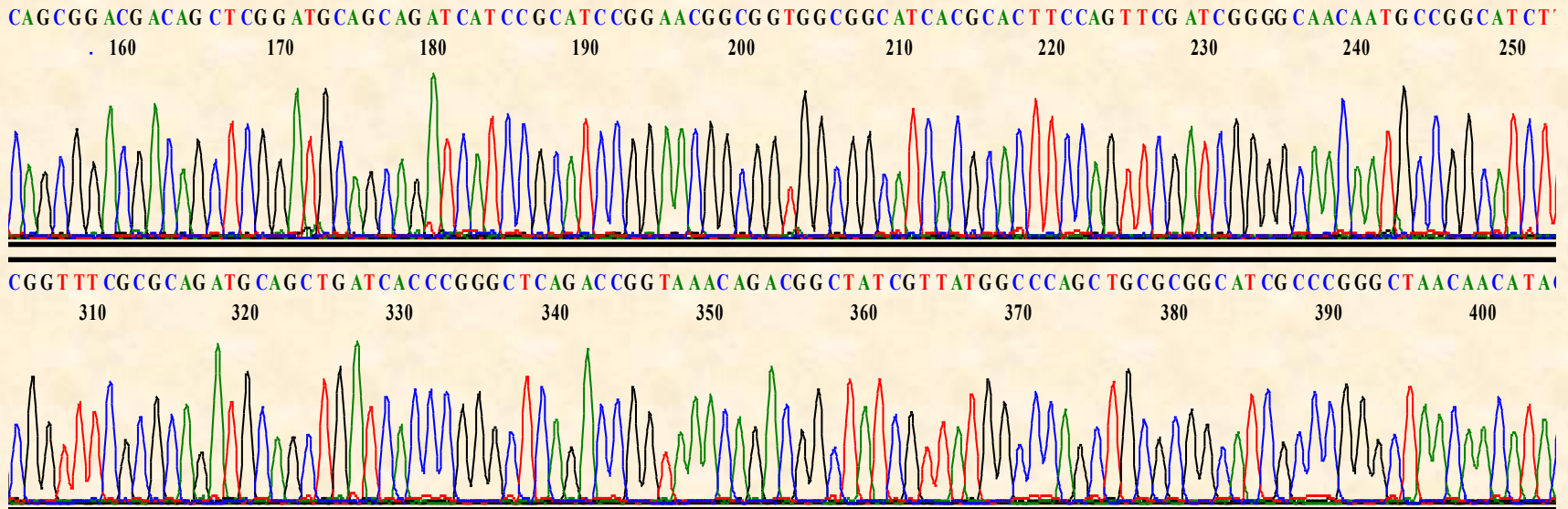


Molekulárně biologické databáze

Pro zajímavost...

Důležité...

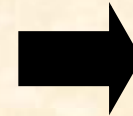
Molekulárně biologická data



GATAGCGTAATGATCGGCTGGCTGCCGCATTTTCATGCTGGTTTCCCAACGAAAAATAACCGCTCACGGTGCCATCACGATCGCACACCGCAAATCGGCGG
TACAGGTGGTCGCGCCCGCCGACACATCGCTGCGCCAATAATGATCTTTCAGCGGACGACAGCTCGGATGCAGCAGATCATCCGCATCCGGAACGGC
GGTGGCGGCATCACGCACCTCCAGTTCGATCGGGGCAACAATGCCGGCATCTTTCAGGGCAAAGCGAATAAACAGCACGCTCACTTCCGCGGCAGCGCC
AGCGCGGTTTCGCGCAGATGCAGCTGATCACCCGGGCTCAGACCGGTAAACAGACGGCTATCGTTATGGCCAGCTGCGCGGCATCGCCCGGGCTAAACA
CATACAGGTGGCGACCATCAATCACGGTCGGGGCGCCGGATCACGGCTGGCTTCCGGATAGGCGCTCAGCAGGGTAACGGCATCCACAATCACCAGCAT

Molekulárně biologická data

MALDI-TOF



Identifikace proteinů



Sekvenace proteinů

MDRNGNFSLPPNTAFKAIIFYANAADRQDLK

LFIDDAPEPAATFVGNSEEDGVRLFTLNSKG

GKIRIEASANGRQSATDARLAPLSAGDTVW

LGWLGAEDGADADYNDGIVILQWPIT

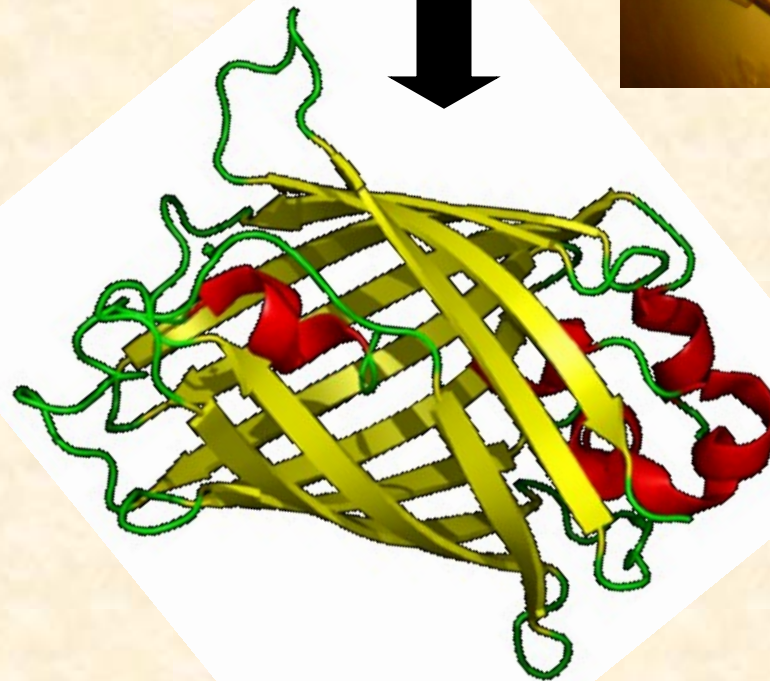
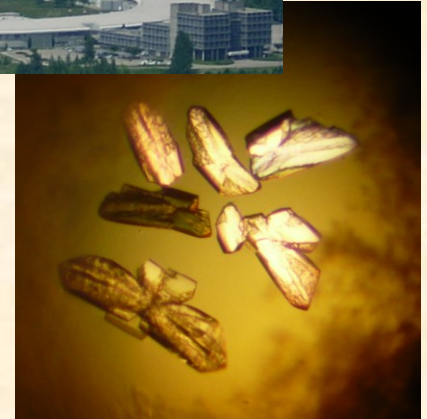
Molekulárně biologická data



NMR spektroskopie



Proteinová
krystalografie



Molekulárně biologická data

- **Výkonné technologie:**

Automatické sekvencování

MALDI-TOF

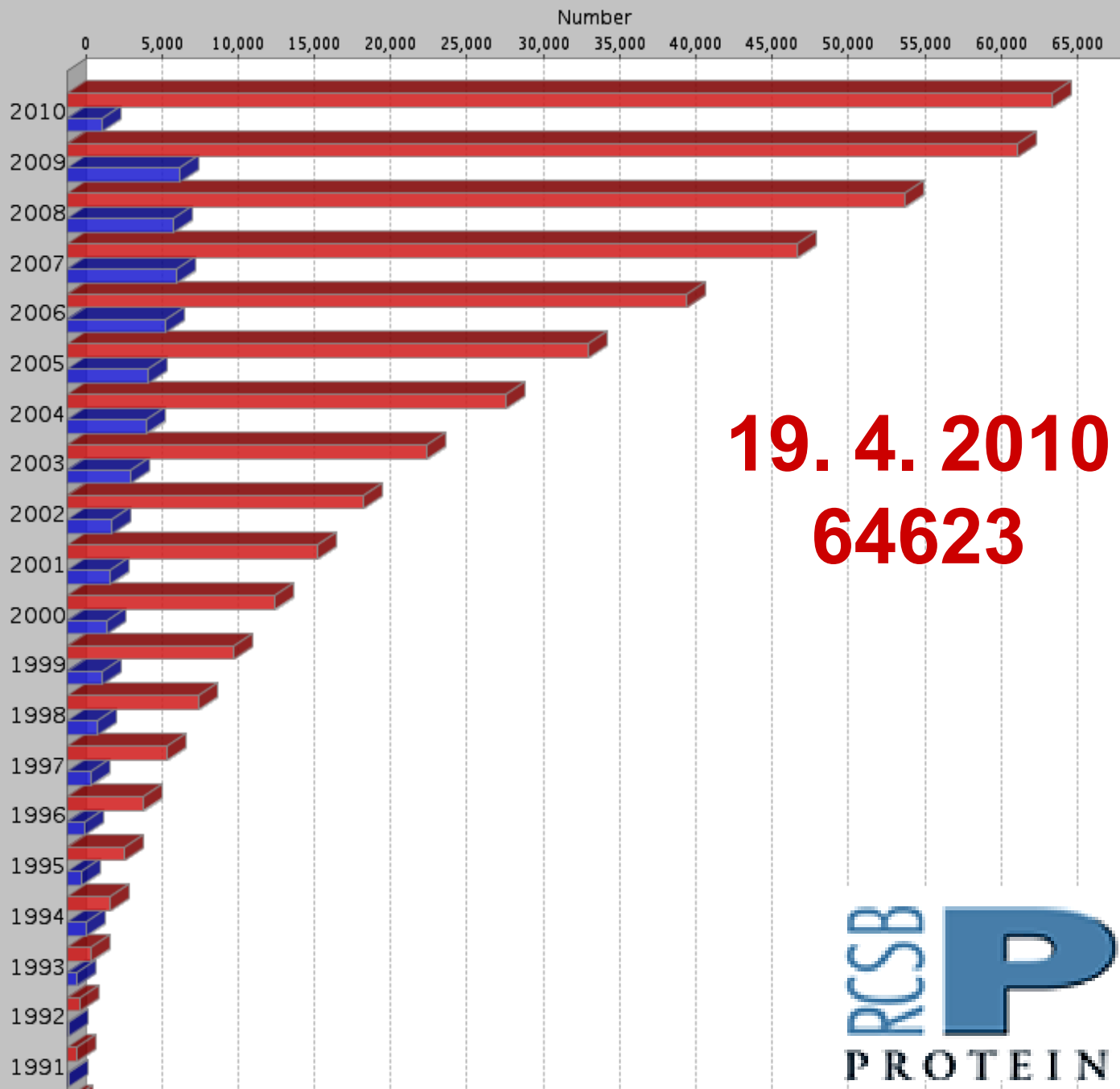
NMR spektroskopie

Proteinová krystalografie

Výrazný nárůst množství biologických dat.

Yearly Growth of Total Structures

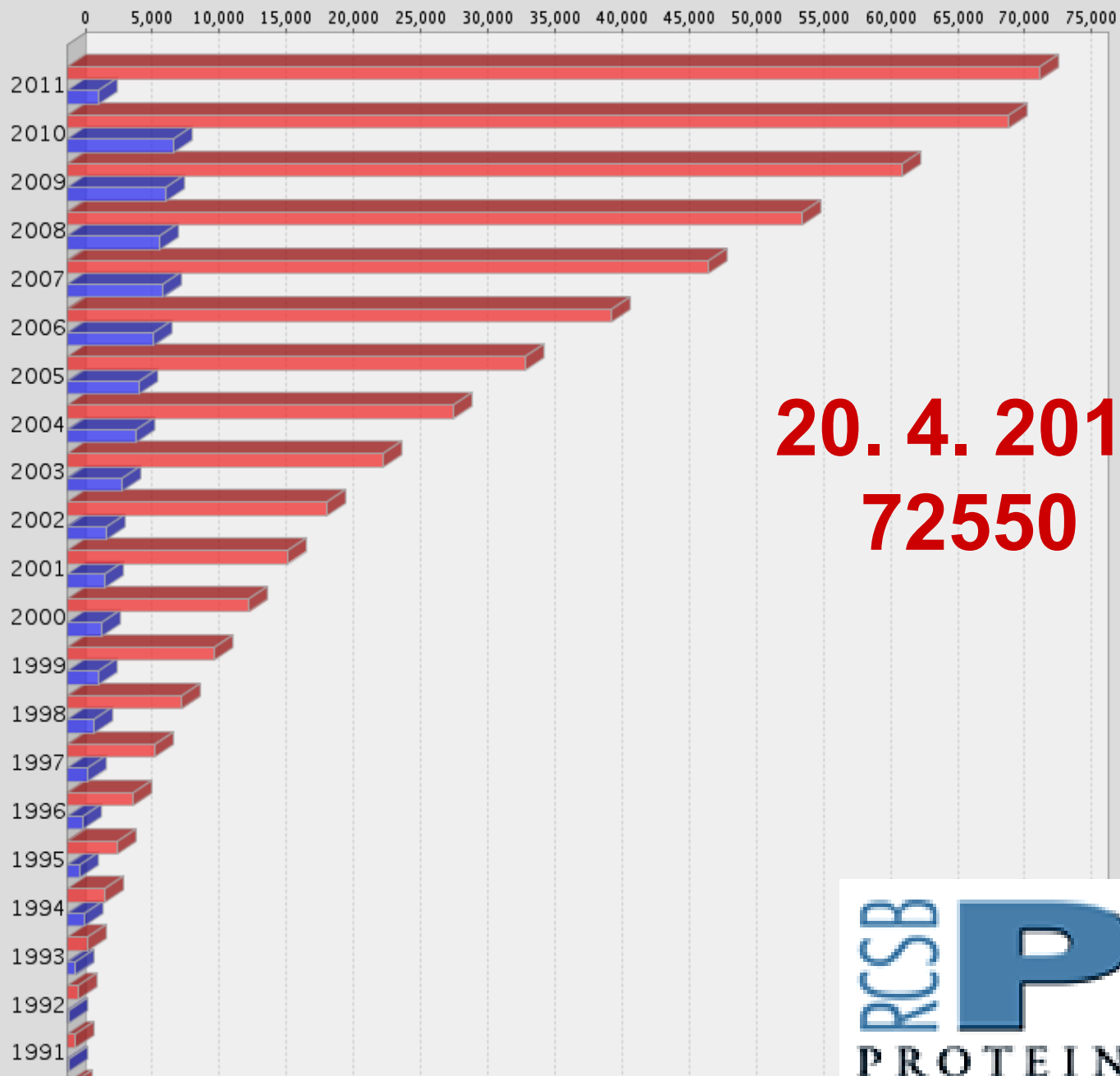
number of structures can be viewed by hovering mouse over the bar



Yearly Growth of Total Structures

number of structures can be viewed by hovering mouse over the bar

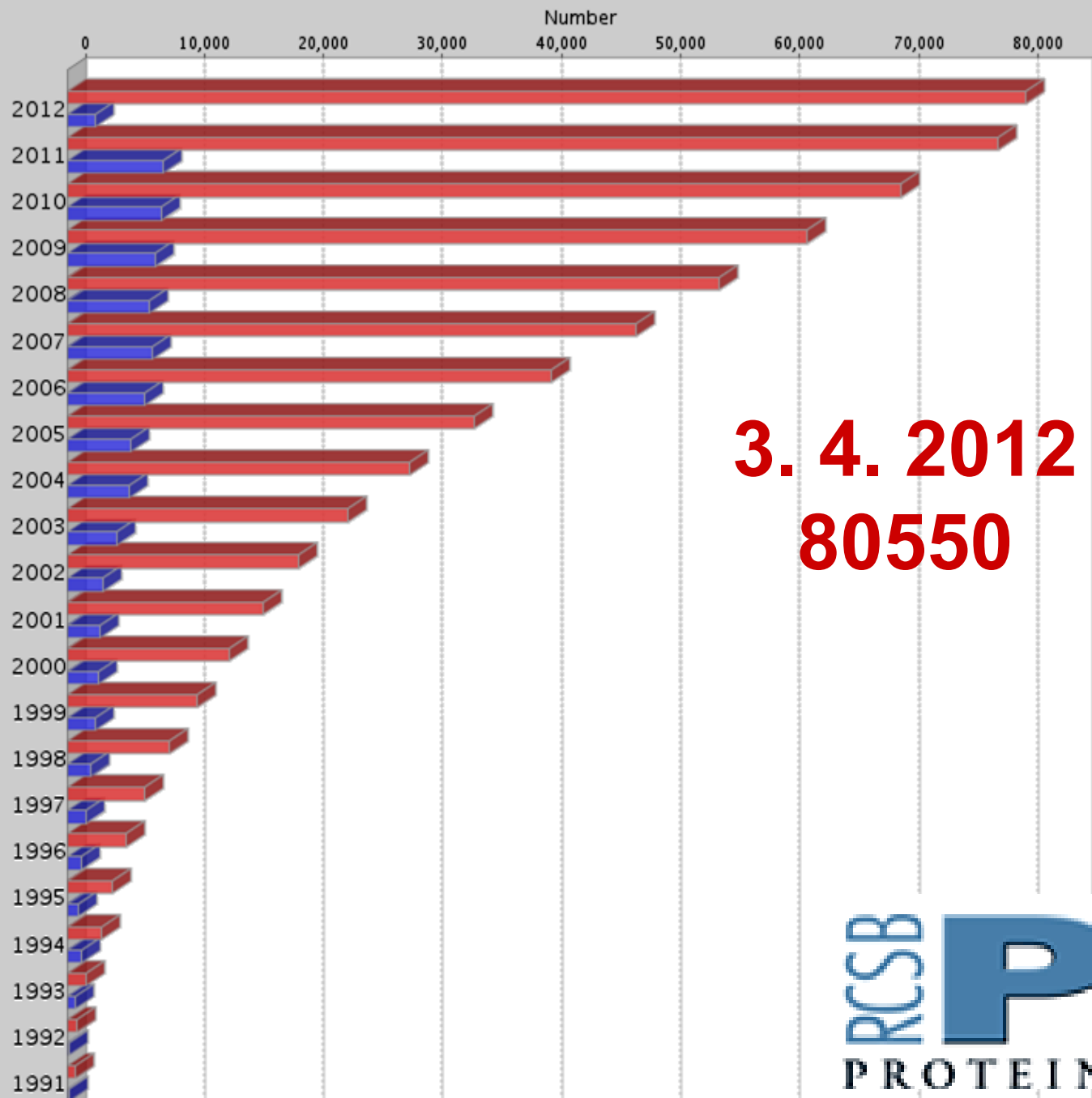
Number



20. 4. 2011
72550

Yearly Growth of Total Structures

number of structures can be viewed by hovering mouse over the bar



3. 4. 2012
80550

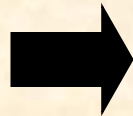
Éra reverzní genetiky

Klasická genetika



GATAGCGTAATGATCGGCTGGCTGCCGATTTT
TACAGGTGGTCGCGCCCGCCAGCACATCGC
GGTGGCGGCATCACGCACTTCCAGTTCGATCGC
AGCGCGGTTTCGCGCAGATGCAGCTGATCACCC

Fenotyp



Genotyp

Éra reverzní genetiky

Klasická genetik



GATAGCGTAATGATCGGCTGGCTGCCGCATTTTC
TACAGGTGGTCGCGCCCGCCGCCAGCACATCGC
GGTGGCGGCATCACGCACTTCCAGTTCGATCGC
AGCGCGGTTTCGCGCAGATGCAGCTGATCACCC

Fenotyp



Genotyp

Reverzní genetik

Automatické DNA
sekvencování



Produkce velkého
množství dat

GATAGCGTAATGATCGGCTGGCTGCCGCAT
TACAGGTGGTCGCGCCCGCCGCCAGCACAT



Genotyp



Fenotyp

Molekulárně biologická data

- **Nutnost organizovaného ukládání a skladování dat.**



Databáze je určitá uspořádaná množina informací (dat) uložená na paměťovém médiu.

Molekulárně biologická data

- **Nutnost organizovaného ukládání a skladování dat.**
- **Nutnost prohlížení a analyzování uložených dat.**



Databáze je určitá uspořádaná množina informací (dat) uložená na paměťovém médiu.

V širším smyslu jsou součástí databáze i softwarové prostředky, které umožňují manipulaci s uloženými daty a přístup k nim.

Analytické nástroje

- **Vyhledávací software**

Nutnost snadného, rychlého a specifického vyhledání informací.

- **Srovnávání dat (sekvencí)**

Sequence alignment – „seřazení“ sekvencí.

```
LPPNTAFKAI FYANAADRQDLKLFIDDAPEPAATFVGNSEDGVRL--FTLNSKGGKIRIE
IPPNTDFRAIFFANAAEQQHIKLFIGDSQEPAA YHKL TTRDGP RE--ATLNSGNGKIRFE
LPPHIKFGVTALTHAANDQTIDIYIDDDPKPAATFKGAGA QDQNLG TKVLD SGN GRV RVI
LPPNIAFGVTALVNSSAPQTIEVFVDDNPKPAATFQGAGTQ DANLNTQIVNSGKGKVRVV
lPPn-aFg---lanaad-QtiklfidD-p-PAAtfkgag-----l-t-tlnSgnGkiRve
```

```
ASANGRQSATDARLAPLSAGD-----TVWLGWLGAE DGADADYNDGIVILQWPIT
VSVNGKPSATDARLAPINGKKS DGSPFTVNF GIVVSE DGHDSDYNDGIVVLQWPIG
VMANGRPSRLGSRQVDIFKKS-----YFGIIGSE DGADDDYNDGIVFLNWPLG
VTANGKPSKIGSRQVDIFKKT-----YFGLVGS EDGGDGDYNDGIAILNWPLG
vsanGrpSat--R---ifkks-----tvyfGivgsEDGaDaDYNDGiviLqWPig
```

Rozdělení molekulárně biologických databází

- **Databáze:**

Primární

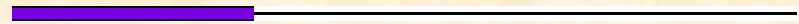
Sekundární

Strukturní

```
EDRPIKFSTEGATSQSYKQFIEALRERLRGGLIHDIPVLPDPTTLQERNRYIT
VELSNSDTESEIEVGIDVTNAYVVAYRAGTQSYFLRDAPSSASDYLFVTGTDQHS
LPFYGTYGDLERWAHQSRQQIPLGLQALTHGISFFRSGGNDNEEKARTLIVII
QMVAEAARFRYISNRVRVSIQTGTAFQPDAAAMISLENNWDNLSRGVQESVQDT
FPNQVTLTNIRNEPVIVDSLHPTVAVLALMLFVCNPPNIVEKSKICSSRYEP
TVRIGGRDGMCDVVDNGYHNGNRIIMWKCKDRLEENQLWTLKSDKTIRSNGK
```



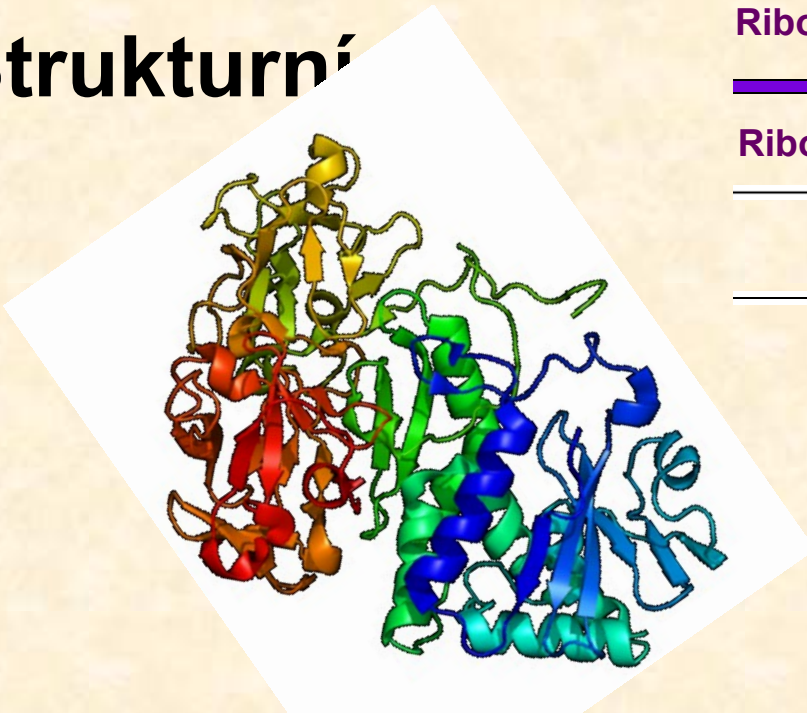
Ribosome-inactivating protein, subdomain 1



Ribosome-inactivating protein, subdomain 2



Ricin B-like lectins



Rozdělení molekulárně biologických databází

- **Databáze:**

Primární

Sekundární

Strukturní

```
EDRPIKFSTEGATSQSYKQFIEALRERLRGGLIHDIPVLPDPTTLQERNRYIT  
VELSNSDTESEIEVGIDVTNAYVVAYRAGTQSYFLRDAPSSASDYLFTGTDQHS  
LPFYGTYGDLERWAHQSRQQIPLGLQALTHGISFFRSGGNDNEEKARTLIVII  
QMVAEAARFRYISNRVRSIQGTAFQPDAAAMISLENNWDNLSRGVQESVQDT  
FPNQVTLTNIRNEPVIVDSL SHPTVAVLALMLFVCNPPNIVEKSKICSSRYEP  
TVRIGGRDGMCDVVDNGYHNGNRIIMWKCKDRLEENQLWTLKSDKTIRSNGK
```

**Primární databáze obsahují anotované sekvence
NA nebo proteinů.**

Rozdělení molekulárně biologických databází

- **Databáze:**
 - Primární**
 - Sekundární**
 - Strukturní**

```
EDRPIKFSTEGATSQSYKQFIEALRERLRGGLIHDIPVLPDPTTLQERNRYIT  
VELSNSDTESEIEVGIDVTNAYVVAYRAGTQSYFLRDAPSSASDYLFRTGTDQHS  
LPFYGTYGDLERWAHQSRQQIPLGLQALTHGISFFRSGGNDNEEKARTLIVII  
QMVAEAAARFRYISNRVRVSIQTGTAFQPDAAAMISLENNWDNLSRGVQESVQDT  
FPNQVTLTNIRNEPVIVDSLHPTVAVLALMLFVCNPPNIVEKSKICSSRYEP  
TVRIGGRDGMCDVVDNGYHNGNRIIMWKCKDRLEENQLWTLKSDKTIRSNGK
```



Ribosome-inactivating protein, subdomain 1



Ribosome-inactivating protein, subdomain 2



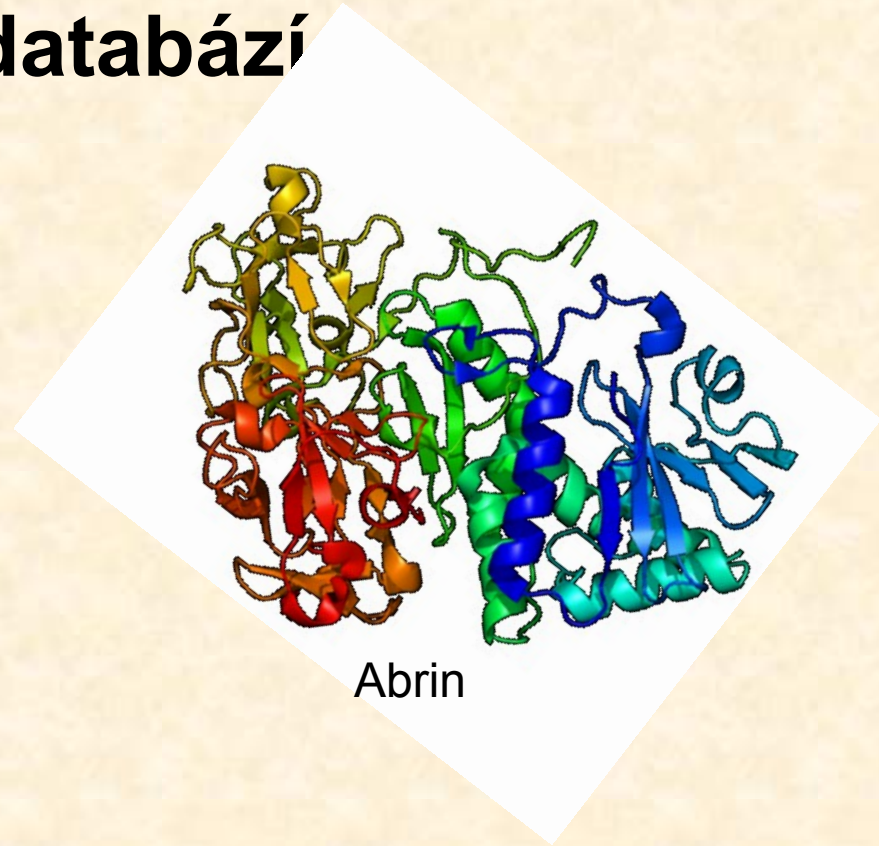
Ricin B-like lectins



Sekundární databáze obsahují informace odvozené z primárních databází ve formě charakteristických vzorů sekvencí, tj. funkčních nebo strukturních motivů získaných srovnáním primárních dat (sekvencí).

Rozdělení molekulárně biologických databází

- **Databáze:**
Primární
Sekundární
Strukturní

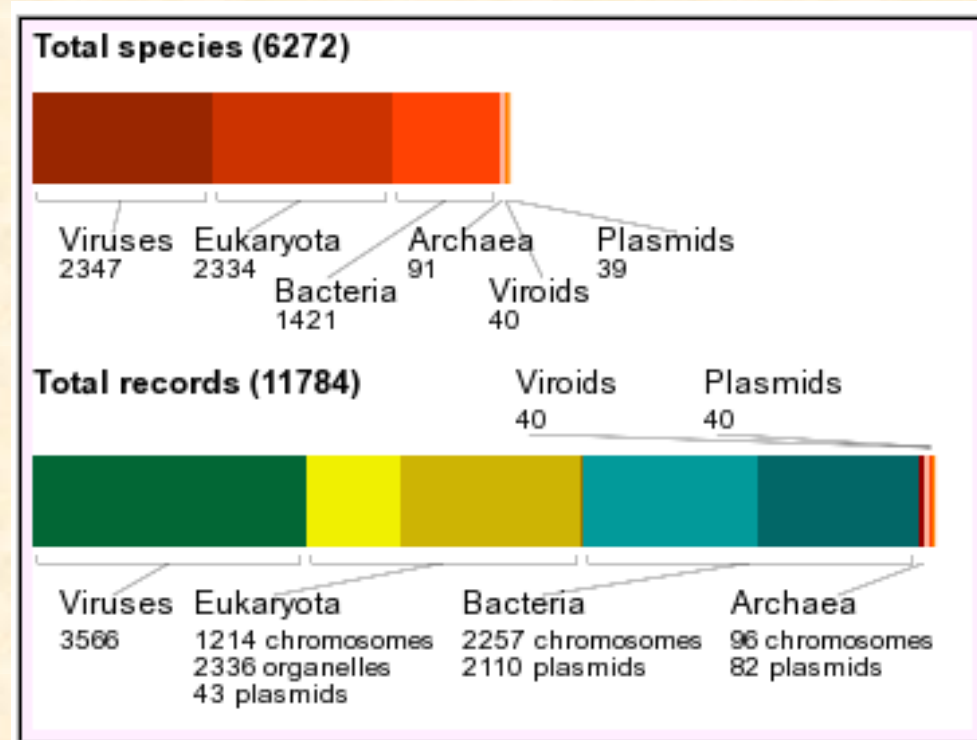


**Obsahují struktury proteinů (nukleových kyselin)
a jejich anotace.**

Rozdělení molekulárně biologických databází

- **Databáze:**
 - Primární
 - Sekundární
 - Strukturní

Genomové zdroje



Rozdělení molekulárně biologických databází

- **Databáze:**
Specializované
Univerzální

Rozdělení molekulárně biologických databází

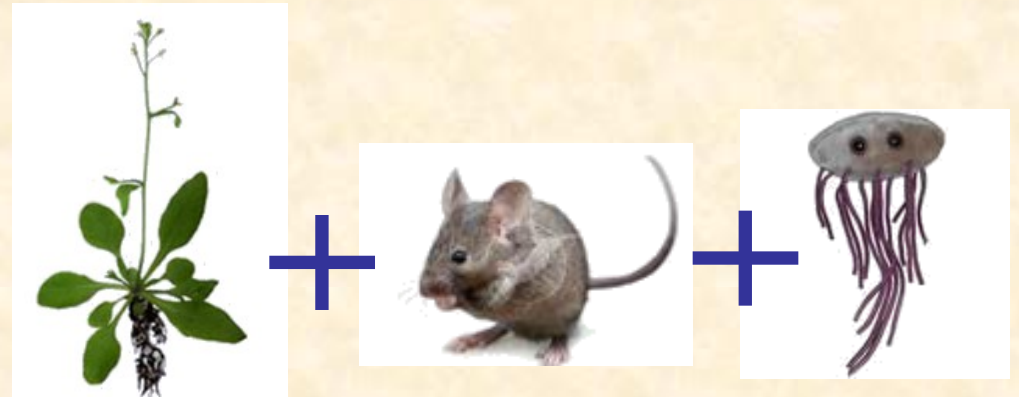
- **Databáze:**
Specializované
Univerzální



Specializované databáze obsahují informace o určité proteinové rodině nebo skupině proteinů, případně o určitém organismu.

Rozdělení molekulárně biologických databází

- **Databáze:**
Specializované
Univerzální



Univerzální databáze obsahují informace o proteinech (NA) ze všech organismů.

Rozdělení univerzálních proteinových databází

- **Univerzální databáze:**

„Skladiště“ sekvencí – sequence repository

„Manuálně“ spravovaná – curated database

Rozdělení univerzálních proteinových databází

- **„Skladiště“ sekvencí – sequence repository**

Kromě sekvencí obsahují málo nebo žádné dodatečné informace.

Záznamy generovány automaticky.

Proteiny mohou být zastoupeny několika různými záznamy (sekvencemi) = „nadbytečnost“ (redundance) sekvencí.

Rozdělení univerzálních proteinových databází

- **Manuálně spravované – curated databases**

Záznamy obsahují dodatečné informace.

Informace jsou před vložením do databáze validovány experty.

Všechny záznamy o stejné proteinové sekvenci jsou sdružovány do jediného = non-redundant dataset.

Rozdělení molekulárně biologických databází

- **Databáze:**

Primární

Sekundární

Strukturní

Genomové zdroje

Složené databáze

Složené databáze

- **Složené (composite) databáze:**

Slučují data z několika primárních databází.

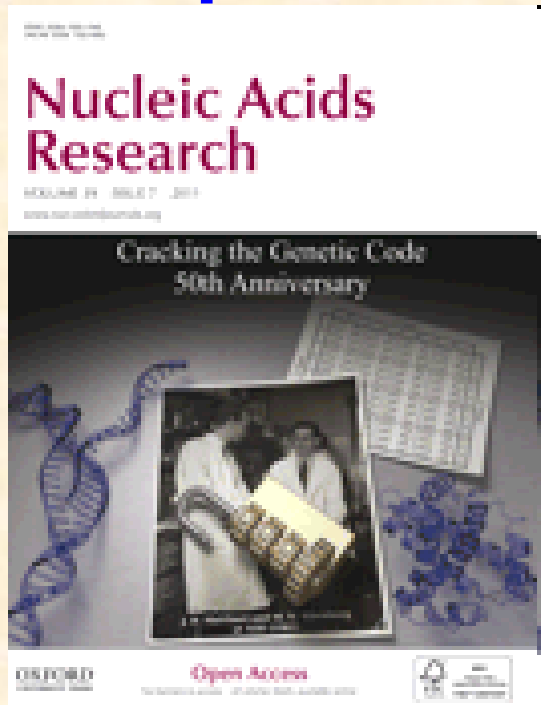
Eliminace redundantních dat.

Různá priorita zdrojových databází podle kvality validace a anotace (eliminace redundantních dat z databáze s nižší prioritou).

Molekulárně biologické databáze

Nucleic Acids Research

<http://www3.oup.co.uk/nar/database/a/>



[Nucleotide Sequence Databases](#)
[International Nucleotide Sequence Database Collaboration](#)
[Coding and non-coding DNA](#)
[Gene structure, introns and exons, splice sites](#)
[Transcriptional regulator sites and transcription factors](#)
[RNA sequence databases](#)
[Protein sequence databases](#)
[Structure Databases](#)

[Genomics Databases \(non-vertebrate\)](#)
[Metabolic and Signaling Pathways](#)
[Human and other Vertebrate Genomes](#)
[Human Genes and Diseases](#)
[Microarray Data and other Gene Expression Databases](#)
[Proteomics Resources](#)
[Other Molecular Biology Databases](#)
[Organelle databases](#)
[Plant databases](#)
[Immunological databases](#)

2011: 1330 databází

Molekulárně biologické databáze

Nucleic Acids Research

<http://www3.oup.co.uk/nar/database/a/>



[Nucleotide Sequence Databases](#)
[International Nucleotide Sequence Database Collaboration](#)
[Coding and non-coding DNA](#)
[Gene structure, introns and exons, splice sites](#)
[Transcriptional regulator sites and transcription factors](#)
[RNA sequence databases](#)
[Protein sequence databases](#)
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[Genomics Databases \(non-vertebrate\)](#)
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[Human Genes and Diseases](#)
[Microarray Data and other Gene Expression Databases](#)
[Proteomics Resources](#)
[Other Molecular Biology Databases](#)
[Organelle databases](#)
[Plant databases](#)
[Immunological databases](#)

2012: 1380 databází

EBI/NCBI/CIB

Institute zabývající se shromažďováním, správou a poskytováním dat a informací a vývojem analytických nástrojů.

EBI

Evropský institut
pro bioinformatiku



European Bioinformatics Institute

<http://www.ebi.ac.uk/>

NCBI

Národní centrum
pro biotechnologické
informace



National Center for Biotechnology Information

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

CIB

Centrum pro informační
biologii



Center for Information Biology

<http://www.cib.nig.ac.jp/>

EBI – Evropský institut pro bioinformatiku



European Bioinformatics Institute

- Založen roku 1992 jako součást European Molecular Biology Laboratory - EMBL.
- Sídlo v Hinxtonu ve Velké Británii.

Welcome to the EBI

The European Bioinformatics Institute (EBI) is a non-profit academic organisation that forms part of the European Molecular Biology Laboratory ([EMBL](#)).

The EBI is a centre for research and services in bioinformatics. The Institute manages databases of biological data including nucleic acid, protein sequences and macromolecular structures.



Our Mission

- To provide freely available data and bioinformatics services to all facets of the scientific community in ways that promote scientific progress
- To contribute to the advancement of biology through basic investigator-driven research in bioinformatics
- To provide advanced bioinformatics training to scientists at all levels, from PhD students to independent investigators
- To help disseminate cutting-edge technologies to industry

NCBI - Národní centrum pro biotechnologické informace



National Center for Biotechnology Information

[National Library of Medicine](#)

[National Institutes of Health](#)

- Založeno v roce 1988 jako oddělení Národní lékařské knihovny (National Library of Medicine – NLM) v USA.
- Součást National Institutes of Health

► What does NCBI do?

Established in 1988 as a national resource for molecular biology information, NCBI creates public databases, conducts research in computational biology, develops software tools for analyzing genome data, and disseminates biomedical information - all for the better understanding of molecular processes affecting human health and disease.



CIB – Centrum pro informační biologii

- Založeno jako oddělení Národního genetického institutu (国立遺伝学研究所, NIG) v Japonsku.




<http://www.nig.ac.jp/>




▶▶ Information/Database

- ▶ DNA Data Bank of Japan
- ▶ National BioResource Project - Information Site
- ▶ WFGC-MIRCEN World Data Centre for Microorganisms
- ▶ Genetic Resources Database (SHIGEN)
- ▶ Nematode Gene Expression Database
- ▶ Mouse Microsatellite Database
- ▶ Rice Genome Database (Oryzabase)
- ▶ E.coli Genome Database (PEC)

 Virtual Museum of Genetics (Japanese)

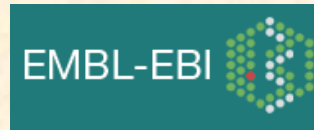
 DNA Data Bank of Japan

 National BioResource Project

 Genome Network Project

Primární databáze NA

- **EMBL** - Evropský institut pro bioinformatiku



- **GenBank** - Národní centrum pro biotechnologické informace

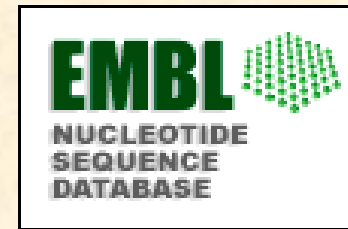


- **DDBJ** - Národní genetický institut (NIG)





EMBL



- **EMBL Nucleotide Sequence Database (EMBL-Bank) byla založena roku 1980 jako první databáze nukleotidových sekvencí.**
- **Obsahuje sekvence RNA a DNA.**
- **Zdroje sekvencí: vloženy přímo autory, genomové projekty, patenty**

**This week the EMBL Database contained
301,588,430,608 nucleotides in 199,575,971 entries**

This week = 20.4.2011



EMBL



- **EMBL Nucleotide Sequence Database (EMBL-Bank)**
– **součást ENA (European Nucleotide Archive).**

About the European Nucleotide Archive

The European Nucleotide Archive ([ENA](#)) captures and presents information relating to experimental workflows that are based around nucleotide sequencing. A typical workflow includes the isolation and preparation of material for sequencing, a run of a sequencing machine in which sequencing data are produced and a subsequent bioinformatic analysis pipeline. ENA records this information in a data model that covers input information (sample, experimental setup, machine configuration), output machine data (sequence traces, reads and quality scores) and interpreted information (assembly, mapping, functional annotation).

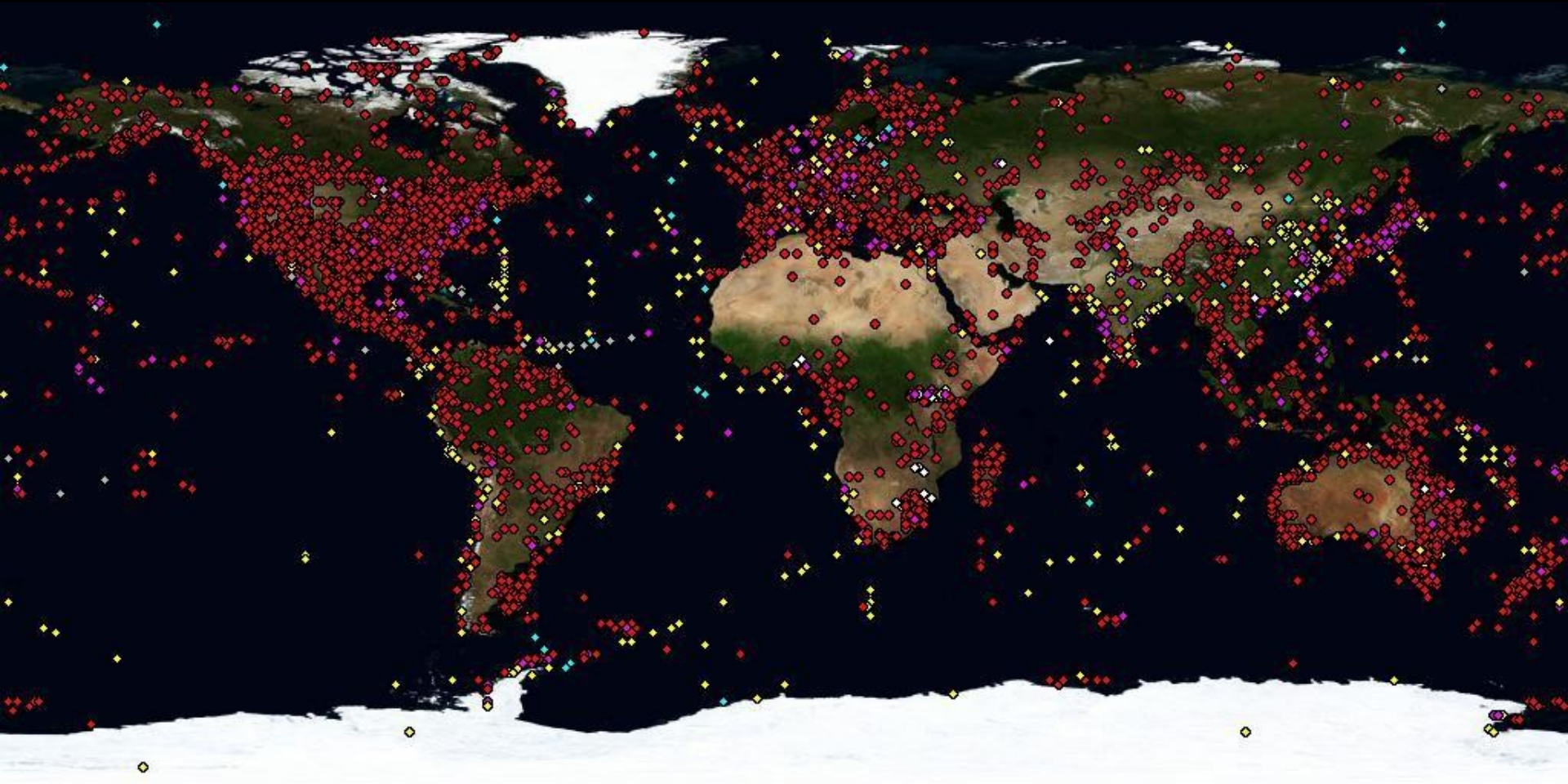
Data arrive at ENA from a variety of sources. These include submissions of raw data, assembled sequences and annotation from small-scale sequencing efforts, data provision from the major European sequencing centres and routine and comprehensive exchange with our partners in the International Nucleotide Sequence Database Collaboration (INSDC).

Provision of nucleotide sequence data to ENA or its INSDC partners has become a central and mandatory step in the dissemination of research findings to the scientific community. ENA works with publishers of scientific literature and funding bodies to ensure compliance with these principles and to provide optimal submission systems and data access tools that work seamlessly with the published literature.

ENA is made up of a number of distinct databases that includes EMBL-Bank, the newly established Sequence Read Archive (SRA) and the Trace Archive each with their own data formats and standards. ENA data classes and formats are described [here](#).

<http://www.ebi.ac.uk/ena/home>

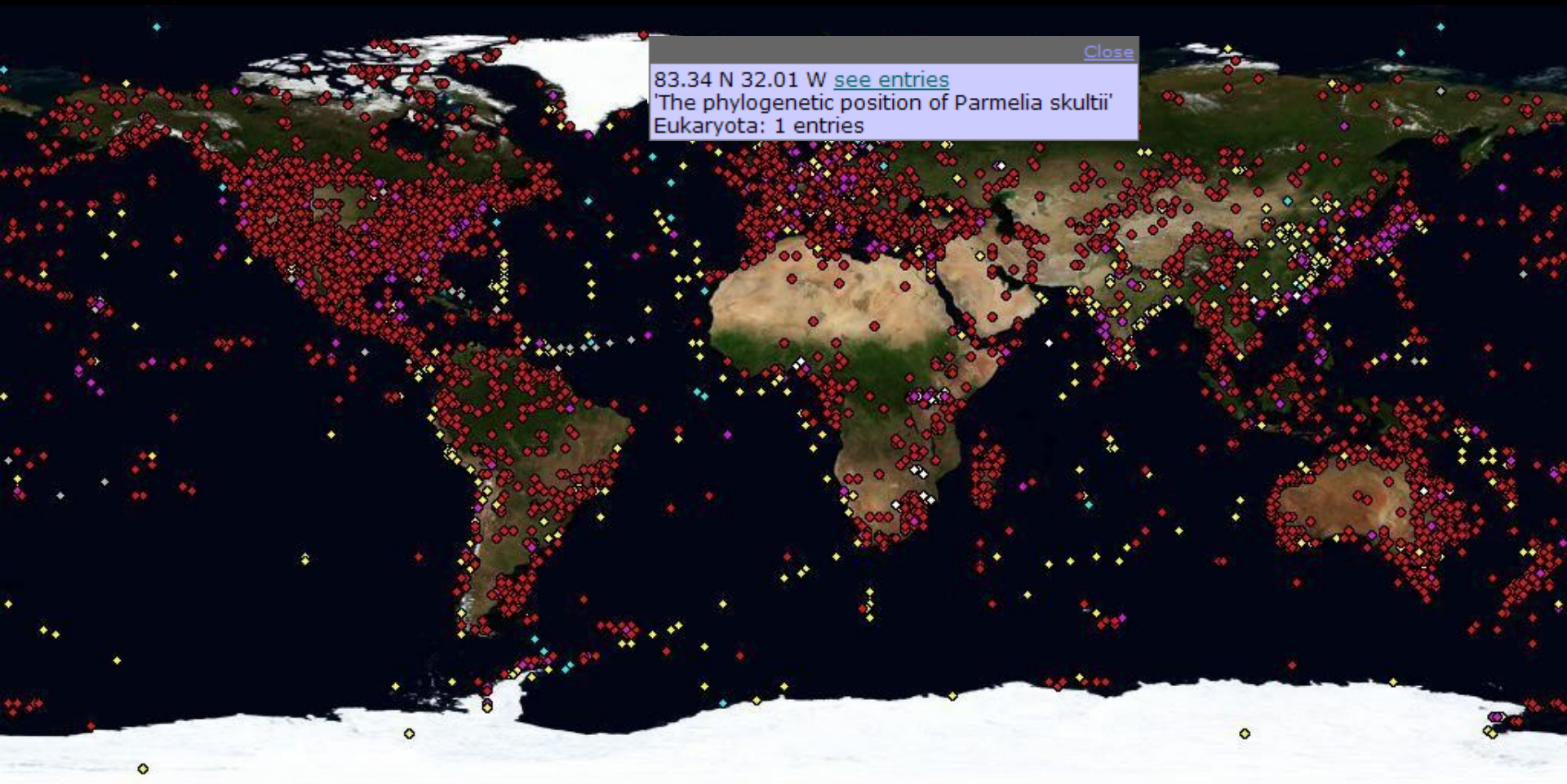
The map shows 18,628,656 entries distributed over 57,974 locations.



The dots on the map have different colours according to the taxonomy of the specimens:

 Eukaryota  Bacteria  Archaea  Other  Mixed

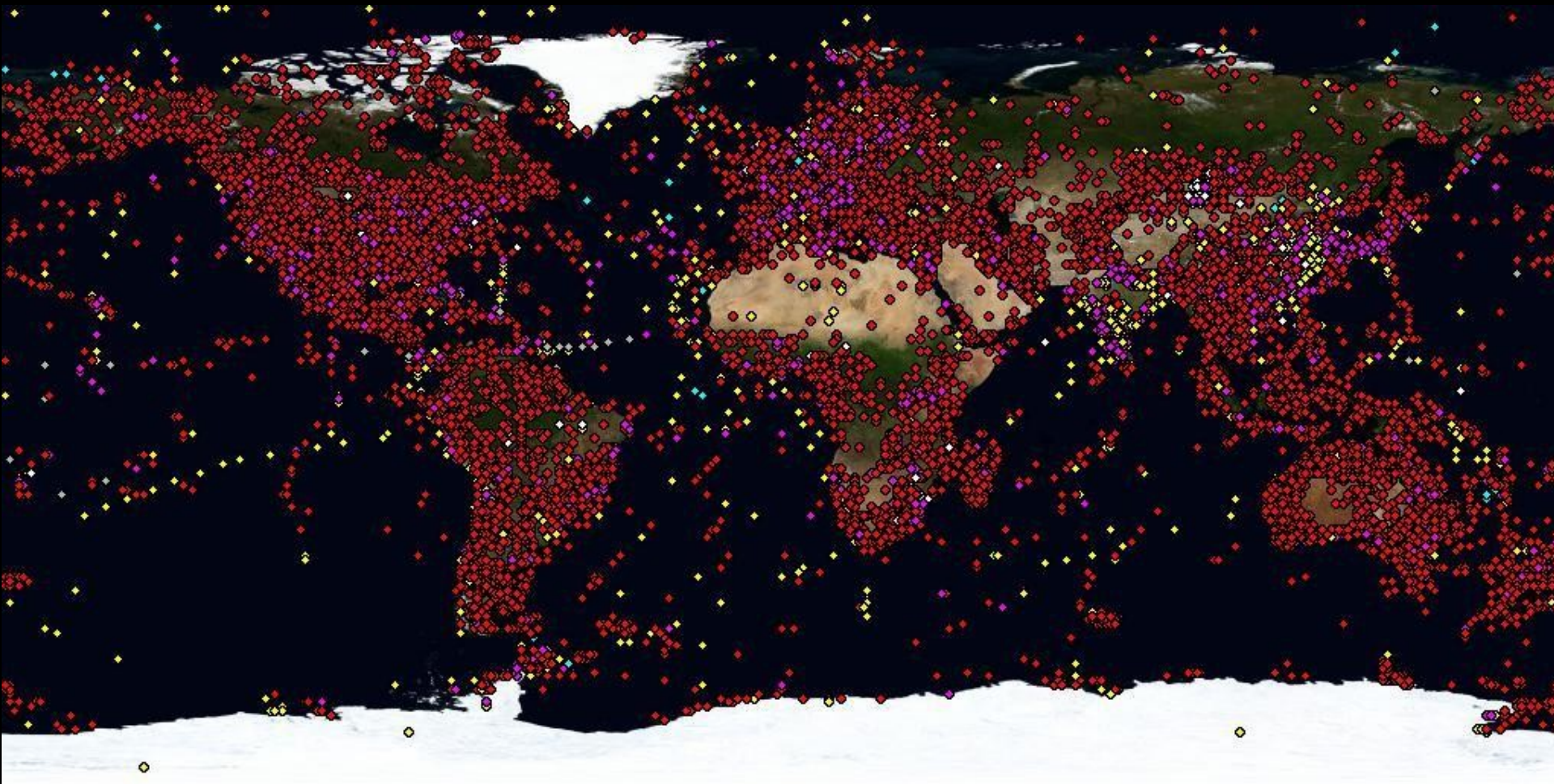
The map shows 18,628,656 entries distributed over 57,974 locations.



The dots on the map have different colours according to the taxonomy of the specimens:

 Eukaryota  Bacteria  Archaea  Other  Mixed

The map shows 18,710,024 entries distributed over 62,882 locations.



The dots on the map have different colours according to the taxonomy of the specimens:

 Eukaryota  Bacteria  Archaea  Other  Mixed

ID X56734; SV 1; linear; mRNA; STD; PLN; 1859 BP.

XX

AC X56734; S46826;

XX

DT 12-SEP-1991 (Rel. 29, Created)

DT 25-NOV-2005 (Rel. 85, Last updated, Version 11)

XX

DE Trifolium repens mRNA for non-cyanogenic beta-glucosidase

XX

KW beta-glucosidase.

XX

OS Trifolium repens (white clover)

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids;

OC eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Trifolium.

XX

RN [5]

RP 1-1859

RX PUBMED; 1907511.

RA Oxtoby E., Dunn M.A., Pancoro A., Hughes M.A.;

RT "Nucleotide and derived amino acid sequence of the cyanogenic

RT beta-glucosidase (linamarase) from white clover (Trifolium repens L.);

RL Plant Mol. Biol. 17(2):209-219(1991).

XX

RN [6]

RP 1-1859

RA Hughes M.A.;

RT ;

RL Submitted (19-NOV-1990) to the EMBL/GenBank/DDBJ databases.

RL Hughes M.A., University of Newcastle Upon Tyne, Medical School, Newcastle

RL Upon Tyne, NE2 4HH, UK

EMBL „entry“

Translation = *proteinová databáze*

```
FT source 1..1859
FT /organism="Trifolium repens"
FT /mol_type="mRNA"
FT /clone_lib="lambda gt10"
FT /clone="TRE361"
FT /tissue_type="leaves"
FT /db_xref="taxon:3899"
FT CDS 14..1495
FT /product="beta-glucosidase"
FT /EC_number="3.2.1.21"
FT /note="non-cyanogenic"
FT /db_xref="GOA:P26204"
FT /db_xref="HSSP:P26205"
FT /db_xref="InterPro:IPR001360"
FT /db_xref="UniProtKB/Swiss-Prot:P26204"
FT /protein_id="CAA40058.1"
FT /translation="MDFIVAI FALFVISSFTITSTNAVEASTLLDIGNLSRSSFPRGFI
FT FGASSSNYQFEGAVNEGGRGPSIWDFTFKHYPEKIRDGSNADITVDQYHRYKEDVGMK
FT DQNMDSYRFSISWPRILPKGKLSGGINHEGIKYNNLINELLANGIQPFVTLFHWDLPO
FT VLEDEYGGFLNSGVINDFRDYTDLCFKEFGDRVRYWSTLNEPWVFSNSGYALGTNAPGR
FT CSASNVAKPGDSGTGPYIVTHNQILAHAEAVHVYKTKYQAYQKKGIGITLVSNWLMPLD
FT DNSIPDIKAAERSLDFQFGLFMEQLTTGDYSKSMRRIVKNRLPKFSKFESSLVNGSFD
FT IGINYSSSYISNAPSHGNAKPSYSTNPMTNISFEKHGIPLGPRASIIWIYVYPYMFIQ
FT EDFEIFCYILKINITILQFSITENGMNEFNATLPVEEALLNTYRIDYYRHLYYIRSA
FT IRAGSNVKGIFYAWSFLDCNEWFAGFTVRFGLNFVD"
FT mRNA 1..1859
FT /experiment="experimental evidence, no additional details
FT recorded"
XX
```

```
SQ Sequence 1859 BP; 609 A; 314 C; 355 G; 581 T; 0 other;
aaacaaacca aatattgatt ttattgtagc catatttgct ctgtttgta ttagctcatt 60
cacaattact tccacaaatg cagttgaagc ttctactctt cttgacatag gtaacctgag 120
tcggagcagt tttcctcgtg gcttcatctt tgggtgctgga tcttcagcat accaatttga 180
aggtgcagta aacgaaggcg gtagaggacc aagtatttgg gataccttca cccataaata 240
tccagaaaaa ataagggatg gaagcaatgc agacatcacg gttgaccaat atcaccgcta 300
caaggaagat gttgggatta tgaaggatca aaatatggat tcgtatagat tctcaatctc 360
ttgqccaaga atactcccaa aqqqaaaagt gacqggaggc ataaatcacg aaggaatcaa 420
```


Formát EMBL databáze

ID	- identification	(begins each entry; 1 per entry)
AC	- accession number	(>=1 per entry)
PR	- project identifier	(0 or 1 per entry)
DT	- date	(2 per entry)
DE	- description	(>=1 per entry)
KW	- keyword	(>=1 per entry)
OS	- organism species	(>=1 per entry)
OC	- organism classification	(>=1 per entry)
OG	- organelle	(0 or 1 per entry)
RN	- reference number	(>=1 per entry)
RC	- reference comment	(>=0 per entry)
RP	- reference positions	(>=1 per entry)
RX	- reference cross-reference	(>=0 per entry)
RG	- reference group	(>=0 per entry)
RA	- reference author(s)	(>=0 per entry)
RT	- reference title	(>=1 per entry)
RL	- reference location	(>=1 per entry)
DR	- database cross-reference	(>=0 per entry)
CC	- comments or notes	(>=0 per entry)
AH	- assembly header	(0 or 1 per entry)
AS	- assembly information	(0 or >=1 per entry)
FH	- feature table header	(2 per entry)
FT	- feature table data	(>=2 per entry)
XX	- spacer line	(many per entry)
SQ	- sequence header	(1 per entry)
CO	- contig/construct line	(0 or >=1 per entry)
bb	- (blanks) sequence data	(>=1 per entry)
//	- termination line	(ends each entry; 1 per entry)

Formát EMBL databáze

```
ID <1>; SV <2>; <3>; <4>; <5>; <6>; <7> BP.
```

The tokens represent:

1. Primary accession number
2. Sequence version number
3. Topology: 'circular' or 'linear'
4. Molecule type
5. Data class
6. Taxonomic division
7. Sequence length

```
ID CD789012; SV 4; linear; genomic DNA; HTG; MAM; 500 BP.
```

Formát EMBL databáze

Class	Definition
CON	Entry constructed from segment entry sequences, drawing annotation from segment entries
ANN	Entry constructed from segment entry sequences with its own annotation
PAT	Patent
EST	Expressed Sequence Tag
GSS	Genome Survey Sequence
HTC	High Throughput CDNA sequencing
HTG	High Throughput Genome sequencing
MGA	Mass Genome Annotation
WGS	Whole Genome Shotgun
TPA	Third Party Annotation
STS	Sequence Tagged Site
STD	Standard (all entries not classified as above)

http://www.ebi.ac.uk/embl/Documentation/User_manual/usrman.html

Formát EMBL databáze

Division	Code
Bacteriophage	PHG
Environmental Sample	ENV
Fungal	FUN
Human	HUM
Invertebrate	INV
Other Mammal	MAM
Other Vertebrate	VRT
Mus musculus	MUS
Plant	PLN
Prokaryote	PRO
Other Rodent	ROD
Synthetic	SYN
Transgenic	TGN
Unclassified	UNC
Viral	VRL

http://www.ebi.ac.uk/embl/Documentation/User_manual/usrman.html



GenBank

- **Založena roku 1982 v rámci institutu NCBI.**

GenBank[®] is the NIH genetic sequence database, an annotated collection of all publicly available DNA sequences (*Nucleic Acids Research*, 2008 Jan;36(Database issue):D25-30). There are approximately 85,759,586,764 bases in 82,853,685 sequence records in the traditional GenBank divisions and 108,635,736,141 bases in 27,439,206 sequence records in the WGS division as of February 2008.



Sample GenBank Record

<http://www.ncbi.nlm.nih.gov/Sitemap/samplerecord.html>



NCBI

Sample GenBank Record

LOCUS SCU49845 5028 bp DNA PLN 21-JUN-1999
DEFINITION Saccharomyces cerevisiae TCP1-beta gene, partial cds, and Axl2p
(AXL2) and Rev7p (REV7) genes, complete cds.
ACCESSION U49845
VERSION U49845.1 GI:1293613
KEYWORDS .
SOURCE Saccharomyces cerevisiae (baker's yeast)
ORGANISM Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE 1 (bases 1 to 5028)
AUTHORS Torpey,L.E., Gibbs,P.E., Nelson,J. and Lawrence,C.W.
TITLE Cloning and sequence of REV7, a gene whose function is required for
DNA damage-induced mutagenesis in Saccharomyces cerevisiae
JOURNAL Yeast 10 (11), 1503-1509 (1994)
PUBMED 7871890
REFERENCE 2 (bases 1 to 5028)
AUTHORS Roemer,T., Madden,K., Chang,J. and Snyder,M.
TITLE Selection of axial growth sites in yeast requires Axl2p, a novel
plasma membrane glycoprotein
JOURNAL Genes Dev. 10 (7), 777-793 (1996)
PUBMED 8846915
REFERENCE 3 (bases 1 to 5028)
AUTHORS Roemer,T.
TITLE Direct Submission
JOURNAL Submitted (22-FEB-1996) Terry Roemer, Biology, Yale University, New
Haven, CT, USA

<http://www.ncbi.nlm.nih.gov/Sitemap/samplerecord.html>



LOCUS SCU49845 5028 bp DNA **PLN** 21-JUN-1999
 DEFINITION *Saccharomyces cerevisiae* TCP1-beta gene, partial cds, and Axl2p
 (AXL2) and Rev7p (REV7) genes, complete cds.

ACCESSION U49845

VERSION U49845.1 GI:1293613

KEYWORDS .

SOURCE *Saccharomyces cerevi*

ORGANISM *Saccharomyces cerevi*

Eukaryota; Fungi; As

Saccharomycetales; S

REFERENCE 1 (bases 1 to 5028)

AUTHORS Torpey,L.E., Gibbs,P

TITLE Cloning and sequence

DNA damage-induced m

JOURNAL *Yeast* 10 (11), 1503-

PUBMED 7871890

REFERENCE 2 (bases 1 to 5028)

AUTHORS Roemer,T., Madden,K.

TITLE Selection of axial g

plasma membrane glyc

JOURNAL *Genes Dev.* 10 (7), 7

PUBMED 8846915

REFERENCE 3 (bases 1 to 5028)

AUTHORS Roemer,T.

TITLE [Direct Submission](#)

JOURNAL Submitted (22-FEB-19

Haven, CT, USA

GenBank Division

The GenBank division to which a record belongs is indicated with a three letter abbreviation. In this example, GenBank division is **PLN**.

The GenBank database is divided into 18 divisions:

1. PRI - primate sequences
2. ROD - rodent sequences
3. MAM - other mammalian sequences
4. VRT - other vertebrate sequences
5. INV - invertebrate sequences
6. PLN - plant, fungal, and algal sequences
7. BCT - bacterial sequences
8. VRL - viral sequences
9. PHG - bacteriophage sequences
10. SYN - synthetic sequences
11. UNA - unannotated sequences
12. EST - EST sequences (expressed sequence tags)
13. PAT - patent sequences
14. STS - STS sequences (sequence tagged sites)
15. GSS - GSS sequences (genome survey sequences)
16. HTG - HTG sequences (high-throughput genomic sequences)
17. HTC - unfinished high-throughput cDNA sequencing
18. ENV - environmental sampling sequences

The DNA Data Bank of Japan

- Původně zahrnovala data především z japonských výzkumů.
- V současnosti úzká spolupráce s ostatními databázemi.





International Nucleotide Sequence Database Collaboration



DDBJ: DNA Data Bank of Japan

CIB-DDBJ: Center for Information Biology and DNA Data Bank of Japan

NIG: National Institute of Genetics

EBI: European Bioinformatics Institute

EMBL: European Molecular Biology Laboratory

NCBI: National Center for Biotechnology Information

NLM: National Library of Medicine

IAC: International Advisory Committee

ICM: International Collaborative Meeting

<http://www.insdc.org/>

Primární databáze proteinů

- **Univerzální databáze:**
„Skladiště“ sekvencí – sequence repository
Manuálně spravovaná – curated database

Příklad: GenBank *versus* RefSeq



National Center for Biotechnology Information

[National Library of Medicine](#)

[National Institutes of Health](#)

Primární databáze proteinů

GenBank

Not curated

Author submits

Only author can revise

Multiple records for same loci common

Records can contradict each other

No limit to species included

Data exchanged among INSDC members

Akin to primary literature

Proteins identified and linked

Access via NCBI Nucleotide databases

RefSeq

Curated

NCBI creates from existing data

NCBI revises as new data emerge

Single records for each molecule of major organisms

Limited to model organisms

Exclusive NCBI database

Akin to review articles

Proteins and transcripts identified and linked

Access via Nucleotide & Protein databases

GenPept - GenBank Gene Products Data Bank

RefSeq - Reference Sequence

Primární databáze proteinů

- **PIR-PSD - Protein Information Resource Protein Sequence Database.**
- **Nejstarší univerzální „curated“ databáze proteinů.**
- **Komplexní, non-redundant data, rozčleněna podle proteinových rodin a nadrodin, doplněna funkčními, strukturními a bibliografickými daty.**

<http://pir.georgetown.edu/>

- **Swiss-Prot** - „Curated“ databáze založená na Univerzitě v Ženevě v roce 1986. Spravovaná Švýcarským institutem pro bioinformatiku (**SIB - Swiss Institute of Bioinformatics**).
- Vysoká úroveň anotace → vkládáno více sekvencí než je možno manuálně anotovat a zařadit do databáze.
- **TrEMBL** – Počítačově anotovaná data, odvozená z kódujících úseku sekvencí v DDBJ/EMBL/GenBank, která **ZATÍM** nejsou zařazena v Swiss-Prot.



Swiss-PROT + TrEMBL



- **Anotace:**
 - Funkce**
 - Katalytická aktivita**
 - Podjednotky**
 - Domény**
 - Biotechnologické využití**
 - Sekvenční homologie**
 - Posttranslační modifikace**
 - Reference atd.**

Složené databáze

- **Databáze:**

Primární

Sekundární

Strukturní

Genomové zdroje

Složené databáze

Složené databáze

- **Složené (composite) databáze:**

Slučují data z několika primárních databází.

Eliminace redundantních dat.

Různá priorita zdrojových databází podle kvality validace a anotace (eliminace redundantních dat z databáze s nižší prioritou).

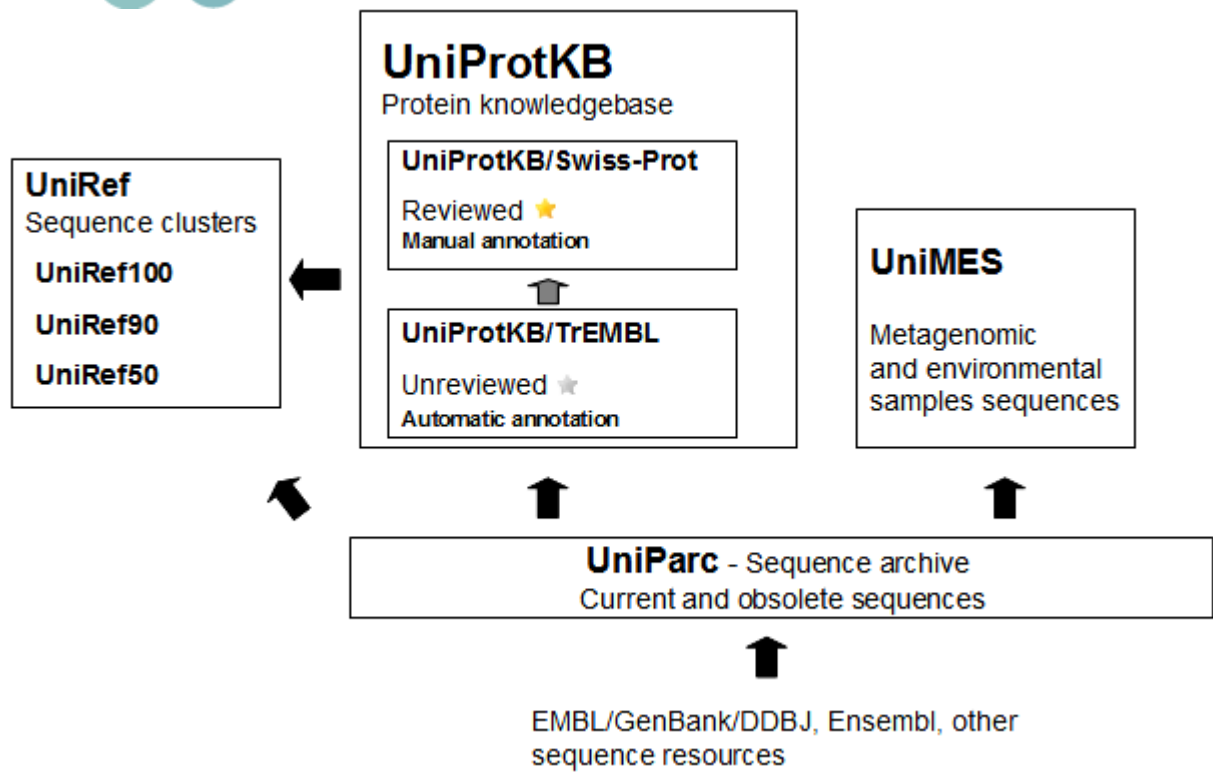


Swiss-PROT + TrEMBL

OWL (Swiss-PROT + PIR + Genbank + NRL-3D)



UniProt



2002- spolupráce mezi EBI, SIB a PIR

<http://www.uniprot.org>

Sekundární databáze NA a proteinů

Sekundární databáze obsahují informace odvozené z primárních databází ve formě charakteristických vzorů sekvencí, tj. funkčních nebo strukturních motivů získaných srovnáním primárních dat (sekvencí).

- Vyhledávání „vzoru“ charakteristického pro určitou skupinu proteinů.
- Možnost predikce funkce proteinů.

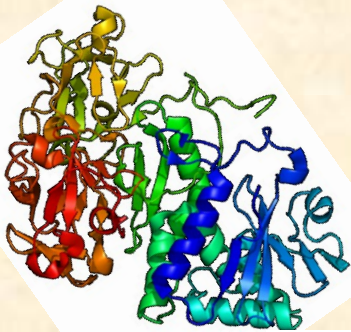
Sekundární databáze NA a proteinů

- **Databáze mohou obsahovat:**

Proteinové **DOMÉNY** odvozené ze známých struktur

Proteinové sekvence seřazené do **SEKVENČNÍCH RODIN**

CHARAKTERISTICKÉ MOTIVY odvozené z těchto sekvencí rodin.



```
LPPNTAFKAI FYANAADRQDLKLFIDD  
IPPNTDFRAIFFANAAEQOHIKLFIGD  
LPPHIKFGVTALTHAANDQTIDIYIDD  
LPPNIAFGVTALVNSSAPQTIEVFVDD
```

[AC]-x-V-x(4)-{ED}.

This pattern is translated as: [Ala or Cys]-any-Val-any-any-any-any-{any but Glu or Asp}

Sekundární databáze NA a proteinů

- **Sekundární proteinové databáze:**
**PROSITE, Pfam, PRINTS, ProDom,
SMART, TIGRFAMS**
V současné době sdruženy do integrované
klasifikační databáze proteinů **InterPro**

<http://www.ebi.ac.uk/interpro/>

[Table View](#)[Raw Output](#)[XML Output](#)[Original Sequences](#)[SUBMIT ANOTHER JOB](#)SEQUENCE: [Sequence_1](#) CRC64: B08AB341813AD2EE LENGTH: 382 aa**InterPro**[IPR000772](#)

Domain

InterPro

**Ricin B lectin**[PF00652](#)

Ricin_B_lectin

[SM00458](#)

RICIN

[PS50231](#)

RICIN_B_LLECTIN

InterPro[IPR001574](#)

Family

InterPro

**Ribosome-inactivating protein**[PF00161](#)

RIP

[SSF56371](#)

Ribosome_inactivat_prot

InterPro[IPR008997](#)

Domain

InterPro

**Ricin B-related lectin**[SSF50370](#)

RicinB_like

InterPro[IPR016139](#)

Domain

InterPro

**Ribosome-inactivating protein, subdomain 2**[G3DSA:4.10.470.10](#)

Ribosome_inactivat_prot_sub2

InterPro[IPR017989](#)

Family

InterPro

**Ribosome-inactivating protein subgroup**[PR00396](#)

SHIGARICIN

Sekundární databáze NA a proteinů

- **Sekundární proteinové databáze:**
**PROSITE, Pfam, PRINTS, ProDom,
SMART, TIGRFAMS**

V současné době sdruženy do integrované klasifikační databáze proteinů **InterPro**

<http://www.ebi.ac.uk/InterProscan/>

- **Sekundární databáze NA**
TRANSFAC

Strukturní databáze

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<http://www3.oup.co.uk/nar/database/a/>

Strukturní databáze proteinů

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[CC+](#)

[CE](#)

[CoC Central](#)

[ColiSNP](#)

[Columba](#)

[ConSurf-DB](#)

[CPDB](#)

[CSA - Catalytic Site Atlas](#)

[DisProt - Database of Protein Disorder](#)

[DMAPS](#)

[Dockground](#)

[DomIns - Database of Domain Insertions](#)

[DSDBASE - Disulfide Database](#)

[DSMM - a Database of Simulated Molecular Motions](#)

[E-MSD - EBI-Macromolecular Structure Database](#)

[eF-site - Electrostatic surface of Functional site](#)

[EzCatDB](#)

[FireDB](#)

[FSN](#)

[Gene3D](#)

[Genomic Threading Database](#)

[GTOP - Genomes To Protein structures](#)

[HOMSTRAD - Homologous Structure Alignment Database](#)

[HotSprint](#)

[IMGT/3Dstructure-DB](#)

[IMOTdb](#)

[JAIL](#)

[Jenalib: Jena Library of Biological Macromolecules](#)

[KineticDB](#)

[LPFC](#)

[MALISAM](#)

[MegaMotifbase](#)

[MMDB](#)

[ModBase](#)

[MolMovDB - Database of Macromolecular Movements](#)

[PASSz](#)

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[PDB-REFRDB](#)

[PDBselect](#)




[PDBsum](#)

PDB - Protein Data Bank



A MEMBER OF THE  PDB

An Information Portal to Biological Macromolecular Structures

As of Tuesday Apr 03, 2012 at 5 PM PDT there are 80550 Structures | [PDB Statistics](#) |   

- Databáze obsahuje experimentálně získané struktury proteinů, **nukleových kyselin** a komplexů informačních biomakromolekul.

PDB Current Holdings Breakdown

Exp.Method	Proteins	Nucleic Acids	Protein/NA Complexes	Other	Total
X-RAY	65950	1346	3261	2	70559
NMR	8185	979	186	7	9357
ELECTRON MICROSCOPY	284	22	116	0	422
HYBRID	44	3	2	1	50
other	140	4	5	13	162
Total	74603	2354	3570	23	80550

<http://www.rcsb.org/pdb/>

PDB formát

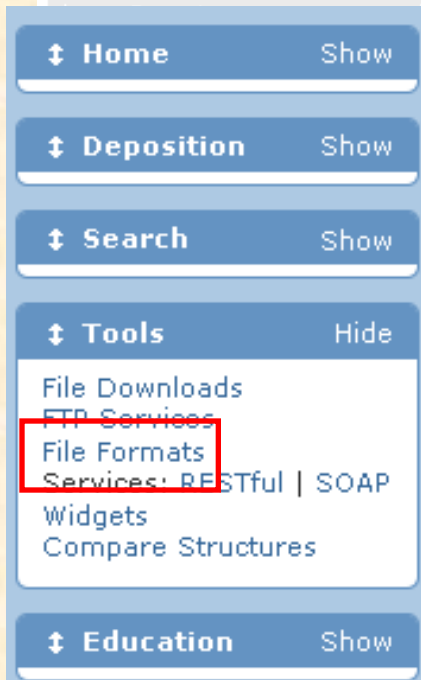
PDB File Format

The Protein Data Bank (PDB) format provides a standard representation for macromolecular structure data derived from X-ray diffraction and NMR studies. This representation was created in the 1970's and a large amount of software using it has been written.

Documentation describing the PDB file format is available from the wwPDB at <http://www.wwpdb.org/docs.html>.

Historical copies of the PDB file format from 1992* and 1996* are available.

- PDB formát – původní formát databáze.
- 1997 – mmCIF (macromolecular Crystallographic Information File).
- Záznamy jsou v databázi uloženy v obou formátech a volně stažitelné.
- PDB formát – rozeznáván téměř všemi programy pro práci se strukturami.



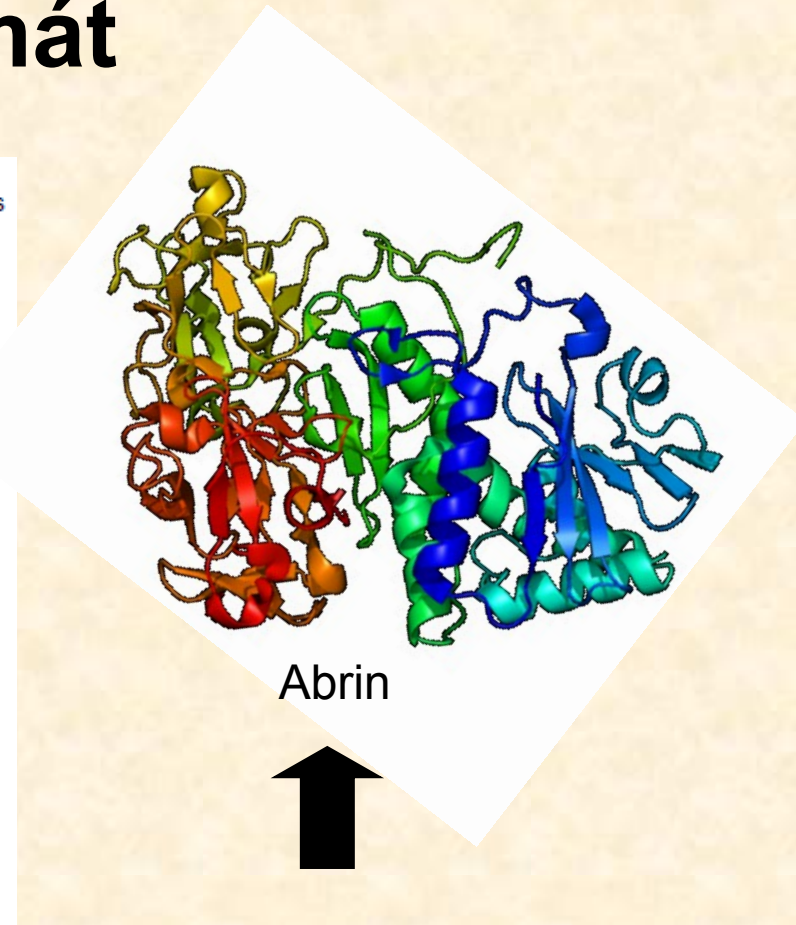
PDB formát

The ATOM records present the atomic coordinates for standard amino acids and nucleotides. They also present the occupancy and temperature factor for each atom. Non-polymer chemical coordinates use the HETATM record type. The element symbol is always present on each ATOM record; charge is optional.

Changes in ATOM/HETATM records result from the standardization atom and residue nomenclature. This nomenclature is described in the Chemical Component Dictionary (<ftp://ftp.wwpdb.org/pub/pdb/data/monomers>).

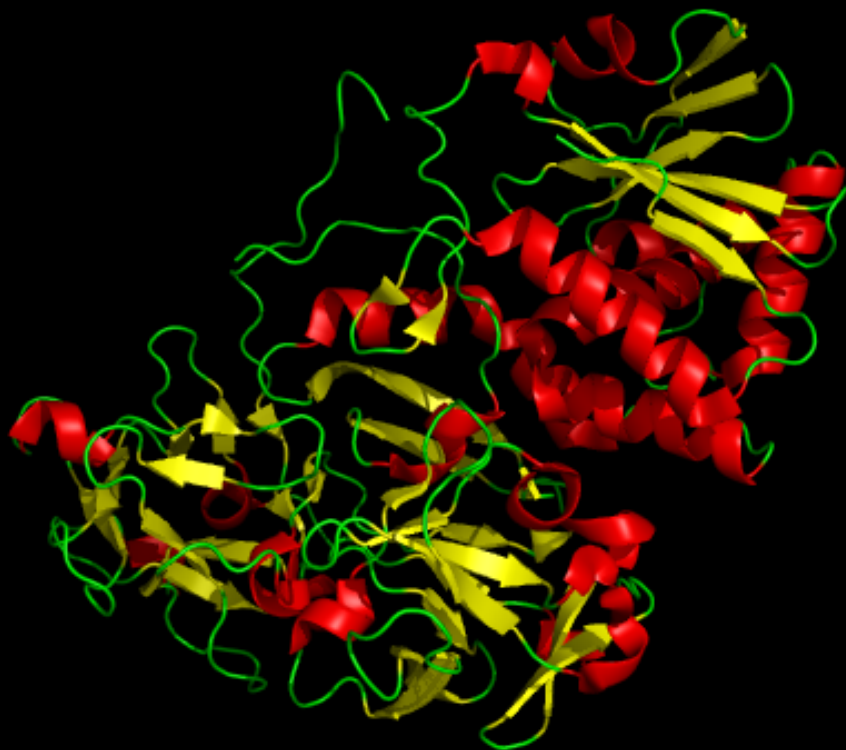
Record Format

COLUMNS	DATA TYPE	FIELD	DEFINITION
1 - 6	Record name	"ATOM "	
7 - 11	Integer	serial	Atom serial number.
13 - 16	Atom	name	Atom name.
17	Character	altLoc	Alternate location indicator.
18 - 20	Residue name	resName	Residue name.
22	Character	chainID	Chain identifier.
23 - 26	Integer	resSeq	Residue sequence number.
27	AChar	iCode	Code for insertion of residues.
31 - 38	Real(8.3)	x	Orthogonal coordinates for X in Angstroms.
39 - 46	Real(8.3)	y	Ortho
47 - 54	Real(8.3)	z	Ortho
55 - 60	Real(6.2)	occupancy	Occup
61 - 66	Real(6.2)	tempFactor	Tempe
77 - 78	LString(2)	element	Elem
79 - 80	LString(2)	charge	Charg



ATOM	2	CA	GLU	A	1	64.373	11.709	60.583	1.00	79.99	C
ATOM	3	C	GLU	A	1	63.512	10.438	60.597	1.00	79.31	C
ATOM	4	O	GLU	A	1	63.540	9.685	61.574	1.00	79.23	O
ATOM	5	CB	GLU	A	1	63.805	12.754	59.603	1.00	79.36	C
ATOM	6	CG	GLU	A	1	62.880	13.819	60.228	1.00	78.52	C
ATOM	7	CD	GLU	A	1	61.525	13.275	60.676	1.00	78.50	C
ATOM	8	OE1	GLU	A	1	60.915	12.482	59.923	1.00	77.14	O
ATOM	9	OE2	GLU	A	1	61.064	13.659	61.776	1.00	77.48	O
ATOM	10	H1	GLU	A	1	66.078	10.648	60.914	1.00	20.00	H
ATOM	11	H2	GLU	A	1	65.776	10.893	59.265	1.00	20.00	H
ATOM	12	H3	GLU	A	1	66.387	12.177	60.222	1.00	20.00	H

/1abr 1 6 11 16 21 26 31 36 41 46 51 56 61 66 71
PPN IVEKSKICSSRYEPTVRIGGRDGMCDVYDNGYHNGNRIIMWKCKDRLEENQLWTLKSDKTIRSNGKCLTTYG



Color:

- by element
- by chain
- by ss
- spectrum
- auto
- reds
- greens
- blues
- yellows
- magentas
- cyans
- oranges
- tints
- grays

By Secondary Structure:

- Helix Sheet Loop
- Helix Sheet Loop

Mouse Mode 3-Button Viewing

Buttons	L	M	R	Wheel
& Keys	Rota	Move	MovZ	Slab
Shft	+Box	-Box	Clip	MovS
Ctrl	+/-	PkAt	Pk1	MvSZ
CtSh	Sele	Orig	Clip	MovZ
SnglClk	+/-	Cent	Menu	
DblClk	Menu	-	PkAt	

Selecting Residues

Frame [1/ 1] 0/sec

Strukturní databáze NA

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[ITS2](#)

[MeRNA](#)

[NCIR - Non-Canonical Interactions in RNA](#)

[NDB](#)

[NNDB](#)

[non-B DB](#)

[NTDB](#)

[QuadBase](#)

[Rfam](#)

[RNA FRABASE](#)

[RNA SSTRAND](#)

[RNAJunction](#)

[SARS-CoV RNA SSS](#)

[SCOR - Structural Classification Of RNA](#)

[Vir-Mir db](#)

NDB - Nucleic Acid Database



WELCOME TO THE NUCLEIC ACID DATABASE

a repository of three-dimensional structural information about nucleic acids

Number of Released Structures:

5817 Structures

Last Update: 04-Apr-2012

NDB ID: AD0001

NMR Atlas X-Ray Atlas

Title: STRUCTURE OF A DNA IN LOW SALT CONDITIONS D
(GACCGCGGTC)

Molecular Description: 5' -D (GpApCpCpGpCpGpGpTpC) -3'

Structural Features: A DOUBLE HELIX

Nucleic Acid Sequence: Chain A: (DG) (DA) (DC) (DC) (DG)
(DC) (DG) (DG) (DT) (DC)

Primary Citation: Finley, J.B., Luo, M.
X-ray crystal structures of half the human papilloma virus E2 binding site: d(GACCGCGGTC).
Nucleic Acids Res., **26**, pp. 5719 - 5727, 1998.

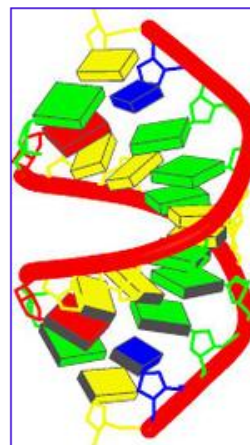
Experimental Information: X-RAY DIFFRACTION

Space Group: P 6₁ 2 2

Cell Constants: a = 38.444 b = 38.444 c = 80.175 (Ångstroms)
 α = 90.00 β = 90.00 γ = 120.00 (degrees)

Crystallization Conditions: Method: VAPOR DIFFUSION
Drop: WATER, MPD, Spermine HCl, Na
Cacodylate
Reservoir: WATER, MPD

Refinement: The structure was refined using the X-PLOR program.
The R value is 21.9 for 1779 reflections in the resolution range 5.000 to 2.200 Ångstroms with Fobs > 3.000 sigma(Fobs).



Biological Unit 1

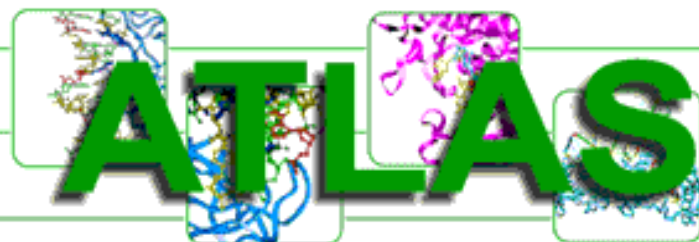
Other Views

Asymmetric Unit

Crystal Packing

Enlarge Biological Unit 1

<http://ndbserver.rutgers.edu/>



of Nucleic Acid Containing Structures

X-Ray Atlas

- [Gallery Index](#)
- [Index Listing](#) [text only]

NMR Atlas

- [Gallery Index](#)
- [Index Listing](#) [text only]

● [Sorted Galleries](#)

● [Musical Atlas](#)

● [About this Atlas](#)

The NDB Atlas provides summary information and images for each structure in the database. These images provide many looks at the varied structures of nucleic acids.

The Atlas is first divided by experimental type, and then by structure type. Features include:

- images of the asymmetric and biological units, and crystal packing pictures for nucleic acid structures from X-ray crystallographic experiments
- images of the average and ensemble structure from NMR experiments
- links to coordinate files, experimental data files
- tables of derived data, including torsion angles and hydrogen bonding classifications
- special features for RNA structures, including images of secondary and tertiary structure

A more detailed description of the NDB Atlas features is available at "[About this Atlas](#)"

Genomové zdroje

Nucleic Acids Research

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[Oxford Journals](#) > [Life Sciences](#) > [Nucleic Acids Research](#) > Database Summary Paper Categories

2011 NAR Database Summary Paper Category List

[Nucleotide Sequence Databases](#)

[RNA sequence databases](#)

[Protein sequence databases](#)

[Structure Databases](#)

[Genomics Databases \(non-vertebrate\)](#)

[MGD - Mouse Genome Database](#)

[TIGR Gene Indices](#)

[Genome annotation terms, ontologies and nomenclature](#)

[Taxonomy and identification](#)

[General genomics databases](#)

[Viral genome databases](#)

[Prokaryotic genome databases](#)

[Unicellular eukaryotes genome databases](#)

[Fungal genome databases](#)

[Invertebrate genome databases](#)

**EBI, NCBI – genomové
databáze**

Vyhledávací systémy

- **Nutnost organizovaného ukládání a skladování dat.**
- **Nutnost prohlížení a analyzování uložených dat.**



Databáze je určitá uspořádaná množina informací (dat) uložená na paměťovém médiu.

V širším smyslu jsou součástí databáze i softwarové prostředky, které umožňují manipulaci s uloženými daty a **přístup k nim.**

Vyhledávací systémy



- **Textové vyhledávání v databázích**

NCBI – Entrez

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

Entrez is the integrated, text-based search and retrieval system used at NCBI for the major databases, including PubMed, Nucleotide and Protein Sequences, Protein Structures, Complete Genomes, Taxonomy, and others.

<http://www.ncbi.nlm.nih.gov/Entrez/tutor.html>



U.S. National Library of Medicine
National Institutes of Health

Welcome to PubMed

PubMed comprises more than 19 million citations for biomedical articles from MEDLINE and life science journals. Citations may include links to full-text articles from PubMed Central or publisher web sites.



Entrez, The Life Sciences Search Engine

HOME SEARCH SITE MAP

PubMed

All Databases

Human Genome

GenBank

Map Viewer

BLAST

Search across databases

















GO

Clear

Help

Welcome to the Entrez cross-database search page

- | | |
|--|---|
|  PubMed: biomedical literature citations and abstracts |  Books: online books |
|  PubMed Central: free, full text journal articles |  OMIM: online Mendelian Inheritance in Man |
|  Site Search: NCBI web and FTP sites |  OMIA: online Mendelian Inheritance in Animals |

- | | |
|---|---|
|  Nucleotide: Core subset of nucleotide sequence records |  dbGaP: genotype and phenotype |
|  EST: Expressed Sequence Tag records |  UniGene: gene-oriented clusters of transcript sequences |
|  GSS: Genome Survey Sequence records |  CDD: conserved protein domain database |
|  Protein: sequence database |  3D Domains: domains from Entrez Structure |
|  Genome: whole genome sequences |  UniSTS: markers and mapping data |
|  Structure: three-dimensional macromolecular structures |  PopSet: population study data sets |
|  Taxonomy: organisms in GenBank |  GEO Profiles: expression and molecular abundance profiles |
|  SNP: single nucleotide polymorphism |  GEO DataSets: experimental sets of GEO data |

Search across databases


abrin





































GO

Clear

Help

Result counts displayed in gray indicate one or more terms not found

298		PubMed: biomedical literature citations and abstracts	
269		PubMed Central: free, full text journal articles	
none		Site Search: NCBI web and FTP sites	
4		Books: online books	
1		OMIM: online Mendelian Inheritance in Man	
none		OMIA: online Mendelian Inheritance in Animals	

15		Nucleotide: Core subset of nucleotide sequence records	
1		EST: Expressed Sequence Tag records	
none		GSS: Genome Survey Sequence records	
26		Protein: sequence database	
none		Genome: whole genome sequences	
2		Structure: three-dimensional macromolecular structures	
none		Taxonomy: organisms in GenBank	
none		SNP: single nucleotide polymorphism	
2		Gene: gene-centered information	
none		dbGaP: genotype and phenotype	
none		UniGene: gene-oriented clusters of transcript sequences	
none		CDD: conserved protein domain database	
10		3D Domains: domains from Entrez Structure	
none		UniSTS: markers and mapping data	
none		PopSet: population study data sets	
none		GEO Profiles: expression and molecular abundance profiles	
none		GEO DataSets: experimental sets of GEO data	
none		Cancer Chromosomes: cytogenetic databases	

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Search Options

1. Select the **databanks** you want to search
2. Enter your **search terms** in the **Quick Search** box, or choose a **query form** from below

[Standard Query Form](#)
[Extended Query Form](#)

You can **browse** through all the **entries** in any **databanks**. First, **select** the **databanks** you want to browse, then click:

[Browse Entries](#)

Tips

- ▶ bookmark this [link](#) to return to your project
- ▶ [Linking to SRS?](#)
- Please read our [Linking to SRS](#) guide for important

Available Databanks

Expand all Collapse all Show databanks tooltips:

Literature, Bibliography and Reference Databases

MEDLINE Taxonomy OMIM OMIM Morbid Map

Patent Abstracts Karyn's Genomes

Literature, Bibliography and Reference Databases - subsections

MEDLINE (Updates) MEDLINE (Main Release 2009) MEDLINE (Main Release 2008) MED2PUB

Gene Dictionaries and Ontologies

Nucleotide sequence databases

EMBL Patent DNA EMBL (Contig)

EMBL (Contigs expanded) EMBL (Annotated Cons) EMBL (Coding Sequences)

EMBL ID/Accession Mapping EMBL MGA IMGTL/LIGM-DB

IMGTL/H Genome Reviews

GR Gen RefSeq Genome

LiveList

Nucleotide s

EMBL (release) EMBL (Whole Genome Shotgun)

EMBL (Whole Genome Shotgun updates) EMBL (Contig release)

EMBL (Contigs expanded release) EMBL (Contigs expanded updates)

EMBL (Annotated Cons release) EMBL (Annotated Cons updates) EMBL (Release, Deleted)

The EMBL nucleotide sequence database constitutes Europe's primary nucleotide sequence resource. The database is produced in an international collaboration with GenBank (USA) and the DNA Database of Japan (DDBJ).

To obtain comprehensive information on this databank, click the link

SRS

• Textové vyhledávání v databázích

EBI– SRS

Sequence Retrieval System

<http://srs.ebi.ac.uk/>

Vyhledávací systémy

- **Vyhledávání podobností sekvencí**

Textové vyhledávání může selhat (nedostatečná anotace).

Vyskytuje se shodná nebo podobná sekvence v databázi? (Identifikace možné funkce na základě homologie.)

- **Specializované nástroje (algoritmy) pro „seřazení“ (alignment) sekvencí.**

```
LPPNTAFKAIIFYANAADRQDLKLFIDDAPFPAAATFVGNSEEDGVRL--FTLNSKGGKIRIE
IPPNTDFRAIFFANAAEQOHIKLFIGDSQEPAAAYHKLTRDGPREE--ATLNSGNGKIRFE
LPPHIKFGVTAALTHAANDQTIDIYIDDDPKPAAATFKGAGAQQDQNLGTTKVLDSGNGRVRVI
LPPNIAFGVTAALVNSSAPQTIEVFVDDNPKPAAATFQGAGTQDANLNTQIVNSGKGKVRVV
lPPn-aFg---lanaad-QtiklfidD-p-PAAatfkgag-----l-t-tlnSgnGkiRve
```

```
ASANGRQSATDARLAPLSAGD-----TVWLGWLGAEEDGADADYNDGIVILQWPIIT
VSVNGKPSATDARLAPINGKKSDDGSPFTVNFQIVVSEEDGHDSYNDGIVVLQWPIG
VMANGRPSRLGSRQVDIFKKS-----YFGIIGSEEDGADDDYNDGIVFLNWPLG
VTANGKPSKIGSRQVDIFKKT-----YFGLVGSSEEDGGDGYNDGIVAILNWPLG
vsaNGrpSat--R---ifkks-----tvyfGivgsEDGaDaDYNDGIViLqWPig
```

Shrnutí

- Výrazný nárůst množství biologických dat vede k nutnosti jejich **organizovaného skladování a analyzování (databáze)**.
- Instituce pro správu dat a vývoj nástrojů pro analýzu: **EBI/NCBI/CIB**
- Základní rozdělení databází: **primární/sekundární/strukturní databáze**
- Textové vyhledávací systémy: **Entrez/SRS**