Gene finding and Genome annotation

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BerkeleyPGA

Bioinformatics Tools for Comparative Analysis

June 12, 2001

What is a Gene?

- Definition: An inheritable trait associated with a region of DNA that codes for a polypeptide chain or specifies an RNA molecule which in turn have an influence on some characteristic phenotype of the organism.

Abstract concept that describes a complex phenomenon

What is Annotation?

- Definition: Extraction, definition, and interpretation of features on the genome sequence derived by integrating computational tools and biological knowledge.

Identifiable features in the sequence

How does an annotation differ from a gene?

- Many annotations describe features that constitute a gene.
- Other annotations may not always directly correspond in this way, e.g., an STS, or sequence overlap

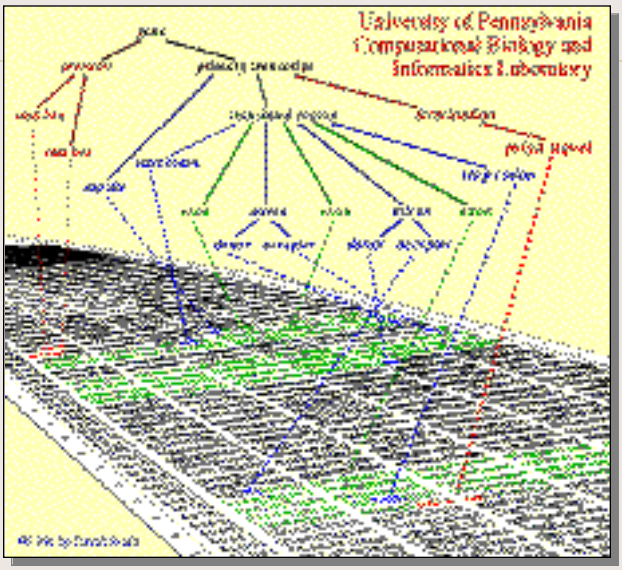
DNA Analysis

- Heuristics
- Statistics
- Artistics

DNA Analysis

- Find the genes
  - Heuristic signals
  - Inherent features
  - Intelligent methods
- Characterize each gene
  - Compare with other genes
  - Find functional components
  - Predict features

What is a Gene?



Heuristic Signals

- DNA contains various recognition sites for internal machinery

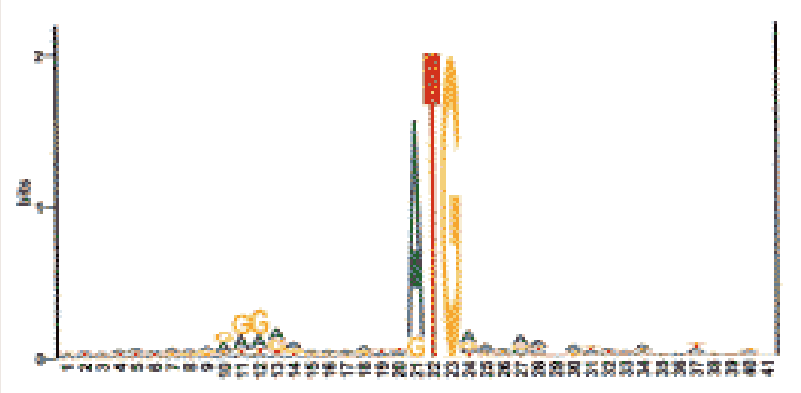
- Promoter signals
- Transcription start signals
- Start Codon
- Exon, Intron boundaries
- Transcription termination signals

Heuristic Signals

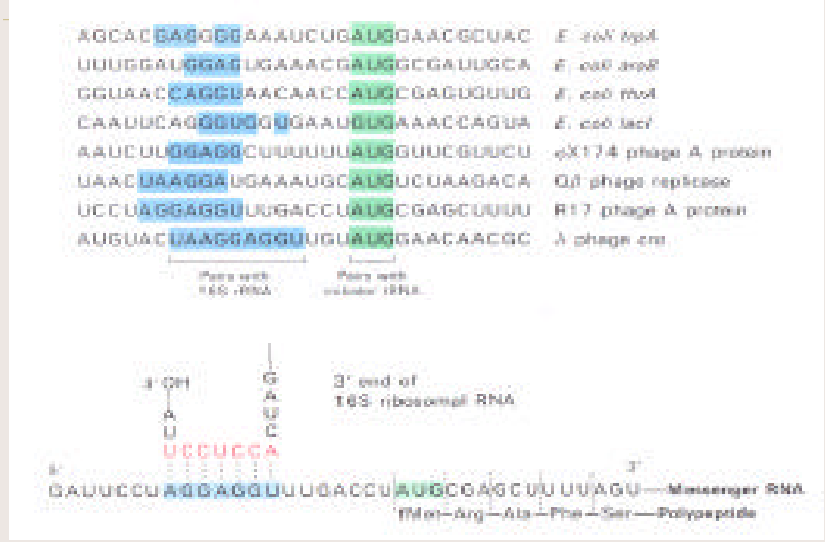
Start of the gene

Heuristic Signals

Start Codon



Initiation

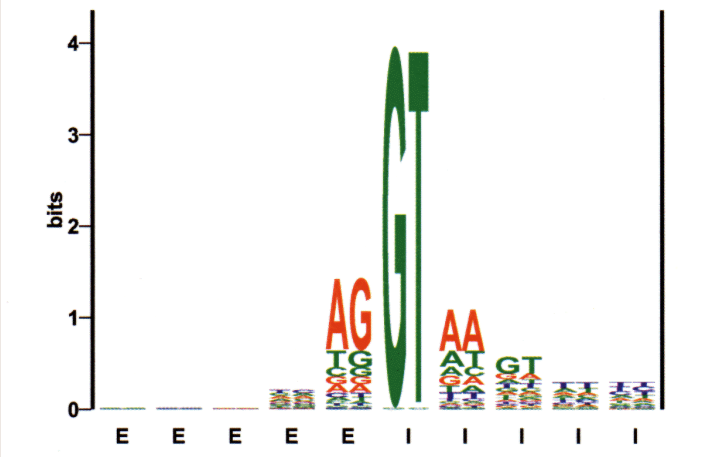


Inherent Features

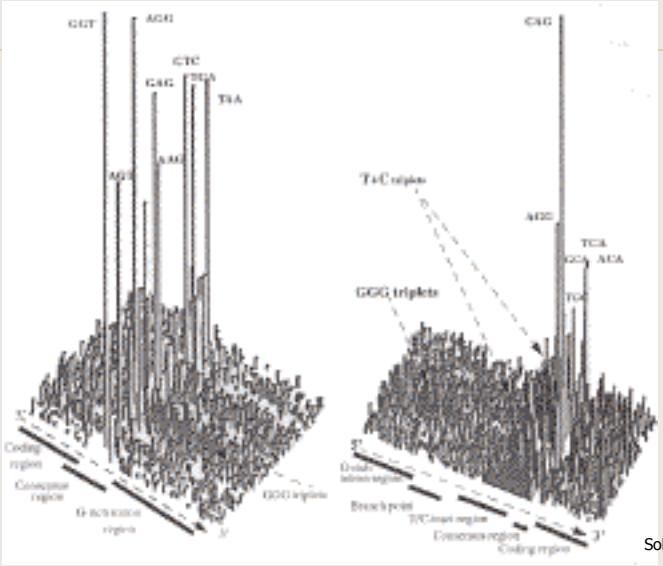
- DNA exhibits certain biases that can be exploited to locate coding regions

- Uneven distribution of bases
- Codon bias
- CpG islands
- In-phase words
- Encoded amino acid sequence
- Imperfect periodicity
- Other global patterns

Donor Splice Site



Inherent Features



Solovyev, 1994

Intelligent Methods

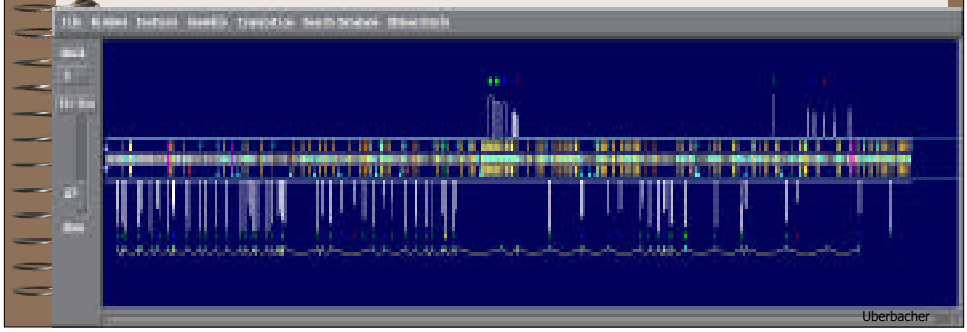
- Pattern recognition methods weigh inputs and predict gene location
  - Content-based methods
  - Site-based methods
  - Comparative methods
- Neural Networks
- Hidden Markov Models
- Stochastic Context-Free Grammar

GRAIL *Uberbacher, Mural*

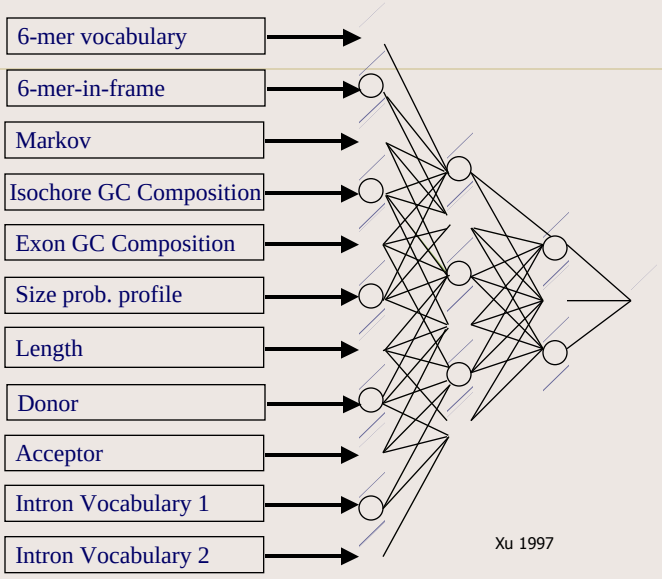
- GRAIL 1
  - Neural network with fixed window length (100 bases)
- GRAIL 1a
  - GRAIL 1 + adjacent information
- GRAIL 2
  - Variable length window, contextual information
- GRAIL-EXP
  - Comparison with partial and complete gene sequences

Analyzing Complex Multi-Gene Regions

- Errors in exon prediction and splice site boundaries
- Gene boundaries uncertain
- Genes can be on both strands

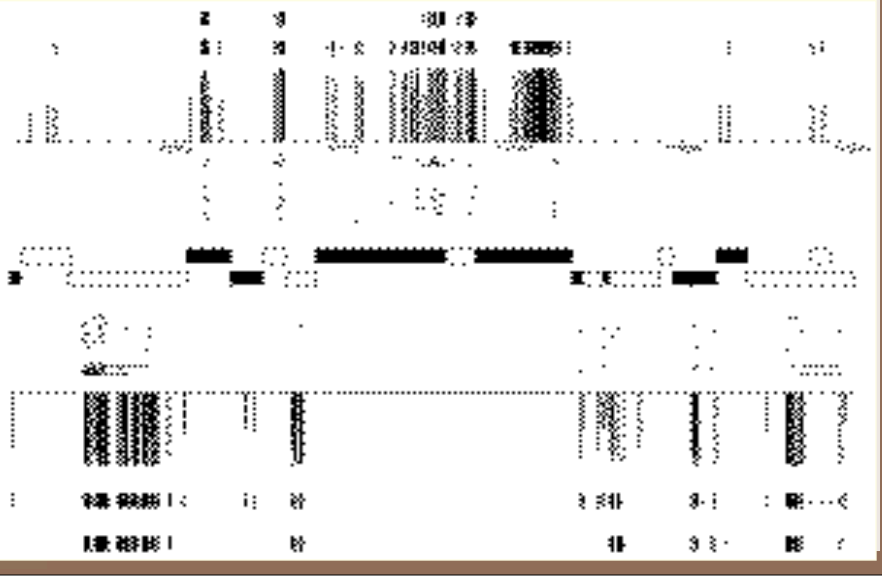


Neural networks



Xu 1997

Grail-EXP



FGENEH/FGENES *Solovyev*

- Looks at several structural features
  - Splice donor/acceptor sites
  - Putative coding regions
  - Intronic regions
- *Linear discriminant analysis* to split exon / non-exon classes
- Dynamic programming to assemble best gene structure

MZEF *Zhang*

- *Quadratic discriminant analysis*
  - Exon length
  - Exon-intron transitions
  - Splice sites
  - Branch sites
  - Exon, strand, frame scores
- Detects internal exons
- No information about gene structure

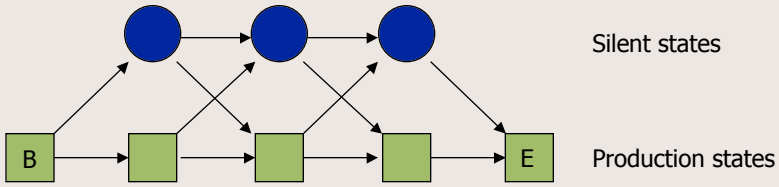
GENSCAN *Burge, Karlin*

- Probabilistic model of sequence composition and gene structure
  - Looks for gene structure descriptions that are consistent with the query sequence to assign probability that sequence stretch is exon, …
  - Best ---> optimal
  - But generates also suboptimal exons

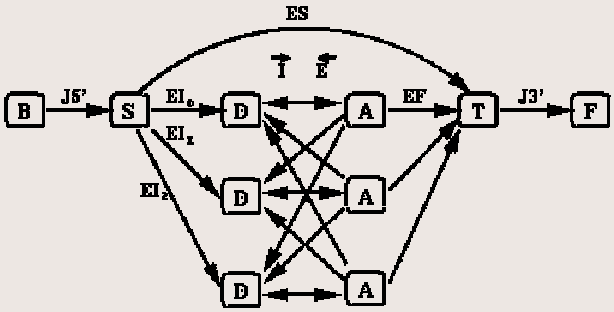
PROCRUSTES *Gelfand*

- Forces sequence into target structure
  - Requires putative gene product
  - Strecthes/shortens sequence to fit into model

Hidden Markov Models



GENIE *Kulp, Reese, Haussler*



Strategies

- Select by correlation coefficient
- Select by review paper
- Select by recommendation
- Use them all

Drawbacks

- Most programs are “trained” on existing data
- It’s awfully hard to find new things this way!
    - NTT
    - IPW

Internet Resources

Banbury Cross	http://igs-server.cnrs-mrs.fr/igs/banbury
FGENEH	http://genomic.sanger.ac.uk/gf/gf.shtml
GeneID	http://www1.imim.es/geneid.html
GeneMachine	http://genome.nhgri.nih.gov/genemachine
GENSCAN	http://genes.mit.edu/GENSCAN.html
Genotator	http://www.fruitfly.org/_nomi/genotator/
GRAIL	http://compbio.ornl.gov/tools/index.shtml
GRAIL-EXP	http://compbio.ornl.gov/grailexp
MZEF	http://www.cshl.org/genefinder
PROCRUSTES	http://www-hto.usc.edu/software/procrustes
RepeatMasker	http://ftp.genome.washington.edu/RM/RepeatMasker.html
HMMgene	http://www.cbs.dtu.dk/services/HMMgene
Chapter 10	http://www.wiley.com/legacy/products/subject/life/bioinformatics/chapterlinks.html

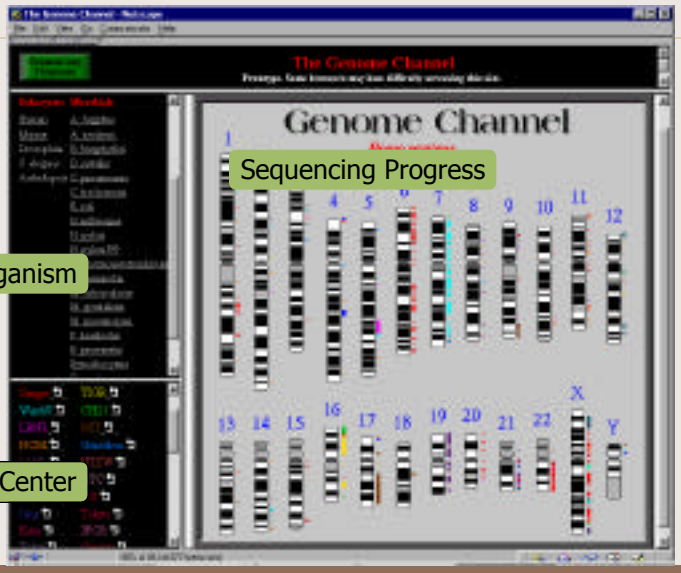
Characterize a Gene

Collect clues for potential function

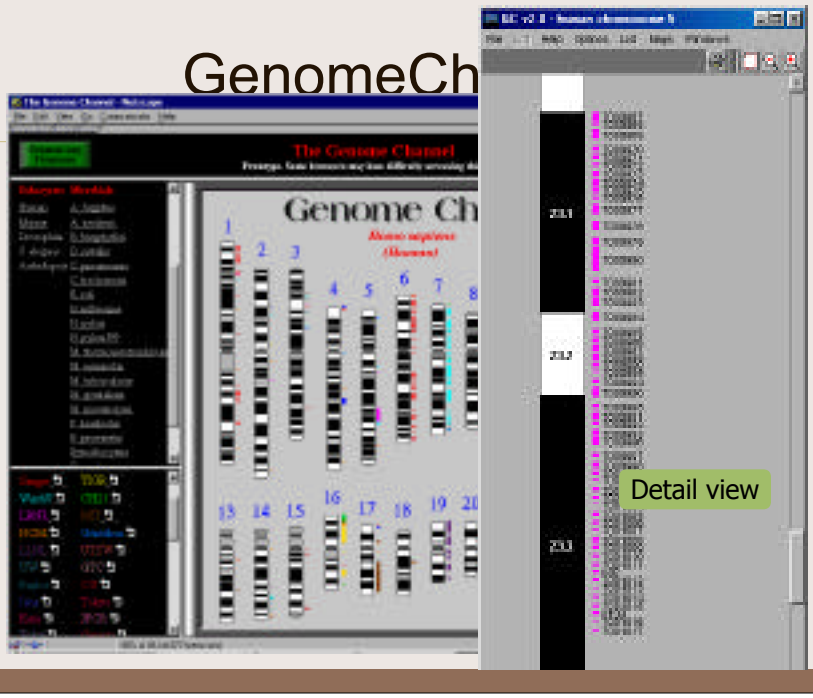
- Comparison with other known genes, proteins
- Predict secondary structure
- Fold classification

- Gene Expression
- Gene Regulatory Networks
- Phylogenetic comparisons
- Metabolic pathways

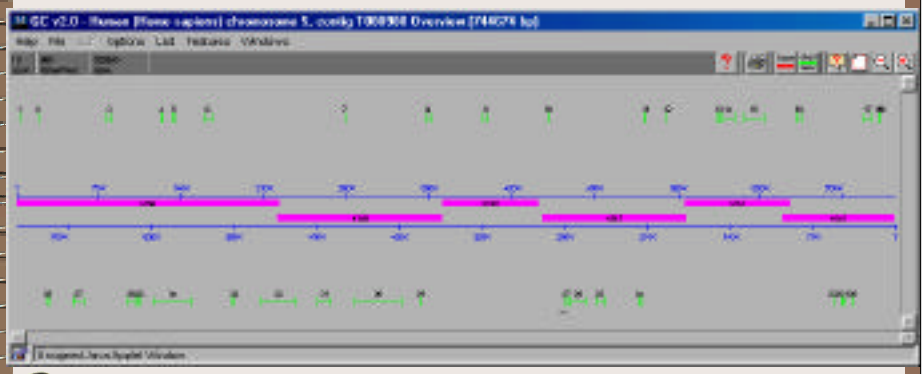
GenomeChannel



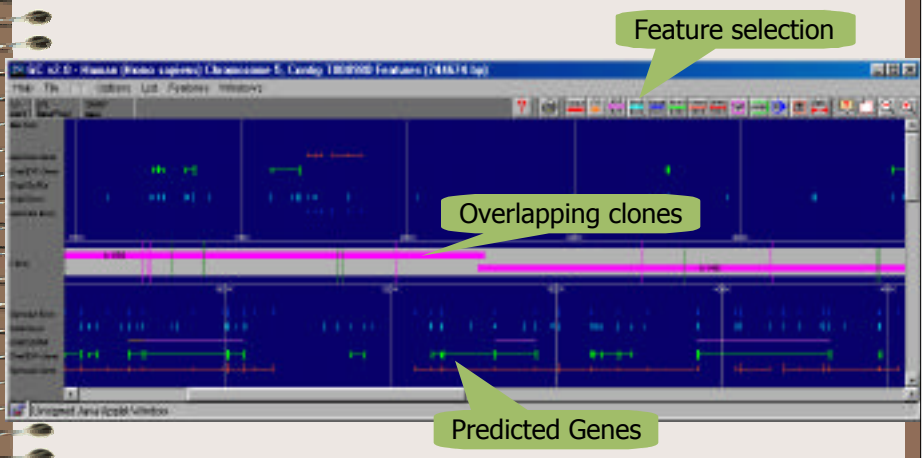
GenomeCh



A Contig Overview

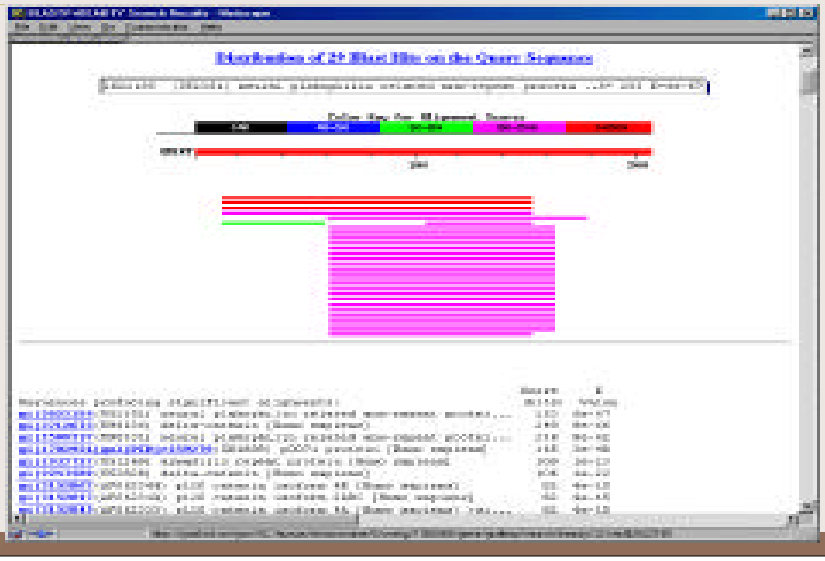


Feature Display



Gene Summary Report

BEAUTY - Gene Search Results

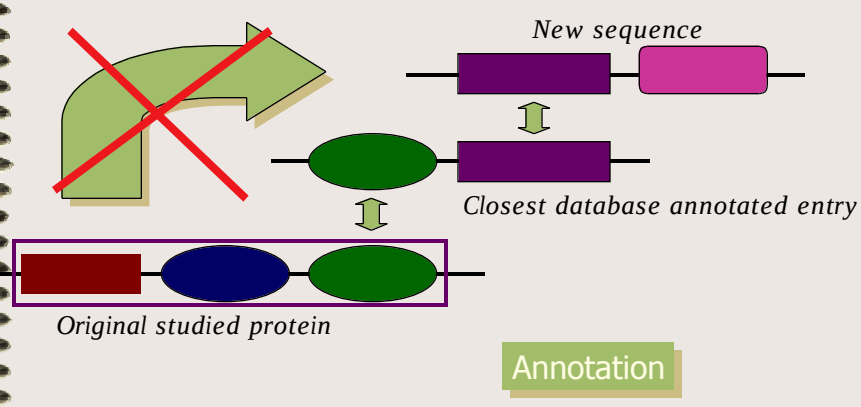


Layers of Information

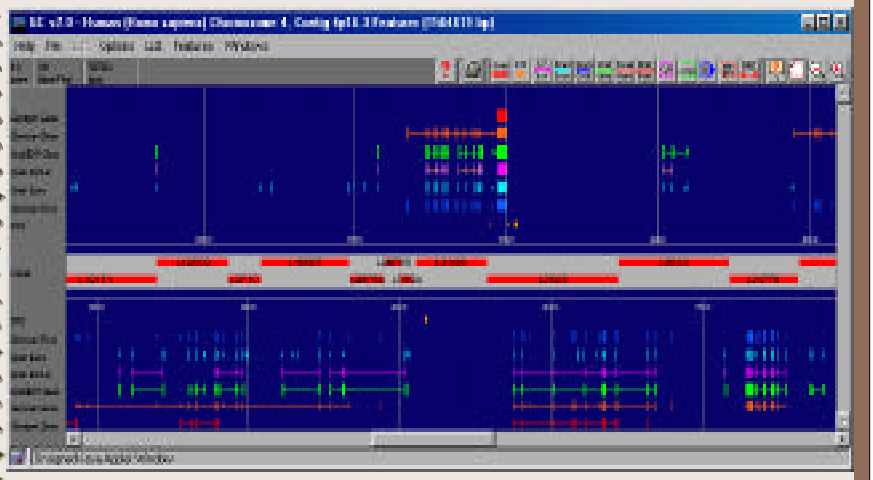
The same base sequence contains many layered instructions!

- Chromosome structure and function
  - Telomers, centromers
- Gene Regulatory information
  - Enhancers, promoters, ...
- Instructions for gene structure
- Instructions for protein
- Instructions for protein post-processing and localization

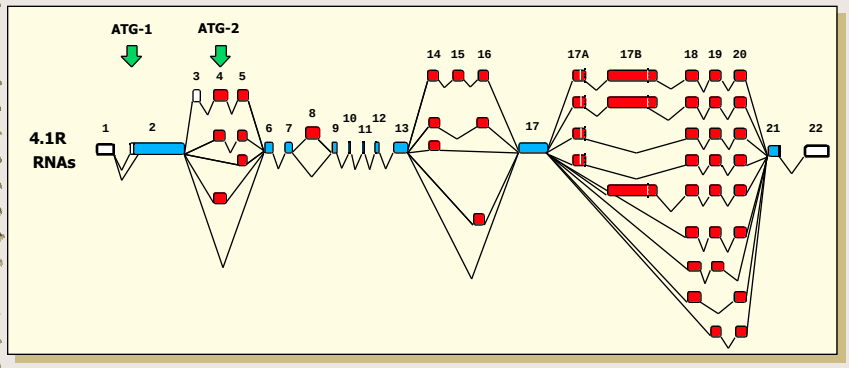
Inherited Annotation Problems in Multi-Domain Proteins



Alternatively Spliced ?



One Gene - Many Proteins



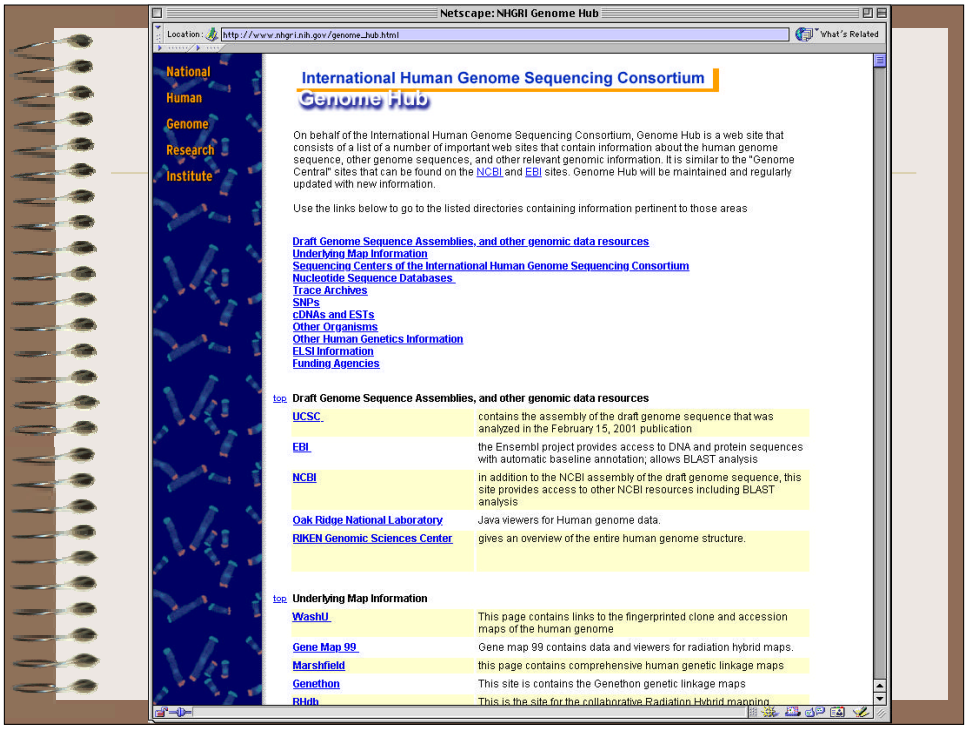
Conboy 1998

As many as 30% of human genes, in particular structural genes, may be alternatively spliced.

Annotated Genomes

Internet Resources

GenomeHub	http://www.nhgri.nih.gov/genome_hub.html
NAR Database Issue	http://nar.oupjournals.org/content/vol29/issue1/


Netscape: NHGRI Genome Hub
Location: http://www.nhgri.nih.gov/genome_hub.html
What's Related
National Human Genome Research Institute
International Human Genome Sequencing Consortium
Genome Hub
On behalf of the International Human Genome Sequencing Consortium, Genome Hub is a web site that consists of a list of a number of important web sites that contain information about the human genome sequence, other genome sequences, and other relevant genomic information. It is similar to the "Genome Central" sites that can be found on the NCBI and EBI sites. Genome Hub will be maintained and regularly updated with new information.
Use the links below to go to the listed directories containing information pertinent to those areas
Draft Genome Sequence Assemblies, and other genomic data resources
Underlying Map Information
Sequencing Centers of the International Human Genome Sequencing Consortium
Nucleotide Sequence Databases
Trace Archives
SNPs
cDNAs and ESTs
Other Organisms
Other Human Genetics Information
ELSI Information
Funding Agencies
top Draft Genome Sequence Assemblies, and other genomic data resources
UCSC contains the assembly of the draft genome sequence that was analyzed in the February 15, 2001 publication
EBI the Ensembl project provides access to DNA and protein sequences with automatic baseline annotation; allows BLAST analysis
NCBI in addition to the NCBI assembly of the draft genome sequence, this site provides access to other NCBI resources including BLAST analysis
Oak Ridge National Laboratory Java viewers for Human genome data.
RIKEN Genomic Sciences Center gives an overview of the entire human genome structure.
top Underlying Map Information
WashU This page contains links to the fingerprinted clone and accession maps of the human genome
Gene Map 99 Gene map 99 contains data and viewers for radiation hybrid maps.
Marshfield this page contains comprehensive human genetic linkage maps
Genethon This site is contains the Genethon genetic linkage maps
RHdb This is the site for the collaborative Radiation Hybrid mapping

GoldenPath
Netscape: Human Genome Browser Gateway
Location: http://genome.cse.ucsc.edu/goldenPath/octTracks.html
What's Related
Human Genome Browser
Web tool created by Jim Kent of UC Santa Cruz
7 Oct 2000 draft assembly of the human genome
Please enter a position in the genome, set your preferred window width, and press the submit button: (Use BLAT Search to locate a particular sequence in the genome.)
genome position: chr17:45247249-45350955 pixel width 610 Submit
A genome position can be specified by the accession number of a sequenced human genomic clone, an mRNA or EST or STS marker, or a cytological band, a chromosomal coordinate range, or keywords from the Genbank description of an mRNA. See the User Guide for more help.
Request: Genome Browser Response:
chr19 Displays all of chromosome 19
20p13 Displays region for band p13 on chr 20
4q28 Displays band q28 on chr 4, gene region determining red hair color
chr3:1-1000000 Displays first million bases of chr 3, counting from p arm telomere
D16S3046 Displays region around STS marker D16S3046 from the Genethon/Marshfield maps (open "STS Markers" track by clicking to see this marker)
AA205474 Displays region of EST with GenBank acc. AA205474 in BRCA1 cancer gene on chr 17 (open "spliced ESTs" track by clicking to see this EST)
ctg13698 Displays region of the fingerprint clone contig ctg13698 from the Wash. U. map (set "FPC contigs" track to "dense" and refresh to see FPC contigs)
AP001670 Displays region of clone with GenBank accession AP001670 (open "coverage" track by clicking to see this clone)
AF083811 Offers 2 coordinate choices on chr 7 and chr 22 for this mitotic checkpoint mRNA
PRNP Offers coordinates choices for nested mRNAs for prion gene, chr 20p
pseudogene mRNA Lists transcribed pseudogenes but not cDNAs
homeobox caudal Lists mRNAs for caudal homeobox genes
valyl-tRNA Lists mRNAs for valyl tRNA synthetases but not unsubmitted tRNA
zinc finger Lists many zinc finger mRNAs
kruppel zinc finger Lists only kruppel-like zinc fingers
huntington Lists candidate genes associated with Huntington's disease
zahler Lists mRNAs deposited by scientist named Zahler
Evans,J.E. Lists mRNAs deposited by co-author J.E. Evans
Use this last format for entry authors -- even though Genbank searches require Evans JE format, GenBank entries themselves use Evans,J.E. internally.

BLAT Search

Netscape: BLAT Search

Location: http://genome.cse.ucsc.edu/cgi-bin/hgBlat?db=hg5

What's Related

BLAT Search Human Genome

Freeze: Oct. 7, 2000

Query type: BLAT's guess

Sort output: query,score

Submit

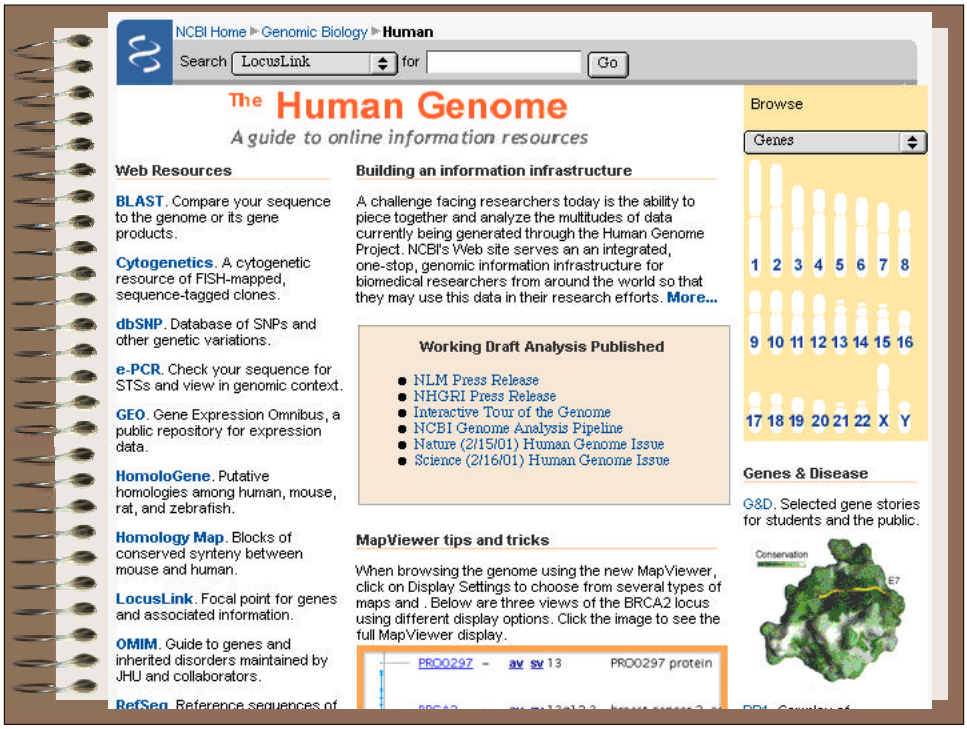
Please paste in a query sequence to see where it is located in the UCSC assembly of the human genome. Multiple sequences can be searched at once if separated by a line starting with > and the sequence name.

Only DNA sequences less than 20,000 bases and protein or translated sequence of less than 4000 letters will be processed. If multiple sequences are submitted at the same time, the total limit is 50,000 bases or 10,000 letters.

BLAT on DNA is designed to quickly find sequences of 95% and greater similarity of length 40 bases or more. It may miss more divergent or shorter sequence alignments. It will find perfect sequence matches of 33 bases, and sometimes find them down to 22 bases. BLAT on proteins finds sequences of 80% and greater similarity of length 20 amino acids or more. In practice DNA BLAT works well on primates, and protein blat on land vertebrates

BLAT is not BLAST. DNA BLAT works by keeping an index of the entire genome in memory. The index consists of all non-overlapping 11-mers except for those heavily involved in repeats. The index takes up a bit less than a gigabyte of RAM. The genome itself is not kept in memory, allowing BLAT to deliver high performance on a reasonably priced Linux box. The index is used to find areas of probable homology, which are then loaded into memory for a detailed alignment. Protein BLAT works in a similar manner, except with 4-mers rather than 11-mers. The protein index takes a little more than 2 gigabytes

BLAT was written by Jim Kent. Like most of Jim's software interactive use on this web server is free to all. Sources and executables to run batch jobs on your own server are available free for academic, personal, and non-profit purposes. Non-exclusive commercial licenses are also available. Contact Jim for details.

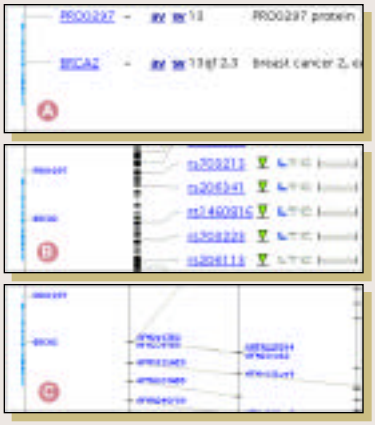


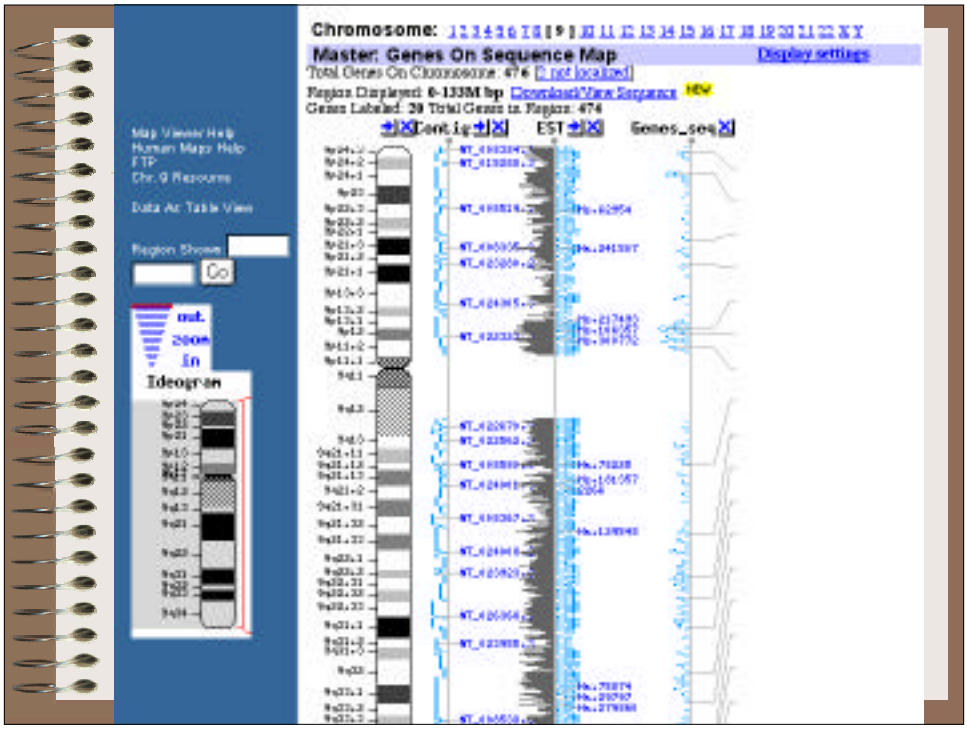
NCBI Display options

A. Genes

B. Variations, juxtaposed with genes

C. Several STS maps, juxtaposed with genes

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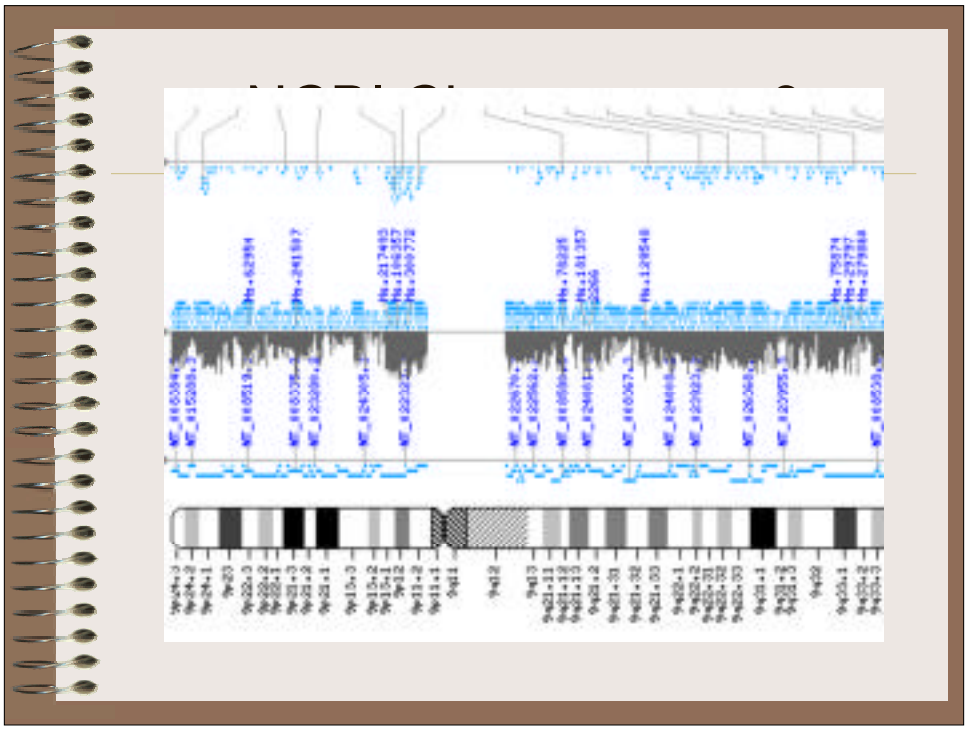
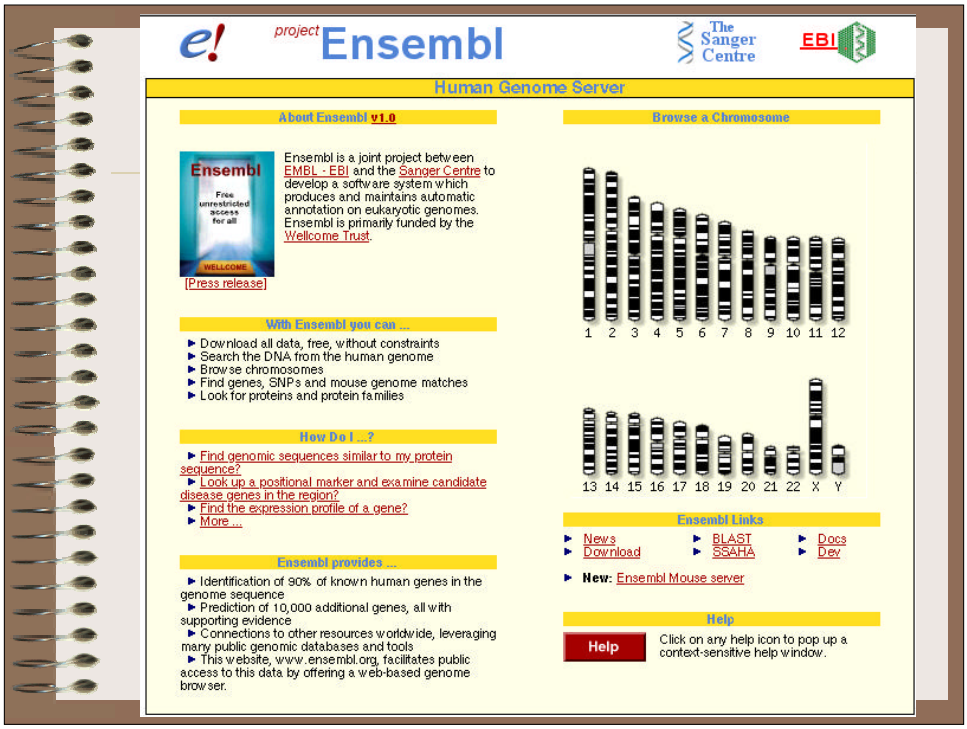
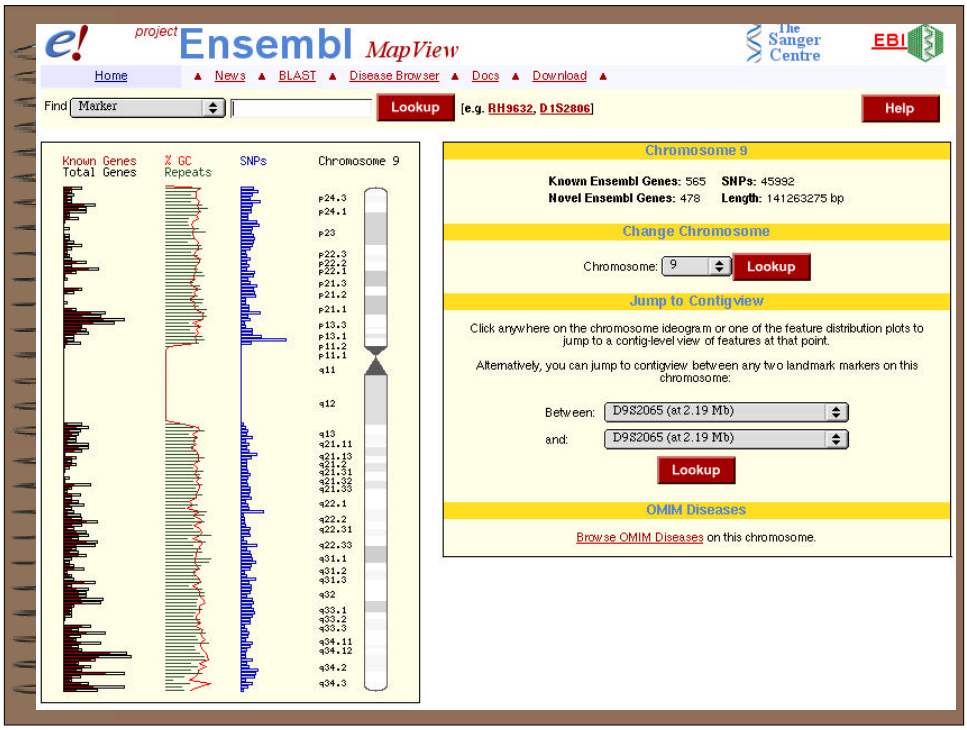
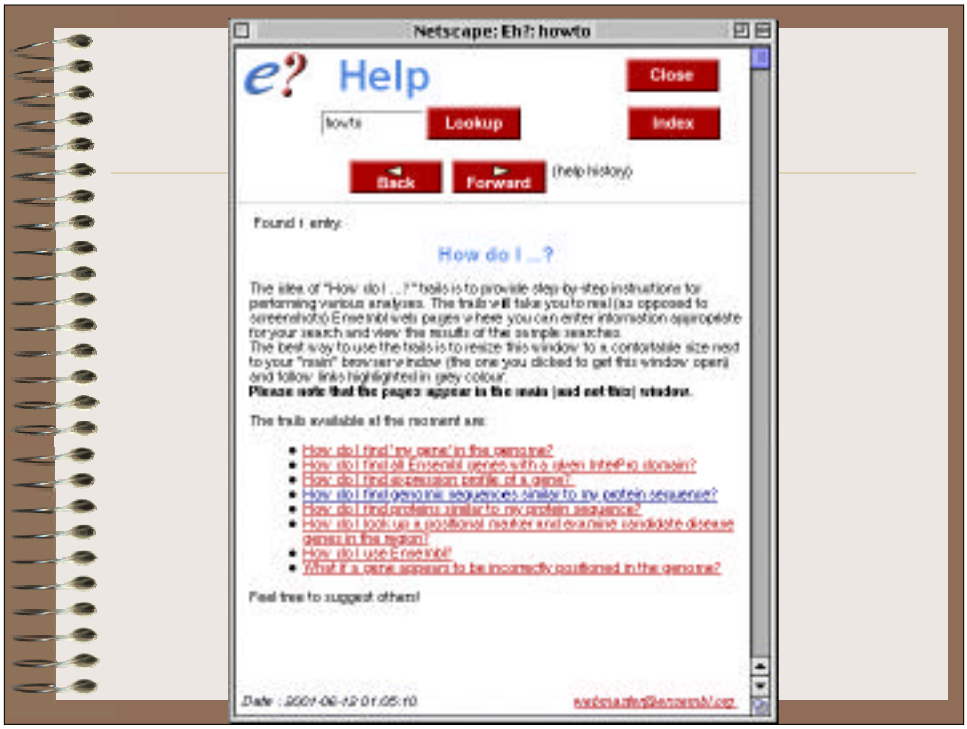
Master: Genes On Sequence Map
Display settings
Total Genes On Chromosome: 476
Region Displayed: 0-133M bp
Genes Labeled: 20 Total Genes in Region: 474
Contig
EST
Genes_seq
Map Viewer Help
Human Maps Help
FTP
Chr. 9 Resources
Data As Table View
Region Shown
Go
out
zoom
in
Ideogram

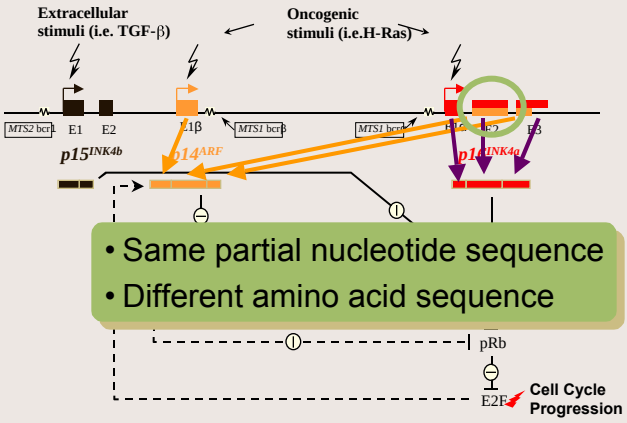



project Ensembl
The Sanger Centre
EBI
Human Genome Server
About Ensembl v1.0
Ensembl is a joint project between EMBL - EBI and the Sanger Centre to develop a software system which produces and maintains automatic annotation on eukaryotic genomes. Ensembl is primarily funded by the Wellcome Trust.
[Press release]
With Ensembl you can ...
Download all data, free, without constraints
Search the DNA from the human genome
Browse chromosomes
Find genes, SNPs and mouse genome matches
Look for proteins and protein families
How Do I ...?
Find genomic sequences similar to my protein sequence?
Look up a positional marker and examine candidate disease genes in the region?
Find the expression profile of a gene?
More ...
Ensembl provides ...
Identification of 90% of known human genes in the genome sequence
Prediction of 10,000 additional genes, all with supporting evidence
Connections to other resources worldwide, leveraging many public genomic databases and tools
This website, www.ensembl.org, facilitates public access to this data by offering a web-based genome browser.
Browse a Chromosome
1 2 3 4 5 6 7 8 9 10 11 12
13 14 15 16 17 18 19 20 21 22 X Y
Ensembl Links
News
Download
BLAST
SSAHA
Docs
Dev
New: Ensembl Mouse server
Help
Help
Click on any help icon to pop up a context-sensitive help window.

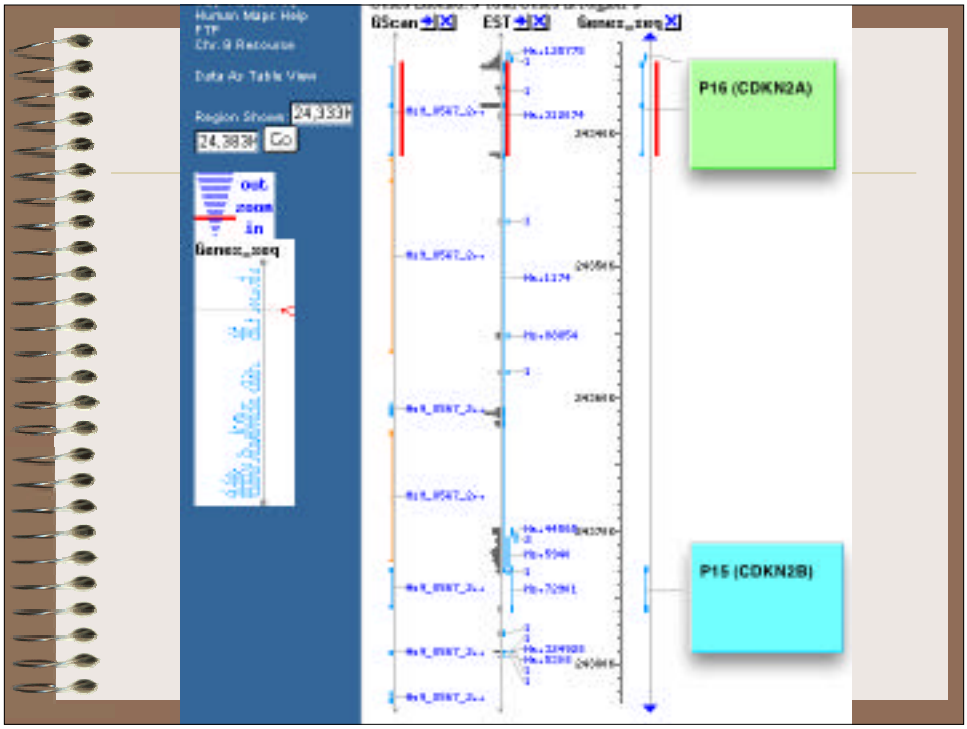

project Ensembl MapView
The Sanger Centre
EBI
Home
News
BLAST
Disease Browser
Docs
Download
Find Marker
Lookup
[e.g. RH9632, D1S2806]
Help
Known Genes
Total Genes
% GC
Repeats
SNPs
Chromosome 9
Chromosome 9
Known Ensembl Genes: 565
SNPs: 45992
Novel Ensembl Genes: 478
Length: 141263275 bp
Change Chromosome
Chromosome: 9
Lookup
Jump to Contigview
Click anywhere on the chromosome ideogram or one of the feature distribution plots to jump to a contig-level view of features at that point.
Alternatively, you can jump to contigview between any two landmark markers on this chromosome:
Between: D9S2065 (at 2.19 Mb)
and: D9S2065 (at 2.19 Mb)
Lookup
OMIM Diseases
Browse OMIM Diseases on this chromosome.



9p21 gene cluster is a nexus of the Rb and p53 pathways



- Same partial nucleotide sequence
- Different amino acid sequence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FTP
Chr. 9 Resource
Data As Table View
Region Shown
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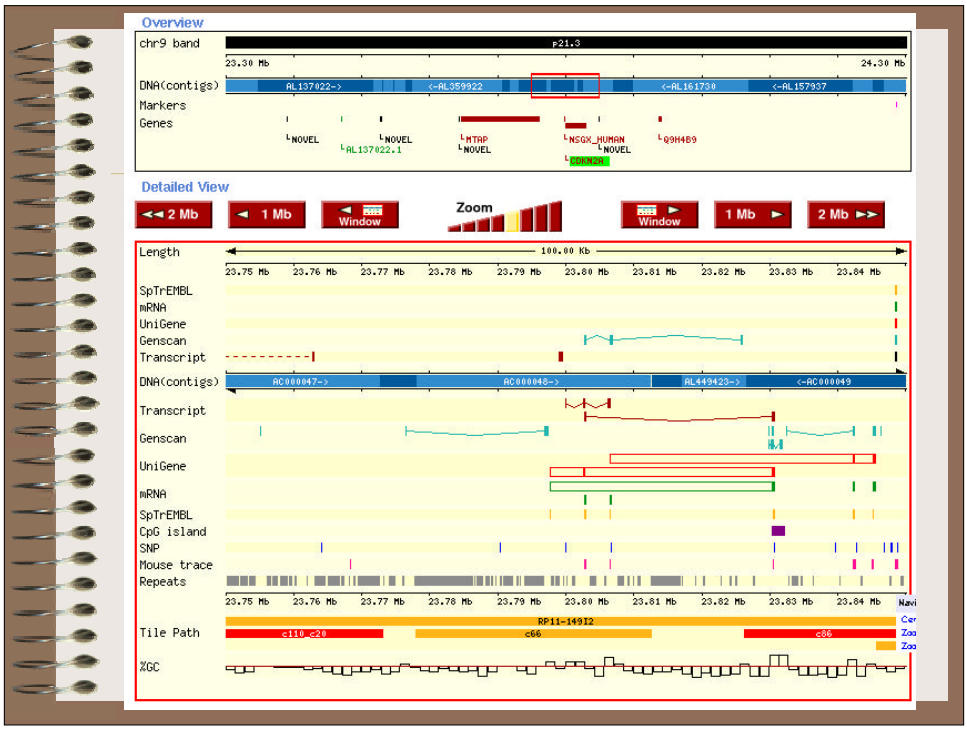
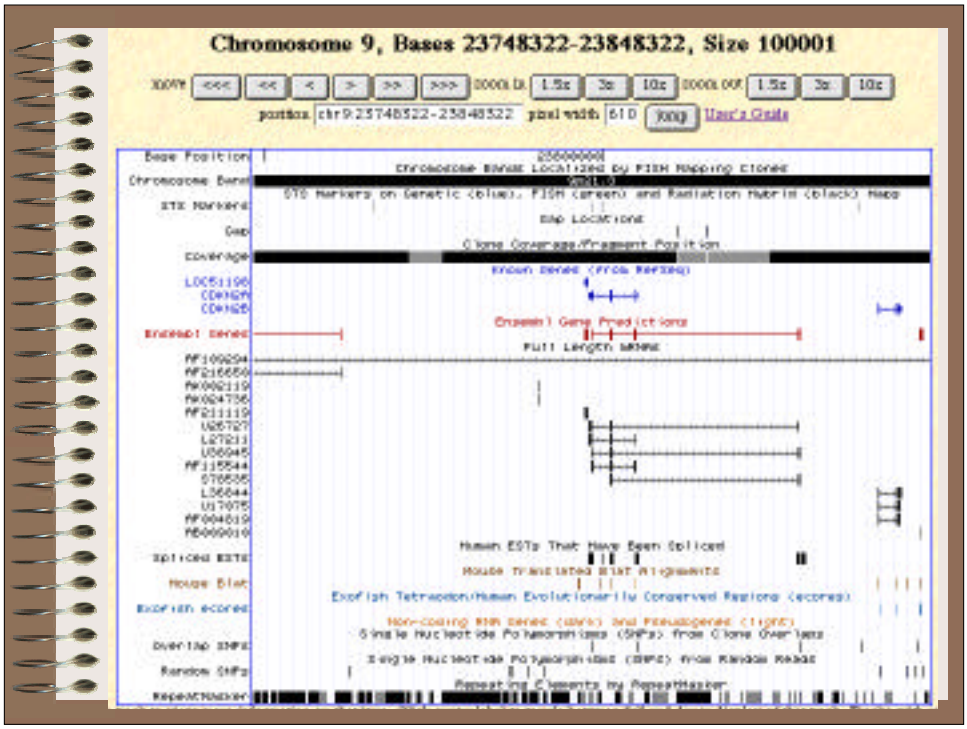
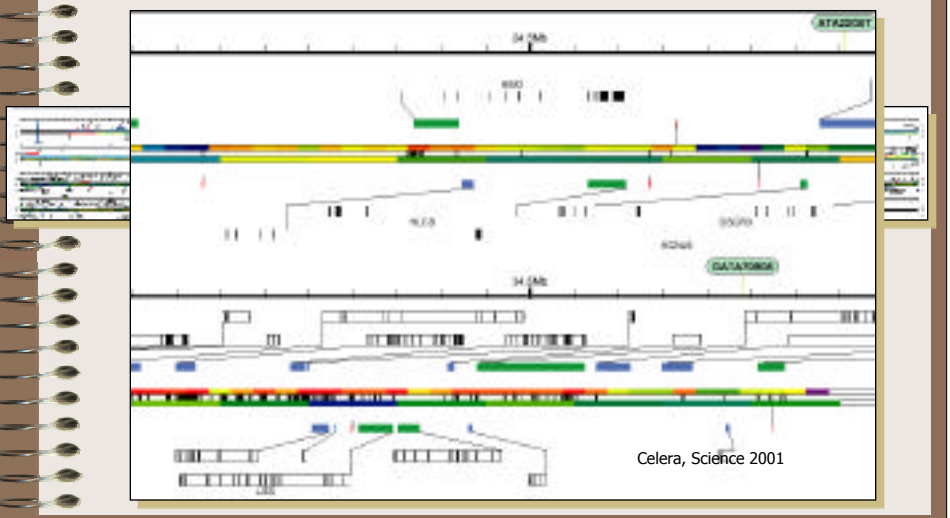
Go
out
zoom
in
Genes_seq
GScan
EST
Genes_seq
P16 (CDKN2A)
P15 (CDKN2B)


Overview
chr9 band
p21.3
23.30 Mb
24.30 Mb
DNA(contigs)
AL137022->
<-AL359922
<-AL161730
<-AL157937
Markers
Genes
NOVEL
AL137022.1
MTAP
NSGX_HUMAN
Q9H4B9
CDKN2A
Detailed View
2 Mb
1 Mb
Window
Zoom
Window
1 Mb
2 Mb
Length
100.00 Kb
23.75 Mb
23.76 Mb
23.77 Mb
23.78 Mb
23.79 Mb
23.80 Mb
23.81 Mb
23.82 Mb
23.83 Mb
23.84 Mb
SpTrEMBL
mRNA
UniGene
Genscan
Transcript
DNA(contigs)
AC000047->
AC000048->
AL449423->
<-AC000049
Transcript
Genscan
UniGene
mRNA
SpTrEMBL
CpG island
SNP
Mouse trace
Repeats
RP11-149I2
Tile Path
c110_c20
c66
c86
%GC



Celera Chromosome 21



Celera, Science 2001

Beyond the Genome

ExPASy Molecular Biology Server

This is the ExPASy (**Ex**pert **P**rotein **A**nalysis **Sy**stem) proteomics server of the Swiss Institute of Bioinformatics (SIB). This server is dedicated to the analysis of protein sequences and structures as well as 2-D PAGE (Disclaimer).

[**Announcements**] [**Job opening**] [**Mirror Sites**]

Databases	Tools and Software Packages

• **SWISS-PROT and TrEMBL** - Protein sequences
• **PROSITE** - Protein families and domains
• **SWISS-2DPAGE** - Two-dimensional polyacrylamide gel electrophoresis
• **SWISS-3DIMAGE** - 3D images of proteins and other biological macromolecules
• **SWISS-MODEL Repository** - Automatically generated protein models
• **CD40Lbase** - CD40 ligand defects
• **ENZYME** - Enzyme nomenclature
• **SeqAnalRef** - Sequence analysis bibliographic references
 	
• **Links to many other molecular biology databases**
	• **Proteomics tools**
	  ○ Identification and characterization
	  ○ DNA -> Protein
	  ○ Similarity searches
	  ○ Pattern and profile searches
	  ○ Post-translational modification prediction
	  ○ Primary structure analysis
	  ○ Secondary structure prediction
	  ○ Tertiary structure
	  ○ Transmembrane regions detection
	  ○ Alignment
	• **Melanie 3** - Software for 2-D PAGE analysis
	• **SWISS-MODEL** - Automated knowledge-based protein modelling server
	• **Swiss-PdbViewer** - Macintosh/PC tool for structure display and analysis
	• **Boehringer Mannheim's Biochemical Pathways**

Education and services	**Documentation**
• **The ExPASy FTP server** • **Swiss-Shop** - automatically obtain (by email) new sequence entries relevant to your field(s) of interest • **Masters Degree in Bioinformatics** • **2-D PAGE training** - attend a one-week course in Geneva • **SWISS-2DSERVICE** - get your 2-D Gels performed according to Swiss standards	• **What's New on ExPASy** • **SWISS-FLASH** electronic bulletins • **SWISS-PROT documents** • **How to create HTML links to ExPASy** • **Complete table of available documents**
Links to lists of molecular biology resources	**Links to some major molecular biology servers**
• **Amos' WWW links** - The ExPASy list of Biomolecular servers • **BioHunt** - Search the internet for molecular biology information • **WORLD-2DPAGE** - Links to 2-D PAGE database servers and 2-D PAGE related servers and services	• **European Bioinformatics Institute (EBI)** • **National Center for Biotechnology Information (NCBI)** • **Japanese GenomeNet** • **Australian National Genomic Information Service**

Physical Properties

Prediction of Physical Properties

- Compute pI/MW http://www.expasy.ch/tools/pitool.html
- MOWSE http://srs.hgmp.mrc.ac.uk/cgi-bin/mowse
- PeptideMass http://www.expasy.ch/tools/peptide-mass.html
- TGREASE ftp://ftp.virginia.edu/pub/fasta/
- SAPS http://www.isrec.isb-sib.ch/software/SAPSform.html

Prediction of Protein Identity Based on Composition

- AACompIdent http://www.expasy.ch/tools/aacomp/
- AACompSim http://www.expasy.ch/tools/aacsim/
- PROPSEARCH http://www.embl-heidelberg.de/prs.html

Motifs and Patterns

- BLOCKS http://blocks.fhcrc.org
- Pfam http://www.sanger.ac.uk/Software/Pfam/
- PRINTS http://www.bioinf.man.ac.uk/dbbrowser/PRINTS/PRINTS.html
- ProfileScan http://www.isrec.isb-sib.ch/software/PFSCANform.html

Protein Structure

Prediciton of Secondary Structure and Folding Classes

- nnpredict http://www.cmpharm.ucsf.edu/_nomi/nnpredict.html
- PredictProtein http://www.embl-heidelberg.de/predictprotein/
- SOPMA http://pbil.ibcp.fr/
- Jpred http://jura.ebi.ac.uk:8888/
- PSIPRED http://insulin.brunel.ac.uk/psipred
- PREDATOR http://www.embl-heidelberg.de/predator/predatorinfo.html

Prediction of Specialized Structures or Features

- COILS http://www.ch.embnet.org/software/COILSform.html
- MacStripe http://www.york.ac.uk/depts/biol/units/coils/mstr2.html
- PHDtopology http://www.embl-heidelberg.de/predictprotein
- SignalP http://www.cbs.dtu.dk/services/SignalP/
- TMpred http://www.isrec.isb-sib.ch/ftp-erver/tmpred/www/TMPREDform.html

Structure Prediction

- DALI http://www2.ebi.ac.uk/dali/
- Bryant-Lawrence ftp://ncbi.nlm.nih.gov/pub/pkb/
- FSSP http://www2.ebi.ac.uk/dali/fssp/
- UCLA-DOE http://fold.doe-mbi.ucla.edu/Home
- SWISS-MODEL http://www.expasy.ch/swissmod/SWISS-MODEL.html
- TOPITS http://www.embl-heidelberg.de/predictprotein/