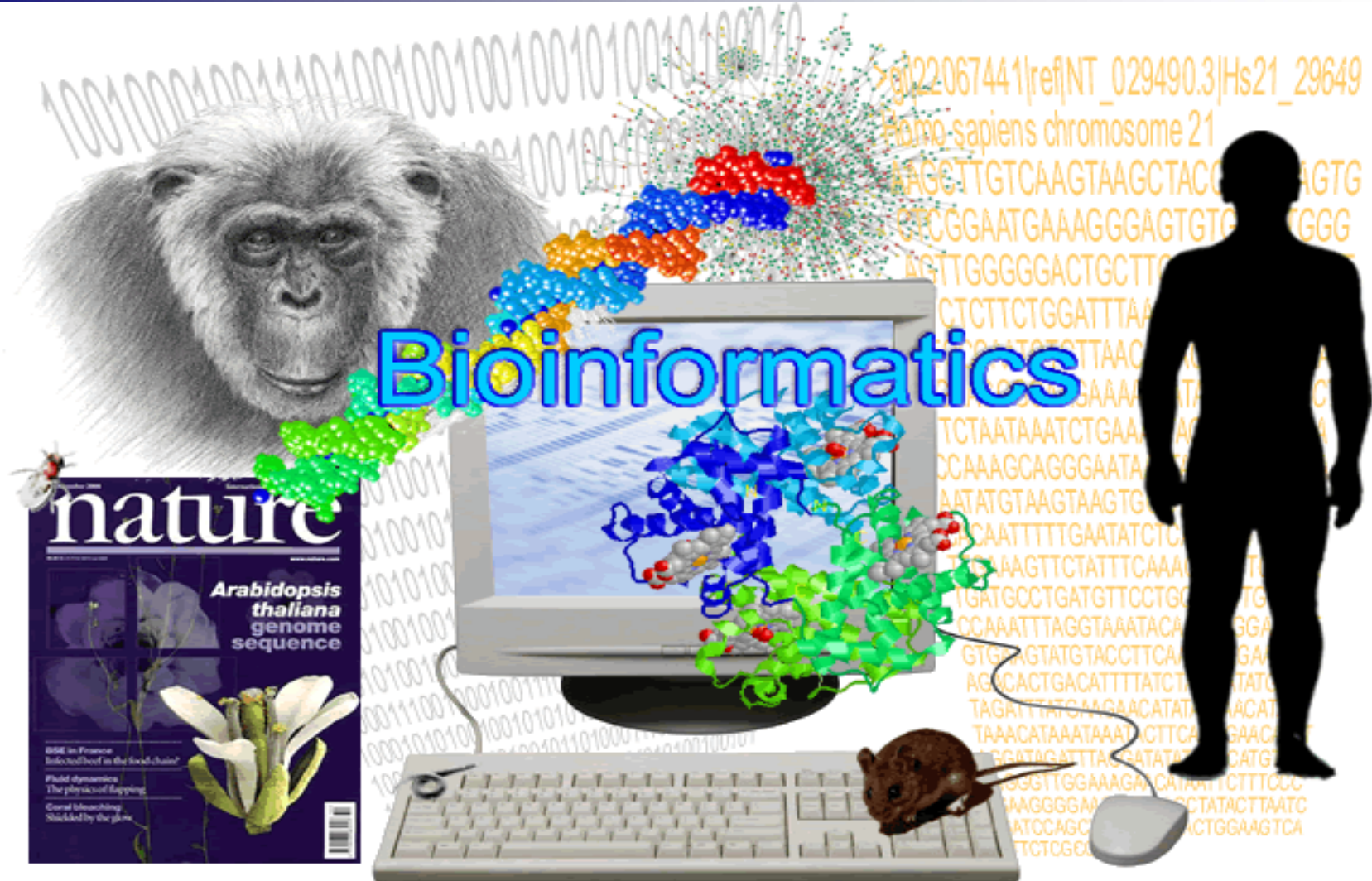
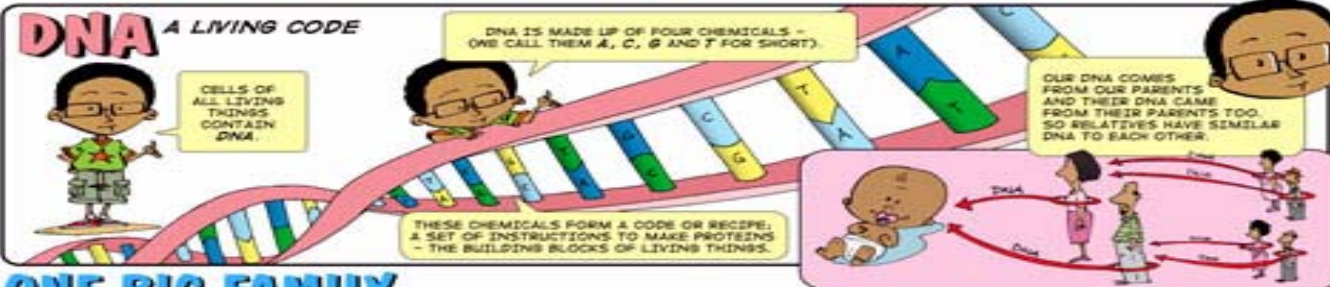




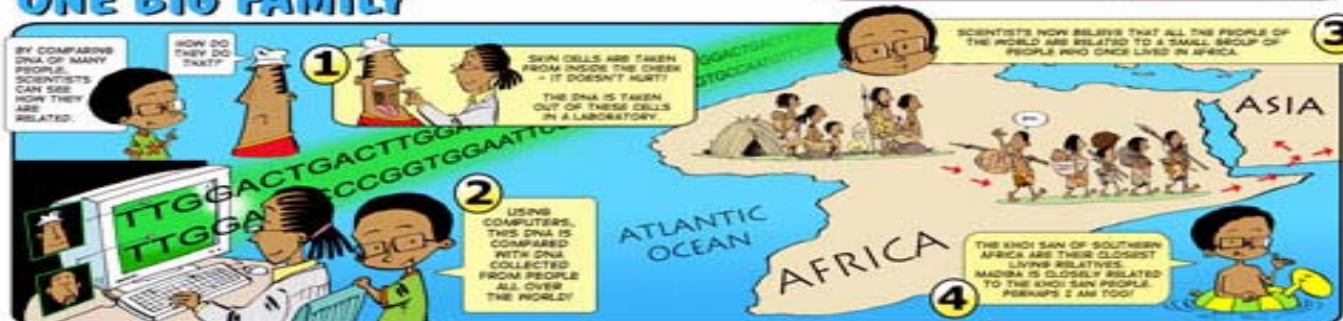
Yard. Doç. Dr. Ercan ARICAN

Moleküler Biyoloji ve Genetik Bölümü

BIOINFORMATICS



ONE BIG FAMILY



BIOINFORMATICS



FIGHTING MALARIA

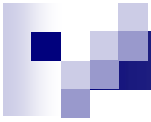
COMPUTERS CAN PREDICT THE SHAPE OF PROTEINS (BUILDING BLOCKS OF LIVING THINGS). THEY CAN BE USED TO CHECK THAT MALARIA TREATMENTS WILL DESTROY MALARIA PROTEINS BUT NOT HUMAN ONES.



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.





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)

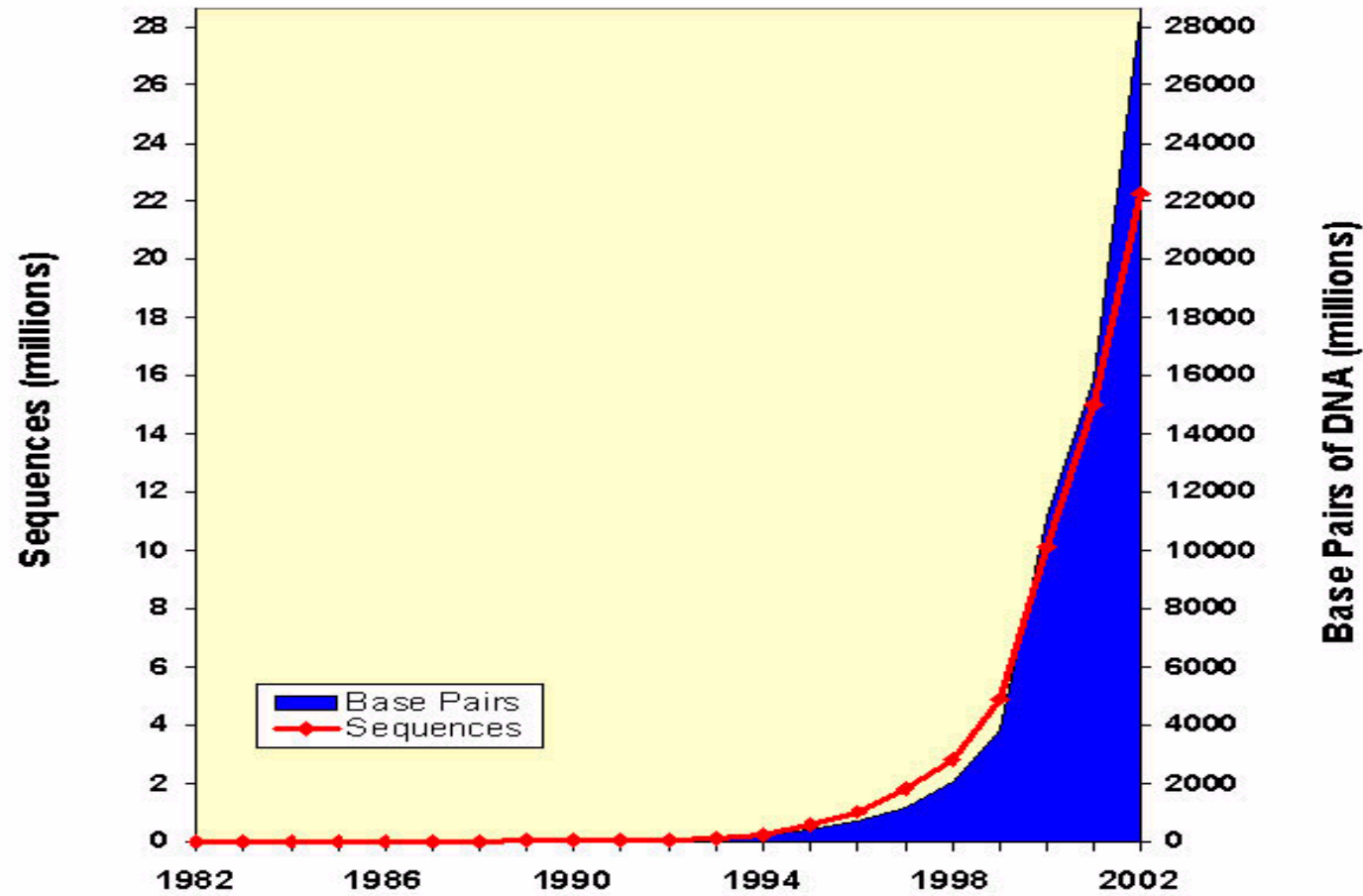


**6. Gen anlatımı ürünleri ve protein
verilerinin eldesi**
(EST, DNA microarray)



7. Varyasyon
(SNP)

Gen Banklarındaki Bilgi Artışı



GOLD: Genomes OnLine Database Homepage - Microsoft Internet Explorer

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GOLDTM

Genomes OnLine Database



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

http://elegans.imbb.forth.gr/GOLD/search.cgi?colcol=all&org_name1=genus&gensp=Oryza&org_domain= - Microsoft Internet Explorer

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Back Forward Stop Home Search Favorites Media Print Mail News RSS Feeds

Links Activity Address Bioexplorer gold genome Google Search Links MolBiolNet Books Forum Literature

Organism	D	Type	Information	Size	DATA-search	Institution	Funding	Genome Database	Publication	Contact	Status
<i>Oryza sativa (rice)</i>	E	ESTs	PLANTS Taxonomy RiceGenes			Monsanto		Monsanto		rice.webmaster	incomplete
<i>Oryza sativa L. ssp. indica</i>	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
<i>Oryza sativa ssp. japonica</i>	E		PLANTS Taxonomy GNN report	420000 Kb 50000 orfs		Syngenta Myriad Genetics		NCBI TMRI	Science 296, 92-100 2002-04-05	Goff SA	complete
<i>Oryza sativa ssp. japonica c.v. Nipponbare</i>	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

Internet

The TIGR Rice Annotation and Informatics - Netscape

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http://www.tigr.org/tdb/e2k1/osa1/annotation.shtml Search

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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 & Rice Markers

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 Ortholog Database.

GlimmerM/A/R server - Netscape

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←

→

↶

✕

http://www.tigr.org/tdb/glimmerm/glmr_form.html

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plant genomics resources on the... IRGSP hmmpfam-search-Fri Nov 14 17:... ONLamp.com: [2003 15, Novem... GlimmerM/A/R server



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[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

☐ Brugia malayi

☐ Entamoeba histolytica

☐ Plasmodium falciparum (malaria)

☐ Schistosoma mansoni

☐ Aspergillus fumigatus

☐ Cryptococcus neoformans

☒ Oryza sativa (rice)

☐ Plasmodium yoelii

☐ Theileria parva

e-Mail results

☒ No, I'll wait

☐ Yes, to:

plant genomics resources on the web - Netscape

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http://www.plantgenome.uga.edu/links.htm#Gene-findingsoftware Search

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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

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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

- 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

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SDSC Biology Workbench IRGSP The GlimmerM Home Page Eukaryotic Projects - The... The Gibbs Motif Sampler ... MEME - Introduction

 **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 secondary 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/

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Search for

ExPASy Molecular Biology Server

The ExPASy (Expert Protein Analysis System) [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	Tools and software packages
• 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	• 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 • Raché Applied Science's Biochemical Pathways

10:50

The National Center for Biotechnology Information (NCBI) Home Page

<http://www.ncbi.nlm.nih.gov>



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

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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

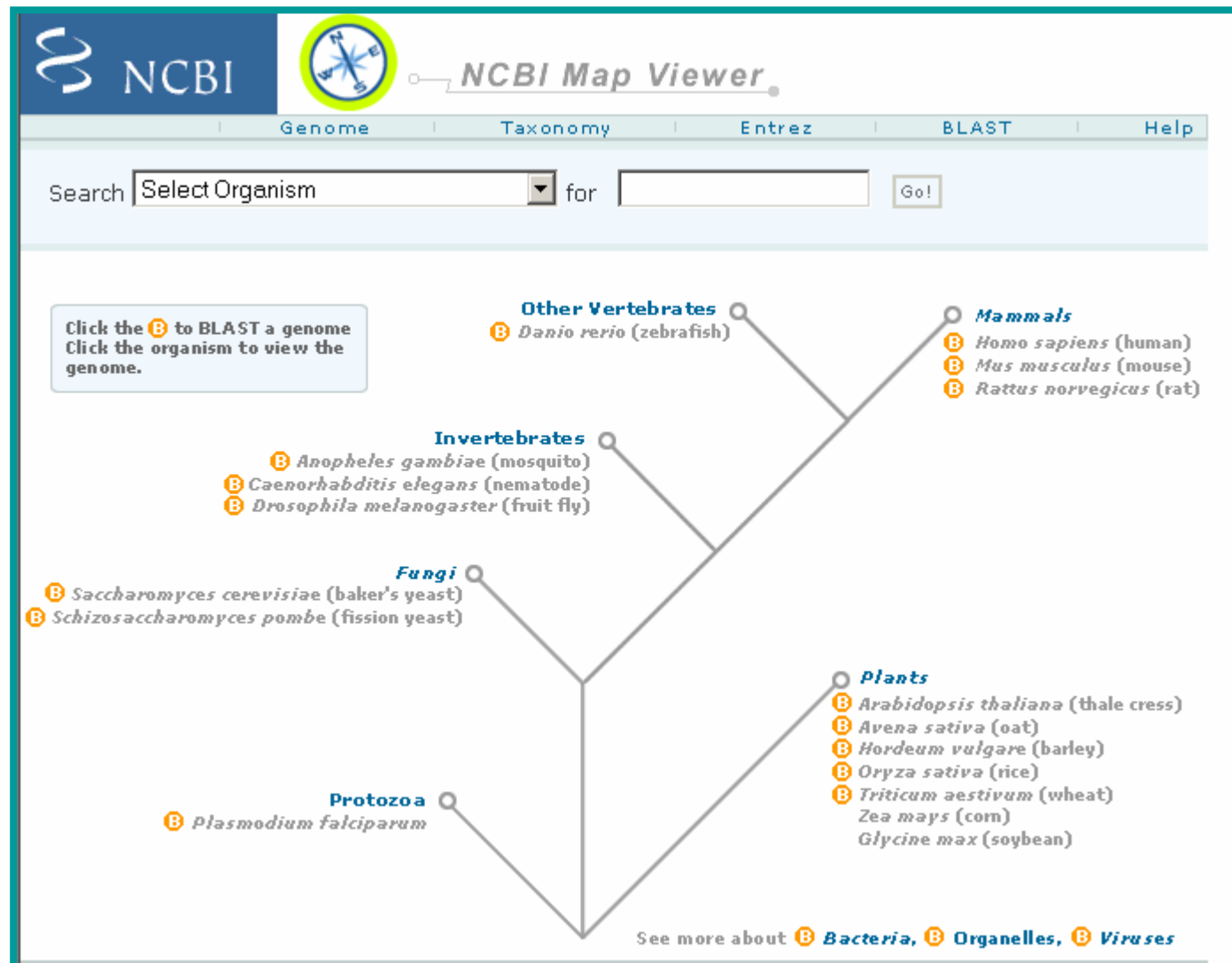
ALPHABETICAL INDEX

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'in nukleotid dizileri veri tabanı

- **Bilgiler işbirliği içerisindeki üç veritabanı arasında paylaşılır.**

- GenBank

- DDBJ (“DNA Database of Japan”)

- www.ddbj.nig.ac.jp

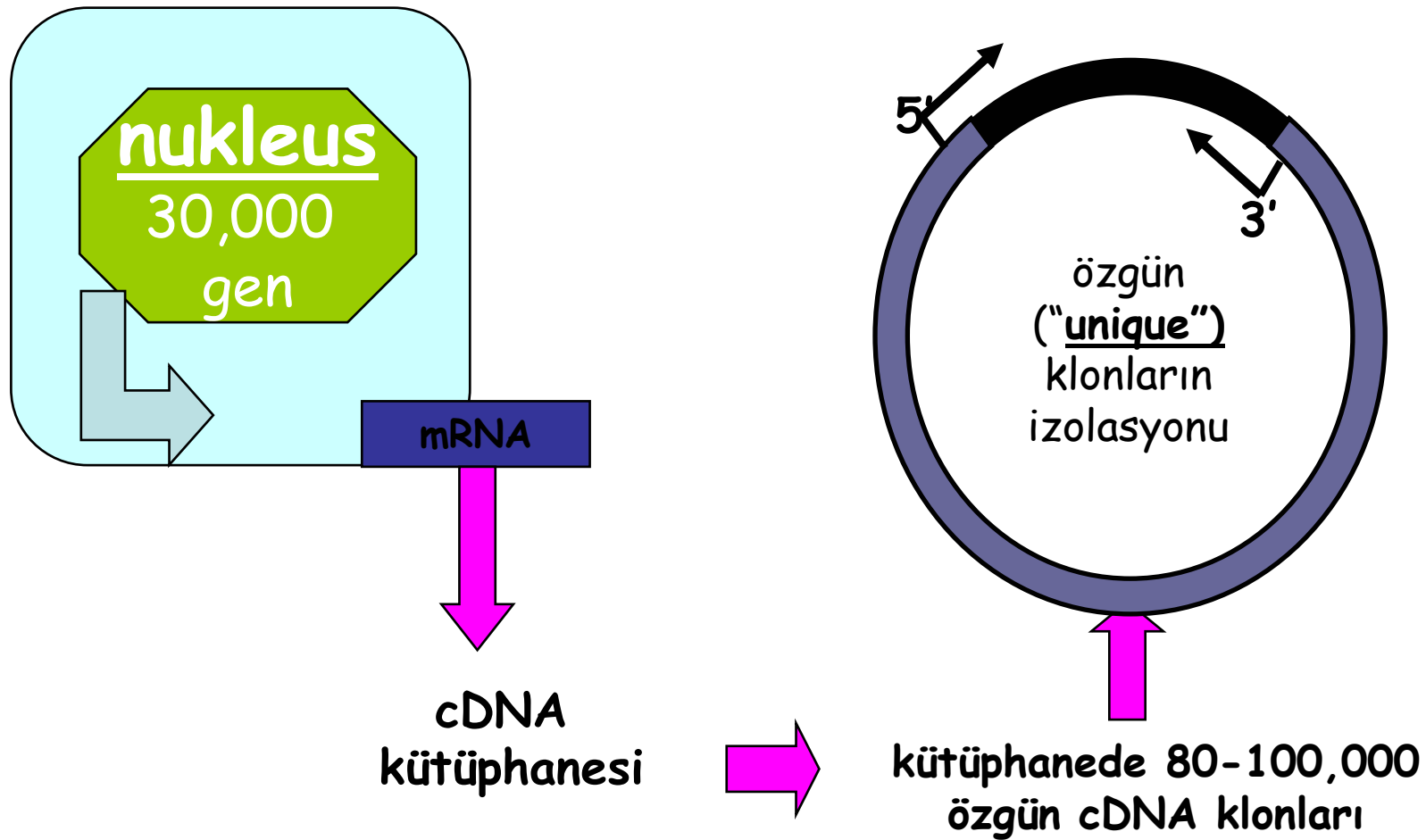
- EMBL (“European Molecular Biology Laboratory Database”)

- 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 Sequences Tags"=cDNA) Bölümü



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

[illegible]

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





[Entrez ProbeSet](#)
[SAGEmap](#)
[PubMed](#)
[UniGene](#)
[LocusLink](#)

Public gene expression data

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Feedback

Retrieval tools
[...by GEO accession](#)
[...by attribute](#)

Deposit / Update
[...via web](#)
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[New account](#)

Brief info
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[...via direct deposit](#)
[Database design](#)

Detailed info
[SOFT guide](#)
[...examples](#)
[Web deposit guide](#)
[...entry fields](#)
[...data tables](#)
[SQL implementation](#)

In order to support the public use and dissemination of gene expression data, NCBI has launched the Gene Expression Omnibus. GEO is a gene expression and hybridization array data repository, as well as an online resource for the retrieval of gene expression data from any organism or artificial source.

Repository contents	
Platforms	176 (160 Mb)
Samples	3899 (2452 Mb)
Series	126

Sun Feb 23 01:30:30 2003 EDT

Many types of gene expression data from platform types such as nucleotide, antibody and tissue arrays and serial analysis of gene expression (SAGE) data, will be accepted, accessioned, and archived as public data sets.

"Briefs" of the various [data retrieval](#) and [data deposit](#) mechanisms as well as [repository design](#) are a good place to start for the new user.

Recent news

May 2, 2002
The platform types of filter, high density oligonucleotide array (HDA), microarray and antibody array have been deprecated (retired). The platform types of commercial nucleotide, commercial antibody, commercial tissue, non-commercial nucleotide, non-commercial antibody, non-commercial tissue and other are their replacements. This change was made in order to increase clarity

Entrez PopSet: Populasyon çalışmaları





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			150	160	170	180	190	200	210
1]	AF501515	> 141	aacaggtaga	atatgcgaca	gtcctcacca	aatccttgat	ggagaaaact	gcacactaat	agatgctc
2]	AF501517	> 141							
3]	AF501518	> 141	a.....		g			g..	
4]	AF501519	> 141							
5]	AF501520	> 141			t..				
6]	AF501521	> 141							
7]	AF501522	> 141							
8]	AF501523	> 141							
9]	AF501524	> 141							
10]	AF501525	> 141			g			g..	
11]	AF501526	> 141						g..	
12]	AF501527	> 141							
13]	AF501528	> 141						c	
14]	AF501529	> 141							
15]	AF501530	> 141							
16]	AF501531	> 141							
17]	AF501532	> 141			g			g..	
18]	AF501533	> 141			c.....g			g..	
19]	AF501534	> 141						g..	
20]	AF501535	> 141							
21]	AF501516	> 141					t		

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[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 | ☐ Hepatitis C virus | ☐ Pneumocystis carinii |
| ☐ Bos taurus | ☐ Homo sapiens | ☐ Rattus norvegicus |
| ☐ Caenorhabditis elegans | ☐ Magnaporthe grisea | ☐ Saccharomyces cerevisiae |
| ☐ Chlamydomonas reinhardtii | ☐ Mus musculus | ☐ Schizosaccharomyces pombe |
| ☐ Danio rerio (zebrafish) | ☐ Mycoplasma pneumoniae | ☐ Takifugu rubripes |
| ☐ Dictyostelium discoideum | ☐ Neurospora crassa | ☐ Xenopus laevis |
| ☐ Drosophila melanogaster | ☐ Oryza sativa | ☐ Zea mays |
| ☐ Escherichia coli | ☐ Plasmodium falciparum | |

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

NCBI

OMIM
Online Mendelian Inheritance in Man

Johns Hopkins University

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM

Search OMIM for Go Clear

Limits Preview/Index History Clipboard Details

Entrez

- Enter one or more search terms.
- Use **Limits** to restrict your search by search field, chromosome, and other criteria.
- Use **Index** to browse terms found in OMIM records.
- Use **History** to retrieve records from previous searches, or to combine searches.

OMIM™ - Online Mendelian Inheritance in Man™

NEW OMIM is now incorporated into NCBI's Entrez system and can be queried using the same approach as the other Entrez databases such as PubMed and GenBank. The previous OMIM pages are still available [here](#).

Welcome to OMIM, Online Mendelian Inheritance in Man. This database is a catalog of human genes and genetic disorders authored and edited by Dr. Victor A. McKusick and his colleagues at Johns Hopkins and elsewhere, and developed for the World Wide Web by NCBI, the National Center for Biotechnology Information. The database contains textual information and references. It also contains copious links to MEDLINE and sequence records in the Entrez system, and links to additional related resources at NCBI and elsewhere.

You can do a search by entering one or more terms in the text box above. Advanced search options are accessible via the Limits, Preview/Index, History, and Clipboard options in the grey bar beneath the text box. The [OMIM help](#) document provides additional information and examples of basic and advanced searches.

OMIM Facts
Statistics
Update Log
Restrictions on Use

Allied Resources
Genetic Alliance
Databases
HGMD
Locus-Specific
Model Organisms

NCBI BLAST - Microsoft Internet Explorer

Dosya Düzen Görünüm Sık Kullanılanlar Araçlar Yardım

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

Adres http://www.ncbi.nlm.nih.gov/BLAST/

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NCBI

BLAST

PubMed Entrez BLAST OMIM Taxonomy Structure

Info

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- References
- Credits

Education

- Program selection guide
- Tutorial
- URL API guide

Download

- Executables
- Databases
- Source code

Support

- Helpdesk
- Mailing list

NEW 15 November 2003 The BLAST databases in FASTA format will move from .Z to .gz compression. [Read more...](#)

Nucleotide

- Discontiguous megablast
- 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)
- Immunoglobulin BLAST (IgBlast)

Meta

- Retrieve results by RID
- Get this page with javascript-free links

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Internet

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NCBI Blast - Microsoft Internet Explorer

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Adres <http://ncbi.nlm.nih.gov/blast/>

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 **NCBI** *nucleotide-nucleotide* **BLAST**

Nucleotide Protein NCBI home page stations Retrieve results for an RID

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[Choose database](#)

Now: **BLAST!** or [Reset query](#) [Reset all](#)

Options for advanced blasting

[Limit by entrez query](#) or select from:

[Choose filter](#) ☒ Low complexity ☐ Human repeats ☐ Mask for lookup table only ☐ Mask lower case

[Format](#)

<http://www.ncbi.nlm.nih.gov/> Internet

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RID=1074675297-13259-129226525381.BLASTQ3, - Microsoft Internet Explorer

Dosya Düzen Görünüm Sık Kullanılanlar Araçlar Yardım

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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	
gi 12578950 emb AJ295605.1 ATH295605 Arabidopsis thaliana p...	856	0.0	
gi 24740478 emb AJ493151.1 ATH493151 Arabidopsis thaliana p...	856	0.0	
gi 24740472 emb AJ493150.1 ATH493150 Arabidopsis thaliana p...	856	0.0	
gi 24740466 emb AJ493149.1 ATH493149 Arabidopsis thaliana p...	856	0.0	
gi 24740461 emb AJ493148.1 ATH493148 Arabidopsis thaliana p...	856	0.0	
gi 24740456 emb AJ493147.1 ATH493147 Arabidopsis thaliana p...	856	0.0	
gi 24740451 emb AJ493146.1 ATH493146 Arabidopsis thaliana p...	856	0.0	
gi 12578948 emb AJ295604.1 ATH295604 Arabidopsis thaliana p...	848	0.0	
gi 24740505 emb AJ493156.1 ATH493156 Arabidopsis thaliana p...	848	0.0	
gi 24740500 emb AJ493155.1 ATH493155 Arabidopsis thaliana p...	848	0.0	
gi 24740488 emb AJ493153.1 ATH493153 Arabidopsis thaliana p...	848	0.0	
gi 24740483 emb AJ493152.1 ATH493152 Arabidopsis thaliana p...	848	0.0	
gi 24740367 emb AJ493129.1 ATH493129 Arabidopsis thaliana p...	848	0.0	
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	
gi 12578942 emb AJ295601.1 ATH295601 Arabidopsis thaliana n...	817	0.0	

Internet

Başlat NCBI Sequence Viewer... Microsoft PowerPoint - [t... ExPASy Molecular Biolo... NCBI Blast - Microsoft In... RID=1074675297-1... 10:59

- NCBI, Google gibi WEB sayfası araması için kullanılabilir.

The screenshot displays the NCBI Site Search interface. At the top, the NCBI logo is on the left, and the title "NCBI- Site Search" is in the center. Below the title is a navigation bar with tabs for PubMed, Nucleotide, Protein, Genome, Structure, Popset, and Taxonomy. A search bar contains the text "cancer" with "Go" and "Clear" buttons. Below the search bar are links for Limits, Preview/Index, History, Clipboard, and Details. On the left side, there is a sidebar with links to Entrez, PubMed Search, NCBI Site Map, Quick Links, Help, and FAQ. The main content area shows the search results for "cancer", indicating 265 matches under 37 home pages. It lists three categories: "Genes and disease", "Cancer", and "Collaborative Cancer Research", each with a brief description and a link to view all results. The "Genes and disease" category is highlighted in blue.

NCBI

NCBI- Site Search

PubMed Nucleotide Protein Genome Structure Popset Taxonomy

Search NCBI Web Site for cancer Go Clear

Limits Preview/Index History Clipboard Details

Display Home Page View Send to Text

Searched for : cancer
265 matches under 37 home pages [View all 265 results](#)

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Genes and disease provides short descriptions of inherited disorders. It is hosted by the National Center for Biotechnology Information (NCBI), a division of the National Library of Medicine (NLM) at the National Institutes of Health (NIH).
Category: [product-service.information.guide](#)[product-service.home page](#)

[Cancer](#) [Related sites](#)
Genes and disease provides short descriptions of inherited disorders. It is hosted by the National Center for Biotechnology Information (NCBI), a division of the National Library of Medicine (NLM) at the National Institutes of Health (NIH).
Category: [product-service.information.article](#)
[[View all 19 results from http://www.ncbi.nlm.nih.gov/disease/](#)]

[Collaborative Cancer Research](#) [Related sites](#)
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- NCBI, eğitim bölümü



EDUCATION



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Similarity searching

Glossary of terms

References

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Information and tutorials

BLAST statistics

Coffee break

What is bioinformatics?

Bioinformatics is the field of science in which biology, computer science, and information technology merge into a single discipline. The ultimate goal of the field is to enable the discovery of new biological insights as well as to create a global perspective from which unifying principles in biology can be discerned. There are three important sub-disciplines within bioinformatics:

- ▶ the development of new algorithms and statistics with which to assess relationships among members of large data sets;
- ▶ the analysis and [interpretation](#) of various [types of data](#) including nucleotide and amino acid sequences, protein domains, and protein structures; and
- ▶ the development and implementation of tools that enable efficient access and management of different types of information. [More...](#)

Information and tutorials at NCBI

Information and tutorials


Nucleotide tutorial


Pubmed tutorial


Book List



Basic Neurochemistry, Molecular, Cellular, and Medical Aspects. 6th ed.

Siegel, George J.; Agranoff, Bernard W.; Albers, R. Wayne; Fisher, Stephen K.; Uhler, Michael D., editors
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ISBN 0 397 51820 X



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National Institutes of Health
[NCBI](#); Not under copyright.



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Kitaplar



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Holzheimer, Rene G.; Mannick, John A., editors;
Munich: [Zuckschwerdt Publishers](#); c2001.
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Chapter 6, Smallpox and Vaccinia.

From: Vaccines. 3rd ed.
Plotkin, Stanley A.; Orenstein, Walter A., editors.
Philadelphia: [W. B. Saunders Company](#); c1999.



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

File Edit View Favorites Tools Help

Back Forward Stop Home Search Favorites Media Print Copy Paste Reload

Links Address Bioexplorer Google Search Links MolBiolNet Books Forum Literature Norton AntiVirus

Primer3

pick primers from a DNA sequence (see [NEW](#))

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 \(repeat library\)](#):

☒ Pick left primer or use left primer below.

☐ Pick hybridization probe (internal oligo) or use oligo below.

☒ Pick right primer or use right primer below (5'-

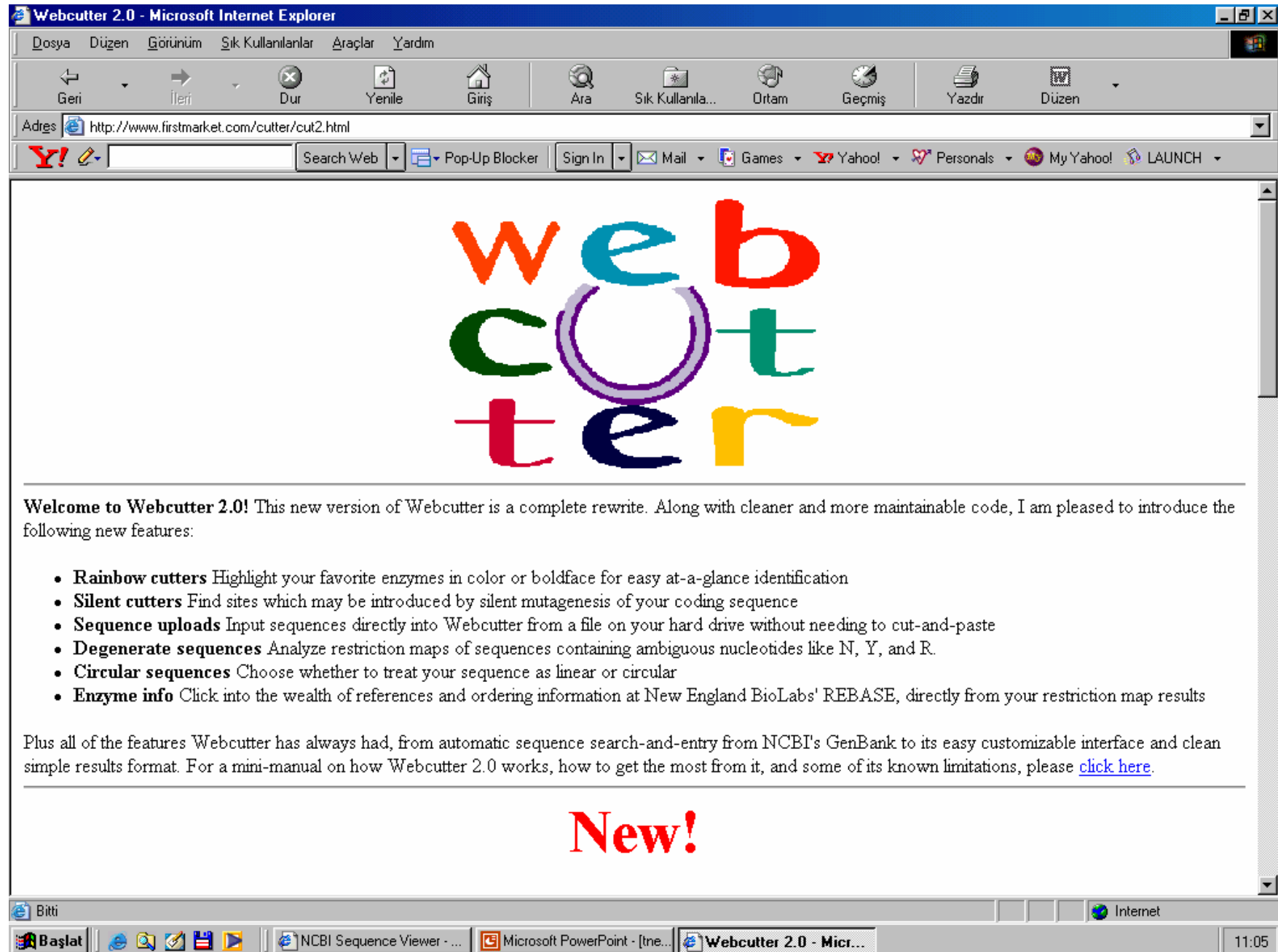
[Sequence Id:](#) A string to identify your output.

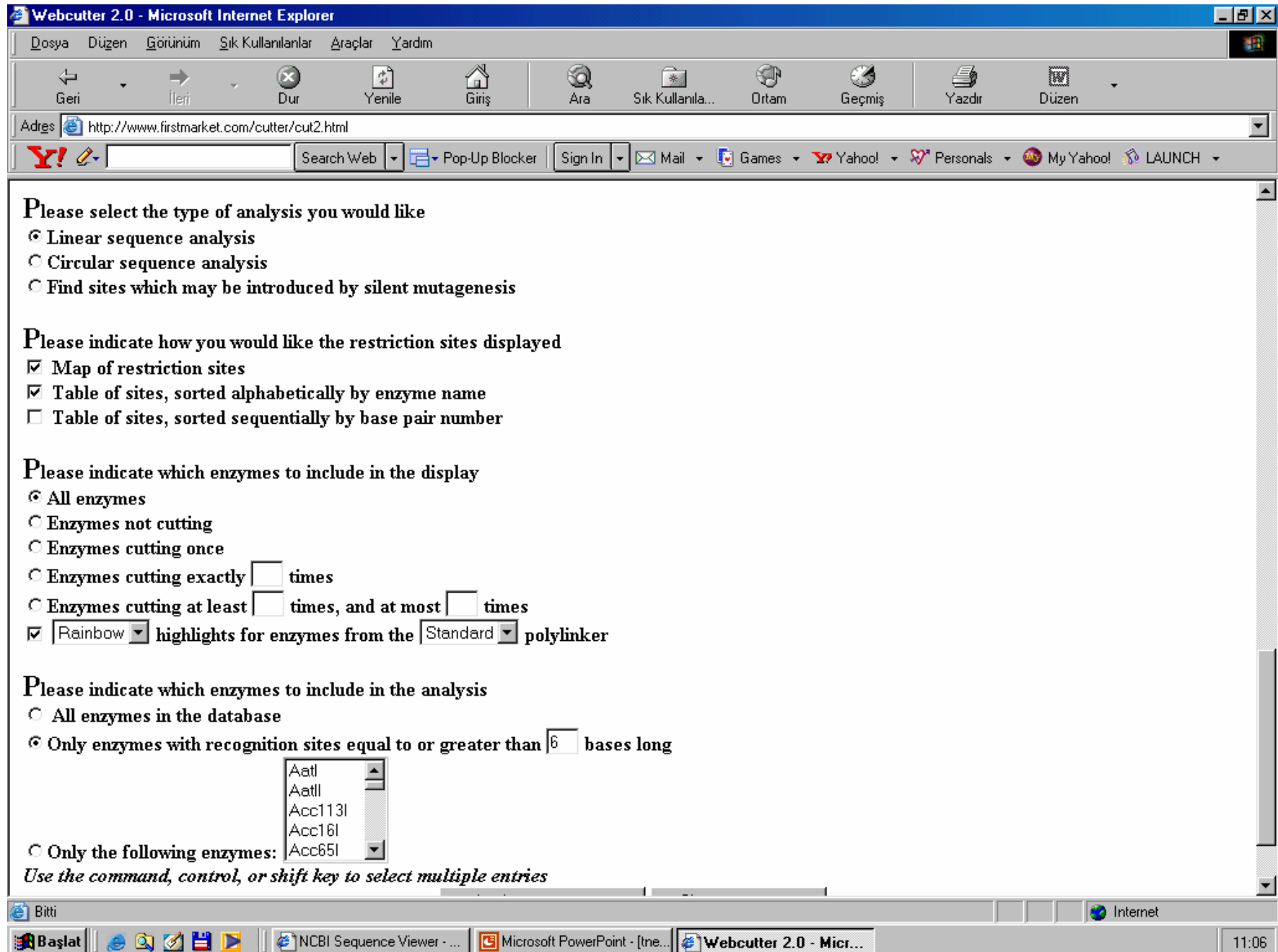
[Targets:](#) E.g. 50,2 requires primers to surround the 2 bases at positions 50 and 51. Or mark the [source sequence](#) with [and]: e.g. ...ATCT[CCCC]TCAT.. means that primers must flank the central CCCC.

[disclaimer](#) [source code](#)
[cautions](#) [old interface](#)

Done Internet

http://www-genome.wi.mit.edu/cgi-bin/primer/primer3.cgi/primer3_www.cgi





- <http://elegans.imbb.forth.gr/GOLD>
- http://www.tigr.org/tdb/glimmerm/glmr_form.html
- www.plantgenome.uga.edu/links.htm
- www.ncbi.nlm.nih.gov/genomes/PLANTS/PlantList.html
- <http://workbench.sdsc.edu/>
- <http://expasy.ch>
- http://www-genome.wi.mit.edu/cgi-bin/primer/primer3.cgi/primer3_www.cgi
- <http://www.firstmarket.com/cutter.cut2.html>