the proteins in UniProt are provided, including basic information (position, id and a brief description) and internet addresses to the relevant data source. The following kinds of protein ID / Accession number can be used: UniProt Accession numbers e.g. O35502 Swiss-Prot IDs e.g. A4_Human TrEMBL IDs e.g. Q12368 IPI IDs e.g. IPI00015171 UniParc IDs e.g. UPI0000125656 For a full description of the service, visit http://www.ebi.ac.uk/uniprot-das/ go to site
				omo sapiens	ensembl genebuild NCBI36 CDS go to site
				equence	Ensembl exon boundary and snp data projected on UniProt sequence. Based on the COMPARA ENSP-UniProt mapping.
					Associated directly or via orthologues or protein families

EMBL-EBI European Bioinformatics Institute

Get Nucleotide sequences for Go ? Site search Go ?

Site Map EBI Database Queries

EBI Home | About EBI | Groups | Services | Toolbox | Databases | Downloads | Submissions

DATABASE BROWSING TOOLS

UniProt DAS

- UniProt DAS Home
- Access DAS Server
- Download DAS Server
- Contact Us

UniProt DAS Services at the EBI

The distributed annotation system (DAS) is a client-server system in which a single client integrates information from multiple servers. The UniProt DAS server allows researchers to show their research results, for example identified peptides or signal sequences, on the UniProt reference sequence server, in the context of UniProt/Swiss-Prot annotation.

The UniProt Protein DAS Reference Server

- Access the UniProt DAS Server

The UniProt DAS Reference Server serves both sequence and feature data from UniProt/Swiss-Prot and UniProt/TrEMBL. In addition to this, feature links to InterPro for all the proteins in UniProt are provided, including basic information (position, id and a brief description) and internet addresses to the relevant data source.

The server can be queried using any of the following:

- *UniProt Accession numbers e.g. O35502 sequence, features
- *Swiss-Prot ID's e.g. A4_Human sequence, features
- *TrEMBL ID's e.g. Q12368 sequence, features
- IPI ID's e.g. IPI00015171 sequence
- UniParc ID's e.g. UPI0000125656 sequence

All of these kinds of identifier will return sequence information. Identifier types marked with an * will also return UniProt and InterPro feature hits.

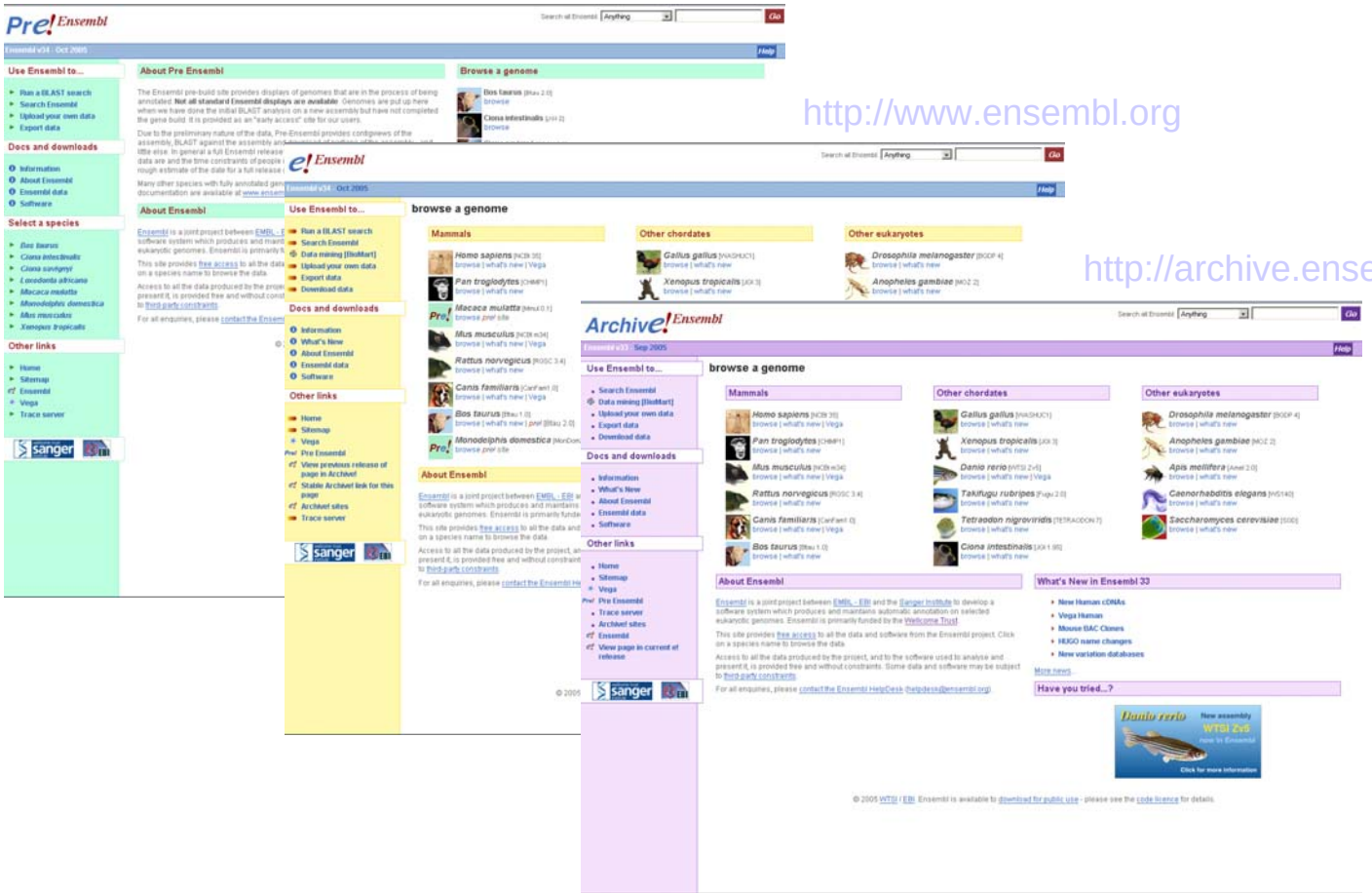
For further details of the UniProt DAS server click on the link above that will take you to the UniProt DAS home page. This includes example requests using the DAS protocol for real proteins that can be found in UniProt.

Pre! and Archive! sites

http://pre.ensembl.org

http://www.ensembl.org

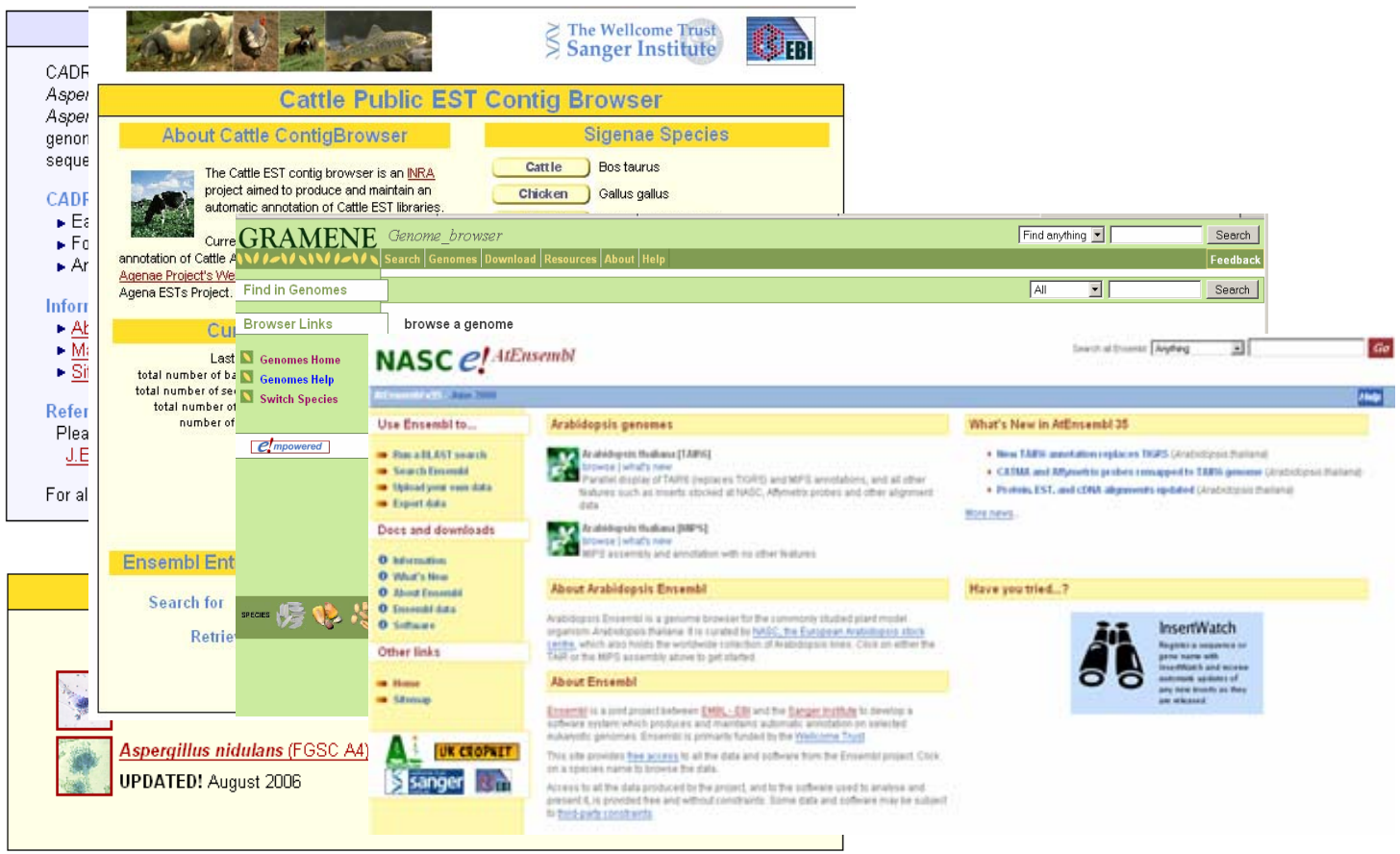
http://archive.ensembl.org



Open source open standards

- Object model
  - **standard interface makes it easy for others to build custom applications on top of Ensembl data**
- Open discussion of design (ensembl-dev@ebi.ac.uk)
- Most major pharma and many academics represented on mailing list and code is being actively developed externally
- Ensembl locally
  - **Both industry & academia**

Ensembl – Open source

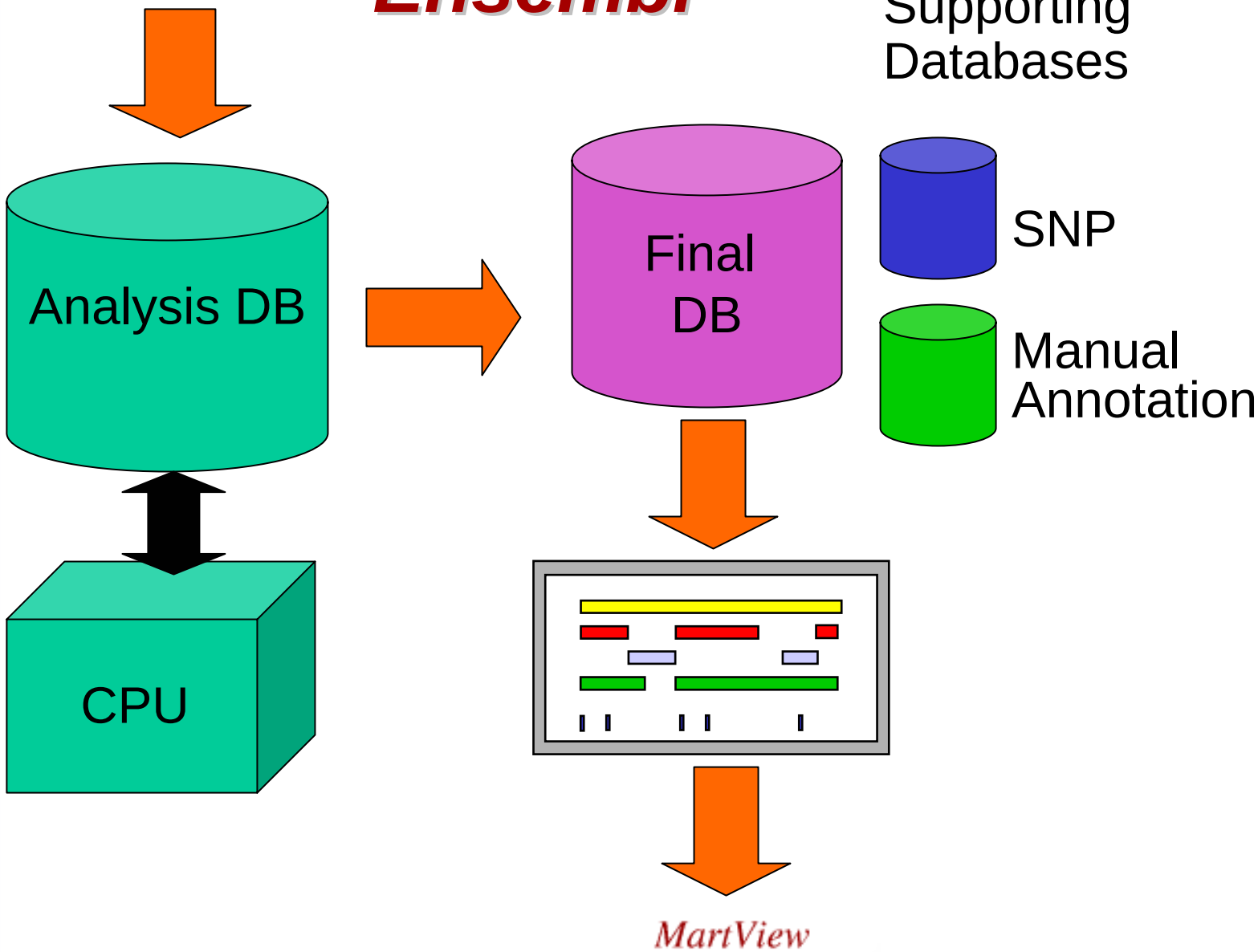


Making genomes useful

- Interpretation
  - Where are the interesting parts of the genome?
  - What do they do?
  - How are they related to elements in other genomes?
- Access
  - for bench biologists
  - for non-programming mid-scale groups
  - for good programming groups

Ensembl

Ensembl



Ensembl

Genome browsing

why present the whole genome?

- Explore what is in a chromosome region
- See features in and around a specific gene
- Search & retrieve across the whole genome
- Investigate genome organization
- Compare to other genomes

Basic Genome Annotation

- **Genes**
  - **Genomic location**
  - **Gene model structures**
    - Exons
    - Introns
    - UTRs
  - **Transcript(s)**
    - Pseudogenes
    - Non-coding RNA
  - **Protein(s)**
  - **Links to other sources of information**

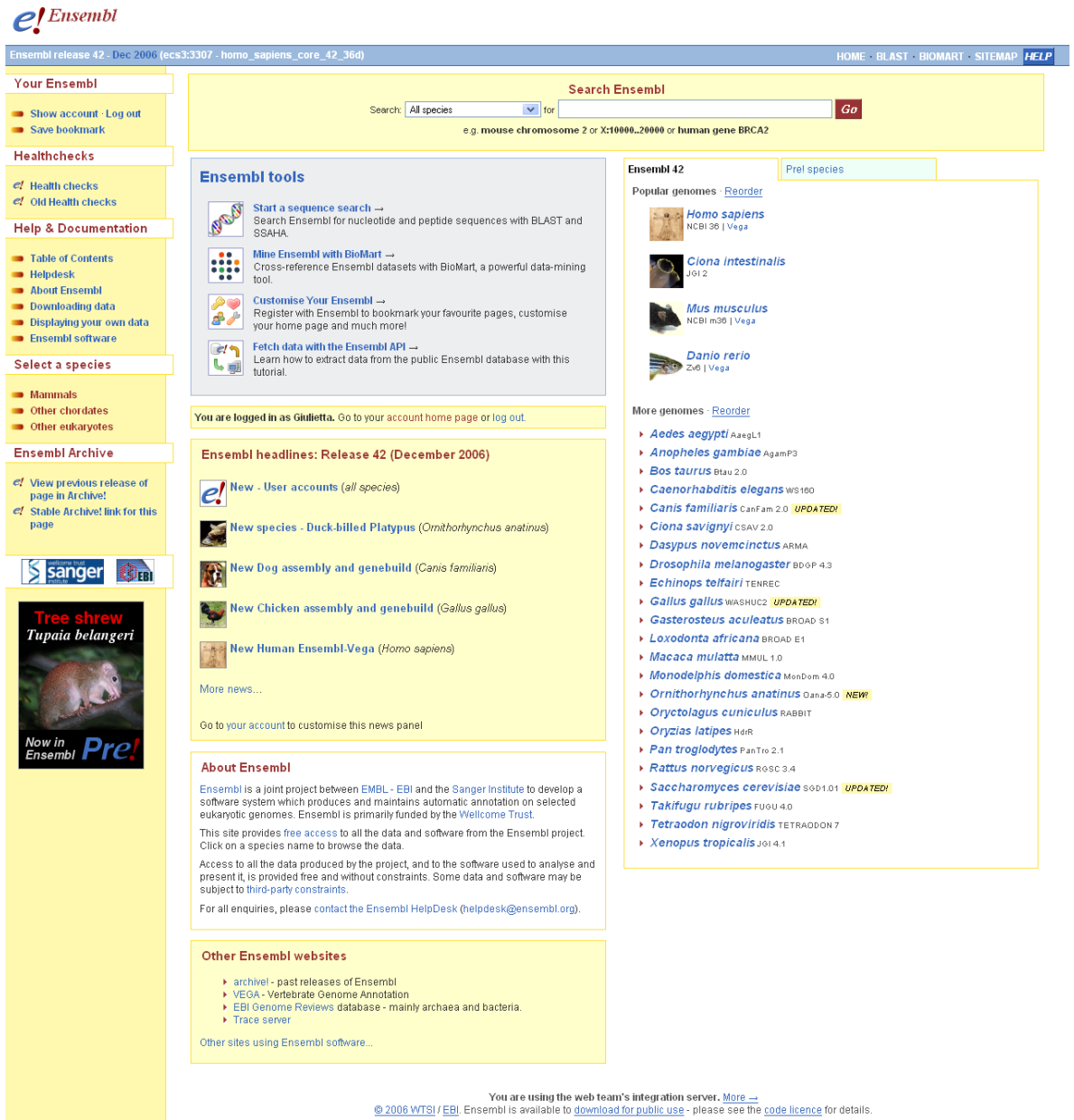
Advanced Genome Annotation

- Cytogenetic bands
- Polymorphic markers
  - Sequence Tagged Sites (STS)
- Genetic variation
  - Single Nucleotide Polymorphisms (SNPs)
  - Deletion-Insertion Polymorphisms (DIPs)
  - Short Tandem Repeats (STRs)
- Repetitive sequences
- Expressed Sequence Tags (ESTs)
- cDNAs or mRNAs from related species
- Regions of sequence homology

How to get started … …

- Species homepage
- Map View
- Text search
- BLAST
- SSAHA

Homepage


Ensembl release 42 - Dec 2006 (ecs3:3307 - homo_sapiens_core_42_36d)
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Now in Ensembl Pre!
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Search: All species for Go
e.g. mouse chromosome 2 or X:10000..20000 or human gene BRCA2
Ensembl tools
Start a sequence search →
Search Ensembl for nucleotide and peptide sequences with BLAST and SSAHA.
Mine Ensembl with BioMart →
Cross-reference Ensembl datasets with BioMart, a powerful data-mining tool.
Customise Your Ensembl →
Register with Ensembl to bookmark your favourite pages, customise your home page and much more!
Fetch data with the Ensembl API →
Learn how to extract data from the public Ensembl database with this tutorial.
You are logged in as Giulietta. Go to your account home page or log out.
Ensembl headlines: Release 42 (December 2006)
New - User accounts (all species)
New species - Duck-billed Platypus (Ornithorhynchus anatinus)
New Dog assembly and genebuild (Canis familiaris)
New Chicken assembly and genebuild (Gallus gallus)
New Human Ensembl-Vega (Homo sapiens)
More news...
Go to your account to customise this news panel
About Ensembl
Ensembl is a joint project between EMBL - EBI and the Sanger Institute to develop a software system which produces and maintains automatic annotation on selected eukaryotic genomes. Ensembl is primarily funded by the Wellcome Trust.
This site provides free access to all the data and software from the Ensembl project. Click on a species name to browse the data.
Access to all the data produced by the project, and to the software used to analyse and present it, is provided free and without constraints. Some data and software may be subject to third-party constraints.
For all enquiries, please contact the Ensembl HelpDesk (helpdesk@ensembl.org).
Other Ensembl websites
archive! - past releases of Ensembl
VEGA - Vertebrate Genome Annotation
EBI Genome Reviews database - mainly archaea and bacteria.
Trace server
Other sites using Ensembl software...
Ensembl 42
Prel species
Popular genomes · Reorder
Homo sapiens NCBI 36 | Vega
Ciona intestinalis JGI 2
Mus musculus NCBI m36 | Vega
Danio rerio Zv6 | Vega
More genomes · Reorder
Aedes aegypti AaegL1
Anopheles gambiae AgamP3
Bos taurus Btau 2.0
Caenorhabditis elegans WS160
Canis familiaris CanFam 2.0 UPDATED!
Ciona savignyi CSAV 2.0
Dasypus novemcinctus ARMA
Drosophila melanogaster BDGP 4.3
Echinops telfairi TENREC
Gallus gallus WASHUC2 UPDATED!
Gasterosteus aculeatus BROAD S1
Loxodonta africana BROAD E1
Macaca mulatta MMUL 1.0
Monodelphis domestica MonDom 4.0
Ornithorhynchus anatinus Oana-5.0 NEW!
Oryctolagus cuniculus RABBIT
Oryzias latipes HdrR
Pan troglodytes PanTro 2.1
Rattus norvegicus RGSC 3.4
Saccharomyces cerevisiae SGD1.01 UPDATED!
Takifugu rubripes FUGU 4.0
Tetraodon nigroviridis TETRAODON 7
Xenopus tropicalis JGI 4.1
You are using the web team's integration server. More →
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MapView

e! Ensembl Human MapView

Search e!Human: Anything Go

e.g. 5, 22

Ensembl v32 - May 2005 Help

Chromosome X

- View Chromosome X
- View Chr X Synteny
- Map your data onto this chromosome
- Browse OMIM diseases

Use Ensembl to...

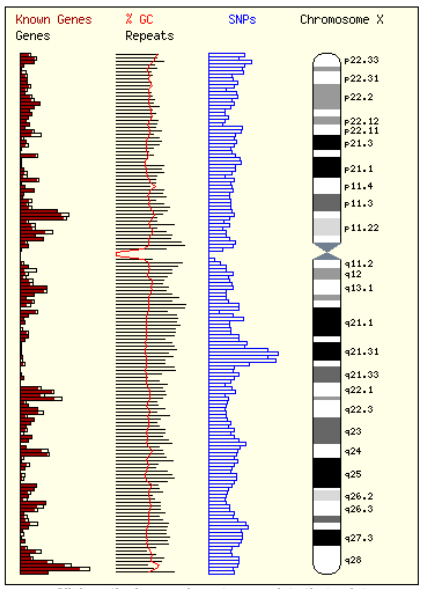
- Run a BLAST search
- Search Ensembl
- Data mining [BioMart]
- Upload your own data
- Download data
- Export data

Docs and downloads

- Information
- About Ensembl
- Using Ensembl data
- Software

Other links

- Home
- Sitemap
- What's New
- Stable (archive) link for this page



Click on the image above to zoom into that point

Chromosome X

Length:	154,824,264	bps
Gene Count:	931	
Known Gene Count:	766	
PseudoGene Count:	380	
SNP Count:	320,997	

Change Chromosome

Chromosome: X

Fields marked with * are required

Jump to ContigView

Choose two features from this chromosome as anchor points and display the region between them. Both features must be mapped to the current Ensembl golden tiling path. If you select "None" for the second feature, the display will be based around the first feature.

Please note that if you select widely spaced features there may be an significant delay while Ensembl builds the DNA display.

Region

From (type): Marker DXS7096 *

To (type): Marker DXS7094

Context

Bp downstream

Bp upstream

Go

Fields marked with * are required

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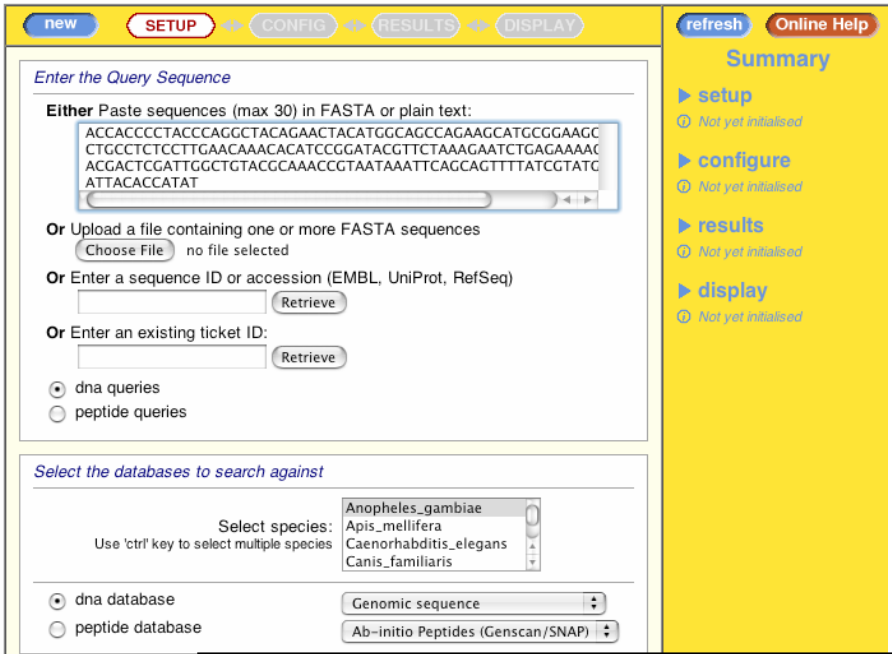
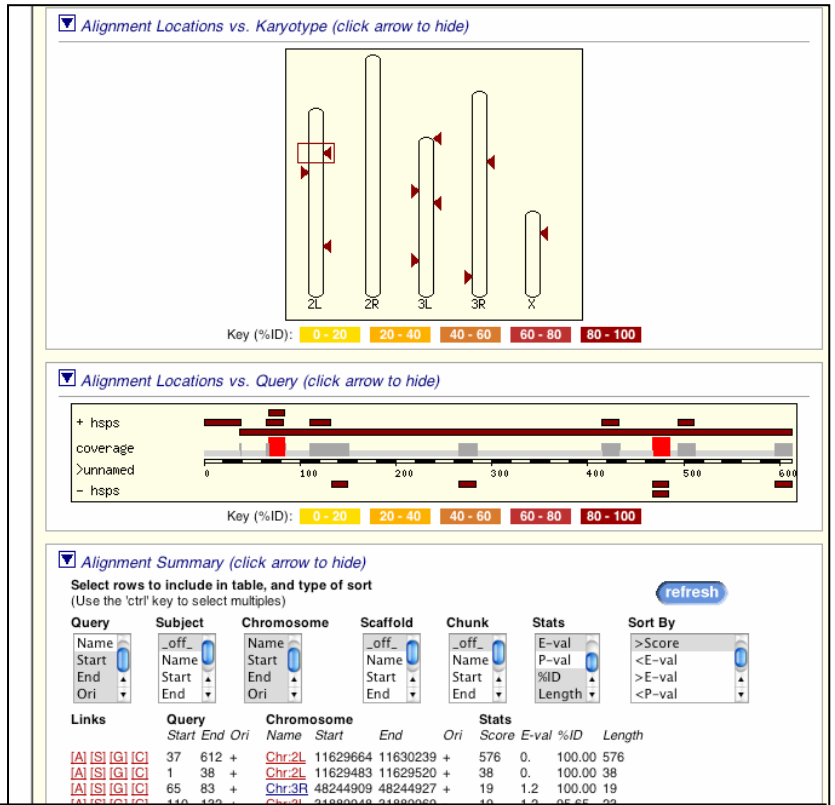
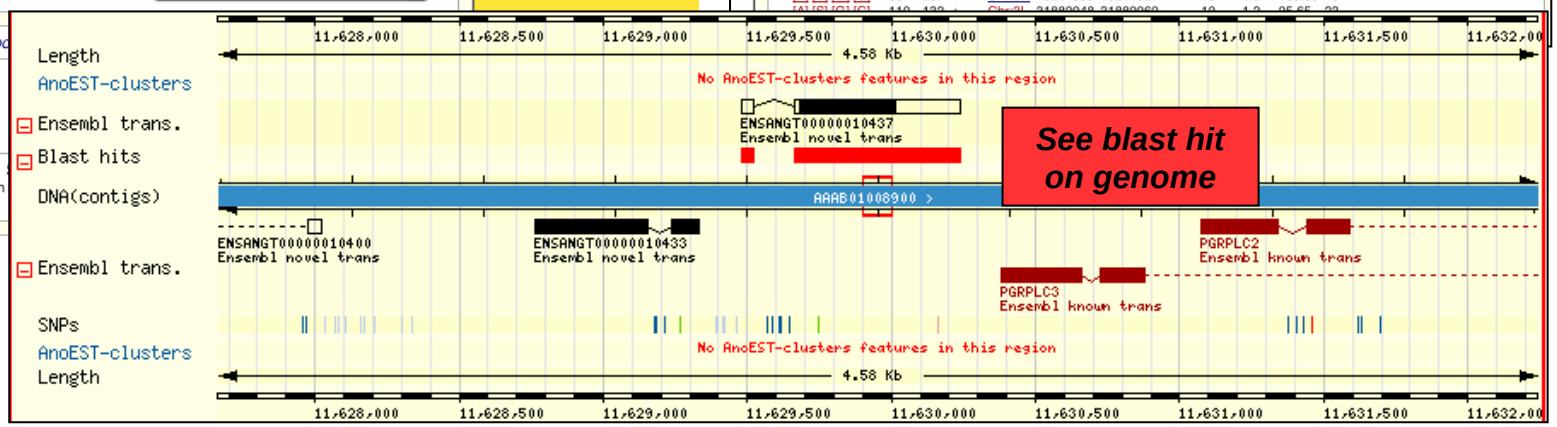
BLAST and SSAHA







Regions, maps and markers

ContigView

CytoView

SyntenyView

MultiContigView

MarkerView

SNPView

GeneSNPView

Chromosome X
138,229,875 - 138,686,223

- View of Chromosome X
- Graphical view
- Graphical overview
- Export sequence as FASTA
- Export EMBL file
- Export Gene info in region
- Export SNP info in region
- Export Vega info in region
- View alongside ...
- View Syntenic regions ...
- View region in NCBI browser
- View region in UCSC browser

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Other links

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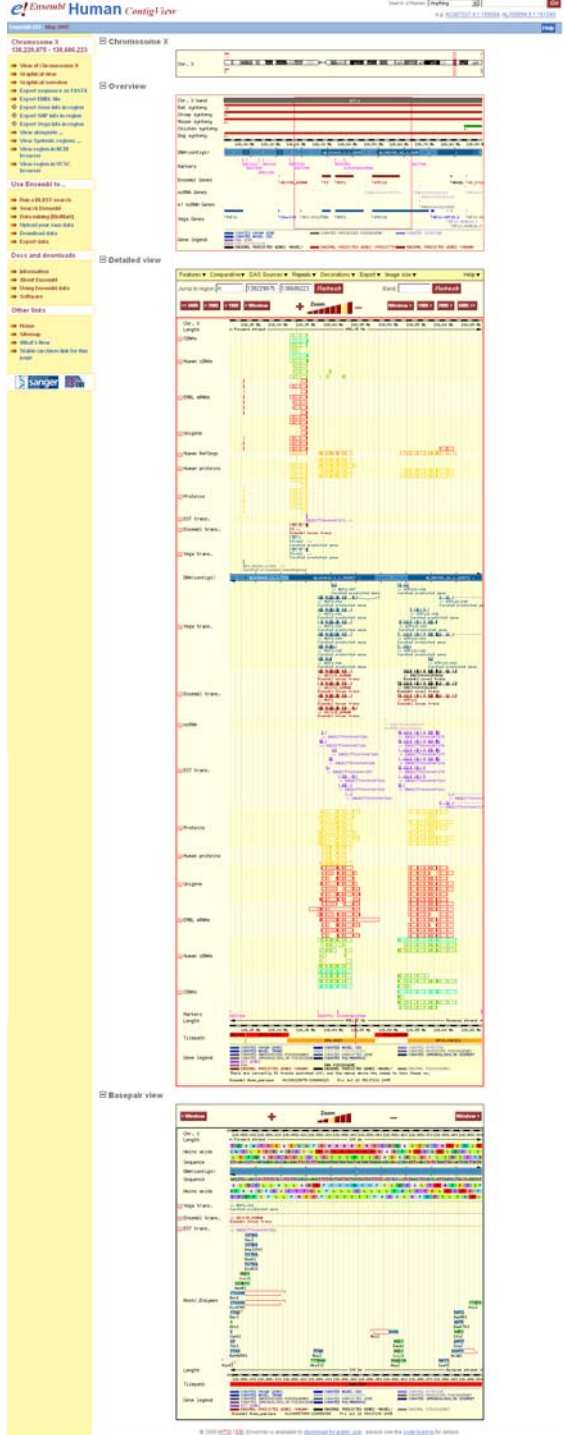
- Stable (archive) link for this page

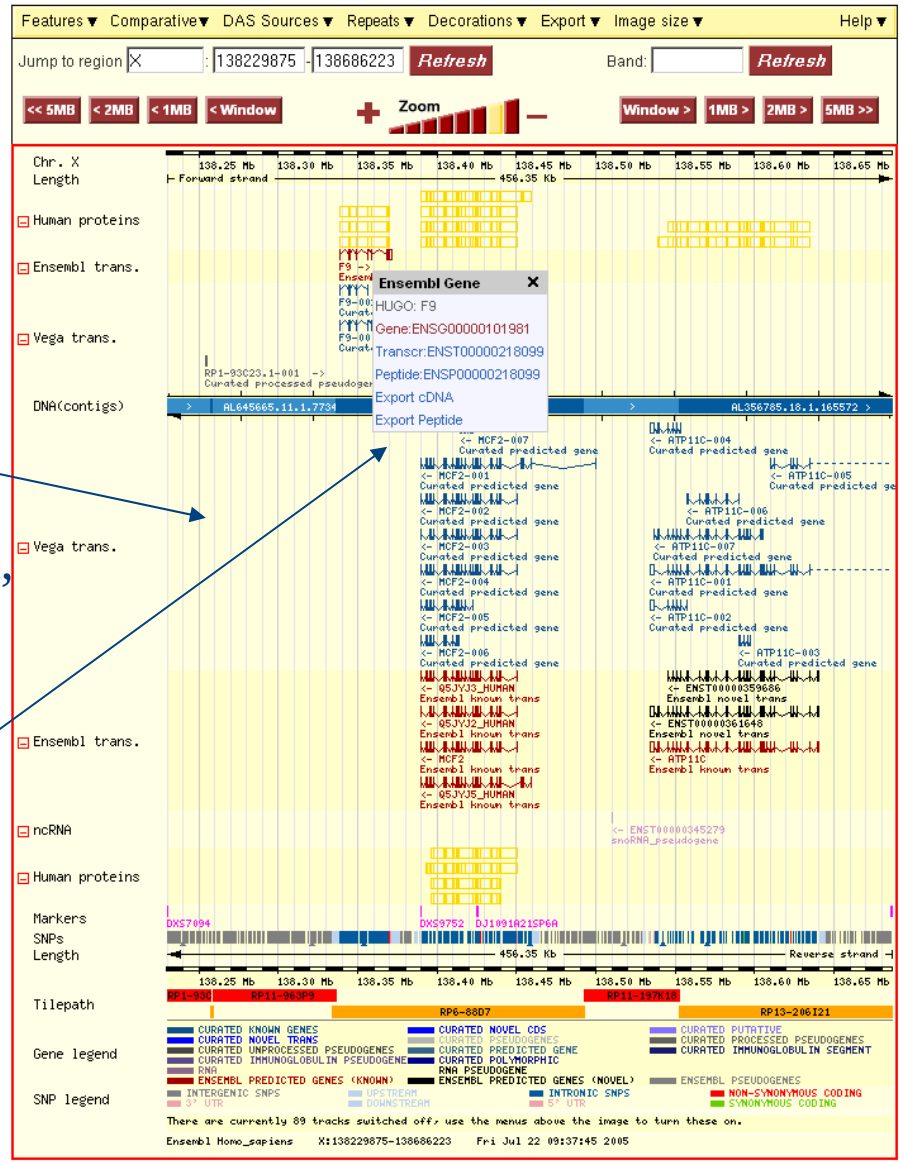
Ensembl
ContigView



ContigView close-up

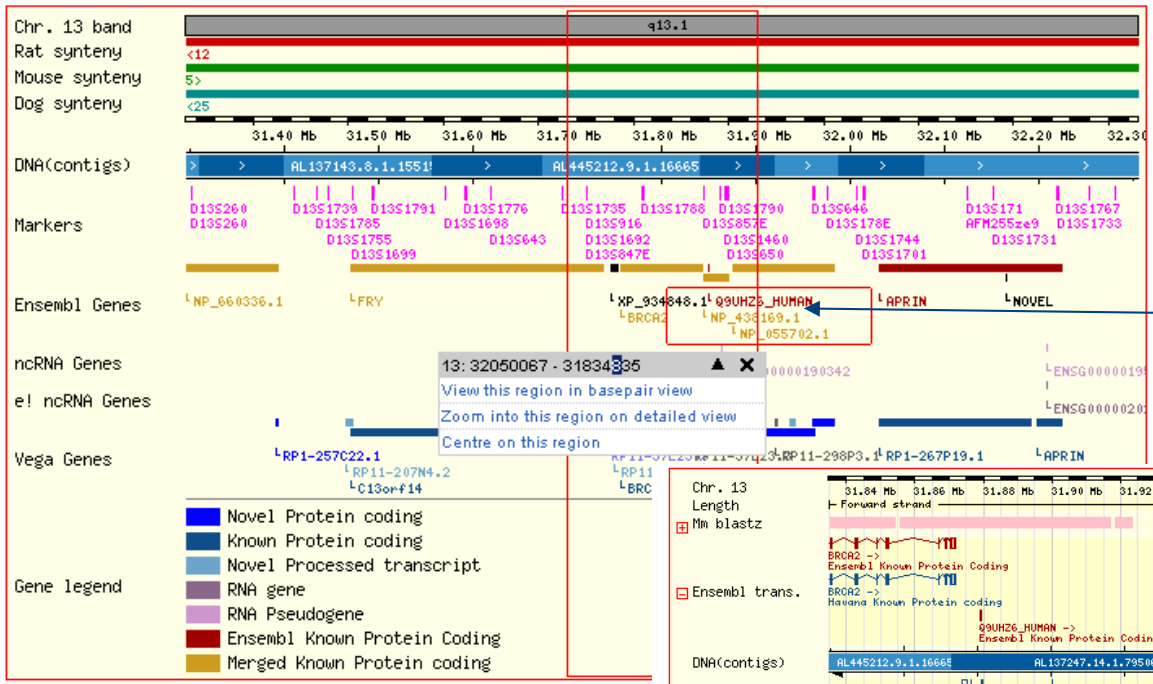
Transcripts
red & black
(Ensembl predictions)
Blue (Vega) & gold (HAVANA,
only in human)

Pop-up menu

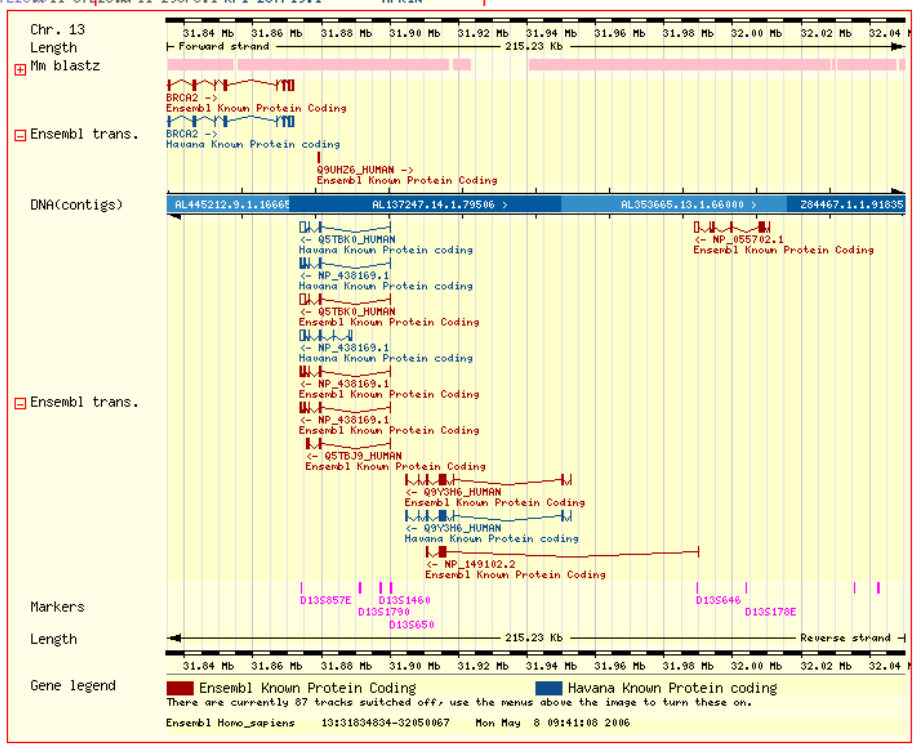


ContigView - Navigation

Overview

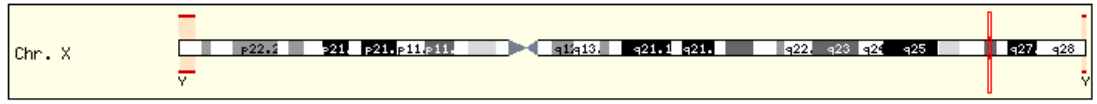


Click and drag mouse to select region

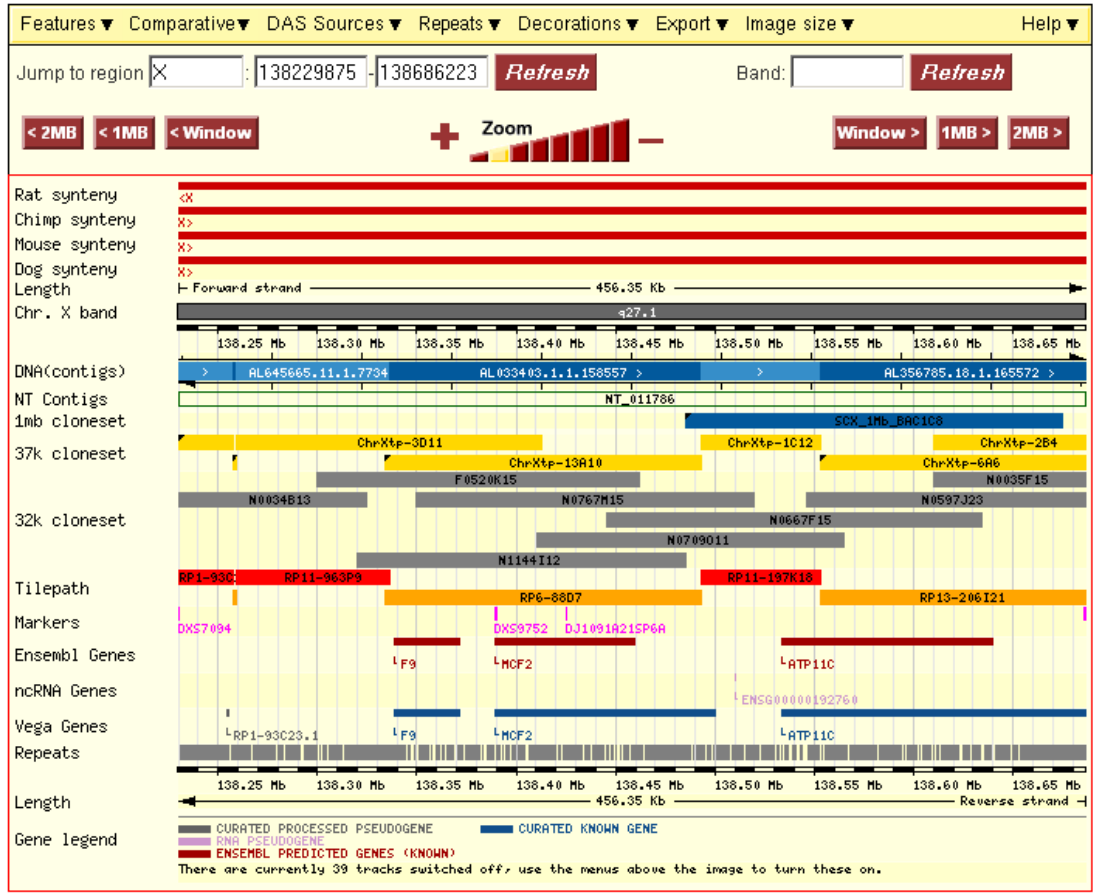


CytoView

Chromosome X



Detailed view



Export data

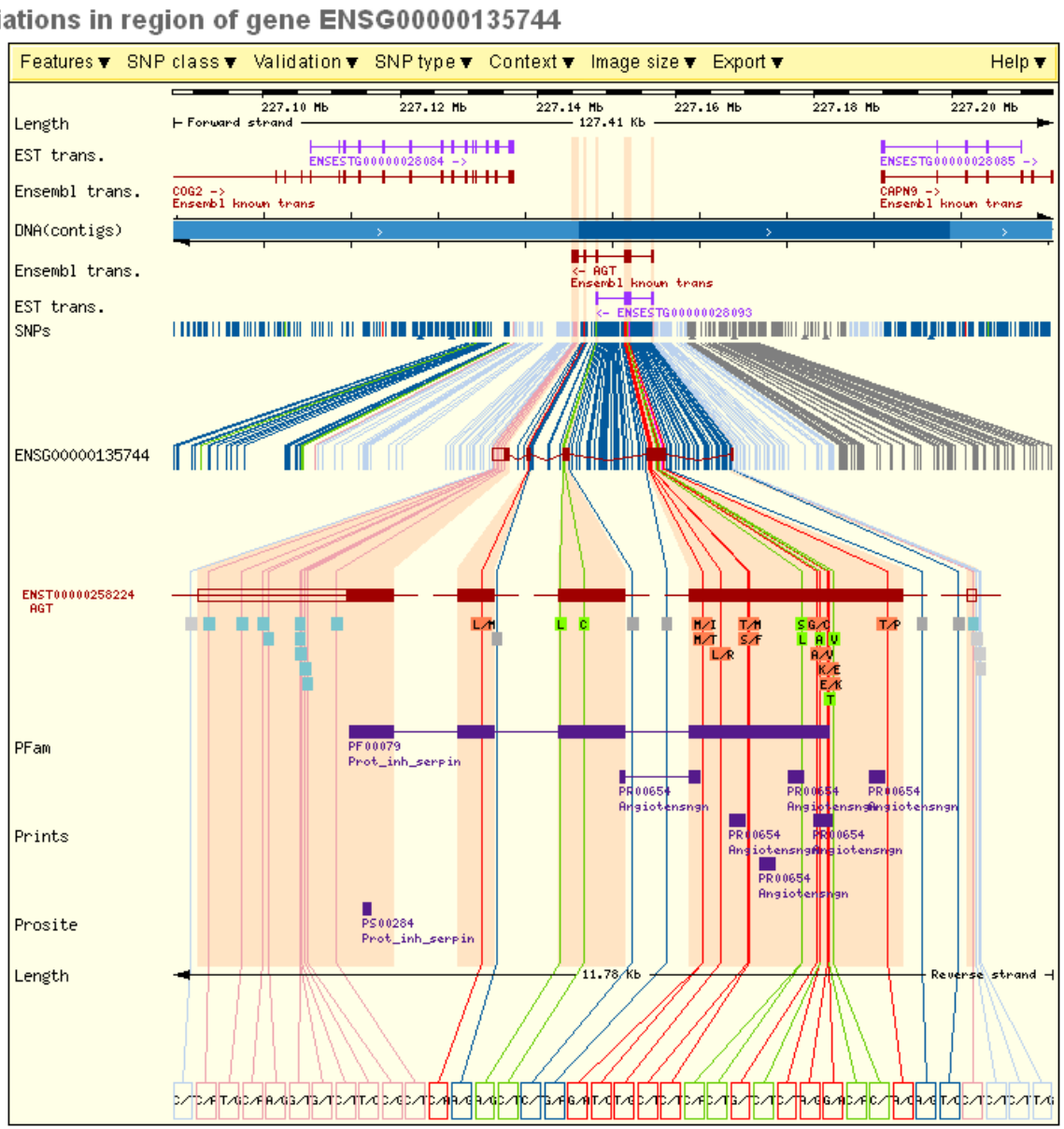
Select Set of features to render: Tile path clones

Output format: HTML

Select type to export: Features on this chromosome

Export

GeneSNP View



SNPView

SNP Report

SNP	rs699 (dbSNP124)
Synonyms	**HGVbase** SNP000000510
Alleles	**T/C** (ambiguity code: **Y**)
Validation status	Proven by **cluster, frequency, doublehit** (*SNP tested and validated by a non-computational method*).
Linkage disequilibrium data	**Links to LDview per population:** PERLEGEN:AFD_CHN_PANEL CSHL-HAPMAP:HapMap-YRI CSHL-HAPMAP:HapMap-JPT CSHL-HAPMAP:HapMap-HCB PERLEGEN:AFD_AFR_PANEL CSHL-HAPMAP:HapMap-CEU PERLEGEN:AFD_EUR_PANEL
Sequence region	CCCTGCAGGCTGTACAGGGCCTGCTAGTGGCCCAGGGCAGGGCTGATAGCCAGGCCCAGC TGCTGCTGTCCACGGTGGTGGGCGTGTTCACAGCCCCAGGCCTGCACCTGAAGCAGCCGT TTGTGCAGGGCCTGGCTCTCTATACCCCTGTGGTCCTCCCACGCTCTCTGGACTTCACAG AACTGGATGTTGCTGCTGAGAAGATTGACAGGTTCATGCAGGCTGTGACAGGATGGAAGA CTGGCTGCTCCCTGAYGGGAGCCAGTGTGGACAGCACCCTGGCTTTCAACACCTACGTCC ACTTCCAAGGTAAGGCAAACCTCTCTGCTGGCTCTGGCCCTAGGACTTAGTATCCAATGT CTAGCTGAGATCAGCCAGTCAGCCTTGGAGATGGGCAGGGGGCCACCCTGCGGACATACC TGGTGACCACCCTTGAGAAGTGGGGAAGTGGCTGCTCCGCTGGGTCCCTGGATGGGCCGT CCACCTCCTGGACCTGCTGCCCTACTATGTG *(SNP highlighted)*

Genotype frequencies per population

Population	Genotypes T/T	Genotypes C/T	Genotypes C/C	Description
PARC:PARC-EUROPEAN-PANEL	0.217	0.652	0.130	This population of 23 individuals 12 male/11 female is composed of CEPH Parent DNA available from the Coriell Cell Repository (CCR).,CCR ID CEPH PEDIGREE ID PARC ID SEX,NA12560 French 12 E001 M,NA12547 French 66 E002 M,NA10846 Utah 1424 E003 M,NA10853 Uta
WIPGA:POP-WIPGA-12-05-2003	0.179	0.436	0.385	Each assay with this population used a subset of the individuals,listed below. To determine which specific individuals were used for a,given polymorphism, please consult the genotypes associated with the polymorphism.,CL420:female,Caucasian,Coriell,CL388
PARC:PARC-AFRICAN-PANEL	0.042	0.250	0.708	This population of 24 individuals (12 male/12 female) is composed of DNA available from the Coriell Cell Repository. These individuals were selected from the human variation panel of 50 African Americans (HD50AA).,CCR ID PARC ID SEX,NA17101 D001 M,NA17102

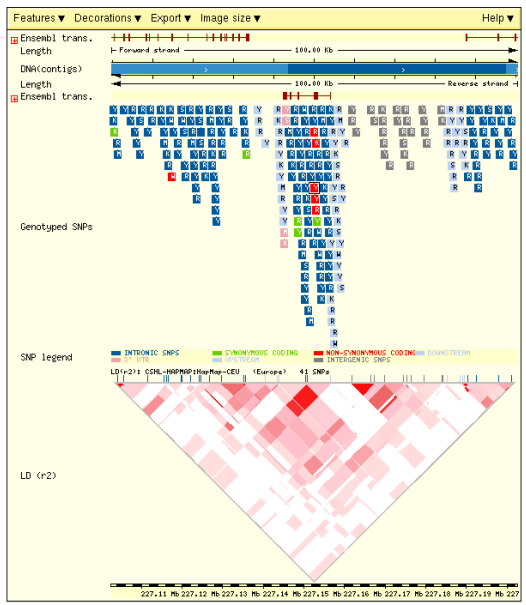
Allele frequencies per population

Population	Alleles T	Alleles C	Description
ARAVINDA:HYP1	0.100	0.900	80 chromosomes are from Harare, Zimbabwe; Samples represent,individuals from both extremes (2.5th percentiles) of a community blood,pressure distribution.
PARC:PARC-EUROPEAN-PANEL	0.543	0.457	This population of 23 individuals 12 male/11 female is composed of CEPH Parent DNA available from the Coriell Cell Repository (CCR).,CCR ID CEPH PEDIGREE ID PARC ID SEX,NA12560 French 12 E001 M,NA12547 French 66 E002 M,NA10846 Utah 1424 E003 M,NA10853 Uta
YUSUKE:JBIC-allele	0.188	0.812	752 anonymous unrelated Japanese volunteers,Nation:Japan
PHARMGKB_PARC:PA128275074	0.351	0.649	-
CGAP-GAI:POOLED_CEPH	0.572	0.428	Pooled genomic DNA from 94 unrelated CEPH individuals (caucasian)
WIPGA:POP-WIPGA-12-05-2003	0.397	0.603	Each assay with this population used a subset of the individuals,listed below. To determine which specific individuals were used for a,given polymorphism, please consult the genotypes associated with the polymorphism.,CL420:female,Caucasian,Coriell,CL388
PARC:PARC-AFRICAN-PANEL	0.167	0.833	This population of 24 individuals (12 male/12 female) is composed of DNA available from the Coriell Cell Repository. These individuals were selected from the human variation panel of 50 African Americans (HD50AA).,CCR ID PARC ID SEX,NA17101 D001 M,NA17102

SNP rs699 is located in the following transcripts

Genomic location (strand)	Transcript: start-end	GeneSNPView link	Translation: start-end	Peptide allele	Consequence
1: 227152529-227152529 (-1)	ENST00000258224: 842-842	SNP in gene context	ENSP00000258224: 268-268	M/T	NON_SYNONYMOUS_CODING

SNP Context - chromosome 1 227152529



MarkerView

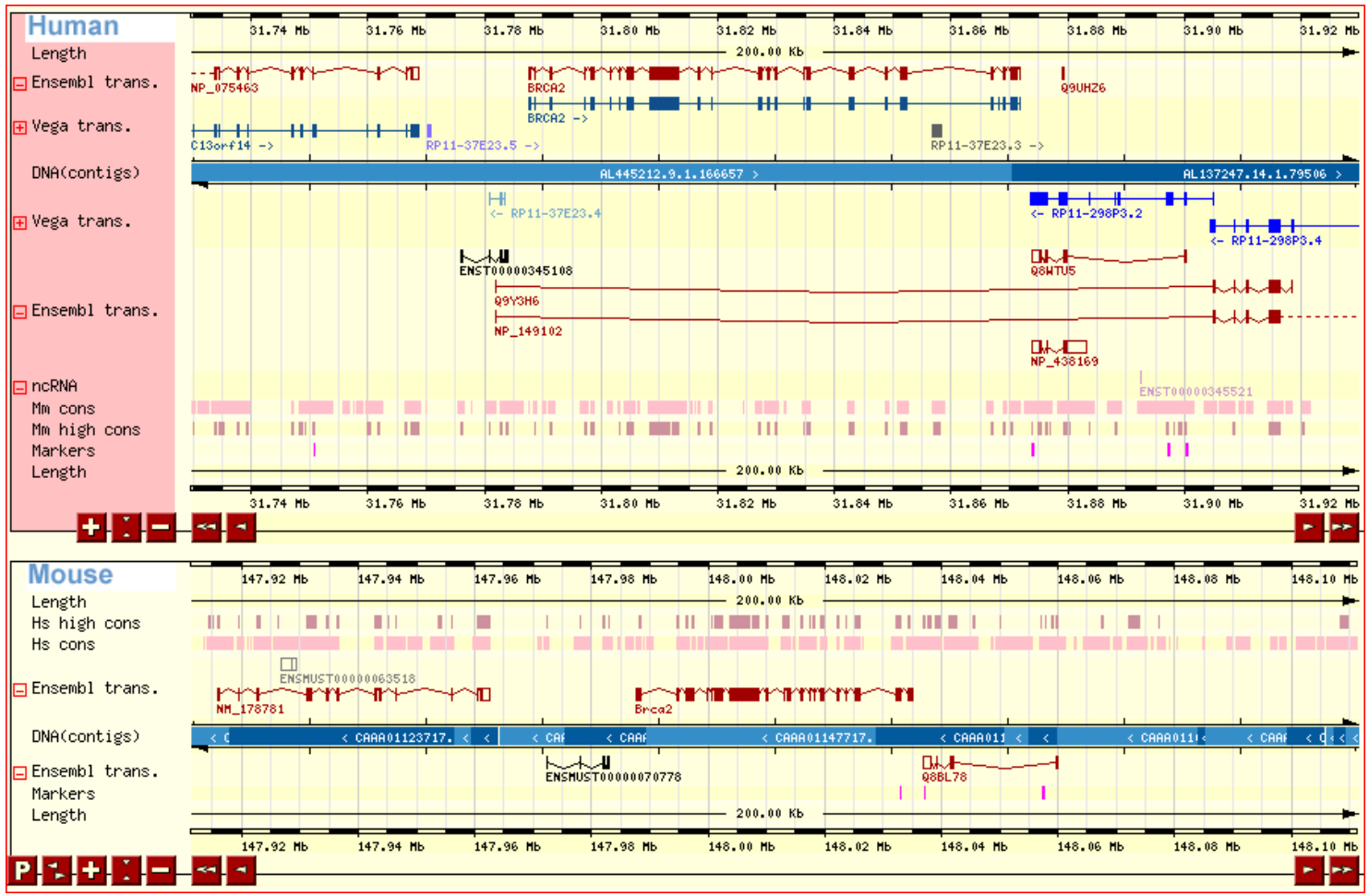
Chromosome Map Marker DXS9752

Marker Source	82913 **(database: unists)**
Marker Location	Basepairs 138389786 - 138390044 on chromosome X [Export data]
Marker Synonyms	**Gdb :** GDB:737728 GDB:738733 **Genbank :** G13636 **Other :** SHGC-11927 DXS9752 RH8108
Marker Primers	**Expected Product Size** **Left Primer** **Right Primer** 259 TTTTCAGGTTAATGGACACGC CCATTTTGCAGCCGTAATTT

Marker DXS9752 map locations

Map Name	Synonym	Chromosome	Position	LOD Score
gm99g3	RH8108	X	4259	3.5

MultiContigView



Genes & gene products

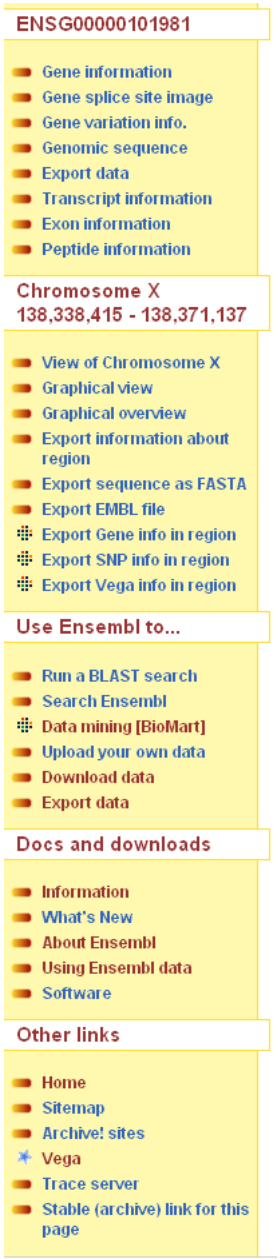
GeneView

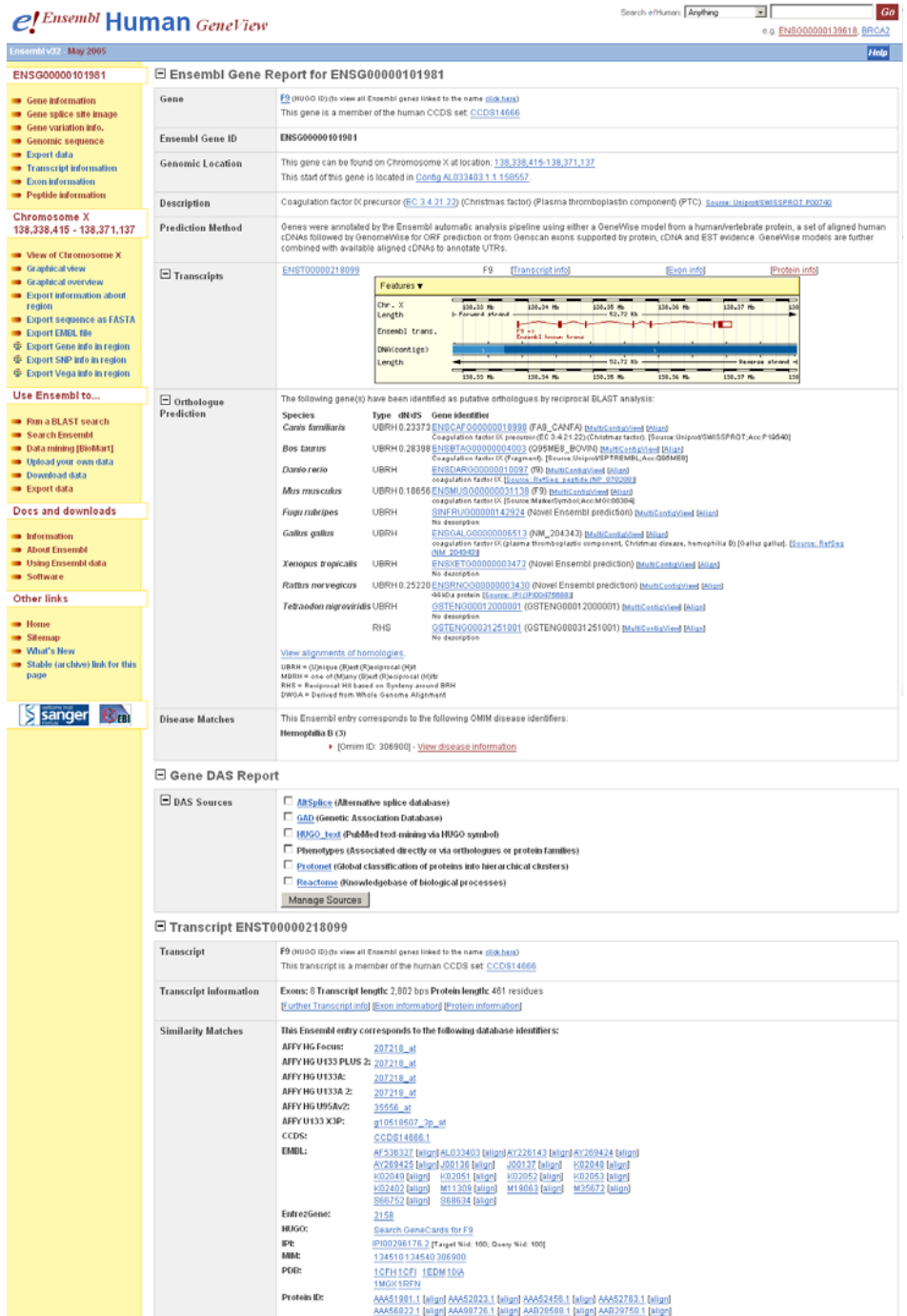
TransView
ExonView
ProteinView

FamilyView

GOView

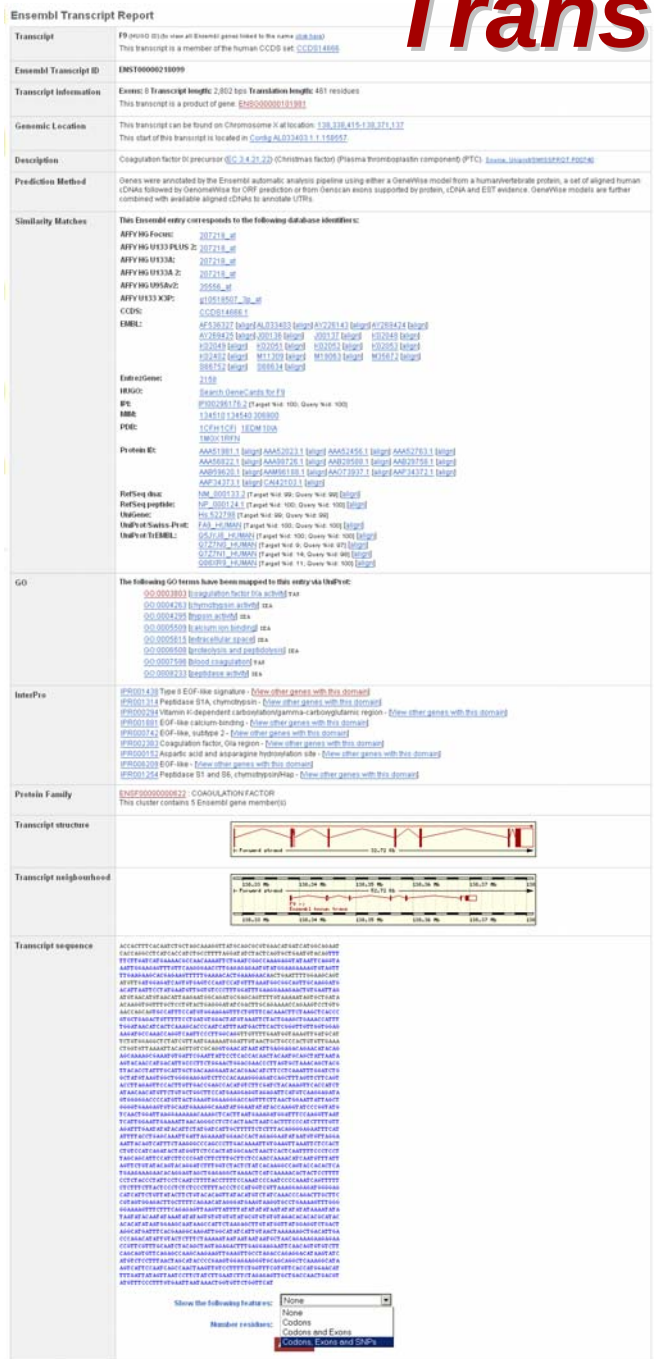
Ensembl GeneView

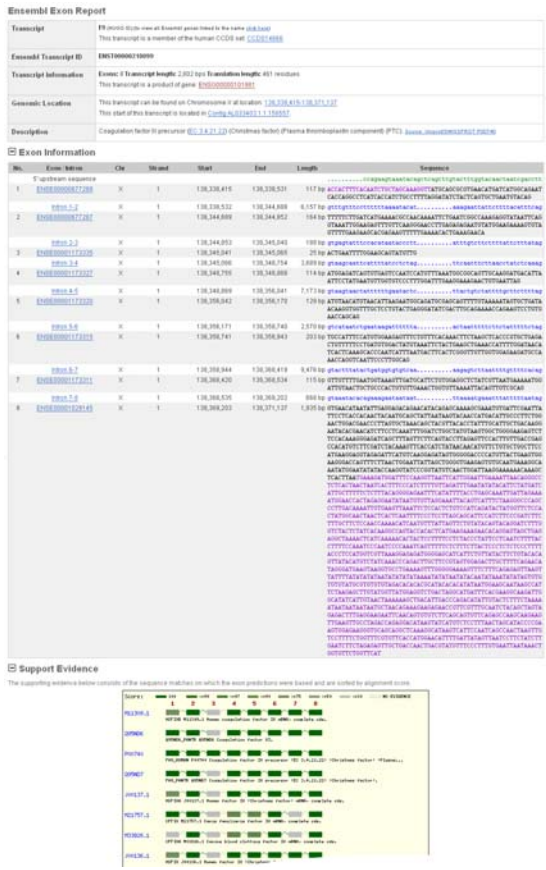




TransView

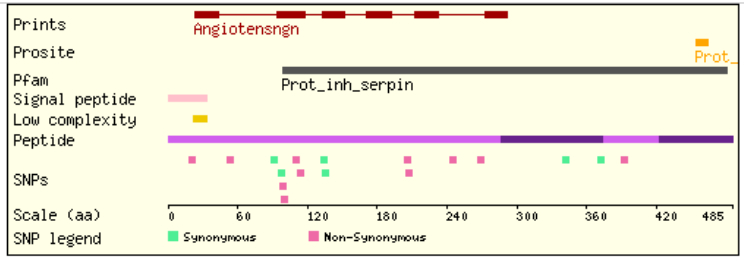
ExonView





Protein View

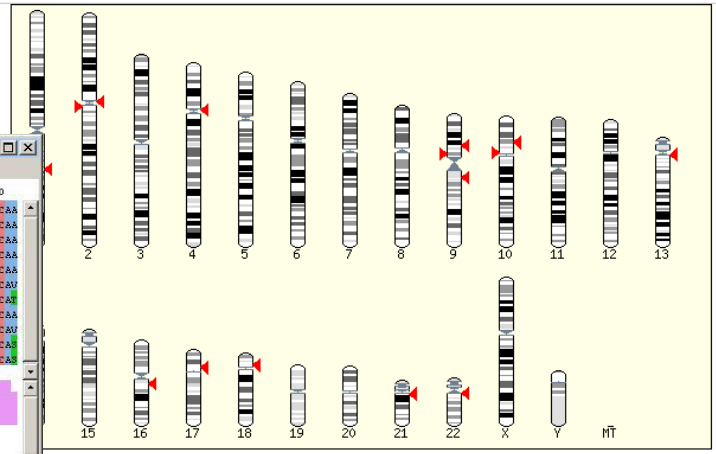
Ensembl Protein Report

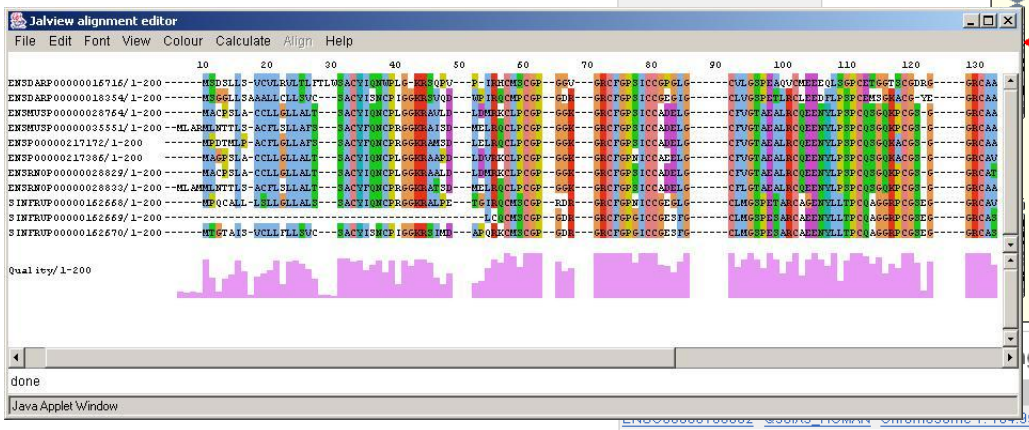
Peptide	**AGT** (HUGO ID) (to view all Ensembl genes linked to the name click here) This peptide is a member of the human CCDS set: CCDS1585
Ensembl Peptide ID	**ENSP00000258224**
Translation information	This peptide is a translation of transcript: ENST00000258224, which is a product of gene: ENSG00000135744 .
Genomic Location	This peptide can be found on Chromosome 1 at location: 227,145,622-227,153,331 This start of this peptide is located in Contig AL158214.33.1.181175.
Description	Angiotensinogen precursor [Contains: Angiotensin I (Ang I); Angiotensin II (Ang II); Angiotensin III (Ang III) (Des-Asp[1]- angiotensin II)]. Source: Uniprot/SWISSPROT P01019
Prediction Method	Genes were annotated by the Ensembl automatic analysis pipeline using either a GeneWise model from a human/vertebrate protein, a set of aligned human cDNAs followed by GenomeWise for ORF prediction or from Genscan exons supported by protein, cDNA and EST evidence. GeneWise models are further combined with available aligned cDNAs to annotate UTRs.
InterPro	IPR000227 Angiotensinogen - [View other genes with this domain] IPR000215 Proteinase inhibitor I4, serpin - [View other genes with this domain]
Protein Family	ENSF00000005553 : ANGIOTENSINOGEN PRECURSOR [CONTAINS: ANGIOTENSIN I ANG I ; ANGIOTENSIN II ANG II ; ANGIOTENSIN III ANG III DES ASP[1] ANGIOTENSIN II] This cluster contains 1 Ensembl gene member(s)
Protein Features	
Peptide Sequence	MRKRAPQSEMAPAGVSLRATILCLLAWAGLAAGDRVYIHPFHLVIHNESTCEQLAKANAG KPKDPTFIPAPIQAKTSPVDEKALQDQLVLVAAKLDTEDKLRAAMVGMLANFLGFRIYGM HSELWGVVHGATVLSPTAVFGTLASLYLGALDHTADRLQAILGVPWKDKNCTSRLDAHKV LSALQAVQGLLVAQGRADSQAQLLLSTVVGVFTAPGLHLKQPFVQGLALYTPVVLPRSLD FTELDVAAEKIDRFMQAVTGWKTGCSLMGASVDSTLAFNTYVHFQGKMKGFSLLAEPQEF WVDNSTSVSVPMLSGMGTFQHWSDIQDNFSVTQVPFTESACLLLIQPHYASDLDKVEGLT FQQNSLNWMKKLSPRTIHLTMPQLVLQGSYDLQDLLAQAELPAILHTELNLQKLSNDRIR VGEVLNSIFFELEADEREPTESTQQLNKPEVLEVTLNRPFLFAVYDQSATALHFLGRVAN PLSTA

Family View

Ensembl Family ENSF00000000497

Family ID	ENSF00000000497
Consensus annotation	AMBIGUOUS
Prediction method	Protein families were generated using the MCL (Markov CLustering) package available at http://micans.org/mcl/. The application of MCL to biological graphs was initially proposed by Enright A.J., Van Dongen S. and Ouzounis C.A. (2002) "An efficient algorithm for large-scale detection of protein families." Nucl. Acids. Res. 30, 1575-1584.
Multiple alignments	Click to view multiple alignments of the 203 Ensembl members of this family. JalView Click to view multiple alignments of the 249 members of this family. JalView
Ensembl genes containing peptides in family ENSF00000000497	





g family ENSF00000000497

			Description(if known)
			MGC12538 protein (Novel protein). [Source:Uniprot/SPTREMBL;Acc:Q96IX9]
ENSG00000177195	-novel-	Chromosome 2: 88.94m	No description
ENSG00000172014	-novel-	Chromosome 2: 94.85m	No description
ENSG00000135976	-novel-	Chromosome 2: 95.94m	No description
ENSG00000174501	KIAA1641	Chromosome 2: 97.30m	No description
ENSG00000187998	NP_066021.1	Chromosome 2: 97.58m	No description
ENSG00000178305	Q8NF67_HUMAN	Chromosome 4: 49.33m	No description
ENSG00000159712	-novel-	Chromosome 9: 33.51m	No description
ENSG00000180071	ANKRD18A	Chromosome 2: 39.53m	Ankyrin repeat domain protein 18A. [Source:Uniprot/SWISSPROT;Acc:Q8IVF6]

GOView

Ensembl GO Search

GO Accession	**GO:0004867** [serine-type endopeptidase inhibitor activity]
GO Database	GO data is provided by the Gene Ontology Consortium
Search GO	**Search GO database for:** GO:0004867 *[e.g. GO:0004867, *vesicle, *calcium binding*] Search Fields marked with * are required
Go Graph	

tree	Ensembl Gene Matches
all [all]	
molecular_function [GO:0003674]	
enzyme regulator activity [GO:0030234]	5 gene(s)
enzyme inhibitor activity [GO:0004857]	22 gene(s)
protease inhibitor activity [GO:0030414]	1 gene(s)
endopeptidase inhibitor activity [GO:0004866]	17 gene(s)
serine-type endopeptidase inhibitor activity [GO:0004867]	80 gene(s)
chymotrypsin inhibitor activity [GO:0030569]	1 gene(s)
plasmin inhibitor activity [GO:0030568]	1 gene(s)
trypsin inhibitor activity [GO:0030304]	3 gene(s)

Data retrieval

BioMart

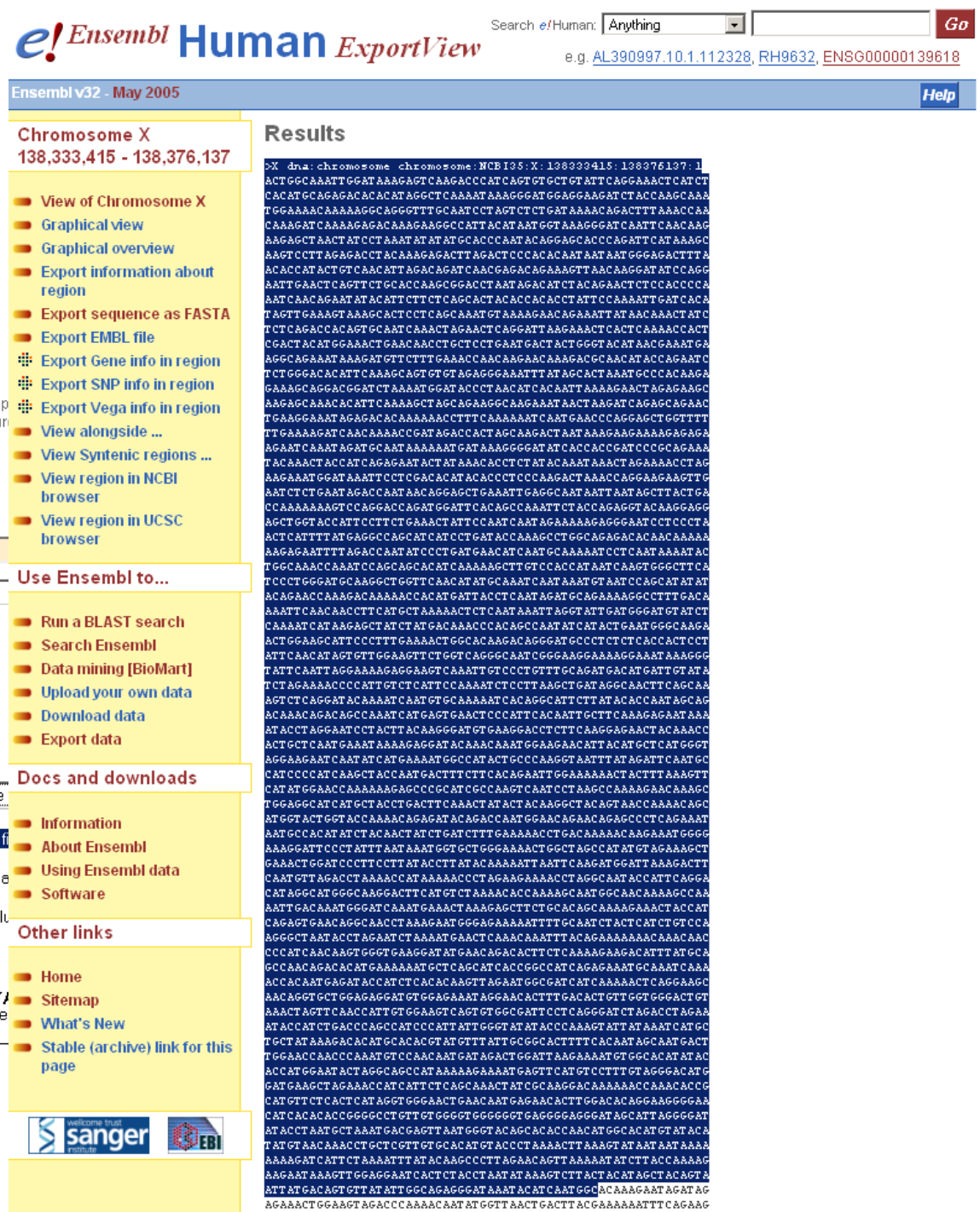
Export View

Data sets on ftp site

MySQL queries of databases

Perl API access to databases

ExportView



Select region/feature to Export

Choose one or two features from the same chromosome as anchor points and disp
select "None" for the second feature, the display will be based around the first featur

Please note that there is an upper limit of 5Mb that we will export.

Region

Chromosome name/fragment:

From (type): Base pair

To (type): Base pair

Context

Bp downstream:

Bp upstream:

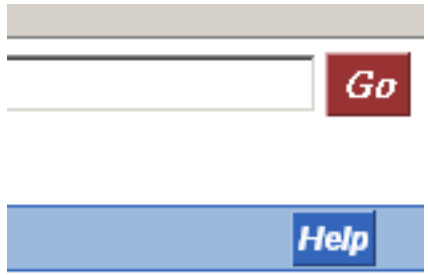
Output format

Output Format: FASTA format text file

- *FASTA File*
  - FASTA format text f
- *Feature List*
  - CSV (Comma Sepa
  - GFF format
  - Tab separated valu
- *Flat File*
  - EMBL
  - GenBank
- *PIP (%age identity*
  - Pipmaker / zPicture
  - Vista Format

© 2005 WTSI / E

Help!



- context sensitive help pages - click Help
- access other documentation via generic home page
- email the helpdesk Contact helpdesk

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VectorBase Annotation	**Martin Hammond, Dan Lawson, Karyn Megy**
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