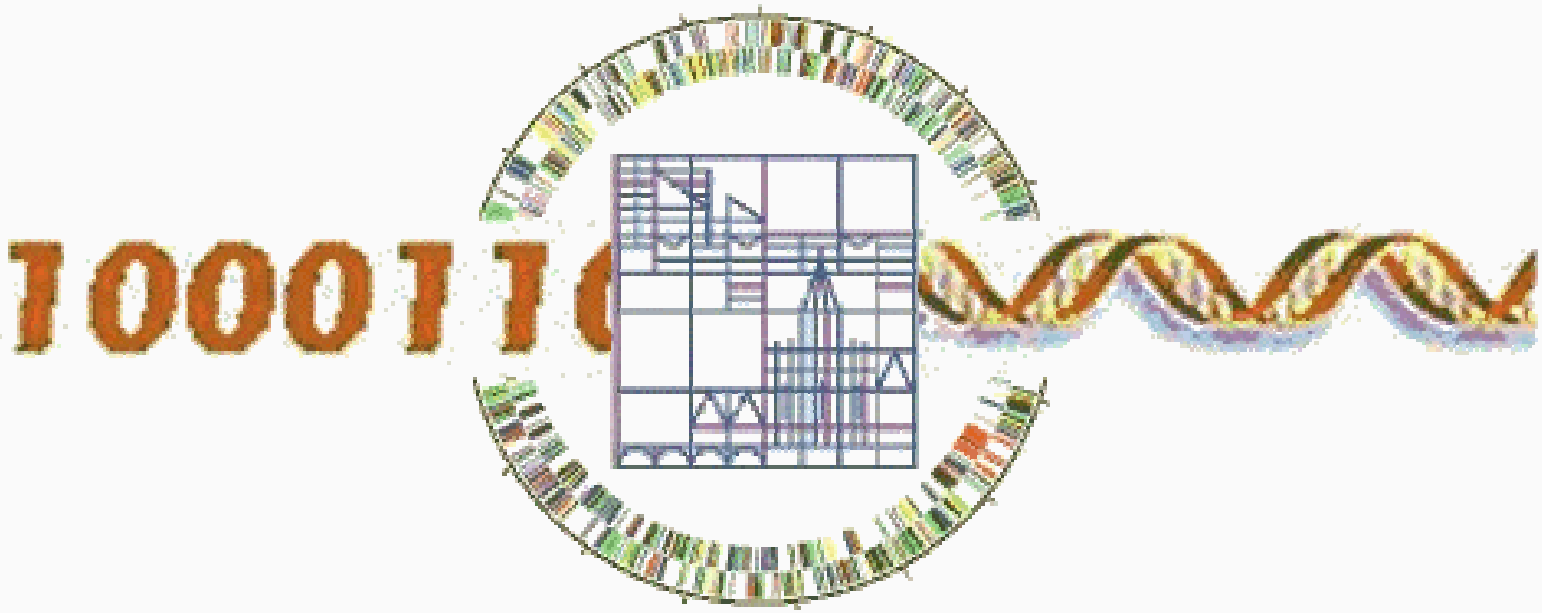
Bioinformatics and Drug Research

Klaus P. Schaefer



Databases Survey

Summer Course - Lecture 05 - Version of May 26, 2003

http://www.uni-konstanz.de/FuF/Bio/Bioinformatik/

A special LinkResource covering various DataBases

BIOINFORMATICS and Drug Research

US English | Bio Info | Audience | Research | Infos | News

Databases in the WWW

NetResources in Bioinformatics

Databases

- TIGR Database (TDB) - The Institute for Genomic Research
  The TIGR Databases are a collection of curated databases containing DNA and protein sequence, gene expression, cellular role, protein family, and taxonomic data for microbes, plants and humans.
- Human Genome Database (DoubleTwist)
  Subscriber-based Human genome Database
- Human Unidentified Gene-Encoded Large Proteins
  HUGE - A Database of Human Unidentified Gene-Encoded Large Proteins
- Human BAC Ends
  Sequences from the ends of bacterial artificial chromosome (BAC) clones provide highly specific markers
- The Phytophthora Genome Initiative
  Phytophthora comprise a group of plant pathogenic organisms (Oomycetes) that attack an extremely broad range of agronomically important species, affecting many major crops worldwide. Their cumulative global damage is estimated at billions of dollars annually.
- Saccharomyces Genome Database
  SGDTM is a scientific database of the molecular biology and genetics of the yeast Saccharomyces cerevisiae, which is commonly known as baker's or budding yeast.
- Yeast Intron DataBase
  The Yeast Intron DataBase (YIDB) contains currently available information about all introns encoded in the nuclear and mitochondrial genomes of the yeast Saccharomyces cerevisiae.
- Database of Arabidopsis thaliana Annotation
  All annotated Coding sequences from Arabidopsis Genomic DNA Sequencing are in this Database.
- ZmDB: Maize Genome Database
  ZmDB (Zea mays DataBase) website, home of
- TRIPLES DataBase
  database of TRansposon-Insertion Phenotypes, Localization, and Expression in Saccharomyces

DataBase Links are given with brief description of content

http://www.uni-konstanz.de/FuF/Bio/Bioinformatik/bivli_db.htm



There are many Types of DataBases

- Just some examples ...
- Organisms
  - → Eukaryotes, Prokaryotes
  - → Animals, Plants
  - → Viruses
- Organelles
  - → Mitochondria, Chloroplasts
- Molecular Classes
  - → mRNA
  - → tRNA etc.
- Special Sequences
  - → Promotors, Attenuators, Enhancers, Introns etc.



Examples of DataBanks covering Organisms – Whole Genomes

- Human Genome
  - → TIGR Site
- Bacteria
  - → *Escherichia coli*
  - → *Helicobacter pylori*
- Plants
  - → Maize
  - → Rice
- Fungi
  - → *Saccharomyces cerevisiae*
  - → Dictyostelium
- Viruses
  - → Adenoviruses
  - → HIV

Always a good Site to start with ... TIGR



WebSite Info - Genome Projects
TIGR's Genome Projects are a collection of curated databases containing DNA and protein sequence, gene expression, cellular role, protein family, and taxonomic data for microbes, plants and humans. Anonymous FTP access to sequence data is also provided.

http://www.tigr.org/tdb/index.shtml

The Human Genome DataBase is still evolving ...



Human Chromosome Genomic Sequencing Status

TIGR has been awarded a grant from the NHGRI to sequence the short arm of chromosome 16. TIGR will shotgun sequence clones from the Caltech BAC Library.

This project is a collaboration between TIGR, Caltech, and Los Alamos National Laboratory. A summary of the status of the map can be found at the CalTech chromosome 16 page

TIGR has completed, annotated, and submitted to GenBank 11,789,414 bp of human genomic sequence.

	Total Clones	Size (bp)
Completed Clones	82	11,789,414
Clones in Progress	9	1,126,000
Clones in Preparation	40	5,080,000

Completed Clones Clones in Progress Clones in Preparation Clones in Other Chromosomes

Clone Name: Search Clear

Chromosome 16 Sequencing Project

- Completed Clones
- Clones in Progress
- Clones in Library Preparation

Other Sequencing Projects

Human Gene Name Search

Search BAC End Sequence Database

http://www.tigr.org/tdb/humgen/humgen.html

WebSite Info - Human Chromosome Genomic Sequencing Status TIGR has been awarded a grant from the NHGRI to sequence the short arm of chromosome 16. TIGR will shotgun sequence clones from the Caltech BAC Library. This project is a collaboration between TIGR, Caltech, and Los Alamos National Laboratory. A summary of the status of the map can be found at the CalTech chromosome 16 page. TIGR has completed, annotated, and submitted to GenBank 11,789,414 bp of human genomic sequence.

A Specialized DataBase for long Human Proteins

HUGE

A Database of Human Unidentified Gene-Encoded Large Proteins Analyzed by Kazusa cDNA Project

Thank you for your interest in our HUGE Protein Database

The HUGE protein database has been created to publicize the fruits of our Human cDNA project at the Kazusa DNA Research Institute. In this project, we plan to sequence and analyze long (>4 kb) human cDNAs and to establish methods by using the sequence data how to predict the primary structure of proteins of various biological activities. Currently, we focus on the analysis of cDNA clones encoding particularly large proteins (>50 kDa). The basic concept underlying our project and the strategies employed have been described elsewhere *(Ohara et al., 1997)*. Our HUGE protein database contains various types of information derived from the predicted primary structure data of newly identified human proteins.

The HUGE protein database are expected to cover various sets of large human proteins of hitherto unidentified functions. They are likely to be involved in cellular structure/motility (such as cytoskeleton, membrane skeleton, and motor proteins), gene expression and nucleic acid metabolism, cell signaling/communication (such as cellular adhesion, signal transduction, channels, and receptors), and so on.

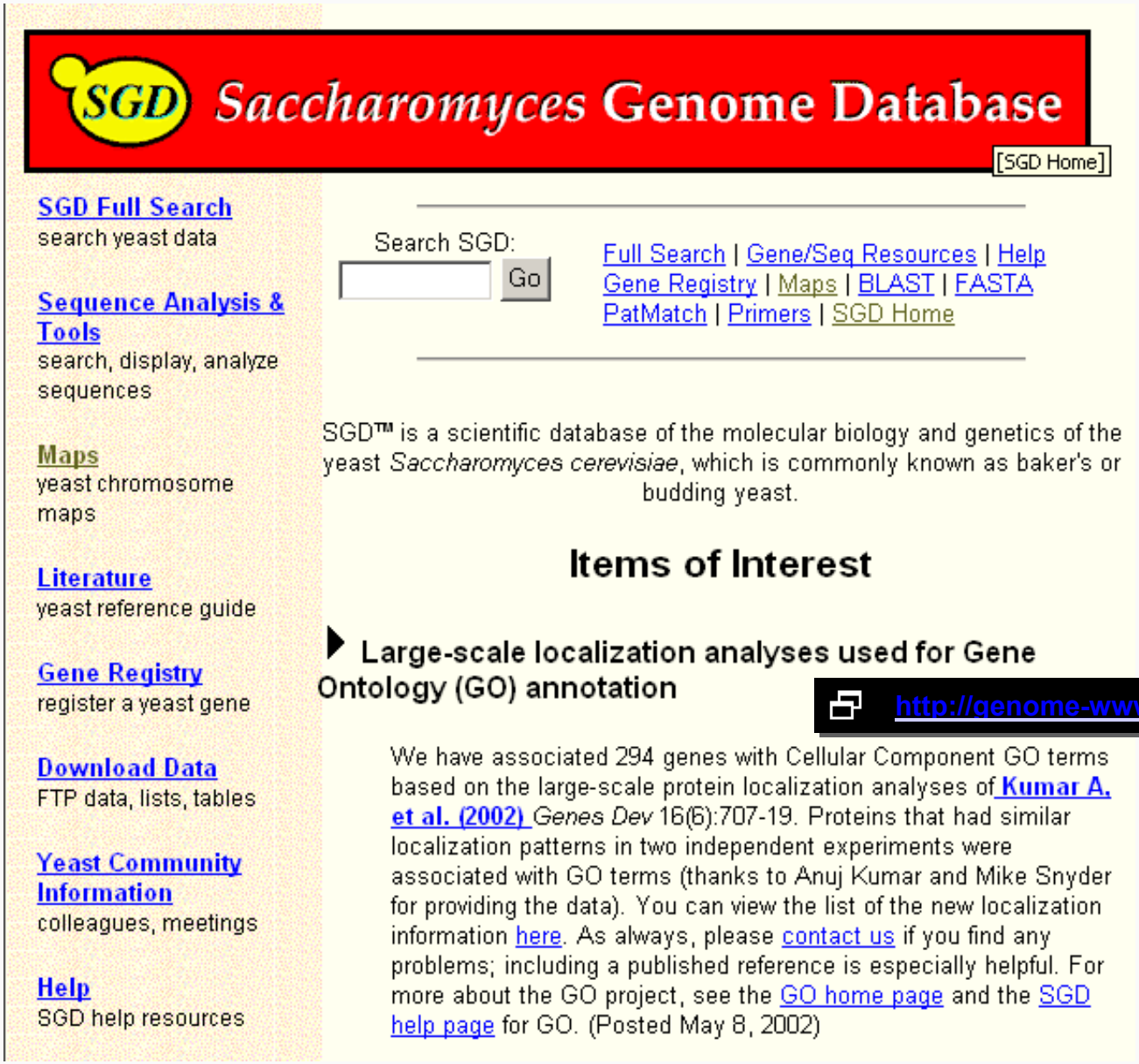
REFERENCES

- Kikuno R., Nagase T., Waki M. et al., HUGE: a database for human large proteins identified in the Kazusa cDNA sequencing project. *Nucleic Acids Res.* **30**, 166-168, (2002).
- Ohara, O., Nagase, T., Ishikawa, K.-I. et al., Construction and characterization of human brain cDNA libraries suitable for analysis of cDNA clones encoding relatively large proteins. *DNA Res.*, **4**, 53-59, (1997).

http://www.kazusa.or.jp/huge/

WebSite Info - The HUGE protein database has been created to publicize the fruits of our Human cDNA project at the Kazusa DNA Research Institute.

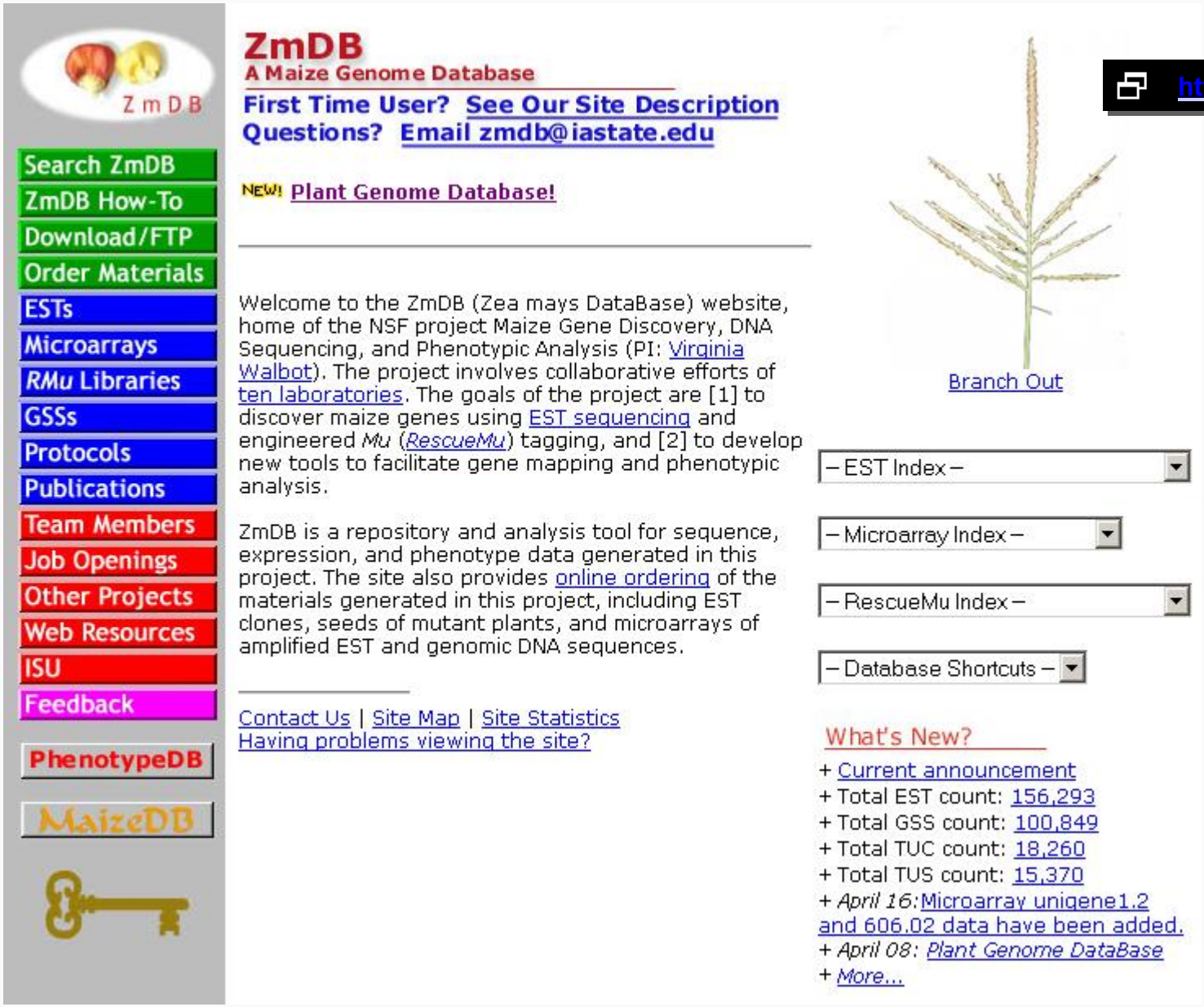
One of the Yeast Genome Sites



Website Info - SGDTM is a scientific database of the molecular biology and genetics of the yeast Saccharomyces cerevisiae, which is commonly known as baker's or budding yeast

http://genome-www.stanford.edu/Saccharomyces/

The Maize Genome DataBase

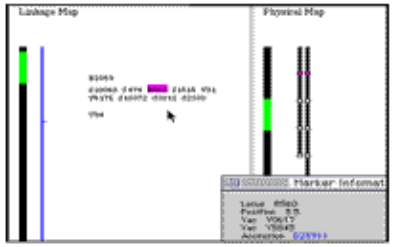


http://zmdb.iastate.edu/

WebSite Info - ZmDB is a repository and analysis tool for sequence, expression, and phenotype data generated in this project. The site also provides online ordering of the materials generated in this project, including EST clones, seeds of mutant plants, and microarrays of amplified EST and genomic DNA sequences.

The Rice Genome DataBase

INE 稲



INE, pronounced [i-ne], is the Japanese word for rice plant. It is used here as an abbreviation for INtegrated rice genome Explorer - a database integrating the genetic map, physical map and sequencing information of rice genome. This database is written in JAVA language.

INE needs Netscape Navigator™ 4.0 or Netscape Communicator™ 4.0 and later.

The integrated maps are presented for each chromosome. Alternatively search marker directly leads to available data on specific DNA clones.

Choose Chromosome Chr.1

go

Search Keyword

search

webmaster@staff.or.jp

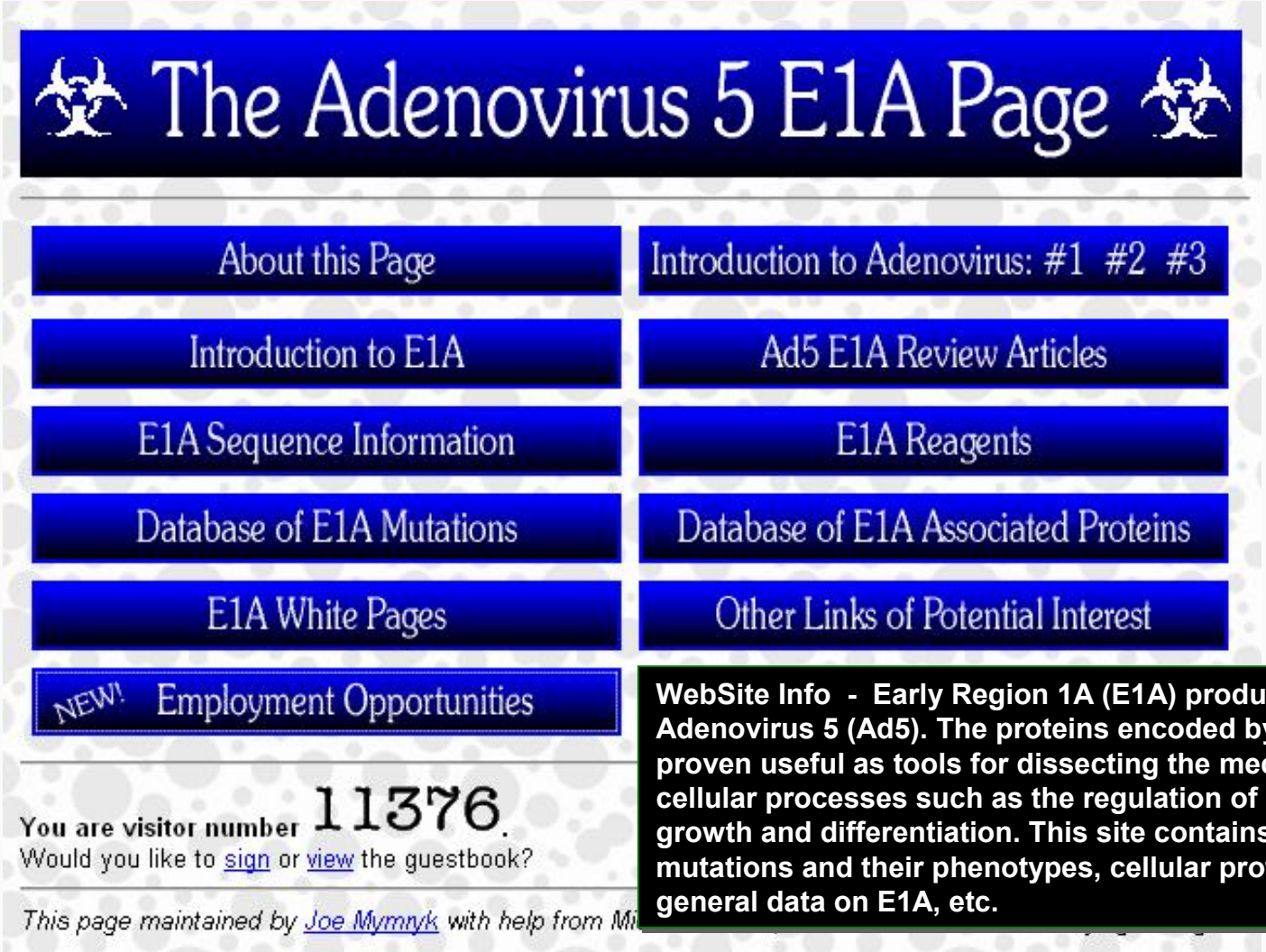
last updated 2000.12.20

Copyright (C) Rice Genome Research Program (RGP). 1999 All rights reserved.

WebSite Info - INE is the Japanese word for rice plant. It is used here as an abbreviation for INtegrated rice genome Explorer - a database integrating the genetic map, physical map and sequencing information of rice genome.
The integrated maps are presented for each chromosome. Alternatively search marker directly leads to available data on specific DNA clones.

http://rgp.dna.affrc.go.jp/giot/INE.html

Adenovirus Sequence Sites



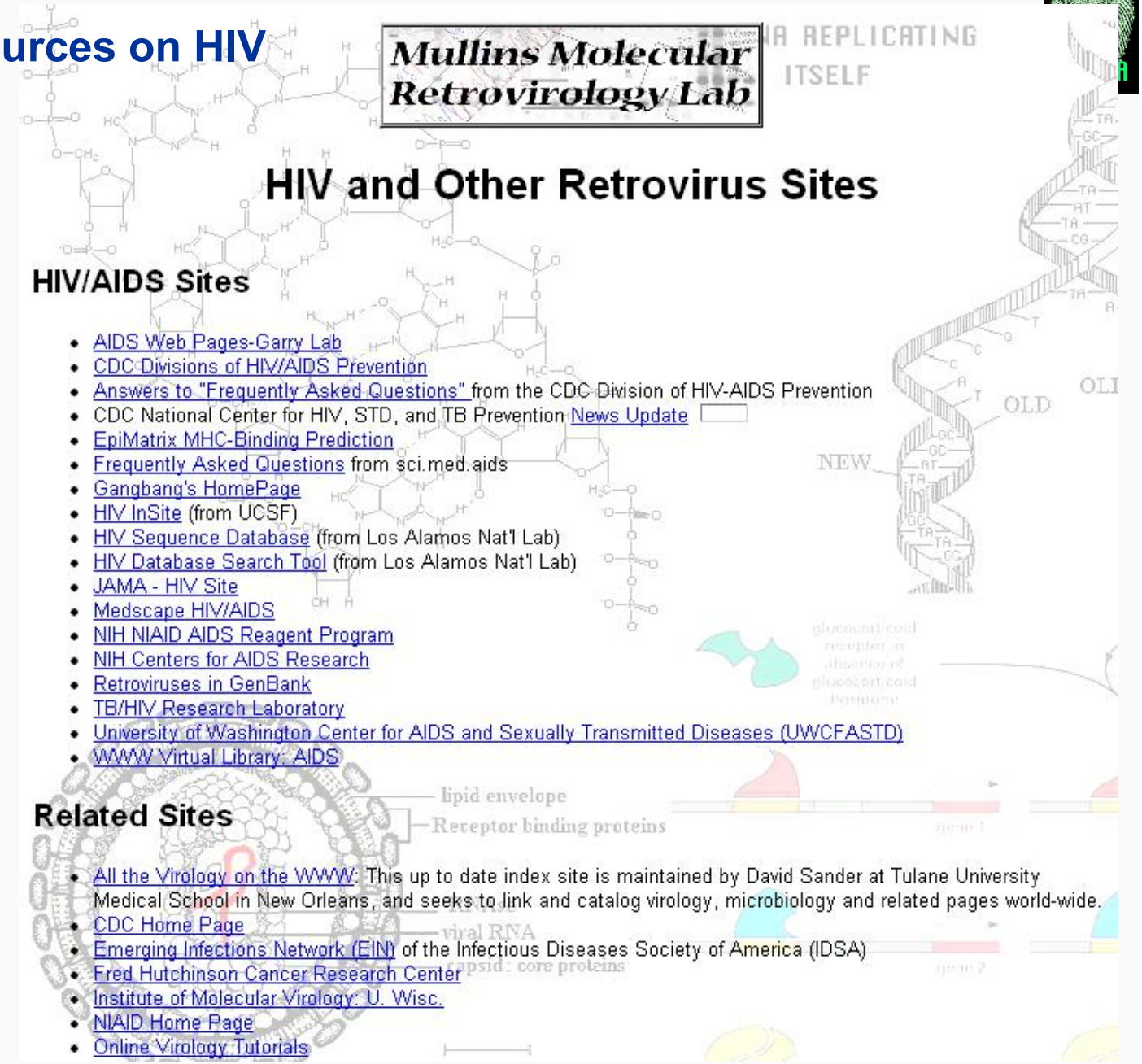
WebSite Info - Early Region 1A (E1A) products of human Adenovirus 5 (Ad5). The proteins encoded by Ad5 E1A have proven useful as tools for dissecting the mechanisms of complex cellular processes such as the regulation of gene expression, cell growth and differentiation. This site contains information on E1A mutations and their phenotypes, cellular proteins targeted by E1A, general data on E1A, etc.

http://www.geocities.com/CapeCanaveral/Hangar/2541/index.html

One of many Resources on HIV

WebSite Info - Internet information resources for HIV/AIDS are numerous and easily accessible through the World Wide Web. Like other subject areas, this vast amount of information has not been adequately organized. For my attempt, I have grouped all the HIV/AIDS sites that we have located into several general categories. These are not exclusive and some sites may appear in more than one area.

http://ubik.microbiol.washington.edu/HIVsites.html



Retroviral Resource

WebSite Info
DB Search does a straightforward search on a large number of database fields.
Ouput comes in the form og Genbank-style sequences.
This interface does allow searches by subtype, and country, and accession number or sequence name, and can produce output file sin Genbank, Fasta, and Intelligenetics format.

http://retro.lanl.gov/

HIV Databases

The HIV databases contain data on HIV genetic sequences, immunological epitopes, drug resistance-associated mutations, and vaccine trials. The website also gives access to a large number of tools that can be used to analyze these data. This project is funded by the Division of AIDS of the National Institute of Allergy and Infectious Diseases (NIAID), a part of the National Institutes of Health (NIH). Click on any of the links below to access a database.

- Sequence Database
- Resistance Database
- Immunology Database
- Vaccine Trials Database

News

- We have new search interfaces for the Immunology and Sequence Databases. The Immunology Database also has new search capabilities. Please try out the new interfaces and let us know what you think about them. March 5, 2002.
- The CTL and Helper databases have been updated for 2001. March 5, 2002.
- The Barcelona meeting is upcoming in July. Check out our meetings page for more information. March 5, 2002.
- We have an interim version of our HIV/SIV Vaccine Trials Database available. We are currently designing a new vaccine trials database which will also include human trials. December 3, 2001.

Old News

Questions or comments? Contact us at seq-info@t10.lanl.gov

Los Alamos NATIONAL LABORATORY

Operated by the University of California for the US Department of Energy
Copyright © 2001 UC | Disclaimer/Privacy

The Helicobacter Genome DataBase

TIGR
THE INSTITUTE FOR GENOMIC RESEARCH

tigr cmr
comprehensive microbial resource

CMR Home | Genomes | CMR Blast | Align Genomes | Related Links | Help
Genome Home | Overview | Analyses | List By Category | Searches | Related Links

Helicobacter pylori 26695

Welcome to the *Helicobacter pylori 26695* genome page. Listed below are some general properties and a chromosomal display of *Helicobacter pylori 26695*. Use the Genome tabs on the menu above to view more information and analyses on this genome.

General Information on *Helicobacter pylori 26695*:

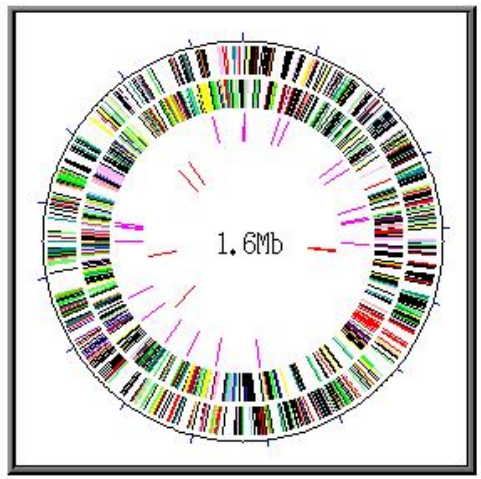
Sequencing Center:	TIGR
Funding Center:	TIGR
Publication:	PubMed Abstract
Sequence & Annotation Acquisition:	CMR Batch Download
	CMR Gene Attribute Download
	Genbank FTP
	TIGR FTP
Completed Genome:	Yes
Other:	Background Information

Taxonomy of *Helicobacter pylori 26695*:

Kingdom: Bacteria

Chromosomal Display:

Below is a schematic representation of the *Helicobacter pylori 26695* chromosome. Choose a DNA molecule from the Select DNA Molecule menu below to get a larger, more detailed view.



WebSite Info - Helicobacter pylori is a micro-aerophilic, Gram-negative, slow-growing, spiral-shaped and flagellated organism. Its most characteristic enzyme is a potent multisubunit urease that is crucial for its survival at acidic pH and for its successful colonization of the gastric environment, a site that few other microbes can colonize. H. pylori is probably the most common chronic bacterial infection of humans, present in almost half of the world population. The presence of the bacterium in the gastric mucosa is associated with chronic active gastritis and is implicated in more severe gastric diseases, including chronic atrophic gastritis (a precursor of gastric carcinomas), peptic ulceration and mucosa-associated lymphoid tissue lymphomas.

http://www.tigr.org/tigr-scripts/CMR2/GenomePage3.spl?database=ghp



The TIGR Genome Sites offer more than just a Sequence

Helicobacter pylori 26695

- Genome Overview
  - **DNA molecule Information:** Provides detailed information on each of the DNA molecules found in the organism (chromosomes, plasmids) including the topology (linear or circular), length, %A, T, G, C and number of genes.
  - **Condensed Genome Display:** Shows all of the genes on a DNA molecule as different colored stars. The colors represent different functional roles.
  - **Codon Usage Chart:** Shows the codon usage for all genes in the genome or for each role category.
  - **Role Category Graph:** Shows the number and percentage of genes in the genome assigned to each of the role categories.
  - **Download TIGR Genomes:** Retrieve this TIGR genome using ftp.

- Genome Analyses
  - **GC Plot:** Shows the %GC for a set "window" of nucleotides across the entire DNA molecule. The user has the option to change the size of the %GC window.
  - **COG/TIGRFAM/PFAM Comparison:** Shows the percentage of genes in the genome assigned a COG, a TIGRFAM, a PFAM or any combination of the three. Links to a listing of genes in each category are also included.
  - **2D gel:** Shows a computer model of a 2-Dimensional gel for the genome.

All of the proteins in the CMR are routinely blasted against one another. We call these the "All v/s All" searches. When a new genome is added to the database the all v/s all searches are re-run. The following programs display the data from the all v/s all searches in different graphs. The user is given the option to view the data based on either "Total Protein Hits" or "Best Protein Hits." The programs that use "Total Protein Hits" display all of the blast results for each protein in the graph. The programs the use "Best Protein Hits" only display the single "best" blast result for each protein. The best blast result is the blast result with the best P value.

- **Genome v/s All Organisms "Total Protein Hits":** This page shows the number of "Total Protein Hits" *Helicobacter pylori 26695* has in common with all of the genomes in the CMR (not including itself), based on all v/s all searches. Each protein in *Helicobacter pylori 26695* may have more than one blast hit and consequently the number of "Total Protein Hits" for two organisms may be higher than the total number of genes in either organism.
- **Genome v/s All Organisms "Best Protein Hits":** This page shows the number of "Best Protein Hits" *Helicobacter pylori 26695* has in common with all of the genomes in the CMR (not including itself), based on all v/s all searches. The "Best Protein Hit" for each *Helicobacter pylori 26695* protein is determined by the protein from the blast search that has the best P value. Because only

The Mitochondrial DataBase

MITOMAP

A human mitochondrial genome database

A compendium of polymorphisms and mutations of the human mitochondrial DNA



Search MITOMAP for information on: Perform search Clear

Gene, disease, enzyme names may be abbreviated, truncated, etc.

Examples of search words: ND1, ND4, NARP, LHON, 11778, 3243, Leu, Lys, etc.

WebSite Info - A human mitochondrial genome database.
A compendium of polymorphisms and mutations of the human mitochondrial DNA

New citations added weekly. If there are publications not yet cited in Mitomap that you wish added, please email the full reference including authors, title, journal, year, volume, page number, relevant nucleotides/disease, etc. to mitocite@gen.emory.edu. We would also appreciate a pdf file of the publication, if available. Complete data sets from articles that are either 'in-press' or already in publication are welcome via email submission. Unpublished lab data may be submitted to Mitomap using the unpublished polymorphisms form.

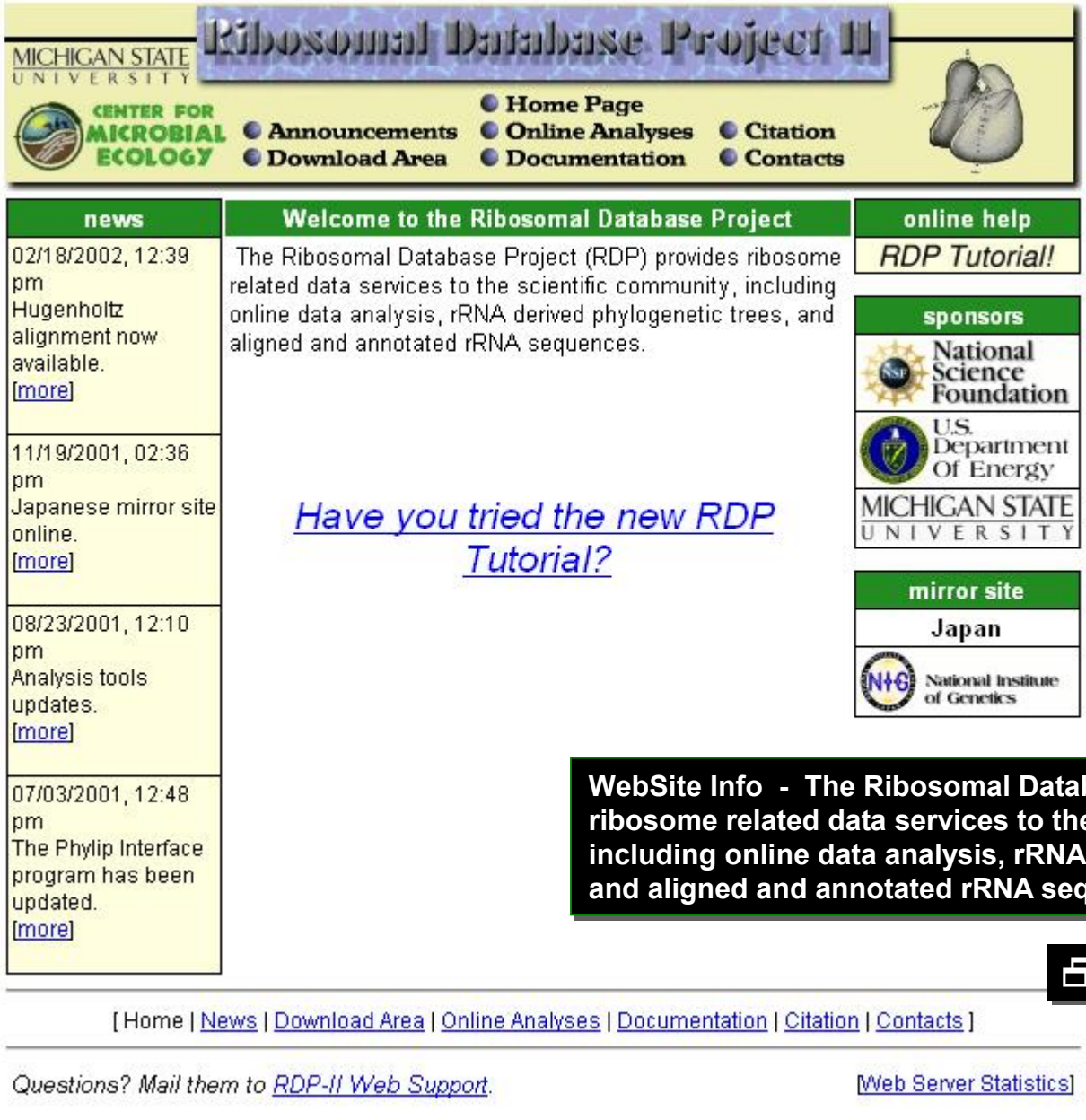
Mitomap Quick Reference

http://www.gen.emory.edu/mitomap.html

The Human Mitochondrial Sequence
Amino Acid Translation Tables
Mitochondrial References (A-Z) (1 MB)
or view only authors A-L or authors M-Z
Mitochondrial Human Genome Report
New! MitoAnalyzer Tool (NIST)

Illustrations
-Mitochondrial DNA Map
-Eleven pathological mutations in $tRNA^{Leu(UUR)}$
-Mitochondrial energetics
-Diabetes metabolism & the mitochondria
-World migrations

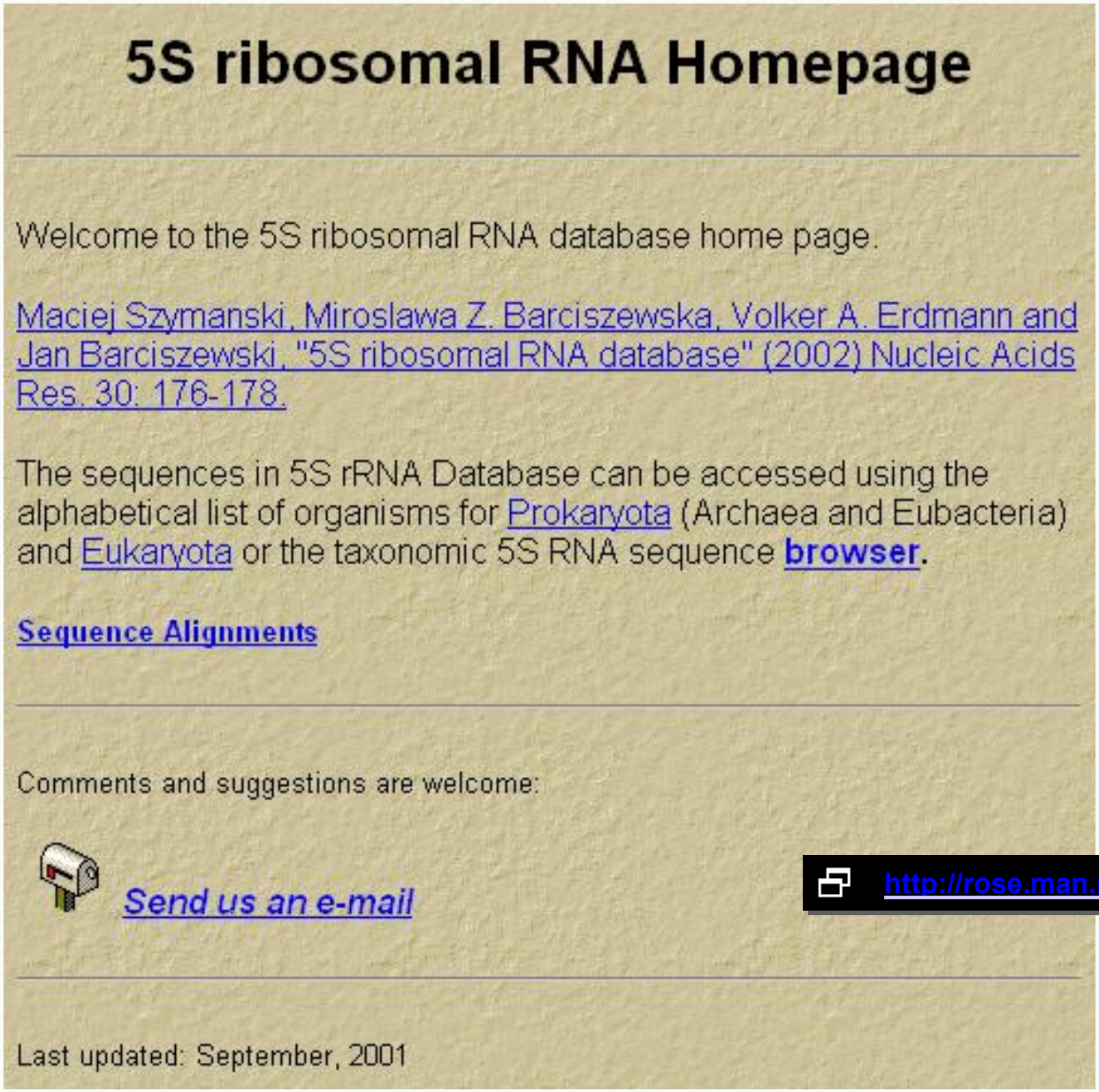
The rRNA DataBase



WebSite Info - The Ribosomal Database Project (RDP) provides ribosome related data services to the scientific community, including online data analysis, rRNA derived phylogenetic trees, and aligned and annotated rRNA sequences.

http://rdp.cme.msu.edu/html/

The 5S rRNA DataBase



5S ribosomal RNA Homepage

Welcome to the 5S ribosomal RNA database home page.

Maciej Szymanski, Miroslawa Z. Barciszewska, Volker A. Erdmann and Jan Barciszewski, "5S ribosomal RNA database" (2002) Nucleic Acids Res. 30: 176-178.

The sequences in 5S rRNA Database can be accessed using the alphabetical list of organisms for Prokaryota (Archaea and Eubacteria) and Eukaryota or the taxonomic 5S RNA sequence **browser**.

Sequence Alignments

Comments and suggestions are welcome:

Send us an e-mail

Last updated: September, 2001

WebSite Info - The sequences in 5S rRNA Database can be accessed using the alphabetical list of organisms for Prokaryota (Archaea and Eubacteria) and Eukaryota or the taxonomic 5S RNA sequence browser.

http://rose.man.poznan.pl/5SData/index.html

An Exon-Intron DataBase

EID (from GenBank 115)

http://mcb.harvard.edu/gilbert/EID/

WebSite Info - The Exon-Intron Database
An exhaustive database of protein-coding intron-containing genes

The Exon-Intron Database

An exhaustive database of protein-coding intron-containing genes

Serge Saxonov, Iraj Daizadeh, Alexei Fedorov, and Walter Gilbert

Nucleic Acids Res. 2000 Jan 1;28(1):185-190.

	Unix gzip-ed	Windows zip-ed	Uncompressed size
The entire distribution. Includes tools, makers and all the databases.	208mb	208mb	800mb
All the protein sequences (58,130):	15mb	16mb	36mb
All the DNA sequences (58,130):	57mb	52mb	195mb
Headers for all the sequences	30mb	30mb	215 mb
Genes that, based on the header information, were experimentally determined (a subset of the above):			
Protein sequences (25,130):	5mb	5mb	13mb
DNA sequences (25,130):	18mb	18mb	63mb
Genes with matches to mRNAs			
Protein sequences (13,021):	3mb	3mb	7mb
DNA sequences (13,021):	16mb	17mb	55mb

A Yeast Intron DataBase

The Séraphin Group left EMBL Heidelberg

The information on this page is **not** maintained at the EMBL any longer.
the hompeage address (as of April 2002) is http://www.cnrs-gif.fr/cgm/epissage/equipe_seraphin.html

---

For your information we provide the old content below. Regards, webmaster@embl-heidelberg.de.

Welcome to

YIDB: the Yeast Intron DataBase

By Pascal J. Lopez and Bertrand Séraphin

http://www.embl-heidelberg.de/ExternalInfo/seraphin/yidb.html

WebSite Info - The Yeast Intron DataBase (YIDB) contains currently available information about all introns encoded in the nuclear and mitochondrial genomes of the yeast Saccharomyces cerevisiae. Introns are divided according to their mechanisms of excision as: pre-mRNA introns, tRNA introns, the HAC1 intron, group I introns, group II introns.
Information about the host genome, the type of RNA in which they are inserted and their primary structure are provided together with references. For nuclear pre-mRNA introns transcription frequencies, as determined by microarray experiments, have also been included.



A DataBase on Non-Coding RNAs

Database of non-coding RNAs

Volker A. Erdmann, Miroslawa Z. Barciszewska, Maciej Szymanski, Abraham Hochberg, Nathan de Groot, and Jan Barciszewski "The non-coding RNAs as riboregulators" (2001) Nucleic Acids Res. 29: 189-193.

| xist; rox, PAT | H19 | CMPD | DGCR5 | G90 | gadd / adapt / vseap | His-1 | IPW | BC200 | BC1 |
| U17HG | U19 | gas5 | sra | hsr-omega | ENOD40 | CR20 | GUT15 | mei | oxyS | aepH | csrB | dsrA | Ibi |

Xist / roX / PAT

http://biobases.ibch.poznan.pl/ncRNA/

RNA	Size	EMBL/GenBank Accession Number	Notes	References
Homo sapiens xist	16,5 kb	M97168		Ref.
Bos taurus xist	n.d.*)	AF104906	partial sequence	Ref.
Mus musculus xist	14.7 kb	L04961		Ref.
Equus caballus xist	n.d.*)	U50911	partial sequence	Ref.
Oryctolagus cuniculus xist	n.d.*)	U50910	partial sequence	Ref.
Drosophila melanogaster roX1	3749 nt	U85980		Ref.
Drosophila melanogaster roX2	1293 nt	U85981		Ref.
Hz-1 virus PAT-1	2937 nt	U03488		Ref.

*) n.d. - not determined

WebSite Info - In last few years much data has accumulated on various non-translatable RNA transcripts that are synthesised in different cells. They are lacking in protein coding capacity and it seems that they work mainly or exclusively at the RNA level. All known non-coding RNA transcripts are collected in the database: http://www.man.poznan.pl/5SData/ncRNA/index.html

A Protein Domain Library

DATABASE INFO



HELP
Links
SBASE article
Back to Main

Welcome to

The SBASE 9.0

protein domain library

These are the well known structural and functional domain types. It has no sequential overlap with any other domain group. This database produced by statistics.

- Browse the list of.
  - SBASE-A: The consolidated domain collection.
  - SBASE-B: Miscellaneous experimental domain groups.
- Find/retrieve sequences by SRS.
- Statistical protein domain prediction.
  (An experimental server based on nearest neighbour statistics,probabilistic scoring and artificial neural network prediction)
- Simple similarity search on SBASE.
  - BLAST 1.4.9.
  - BLAST 2.0.
  - PSI-BLAST.
- Domain prediction in a protein sequence (tabulated and graphic output).
  - BLAST Search on Swiss-Prot+PIR for SBASE domain similarities.
  - BLAST Search on PIR for Protfam similarities.
  - BLAST Search on SBASE (experimental).
- Search and optimization motifs on SBASE.
  - Find and optimize a known motif in your sequence by PHI-PSI-BLAST.
    PROSITE // Your own reg. expr.
  - Find all Prosite motifs in your sequence.
  - Find a motif in all SBASE sequences.
    PROSITE // Your own reg. expr.

WebSite Infos - SBASE entries are currently grouped by Standard names (SN groups) that designate various functional and structural domains of protein sequences.

http://www3.icgeb.trieste.it/~sbasesrv/

A 2D DataBase

Nucleic Acids Research

OXFORD Journals online

HOME | HELP | FEEDBACK | SUBSCRIPTIONS | ARCHIVE | SEARCH | TABLE OF CONTENTS

Institution: Agent: Schnetztor - Verlag Kunde: Byk Gulden Lomberg Chemische Fabrik GmbH || Sign In as Personal Subscriber || Contact Subscription Administrator at your institution || FAQ

Nucleic Acids Research, 2000, Vol. 28, No. 1 **286-288**
© 2000 Oxford University Press

The 1999 SWISS-2DPAGE database update

Christine Hoogland[1,*], Jean-Charles Sanchez[2], Luisa Tonella[2], Pierre-Alain Binz[1,2,3], Amos Bairoch[3], Denis F. Hochstrasser[2] and Ron D. Appel[1]

[1]Swiss Institute of Bioinformatics, 1 rue Michel-Servet, CH-1211 Genève 4, Switzerland, [2]Central Clinical Chemistry Laboratory, Geneva University Hospital, Geneva, Switzerland and [3]Department of Medical Biochemistry, University of Geneva, Geneva, Switzerland

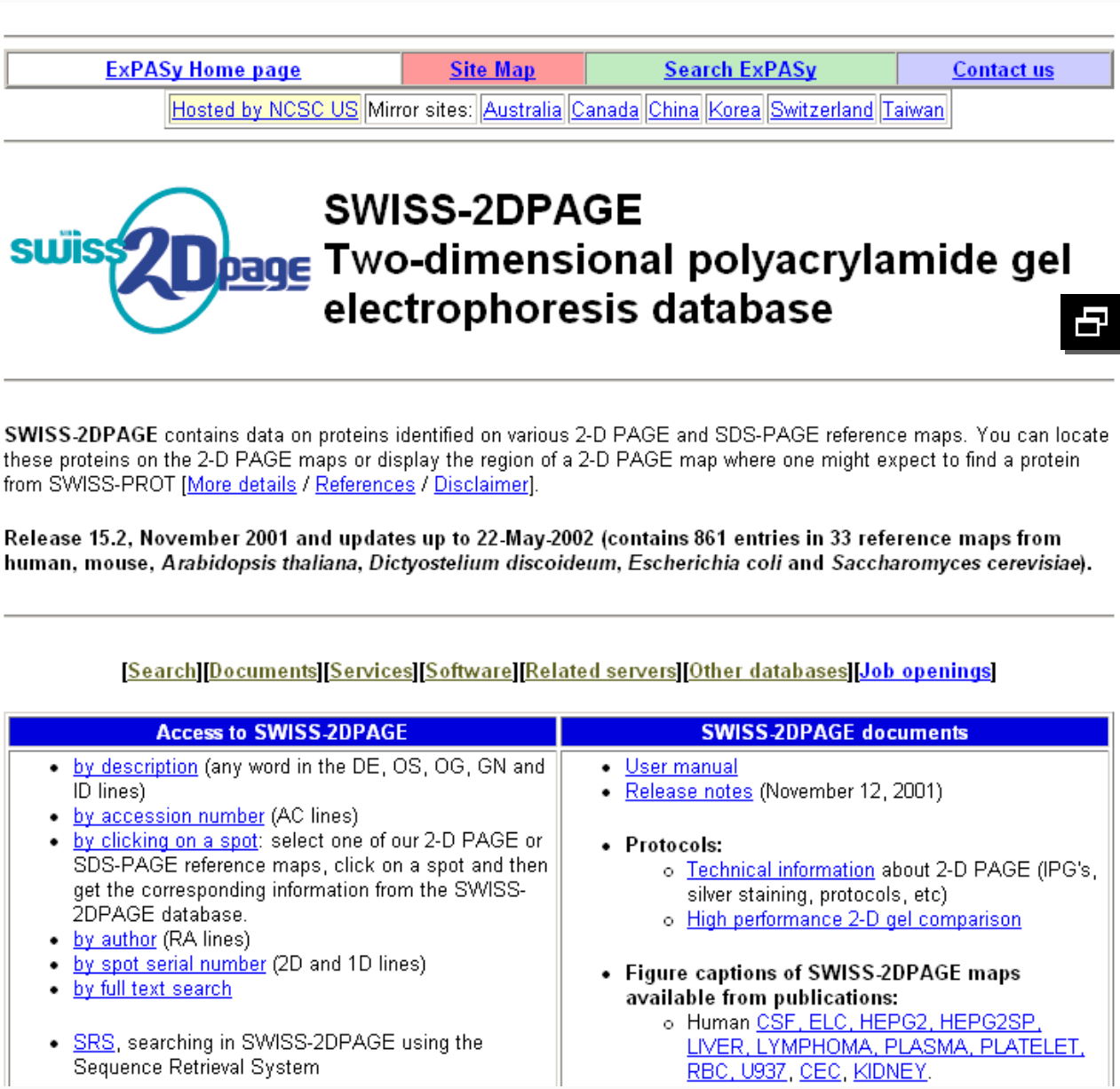
- **Full Text of this Article**
- Reprint (PDF) Version of this Article
- Similar articles found in:
  Nucl. Acids. Res. Online
  PubMed
- PubMed Citation
- Search Medline for articles by:
  Hoogland, C. || Appel, R. D.
- Alert me when:
  new articles cite this article
- Download to Citation Manager

SWISS-2DPAGE (http://www.expasy.ch/ch2d/) is an annotated two-dimensional polyacrylamide gel electrophoresis (2-DE) database established in 1993. The current release contains 24 reference maps from human and mouse biological samples, as well as from *Saccharomyces cerevisiae*, *Escherichia coli* and *Dictyostelium discoideum* origin. These reference maps have now 2824 identified spots, corresponding to 614 separate protein entries in the database, in addition to virtual entries for each SWISS-PROT sequence or any user-entered amino acids sequence. Last year improvements in the SWISS-2DPAGE database are as follows: three new maps have been created and several others have been updated; cross-references to newly built federated 2-DE databases have been added; new functions to
ExPASy proteomics server.

http://nar.oupjournals.org/cgi/content/abstract/28/1/286

WebSite Info - SWISS-2DPAGE (http://www.expasy.ch/ch2d/) is an annotated two-dimensional polyacrylamide gel electro-phoresis (2-DE) database established in 1993.

The SWISSPROT 2DPAGE Resource



ExPASy Home page | Site Map | Search ExPASy | Contact us

Hosted by NCSC US | Mirror sites: Australia Canada China Korea Switzerland Taiwan

swiss 2Dpage

SWISS-2DPAGE
Two-dimensional polyacrylamide gel electrophoresis database

SWISS-2DPAGE contains data on proteins identified on various 2-D PAGE and SDS-PAGE reference maps. You can locate these proteins on the 2-D PAGE maps or display the region of a 2-D PAGE map where one might expect to find a protein from SWISS-PROT [More details / References / Disclaimer].

Release 15.2, November 2001 and updates up to 22-May-2002 (contains 861 entries in 33 reference maps from human, mouse, *Arabidopsis thaliana*, *Dictyostelium discoideum*, *Escherichia coli* and *Saccharomyces cerevisiae*).

[Search][Documents][Services][Software][Related servers][Other databases][Job openings]

Access to SWISS-2DPAGE

- by description (any word in the DE, OS, OG, GN and ID lines)
- by accession number (AC lines)
- by clicking on a spot: select one of our 2-D PAGE or SDS-PAGE reference maps, click on a spot and then get the corresponding information from the SWISS-2DPAGE database.
- by author (RA lines)
- by spot serial number (2D and 1D lines)
- by full text search

- SRS, searching in SWISS-2DPAGE using the Sequence Retrieval System

SWISS-2DPAGE documents

- User manual
- Release notes (November 12, 2001)

- **Protocols:**
  - Technical information about 2-D PAGE (IPG's, silver staining, protocols, etc)
  - High performance 2-D gel comparison

- **Figure captions of SWISS-2DPAGE maps available from publications:**
  - Human CSF, ELC, HEPG2, HEPG2SP, LIVER, LYMPHOMA, PLASMA, PLATELET, RBC, U937, CEC, KIDNEY.

http://www.expasy.ch/ch2d/

WebSite Info - SWISS-2DPAGE - Two-dimensional polyacrylamide gel electrophoresis database. SWISS-2DPAGE contains data on proteins identified on various 2-D PAGE reference maps.

A Resource of Gene Regulatory Sequences

GRESA

Project

Gene REgulatory Sequence Analysis

Laboratory of Molecular Genetic Systems

Institute of Cytology and Genetics SB RAS

ИЦГ

FunSite

FunSite Computer System

Classification Database

Classification Database

Match

Match: matrix search

Databases on transcriptional regulation

TRRD database

TRANSFAC database

COMPEL

COMPEL

Database on composite regulatory elements affecting gene transcription in eukaryotes

- About composite regulatory elements
- Documentation: status of the COMPEL and field description
- How to cite COMPEL
- Download release 2.4
- Browse release 3.0
- Search release 3.0

http://compel.bionet.nsc.ru/

PATTERN_SEARCH

Program for searching potential composite elements similar to the COMPEL collection

WebSite Info - Composite regulatory elements: structure, function and classification. Composite regulatory elements contain two closely situated binding sites for distinct transcription factors, and actually are minimal functional units providing combinatorial transcriptional regulation.