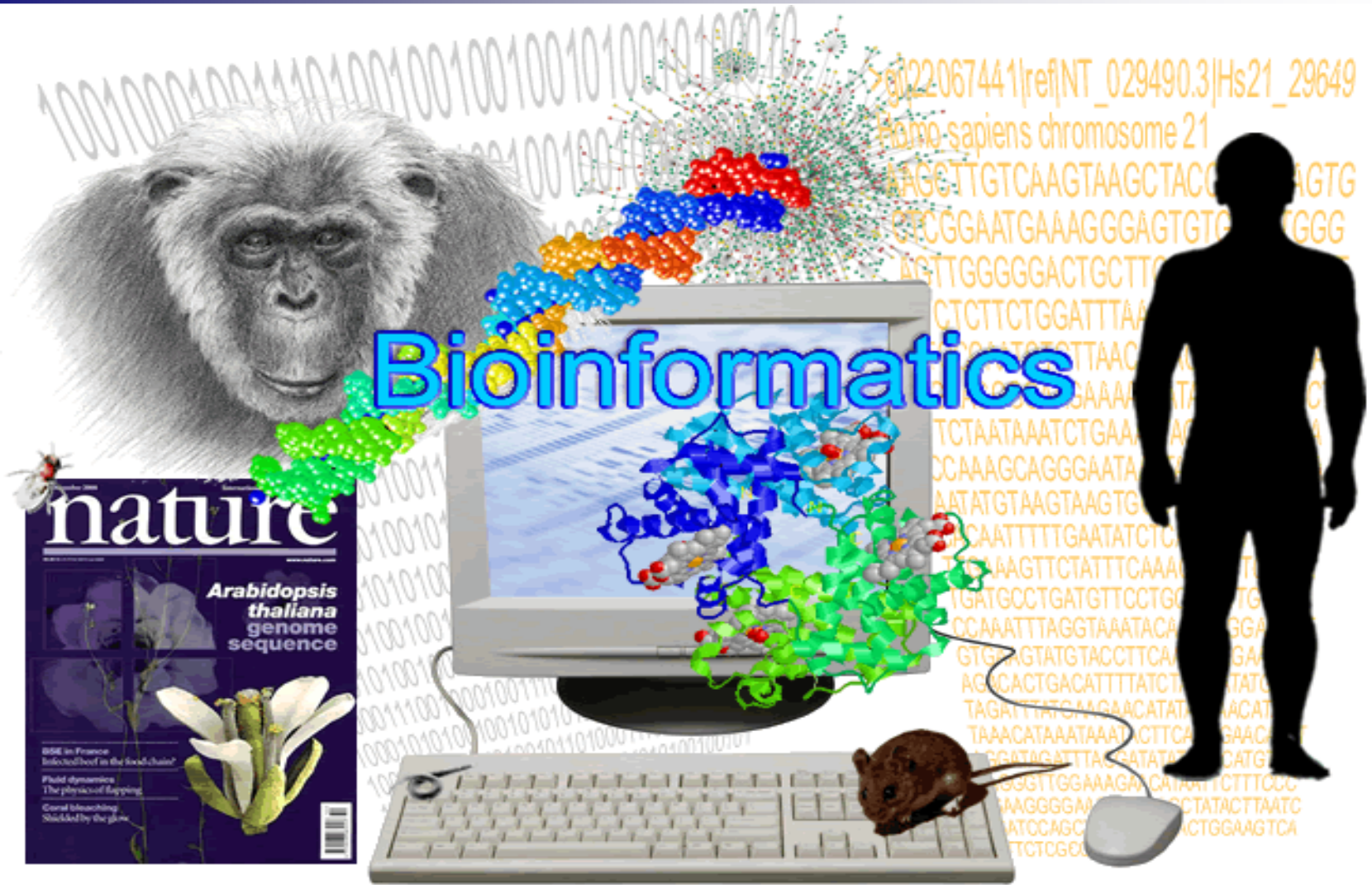
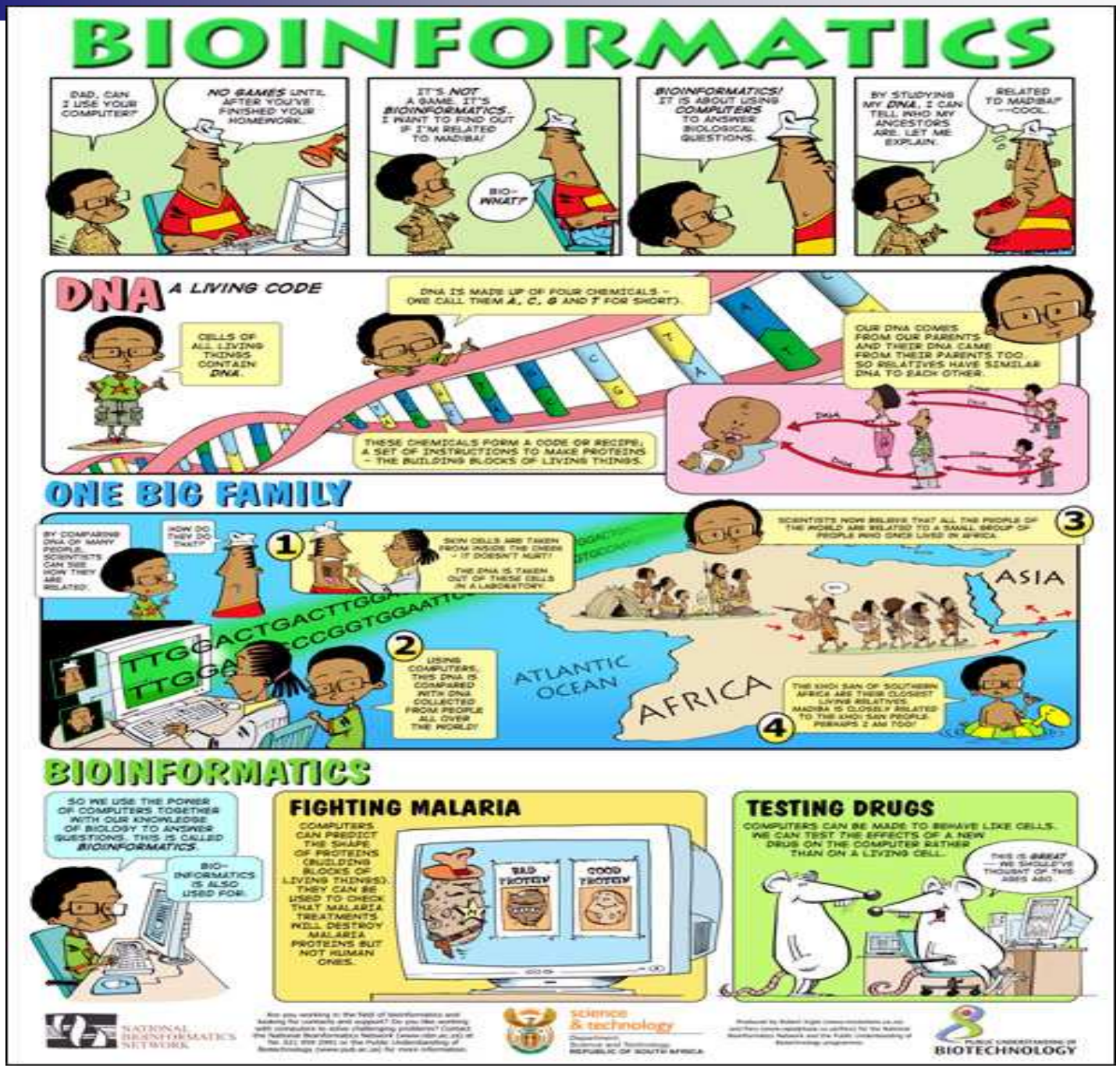


Doç. Dr. Ercan ARICAN

Moleküler Biyoloji ve Genetik Bölümü


BIOINFORMATICS
DAD, CAN I USE YOUR COMPUTER?
NO GAMES UNTIL AFTER YOU'VE FINISHED YOUR HOMEWORK.
IT'S NOT A GAME. IT'S BIOINFORMATICS. I WANT TO FIND OUT IF I'M RELATED TO MADIBA!
BIO- WHAT?
BIOINFORMATICS! IT IS ABOUT USING COMPUTERS TO ANSWER BIOLOGICAL QUESTIONS.
BY STUDYING MY DNA, I CAN TELL WHO MY ANCESTORS ARE. LET ME EXPLAIN.
RELATED TO MADIBA? —COOL.
DNA A LIVING CODE
CELLS OF ALL LIVING THINGS CONTAIN DNA.
DNA IS MADE UP OF FOUR CHEMICALS – ONE CALL THEM A, C, G AND T FOR SHORT).
THESE CHEMICALS FORM A CODE OR RECIPE; A SET OF INSTRUCTIONS TO MAKE PROTEINS – THE BUILDING BLOCKS OF LIVING THINGS.
OUR DNA COMES FROM OUR PARENTS AND THEIR DNA CAME FROM THEIR PARENTS TOO. SO RELATIVES HAVE SIMILAR DNA TO EACH OTHER.
DNA
ONE BIG FAMILY
BY COMPARING DNA OF MANY PEOPLE, SCIENTISTS CAN SEE HOW THEY ARE RELATED.
HOW DO THEY DO THAT?
1
SKIN CELLS ARE TAKEN FROM INSIDE THE CHEEK – IT DOESN'T HURT!
THE DNA IS TAKEN OUT OF THESE CELLS IN A LABORATORY.
TTGGACTGACTTGGA
TTGGA CCGGTGGAATTC
2
USING COMPUTERS, THIS DNA IS COMPARED WITH DNA COLLECTED FROM PEOPLE ALL OVER THE WORLD!
ATLANTIC OCEAN
AFRICA
ASIA
3
SCIENTISTS NOW BELIEVE THAT ALL THE PEOPLE OF THE WORLD ARE RELATED TO A SMALL GROUP OF PEOPLE WHO ONCE LIVED IN AFRICA.
4
THE KHOI SAN OF SOUTHERN AFRICA ARE THEIR CLOSEST LIVING RELATIVES. MADIBA IS CLOSELY RELATED TO THE KHOI SAN PEOPLE. PERHAPS I AM TOO!
BIOINFORMATICS
SO WE USE THE POWER OF COMPUTERS TOGETHER WITH OUR KNOWLEDGE OF BIOLOGY TO ANSWER QUESTIONS. THIS IS CALLED BIOINFORMATICS.
BIO-INFORMATICS IS ALSO USED FOR:
FIGHTING MALARIA
COMPUTERS CAN PREDICT THE SHAPE OF PROTEINS (BUILDING BLOCKS OF LIVING THINGS). THEY CAN BE USED TO CHECK THAT MALARIA TREATMENTS WILL DESTROY MALARIA PROTEINS BUT NOT HUMAN ONES.
BAD PROTEIN
GOOD PROTEIN
TESTING DRUGS
COMPUTERS CAN BE MADE TO BEHAVE LIKE CELLS. WE CAN TEST THE EFFECTS OF A NEW DRUG ON THE COMPUTER RATHER THAN ON A LIVING CELL.
THIS IS GREAT — WE SHOULD'VE THOUGHT OF THIS 1000S AGO.
NATIONAL BIOINFORMATICS NETWORK
science & technology
REPUBLIC OF SOUTH AFRICA
BIOTECHNOLOGY

Biyoinformatik;

- çeşitli biyoloji veri bankalarından gelen bilginin anlaşılır ve organize hale getirilmesi için informatik tekniklerin kullanımı



Biyoinformatik (Bilgi Akışı)

1. Nükleik asit dizilemesi ve analizi
(dizilerin karşılaştırılması, genlerin belirlenmesi)

↓

2. Proteinlerin analizi (Dizi bilgisi)

↓

3. Moleküler yapı tayini (3-boyutlu modelleme)

↓

4. Moleküler ilişkiler (protein-protein ilişkileri)

5. Bilgi ağlarının kurulması
(Metabolik yolların aydınlanması amaçlı)

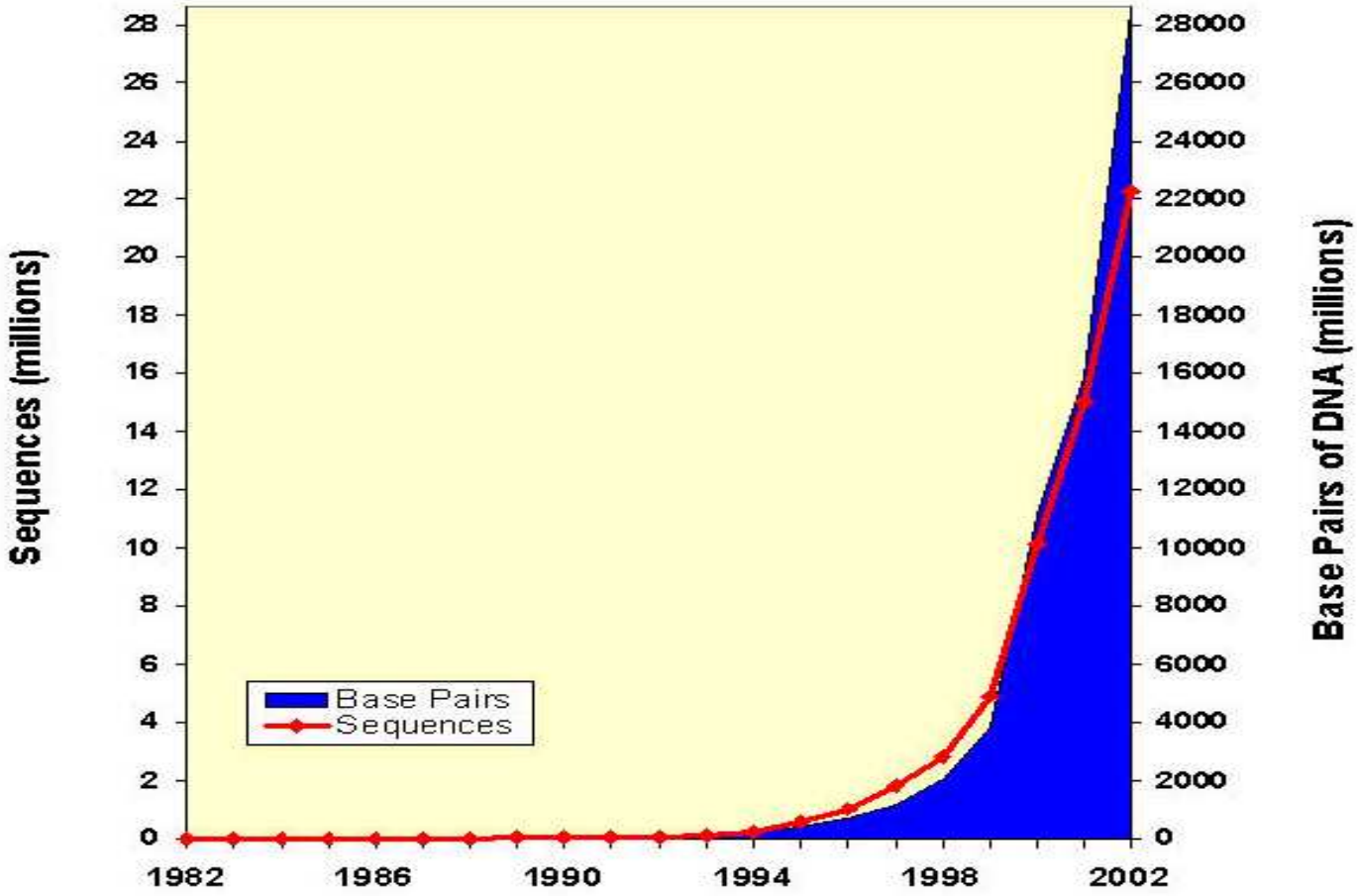
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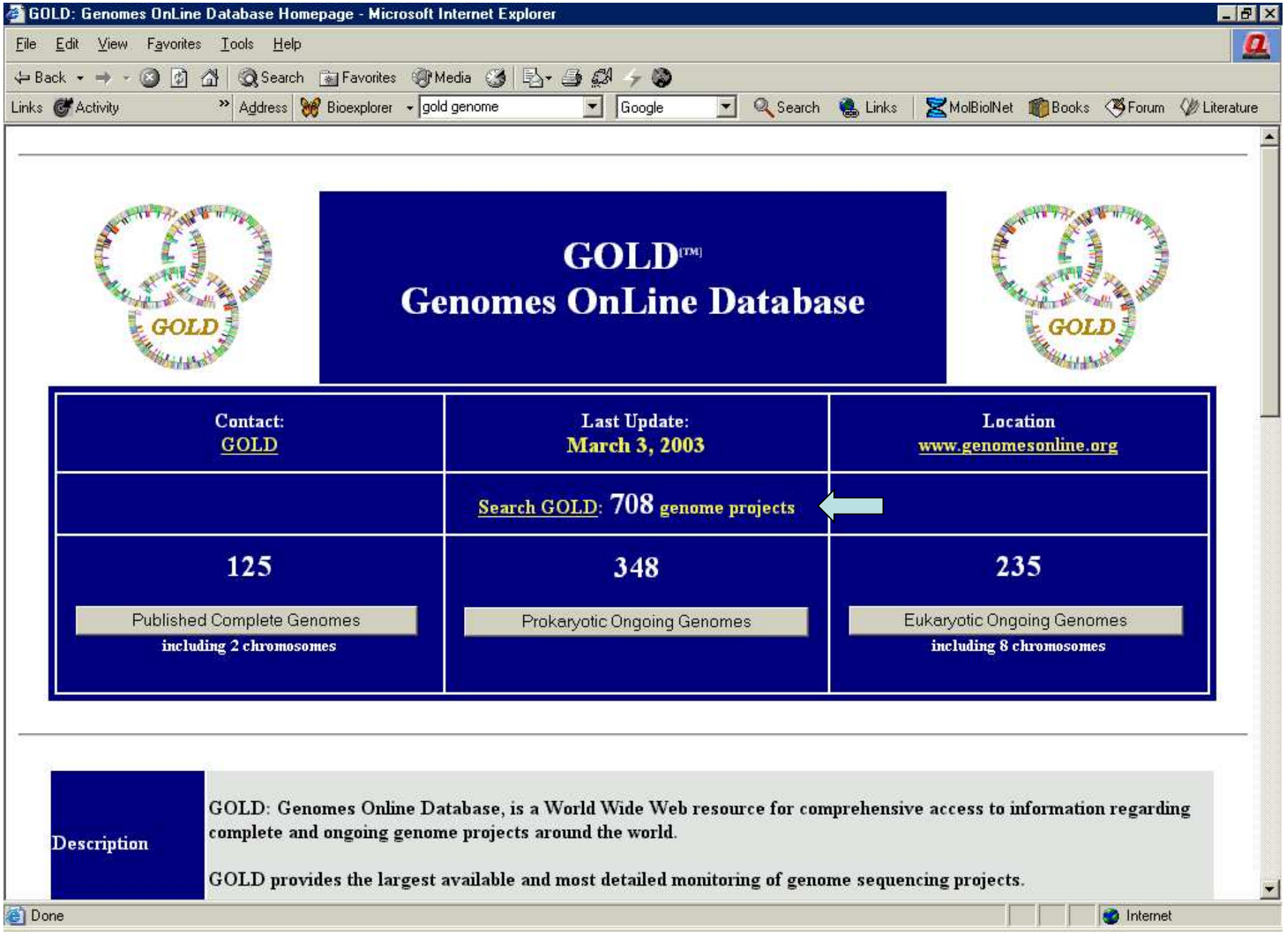
6. Gen anlatımı ürünleri ve protein verilerinin eldesi
(EST, DNA microarray)

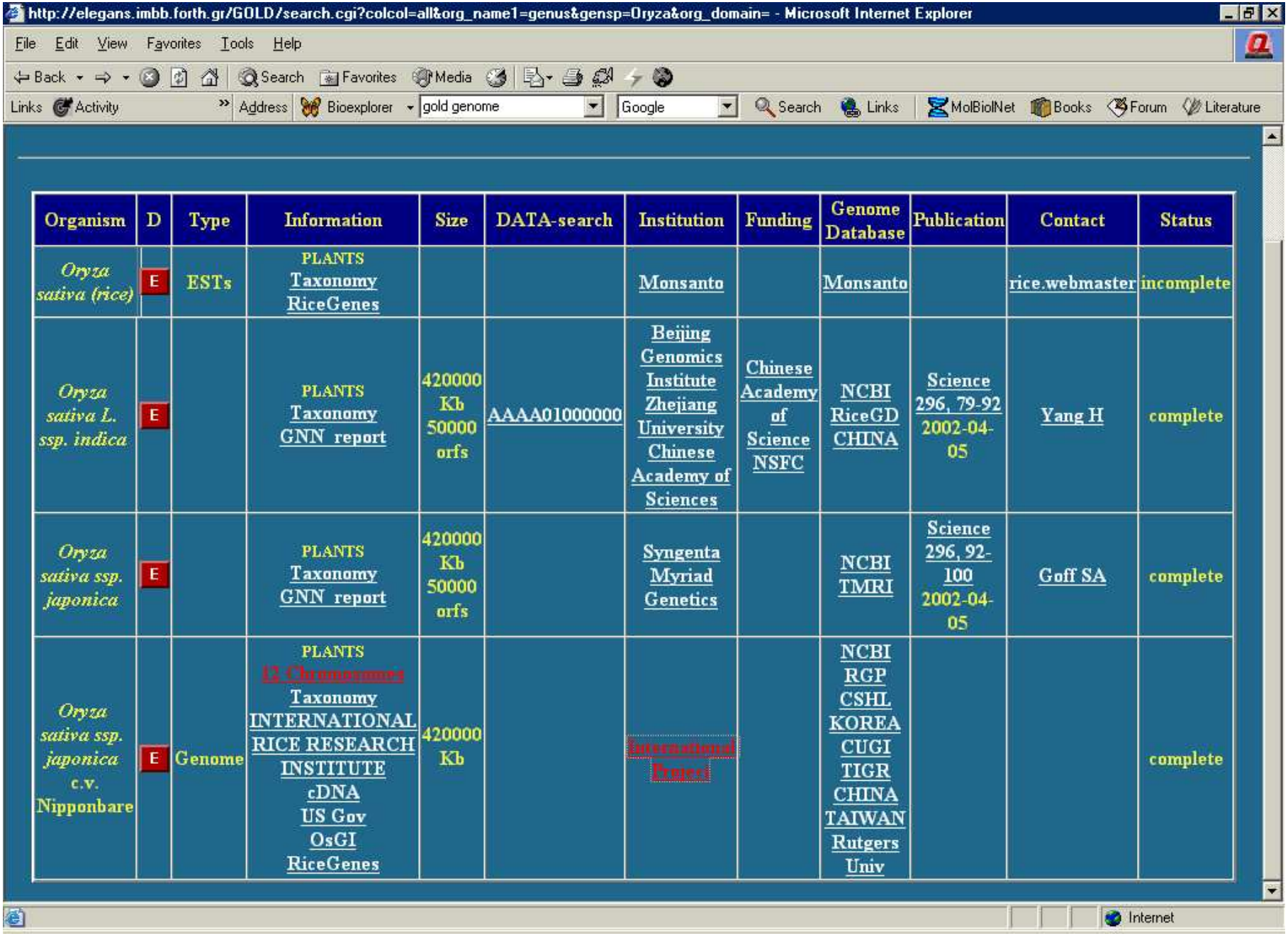
↓

7.Varyasyon
(SNP)

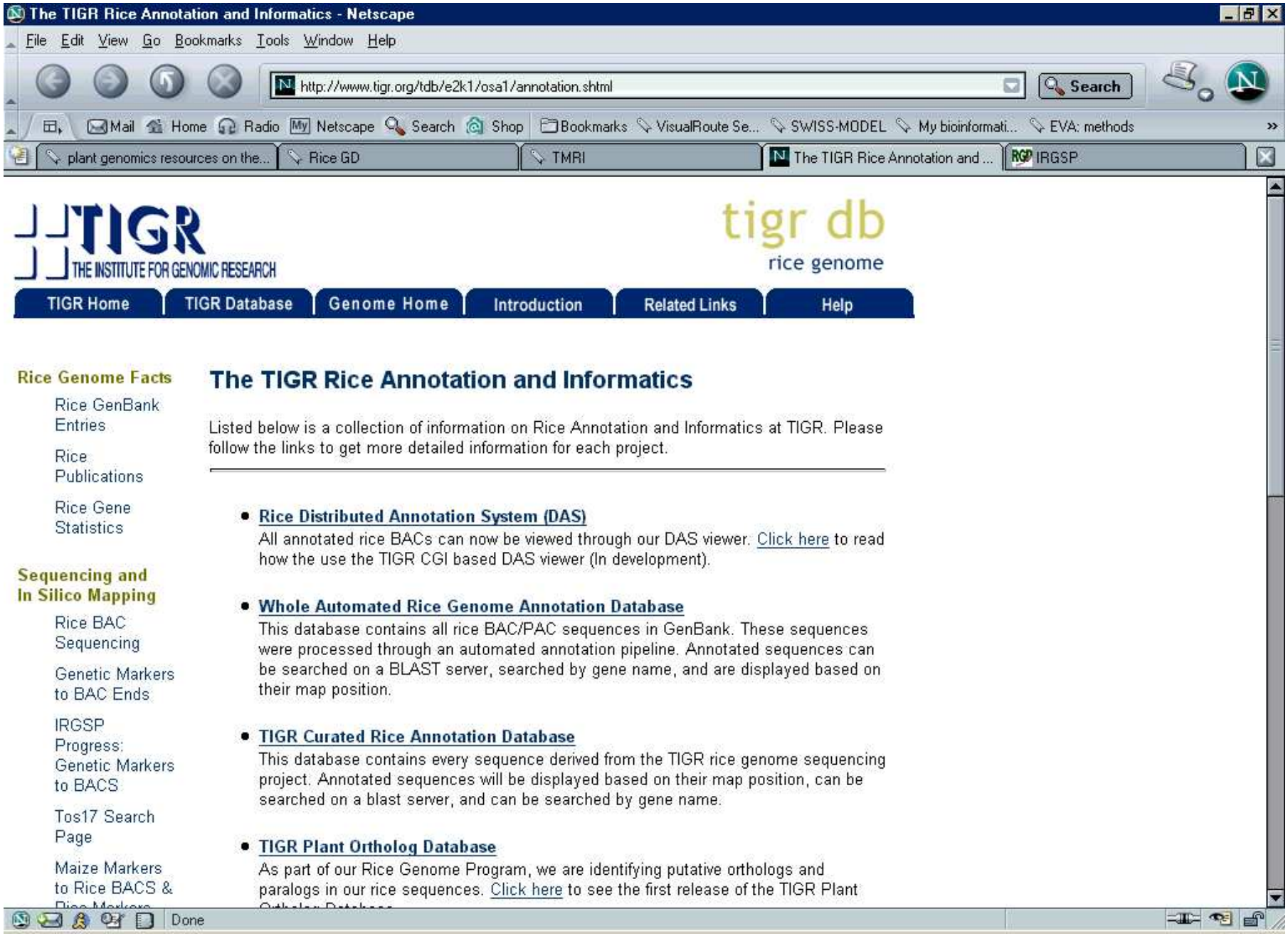
Gen Bankalarındaki Bilgi Artışı

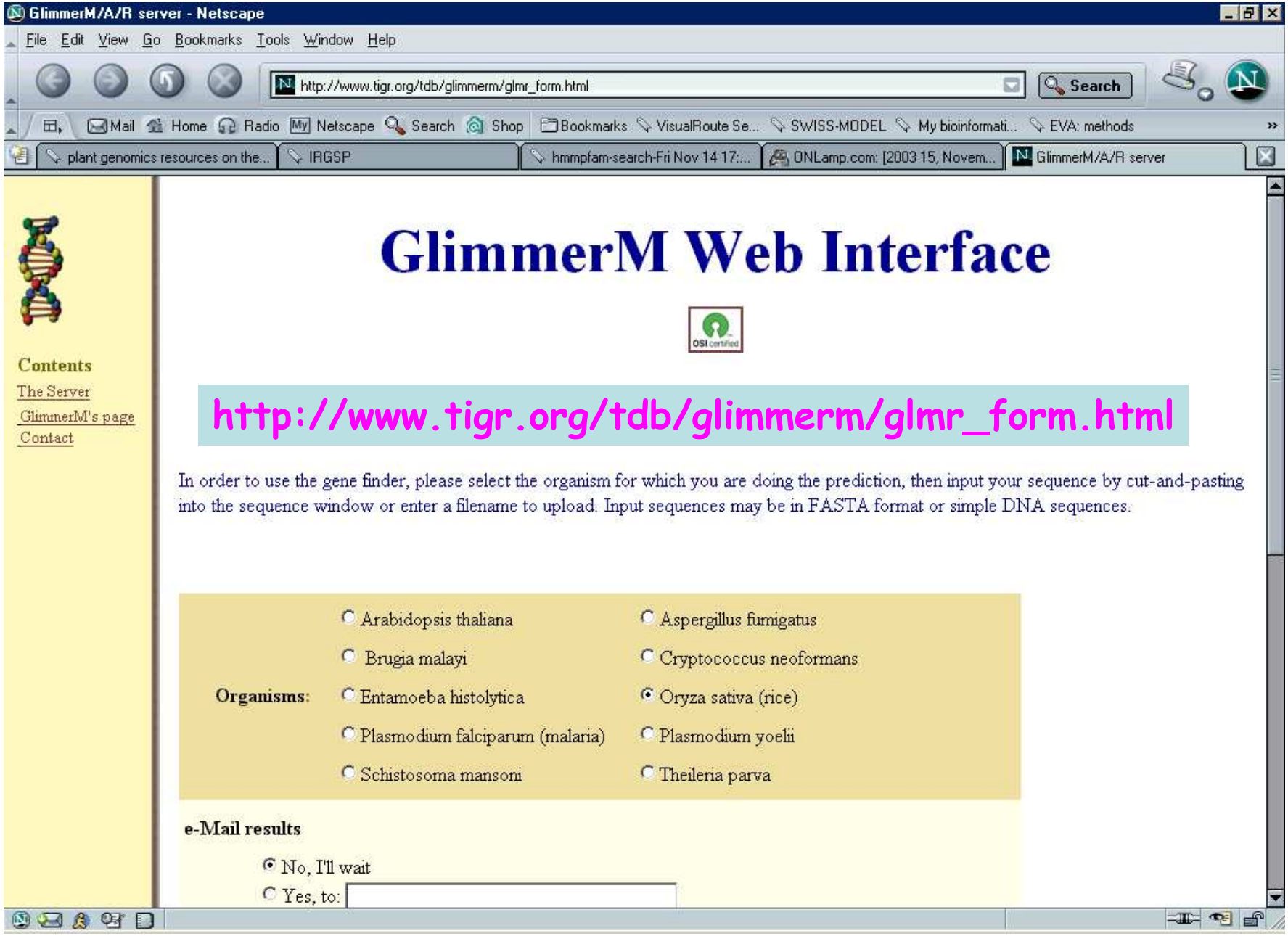


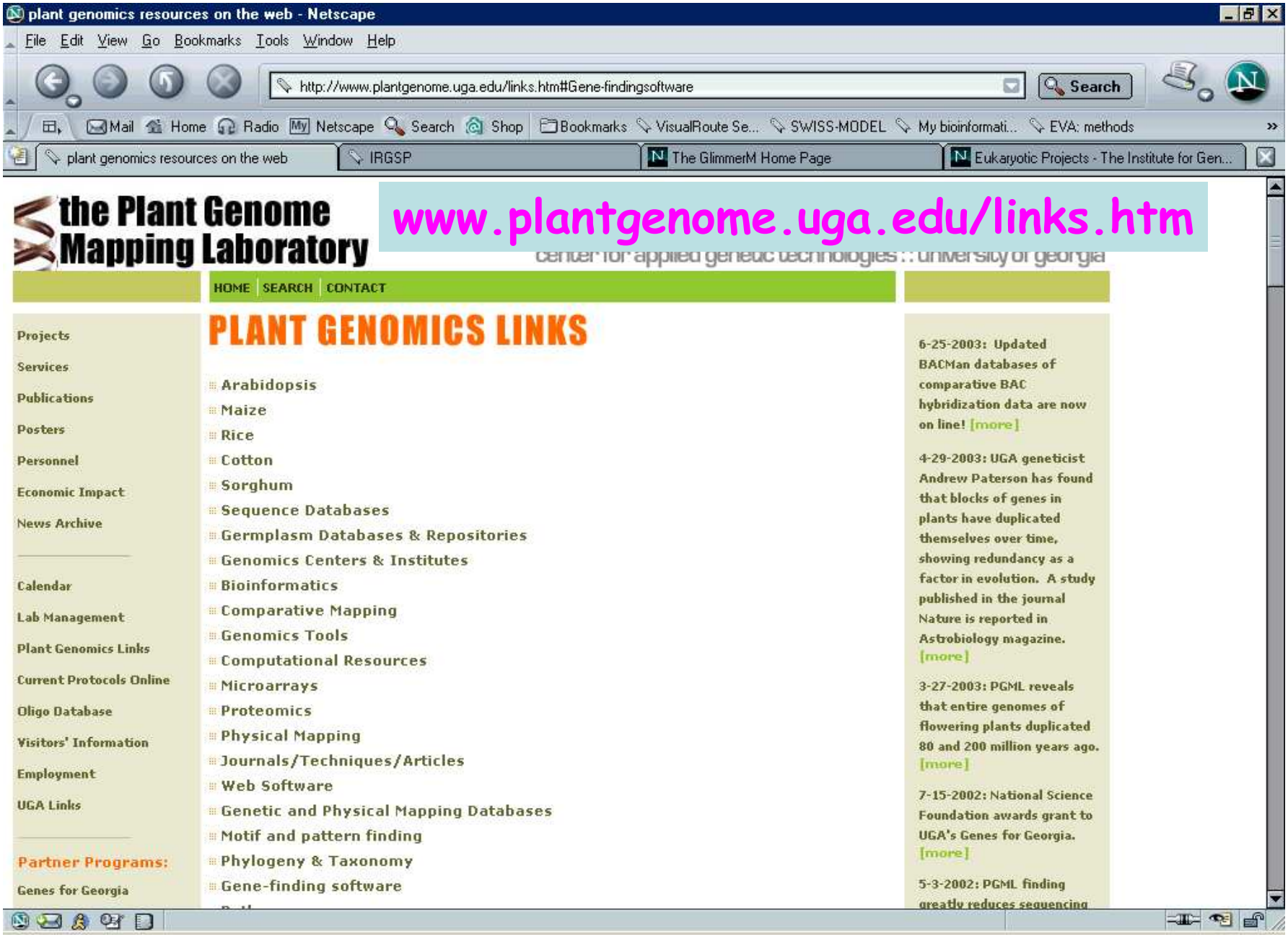

GOLD: Genomes OnLine Database Homepage - Microsoft Internet Explorer
File Edit View Favorites Tools Help
Back Search Favorites Media
Links Activity Address Bioexplorer gold genome Google Search Links MolBiolNet Books Forum Literature
GOLD
GOLD™
Genomes OnLine Database
GOLD
Contact:
GOLD
Last Update:
March 3, 2003
Location
www.genomesonline.org
Search GOLD: 708 genome projects
125
Published Complete Genomes
including 2 chromosomes
348
Prokaryotic Ongoing Genomes
235
Eukaryotic Ongoing Genomes
including 8 chromosomes
Description
GOLD: Genomes Online Database, is a World Wide Web resource for comprehensive access to information regarding complete and ongoing genome projects around the world.
GOLD provides the largest available and most detailed monitoring of genome sequencing projects.
Done
Internet

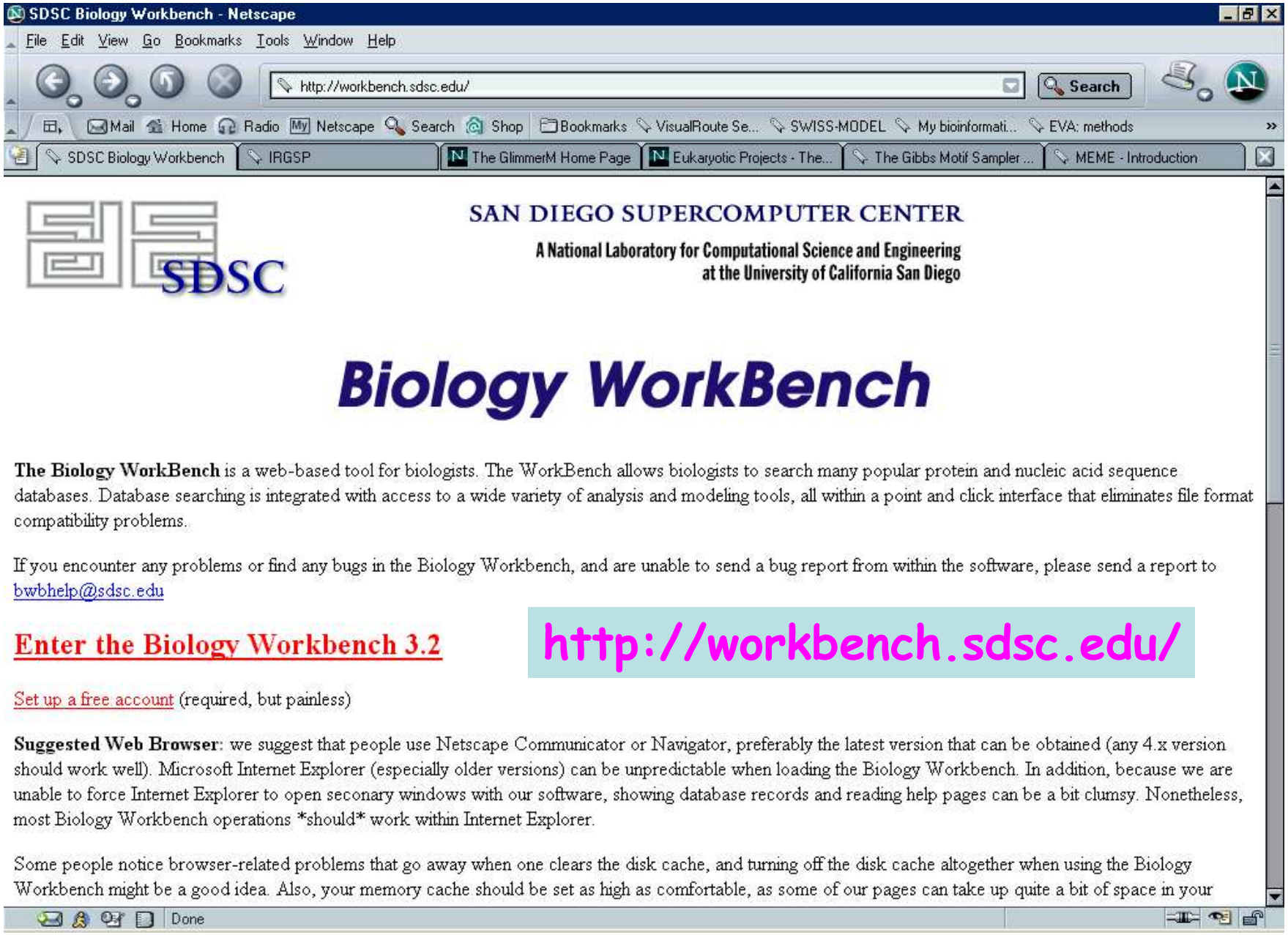


Organism	D	Type	Information	Size	DATA-search	Institution	Funding	Genome Database	Publication	Contact	Status
Oryza sativa (rice)	E	ESTs	PLANTS Taxonomy RiceGenes			Monsanto		Monsanto		rice.webmaster	incomplete
Oryza sativa L. ssp. indica	E		PLANTS Taxonomy GNN report	420000 Kb 50000 orfs	AAAA01000000	Beijing Genomics Institute Zhejiang University Chinese Academy of Sciences	Chinese Academy of Science NSFC	NCBI RiceGD CHINA	Science 296, 79-92 2002-04-05	Yang H	complete
Oryza sativa ssp. japonica	E		PLANTS Taxonomy GNN report	420000 Kb 50000 orfs		Syngenta Myriad Genetics		NCBI TMRI	Science 296, 92-100 2002-04-05	Goff SA	complete
Oryza sativa ssp. japonica c.v. Nipponbare	E	Genome	PLANTS 12 Chromosomes Taxonomy INTERNATIONAL RICE RESEARCH INSTITUTE cDNA US Gov OsGI RiceGenes	420000 Kb		International Project		NCBI RGP CSHL KOREA CUGI TIGR CHINA TAIWAN Rutgers Univ			complete


The TIGR Rice Annotation and Informatics - Netscape
File Edit View Go Bookmarks Tools Window Help
http://www.tigr.org/tdb/e2k1/osa1/annotation.shtml
Search
Mail Home Radio Netscape Search Shop Bookmarks VisualRoute Se... SWISS-MODEL My bioinformati... EVA: methods
plant genomics resources on the... Rice GD TMRI The TIGR Rice Annotation and ... IRGSP
TIGR
THE INSTITUTE FOR GENOMIC RESEARCH
tigr db
rice genome
TIGR Home
TIGR Database
Genome Home
Introduction
Related Links
Help
Rice Genome Facts
Rice GenBank Entries
Rice Publications
Rice Gene Statistics
Sequencing and In Silico Mapping
Rice BAC Sequencing
Genetic Markers to BAC Ends
IRGSP Progress: Genetic Markers to BACS
Tos17 Search Page
Maize Markers to Rice BACS &
The TIGR Rice Annotation and Informatics
Listed below is a collection of information on Rice Annotation and Informatics at TIGR. Please follow the links to get more detailed information for each project.
Rice Distributed Annotation System (DAS)
All annotated rice BACs can now be viewed through our DAS viewer. Click here to read how the use the TIGR CGI based DAS viewer (In development).
Whole Automated Rice Genome Annotation Database
This database contains all rice BAC/PAC sequences in GenBank. These sequences were processed through an automated annotation pipeline. Annotated sequences can be searched on a BLAST server, searched by gene name, and are displayed based on their map position.
TIGR Curated Rice Annotation Database
This database contains every sequence derived from the TIGR rice genome sequencing project. Annotated sequences will be displayed based on their map position, can be searched on a blast server, and can be searched by gene name.
TIGR Plant Ortholog Database
As part of our Rice Genome Program, we are identifying putative orthologs and paralogs in our rice sequences. Click here to see the first release of the TIGR Plant
Done


GlimmerM/A/R server - Netscape
File Edit View Go Bookmarks Tools Window Help
http://www.tigr.org/tdb/glimmerm/glmr_form.html
Search
Mail Home Radio Netscape Search Shop Bookmarks VisualRoute Se... SWISS-MODEL My bioinformati... EVA: methods
plant genomics resources on the... IRGSP hmmpfam-search-Fri Nov 14 17:... ONLamp.com: [2003 15, Novem... GlimmerM/A/R server
Contents
The Server
GlimmerM's page
Contact
GlimmerM Web Interface
http://www.tigr.org/tdb/glimmerm/glmr_form.html
In order to use the gene finder, please select the organism for which you are doing the prediction, then input your sequence by cut-and-pasting into the sequence window or enter a filename to upload. Input sequences may be in FASTA format or simple DNA sequences.
Organisms:
Arabidopsis thaliana
Aspergillus fumigatus
Brugia malayi
Cryptococcus neoformans
Entamoeba histolytica
Oryza sativa (rice)
Plasmodium falciparum (malaria)
Plasmodium yoelii
Schistosoma mansoni
Theileria parva
e-Mail results
No, I'll wait
Yes, to:


plant genomics resources on the web - Netscape
File Edit View Go Bookmarks Tools Window Help
http://www.plantgenome.uga.edu/links.htm#Gene-findingsoftware
Search
Mail Home Radio Netscape Search Shop Bookmarks VisualRoute Se... SWISS-MODEL My bioinformati... EVA: methods
plant genomics resources on the web
IRGSP
The GlimmerM Home Page
Eukaryotic Projects - The Institute for Gen...
the Plant Genome Mapping Laboratory
www.plantgenome.uga.edu/links.htm
center for applied genetic technologies :: university of georgia
HOME | SEARCH | CONTACT
Projects
Services
Publications
Posters
Personnel
Economic Impact
News Archive
Calendar
Lab Management
Plant Genomics Links
Current Protocols Online
Oligo Database
Visitors' Information
Employment
UGA Links
Partner Programs:
Genes for Georgia
PLANT GENOMICS LINKS
Arabidopsis
Maize
Rice
Cotton
Sorghum
Sequence Databases
Germplasm Databases & Repositories
Genomics Centers & Institutes
Bioinformatics
Comparative Mapping
Genomics Tools
Computational Resources
Microarrays
Proteomics
Physical Mapping
Journals/Techniques/Articles
Web Software
Genetic and Physical Mapping Databases
Motif and pattern finding
Phylogeny & Taxonomy
Gene-finding software
6-25-2003: Updated BACMan databases of comparative BAC hybridization data are now on line! [more]
4-29-2003: UGA geneticist Andrew Paterson has found that blocks of genes in plants have duplicated themselves over time, showing redundancy as a factor in evolution. A study published in the journal Nature is reported in Astrobiology magazine. [more]
3-27-2003: PGML reveals that entire genomes of flowering plants duplicated 80 and 200 million years ago. [more]
7-15-2002: National Science Foundation awards grant to UGA's Genes for Georgia. [more]
5-3-2002: PGML finding greatly reduces sequencing


SDSC Biology Workbench - Netscape
File Edit View Go Bookmarks Tools Window Help
http://workbench.sdsc.edu/
Search
Mail Home Radio Netscape Search Shop Bookmarks VisualRoute Se... SWISS-MODEL My bioinformati... EVA: methods
SDSC Biology Workbench
IRGSP
The GlimmerM Home Page
Eukaryotic Projects - The...
The Gibbs Motif Sampler ...
MEME - Introduction
SDSC
SAN DIEGO SUPERCOMPUTER CENTER
A National Laboratory for Computational Science and Engineering
at the University of California San Diego
Biology WorkBench
The Biology WorkBench is a web-based tool for biologists. The WorkBench allows biologists to search many popular protein and nucleic acid sequence databases. Database searching is integrated with access to a wide variety of analysis and modeling tools, all within a point and click interface that eliminates file format compatibility problems.
If you encounter any problems or find any bugs in the Biology Workbench, and are unable to send a bug report from within the software, please send a report to bwbhelp@sdsc.edu
Enter the Biology Workbench 3.2
http://workbench.sdsc.edu/
Set up a free account (required, but painless)
Suggested Web Browser: we suggest that people use Netscape Communicator or Navigator, preferably the latest version that can be obtained (any 4.x version should work well). Microsoft Internet Explorer (especially older versions) can be unpredictable when loading the Biology Workbench. In addition, because we are unable to force Internet Explorer to open seconary windows with our software, showing database records and reading help pages can be a bit clumsy. Nonetheless, most Biology Workbench operations *should* work within Internet Explorer.
Some people notice browser-related problems that go away when one clears the disk cache, and turning off the disk cache altogether when using the Biology Workbench might be a good idea. Also, your memory cache should be set as high as comfortable, as some of our pages can take up quite a bit of space in your
Done

Biyologların bilmesi gereken beş WEB sitesi

- NCBI ("The National Center for Biotechnology Information")
  - http://www.ncbi.nlm.nih.gov/
- SwissProt/ExPASy ("Swiss Bioinformatics Resource")
  - http://expasy.cbr.nrc.ca/sprot/
- EBI ("The European Bioinformatics Institute"")
  - http://www.ebi.ac.uk/
- "The Canadian Bioinformatics Resource"
  - http://www.cbr.nrc.ca/
- PDB ("The Protein Databank")
  - http://www.rcsb.org/PDB/

ExPASy Molecular Biology Server - Microsoft Internet Explorer

Dosya Düzen Görünüm Sık Kullanılanlar Araçlar Yardım

Geri İleri Dur Yenile Giriş Ara Sık Kullanıla... Ortam Geçmiş Yazdır Düzen

Adres http://au.expasy.org/

Search Web Pop-Up Blocker Sign In Mail Games Yahoo! Personals My Yahoo! LAUNCH

Site Map | Search ExPASy | Contact us

Hosted by APAF Australia | Mirror sites: Bolivia Canada China Korea Switzerland Taiwan USA

Search Swiss-Prot/TrEMBL for Go Clear

ExPASy Molecular Biology Server

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

ExPASy celebrates 10 years of continuing service!
What do you like best on ExPASy, what do you like least?



[Announcements] [Job opening] [Mirror Sites]

Databases

- **Swiss-Prot and TrEMBL** - Protein knowledgebase
- **PROSITE** - Protein families and domains
- **SWISS-2DPAGE** - Two-dimensional polyacrylamide gel electrophoresis
- **ENZYME** - Enzyme nomenclature
- **SWISS-3DIMAGE** - 3D images of proteins and other biological macromolecules
- **SWISS-MODEL Repository** - Automatically generated protein models
- **CD40Lbase** - CD40 ligand defects
- **SeqAnalRef** - Sequence analysis bibliographic references

- **Links to many other molecular biology databases**

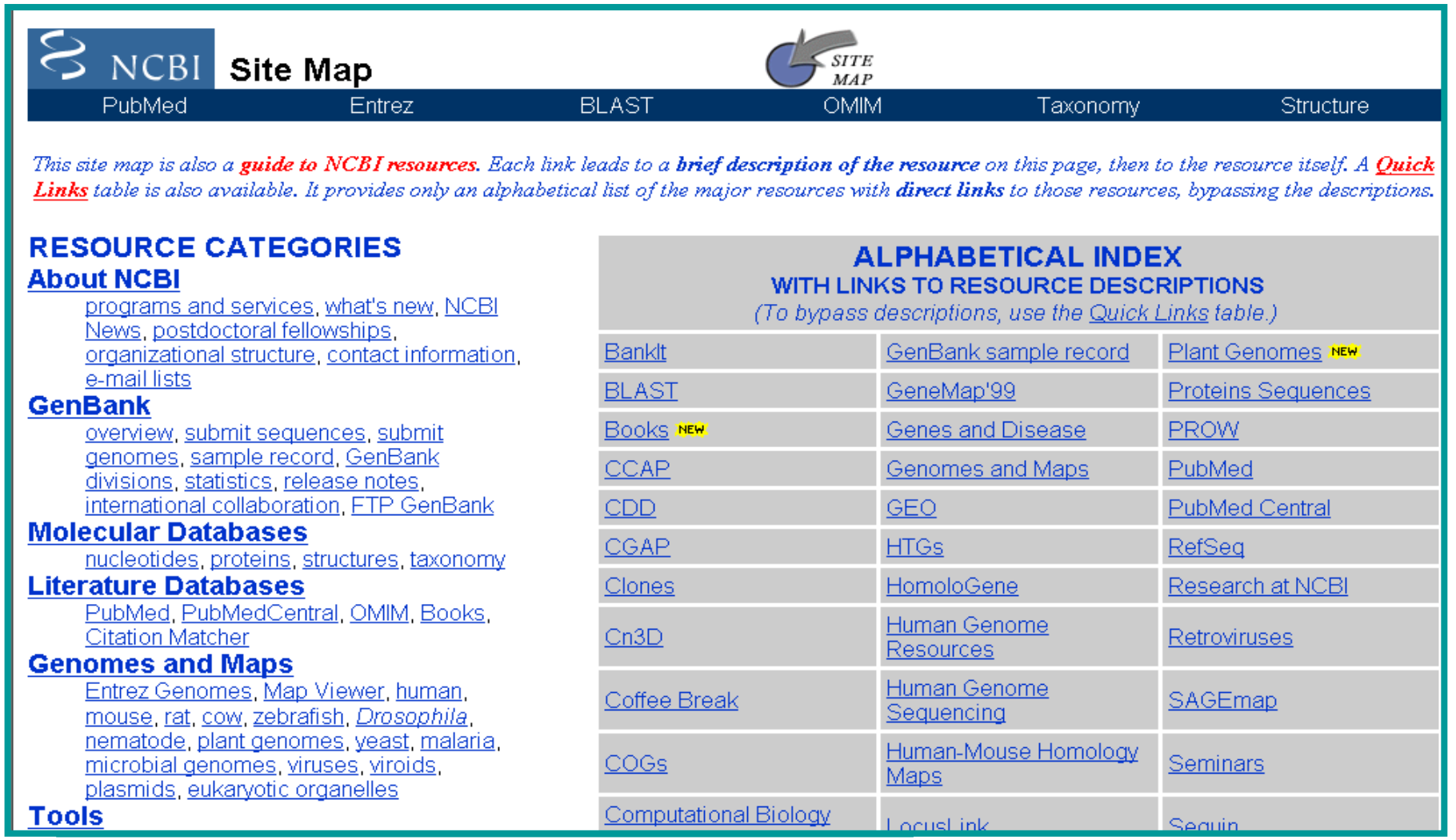
Tools and software packages

- **Proteomics and sequence analysis tools**
  - Proteomics [PeptIdent, PeptideMass, ...]
  - DNA -> Protein [Translate]
  - Similarity searches [BLAST]
  - Pattern and profile searches [ScanProsite]
  - Post-translational modification and topology prediction
  - Primary structure analysis [ProtParam, pI/MW, ProtScale]
  - Secondary and tertiary structure prediction [SWISS-MODEL, Swiss-PdbViewer]
  - Alignment [T-COFFEE, SIM]
  - Biological text analysis
- **Melanie 4** - Software for 2-D PAGE analysis
- **Roche Applied Science's Biochemical Pathways**

Internet

Başlat ExPASy Molecular Biology ... Microsoft PowerPoint... 10:50

The National Center for Biotechnology Information (NCBI) Home Page http://www.ncbi.nlm.nih.gov



NCBI **Site Map**

SITE MAP

PubMed | Entrez | BLAST | OMIM | Taxonomy | Structure

*This site map is also a **guide to NCBI resources**. Each link leads to a **brief description of the resource** on this page, then to the resource itself. A **Quick Links** table is also available. It provides only an alphabetical list of the major resources with **direct links** to those resources, bypassing the descriptions.*

RESOURCE CATEGORIES

About NCBI
programs and services, what's new, NCBI News, postdoctoral fellowships, organizational structure, contact information, e-mail lists

GenBank
overview, submit sequences, submit genomes, sample record, GenBank divisions, statistics, release notes, international collaboration, FTP GenBank

Molecular Databases
nucleotides, proteins, structures, taxonomy

Literature Databases
PubMed, PubMedCentral, OMIM, Books, Citation Matcher

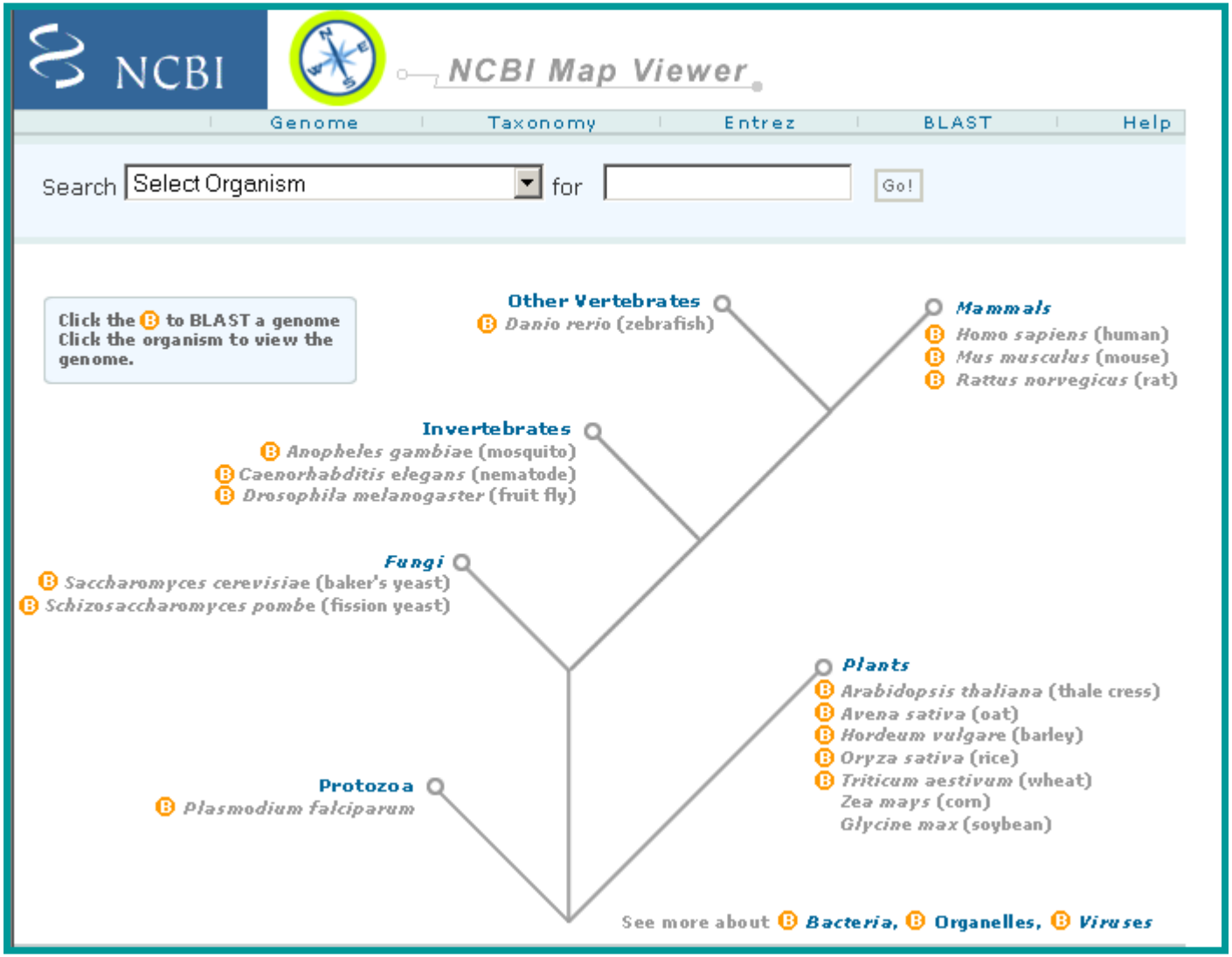
Genomes and Maps
Entrez Genomes, Map Viewer, human, mouse, rat, cow, zebrafish, *Drosophila*, nematode, plant genomes, yeast, malaria, microbial genomes, viruses, viroids, plasmids, eukaryotic organelles

Tools

ALPHABETICAL INDEX
WITH LINKS TO RESOURCE DESCRIPTIONS
(To bypass descriptions, use the Quick Links table.)

BankIt	GenBank sample record	Plant Genomes NEW
BLAST	GeneMap'99	Proteins Sequences
Books NEW	Genes and Disease	PROW
CCAP	Genomes and Maps	PubMed
CDD	GEO	PubMed Central
CGAP	HTGs	RefSeq
Clones	HomoloGene	Research at NCBI
Cn3D	Human Genome Resources	Retroviruses
Coffee Break	Human Genome Sequencing	SAGEmap
COGs	Human-Mouse Homology Maps	Seminars
Computational Biology	LocusLink	Sequin

- **Map Viewer: NCBI'da bulunan genomlara genel bakış**



- GenBank: NCBI'ın nukleotid dizileri veri tabanı

- **Bilgiler işbirliği içerisindeki üç veritabanı arasında paylaşılır.**
  - **GenBank**
  - **DDBJ ("DNA Database of Japan")**

  www.ddbj.nig.ac.jp
  - **EMBL ("European Molecular Biology Laboratory Database")**

  www.ebi.ac.uk/embl/index.html

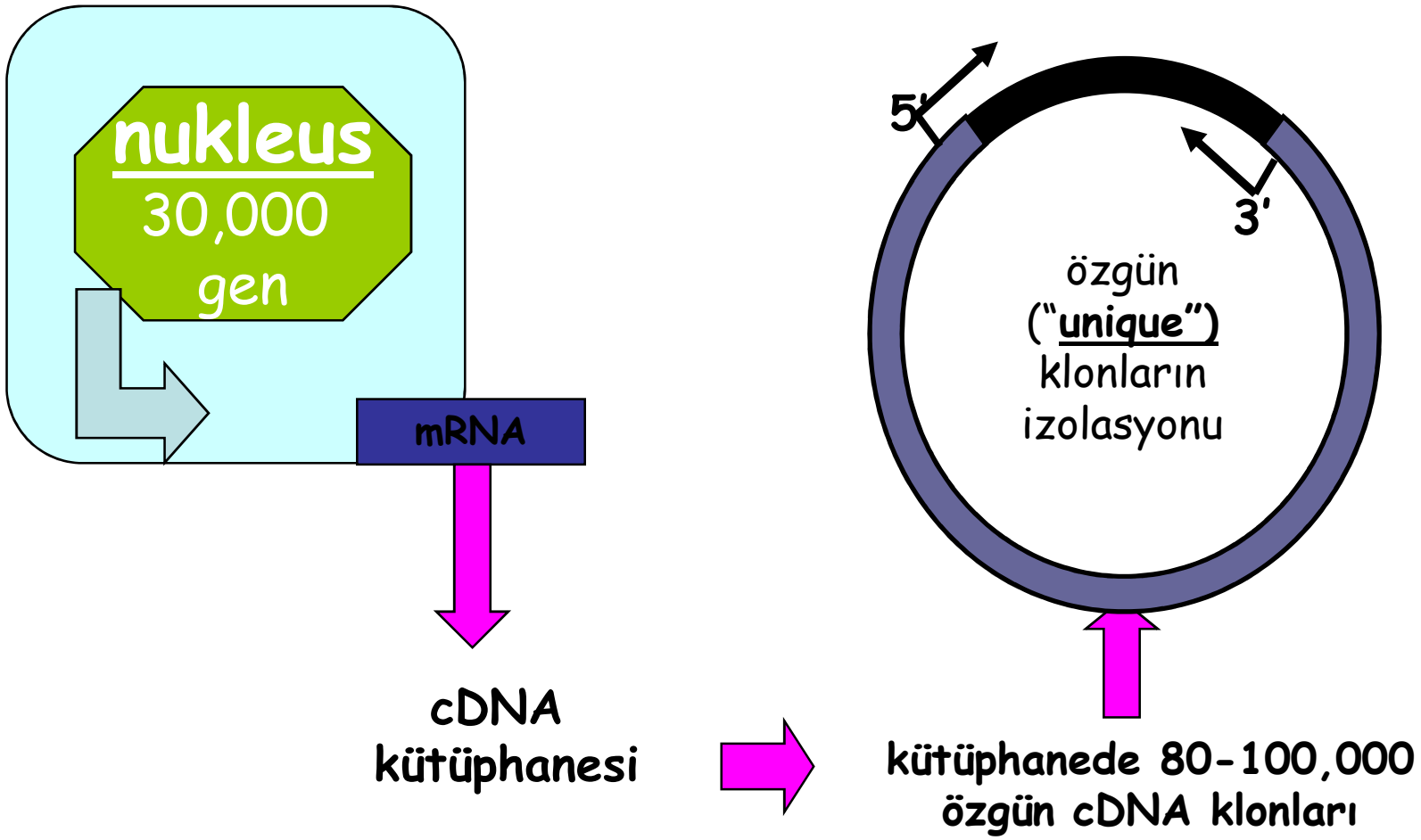
- Özgün Gen (“UniGene”)

·Dokuya özgü anlatım bilgisi ve haritalamadaki lokus bilgisinin sağlanması için kullanılabilir.

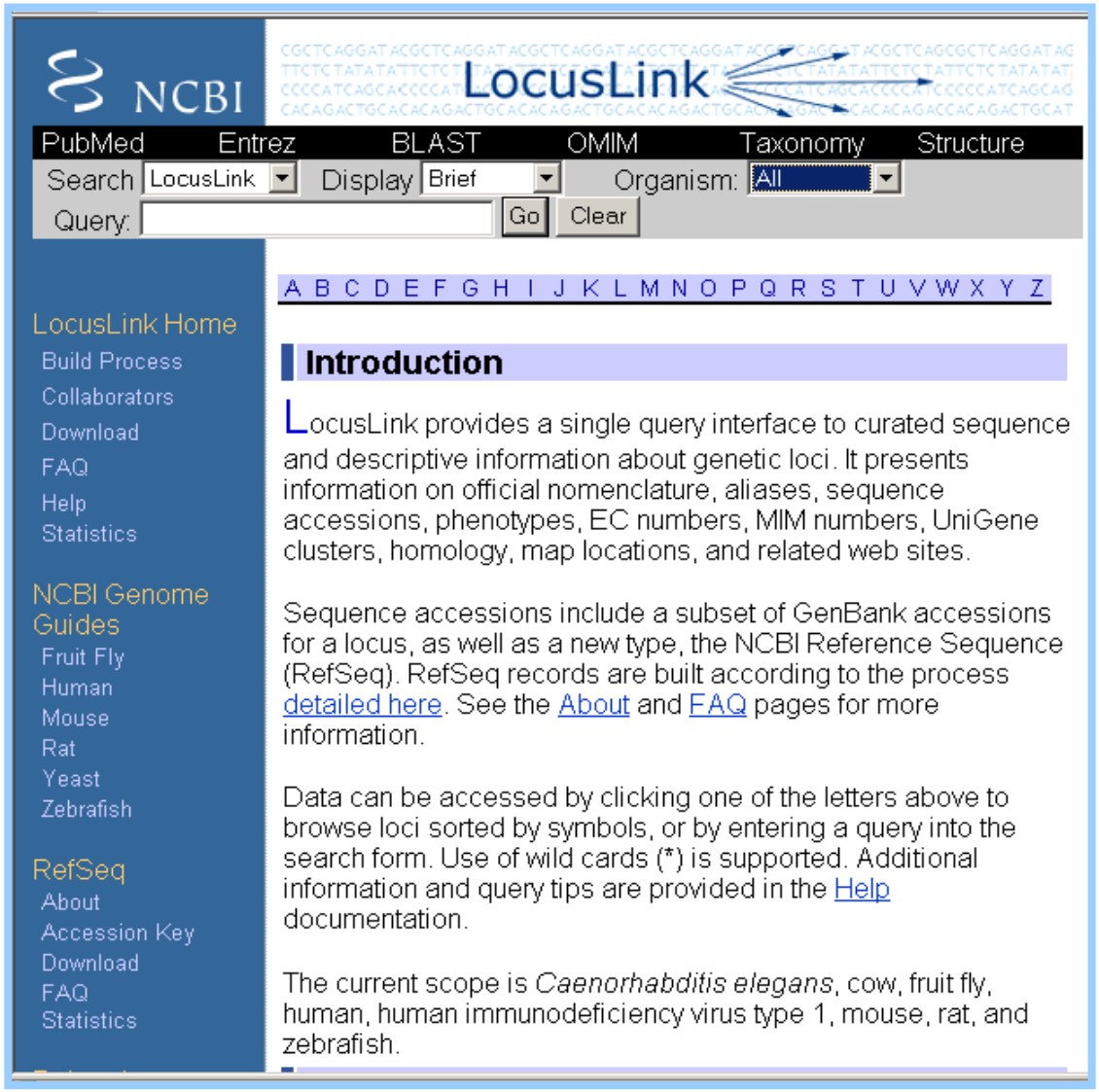
· İyi karakterize edilmiş genleri ve yeni ESTleri kapsar.

· Yeni genlerin keşfi için uygundur.

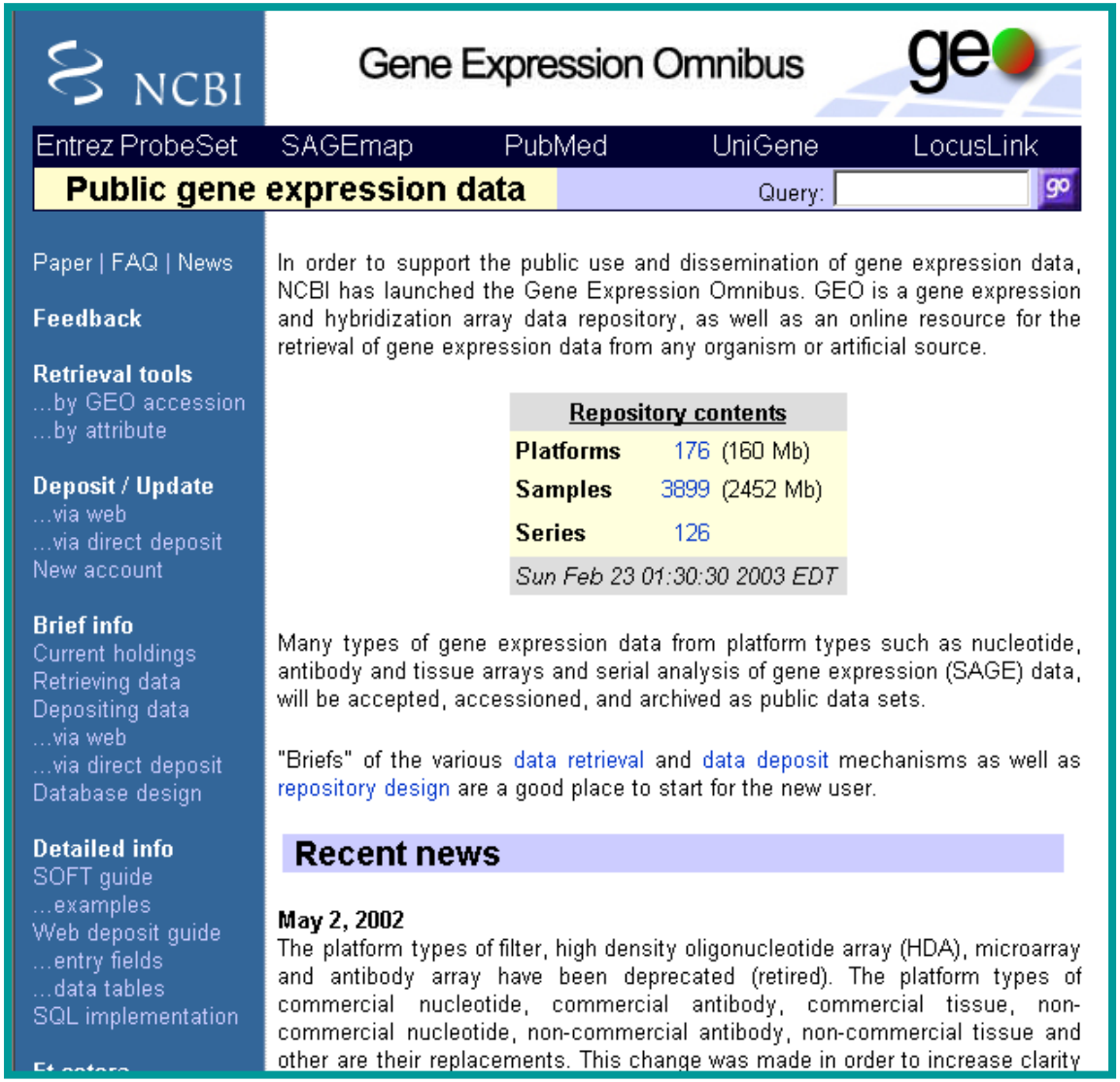
- **EST (”Expressed Sequence Tags”=cDNA) Bölümü**



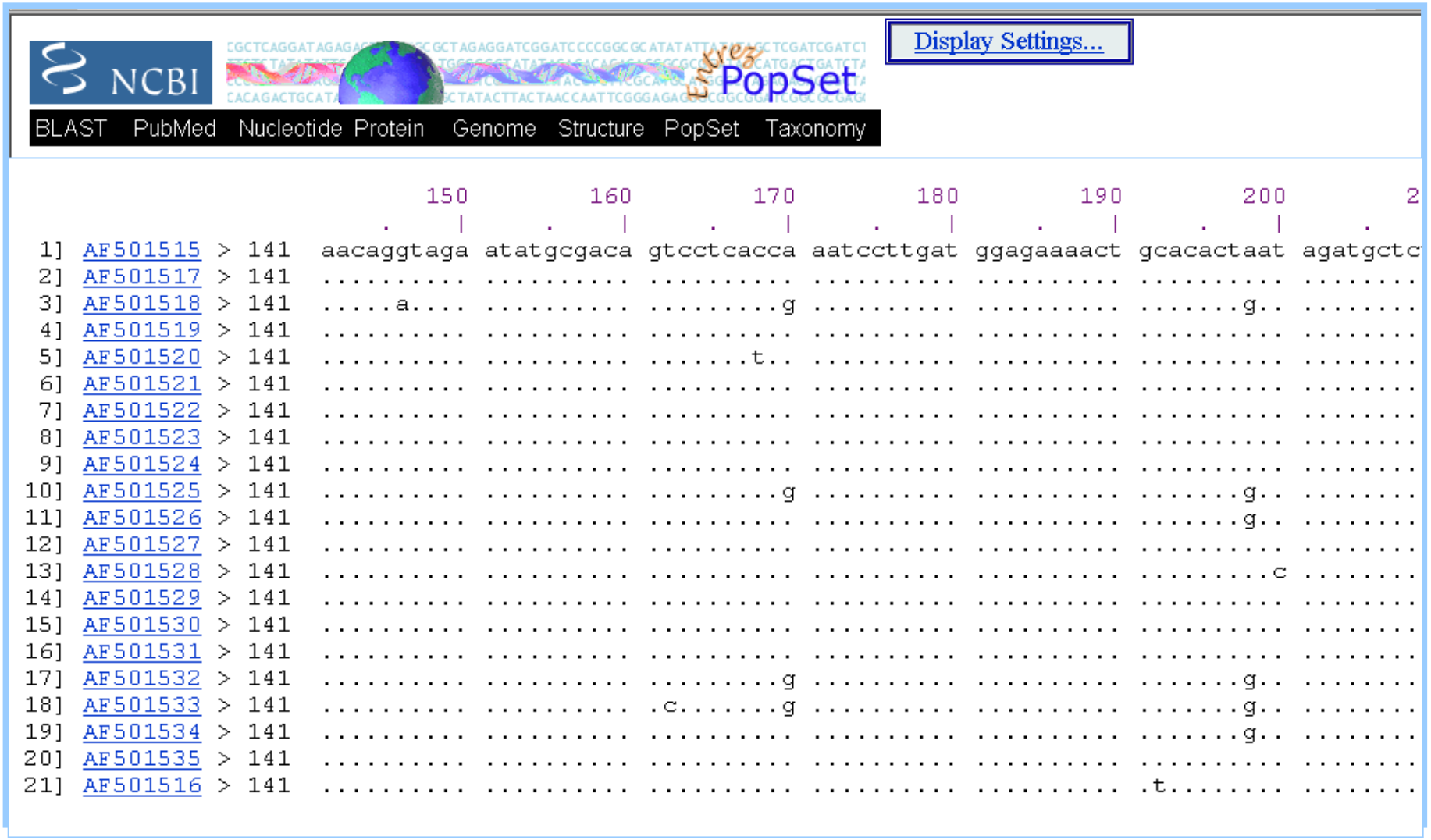
- **Locus Link: Genin bulunduğu lokus hakkında bilgi**

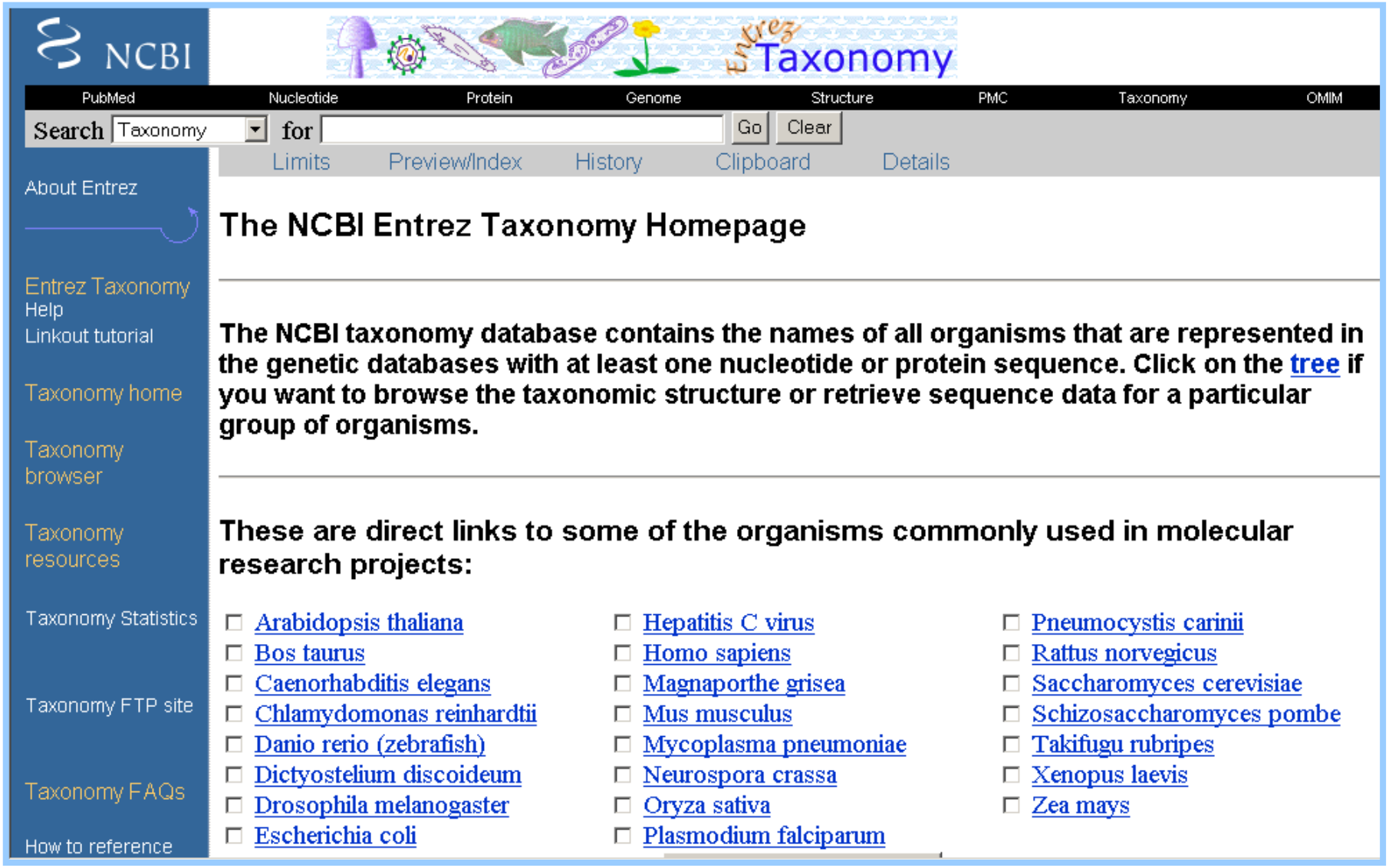


- **GEO (“Gene Expression Omnibus”): Gen anlatım bilgileri**

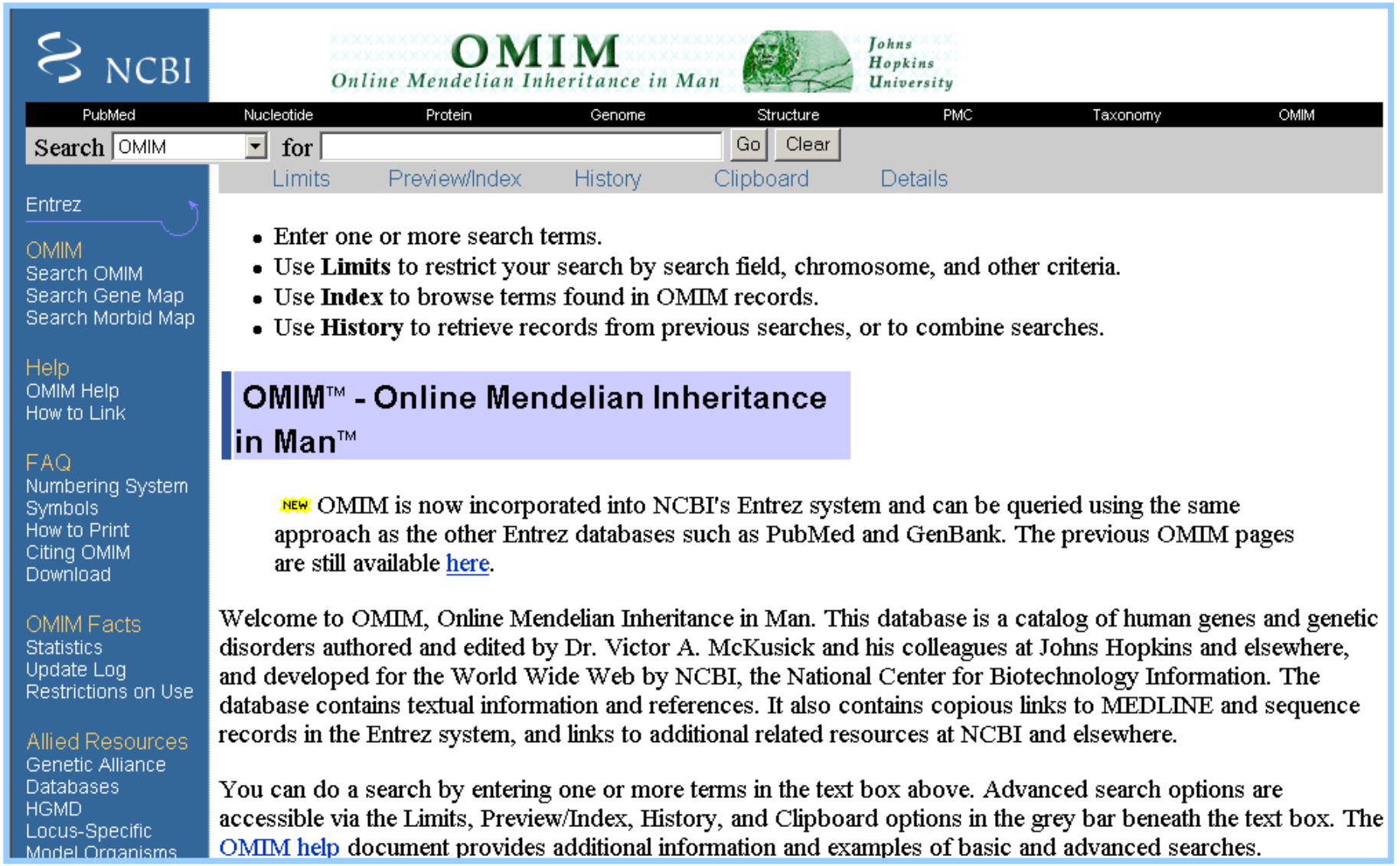


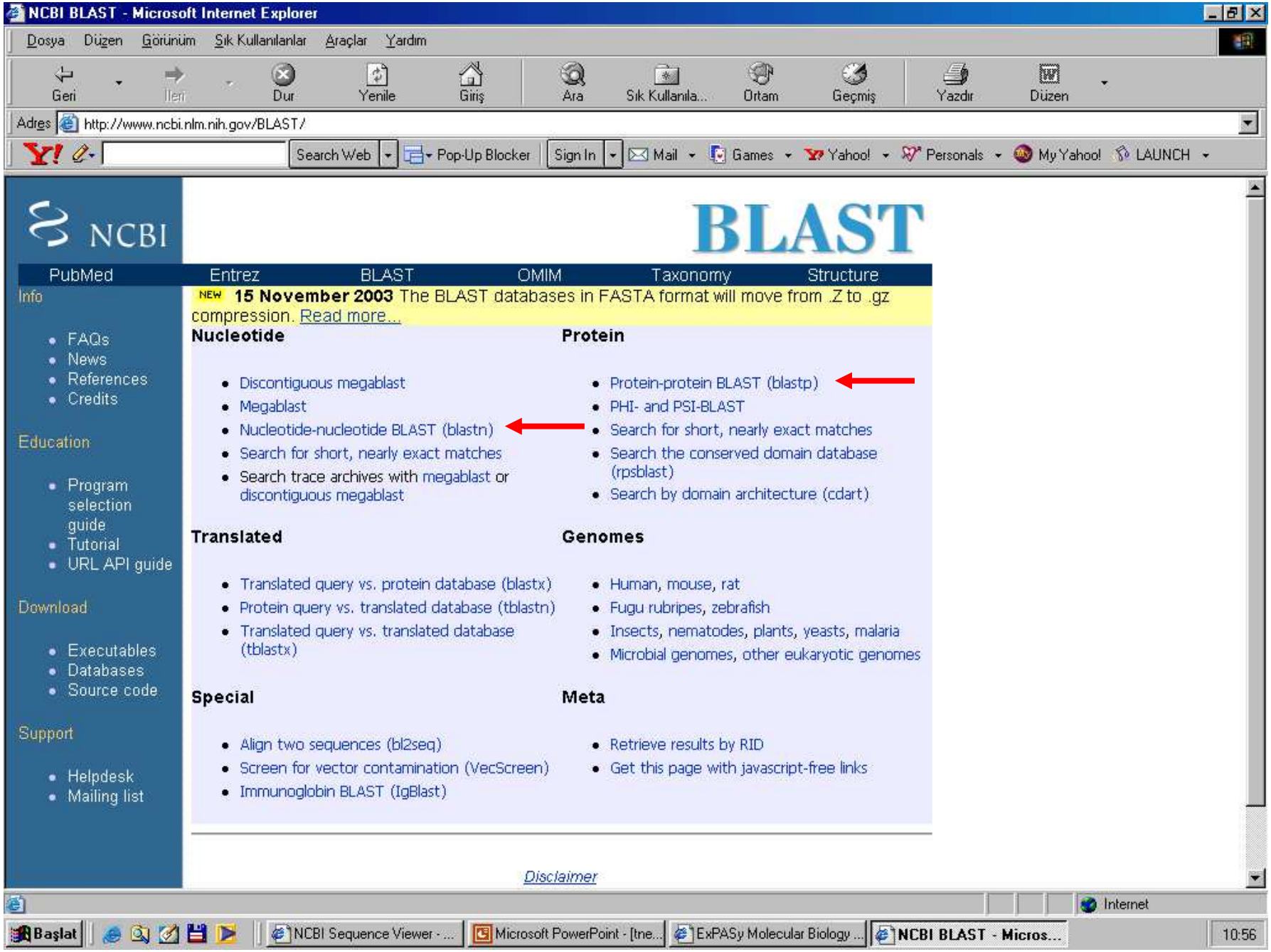
Entrez PopSet:
Populasyon çalışmaları

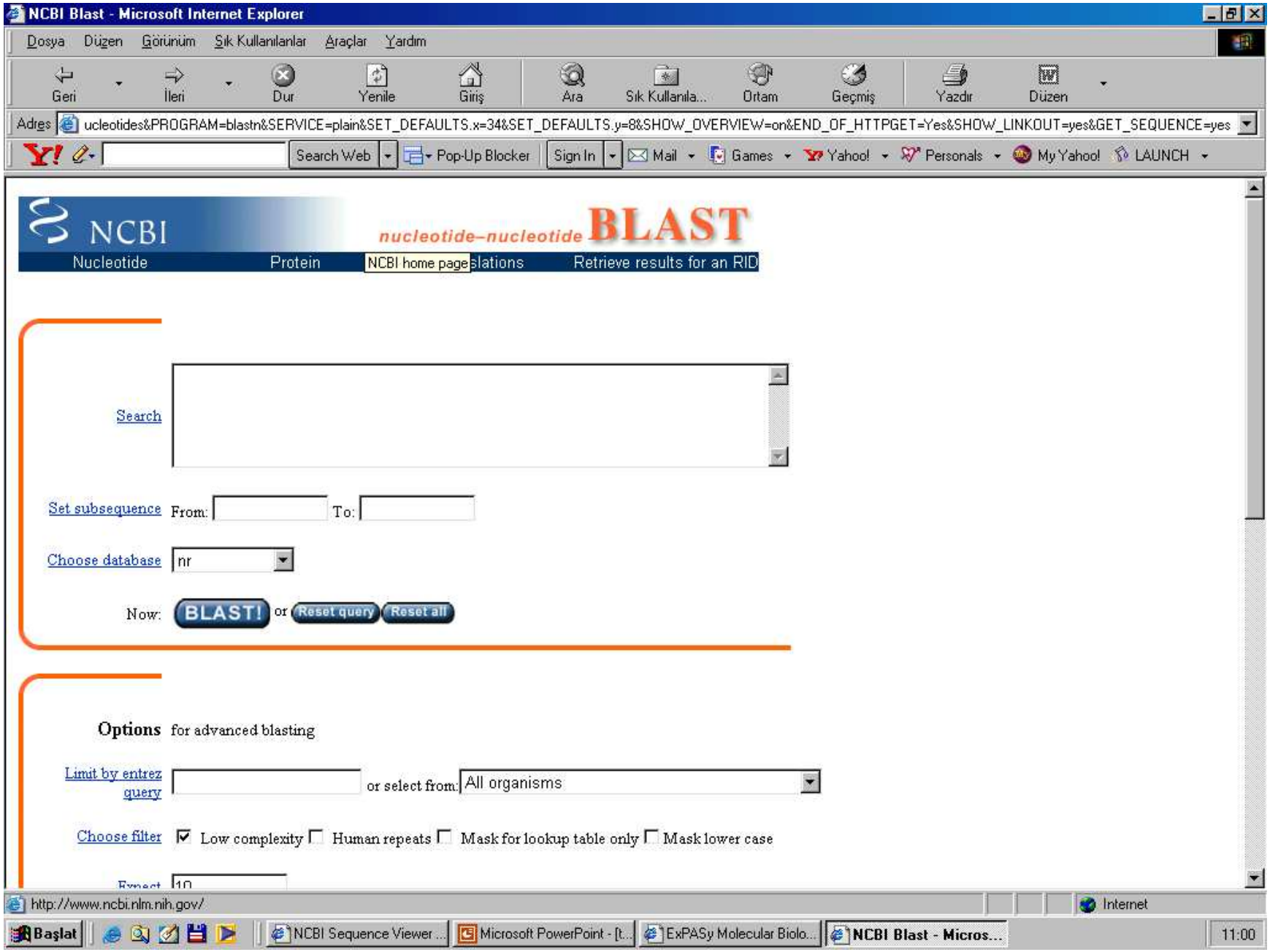


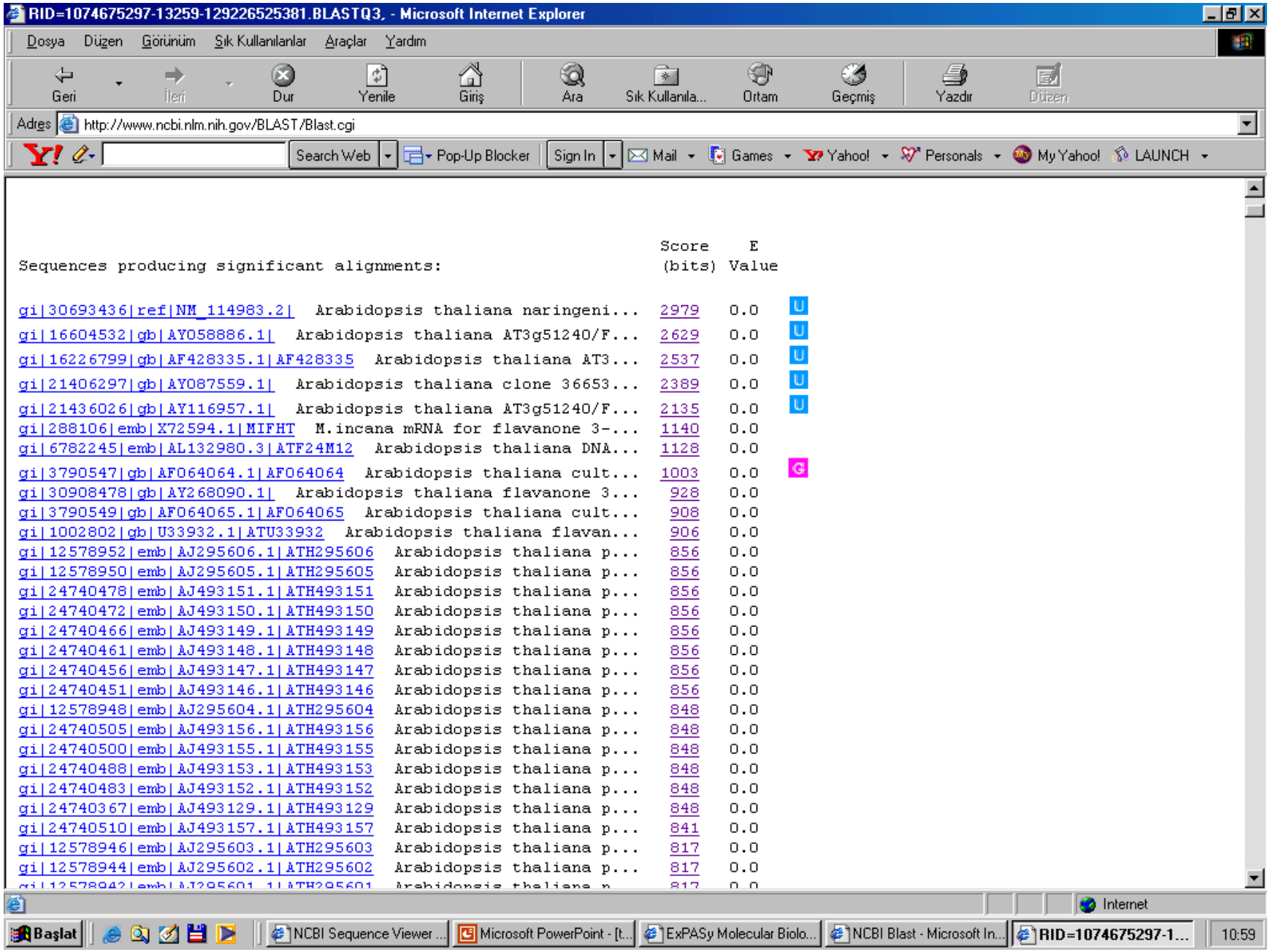

NCBI
Entrez Taxonomy
PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM
Search Taxonomy for Go Clear
Limits Preview/Index History Clipboard Details
About Entrez
Entrez Taxonomy Help
Linkout tutorial
Taxonomy home
Taxonomy browser
Taxonomy resources
Taxonomy Statistics
Taxonomy FTP site
Taxonomy FAQs
How to reference
The NCBI Entrez Taxonomy Homepage
The NCBI taxonomy database contains the names of all organisms that are represented in the genetic databases with at least one nucleotide or protein sequence. Click on the tree if you want to browse the taxonomic structure or retrieve sequence data for a particular group of organisms.
These are direct links to some of the organisms commonly used in molecular research projects:
Arabidopsis thaliana
Bos taurus
Caenorhabditis elegans
Chlamydomonas reinhardtii
Danio rerio (zebrafish)
Dictyostelium discoideum
Drosophila melanogaster
Escherichia coli
Hepatitis C virus
Homo sapiens
Magnaporthe grisea
Mus musculus
Mycoplasma pneumoniae
Neurospora crassa
Oryza sativa
Plasmodium falciparum
Pneumocystis carinii
Rattus norvegicus
Saccharomyces cerevisiae
Schizosaccharomyces pombe
Takifugu rubripes
Xenopus laevis
Zea mays

OMIM (“On-line Mendelian Inheritance in Man”): İnsan genleri ve genetik hastalıkları




NCBI BLAST - Microsoft Internet Explorer
Dosya Düzen Görünüm Sık Kullanılanlar Araçlar Yardım
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Megablast
Nucleotide-nucleotide BLAST (blastn)
Search for short, nearly exact matches
Search trace archives with megablast or discontiguous megablast
Protein
Protein-protein BLAST (blastp)
PHI- and PSI-BLAST
Search for short, nearly exact matches
Search the conserved domain database (rpsblast)
Search by domain architecture (cdart)
Translated
Translated query vs. protein database (blastx)
Protein query vs. translated database (tblastn)
Translated query vs. translated database (tblastx)
Genomes
Human, mouse, rat
Fugu rubripes, zebrafish
Insects, nematodes, plants, yeasts, malaria
Microbial genomes, other eukaryotic genomes
Special
Align two sequences (bl2seq)
Screen for vector contamination (VecScreen)
Immunoglobin BLAST (IgBlast)
Meta
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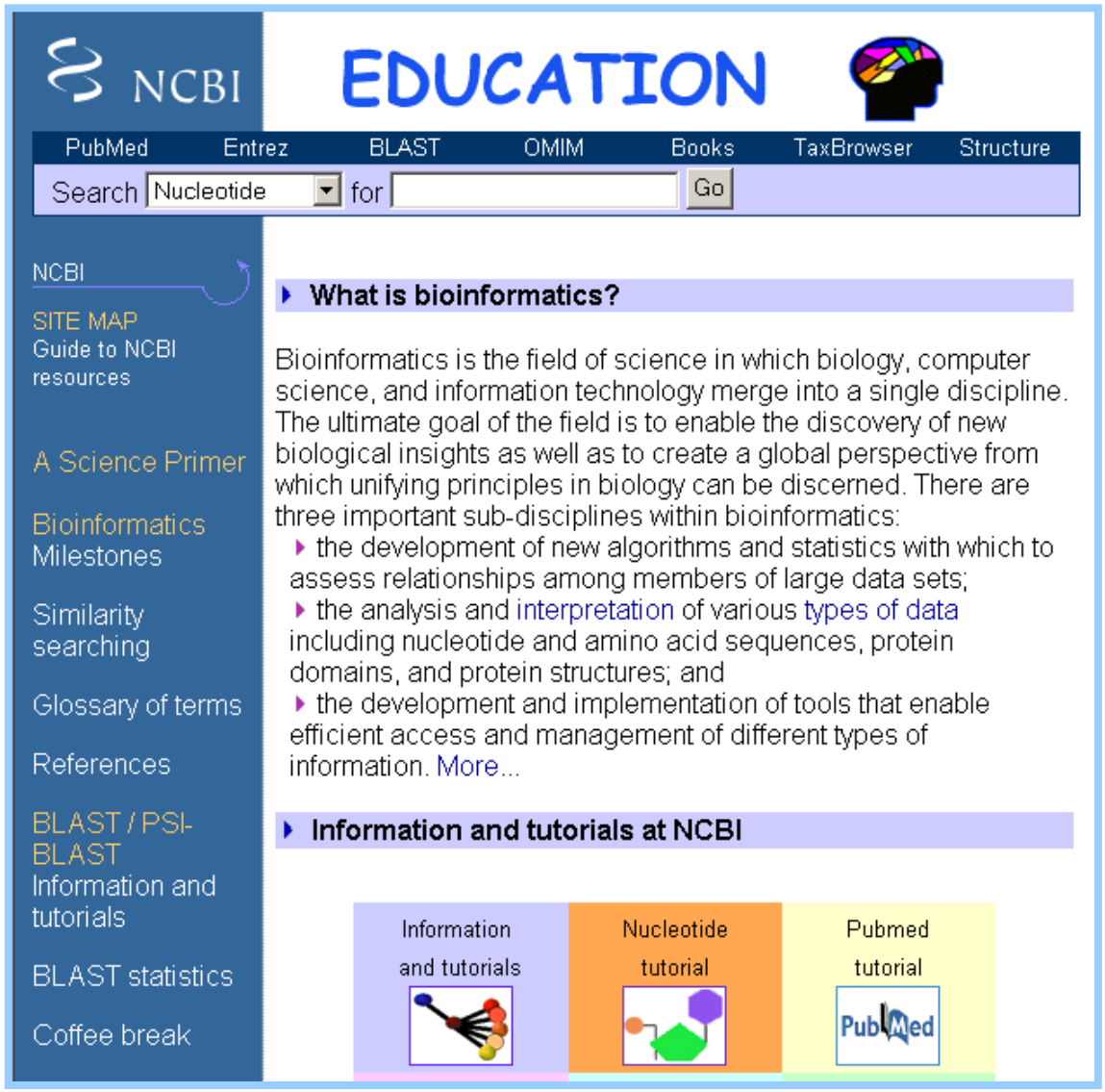

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Adres http://www.ncbi.nlm.nih.gov/BLAST/Blast.cgi
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Sequences producing significant alignments: Score (bits) E Value
gi|30693436|ref|NM_114983.2| Arabidopsis thaliana naringeni... 2979 0.0 U
gi|16604532|gb|AY058886.1| Arabidopsis thaliana AT3g51240/F... 2629 0.0 U
gi|16226799|gb|AF428335.1|AF428335 Arabidopsis thaliana AT3... 2537 0.0 U
gi|21406297|gb|AY087559.1| Arabidopsis thaliana clone 36653... 2389 0.0 U
gi|21436026|gb|AY116957.1| Arabidopsis thaliana AT3g51240/F... 2135 0.0 U
gi|288106|emb|X72594.1|MIFHT M.incana mRNA for flavanone 3-... 1140 0.0
gi|6782245|emb|AL132980.3|ATF24M12 Arabidopsis thaliana DNA... 1128 0.0
gi|3790547|gb|AF064064.1|AF064064 Arabidopsis thaliana cult... 1003 0.0 G
gi|30908478|gb|AY268090.1| Arabidopsis thaliana flavanone 3... 928 0.0
gi|3790549|gb|AF064065.1|AF064065 Arabidopsis thaliana cult... 908 0.0
gi|1002802|gb|U33932.1|ATU33932 Arabidopsis thaliana flavan... 906 0.0
gi|12578952|emb|AJ295606.1|ATH295606 Arabidopsis thaliana p... 856 0.0
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gi|24740478|emb|AJ493151.1|ATH493151 Arabidopsis thaliana p... 856 0.0
gi|24740472|emb|AJ493150.1|ATH493150 Arabidopsis thaliana p... 856 0.0
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gi|24740510|emb|AJ493157.1|ATH493157 Arabidopsis thaliana p... 841 0.0
gi|12578946|emb|AJ295603.1|ATH295603 Arabidopsis thaliana p... 817 0.0
gi|12578944|emb|AJ295602.1|ATH295602 Arabidopsis thaliana p... 817 0.0
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- **NCBI, Google gibi WEB sayfası araması için kullanılabilir.**



- NCBI, eğitim bölümü



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National Institutes of Health
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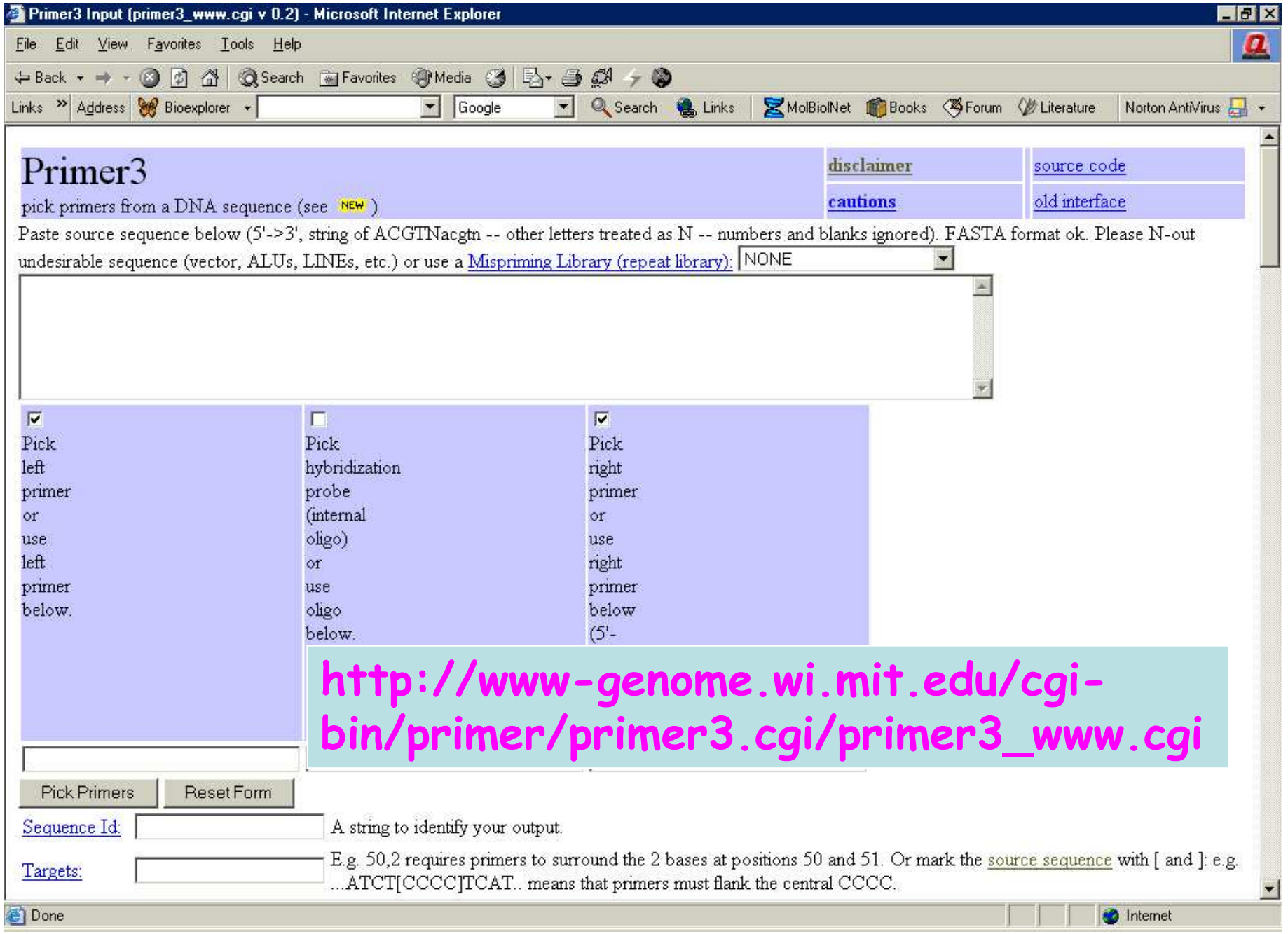


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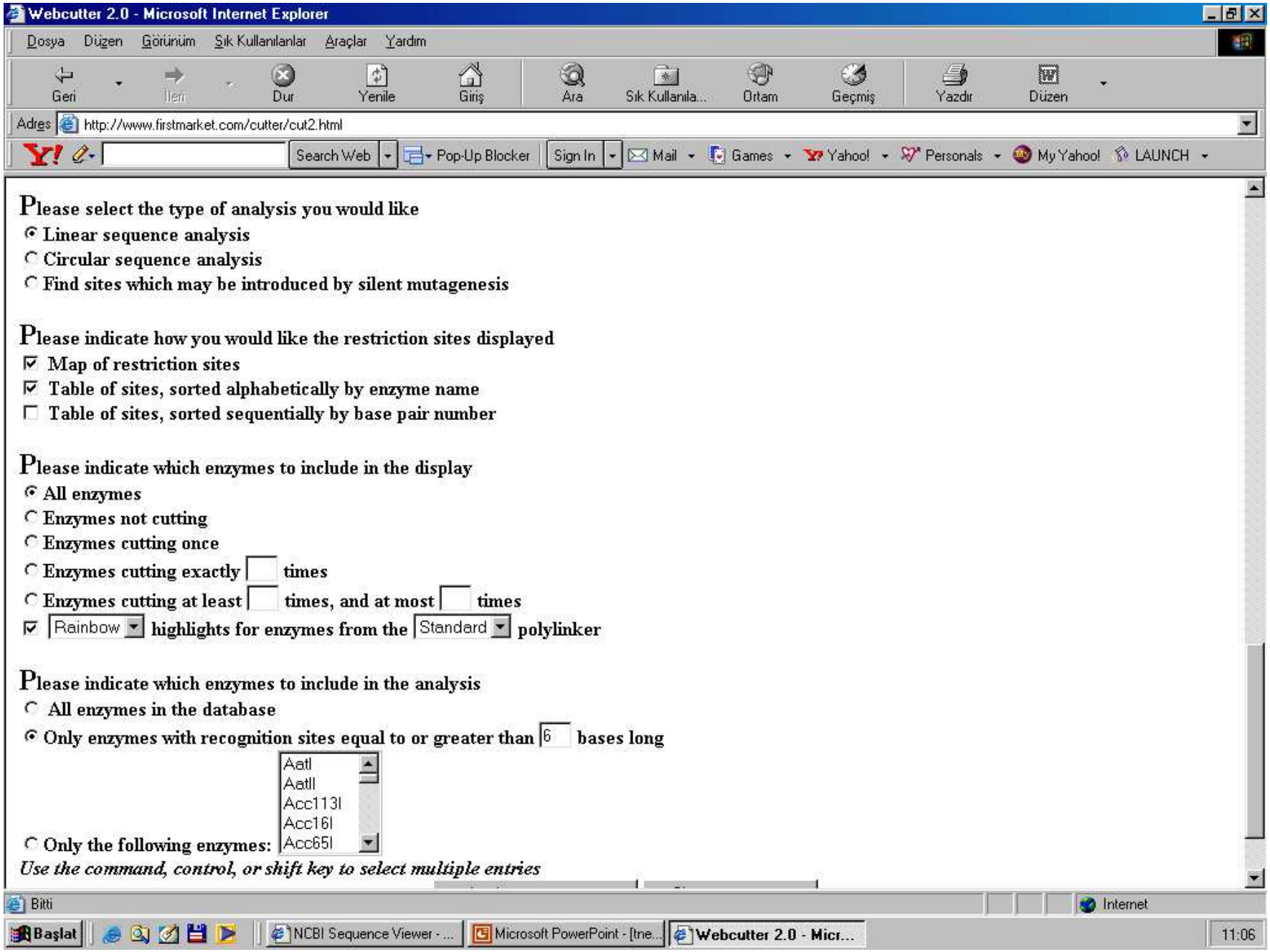
Primer dizayn programları

- **Macvector**
- **Seqlab**
- **Prime (GCG)**
- **Primer3 (ücretsiz)**
- **Primerquest (ücretsiz)**
- **OligoAnalyser**

• Primer dizayn edilirken; primer uzunluğu, GC içeriği, Tm değeri, çoğaltılacak dizinin konumu gibi kriterlerde istenen değişiklikler yapılabilir.


Primer3 Input (primer3_www.cgi v 0.2) - Microsoft Internet Explorer
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Back Search Favorites Media
Links Address Bioexplorer Google Search Links MolBiolNet Books Forum Literature Norton AntiVirus
Primer3
pick primers from a DNA sequence (see NEW)
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Paste source sequence below (5'->3', string of ACGTNacgtn -- other letters treated as N -- numbers and blanks ignored). FASTA format ok. Please N-out undesirable sequence (vector, ALUs, LINEs, etc.) or use a Mispriming Library (repeat library): NONE
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A string to identify your output.
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E.g. 50,2 requires primers to surround the 2 bases at positions 50 and 51. Or mark the source sequence with [and]: e.g. ...ATCT[CCCC]TCAT.. means that primers must flank the central CCCC.
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web cutter
Welcome to Webcutter 2.0! This new version of Webcutter is a complete rewrite. Along with cleaner and more maintainable code, I am pleased to introduce the following new features:
Rainbow cutters Highlight your favorite enzymes in color or boldface for easy at-a-glance identification
Silent cutters Find sites which may be introduced by silent mutagenesis of your coding sequence
Sequence uploads Input sequences directly into Webcutter from a file on your hard drive without needing to cut-and-paste
Degenerate sequences Analyze restriction maps of sequences containing ambiguous nucleotides like N, Y, and R.
Circular sequences Choose whether to treat your sequence as linear or circular
Enzyme info Click into the wealth of references and ordering information at New England BioLabs' REBASE, directly from your restriction map results
Plus all of the features Webcutter has always had, from automatic sequence search-and-entry from NCBI's GenBank to its easy customizable interface and clean simple results format. For a mini-manual on how Webcutter 2.0 works, how to get the most from it, and some of its known limitations, please click here.
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Circular sequence analysis
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Please indicate how you would like the restriction sites displayed
Map of restriction sites
Table of sites, sorted alphabetically by enzyme name
Table of sites, sorted sequentially by base pair number
Please indicate which enzymes to include in the display
All enzymes
Enzymes not cutting
Enzymes cutting once
Enzymes cutting exactly times
Enzymes cutting at least times, and at most times
Rainbow highlights for enzymes from the Standard polylinker
Please indicate which enzymes to include in the analysis
All enzymes in the database
Only enzymes with recognition sites equal to or greater than 6 bases long
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AatII
Acc113I
Acc16I
Acc65I
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- www.plantgenome.uga.edu/links.htm
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