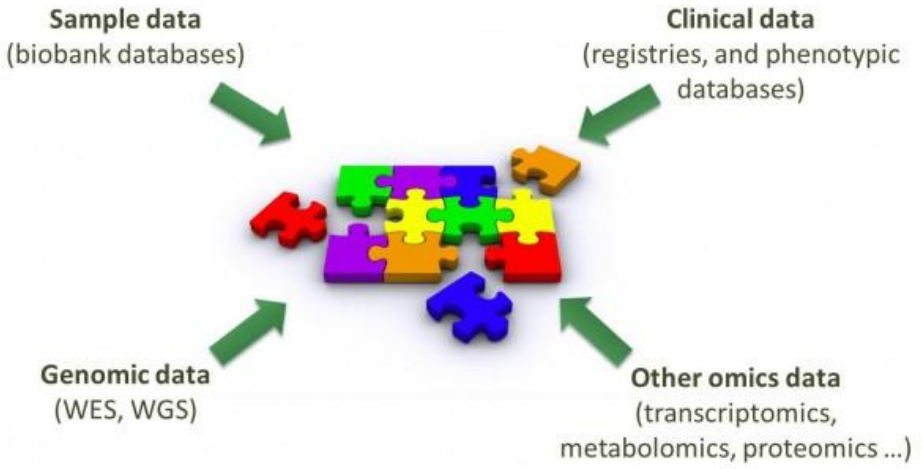
生物信息学：
组学时代的生物信息数据挖掘和理解

2020年秋



有关信息

- 授课教师：宁康，张礼斌，陈鹏
  - Email: ningkang@hust.edu.cn
  - Office: 华中科技大学东十一楼504室
  - Phone: 87793041, 18627968927

- 课程网页
  - http://www.microbioinformatics.org/Bioinformcs.html
  - QQ群：

课程安排

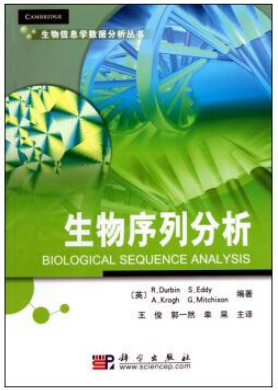
（生物信息中的算法设计与概率统计模型）

- 生物背景和课程简介
- 生物信息学和生物数据挖掘
  - 生物数据的格式及其意义
    - 序列数据
    - 树状数据
    - 网络数据
    - 表达数据等
  - 生物数据库及其用法
  - 生物信息基本算法
    - 双序列联配
    - 多序列联配
    - 基因组组装算法
    - 基因预测和功能注释
    - 系统发育树构建
    - 蛋白质结构预测
    - 生物调控网络解析
  - 组学数据分析方法
    - 基因组变异分析
    - 基因表达和比较分析
    - 非编码RNA分析
    - 蛋白组分析
    - 宏基因组分析
  - 系统生物学与交叉科学
- 面向生物大数据挖掘的深度学习

研究对象：
生物序列，
进化树，
生物网络，
基因表达
…

方法：
生物计算与生物信息

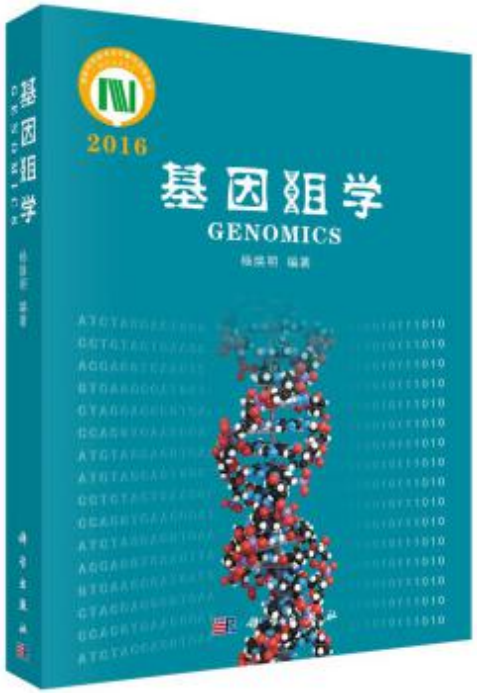
教材及参考书目

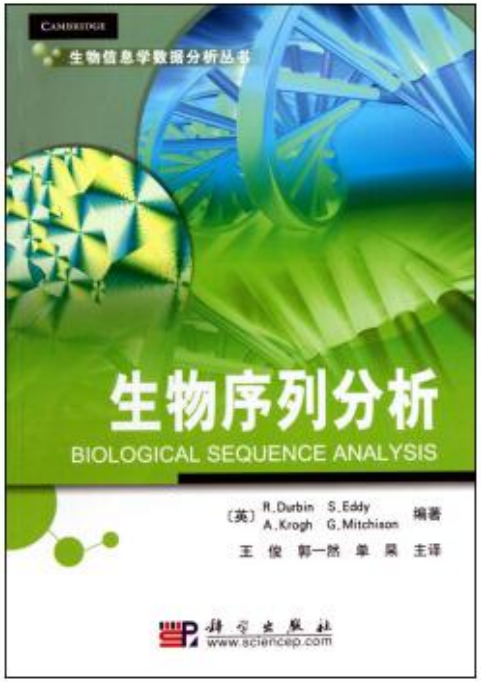


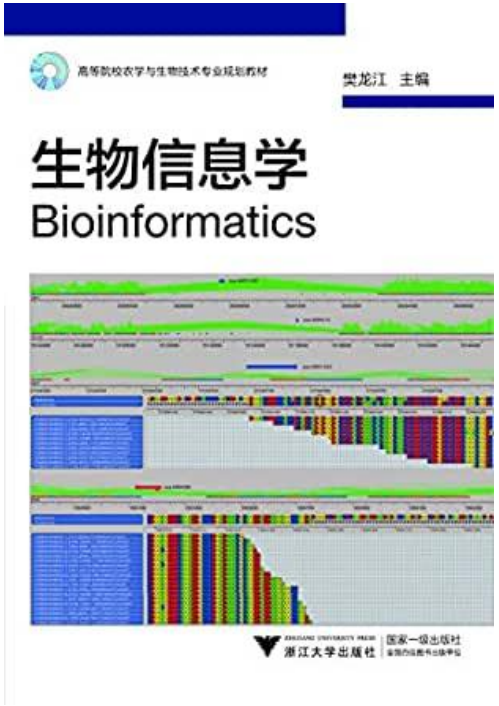
- **教学参考书：**
- 《生物序列分析》（第1版）.科学出版社. 2010年8月出版. R. Durbin等编著，王俊等主译.

- **课外文献阅读：**
- 《生物信息学》（第1版）. 浙江大学出版社. 2017年3月出版. 樊龙江主编.
- 《基因组学》（第1版）. 科学出版社. 2016年10月出版. 杨焕明主编.

References


2016
基因组学
GENOMICS


CAMBRIDGE
生物信息学数据分析丛书
生物序列分析
BIOLOGICAL SEQUENCE ANALYSIS
R.Durbin S.Eddy
A.Krogh G.Mitchison
编著
王俊 郭一然 单渠 主译
www.sciencep.com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生物信息学
Bioinformatics
浙江大学出版社

Slides credits

——生物信息学研究方法概述：北京大学生物信息中心

——生物统计学：卜东波@中国科学院计算技术研究所，邓明华@北京大学

——神经网络与深度学习: 邱锡鹏@复旦大学

——Introduction to Computational Biology and Bioinformatics: Xiaole Shirley Liu Lab@Havard University

——Combinatorial Methods in Computation Biology: Ken Sung Lab@NUS

——Deep Learning in the Life Sciences: MIT

Omics databases

基因组可视化：Genome Browser，(http://genome.ucsc.edu/), (tracks, annotations, etc.)

序列保守性：WebLogo，(http://weblogo.berkeley.edu/logo.cgi),

基因预测：MEME, (http://meme-suite.org/).

进化树：iTOL, (https://itol.embl.de/),

基因调控网络： GeneNetwork, (http://gn2.genenetwork.org/), Cytoscape, (https://cytoscape.org/),

代谢通路：KEGG, (https://www.kegg.jp/); iPATH, (https://pathways.embl.de/),

蛋白结构与功能：PDB，(http://www.rcsb.org); pFAM, (http://pfam.xfam.org/),

微生物组: EBI Magnify. (https://www.ebi.ac.uk/metagenomics/),

蛋白和小分子互作数据：STITCH，(http://stitch.embl.de/); STRING, (http://string-db.org),

药物数据库：DrugBank, (https://www.drugbank.ca/),

生物数据分析平台：Galaxy, (https://usegalaxy.org/),

生物数据可视化：Echart, (https://www.echartsjs.com/examples/zh/index.html),

生物信息学常用数据库

- 一级数据库
  - 数据库中的数据直接来源于实验获得的原始数据，只经过简单的归类整理和注释。

- 二级数据库
  - 对原始生物分子数据进行整理、分类的结果，是在一级数据库、实验数据和理论分析的基础上针对特定的应用目标而建立的。

1.Nucleotide Sequence Databases

（1）美国生物技术信息中心的GenBank

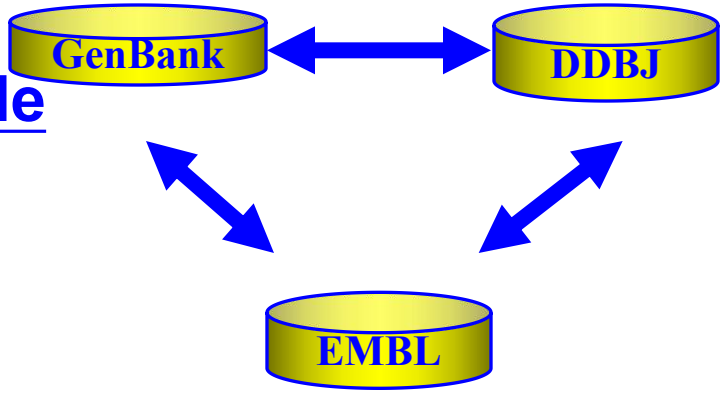
http://www.ncbi.nlm.nih.gov/Web/Genbank/index.html

（2）欧洲分子生物学实验室的EMBL

http://www.embl-heidelberg.de

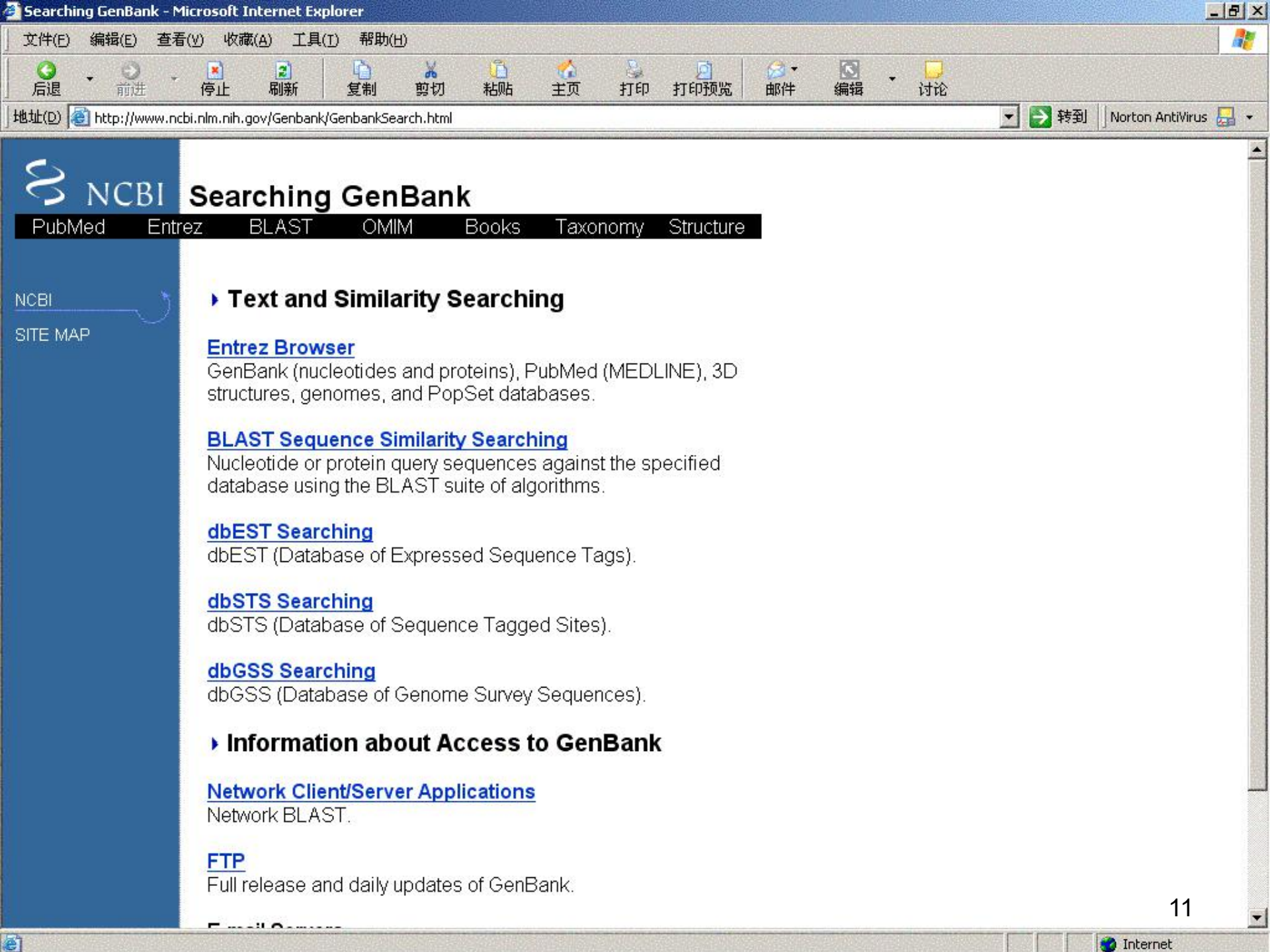
（3）日本遗传研究所的DDBJ

http://www.ddbj.nig.ac.jp/



- 三个数据库中的数据基本一致，仅在数据格式上有所差别，对于特定的查询，三个数据库的响应结果一样。

GenBank 1979年建设，1982年运行


Searching GenBank - Microsoft Internet Explorer
文件(F) 编辑(E) 查看(V) 收藏(A) 工具(T) 帮助(H)
后退 前进 停止 刷新 复制 剪切 粘贴 主页 打印 打印预览 邮件 编辑 讨论
地址(D) http://www.ncbi.nlm.nih.gov/Genbank/GenbankSearch.html
转到 Norton AntiVirus
NCBI
Searching GenBank
PubMed Entrez BLAST OMIM Books Taxonomy Structure
NCBI
SITE MAP
Text and Similarity Searching
Entrez Browser
GenBank (nucleotides and proteins), PubMed (MEDLINE), 3D structures, genomes, and PopSet databases.
BLAST Sequence Similarity Searching
Nucleotide or protein query sequences against the specified database using the BLAST suite of algorithms.
dbEST Searching
dbEST (Database of Expressed Sequence Tags).
dbSTS Searching
dbSTS (Database of Sequence Tagged Sites).
dbGSS Searching
dbGSS (Database of Genome Survey Sequences).
Information about Access to GenBank
Network Client/Server Applications
Network BLAST.
FTP
Full release and daily updates of GenBank.
Internet

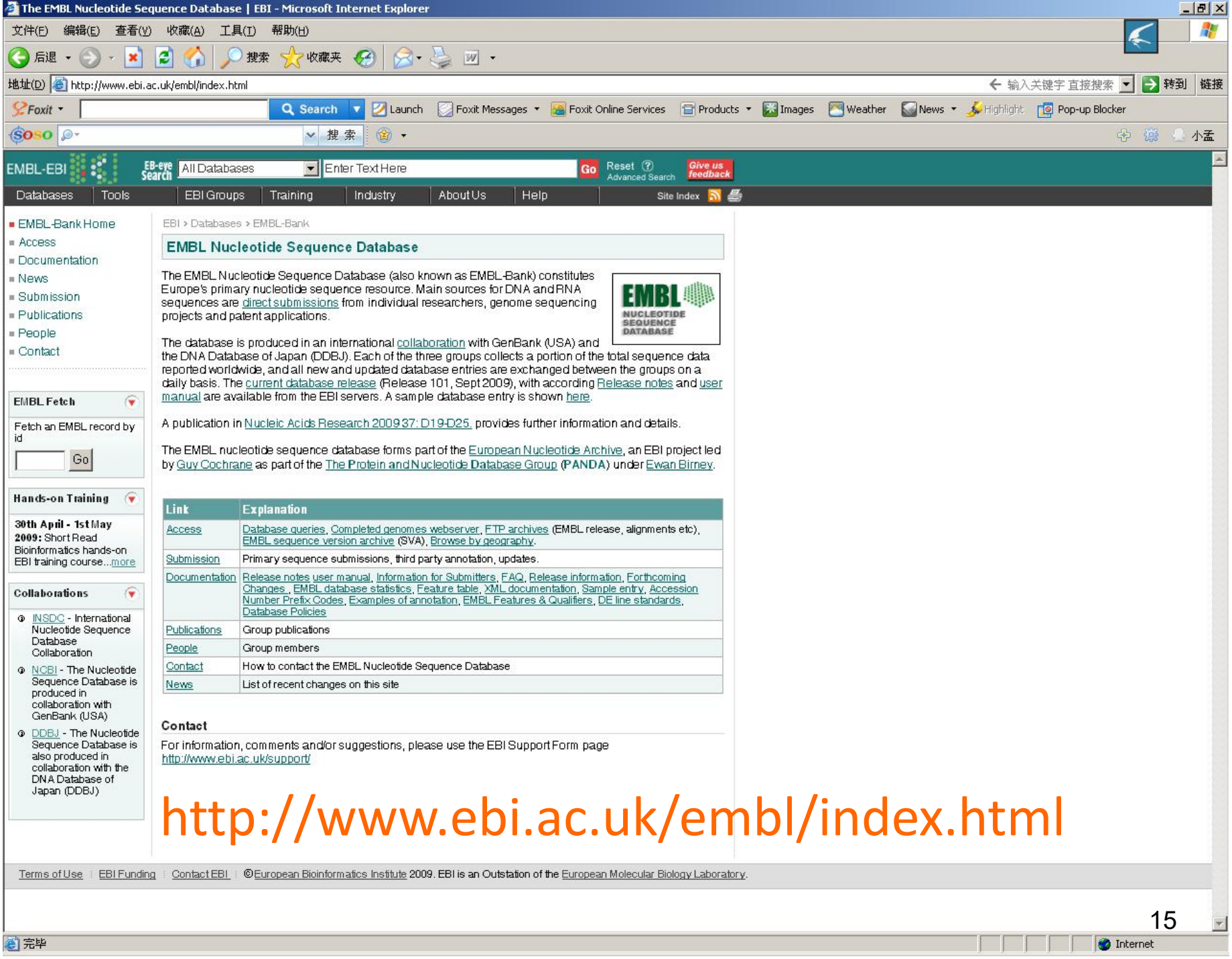
- **Submissions to GenBank**
- Many journals require submission of sequence information to a database prior to publication so that an accession number may appear in the paper. NCBI has a WWW form, called BankIt, for convenient and quick submission of sequence data. Sequin, NCBI's stand-alone submission software for MAC, PC, and UNIX platforms, is also available by FTP. When using Sequin, the output files for direct submission should be sent to GenBank by electronic mail.
- There are specialized, streamlined procedures for batch submissions of sequences, such as EST, STS, and HTG sequences.

- **Updating or Revising a Sequence**
- Revisions or updates to GenBank entries can be made at any time and can be accepted as BankIt or Sequin files or as the text of an e-mail message. Click on the link for more information about updating information on GenBank records.

- **Access to GenBank**
- GenBank is available for searching at NCBI via several methods.
- The GenBank database is designed to provide and encourage access within the scientific community to the most up to date and comprehensive DNA sequence information. Therefore, NCBI places no restrictions on the use or distribution of the GenBank data. However, some submitters may claim patent, copyright, or other intellectual property rights in all or a portion of the data they have submitted. NCBI is not in a position to assess the validity of such claims, and therefore cannot provide comment or unrestricted permission concerning the use, copying, or distribution of the information contained in GenBank.

- **New Developments**
- NCBI is continuously developing new tools and enhancing existing ones to improve both submission and access to GenBank. The easiest way to keep abreast of these and other developments is to check the "What's New" section of the NCBI Web page and to read the *NCBI News*, which is also available by free subscription.

EMBL1982年 运行


The EMBL Nucleotide Sequence Database | EBI - Microsoft Internet Explorer
文件(F) 编辑(E) 查看(V) 收藏(A) 工具(T) 帮助(H)
后退 搜索 收藏夹
地址(D) http://www.ebi.ac.uk/embl/index.html
Foxit Search Launch Foxit Messages Foxit Online Services Products Images Weather News Highlight Pop-up Blocker
EMBL-EBI EB-eye Search All Databases Enter Text Here Go Reset Advanced Search Give us feedback
Databases Tools EBI Groups Training Industry About Us Help Site Index
EMBL-Bank Home
Access
Documentation
News
Submission
Publications
People
Contact
EMBL Fetch
Fetch an EMBL record by id
Go
Hands-on Training
30th April - 1st May 2009: Short Read Bioinformatics hands-on EBI training course...more
Collaborations
INSDC - International Nucleotide Sequence Database Collaboration
NCBI - The Nucleotide Sequence Database is produced in collaboration with GenBank (USA)
DDBJ - The Nucleotide Sequence Database is also produced in collaboration with the DNA Database of Japan (DDBJ)
EBI › Databases › EMBL-Bank
EMBL Nucleotide Sequence Database
The EMBL Nucleotide Sequence Database (also known as EMBL-Bank) constitutes Europe's primary nucleotide sequence resource. Main sources for DNA and RNA sequences are direct submissions from individual researchers, genome sequencing projects and patent applications.
EMBL NUCLEOTIDE SEQUENCE DATABASE
The database is produced in an international collaboration with GenBank (USA) and the DNA Database of Japan (DDBJ). Each of the three groups collects a portion of the total sequence data reported worldwide, and all new and updated database entries are exchanged between the groups on a daily basis. The current database release (Release 101, Sept 2009), with according Release notes and user manual are available from the EBI servers. A sample database entry is shown here.
A publication in Nucleic Acids Research 2009 37: D19-D25. provides further information and details.
The EMBL nucleotide sequence database forms part of the European Nucleotide Archive, an EBI project led by Guy Cochrane as part of the The Protein and Nucleotide Database Group (PANDA) under Ewan Birney.
Link
Explanation
Access
Database queries, Completed genomes webserver, FTP archives (EMBL release, alignments etc), EMBL sequence version archive (SVA), Browse by geography.
Submission
Primary sequence submissions, third party annotation, updates.
Documentation
Release notes user manual, Information for Submitters, FAQ, Release information, Forthcoming Changes, EMBL database statistics, Feature table, XML documentation, Sample entry, Accession Number Prefix Codes, Examples of annotation, EMBL Features & Qualifiers, DE line standards, Database Policies
Publications
Group publications
People
Group members
Contact
How to contact the EMBL Nucleotide Sequence Database
News
List of recent changes on this site
Contact
For information, comments and/or suggestions, please use the EBI Support Form page http://www.ebi.ac.uk/support/
http://www.ebi.ac.uk/embl/index.html
Terms of Use EBI Funding Contact EBI ©European Bioinformatics Institute 2009. EBI is an Outstation of the European Molecular Biology Laboratory.
完毕
Internet

DDBJ 1984年建立, 1987年启用

2. Genome Databases

小鼠(Mouse) http://www.informatics.jax.org/mgd.html
大鼠(Rat) http://ratmap.gen.gu.se
狗(Dog) http://mendel.berkeley.edu/dog.html
牛(Cow) http://locus.jouy.inra.fr/cgi-bin/bovmap/intro2.pl
猪(Pig) http://www.ri.bbsrc.ac.uk/pigmap/pigbase/pigbase.html
羊(Sheep) http://dirk.invermay.cri.nz
鸡(Chicken) http://www.ri.bbsrc.ac.uk/chickmap/chickbase/manager.html
斑马鱼(Zebra fish) http://zfish.uoregon.edu
线虫(C. elegans) http://www.ddbj.nig.ac.jp/htmls/celegans/html/CE_INDEX.html
果蝇(Drosophila) http://morgan.harvard.edu
蚊子(Mosquito) http://klab.agsci.colostate.edu
拟南芥(Arabidopsis) http://genome-www.stanford.edu/Arabidopsis
棉花(Cotton) http://algodon.tamu.edu
玉米(Maize) http://www.agron.missouri.edu
水稻(Rice) http://www.staff.or.jp
大豆(Soya) http://mendel.agron.iastate.edu:8000/main.html
杨树(Trees) http://s27w007.pswfs.gov

Model organism

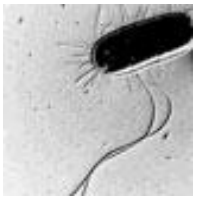
Ureaplasma urealyticum

Bacillus subtilis

Drosophila melanogaster

Rickettsia prowazekii

Helicobacter pylori



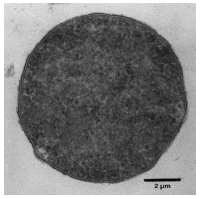
***Buchnera*sp. APS**

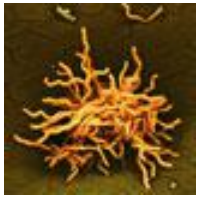
Escherichia coli

human

Arabidopsis

Thermotoga maritima





Thermoplasma acidophilum

mouse

Caenorhabitis elegans

rat

Borrelia burgorferi

Plasmodium falciparum

Borrelia burgorferi

Aquifex aeolicus

***Neisseria meningitidis* Z2491**

Mycobacterium tuberculosis

Model organism databases

- *Escherichia coli*
  - *E. coli* Genome Center (Wisconsin University, USA)
  - The *E. coli* index (University of Birmingham, UK)
- *S. cerevisiae* (Baker's yeast)
  - SGD (Yeast genome database at Stanford, USA)
  - CYGD (MIPS Comprehensive Yeast Genome Database, Neuherberg, Germany)
- *Arabidopsis thaliana*
  - MATDB (MIPS *A. thaliana* database, Munich, Germ.)
  - TAIR (The Arabidopsis Information Resource, previously AtDB, at Stanford, USA)
  - KAOS (Kazusa Arabidopsis data Opening Site at Kazusa DNA Research Institute, Jp)
  - Arabidopsis Genome Analysis (at Cold Spring Harbor laboratories, USA)
  - TIGR Arabidopsis thaliana Database (TIGR, Rockeville MD, USA)
- *Oryza sativa* (Rice)
  - RGP (Rice Genome Research Programme, Jp)
  - Gramene (Comparative mapping resource for graines)
  - INE (Integrated rice genome explorer: common database of the International Rice Genome Sequencing Project, IRGSP, Jp)

Model organism databases

- *Caenorhabditis elegans*
  - WormBase (*C. elegans* database at Cold Spring Harbor Laboratories, USA)
- *Drosophila melanogaster* (Fruit fly)
  - FlyBase (*Drosophila* genome database)
  - BDGP (Berkeley Drosphila genome project)
- *Danio rerio* (Zebrafish)
  - ZFIN (Zebrafish Information Network at University of Oregon, USA)
  - WashU-Zebrafish Genome Resources (Zebrafish EST database at Washington University, USA)
- *Mus musculus* (Mouse)
  - MGI (Mouse genome informatics)
- *Homo sapiens*
  - GDB (The human Genome Database, Toronto, Canada)
  - HIB (HumanInfoBase of annotated UniGene clusters - putative human gene transcripts - at MIPS, Germany)
  - Human genome resources (at NCBI, USA)
  - Human genome browser (at the University of California Santa Cruz, USA)
  - HGP (Human Genome Project at the Sanger Institute, Cambridge, UK)
  - GeneLinks (Portal to hyperlinks for each human gene at the Center for Genomics and Bioinformatics, Karolinska Institutet, Stockholm, Sweden)

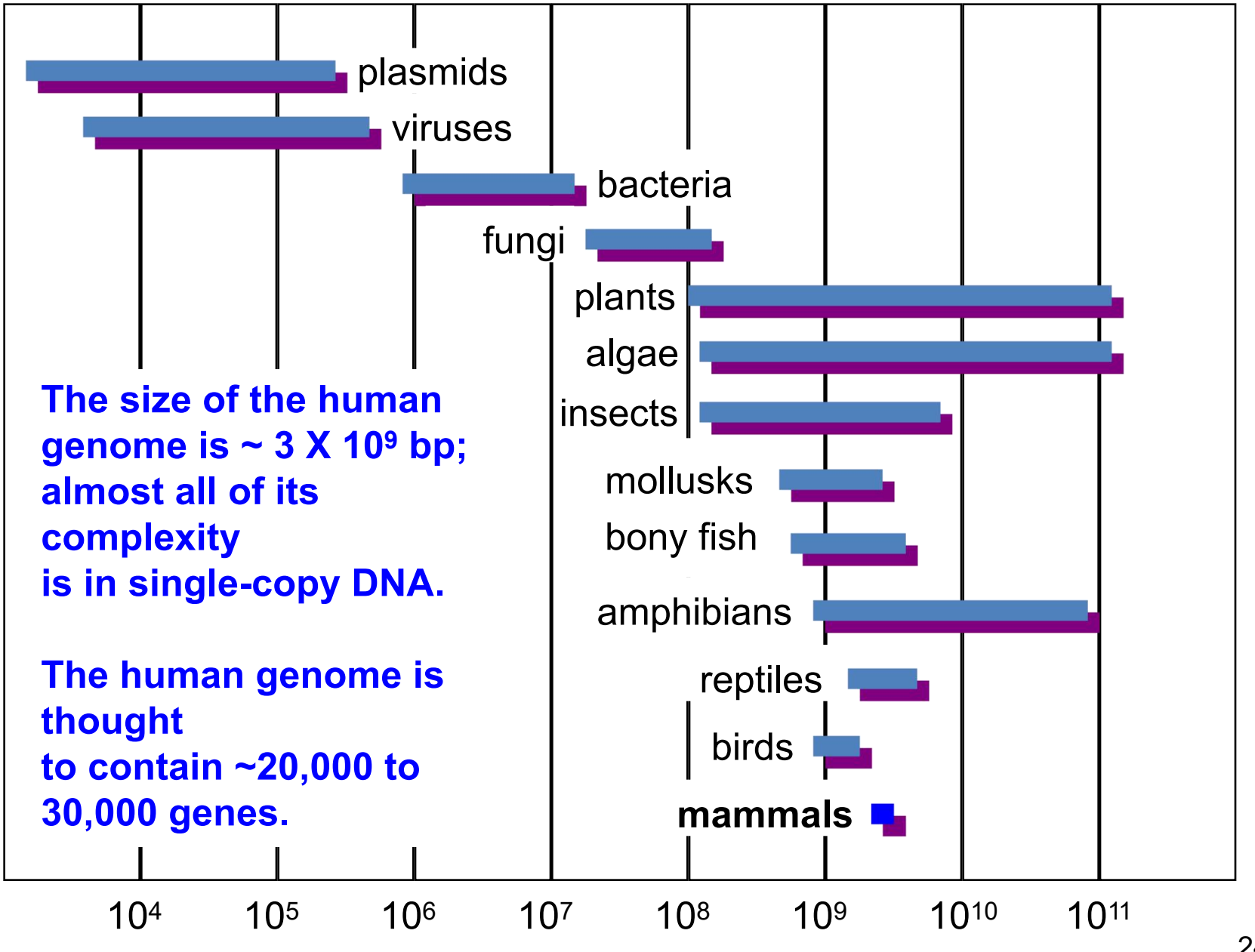
- Prokaryotes include:
  - *Escherichia coli* (*E. coli*) - This common, Gram-negative gut bacterium is the most widely-used organism in molecular genetics.
  - *Bacillus subtilis* - an endospore forming Gram-positive bacterium

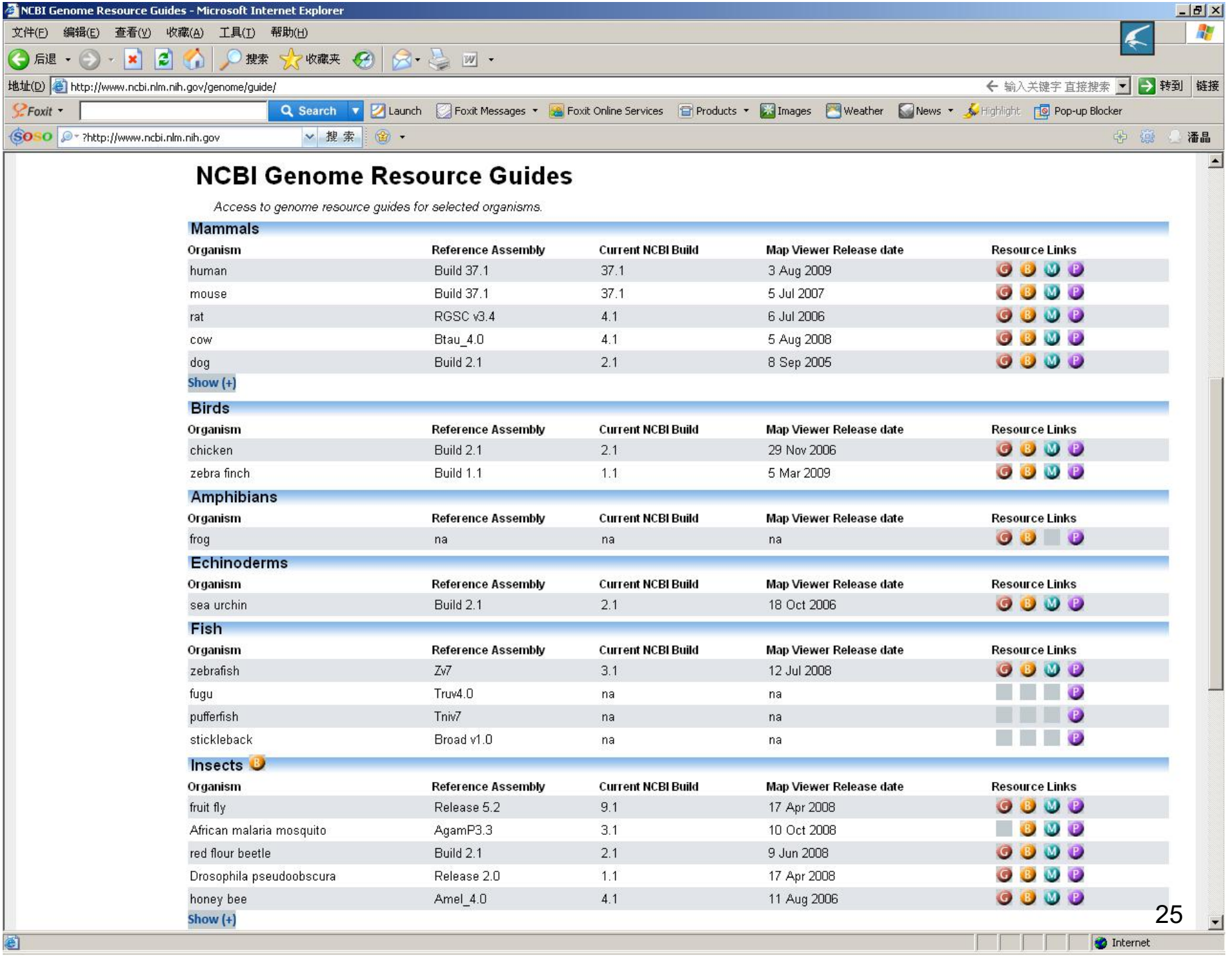
Table of model genetic organisms

Organism	Genome Sequenced	Homologous Recombination	Biochemistry
Prokaryote			
Escherichia coli	Yes	Yes	Excellent
Eukaryote, unicellular			
Dictyostelium discoideum	Yes	Yes	Excellent
Saccharomyces cerevisiae	Yes	Yes	Good
Schizosaccharomyces pombe	Yes	Yes	Good
Chlamydomonas reinhardtii	Yes	No	Good
Tetrahymena thermophila	Yes	Yes	Good
Eukaryote, multicellular			
Caenorhabditis elegans	Yes	Difficult	Not so good
Drosophila melanogaster	Yes	Difficult	Good
Arabidopsis thaliana	Yes	No	Poor
Vertebrate			
Danio rerio	Yes	Difficult?	Good
Mus musculus	Yes	Yes	Good
Homo sapiens	Yes	Yes	Good

• The Genome database provides views for a variety of genomes, complete chromosomes, sequence maps with contigs, and integrated genetic and physical maps.
• The database is organized in six major organism groups: Archaea, Bacteria, Eukaryotae, Viruses, Viroids, and Plasmids and includes complete chromosomes, organelles and plasmids as well as draft genome assemblies.

Genome sizes in nucleotide pairs (base-pairs)





NCBI Genome Resource Guides

Access to genome resource guides for selected organisms.

Mammals

Organism	Reference Assembly	Current NCBI Build	Map Viewer Release date	Resource Links
human	Build 37.1	37.1	3 Aug 2009	G B M P
mouse	Build 37.1	37.1	5 Jul 2007	G B M P
rat	RGSC v3.4	4.1	6 Jul 2006	G B M P
cow	Btau_4.0	4.1	5 Aug 2008	G B M P
dog	Build 2.1	2.1	8 Sep 2005	G B M P

Show (+)

Birds

Organism	Reference Assembly	Current NCBI Build	Map Viewer Release date	Resource Links
chicken	Build 2.1	2.1	29 Nov 2006	G B M P
zebra finch	Build 1.1	1.1	5 Mar 2009	G B M P

Amphibians

Organism	Reference Assembly	Current NCBI Build	Map Viewer Release date	Resource Links
frog	na	na	na	G B P

Echinoderms

Organism	Reference Assembly	Current NCBI Build	Map Viewer Release date	Resource Links
sea urchin	Build 2.1	2.1	18 Oct 2006	G B M P

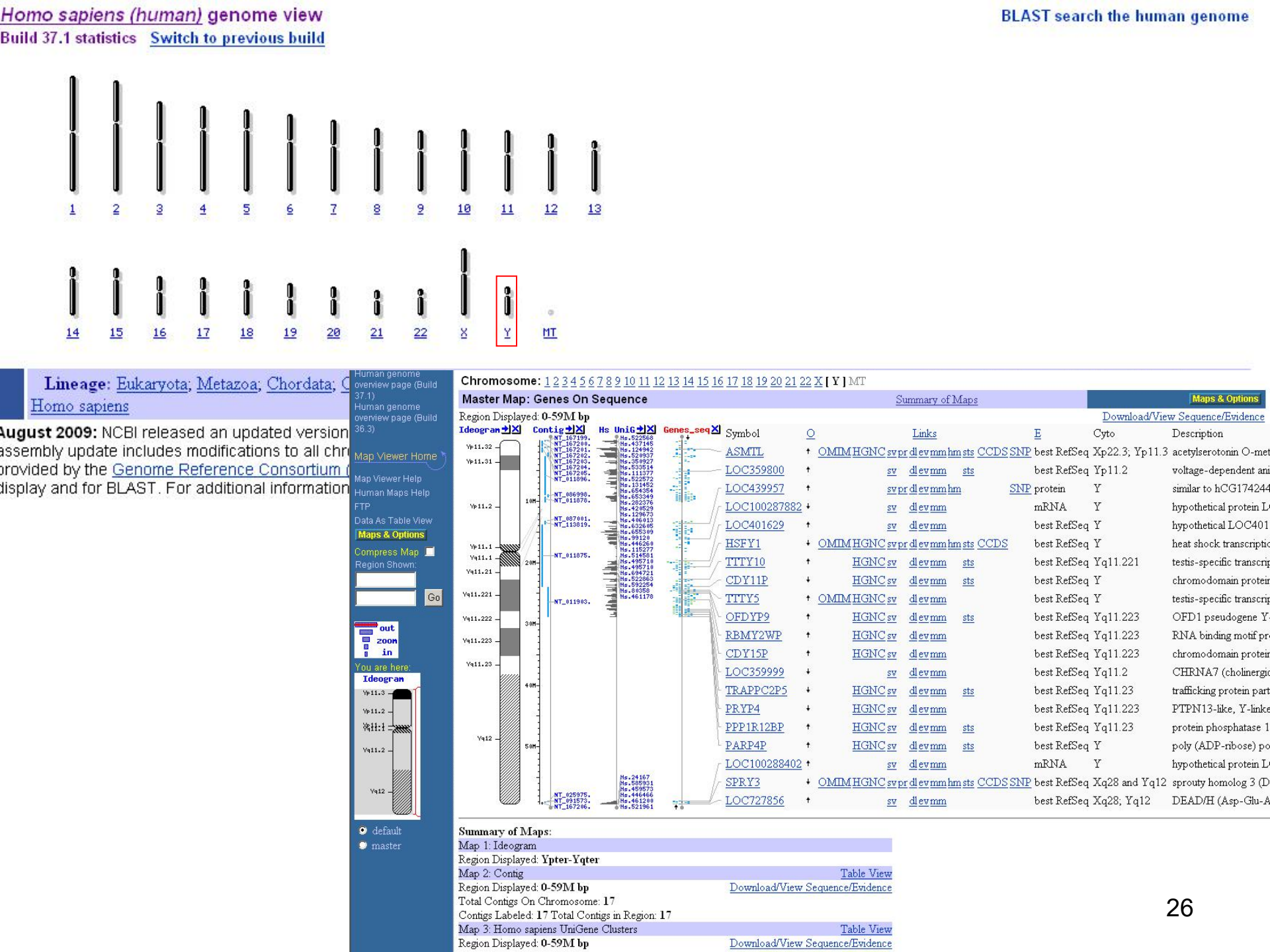
Fish

Organism	Reference Assembly	Current NCBI Build	Map Viewer Release date	Resource Links
zebrafish	Zv7	3.1	12 Jul 2008	G B M P
fugu	Truv4.0	na	na	P
pufferfish	Tniv7	na	na	P
stickleback	Broad v1.0	na	na	P

Insects

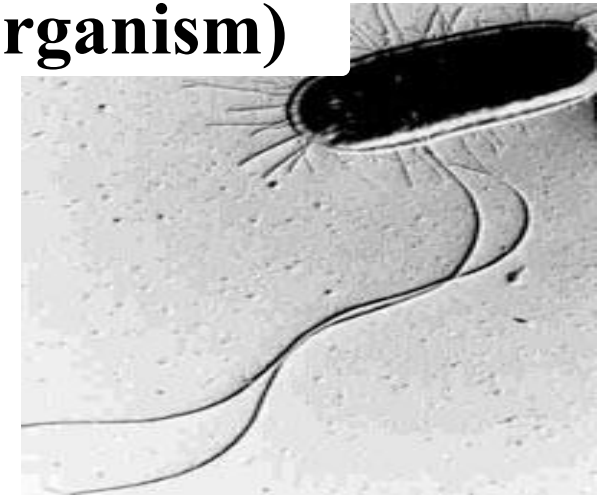
Organism	Reference Assembly	Current NCBI Build	Map Viewer Release date	Resource Links
fruit fly	Release 5.2	9.1	17 Apr 2008	G B M P
African malaria mosquito	AgamP3.3	3.1	10 Oct 2008	B M P
red flour beetle	Build 2.1	2.1	9 Jun 2008	G B M P
Drosophila pseudoobscura	Release 2.0	1.1	17 Apr 2008	G B M P
honey bee	Amel_4.0	4.1	11 Aug 2006	G B M P

Show (+)


Homo sapiens (human) genome view
Build 37.1 statistics
Switch to previous build
BLAST search the human genome
1 2 3 4 5 6 7 8 9 10 11 12 13
14 15 16 17 18 19 20 21 22 X Y MT
Lineage: Eukaryota; Metazoa; Chordata;
Homo sapiens
August 2009: NCBI released an updated version
assembly update includes modifications to all chr
provided by the Genome Reference Consortium
display and for BLAST. For additional information
Human genome overview page (Build 37.1)
Human genome overview page (Build 36.3)
Map Viewer Home
Map Viewer Help
Human Maps Help
FTP
Data As Table View
Maps & Options
Compress Map
Region Shown:
Go
out
zoom
in
You are here:
Ideogram
default
master
Chromosome: 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X [Y] MT
Master Map: Genes On Sequence
Summary of Maps
Maps & Options
Region Displayed: 0-59M bp
Download/View Sequence/Evidence
Ideogram
Contig
Hs UniG
Genes_seq
Symbol
Links
Cyto
Description
ASMTL
LOC359800
LOC439957
LOC100287882
LOC401629
HSFY1
TTTY10
CDY11P
TTTY5
OFDYP9
RBMY2WP
CDY15P
LOC359999
TRAPPC2P5
PRYP4
PPP1R12BP
PARP4P
LOC100288402
SPRY3
LOC727856
Summary of Maps:
Map 1: Ideogram
Region Displayed: Ypter-Yqter
Map 2: Contig
Table View
Region Displayed: 0-59M bp
Download/View Sequence/Evidence
Total Contigs On Chromosome: 17
Contigs Labeled: 17 Total Contigs in Region: 17
Map 3: Homo sapiens UniGene Clusters
Table View
Region Displayed: 0-59M bp
Download/View Sequence/Evidence

模式生物(Model Organism)

Escherichia coli
大肠杆菌



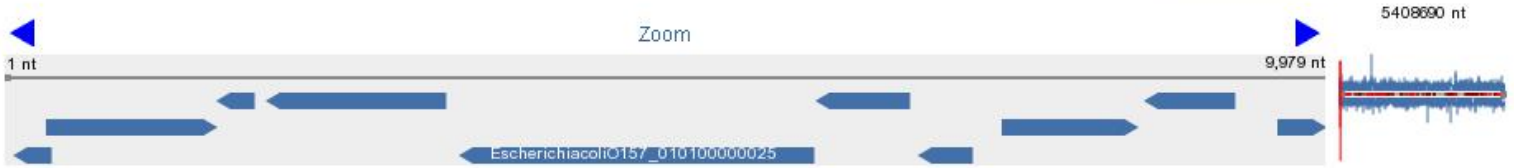
Genome > **Bacteria** > ***Escherichia coli O157:H7 str. FRIK2000, whole genome shotgun sequencing project***

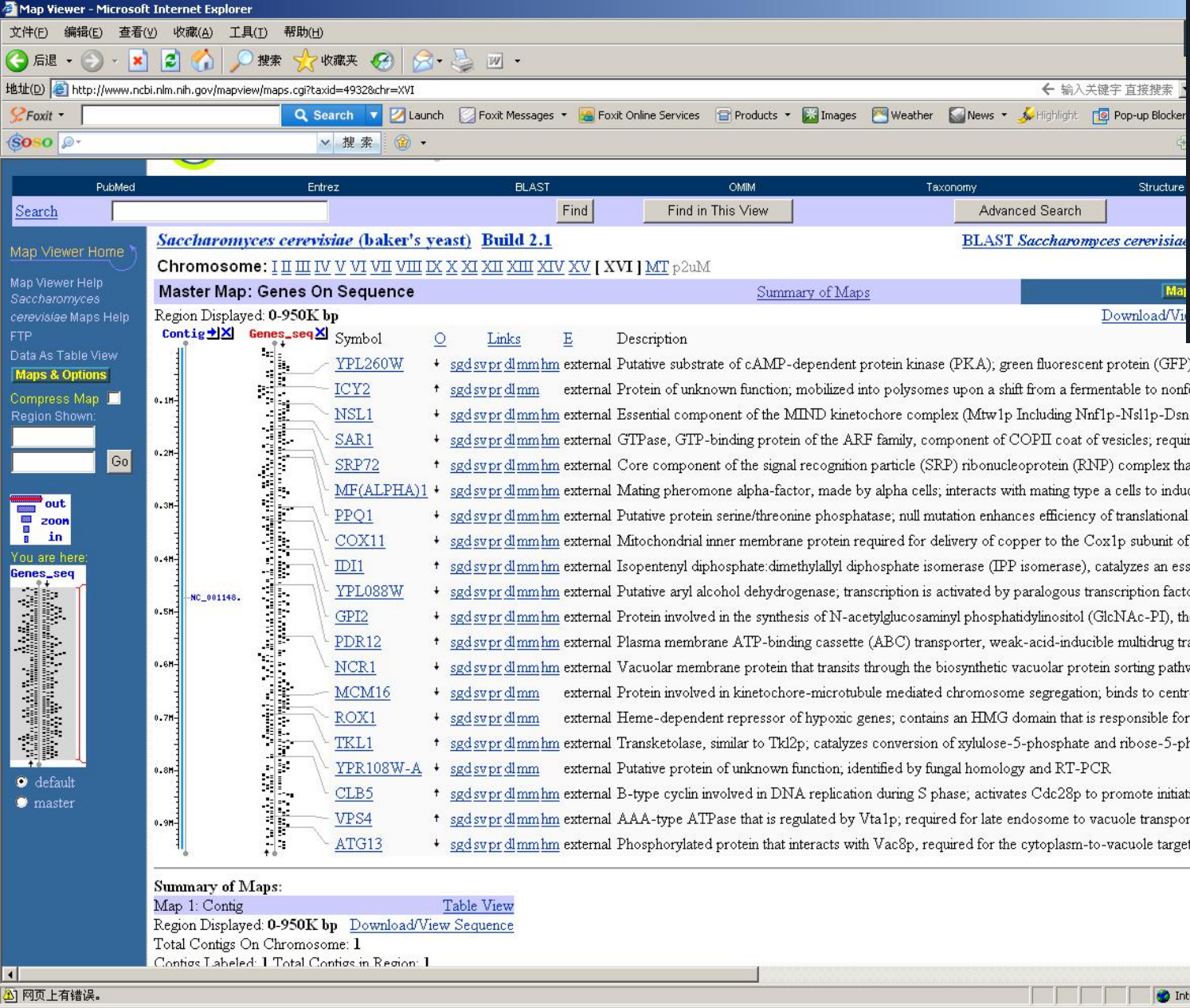
Lineage: Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia; Escherichia coli; Escherichia coli O157:H7; Escherichia coli O

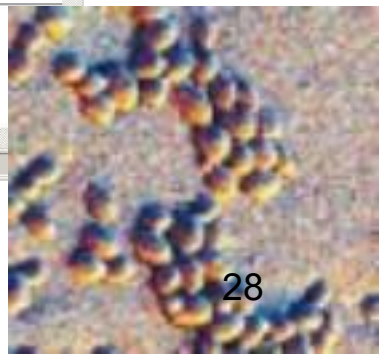
Genome Info:	Features:	BLAST homologs:	Links:	Review Info:
Refseq: NZ_ACXO00000000	Genes: **5383**	COG	Genome Project	Publications: **None**
GenBank: ACXO00000000	Protein coding: 5300	TaxMap	Refseq FTP	Refseq Status: **WGS**
Length: **5,408,690 nt**	Structural RNAs: 83	TaxPlot	GenBank FTP	Seq.Status: **Draft**
GC Content: **50%**	Pseudo genes: **None**	GenePlot	BLAST	Sequencing center: Medical Biofilm Research Institute
% Coding: **85%**	Others: **56**	gMap	TraceAssembly	Completed: **2009/08/20**
Topology: **other**	Contigs: 247		CDD	Organism Group
Molecule: **DNA**			Other genomes for species: 170	

Gene Classification based on COG functional categories

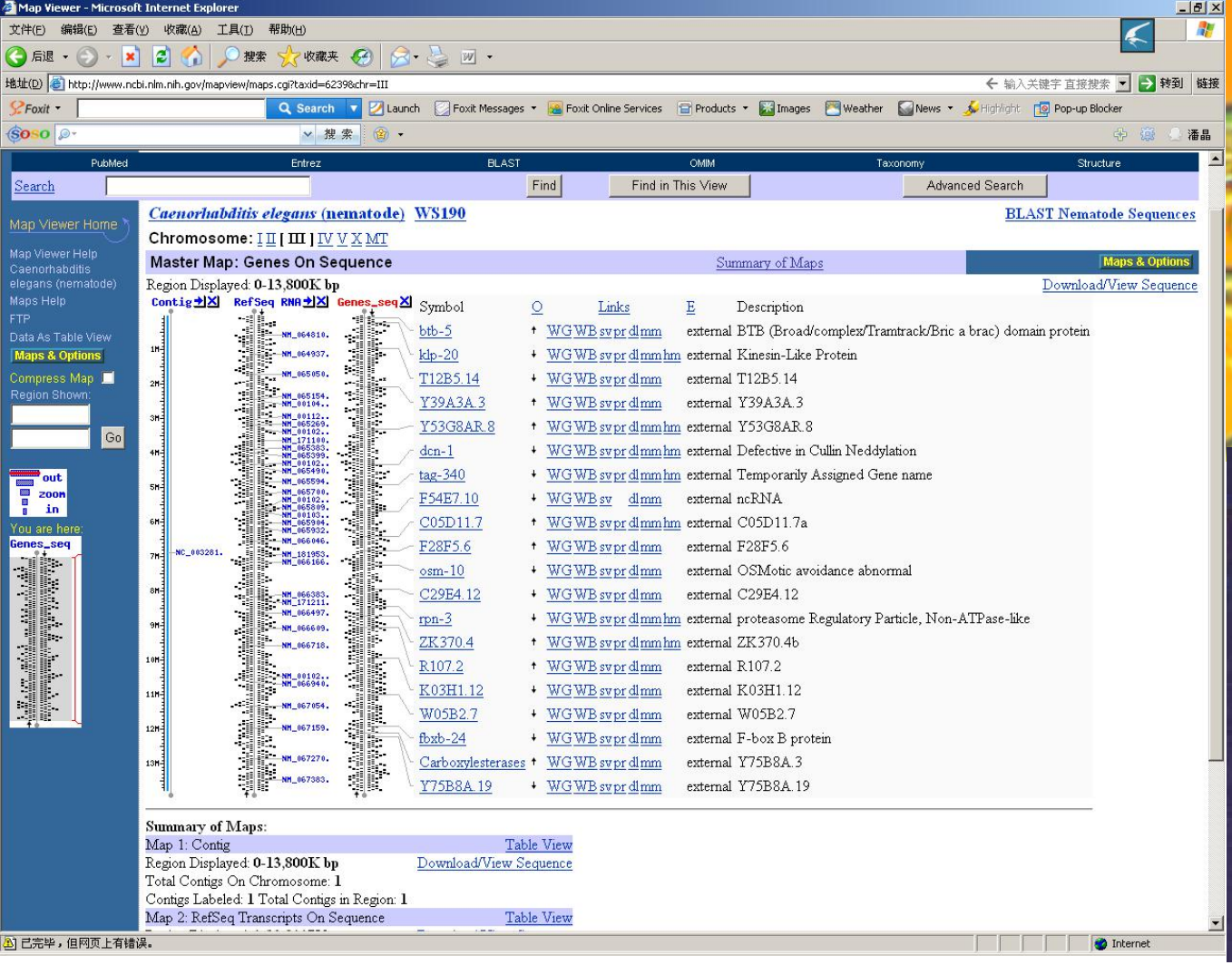
Search gene, GeneID or locus_tag: Find Gene







酿酒酵母：16个染色体，全基因组1996年测定。



秀丽线虫：

雌雄同体成虫细胞数目只有959个，其中包括302个神经元；6条染色体，全基因组于1998年测定，长9.7Mb

果蝇：繁殖很快，基因组：180Mb。

uid=6185 Genome Result - Microsoft Internet Explorer

文件(F) 编辑(E) 查看(V) 收藏(A) 工具(T) 帮助(H)

地址(D) http://www.ncbi.nlm.nih.gov/sites/entrez?Db=genome&Cmd=ShowDetailView&TermToSearch=6185

All Databases | PubMed | Nucleotide | Protein | Genome | Structure | OMIM | PMC | Journals | Books

Search Genome for [ ] Go Clear

Limits | Preview/Index | History | Clipboard | Details

Display Overview Show 20 Send to

All: 1

Genome > ***Eukaryota > Drosophila melanogaster, whole genome shotgun sequencing project***

Links

Lineage: Eukaryota; Fungi/Metazoa group; Metazoa; Eumetazoa; Bilateria; Coelomata; Protostomia; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Eremoneura; Cyclorrhapha; Schizophora; Acalyptratae; Ephydroidea; Drosophilidae; Drosophilinae; Drosophilini; Drosophilina; Drosophiliti; Drosophila; Sophophora; melanogaster group; melanogaster subgroup; Drosophila melanogaster

Chromosomes: *master WGS*, 2L, 2R, 3L, 3R, 4, X, Un
Organelles: mitochondrial-MT

Genome Info:	Features:	BLAST homologs:	Links:	Review Info:
Refseq: NZ_AABU00000000	Genes: **837**	COG	Genome Project	Publications: [8]
GenBank: AABU00000000	Protein coding: 702	TaxMap	Refseq FTP	Refseq Status: **WGS**
Length: **137,586,636 nt**	Structural RNAs: 218	TaxPlot	GenBank FTP	Seq.Status: **Draft**
GC Content: **39%**	Pseudo genes: **43**	GenePlot	BLAST	Sequencing center: The FlyBase Consortium/Berkeley Drosophila Genome Project/Celera Genomics
% Coding: **N/A**	Others: **132**	gMap	TraceAssembly	Completed: **2009/01/27**
Topology: **other**	Contigs: 2756		CDD	Organism Group
Molecule: **DNA**			Other genomes for species	

Gene Classification based on COG functional categories

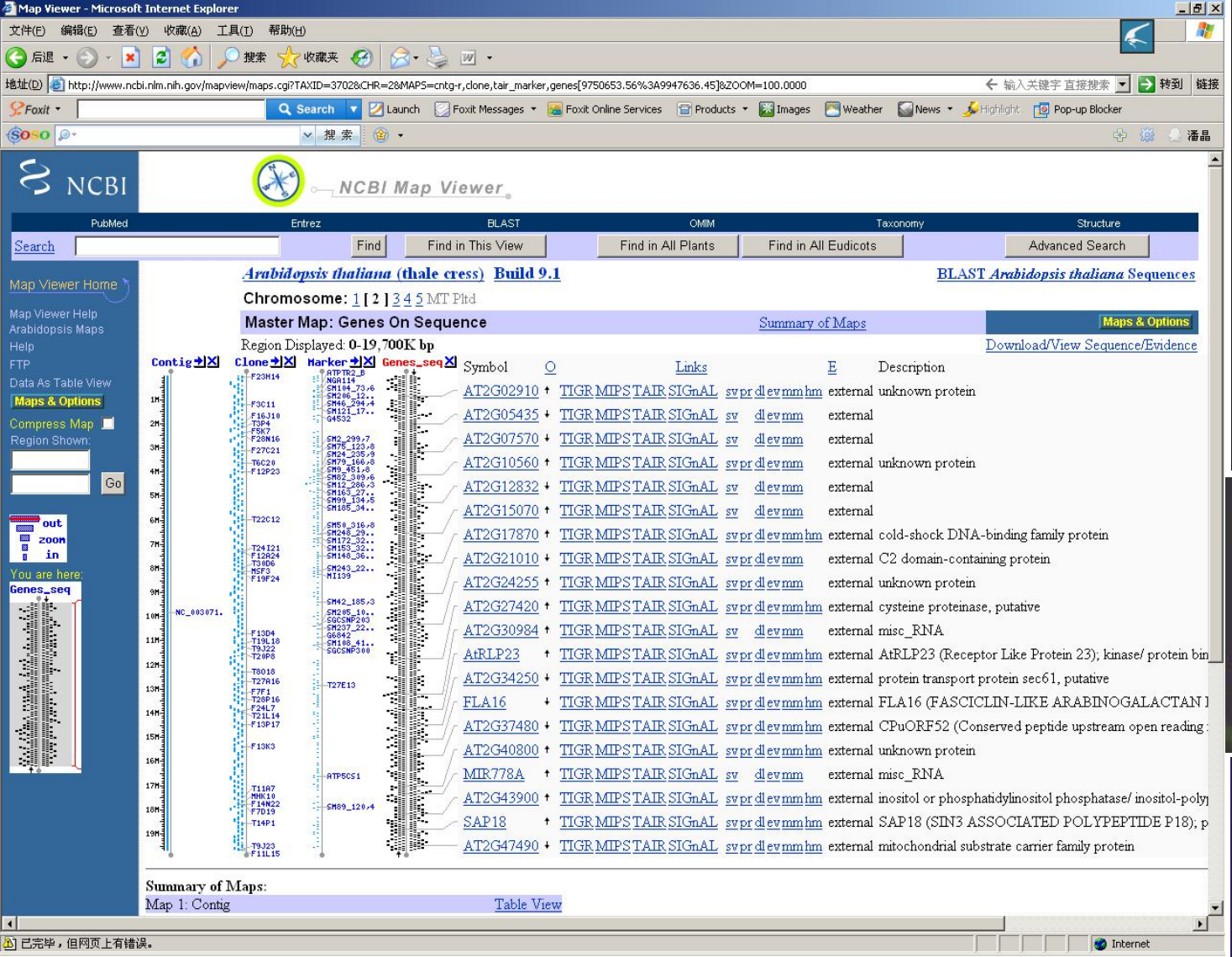
Search gene, GeneID or locus_tag: [ ] Find Gene

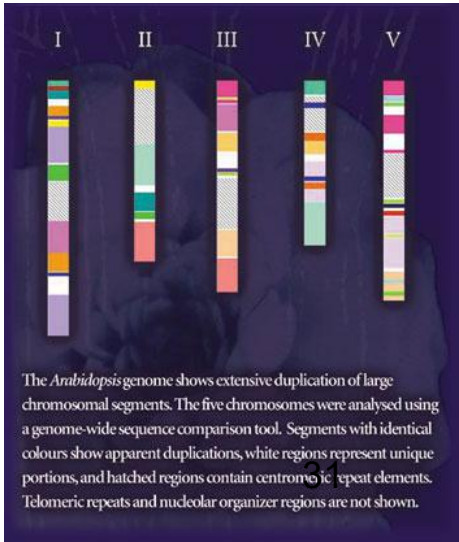
137586636 nt

Zoom

1 nt 50,001 nt

Internet

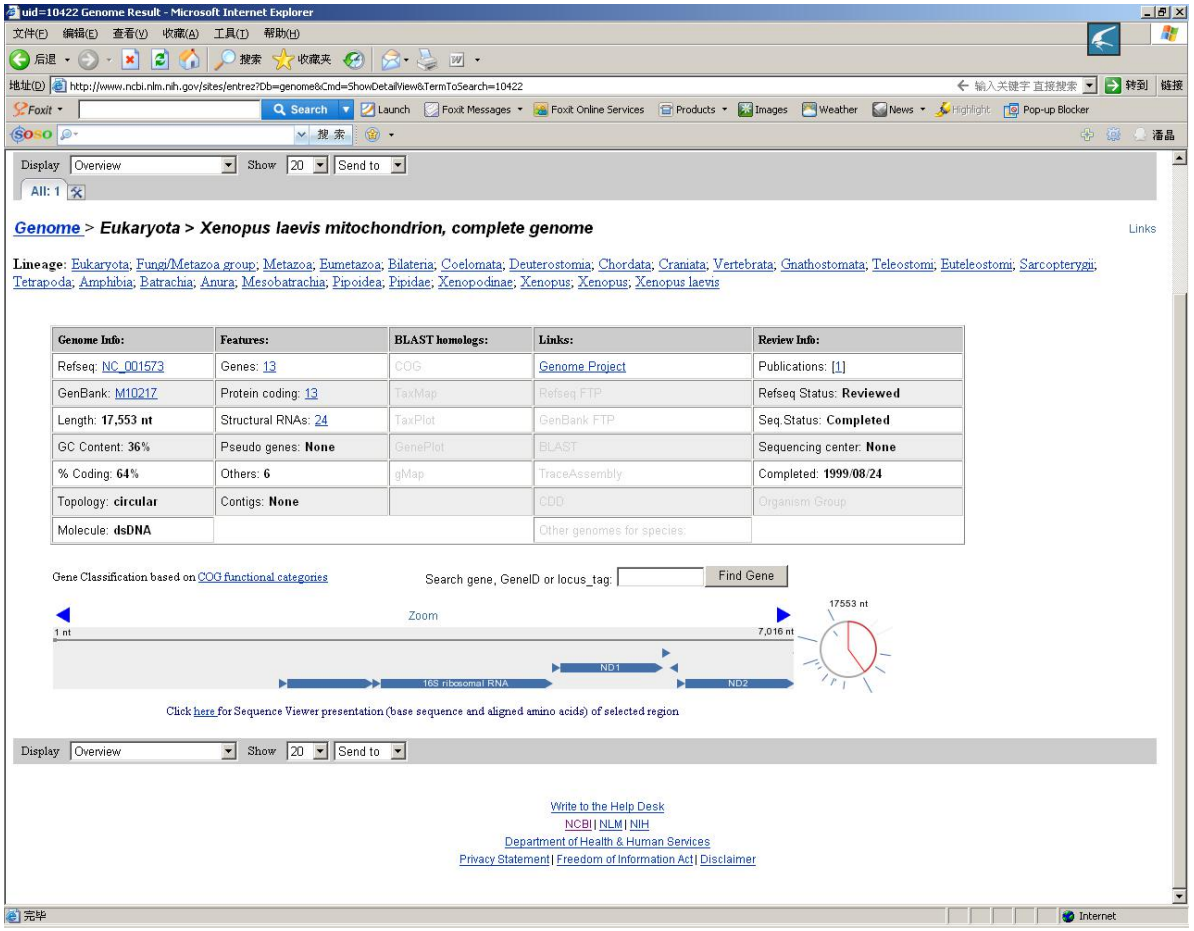


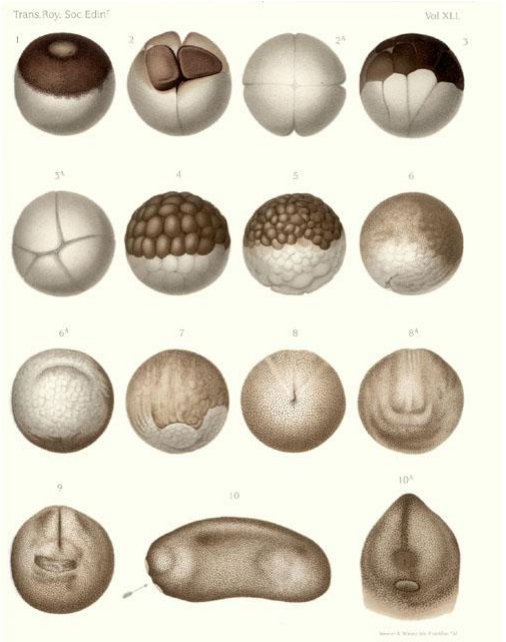


拟南芥：个体生活周期只有6周的十字花科小草，是一种理想的模式植物。

非洲爪蟾（*Xenopus lavias*）

1个受精卵在24小时内分裂到各种器官初具雏形的程度；





斑马鱼（*Danio rerio*）

身体透明的小鱼，生活周期约3个月，是研究脊椎动物发育过程的良好对象。

NCBI

NCBI Map Viewer

PubMed | Entrez | BLAST | OMIM | Taxonomy | Structure

Search | Find | Find in This View | Advanced Search

Map Viewer Home

Map Viewer Help
Zebrafish Maps Help
FTP
Data As Table View
Maps & Options
Compress Map
Region Shown:
Go

out
zoom
in

You are here:
Genes_seq

Danio rerio (zebrafish) Zv7

BLAST Zebrafish Sequences

Chromosome: 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 [25] MT

Master Map: Genes On Sequence

Summary of Maps | Maps & Options

Region Displayed: **0-33M bp**

Download/View Sequence/Evidence

Contig | Dr UniG | Genes_seq

Symbol	O	Links	E	Description
zgc:153678	↑	ZFIN ug sv pr dl ev mm	hm	best RefSeq zgc:153678
LOC100148837	↑	sv pr dl ev mm		mRNA similar to solute carrier family 35, member B4
cyp19a1b	↓	ZFIN ug sv pr dl ev mm sts	hm	best RefSeq cytochrome P450, family 19, subfamily A, polypeptide 1b
met	↓	ZFIN ug sv pr dl ev mm	hm	best RefSeq met proto-oncogene (hepatocyte growth factor receptor)
LOC558687	↓	sv pr dl ev mm	hm	mRNA similar to type II CAX cation/proton exchanger
LOC569055	↑	ug sv pr dl ev mm	hm	mRNA hypothetical LOC569055
LOC795008	↑	sv pr dl ev mm	hm	mRNA hypothetical protein LOC795008
ergic2	↓	ZFIN ug sv pr dl ev mm sts	hm	best RefSeq ERGIC and golgi 2
zgc:91794	↓	ZFIN ug sv pr dl ev mm sts	hm	best RefSeq zgc:91794
LOC797354	↓	ug sv pr dl ev mm	hm	mRNA similar to SMC1 beta protein
si:dkey-80c24.6	↓	ZFIN ug sv pr dl ev mm		best RefSeq si:dkey-80c24.6
LOC569672	↑	ug sv pr dl ev mm	hm	mRNA similar to novel serine/threonine protein kinase
LOC100001260	↑	sv pr dl ev mm		mRNA similar to type-1 protein phosphatase skeletal muscle glycogen targeting sub
wu:fd21f07	↓	ZFIN ug sv pr dl ev mm	hm	best RefSeq wu:fd21f07
zgc:110459	↑	ZFIN ug sv pr dl ev mm	hm	best RefSeq zgc:110459
LOC100150336	↓	sv pr dl ev mm		protein similar to pol polyprotein
LOC564485	↑	sv pr dl ev mm		mRNA hypothetical LOC564485
cox5aa	↑	ZFIN ug sv pr dl ev mm		best RefSeq cytochrome c oxidase subunit Vaa
LOC792268	↓	ug sv pr dl ev mm	hm	best RefSeq hypothetical protein LOC792268
zgc:114037	↑	ZFIN ug sv pr dl ev mm	hm	best RefSeq zgc:114037

Summary of Maps:

Map 1: Contig | Table View

小鼠（*Mus musculus*）
基因组大小与人类相近，有19条常染色体；

NCBI Map Viewer

PubMed | Entrez | BLAST | OMIM | Taxonomy | Structure

Search | Find | Find in This View | Advanced Search

Mus musculus (laboratory mouse) **Build 37.1 (Current)** — BLAST The Mouse Genome

Chromosome: 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 [19] X Y MT

Master Map: Genes On Sequence — Summary of Maps — Maps & Options

Region Displayed: 0-61M bp — Download/View Sequence/Evidence

Mouse genome overview page (Build 37.1)
Mouse genome overview page (Build 36.1)
Map Viewer Home
Map Viewer Help
Mouse Maps Help
FTP
Data As Table View
Maps & Options
Compress Map
Region Shown:
Go
out
zoom
in
You are here:
Ideogram
default
master

Symbol	O	Links	E	Description
Fosl1	↓	MGI sv pr dl ev mm hm sts CCDS SNP	best RefSeq	fos-like antigen 1
Map3k11	↓	MGI sv pr dl ev mm hm sts CCDS SNP	best RefSeq	mitogen activated protein kinase kinase kina
Rcor2	↓	MGI sv pr dl ev mm hm sts CCDS SNP GENSAT	best RefSeq	REST corepressor 2
BC014805	↑	MGI sv pr dl ev mm hm CCDS	best RefSeq	cDNA sequence BC014805
Slc3a2	↑	MGI sv pr dl ev mm hm sts CCDS SNP	best RefSeq	solute carrier family 3 (activators of dibasic
Stxbp3b	↑	MGI sv pr dl ev mm	mRNA	syntaxin-binding protein 3B
LOC100040203	↓	sv pr dl ev mm hm	protein	similar to prostatein C3 subunit
Fads2	↑	MGI sv pr dl ev mm hm CCDS SNP	best RefSeq	fatty acid desaturase 2
2810441K11Rik	↑	MGI sv pr dl ev mm hm sts CCDS	best RefSeq	RIKEN cDNA 2810441K11 gene
Plac1l	↑	MGI sv pr dl ev mm hm CCDS SNP GENSAT	best RefSeq	placenta-specific 1-like
Zfp91	↑	MGI sv pr dl ev mm hm sts CCDS SNP	best RefSeq	zinc finger protein 91
Olfr1454	↓	MGI sv pr dl ev mm hm CCDS	best RefSeq	olfactory receptor 1454
Olfr1470-ps1	↑	MGI sv dl ev mm SNP	best RefSeq	olfactory receptor 1470, pseudogene 1
Ankrd15	↓	MGI sv pr dl ev mm hm sts CCDS SNP	best RefSeq	ankyrin repeat domain 15
Rln1	↑	MGI sv pr dl ev mm hm CCDS	best RefSeq	relaxin 1
Trpd52l3	↓	MGI sv pr dl ev mm hm CCDS	best RefSeq	tumor protein D52-like 3
Mms19l	↑	MGI sv pr dl ev mm hm sts CCDS SNP	best RefSeq	MMS19 (MET18 S. cerevisiae)-like
EG627889	↑	MGI sv pr dl ev mm hm SNP	mRNA	predicted gene, EG627889
1700011F14Rik	↓	MGI sv pr dl ev mm hm CCDS SNP	best RefSeq	RIKEN cDNA 1700011F14 gene
Emx2os	↑	MGI sv dl ev mm sts SNP	best RefSeq	empty spiracles homolog 2 (Drosophila) op

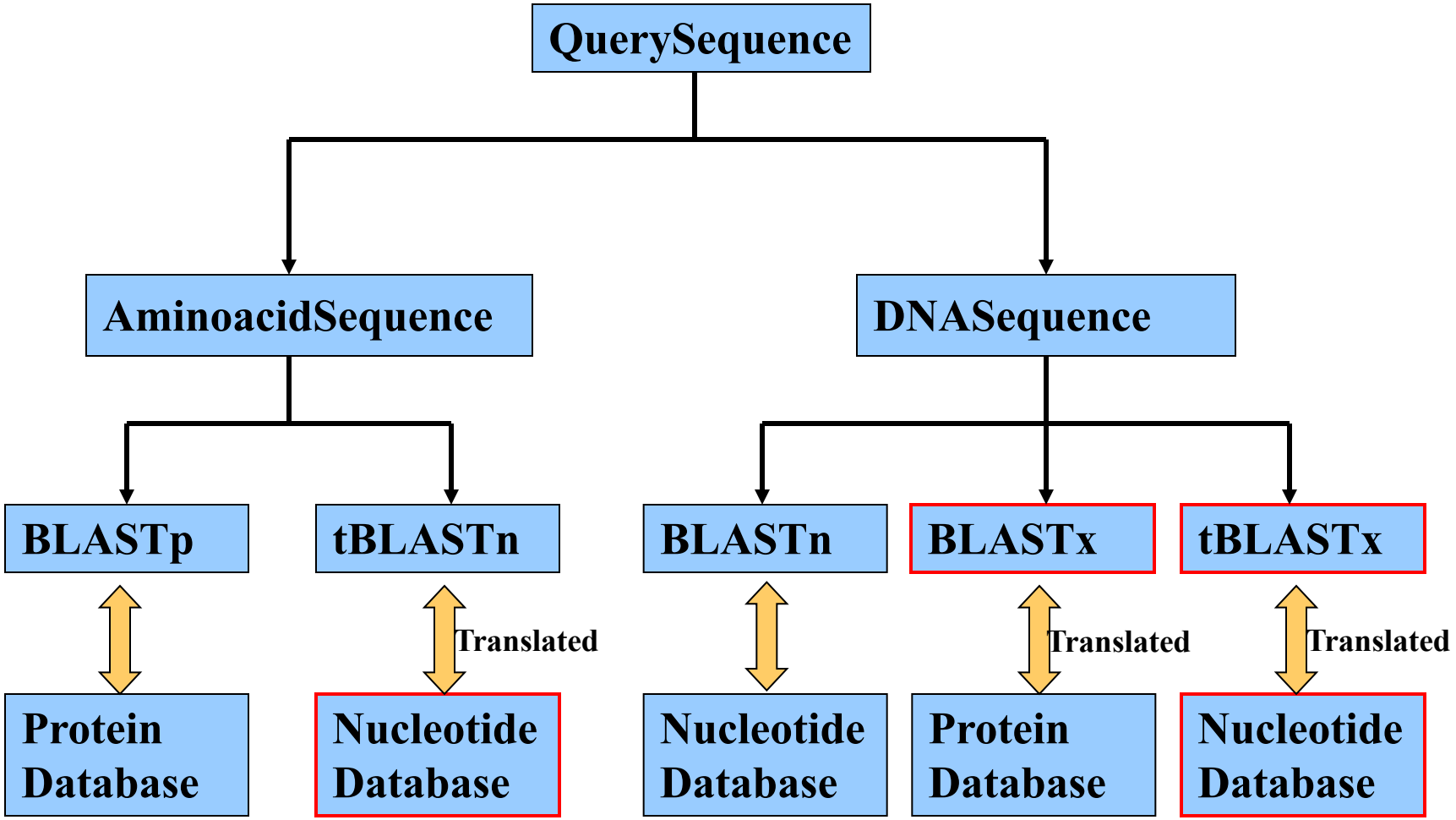
Summary of Maps:
Map 1: Assembly — Table View

BLAST

- 基本局部比对搜索工具
  (Basic Local Alignment Search Tool)
- **NCBI上BLAST服务的网址：**
- **http://blast.ncbi.nlm.nih.gov/**
- **NCBI上BLAST程序的下载：**
  ftp://ftp.ncbi.nlm.nih.gov/blast/executables/release/
- **NCBI的BLAST数据库下载网址：**
  ftp://ftp.ncbi.nlm.nih.gov/blast/db/

选择物种

选择blast程序


QuerySequence
AminoacidSequence
DNASequence
BLASTp
tBLASTn
BLASTn
BLASTx
tBLASTx
Translated
Translated
Translated
Protein Database
Nucleotide Database
Nucleotide Database
Protein Database
Nucleotide Database

程序名	搜索序列	数据库	内容	备注
blastp	**Protein**	**Protein**	比较氨基酸序列与蛋白质数据库	使用取代矩阵寻找较远的关系，进行**SEG**过滤
blastn	**Nucleotide**	**Nucleotide**	比较核酸序列与核酸数据库	寻找较高分值的匹配，对较远的关系不太适用
blastx	**Nucleotide**	**Protein**	比较核酸序列理论上的六个读码框的所有转换结果和蛋白质数据库	用于新的**DNA**序列和**ESTs**的分析，可转译搜索序列
tblastn	**Protein**	**Nucleotide**	比较蛋白质序列和核酸序列数据库，动态转换为六个读码框的结果	用于寻找数据库中没有标注的编码区，可转译数据库序列
tblastx	**Nucleotide**	**Nucleotide**	比较核酸序列和核酸序列数据库，经过两次动态转换为六个读码框的结果	转译搜索序列与数据库序列

以Blastx为例：

目标序列为**ATG AGT ACC GCT AAA TTA GTT AAA TCA AAA GCG ACC AAT CTG CTT TAT ACC CGC**

6个读码框翻译

5’端到3’端

第一位起始：

ATG AGT ACC GCT AAA TTA GTT AAA TCA AAA GCG ACC AAT CTG CTT TAT ACC CGC

第二位起始：

TGA GTA CCG CTA AAT TAG TTA AAT CAA AAG CGA CCA ATC TGC TTT ATA CCC GC

第三位起始：

GAG TAC CGC TAA ATT AGT TAA ATC AAA AGC GAC CAA TCT GCT TTA TAC CCG C

3’端到5’端

第一位起始：

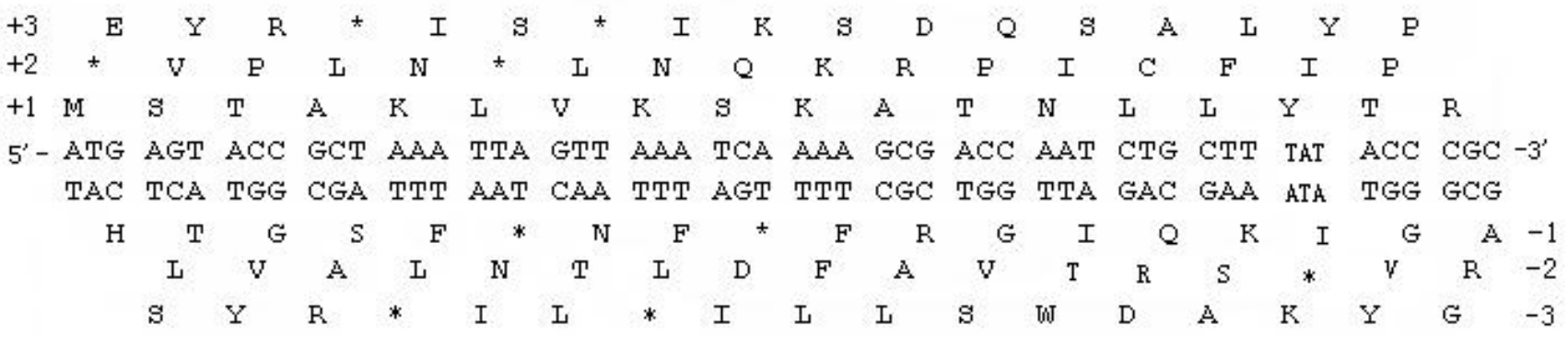
GCG GGT ATA AAG CAG ATT GGT CGC TTT TGA TTT AAC TAA TTT AGC GGT ACT CAT

第二位起始：

CGG GTA TAA AGC AGA TTG GTC GCT TTT GAT TTA ACT AAT TTA GCG GTA CTC AT

第三位起始：

GGG TAT AAA GCA GAT TGG TCG CTT TTG ATT TAA CTA ATT TAG CGG TAC TCA T



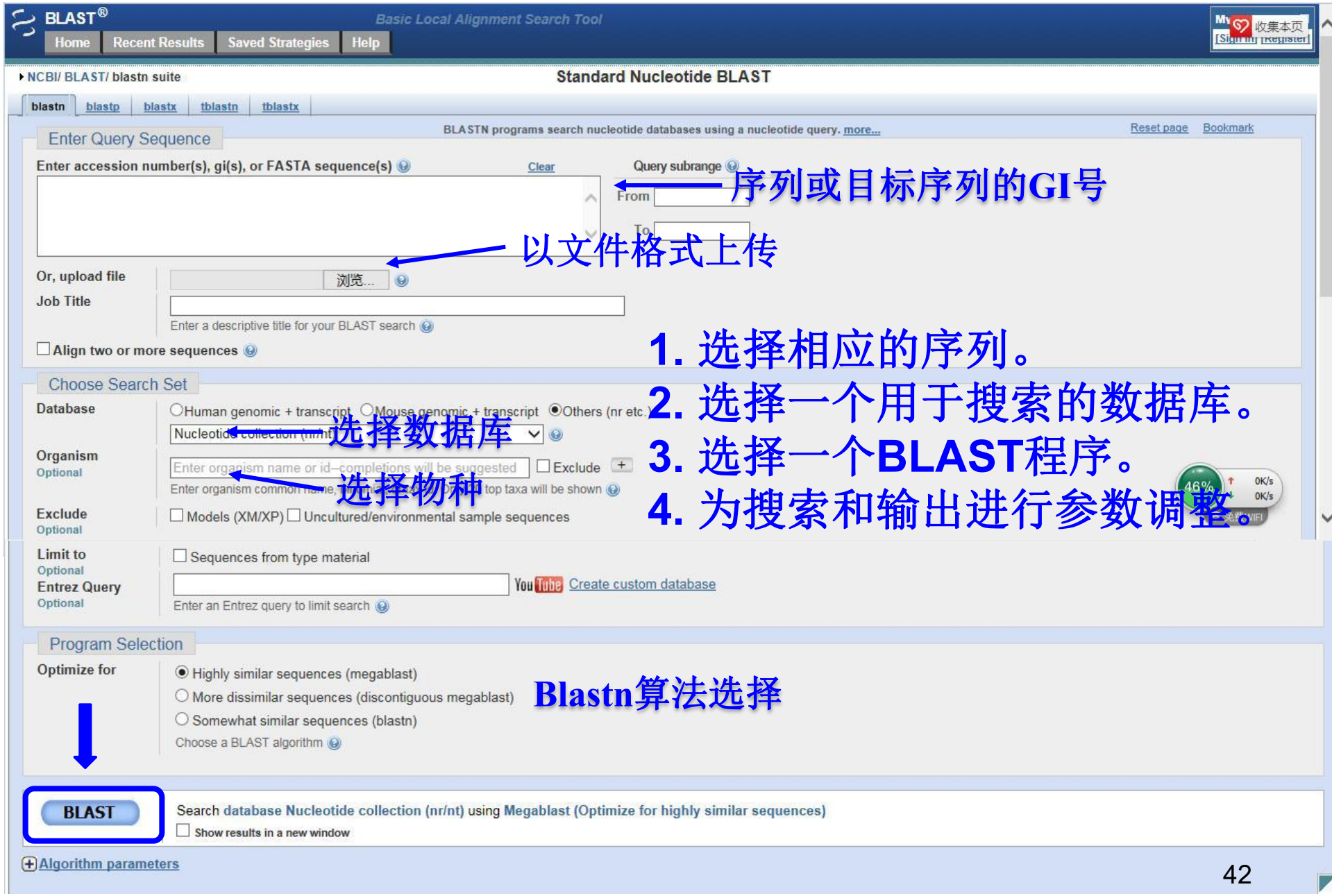
>ref|YP_688332.1| DNA starvation/stationary phase protection protein Dps [Shigella flexneri 5 str. 8401]
gb|ABF03027.1| global regulator, starvation conditions [Shigella flexneri 5 str. 8401]
Length=208

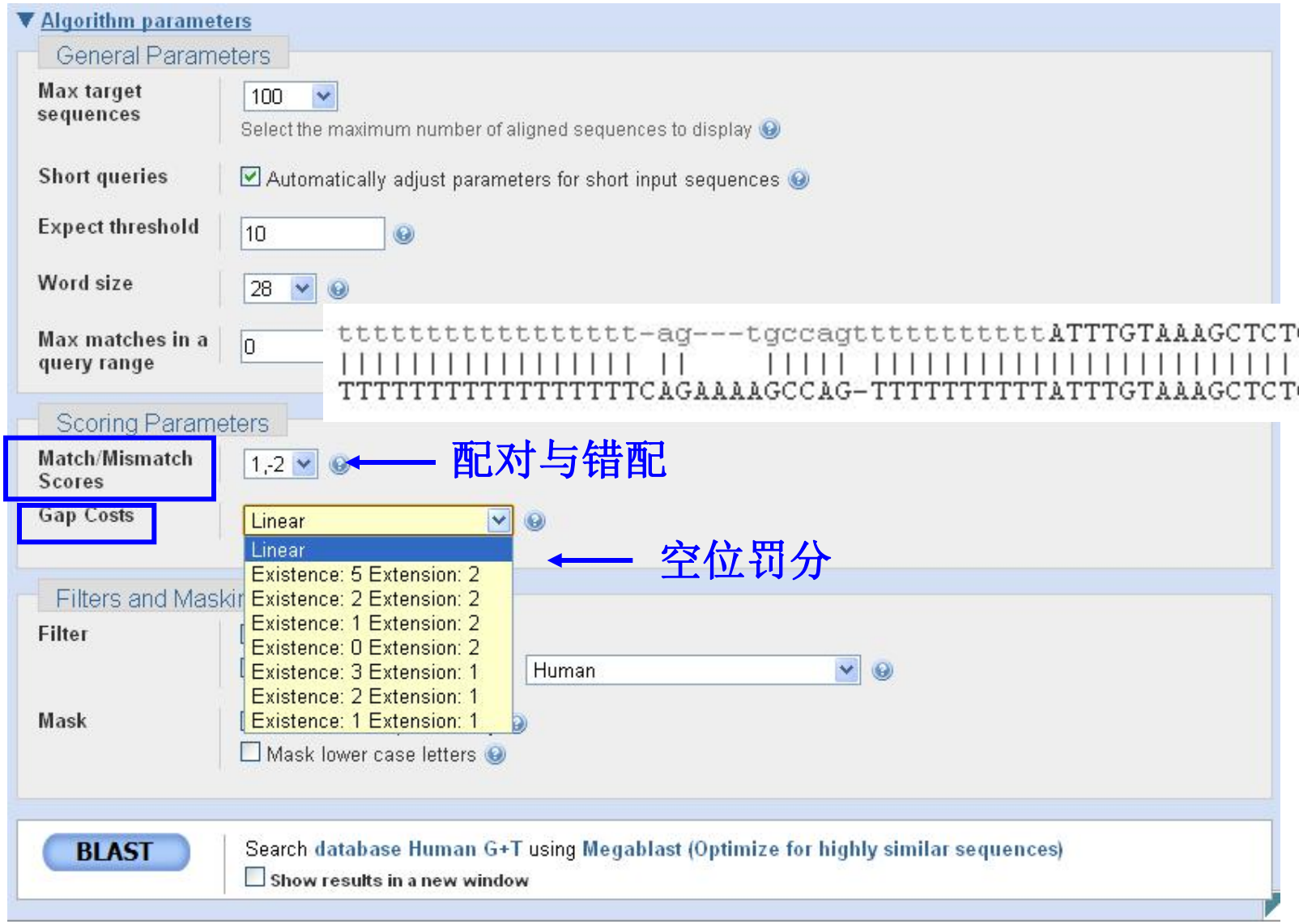
GENE ID: 4209430 dps | DNA starvation/stationary phase protection protein Dps [Shigella flexneri 5 str. 8401] **(10 or fewer PubMed links)**

Score = 37.4 bits (85), Expect = 0.36
Identities = 18/18 (100%), Positives = 18/18 (100%), Gaps = 0/18 (0%)
Frame = +1

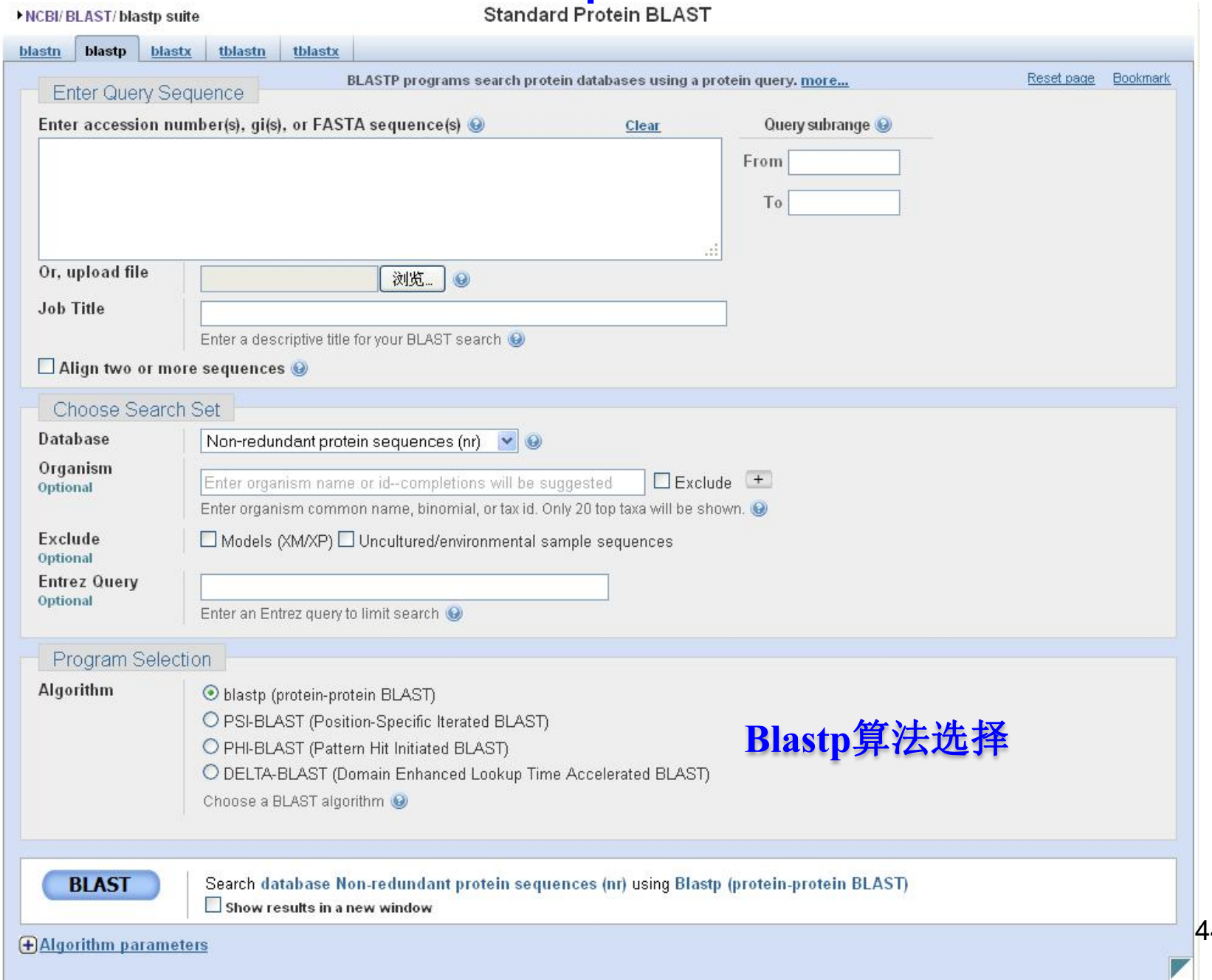
```
Query  1   MSTAKLVKSKATNLLYTR  54
           MSTAKLVKSKATNLLYTR
Sbjct  42  MSTAKLVKSKATNLLYTR  59
```

blastn

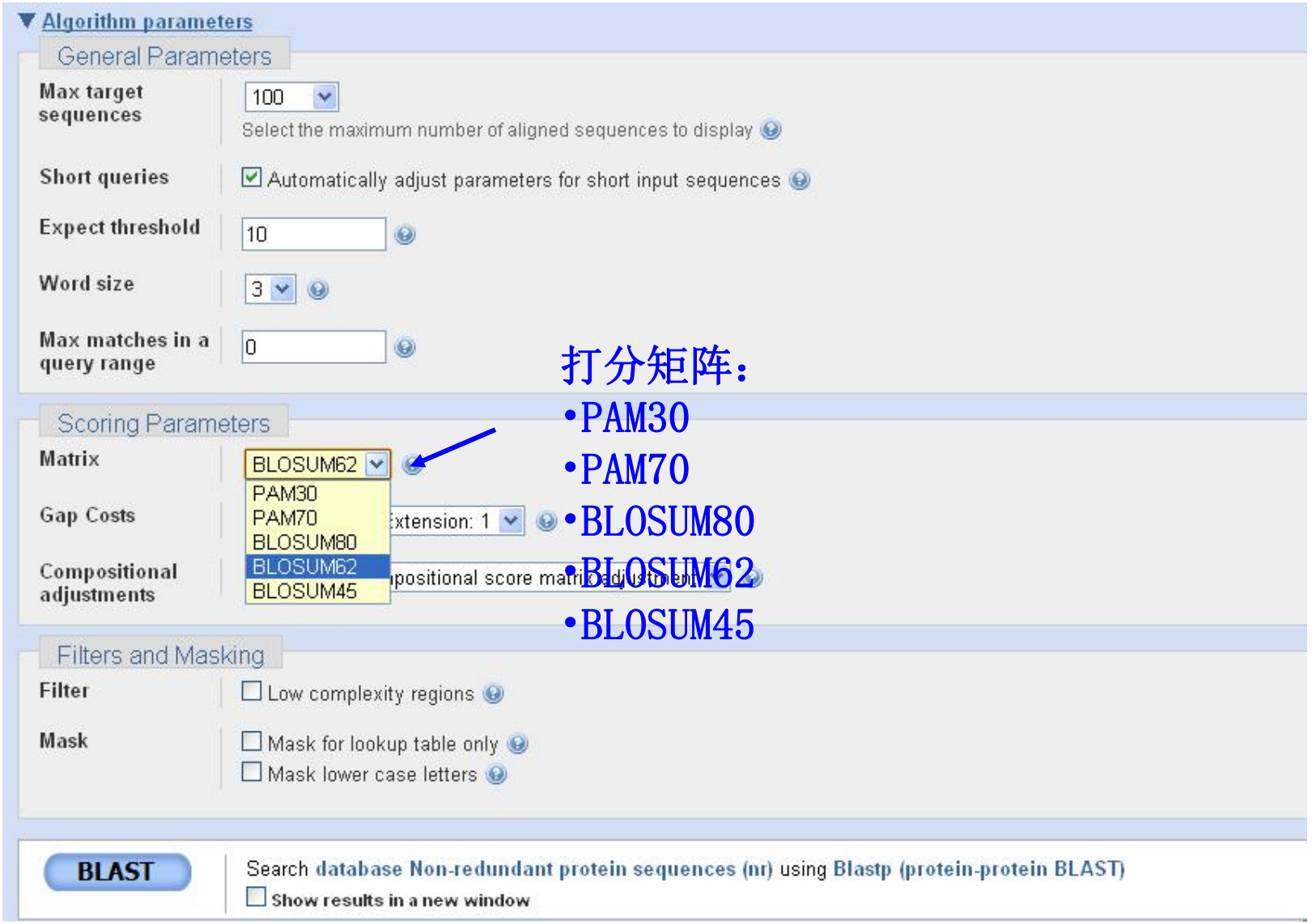

BLAST®
Basic Local Alignment Search Tool
Home
Recent Results
Saved Strategies
Help
NCBI/ BLAST/ blastn suite
Standard Nucleotide BLAST
blastn
blastp
blastx
tblastn
tblastx
BLASTN programs search nucleotide databases using a nucleotide query. more...
Reset page
Bookmark
Enter Query Sequence
Enter accession number(s), gi(s), or FASTA sequence(s)
Clear
Query subrange
From
To
序列或目标序列的GI号
以文件格式上传
Or, upload file
浏览...
Job Title
Enter a descriptive title for your BLAST search
Align two or more sequences
Choose Search Set
Database
Human genomic + transcript
Mouse genomic + transcript
Others (nr etc.)
选择数据库
Organism
Optional
Enter organism name or id--completions will be suggested
Exclude
选择物种
Exclude
Optional
Models (XM/XP)
Uncultured/environmental sample sequences
Limit to
Optional
Sequences from type material
Entrez Query
Optional
Create custom database
Enter an Entrez query to limit search
1. 选择相应的序列。
2. 选择一个用于搜索的数据库。
3. 选择一个BLAST程序。
4. 为搜索和输出进行参数调整。
Program Selection
Optimize for
Highly similar sequences (megablast)
More dissimilar sequences (discontiguous megablast)
Somewhat similar sequences (blastn)
Choose a BLAST algorithm
Blastn算法选择
BLAST
Search database Nucleotide collection (nr/nt) using Megablast (Optimize for highly similar sequences)
Show results in a new window
Algorithm parameters


Algorithm parameters
General Parameters
Max target sequences
100
Select the maximum number of aligned sequences to display
Short queries
Automatically adjust parameters for short input sequences
Expect threshold
10
Word size
28
Max matches in a query range
0
tttttttttttttttttt-ag---tgccagttttttttttATTTGTAAAGCTCTGCCATA
TTTTTTTTTTTTTTTTTCAGAAAAGCCAG-TTTTTTTTTTATTTGTAAAGCTCTGCCATA
Scoring Parameters
Match/Mismatch Scores
1,-2
配对与错配
Gap Costs
Linear
空位罚分
Linear
Existence: 5 Extension: 2
Existence: 2 Extension: 2
Existence: 1 Extension: 2
Existence: 0 Extension: 2
Existence: 3 Extension: 1
Existence: 2 Extension: 1
Existence: 1 Extension: 1
Filters and Maskir
Filter
Human
Mask
Mask lower case letters
BLAST
Search database Human G+T using Megablast (Optimize for highly similar sequences)
Show results in a new window

blastp



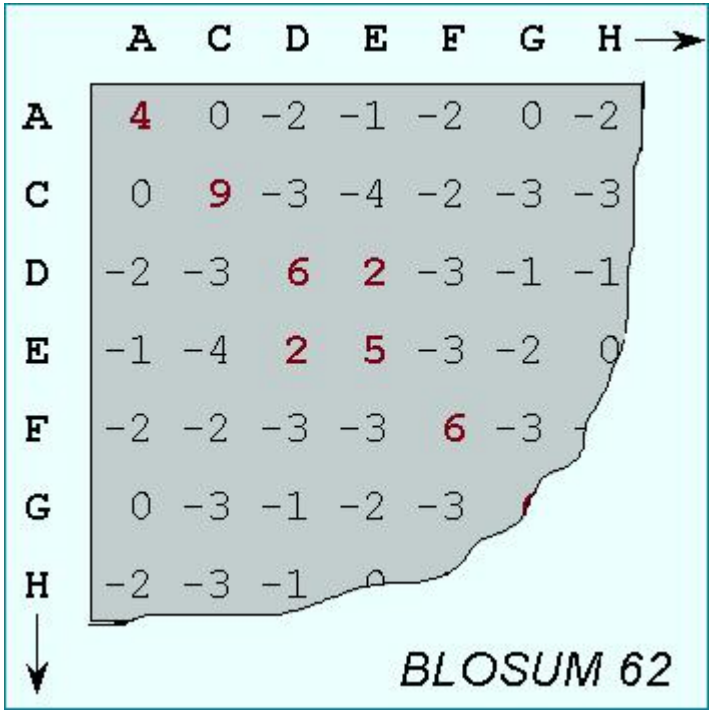
Blastp算法选择



打分矩阵：

- PAM30
- PAM70
- BLOSUM80
- BLOSUM62
- BLOSUM45

选择打分矩阵（scoring matrix）

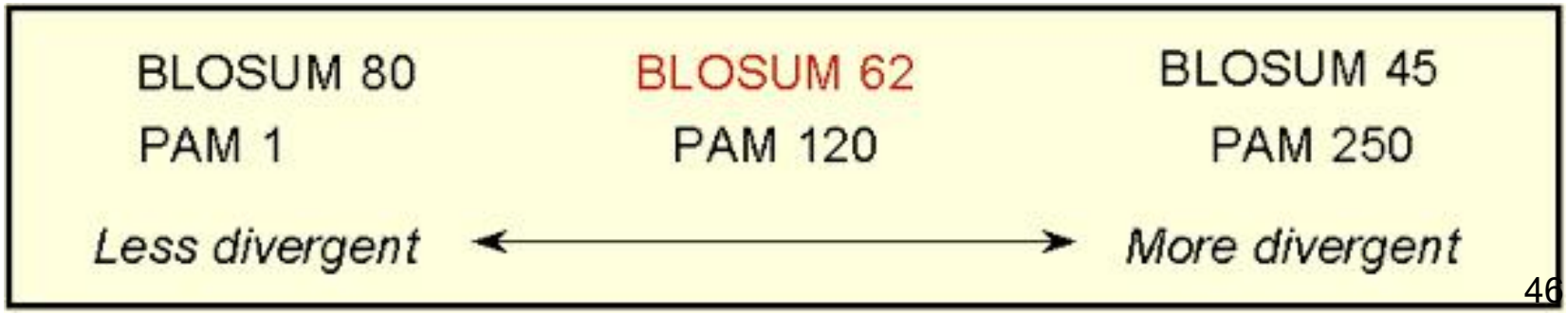


The PAM family

- Based on global alignments
- The PAM1 is the matrix calculated from comparisons of sequences with no more than 1% divergence.
- Other PAM matrices are extrapolated from PAM1.

The BLOSUM family

- Based on local alignments.
- BLOSUM62 is a matrix calculated from comparisons of sequences with no less than 62% divergence.
- All BLOSUM matrices are based on observed alignments ;they are not extrapolated from comparisons of closely related proteins.



blastn结果

NCBI/ BLAST/ blastn suite/ Formatting Results - XD5X1JDU016

Edit and Resubmit | Save Search Strategies | ▶Formatting options | ▶Download

lesson.seq.screen.Contig34

检索序列信息

Query ID	lcl|30513
Description	lesson.seq.screen.Contig34
Molecule type	nucleic acid
Query Length	1093

比对的数据库信息

Database Name	nr
Description	All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS,environmental samples or phase 0, 1 or 2 HTGS sequences)
Program	BLASTN 2.2.25+ ▶Citation

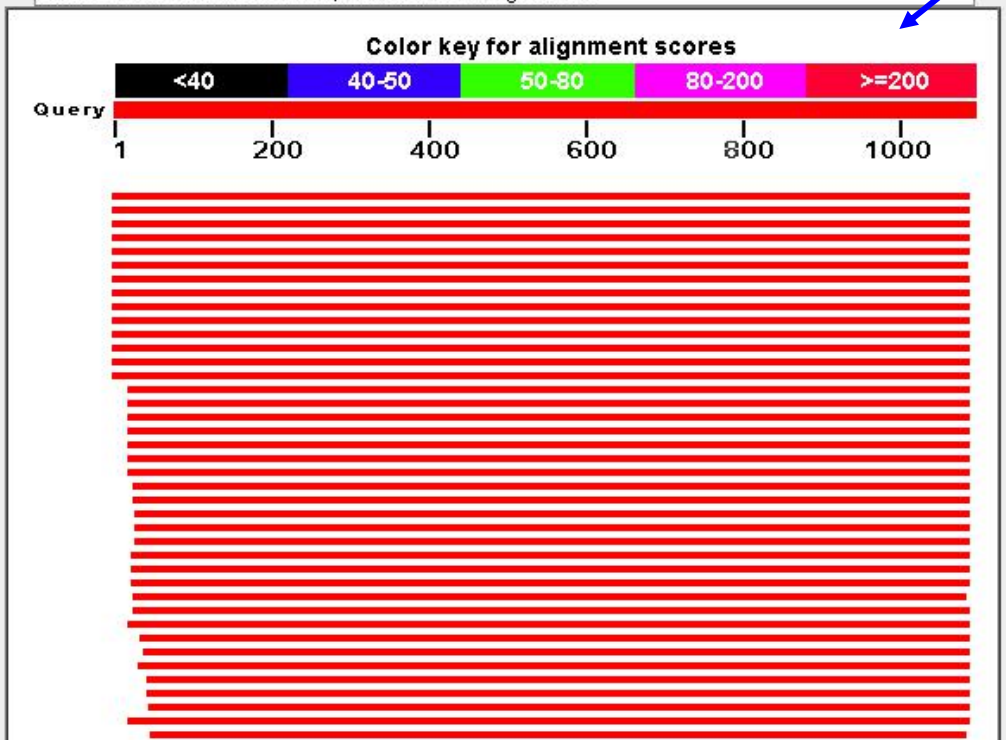
Other reports: ▶Search Summary [Taxonomy reports] [Distance tree of results]

▼ Graphic Summary

图形化结果

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments



blastn结果

Descriptions

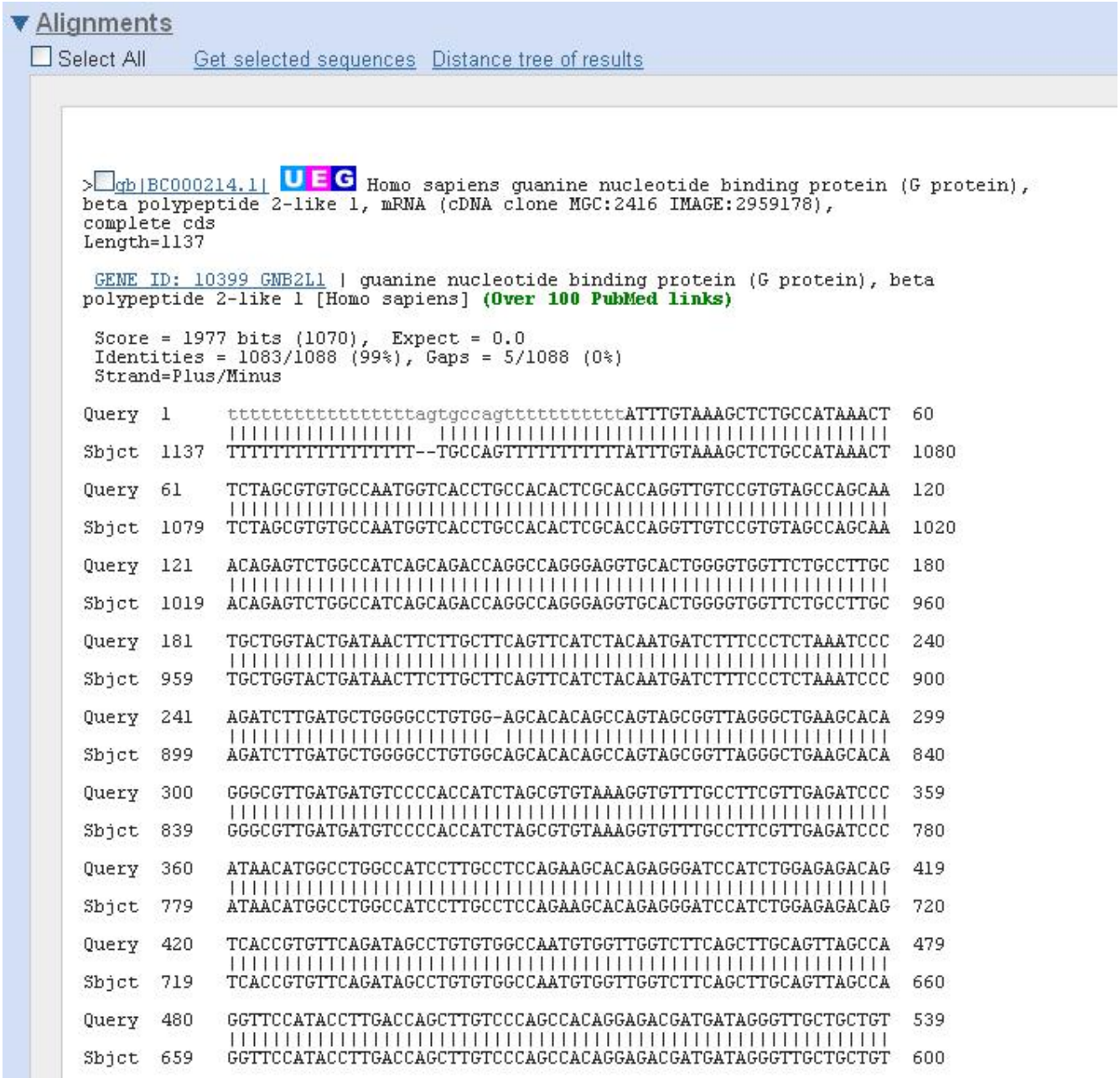
Legend for links to other resources: U UniGene E GEO G Gene S Structure M Map Viewer PubChem BioAssay

Sequences producing significant alignments:

Accession	Description	Max score	Total score	Query coverage	E value	Max ident	Links
BC000214.1	Homo sapiens guanine nucleotide binding protein (G protein	1977	1977	99%	0.0	99%	UEG
BC000366.2	Homo sapiens guanine nucleotide binding protein (G protein	1973	1973	99%	0.0	99%	UEG
BC010119.2	Homo sapiens guanine nucleotide binding protein (G protein	1973	1973	99%	0.0	99%	UEG
BC002620.1	Homo sapiens mRNA similar to guanine nucleotide binding pr	1971	1971	99%	0.0	99%	
BC014256.1	Homo sapiens guanine nucleotide binding protein (G protein	1971	1971	99%	0.0	99%	UEG
BC017287.2	Homo sapiens guanine nucleotide binding protein (G protein	1969	1969	99%	0.0	99%	UEG
BC000672.1	Homo sapiens cDNA clone IMAGE:3350045, **** WARNING	1960	1960	99%	0.0	99%	E
BC073781.1	Homo sapiens guanine nucleotide binding protein (G protein	1960	1960	99%	0.0	99%	
BC021034.1	Homo sapiens cDNA clone IMAGE:3834363, **** WARNING	1960	1960	99%	0.0	99%	
BC019093.2	Homo sapiens guanine nucleotide binding protein (G protein	1960	1960	99%	0.0	99%	UEG
BC019362.1	Homo sapiens guanine nucleotide binding protein (G protein	1960	1960	99%	0.0	99%	UEG
BC032006.1	Homo sapiens guanine nucleotide binding protein (G protein	1960	1960	99%	0.0	99%	UEG
NM_006098.4	Homo sapiens guanine nucleotide binding protein (G protein	1954	1954	99%	0.0	99%	UEGM
AY159316.1	Homo sapiens lung cancer oncogene 7 mRNA, complete cds	1954	1954	99%	0.0	99%	E
BC021993.1	Homo sapiens guanine nucleotide binding protein (G protein	1947	1947	97%	0.0	99%	UEG
CR607176.1	full-length cDNA clone CS0DA001YP03 of Neuroblastoma of	1947	1947	97%	0.0	99%	UG
CR603958.1	full-length cDNA clone CL0BB005ZG08 of Neuroblastoma of	1947	1947	97%	0.0	99%	UG
CR602411.1	full-length cDNA clone CL0BB012ZF09 of Neuroblastoma of	1947	1947	97%	0.0	99%	UG
CR601263.1	full-length cDNA clone CS0DI076YI19 of Placenta Cot 25-no	1947	1947	97%	0.0	99%	UG
CR600581.1	full-length cDNA clone CL0BB012ZC07 of Neuroblastoma of	1947	1947	97%	0.0	99%	UG
CR594655.1	full-length cDNA clone CS0DI053YK19 of Placenta Cot 25-n	1947	1947	97%	0.0	99%	UG
CR625098.1	full-length cDNA clone CS0DE012YB19 of Placenta of Homo	1940	1940	96%	0.0	99%	UG
CR604224.1	full-length cDNA clone CS0DH004YB11 of T cells (Jurkat cel	1940	1940	96%	0.0	99%	UG
CR616532.1	full-length cDNA clone CS0DE003YP09 of Placenta of Homo	1938	1938	96%	0.0	99%	UG
CR613365.1	full-length cDNA clone CS0DE012YI17 of Placenta of Homo	1938	1938	96%	0.0	99%	UG
CR594601.1	full-length cDNA clone CL0BB009ZE04 of Neuroblastoma of	1938	1938	96%	0.0	99%	UG

E值（E-value）表示仅仅因为随机性造成获得这一 比对结果的可能性。这一数值越接近零，随机发生这一事件的可能性越小，结果可靠性越高。

blastn结果



▼ Alignments

☐ Select All Get selected sequences Distance tree of results

>☐gb|BC000214.1| UEG Homo sapiens guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1, mRNA (cDNA clone MGC:2416 IMAGE:2959178), complete cds
Length=1137

GENE ID: 10399 GNB2L1 | guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1 [Homo sapiens] **(Over 100 PubMed links)**

Score = 1977 bits (1070), Expect = 0.0
Identities = 1083/1088 (99%), Gaps = 5/1088 (0%)
Strand=Plus/Minus

```
Query  1     tttttttttttttttttagtgccagttttttttttATTTGTAAAGCTCTGCCATAAACT  60
             ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Sbjct  1137  TTTTTTTTTTTTTTTTT--TGCCAGTTTTTTTTTTATTTGTAAAGCTCTGCCATAAACT  1080

Query  61    TCTAGCGTGTGCCAATGGTCACCTGCCACACTCGCACCAGGTTGTCCGTGTAGCCAGCAA  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1079  TCTAGCGTGTGCCAATGGTCACCTGCCACACTCGCACCAGGTTGTCCGTGTAGCCAGCAA  1020

Query  121   ACAGAGTCTGGCCATCAGCAGACCAGGCCAGGGAGGTGCACTGGGGTGGTTCTGCCTTGC  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1019  ACAGAGTCTGGCCATCAGCAGACCAGGCCAGGGAGGTGCACTGGGGTGGTTCTGCCTTGC  960

Query  181   TGCTGGTACTGATAACTTCTTGCTTCAGTTCATCTACAATGATCTTTCCCTCTAAATCCC  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  959   TGCTGGTACTGATAACTTCTTGCTTCAGTTCATCTACAATGATCTTTCCCTCTAAATCCC  900

Query  241   AGATCTTGATGCTGGGGCCTGTGG-AGCACACAGCCAGTAGCGGTTAGGGCTGAAGCACA  299
             |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  899   AGATCTTGATGCTGGGGCCTGTGGCAGCACACAGCCAGTAGCGGTTAGGGCTGAAGCACA  840

Query  300   GGGCGTTGATGATGTCCCCACCATCTAGCGTGTAAAGGTGTTTGCCTTCGTTGAGATCCC  359
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  839   GGGCGTTGATGATGTCCCCACCATCTAGCGTGTAAAGGTGTTTGCCTTCGTTGAGATCCC  780

Query  360   ATAACATGGCCTGGCCATCCTTGCCTCCAGAAGCACAGAGGGATCCATCTGGAGAGACAG  419
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  779   ATAACATGGCCTGGCCATCCTTGCCTCCAGAAGCACAGAGGGATCCATCTGGAGAGACAG  720

Query  420   TCACCGTGTTCAGATAGCCTGTGTGGCCAATGTGGTTGGTCTTCAGCTTGCAGTTAGCCA  479
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  719   TCACCGTGTTCAGATAGCCTGTGTGGCCAATGTGGTTGGTCTTCAGCTTGCAGTTAGCCA  660

Query  480   GGTTCCATACCTTGACCAGCTTGTCCCAGCCACAGGAGACGATGATAGGGTTGCTGCTGT  539
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  659   GGTTCCATACCTTGACCAGCTTGTCCCAGCCACAGGAGACGATGATAGGGTTGCTGCTGT  600
```

练习1：网上运行blastx和blastn

（NCBIblast网址：http://blast.ncbi.nlm.nih.gov/）

>lesson.seq.screen.Contig34

TTTTTTTTTTTTTTTTTAGTGCCAGTTTTTTTTTTATTTGTAAAGCTCTGCCATAAACTTCTAGCGTGTGCCAATGGTCACCTGCCACA
CTCGCACCAGGTTGTCCGTGTAGCCAGCAAACAGAGTCTGGCCATCAGCAGACCAGGCCAGGGAGGTGCACTGGGGTGGTTCTGCCTTGC
TGCTGGTACTGATAACTTCTTGCTTCAGTTCATCTACAATGATCTTTCCCTCTAAATCCCAGATCTTGATGCTGGGGCCTGTGGAGCACA
CAGCCAGTAGCGGTTAGGGCTGAAGCACAGGGCGTTGATGATGTCCCCACCATCTAGCGTGTAAAGGTGTTTGCCTTCGTTGAGATCCCA
TAACATGGCCTGGCCATCCTTGCCTCCAGAAGCACAGAGGGATCCATCTGGAGAGACAGTCACCGTGTTCAGATAGCCTGTGTGGCCAAT
GTGGTTGGTCTTCAGCTTGCAGTTAGCCAGGTTCCATACCTTGACCAGCTTGTCCCAGCCACAGGAGACGATGATAGGGTTGCTGCTGTT
GGGCGAGAAGCGGACACAAGACACCCACTCTGAGTGGCTCTCATCCTGGACAGTGTATTTGCACACACCCAGGGTATTCCATAGCTTGAT
GGTTTTATCTCGAGATCCAGAGACAATCTGCCGGTTGTCAGAGGAGAAGGCCACACTCAGCACATCCTTGGTATGGCCCACAAATCGCCT
CGTGGTGGTGCCCGTTGTGAGATCCCAGAAGGCGCAGGGTTCCATCCCAGGAGCCTGAGAGGGCAAACTGGCCATCTGAGGAGATAACCA
CATCACTAACAAAGTGGGAGTGACCCCGCAGAGCACGCTGTGGAATTCCATAGTTGGTCTCATCCCTGGTCAGTTTCCACATGATGATGG
TCTTATCTCGAGAGGCGGAGAGGATCATGTCCGGGAACTGCGGGGTAGTAGCGATCTGGGTTACCCAGCCGTTGTGGCCCTTGAGGGTGC
CACGAAGGGTCATCTGCTCAGTCATGGCGGCGGCGAGAGCGTGTTCGCTGCAGCGACGAGGATGGCACTGGATGGCTTAGAGAAACTAGC
ACCACAGTCGACC

1. 对contig34进行网上blastn（演示），
2. blastx（自行操作）比对

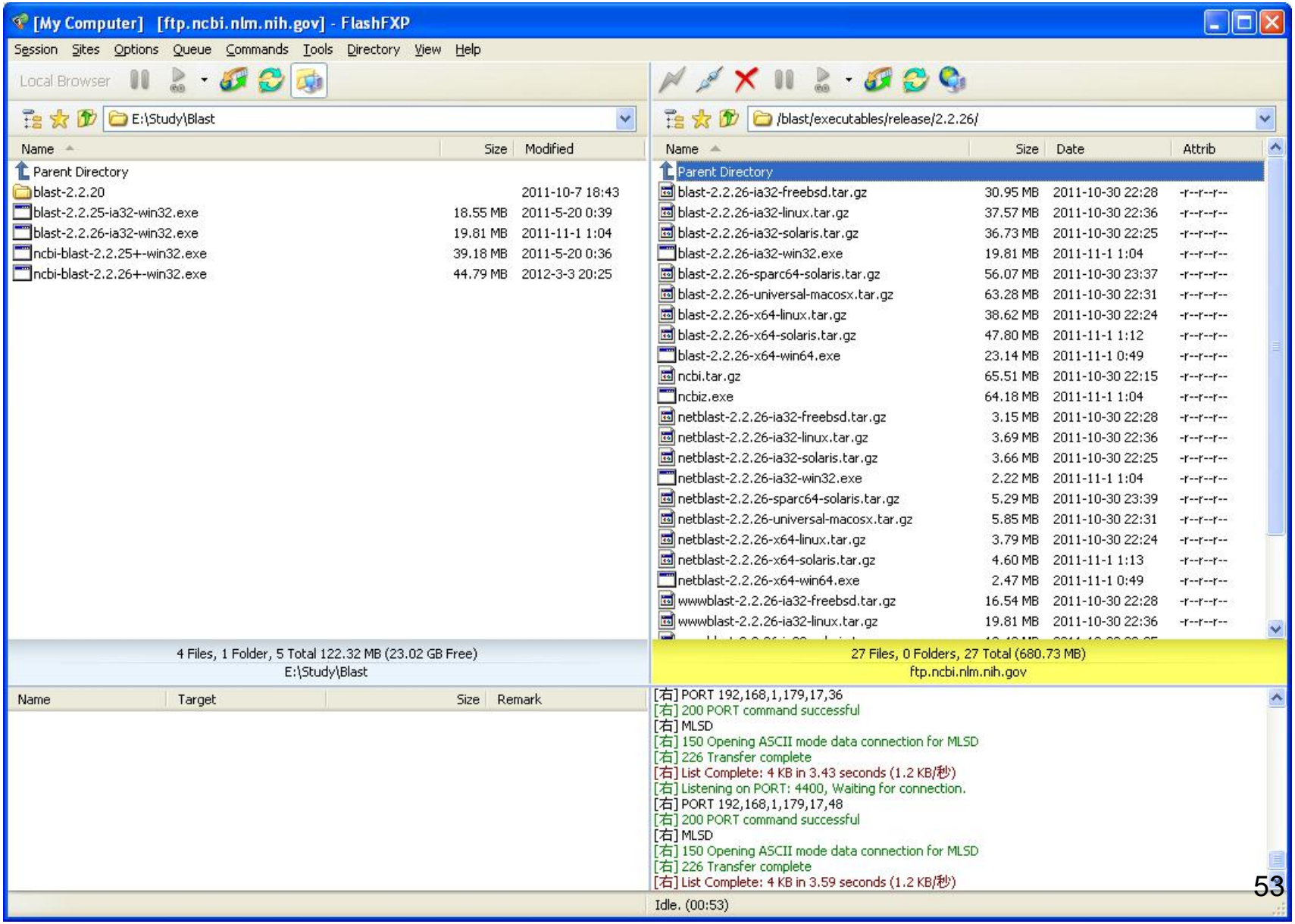
网页版BLAST的优缺点：

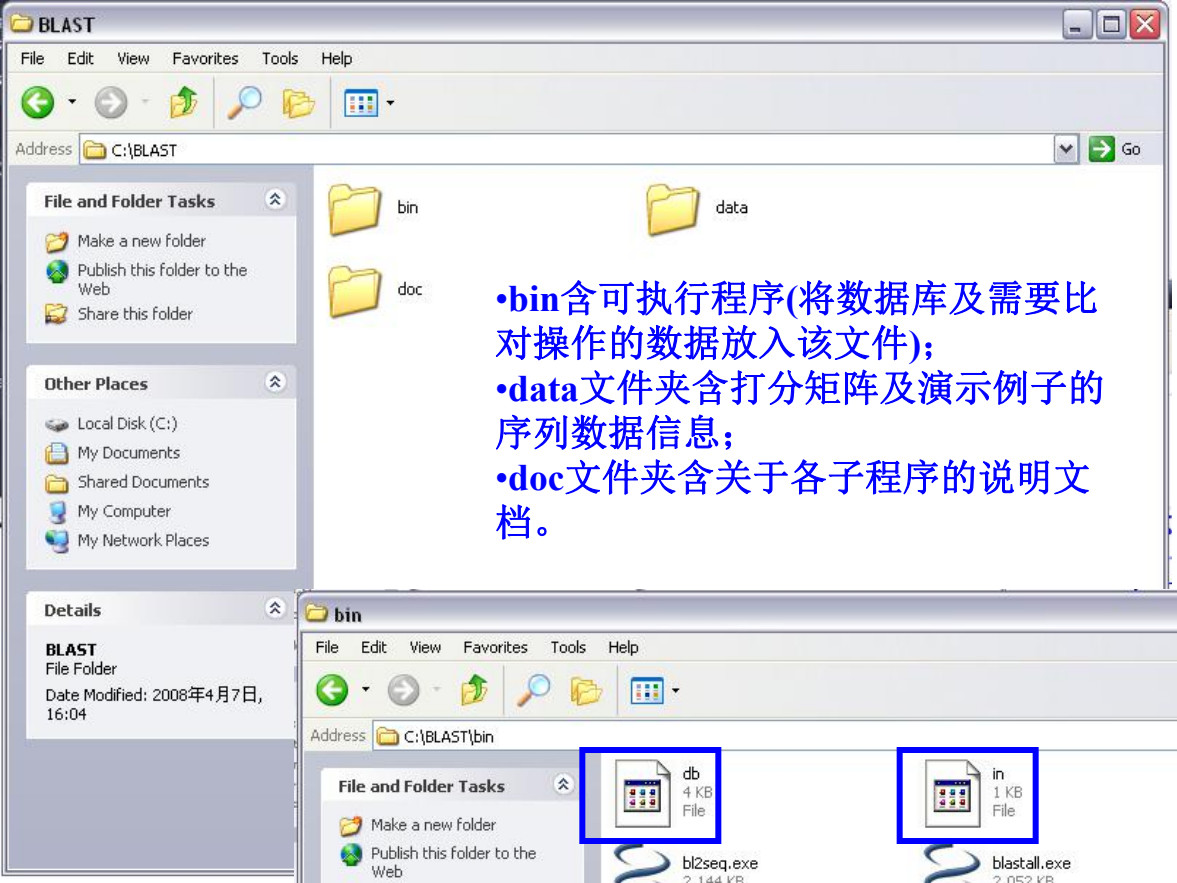
- 优点：直观方便，容易操作，数据库同步更新
- 缺点：不利于操作大批量的数据，同时也不能自己定义搜索的数据库，对网络依赖性太大。

本地运行BLAST

- 下载**NCBI**上**blast**程序：
- **ftp://ftp.ncbi.nlm.nih.gov/blast/executables/release/**
- 安装（安装到C:\blast）
- 数据库的格式化（formatdb）
- 程序运行（blastall）

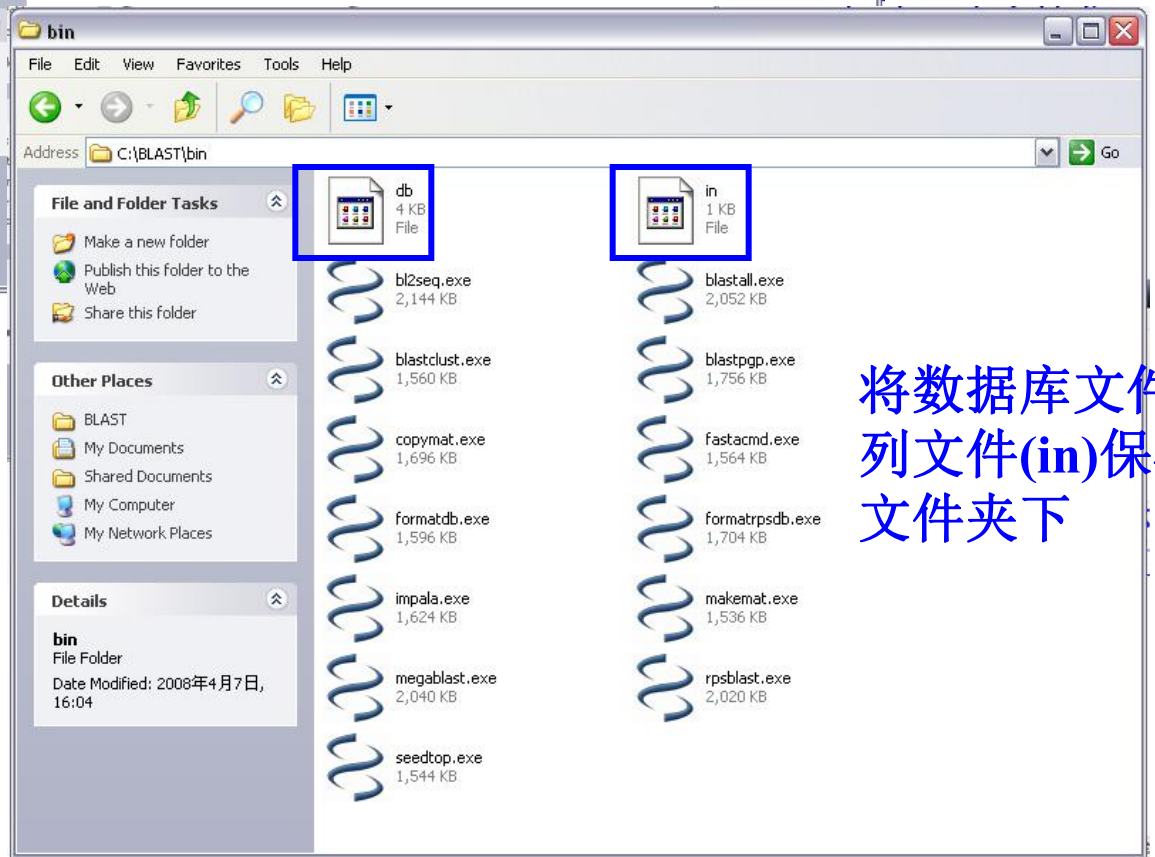
登陆NCBI的FTP下载blast程序





•bin含可执行程序(将数据库及需要比对操作的数据放入该文件)；
•data文件夹含打分矩阵及演示例子的序列数据信息；
•doc文件夹含关于各子程序的说明文档。

双击安装到C盘
产生三个文件夹
•bin
•data
•doc



将数据库文件(db)及目标序列文件(in)保存在Blast/bin文件夹下

本地数据库的构建

- 查看db文件

由fasta格式的序列组成，以“>”开头，紧接着是序列描述信息，换行后即是核苷酸或蛋白质序列，直至下一个“>”前为止。

```
>gi|9506859|ref|NP_061932.1| 6.2 kd protein [Homo sapiens]
MVKLSKEAKQRLQQLFKGSQFAIRWGFIPLVIYLGFKRGADPGMPEPTVLSLLWG
>gi|5441539|emb|CAB46824.1| Ribosomal protein [Canis familiaris]
EIANANSRQQILKLIKDGLIIRKPVTVHSRARCRKNTLARRKGRHMGIGKRKGTANARMPEKVTWMRRMR
ILRRLLTRYRESKKIDRHMYHSLYLKVKGNVFKNKRILMEHIH
>gi|13929184|ref|NP_114016.1| potassium large conductance calcium-activated channel, subfamily M, alpha
member 1 [Rattus norvegicus]
MANGGGGGGGSSGSSGGGGGGGGGETALRMSSNIHANHLSLDASSSSSSSSSSSSSSSSSVHEPKMDAL
IIPVTMEVPCDSRGQRMWWAFLASSMVTFFGGLFIILLWRTLKYLWTVCCHCGGKTKEAQKINNGSSQAD
GTLKPVDEKEEVVAAEVGWMTSVKDWAGVMISAQTLTGRVLVVLVFALSIGALVIYFIDSSNPIESCQNF
YKDFTLQIDMAFNVFFLLYFGLRFIAANDKLWFWLEVNSVVDFFTVPPVFVSVYLNRSWLGLRFLRALRL
IQFSEILQFLNILKTSNSIKLVNLLSIFISTWLTAAGFIHLVENSGDPWENFQNNQALTYWECVYLLMVT
MSTVGYGDVYAKTTLGRLFMVFFILGGLAMFASYVPEIIELIGNRKKYGGSYSAVSGRKHIVVCGHITLE
SVSNFLKDFLHKDRDDVNVEIVFLHNISPNLELEALFKRHFTQVEFYQGSVLNPHDLARVKIESADACLI
LANKYCADPDAEDASNIMRVISIKNYHPKIRIITQMLQYHNKAHLLNIPSWNWKEGDDAICLAELKLGFI
AQSCLAQGLSTMLANLFSMRSFIKIEEDTWQKYYLEGVSNEMYTEYLSSAFVGLSFPTVCELCFVKLKLL
MIAIEYKSANRESRSRKRILINPGNHLKTQEGTLGFFIASDAKEVKRAFFYCKACHDDVTDPKRIKKCGC
RRLIYSKMSIYKRMSRACCFDCGRSERDCSCMSGRVRGNVDTLERNFPLSSVSVNDCSTSFRAFEDEQPP
TLSPKKKQRNGGMRNSPNTSPKLMRHDPLLIPGNDQIDNMDSNVKKYDSTGMFHWCAPKEIEKVILTRSE
AAMTVLSGHVVVCIFGDVSSALIGLRNLVMPLRASNFHYHELKHIVFVGSIEYLKREWETLHNFPKVSIL
PGTPLSRADLRAVNINLCDMCVILSANQNNIDDTSLQDKECILASLNIKSMQFDDSIGVLQANSQGFTPP
GMDRSSPDNSPVHGMLRQPSITTGVNIPIITELVNDTNVQFLDQDDDDDPDTELYLTQPFACGTAFAVSV
LDSLMSATYFNDNILTLIRTLVTGGATPELEALIAEENALRGGYSTPQTLANRDRCRVAQLALLDGPFAD
LGDGGCYGDLFCKALKTYNMLCFGIYRLRDAHLSTPSQCTKRYVITNPPYEFELVPTDLIFCLMQFDHNA
GQSRASLSHSSHSSQSSSKKSSSVHSIPSTANRPNRPKSRESRDKQKKEMVYR
>gi|627367|pir||A45259 desmoyokin - human (fragments)
MPGIKVGGSGVNVNAKGLDLGGRGGVQVPAVDISSSLGGRPVEVQGPSLESGDHAKIKFPTMKVPKFGVS
TGREGQTPKAGLRVSAPEVSVGHKGGKPGLTIQAPQLEVSVPSANIEGLEGKLKGPQITGPSLEGDLGLK
GAKPQGHIGVDASAPQIGGSITGPSVEVQAPDIDVQGPGSKLNVPKMKVPKFSVSGAKGEETGIDVTLPT
GEVTVPGVSGDVSLPEIATGGLEGKMKGTKVKTPEMIIQKPKISMQDVDLSLGSPKLKGDIKVSAPGVQG
DVKGPQVALKGSRVDIETPNLEGTLTGPRLGSPSGKTGTCRISMSEVDLNVAAPKVKGGVDVTLPRVEGK
```

数据库的格式化

formatdb命令用于数据库的格式化：

formatdb [option1] [option2] [option3]…

formatdb常用参数

-i database_name 需要格式化的数据库名称

-p T\F 待格式化数据库的序列类型

（核苷酸选F；蛋白质选T；默认值为T)

例：formatdb -i db -p T

对蛋白质数据库“**db**”进行格式化

程序运行

blastall命令用于运行五个blast子程序:
blastall [option1] [option2] [option3]
*可在dos下输入blastall查看各个参数的意义及使用

- blastall常用参数

  - 四个必需参数

  -p program_name, 程序名，根据数据库及搜索文件序列性质进行选择；
  -d database_name, 数据库名称, 比对完成格式化的数据库；
  -i input_file, 搜索文件名称；
  -o output_file,BLAST结果文件名称；

  - 两个常用参数

  -e expectation，期待值, 默认值为10.0，可采用科学计数法来表示，如2e-5；
  -m alignment view options: 比对显示选项，其具体的说明可以用以下的比对实例说明

例：**blastall -p blastx -d db -i in -o out -e 2e-5 -m 9 (表格显示比对结果)**

采用**blastx**程序，将**in**中的序列到数据库**db**中进行比对，结果以表格形式输入到**out**文件

练习2:本地运行blastx

- 进入DOS命令行提示符状态（“运行”→输入cmd）
- 进入C盘，输入：cd\
- 进入包含序列数据的bin目录下，输入：cd blast\bin
- 查看目录下内容，输入：dir

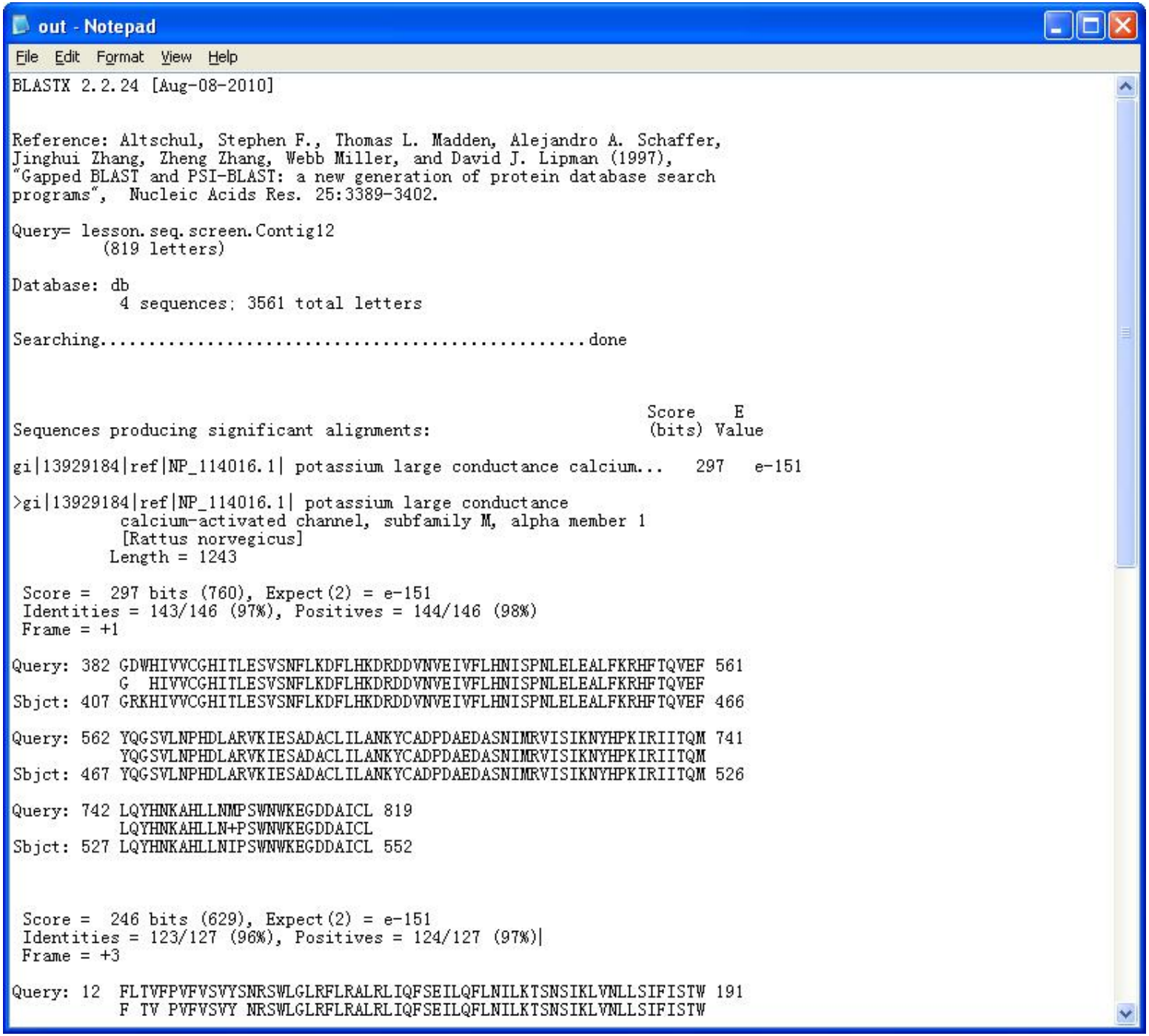
- 格式化数据库db：formatdb -i db -p T

输入　数据库类型：F/T

- 运行blastx
  - blastall -p blastx -i in -d db -o out -e 2e-5 -m 9

Blast程序 序列输入 数据库 结果输出

- 查看结果：用写字板或者记事本打开out文件



out - Notepad

File Edit Format View Help

```
BLASTX 2.2.24 [Aug-08-2010]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= lesson.seq.screen.Contig12
         (819 letters)

Database: db
           4 sequences; 3561 total letters

Searching.....................................................done



                                                                  Score    E
Sequences producing significant alignments:                       (bits) Value

gi|13929184|ref|NP_114016.1| potassium large conductance calcium...   297   e-151

>gi|13929184|ref|NP_114016.1| potassium large conductance
           calcium-activated channel, subfamily M, alpha member 1
           [Rattus norvegicus]
          Length = 1243

 Score =  297 bits (760), Expect(2) = e-151
 Identities = 143/146 (97%), Positives = 144/146 (98%)
 Frame = +1

Query: 382 GDWHIVVCGHITLESVSNFLKDFLHKDRDDVNVEIVFLHNISPNLELEALFKRHFTQVEF 561
           G  HIVVCGHITLESVSNFLKDFLHKDRDDVNVEIVFLHNISPNLELEALFKRHFTQVEF
Sbjct: 407 GRKHIVVCGHITLESVSNFLKDFLHKDRDDVNVEIVFLHNISPNLELEALFKRHFTQVEF 466

Query: 562 YQGSVLNPHDLARVKIESADACLILANKYCADPDAEDASNIMRVISIKNYHPKIRIITQM 741
           YQGSVLNPHDLARVKIESADACLILANKYCADPDAEDASNIMRVISIKNYHPKIRIITQM
Sbjct: 467 YQGSVLNPHDLARVKIESADACLILANKYCADPDAEDASNIMRVISIKNYHPKIRIITQM 526

Query: 742 LQYHNKAHLLNMPSWNWKEGDDAICL 819
           LQYHNKAHLLN+PSWNWKEGDDAICL
Sbjct: 527 LQYHNKAHLLNIPSWNWKEGDDAICL 552



 Score =  246 bits (629), Expect(2) = e-151
 Identities = 123/127 (96%), Positives = 124/127 (97%)|
 Frame = +3

Query: 12  FLTVFPVFVSVYSNRSWLGLRFLRALRLIQFSEILQFLNILKTSNSIKLVNLLSIFISTW 191
           F TV PVFVSVY NRSWLGLRFLRALRLIQFSEILQFLNILKTSNSIKLVNLLSIFISTW
```

3. 蛋白质序列数据库

- SWISS－PROT(欧洲)
- PIR(美国)

- **Protein Sequence Databases**
- UniProt: United Protein Databases
  A single database that combines the information of the major international databases, European Bioinformatics Institute (EBI), Cambridge, UK; Protein Information Resource (PIR) - Georgetown University Medical Center (GUMC) & National Biomedical Research Foundation (NBRF), Washington, D.C.; and Swiss Institute of Bioinformatics (SIB) - Geneva, Switzerland. "The Universal Protein Resource (UniProt) provides the scientific community with a single, centralized, authoritative resource for protein sequences and functional information."
- PIR Protein Sequence Database
  The database is described by its sponsor as "functionally annotated protein sequences, which grew out of the Atlas of Protein Sequence and Structure (1965-1978) edited by Margaret Dayhoff and has been incorporated into an integrated knowledge base system of value-added databases and analytical tools." From the Protein Information Resource, the major U.S. source of protein informatics.
- Swiss-Prot
  The major European protein sequence database, with accompanying annotations, from the Swiss Institute of Bioinformatics. "Swiss-Prot is a curated protein sequence database which strives to provide a high level of annotations (such as the description of the function of a protein, its domains structure, post-translational modifications, variants, etc.), a minimal level of redundancy and high level of integration with other databases." Also at this site is TrEMBL, which contains all translated nucleic acid protein coding sequences in EMBL that have not yet been annotated and incorporated into Swiss-Prot.

- SWISS-PROT
  - 只收录实际存在的蛋白质，有详细的注释（包括功能、结构域、翻译后的修饰等）及齐全的引文和到其它数据库的链接。
  - http://www.expasy.org/sprot/
  - ftp://ftp.expasy.ch/databases/swiss-prot/
- TrEMBL
  - 从EMBL库中的核酸序列翻译出来的氨基酸序列，已经完成自动注释。其中SP-TrEMBL条目已由专家人工分类并赋予SWISS-PROT索引号，但未通过人工审读被最终收入SWISS-PROT。
  - SWISS-PROT+TrEMBL非冗余库
    - http://www.expasy.ch/sprot/
    - ftp://ftp.expasy.ch/databases/sp_tr_nrdb/

- **SWISS－PROT**

1. 瑞士日内瓦大学医学生物化学系和欧洲生物信息学研究所(EBI)合作维护（1986年）；

2. 在EMBL和GenBank数据库上均建立了镜像站点;

3. 数据库包括了从EMBL翻译而来的蛋白质序列，这些序列经过检验和注释；

4. 数据记录包括两部分：

   序列

   注释(结构域、功能位点、跨膜区域、二硫键位置、翻译后的修饰、突变体等)

5. 数据存在滞后性 ➡ TrEMBL数据库的建立

SWISS-PROT的网址： http://cn.expasy.org/sprot
TrEMBL的网址： http://www.ebi.ac.uk/trembl/index.html

SWISS-PROT (http://www.expasy.ch/sprot/sprot-top.html）是目前国际上比较权威的蛋白质序列数据库,其中的蛋白质序列是经过注释的

SWISS-PROT中的数据来源于不同源地：

（1）从核酸数据库经过翻译推导而来；

（2）从蛋白质数据库PIR挑选出合适的数据；

（3）从科学文献中摘录；

（4）研究人员直接提交的蛋白质序列数据

SWISS-PROT有三个明显的特点 ：

（1）注释

在SWISS-PROT中，数据分为核心数据和注释两大类。

核心数据包括：
序列数据、参考文献、分类信息（蛋白质生物来源的描述）

注释包括：

(A)蛋白质的功能描述；
(B)翻译后修饰；
(C)域和功能位点，如钙结合区域、ATP结合位点等；
(D)蛋白质的二级结构；
(E)蛋白质的四级结构，如同构二聚体、异构三聚体等；
(F)与其它蛋白质的相似性；
(G)由于缺乏该蛋白质而引起的疾病；
(H)序列的矛盾、变化等。

（2）最小冗余

- 尽量将相关的数据归并，降低数据库的冗余程度。
- 如果不同来源的原始数据有矛盾，则在相应序列特征表中加以注释。

（3）与其它数据库的连接

•对于每一个登录项，有许多指向其它数据库相关数据的指针，这便于用户迅速得到相关的信息。

•现有的交叉索引有：

到EMBL核酸序列数据库的索引，

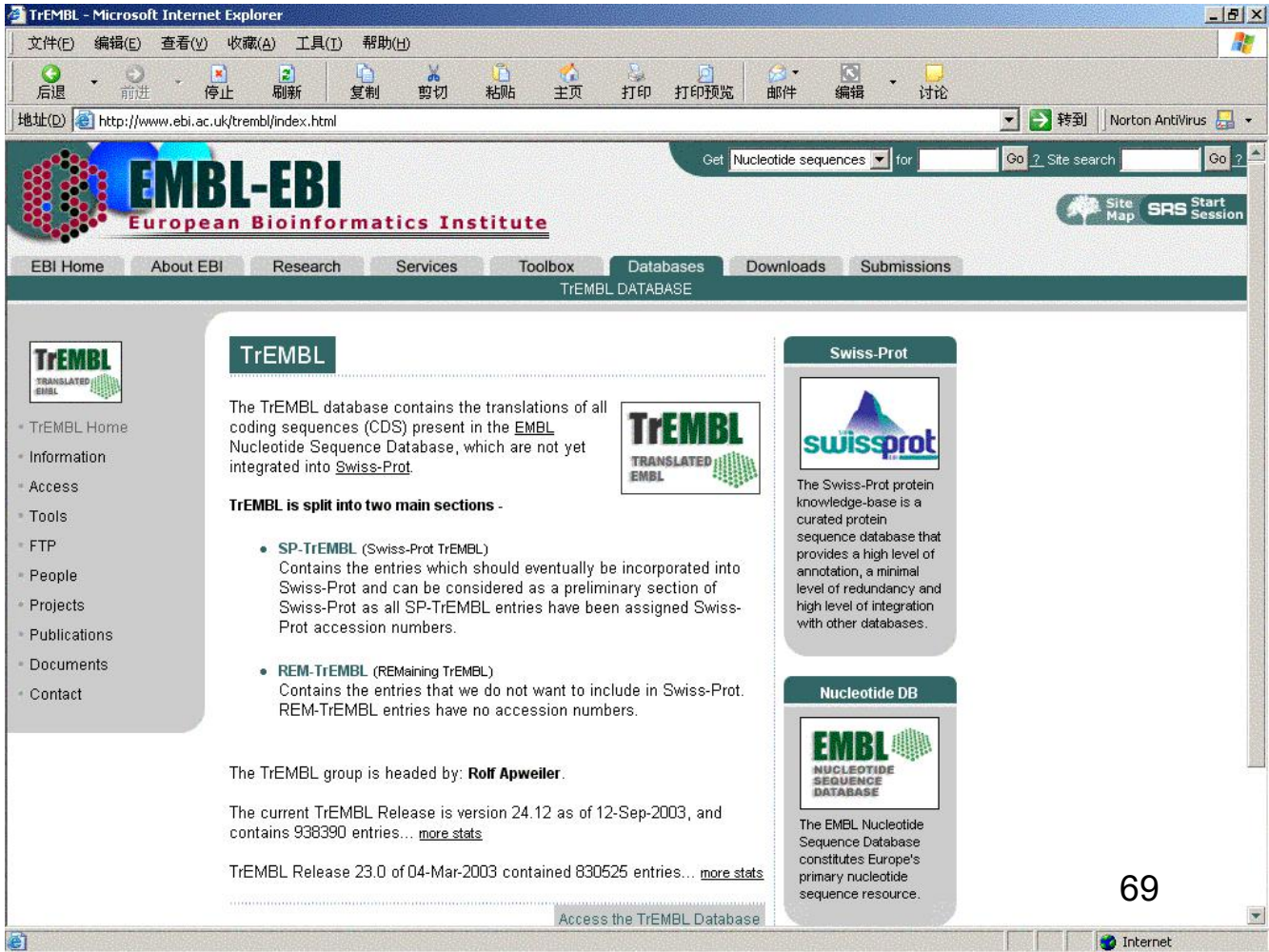
到PROSITE模式数据库的索引，

到生物大分子结构数据库PDB的索引等 。

TrEMBL (http://www.ebi.ac.uk/trembl/index.html) 是与SWISS-PROT相关的一个数据库。
包含从EMBL核酸数据库中根据编码序列(CDS)翻译而得到的蛋白质序列，并且这些序列尚未集成到SWISS-PROT数据库中。

TrEMBL有两个部分：
（1）SP-TrEMBL(SWISS-PROT TrEMBL)
包含最终将要集成到SWISS-PROT的数据，所有的SP-TrEMBL序列都已被赋予SWISS-PROT的登录号。

（2）REM-TrEMBL(REMaining TrEMBL)
包括所有不准备放入SWISS-PROT的数据，因此这部分数据都没有登录号。


TrEMBL - Microsoft Internet Explorer
文件(F) 编辑(E) 查看(V) 收藏(A) 工具(T) 帮助(H)
后退 前进 停止 刷新 复制 剪切 粘贴 主页 打印 打印预览 邮件 编辑 讨论
地址(D) http://www.ebi.ac.uk/trembl/index.html
转到 Norton AntiVirus
EMBL-EBI
European Bioinformatics Institute
Get Nucleotide sequences for Go ? Site search Go ?
Site Map SRS Start Session
EBI Home About EBI Research Services Toolbox Databases Downloads Submissions
TrEMBL DATABASE
TrEMBL
TrEMBL Home
Information
Access
Tools
FTP
People
Projects
Publications
Documents
Contact
TrEMBL
The TrEMBL database contains the translations of all coding sequences (CDS) present in the EMBL Nucleotide Sequence Database, which are not yet integrated into Swiss-Prot.
TrEMBL is split into two main sections -
SP-TrEMBL (Swiss-Prot TrEMBL)
Contains the entries which should eventually be incorporated into Swiss-Prot and can be considered as a preliminary section of Swiss-Prot as all SP-TrEMBL entries have been assigned Swiss-Prot accession numbers.
REM-TrEMBL (REMaining TrEMBL)
Contains the entries that we do not want to include in Swiss-Prot. REM-TrEMBL entries have no accession numbers.
The TrEMBL group is headed by: Rolf Apweiler.
The current TrEMBL Release is version 24.12 as of 12-Sep-2003, and contains 938390 entries... more stats
TrEMBL Release 23.0 of 04-Mar-2003 contained 830525 entries... more stats
Access the TrEMBL Database
Swiss-Prot
swissprot
The Swiss-Prot protein knowledge-base is a curated protein sequence database that provides a high level of annotation, a minimal level of redundancy and high level of integration with other databases.
Nucleotide DB
EMBL NUCLEOTIDE SEQUENCE DATABASE
The EMBL Nucleotide Sequence Database constitutes Europe's primary nucleotide sequence resource.
Internet

http://www.expasy.org/proteomics

UniProt › UniProtKB

Downloads · Contact · Documentation/Help

Search | Blast | Align | Retrieve | ID Mapping *

Search in: Protein Knowledgebase (UniProtKB)

Query: hbsag

Search | Advanced | Clear

1 - 25 of 2,396 results for **hbsag** in **UniProtKB** sorted by **score** descending

Download

Browse by taxonomy, keyword, gene ontology, enzyme class or pathway |

Reduce sequence redundancy to 100%, 90% or 50%

Page 1 of 96 | Next »

Results Customize

› Show only reviewed (86) (UniProtKB/Swiss-Prot) or unreviewed (2,310) (UniProtKB/TrEMBL) entries

› Did you mean bsag (4,791)?

› Restrict term "hbsag" to gene name (184), protein name (1,228), strain (5), taxonomy (5), tissue (5)

Entry	Entry name	Status	Protein names	Gene names	Organism	Length
P03138	HBSAG_HBVD3	★	**Large envelope protein**	S	Hepatitis B virus genotype D subtype ayw (isolate France/Tiollais/1979) (HBV-D)	389
P03141	HBSAG_HBVA3	★	**Large envelope protein**	S	Hepatitis B virus genotype A2 subtype adw2 (strain Rutter 1979) (HBV-A)	400
Q9E6S4	HBSAG_HBVC0	★	**Large envelope protein**	S	Hepatitis B virus genotype C (isolate Vietnam/3270/2000) (HBV-C)	400
P31869	HBSAG_HBVC2	★	**Large envelope protein**	S	Hepatitis B virus genotype C subtype ar (isolate Japan/S-207/1988) (HBV-C)	400
P03140	HBSAG_HBVC5	★	**Large envelope protein**	S	Hepatitis B virus genotype C subtype ad (isolate Japan/S-179/1988) (HBV-C)	400
P31873	HBSAG_HBVA1	★	**Large envelope protein**	S	Hepatitis B virus genotype A1 subtype adw2 (isolate Southern-Africa/Cai) (HBV-A)	400
Q91C35	HBSAG_HBVA6	★	**Large envelope protein**	S	Hepatitis B virus genotype A1 subtype adw2 (isolate South Africa/84/2001) (HBV-A)	389
O91534	HBSAG_HBVA7	★	**Large envelope protein**	S	Hepatitis B virus genotype A2 (isolate Japan/11D11HCCW/1998) (HBV-A)	400
Q9PWW3	HBSAG_HBVB5	★	**Large envelope protein**	S	Hepatitis B virus genotype B2 (isolate Vietnam/16091/1992) (HBV-B)	400
P31868	HBSAG_HBVC1	★	**Large envelope protein**	S	Hepatitis B virus genotype C subtype adr (isolate Japan/Nishioka/1983) (HBV-C)	400
Q913A6	HBSAG_HBVC7	★	**Large envelope protein**	S	Hepatitis B virus genotype C subtype ayw (isolate China/Tibet127/2002) (HBV-C)	400
Q81162	HBSAG_HBVC8	★	**Large envelope protein**	S	Hepatitis B virus genotype C subtype adr (isolate Japan/A4/1994) (HBV-C)	389
Q9QMI0	HBSAG_HBVD4	★	**Large envelope protein**	S	Hepatitis B virus genotype D subtype ayw (isolate Japan/JYW796/1988) (HBV-D)	389
Q998M2	HBSAG_HBVD5	★	**Large envelope protein**	S	Hepatitis B virus genotype D subtype ayw (isolate Australia/AustKW/1991) (HBV-D)	389
O92921	HBSAG_HBVD7	★	**Large envelope protein**	S	Hepatitis B virus genotype D (isolate Germany/1-91/1991) (HBV-D)	389
Q69603	HBSAG_HBVE1	★	**Large envelope protein**	S	Hepatitis B virus genotype E subtype ayw4 (isolate Kou) (HBV-E)	399
Q99HS3	HBSAG_HBVF3	★	**Large envelope protein**	S	Hepatitis B virus genotype F1 (isolate Argentina/sa11/2000) (HBV-F)	400

http://www.uniprot.org/uniprot/?query=hbsag&sort=score

- PIR (Protein Information Resource)
  - 国际蛋白质序列数据库，包含所有序列已知的自然界中野生型蛋白质信息。提供同源性和分类学组织的综合、非冗余的数据库。每周更新，每季度发行新版。
  - http://pir.georgetown.edu/
  - ftp://ftp.pir.georgetown.edu/pir_databases/
- UniProt
  - SWISS-PROT+TrEMBL+PIR
  - http://www.ebi.uniprot.org/
  - ftp://ftp.ebi.ac.uk/pub/databases/uniprot/

- **PIR(protein information resource)**

1. 由美国NCBI翻译自GenBank的DNA序列(1984年)；
2. 在EMBL和GenBank数据库上均建立了镜像站点；
3. 数据依据注释的质量分为4类。

网址： http://www-nbrf.georgetown.edu/

PIR数据库的分类情况(Release 51.03)

分类名称 (Name)	说明 (Comment)	记录数 (Number of entries)
PIR1	已分类、已注释 (Classified and annotated)	13572
PIR2	已注释(Annotated)	69368
PIR3	未核实(Unverified)	7508
PIR4	未翻译(Unencoded or untranslated)	196

PIR（Protein Information Resource）

- 目的：

  帮助研究者鉴别和解释蛋白质序列信息，

  研究分子进化、功能基因组。

- 它是一个全面的、经过注释的、非冗余的蛋白质序列数据库。

- 所有序列数据都经过整理，超过99%的序列已按蛋白质家族分类，一半以上还按蛋白质超家族进行了分类。

Protein Information Resource Home Page - Protein Sequence Database - iProClass - Microsoft Internet Explorer

文件(F) 编辑(E) 查看(V) 收藏(A) 工具(T) 帮助(H)

后退 前进 停止 刷新 复制 剪切 粘贴 主页 打印 打印预览 邮件 编辑 讨论

地址(D) http://www-nbrf.georgetown.edu/ 转到 Norton AntiVirus

pir.georgetown.edu

PIR Protein Information Resource

About PIR | Databases | Search and Retrieval | Download | Support

An Integrated Public Resource of Protein Informatics to Support Genomic and Proteomic Research and Scientific Discovery

PIR produces the **Protein Sequence Database (PSD)** of functionally annotated protein sequences, which grew out of the *Atlas of Protein Sequence and Structure* (1965-1978) edited by Margaret Dayhoff and has been incorporated into an integrated knowledge base system of value-added databases and analytical tools.

iProClass, a central point for exploration of protein information, provides summary descriptions of protein family, function and structure for PIR-PSD, Swiss-Prot, and TrEMBL sequences, with links to over 50 biological databases . Release 2.30, 8-Sep-2003, contains 1094,018 entries.

PIR-NREF, a comprehensive database for sequence searching and protein identification, contains non-redundant protein sequences from PIR-PSD, Swiss-Prot, TrEMBL, RefSeq, GenPept, and PDB. Release 1.30, 8-Sep-2003, contains 1,332,284 entries.

PIR News Flash

PIR featured in Georgetown Blue & Gray newsletter

Text Search Protein Databases: GO!

Find an Exact Peptide Match: GO!

Type in a string of single letter amino acid code (at least 3 letters)

PIR has recently joined forces with EBI (European Bioinformatics Institute) and SIB (Swiss Institute of Bioinformatics) to establish the UniProt (United Protein Databases), the central resource of protein sequence and function.

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3900 Reservoir Rd., NW, Box 571414, Washington, DC 20057-1414, USA
Phone: (202) 687-2121 Fax: (202) 687-1662
pirmail@georgetown.edu

Internet

除了蛋白质序列数据之外，PIR还包含以下信息：

(1)蛋白质名称、蛋白质的分类、蛋白质的来源；

(2)关于原始数据的参考文献；

(3)蛋白质功能和蛋白质的一般特征，包括基因表达、翻译后处理、活化等；

(4)序列中相关的位点、功能区域。

```
ENTRY          G00016  #type fragment
TITLE          FGF-receptor - common marmoset (fragment)
ORGANISM       #formal_name Callithrix jacchus #common_name common
               marmoset
DATE           13-Mar-1997 #sequence_revision 13-Mar-1997 #text_change
               18-Jul-1997
ACCESSIONS     G00016
REFERENCE      H00018
  #authors     Einspanier, R.
  #submission  submitted to the EMBL Data Library, December 1995
  #accession   G00016
    ##status preliminary; translated from GB/EMBL/DDBJ
    ##molecule_type mRNA
    ##residues 1-157 ##label EIN
    ##cross-references EMBL:Z68149; NID:g1279349
CLASSIFICATION #superfamily basic fibroblast growth factor receptor 1;
               immunoglobulin homology; protein kinase homology
FEATURES
  1-157        #domain protein kinase homology (fragment) #label
               KIN
SUMMARY        #length 157
SEQUENCE
             5         10         15         20         25         30
   1/E M E V M K M I G K H K N I I N L L G A C T Q D G P L Y V I
  31 V E Y A S K G N L R E Y L R A R R P P G M E Y S Y D I N R V
  61 P E E Q M T F K D L V S C T Y Q L A R A M E Y L A S Q K C I
  91 H R D L A A R N V L V T E N N V M K I A D F G L A R D I N N
 121 I D Y Y K K T T N G R L P V K W M A P E A L F D R V Y T H Q
 151 S D V W S F G/

Associated Alignments:
DA0934  protein kinase homology
DA1564  immunoglobulin homology - C2 type
DA1565  immunoglobulin homology - V-type, Ig V regions
FA1349  basic fibroblast growth factor receptor 1 - 555.0 1.0
MO6341  basic fibroblast growth factor receptor 1 - 524.0 1.0

Related Links (Superfamily classification and Alignment):
Protein Classification for Entry=G00016 at MIPS, Germany.
ProClass for Entry=G00016 at Univ. of Texas, USA.
```

图4.4 PIR文件实例

PIR提供三种类型的检索服务：

一是基于文本的交互式查询，用户通过关键字进行数据查询。

二是标准的序列相似性搜索，包括BLAST、FastA等。

三是结合序列相似性、注释信息和蛋白质家族信息的高级搜索，包括按注释分类的相似性搜索、结构域搜索等。

http://pir.georgetown.edu/iproclass/

http://pir.georgetown.edu/pirwww/dbinfo/uniprot.shtml

- PROSITE
  - 由专家审编的SWISS-PROT蛋白质序列中有生物意义的sites、patterns和profiles的数据库，可帮助确定新的蛋白质序列是否属于已知的家族。提供PrositeScan服务器搜索PROSITE库。
  - http://www.expasy.ch/prosite/
  - ftp://au.expasy.org/databases/prosite/
- ENZYME
  - 基于命名系统的酶数据库。可按酶的EC号、分类、学名和俗名、化合物、辅助因子等查询。每个条目下列出所催化的反应和酶的来源、功能等，并提供到其它数据库、MEDLINE和代谢途径图的链接。
  - http://au.expasy.org/enzyme/
  - ftp://au.expasy.org/databases/enzyme/

ExPASy Bioinformatics Resource Portal

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PROSITE

Home ScanProsite ProRule Documents Downloads Links Funding

Database of protein domains, families and functional sites

PROSITE consists of documentation entries describing protein domains, families and functional sites as well as associated patterns and profiles to identify them [More details / References / Commercial users].
PROSITE is complemented by **ProRule**, a collection of rules based on profiles and patterns, which increases the discriminatory power of profiles and patterns by providing additional information about functionally and/or structurally critical amino acids [More details].

Release 20.76, of 17-Oct-2011 (1627 documentation entries, 1308 patterns, 946 profiles and 944 ProRule)

PROSITE access

e.g: PDOC00022, PS50089, SH3, zinc finger

Search

add wildcard '*'

Browse:

- by documentation entry
- by ProRule description
- by taxonomic scope
- by number of positive hit

PROSITE tools

Scan a sequence against PROSITE patterns and profiles - quick scan

(Output includes graphical view and feature detection)

- **ScanProsite** - advanced scan
- **PRATT** - allows to interactively generate conserved patterns from a series of unaligned proteins.
- **MyDomains - Image Creator** new - allows to generate custom domain figures.

Enter your sequence or a UniProtKB (Swiss-Prot or TrEMBL) ID or AC [help]:

Scan Clear

exclude patterns with a high probability of occurrence

http://prosite.expasy.org/

http://enzyme.expasy.org/

4. 蛋白质结构数据库

显示分子结构（RasMol， ChemView ）

RasMol :Molecular Visualization Freeware for proteins, dna and macromolecules.

蛋白质结构数据库

- PDB
  - 蛋白质结构数据库，搜集由X射线衍射和核磁共振实验测定的生物大分子三维结构数据。
  - http://www.rcsb.org/pdb/
  - ftp://ftp.rcsb.org/pub/pdb/
- NRL-3D(The NRL-3D database has been replaced with PDB.)
  - 三维结构已经确定的蛋白质序列库，可以将新蛋白序列与库中序列比较，以判断是否与结构已知的蛋白质相似。
  - http://pir.georgetown.edu/pirwww/dbinfo/nrl3d.html
  - ftp://ftp.pir.georgetown.edu/pir_databases/other_databases/nrl_3d/

http://www.pdb.org/pdb/home/home.do

PDB（protein data bank）

⑴ 目前最主要的蛋白质分子结构数据库；

⑵ 1970年代建立，美国Brookhaven国家实验室维护管理;

⑶ 1988年，由美国RCSB(research collaboratory for structural biology)管理；

⑷ 以文本格式存放数据，包括原子坐标、物种来源、测定方法、提交者信息、一级结构、二级结构等；

⑸ PDBsum数据库：PDB注释信息综合数据库，具有检索、分析、可视化的功能。

PDB的网址：http://www.rcsb.org/pdb(美国)

PDBsum的网址：http://www.biochem.ucl.ac.uk/bsm/pdbsum

PDB（Protein Data Bank）

PDB中含有通过实验（X射线晶体衍射，核磁共振NMR）测定的生物大分子的三维结构

- 蛋白质
- 核酸
- 糖类
- 其它复合物

- **隐式序列信息（ implicit sequence ）**

  PDB的隐式序列即为立体化学数据，包括每个原子的名称和原子的三维坐标。

- **显式序列信息（explicit sequence）**

  在PDB文件中，以关键字SEQRES作为显式序列标记，以该关键字打头的每一行都是关于序列的信息。

http://www.rcsb.org/pdb/home/home.do

RCSB PDB PROTEIN DATA BANK

A MEMBER OF THE PDB

An Information Portal to Biological Macromolecular Structures

As of Tuesday Oct 05, 2010 at 5 PM PDT there are 68421 Structures | PDB Statistics

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PDB ID or Text | Search | Advanced Search

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- Sitemap
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- Electron Microscopy
- X-ray | NMR
- Validation Server
- BioSync Beamline
- Related Tools

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- Advanced Search
- Latest Release
- New Structure Papers
- Sequence Search
- Chemical Components
- Unreleased Entries
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Tools Hide
- File Downloads
- Compare Structures
- FTP Services
- File Formats
- Services: RESTful | SOAP
- Widgets

A Resource for Studying Biological Macromolecules

The PDB archive contains information about experimentally-determined structures of proteins, nucleic acids, and complex assemblies. As a member of the wwPDB, the RCSB PDB curates and annotates PDB data according to agreed upon standards.

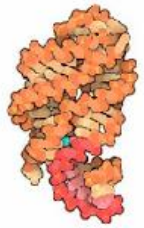
The RCSB PDB also provides a variety of tools and resources. Users can perform simple and advanced searches based on annotations relating to sequence, structure and function. These molecules are visualized, downloaded, and analyzed by users who range from students to specialized scientists.

Hide Welcome Message

Featured Molecules (MotM Category View / Previous Features: MotM | PSI) Hide

Structural View of Biology

Protein Synthesis



Molecule of the Month:
Riboswitches

Why use two or more molecules when one will do? In our own cells, protein synthesis is controlled by thousands of regulatory proteins, which work together to decide when a particular protein will be made. Bacteria are masters of economy, however, and in some cases, they have figured out a way for messenger RNA to control itself, without the need for help by proteins.

Full Article...

Protein Structure Initiative Featured Molecule:
Alpha and beta barrels

Analysis of the metabolic network of the bacterium Thermatoga maritima reveals the evolution of enzyme folding and function.

Full Article | PSI Structural Biology Knowledgebase

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PDB*Mobile*: Save MyPDB Queries

Latest features released:

Website Release Archive:

RCSB PDB News Hide

Weekly | Quarterly | Yearly

2010-10-05

Latest Website Release

New and enhanced features are available, including improved navigation of the Molecule of the Month archive, PDBMobile for the iPhone, and new ways to explore search results using data distribution summaries.

- Poster Prize Awarded at ECM
- Analyze small molecule interactions in the PDB with Ligand Explorer
- Redesigned BioSync
- Exploring Search Results

wwPDB News Hide

Statement on Retraction of PDB Entries

2010-10-05

Announcement: Chemical Shift Data Required for NMR Depositions Starting December 6, 2010

- Upcoming Meeting: PDB Symposium at ACS

● 转录因子数据库

RANSFAChttp://transfac.gbf.de

ooTFDhttp://www.ifti.org

● 基因分类数据库

Gene Ontology (GO)http://www.geneontology.org

● 酶、代谢和调控路径数据库

KEGG http://www.genome.ad.jp/kegg/

Enzyme Nomenclature Database

http://expasy.hcuge.ch/sprot/enzyme.html

Protein Kinase Resource (PKR)

http://www.sdsc.edu/kinases/

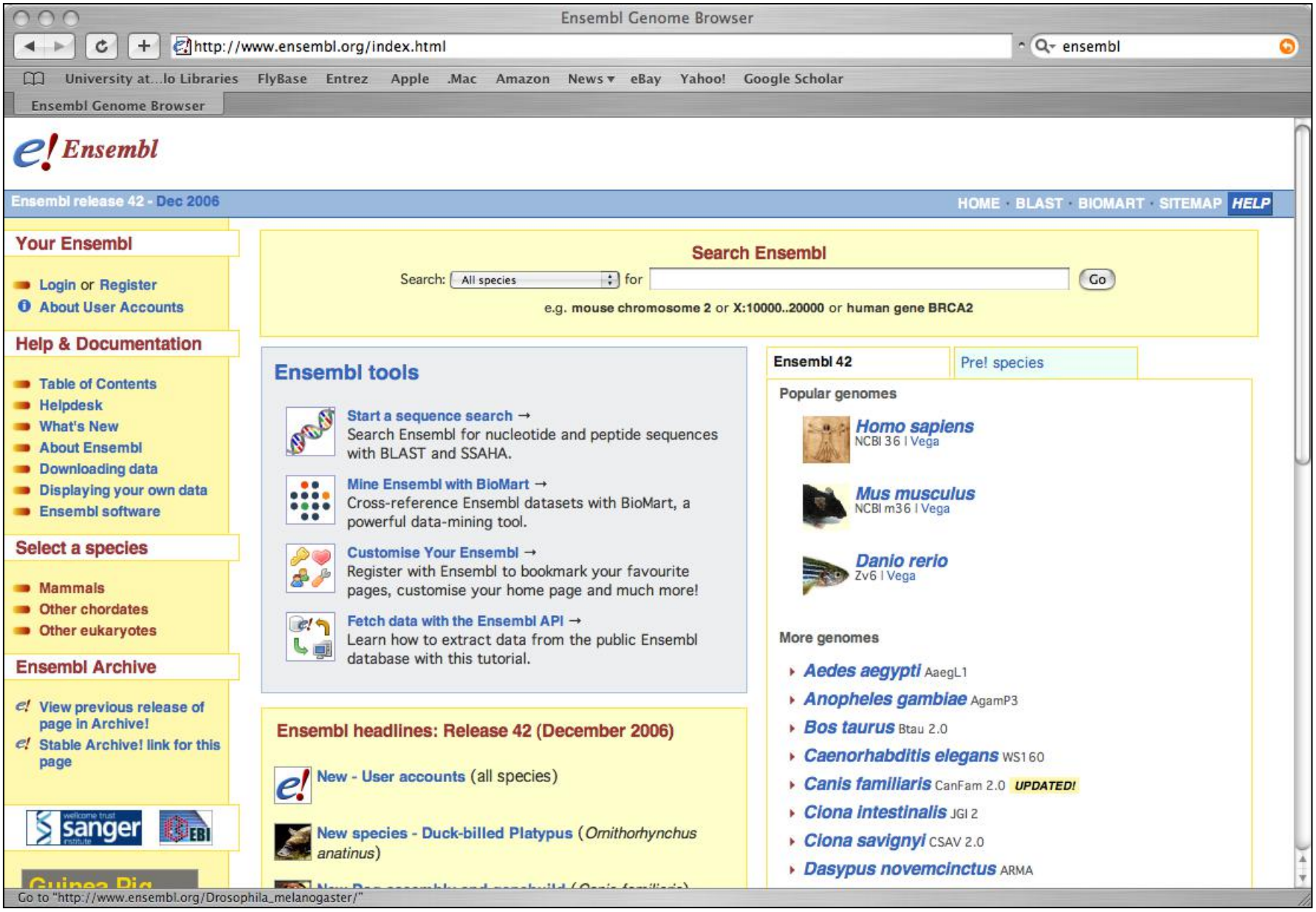
● RNA数据库

miRBase http://www.mirbase.org/

mirna database http://mirnadatabase.com/

lncRNAdb http://www.lncrna.org/Help.aspx

Ensembl


Ensembl Genome Browser
http://www.ensembl.org/index.html
ensembl
University at...lo Libraries FlyBase Entrez Apple .Mac Amazon News eBay Yahoo! Google Scholar
Ensembl Genome Browser
e! Ensembl
Ensembl release 42 - Dec 2006
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Downloading data
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Mammals
Other chordates
Other eukaryotes
Ensembl Archive
View previous release of page in Archive!
Stable Archive! link for this page
Search Ensembl
Search: All species for Go
e.g. mouse chromosome 2 or X:10000..20000 or human gene BRCA2
Ensembl tools
Start a sequence search →
Search Ensembl for nucleotide and peptide sequences with BLAST and SSAHA.
Mine Ensembl with BioMart →
Cross-reference Ensembl datasets with BioMart, a powerful data-mining tool.
Customise Your Ensembl →
Register with Ensembl to bookmark your favourite pages, customise your home page and much more!
Fetch data with the Ensembl API →
Learn how to extract data from the public Ensembl database with this tutorial.
Ensembl headlines: Release 42 (December 2006)
New - User accounts (all species)
New species - Duck-billed Platypus (Ornithorhynchus anatinus)
Ensembl 42
Pre! species
Popular genomes
Homo sapiens
NCBI 36 | Vega
Mus musculus
NCBI m36 | Vega
Danio rerio
Zv6 | Vega
More genomes
Aedes aegypti AaegL1
Anopheles gambiae AgamP3
Bos taurus Btau 2.0
Caenorhabditis elegans WS160
Canis familiaris CanFam 2.0 UPDATED!
Ciona intestinalis JGI 2
Ciona savignyi CSAV 2.0
Dasypus novemcinctus ARMA
Go to "http://www.ensembl.org/Drosophila_melanogaster/"

KEGG Pathway database

- http://www.genome.jp/kegg/pathway.html
- Breakdown into major categories:
  - metabolism (the most important one),
  - genetic information processing (including protein folding and sorting),
  - environmental information processing (including membrane transport and intracellular signaling),
  - cellular processes,
  - plus some others
- Broken down into subcategories, e.g. carbohydrate metabolism, and then into individual pathways, e.g. glycolysis/gluconeogenesis
  - (http://www.genome.jp/kegg/pathway/map/map00010.html)

Omics databases