

CG920 Genomics

Lesson 1

Introduction into Bioinformatics

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INVESTICE DO ROZVOJE VZDĚLÁVÁNÍ

Tato prezentace je spolufinancována
Evropským sociálním fondem
a státním rozpočtem České republiky

Outline

- Syllabus Of The Course
- Definition Of Genomics
- Role Of Bioinformatics In Functional Genomics
- Databases
 - Spectre Of „On-line“ Resources
 - PRIMARY, SECONDARY and STRUCURAL Databases
 - GENOME Resources
- Analytical Tools
 - Homologies Searching
 - Searching Of Sequence Motifs, Open Reading Frames, Restriction Sites...
 - Other On-line Genome Tools



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Course Syllabus

- **Chapter 01**
 - Introduction into Bioinformatics
- **Chapter 02**
 - Identification of Genes
- **Chapter 03**
 - Reverse Genetics Approaches
- **Chapter 04**
 - Forward Genetics Approaches



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Course Syllabus

- **Chapter 05**
 - Functional Genomics Approaches
- **Chapter 06**
 - Protein-Protein Interactions And Their Analysis
- **Chapter 07**
 - Current Methods of DNA Sequencing
- **Chapter 08**
 - Structure of genomes



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Course Syllabus

- **Chapter 09**
 - Genome evolution

- **Chapter 10**
 - Genomics and Systems Biology

- **Chapter 11**
 - Practical Aspects Of Functional Genomics
 - Model Organisms,
 - PCR and Primer Design



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Literature

- Literature resources for **Chapter 01**:
 - **Bioinformatics and Functional Genomics**, 3rd Edition, Jonathan Pevsner, Wiley-Blackwell, 2015
<http://www.bioinfbook.org/php/?q=book3>
 - **Úvod do praktické bioinformatiky**, Fatima Cvrčková, 2006, Academia, Praha
 - **Plant Functional Genomics**, ed. Erich Grotewold, 2003, Humana Press, Totowa, New Jersey



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OP Vzdělávání
pro konkurenceschopnost



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GENOMICS – What is it?

- *Sensu lato* (in the broad sense) – it is interested in **STRUCTURE and FUNCTION** of genomes
 - Necessary prerequisite: knowledge of the genome (sequence) – work with databases
- *Sensu stricto* (in the narrow sense) – it is interested in **FUNCTION** of **INDIVIDUAL GENES** – **FUNCTIONAL GENOMICS**
 - It uses mainly the reverse genetics approaches



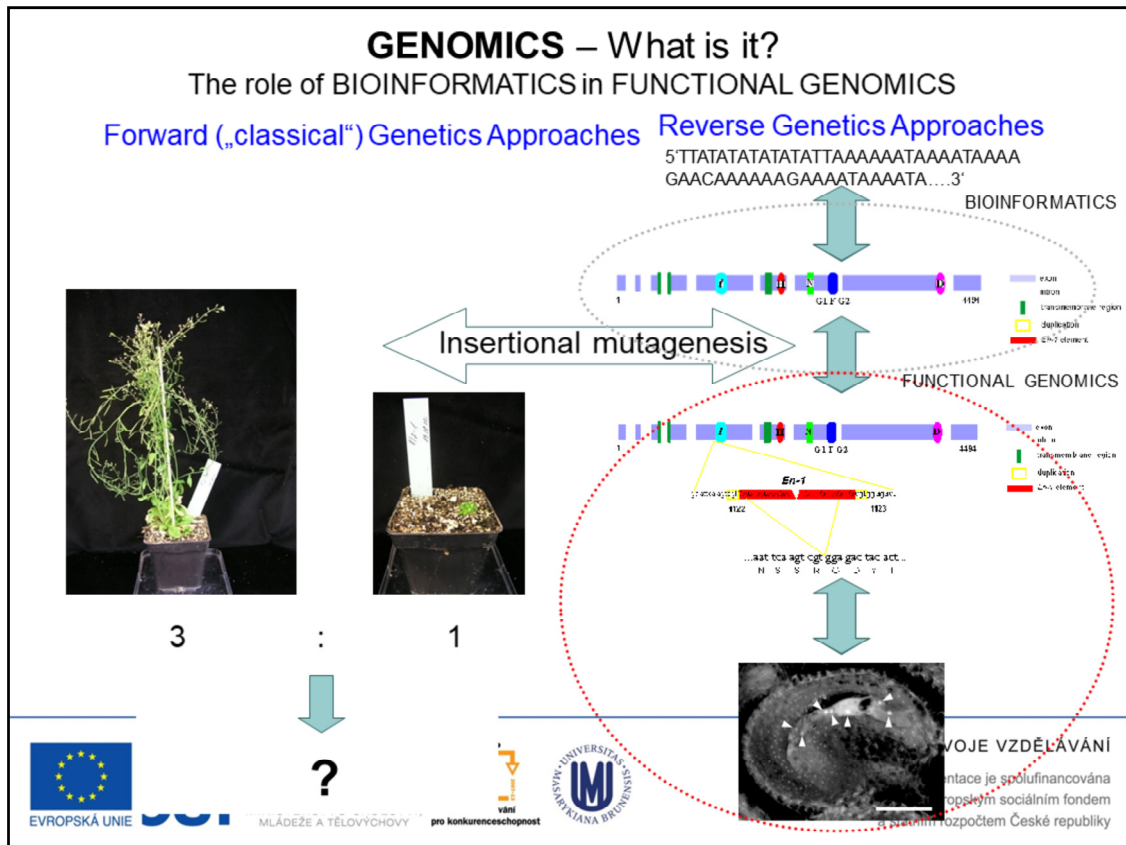
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Genomics is a science discipline that is interested in the analysis of genomes. Genome of each organism is a complex of all genes of the respective organism. The genes could be located in cytoplasm (prokaryotes) nucleus (in most eukaryotic organisms), mitochondria or chloroplasts (in plants).

The critical prerequisite of genomics is the knowledge of gene sequences.

Functional genomics is interested in function of individual genes.



With the knowledge of gene sequences (or the knowledge of the gene files in the individual organisms, i.e. the knowledge of genomes), **Reverse Genetics** appears that allows study their function.

In comparison to "classical" or **Forward Genetics**, starting with the phenotype, the reverse genetics starts with the sequence identified as a gene in the sequenced genome. The gene identification using approaches of **Bioinformatics** will be described later (see Lesson 02).

Reverse genetics uses a spectrum of approaches that will be described in the Lesson 03 that allow isolation of sequence-specific mutants and thus their phenotype analysis.

The necessity of having phenotype alterations in the forward genomics approach introduces important difference between those two approaches. Thus, the gene is no longer understood as a factor (*trait*) determining *phenotype*, but rather as a piece of DNA characterized by the unique *string of nucleotides*. i.e. **physical DNA molecule**.

Outline

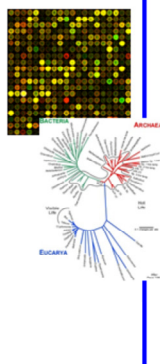
- Syllabus of this course
- Definition of genomics
- Role of BIOINFORMATICS in FUNCTIONAL GENOMICS



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Bioinformatics



- **Definition of Bioinformatics** (according to NIH Biomedical Information Science and Technology Initiative Consortium)

Research, development, or application of computational tools and approaches for expanding the use of **biological, medical, behavioral or health data**, including those to **acquire, store, organize, archive, analyze, or visualize such data.**



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NIH WORKING DEFINITION OF BIOINFORMATICS AND COMPUTATIONAL BIOLOGY

July 17, 2000

The following working definition of bioinformatics and computational biology were developed by the BISTIC Definition Committee and released on July 17, 2000. The committee was chaired by Dr. Michael Huerta of the National Institute of Mental Health and consisted of the following members:

Bioinformatics Definition Committee BISTIC Members Expert Members

Michael Huerta (Chair) Gregory Downing
Florence Haseltine Belinda Seto
Yuan Liu

Preamble

Bioinformatics and computational biology are rooted in life sciences as well as computer and information sciences and technologies. Both of these interdisciplinary approaches draw from specific disciplines such as mathematics, physics, computer science and engineering, biology, and behavioral science. Bioinformatics and computational biology each maintain close interactions with life sciences to realize their full potential. Bioinformatics applies principles of information sciences and technologies to make the vast, diverse, and complex life sciences data more understandable and useful. Computational biology uses mathematical and computational approaches to address theoretical and experimental questions in biology. Although bioinformatics and computational biology are distinct, there is also significant overlap and activity at their interface.

Definition

The NIH Biomedical Information Science and Technology Initiative Consortium agreed on the following definitions of bioinformatics and computational biology recognizing that no definition could completely eliminate overlap with other activities or preclude variations in interpretation by different individuals and organizations.

Bioinformatics: Research, development, or application of computational tools and approaches for expanding the use of biological, medical, behavioral or health data, including those to acquire, store, organize, archive, analyze, or visualize such data.

Computational Biology: The development and application of data-analytical and theoretical methods, mathematical modeling and computational simulation techniques to the study of biological, behavioral, and social systems.

What is bioinformatics?

- **Interface** between the **biology** and **computers**
- **Analysis** of **proteins, genes** and **genomes** using **computer algorithms** and **databases**
- **Genomics** is the **analysis** of **genomes**.

The **tools of bioinformatics** are used to make **sense** of the **billions** of **base pairs** of **DNA** that are sequenced by genomics projects.

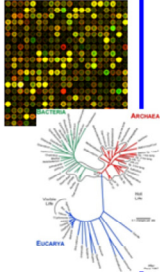
J. Pevsner,
<http://www.bioinfbook.org/index.php>



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Bioinformatics



- **Bioinformatics in functional genomics**
 - **Processing and analysis of sequencing data**
 - Identification of reference sequences
 - Identification of genes
 - Identification of homologues, orthologues and paralogues
 - Correlative analysis of genomes and phenotypes (incl. human)
 - **Processing and analysis of transcriptional data**
 - Transcriptional profiling using DNA chips or next-gen sequencing
 - **Evaluation of experimental data and prediction of new regulations in systems biology approaches**
 - Mathematical modelling of gene regulatory networks



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- Databases
 - Spectre of „on-line“ resources



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Spectre of on-line Resources

EMBLnet National Nodes		
Vienne BioCenter	Austria	http://www.at.emblnet.org/
BBN	Belgium	http://www.be.emblnet.org/
BioBase	Denmark	http://biobase.dk/
CSC	Finland	http://www.fi.emblnet.org/
INFODIGEN	France	http://www.infodigen.fr/
CRISOLINET	Germany	http://genome.zibb-helmholtz.de/biocom/
IMBB	Greece	http://www.imbb.forth.gr/
HIN	Hungary	http://www.hu.emblnet.org/
INCEI	Ireland	http://www.incei.tcd.ie/
JNN	Israel	http://dapsil.wellman.ac.il/bcd/inn.html
JIB-ADN	Italy	http://jib-www.ba.cnr.it/8000/BioWWW/Bio-WWW.htm
CAS/CQARN	Netherlands	http://www.cas.kun.nl/
IBO	Norway	http://www.no.emblnet.org/
IBB	Poland	http://www.ibb.wzpa.pl/
ISC	Portugal	http://www.ig.gulbenkian.pt/
GeneBee	Russia	http://www.genebee.msu.ru/
CNB-CSC	Spain	http://www.es.emblnet.org/
BNC	Sweden	http://www.se.emblnet.org/
SIB	Switzerland	http://www.ch.emblnet.org/
SIGNET	UK	http://www.signet.dl.ac.uk/
EMBLnet Specialist Nodes		
MPS	Germany	http://www.mips.biochem.mpg.de/
IGCB	Italy	http://www.igcb.intec.it/
Pharmacia Uppsala	Sweden	http://www.gnu.com/
FaH/Faasac-La Roche	Switzerland	http://www.roche.com/
EBI	UK	http://www.ebi.ac.uk/
HGMP-BC	UK	http://www.hgmp.mrc.ac.uk/
Sanger	UK	http://www.sanger.ac.uk/
IMBER	UK	http://www.imber.mrc.ac.uk/ibbrowser
EMBLnet Associate Nodes		
IBBN	Argentina	http://iui.biot.unip.edu.ar/emblnet
ANGS	Australia	http://www.angs.usc.edu.au/
CEI	China	http://www.cei.cbi.cas.edu.cn/
CISB	Cuba	http://ibc.cigb.edu.cu/
CFDQ	India	http://falarjung.emblnet.org.in/
SANBE	South Africa	http://www.sanbi.ac.za
USA Information Providers		
NCBI	USA	http://www.ncbi.nlm.nih.gov/
HLM	USA	http://www.nlm.nih.gov/
NDH	USA	http://www.nih.gov/



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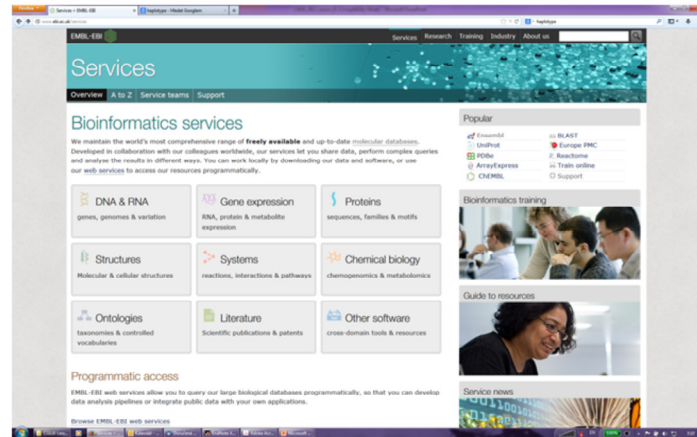
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There are many of on-line resources that could be used.

Spectre of on-line Resources

- EBI <http://www.ebi.ac.uk/services>



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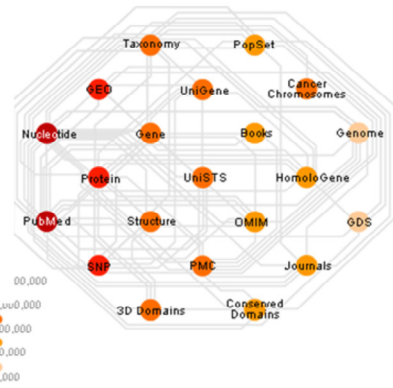
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Nowadays, the resources are interconnected and could be accessed via dedicated web pages. Among the best and mostly used www resources integrating plenty of database resources belong www portal of European Bioinformatics Institute (EBI) in Europe (Germany) and National Center of Biotechnology Information (NCBI) in the USA (

Spectre of on-line Resources

□ NCBI <http://www.ncbi.nlm.nih.gov/>

The screenshot shows the NCBI homepage with a search bar at the top. The main content area includes a 'Welcome to NCBI' message, a 'Get Started' section with links to 'Tools', 'Downloads', 'How-To's', and 'Submissions', and a 'NCBI YouTube channel' section with a 'GO' button. A sidebar on the left lists various resources like 'All Databases', 'Chemicals & Bioassays', 'DNA & RNA', 'Genes & Expression', 'Genetics & Medicine', 'Genomes & Maps', 'Homology', 'Literature', 'Proteins', 'Sequence Analysis', 'Taxonomy', 'Training & Tutorials', and 'Variation'. A 'Popular Resources' list on the right includes PubMed, Bookshelf, PubMed Central, PubMed Health, BLAST, Nucleotide, Genome, SNP, Gene, Protein, and PubChem.



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 - **PRIMARY, SECONDARY and STRUCURAL databases**



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Primary Databases

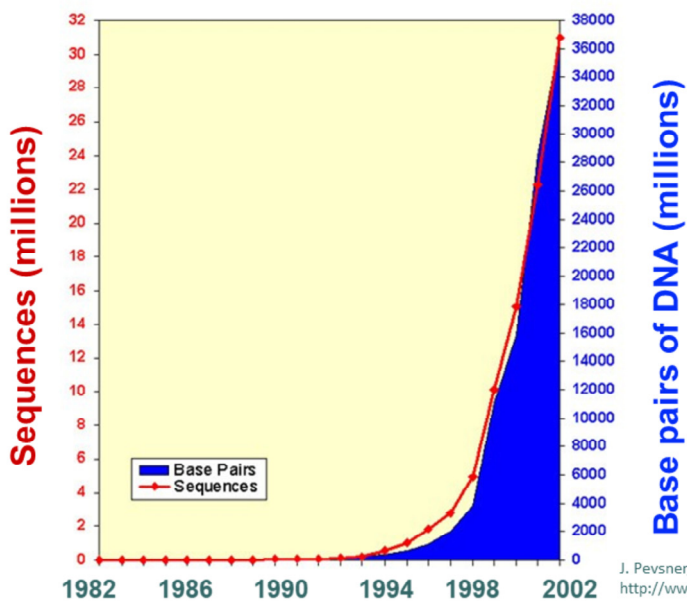
- Include primary datasets – DNA and Protein sequences
 - Sequences in databases of „The Big Three“:
 - EMBL
 - <http://www.ebi.ac.uk/embl/>
 - GenBank,
 - <http://www.ncbi.nih.gov/Genbank/GenbankSearch.html>
 - DDBJ,
 - <http://www.ddbj.nig.ac.jp>
 - Daily mutual exchange and backup of data
 - Works with large amount of data (capacity and software requirements)
 - September 2003 $27,2 \times 10^6$ entries (approx. 33×10^9 bp)
 - August 2005 100×10^9 bp from 165.000 organisms



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Growth of GenBank



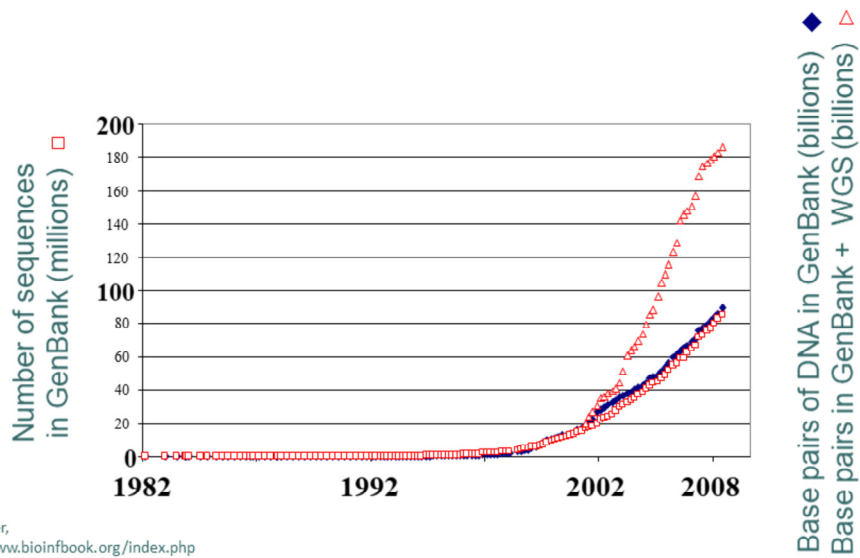
J. Pevsner,
<http://www.bioinfbook.org/index.php>



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Growth of GenBank + Whole Genome Shotgun (1982-November 2008): we reached **0.2 terabases**



J. Pevsner,
<http://www.bioinfbook.org/index.php>

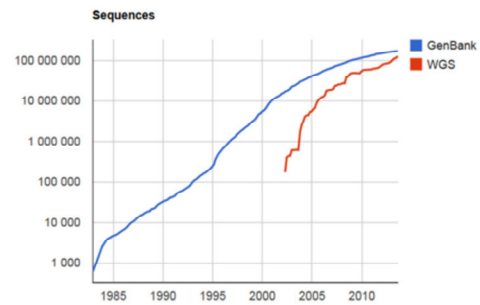
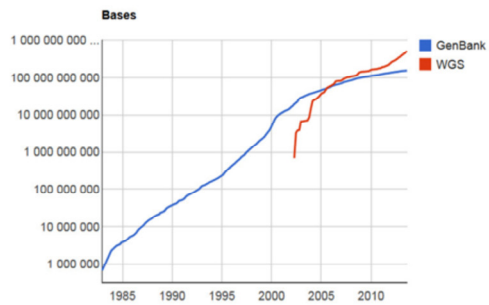


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Growth of GenBank

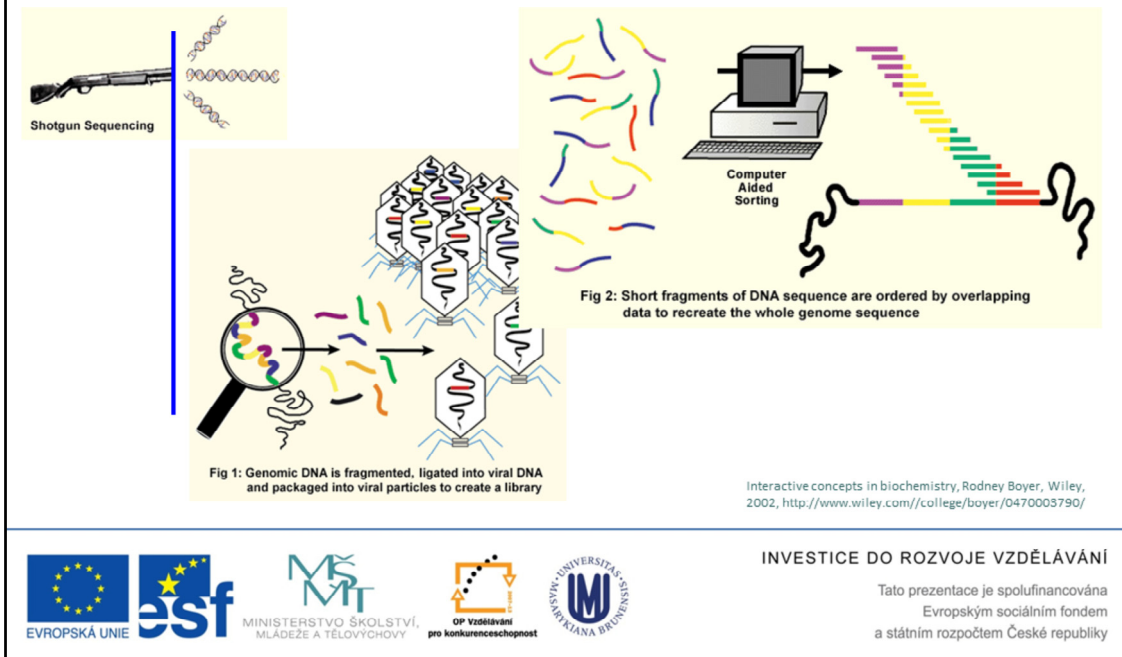
Feb 15 2013



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WGS

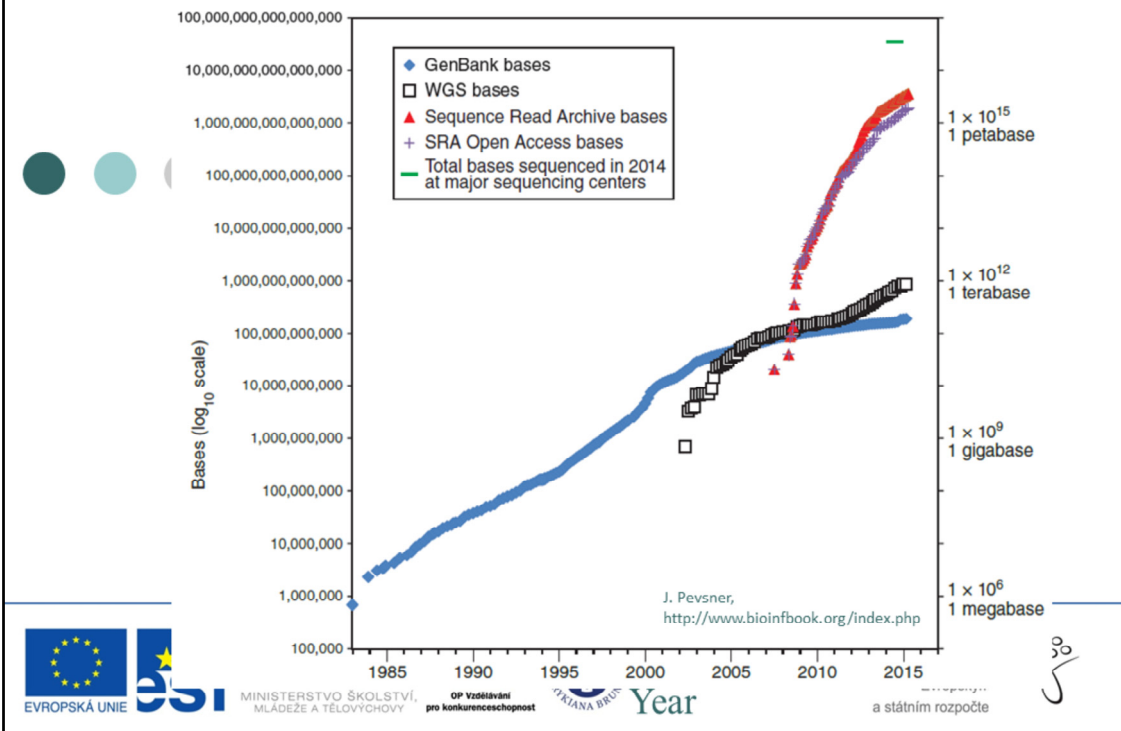


Shotgun sequencing allows a scientist to rapidly determine the sequence of very long stretches of DNA. The key to this process is fragmenting of the genome into smaller pieces that are then sequenced side by side, rather than trying to read the entire genome in order from beginning to end. The genomic DNA is usually first divided into its individual chromosomes. Each chromosome is then randomly broken into small strands of hundreds to several thousand base pairs, usually accomplished by mechanical shearing of the purified genetic material. Each of the short DNA pieces is then inserted into a DNA vector (a viral genome), resulting in a viral particle containing "cloned" genomic DNA (Fig. 1).

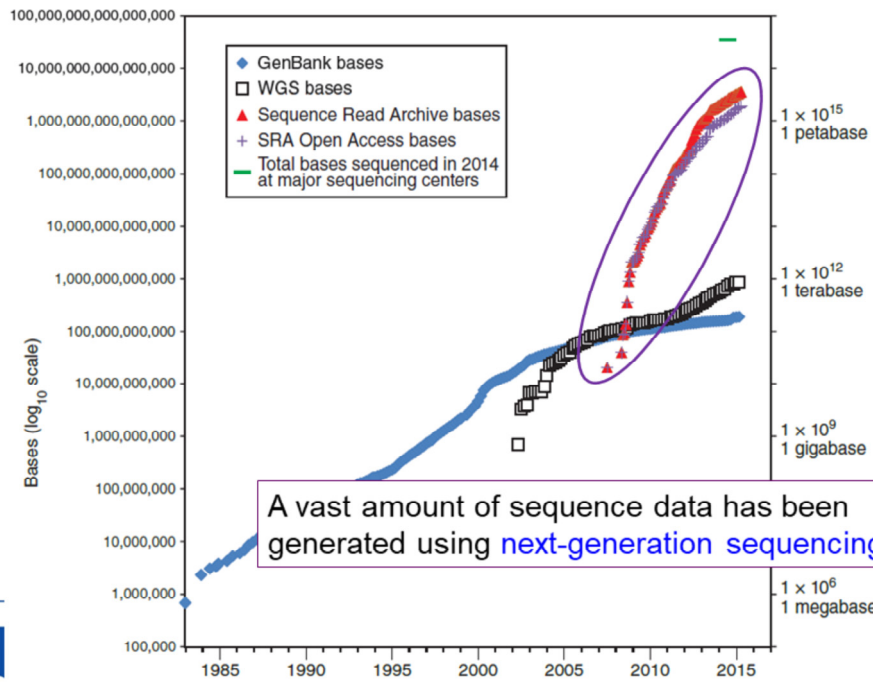
The collection of all the viral particles with all the different genomic DNA pieces is referred to as a library. Just as a library consists of a set of books that together make up all of human knowledge, a genomic library consists of a set of DNA pieces that together make up the entire genome sequence. Placing the genomic DNA within the viral genome allows bacteria infected with the virus to faithfully replicate the genomic DNA pieces. Additionally, since a little bit of known sequence is needed to start the sequencing reaction, the reaction can be primed off the known flanking viral DNA.

In order to read all the nucleotides of one organism, millions of individual clones are sequenced. The data is sorted by computer, which compares the sequences of all the small DNA pieces at once (in a "shotgun" approach) and places them in order by virtue of their overlapping sequences to generate the full-length sequence of the genome (Fig. 2). To statistically ensure that the whole genome sequence is acquired by this method, an amount of DNA equal to five to ten times the length of the genome must be sequenced. (Interactive concepts in biochemistry, Rodney Boyer, Wiley, 2002, <http://www.wiley.com/college/boyer/0470003790/>)

Growth of DNA Sequence in Repositories



Growth of DNA Sequence in Repositories



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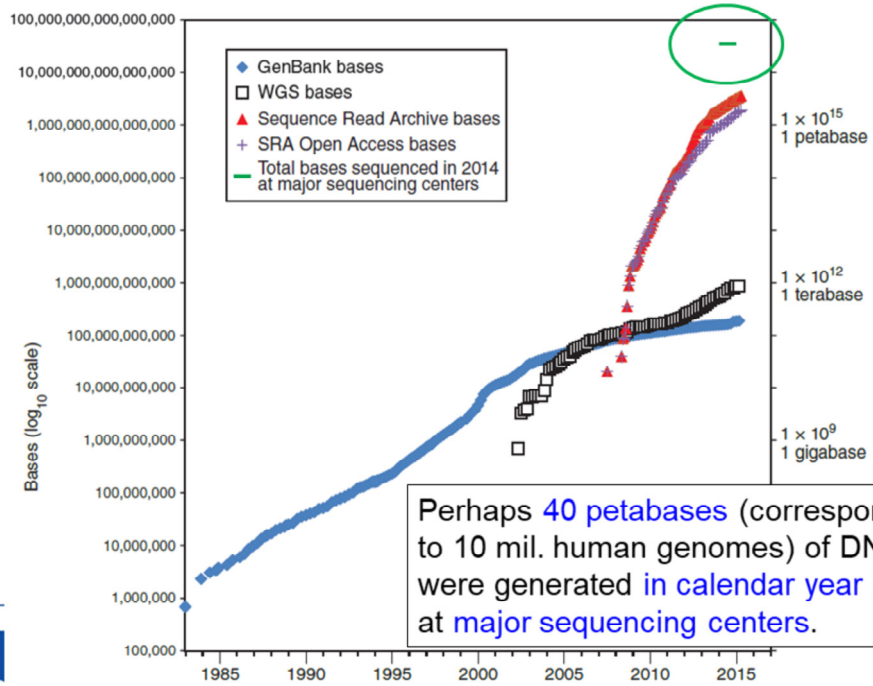
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pro konkurenceschopnost

EVROPSKÝ
ROK
2010

a státním rozpočte



Growth of DNA Sequence in Repositories



Perhaps 40 petabases (corresponding to 10 mil. human genomes) of DNA were generated in calendar year 2014 at major sequencing centers.



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OP Vzdělávání pro konkurenceschopnost

Year

a státním rozpočte

Primary Databases

- They include sets of primary data – [DNA](#) and [Protein](#) sequences
 - Protein sequences:
 - PIR, <http://pir.georgetown.edu/>
 - MIPS, <http://www.mips.biochem.mpg.de>
 - SWISS-PROT, <http://www.expasy.org/sprot/>



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Primary Databases

- Types of sequences in primary databases
 - Standard nucleotide sequences acquired by high quality sequencing
 - **ESTs** (**E**xpressed **S**equences **T**ags)
 - **HGTS** (**H**igh **T**hroughput **G**enome **S**equencing)
 - Results of sequencing projects without annotation
 - **Reference Sequences** of annotated genomes
 - **TPAs** (**T**hird **P**arty **A**nnotation)
 - sequences annotated by third party (by someone else, not the original authors)

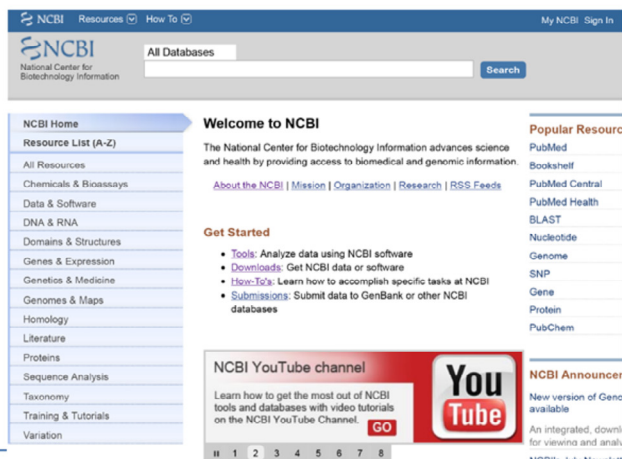


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Primary Databases

GenBank (NCBI) <http://www.ncbi.nlm.nih.gov/>



The screenshot shows the NCBI homepage with a search bar at the top. The main content area includes a 'Welcome to NCBI' message, a 'Get Started' section with links to Tools, Downloads, How-To's, and Submissions, and a 'Popular Resources' list on the right. A 'NCBI YouTube channel' banner is also visible.



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Primary Databases

The screenshot displays the NCBI Gene database entry for the 'suk' gene. Key information includes:

- Gene symbol:** suk
- Gene description:** non-component VWA-like sensor kinase
- Location:** plasmid 01
- Sequence:** NC_023771 (146584..146783)
- Genomic context:** A linear map showing the gene's location on the plasmid.
- Genomic regions, transcripts, and products:** A detailed view of the gene structure with exons and introns.
- Related articles:** A list of four scientific papers related to the gene, with the first article highlighted by a yellow circle.



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Primary Databases

NC_002377.1: 145K..148K (2.9Kbp)

Genes

NP_059797.1

NP_059797.1: two-component VirA-like sensor kinase
total range: NC_002377.1 (145,694..148,183)
total length: 2,490
strand: plus
protein product length: 829

Links & Tools

GenBank View: [NC_002377.1 \(145,694..148,183\)](#), [NP_059797.1 \(145,694..148,183\)](#)
FASTA View: [NC_002377.1 \(145,694..148,183\)](#), [NP_059797.1 \(145,694..148,183\)](#)
BLAST Genomic: [NC_002377.1 \(145,694..148,183\)](#)
Graphical View: [NP_059797.1](#)
BLAST Protein: [NP_059797.1](#)
BLINK Results: [NP_059797.1](#)

Bibliography

Related articles in PubMed



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What is an **Accession Number**?

An accession number is label that used to identify a sequence. It is a string of letters and/or numbers that corresponds to a molecular sequence.

Examples (all for retinol-binding protein, RBP4):

X02775	GenBank genomic DNA sequence	DNA
NT_030059	Genomic contig	
Rs7079946	dbSNP (single nucleotide polymorphism)	
N91759.1	An expressed sequence tag (1 of 170)	RNA
NM_006744	RefSeq DNA sequence (from a transcript)	
NP_007635	RefSeq protein	Protein
AAC02945	GenBank protein	
Q28369	SwissProt protein	
1KT7	Protein Data Bank structure record	

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<http://www.bioinfbook.org/index.php>



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NCBI's important **RefSeq** project: best **representative sequences**

RefSeq (accessible via the main page of NCBI) provides an **expertly curated accession number** that corresponds to **the most stable, agreed-upon "reference" version of a sequence**.

RefSeq identifiers include the following formats:

Complete genome	NC_#####
Complete chromosome	NC_#####
Genomic contig	NT_#####
mRNA (DNA format)	NM_##### e.g. NM_006744
Protein	NP_##### e.g. NP_006735

J. Pevsner,
<http://www.bioinfbook.org/index.php>



INVESTICE DO ROZVOJE VZDĚLÁVÁNÍ

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RefSeq

two-component VIA-like sensor kinase

NCBI Reference Sequences (RefSeq)

Genome Annotation

The following sections contain reference sequences that belong to a specific genome build. [Explain](#)

Reference assembly

Genomic

1. **NC_003065.3**

Range: 18031..18332

Download: [GenBank](#), [FASTA](#), [Sequence Viewer](#), [Graphics](#)

mRNA and Protein(s)

1. **NP_396486.1** two component sensor kinase [Agrobacterium tumefaciens str. C58]

UniProtKB/Swiss-Prot: [E18640](#)

Conserved Domains (3) [summary](#)

cd00075	HATPase_C: Histidine kinase-like ATPases. This family includes several ATP-binding proteins for example: histidine kinase, DNA gyrase B, topoisomerases, heat shock protein HSP90, phytochrome-like ATPases and DNA mismatch repair proteins.
cd00082	HistK: Histidine Kinase A (dimerization/phosphoreceptor) domain: Histidine Kinase A dimers are formed through parallel association of 2 domains creating 4-helix bundles; usually these domains contain a conserved His residue and are activated via ...
PRK13637	PRK13637: two-component VIA-like sensor kinase. Provisional

Location:14 - 833
Blast Score: 2944

Related Sequences



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NCBI's RefSeq project: many accession number formats for genomic, mRNA, protein sequences

<u>Accession</u>	<u>Molecule</u>	<u>Method</u>	<u>Note</u>
AC_123456	Genomic	Mixed	Alternate complete genomic
AP_123456	Protein	Mixed	Protein products; alternate
NC_123456	Genomic	Mixed	Complete genomic molecules
NG_123456	Genomic	Mixed	Incomplete genomic regions
NM_123456	mRNA	Mixed	Transcript products; mRNA
NM_123456789	mRNA	Mixed	Transcript products; 9-digit
NP_123456	Protein	Mixed	Protein products;
NP_123456789	Protein	Curation	Protein products; 9-digit
NR_123456	RNA	Mixed	Non-coding transcripts
NT_123456	Genomic	Automated	Genomic assemblies
NW_123456	Genomic	Automated	Genomic assemblies
NZ_ABCD12345678	Genomic	Automated	Whole genome shotgun data
XM_123456	mRNA	Automated	Transcript products
XP_123456	Protein	Automated	Protein products
XR_123456	RNA	Automated	Transcript products
YP_123456	Protein	Auto. & Curated	Protein products
ZP_12345678	Protein	Automated	Protein products

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Primary Databases

The screenshot displays the NCBI GenBank database interface. The main window shows a genomic map for NC_002377.1 (145K..148K, 2.9Kbp). A gene entry, NP_059797.1, is highlighted in red. A tooltip window is open over this entry, providing the following details:

- NP_059797.1**
- NP_059797.1: two-component VirA-like sensor kinase
- total range: NC_002377.1 (145,694..148,183)
- total length: 2,490
- strand: plus
- protein product length: 829
- Links & Tools**
- GenBank View: [NC_002377.1 \(145,694..148,183\)](#), [NP_059797.1 \(145,694..148,183\)](#)
- FASTA View: [NC_002377.1 \(145,694..148,183\)](#), [NP_059797.1 \(145,694..148,183\)](#)
- BLAST Genomic: [NC_002377.1 \(145,694..148,183\)](#)
- Graphical View: [NP_059797.1](#)
- BLAST Protein: [NP_059797.1](#)
- BLINK Results: [NP_059797.1](#)

Below the tooltip, there are sections for **Bibliography** and **Related articles in PubMed**.



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Secondary Databases

- Databases of **functional** or **structural motifs**, acquired by **primary data** (sequences) **comparison**
- PROSITE, <http://www.expasy.org/prosite/>

[Go to EMBL Home page](#) | [Site Map](#) | [Search EAFAs](#) | [Contact us](#) | [Swiss-Prot](#) | [PROSITE](#) | [Eukaryotic motifs](#)
[Send Us Your Sequence](#) | [Clear site](#) | [Home](#) | [Contact](#) | [Swiss-Prot](#) | [PROSITE](#) | [Eukaryotic motifs](#)

prosite ScanProsite

This program allows to scan a protein sequence (either from [Swiss-Prot](#) or [TrEMBL](#), or provided by the user) for the occurrence of patterns and profiles stored in the [PROSITE](#) database, or to search protein databases with a user-entered pattern ([Reference](#) / [Download ps_scan, the standalone version](#)). The program [PROSITE](#) can be used to generate your own patterns. You may either:

- enter a PROSITE accession number or pattern to search the Swiss-Prot/TrEMBL, and/or PDB databases with a pattern, OR
- enter a sequence or a Swiss-Prot/TrEMBL accession number to scan the sequence with all patterns, profiles and rules in PROSITE, OR
- fill in both fields to find all occurrences of a pattern or profile in a sequence.

Scan a protein for PROSITE matches	Search Swiss-Prot with a PROSITE entry
Enter a Swiss-Prot/TrEMBL accession number (e.g. P01301) or a sequence identifier ID (for example MDIC, BRDML, or a PDB identifier, or paste your own protein sequence in the box below): <input type="text" value="P01301"/> <input type="button" value="Clear"/>	Enter a PROSITE accession number (for example P08125S), or type your pattern in PROSITE format: <input type="text" value=""/> <input type="button" value="Clear"/>
and specify which motifs to use: <input type="checkbox"/> patterns <input type="checkbox"/> profiles <input type="checkbox"/> rules (User Manual) (You may also specify a PROSITE entry in the box to the right) <input type="checkbox"/> Find linked systems with a high probability of occurrence	and specify your search limits: <input type="checkbox"/> The <input type="checkbox"/> Swiss-Prot <input type="checkbox"/> TrEMBL <input type="checkbox"/> TrEMBL/Expasy <input type="checkbox"/> PDB databases (You may also specify a pattern in the box to the left) <input type="checkbox"/> including signal regions <input type="checkbox"/> The following data: <input type="checkbox"/> FASTA format - reports multiple hits with a connection, e.g. Blotting register , Disruption , Not available , in PDB <input type="checkbox"/> Sequences with at least <input type="text" value="100"/> hits <input type="checkbox"/> At most <input type="text" value="1000"/> matches
Your e-mail (optional): <input type="text" value=""/> <input type="checkbox"/> plain text output <input type="button" value="START THE SCAN"/> <input type="button" value="RESET"/>	Advanced options: <input type="checkbox"/> FASTA output <input type="checkbox"/> retrieve complete sequences <input type="checkbox"/> allow at most <input type="text" value="1"/> X sequence characters to match a conserved position in the pattern <input type="checkbox"/> match <input type="checkbox"/> motifs, <input type="checkbox"/> priority overlaps, <input type="checkbox"/> no includes <input type="checkbox"/> the pattern, no-help Prosite database , CDS <input type="checkbox"/> Send us a pattern, see help



MINISTERSTVO ŠKOLSTVÍ,
MLÁDEŽE A TĚLOVÝCHOVY



OP Vzdělávání
pro konkurenceschopnost



MASARYKŮVA UNIVERZITA
BRNO

INVESTICE DO ROZVOJE VZDĚLÁVÁNÍ

Tato prezentace je spolufinancována
Evropským sociálním fondem
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Secondary Databases

- Databases of **functional** or **structural motifs**, acquired by **primary data** (sequences) **comparison**
- PROSITE, <http://www.expasy.org/prosite/>

```
>PDOC00003 PS00003 SULFATION Tyrosine sulfation site [rule] [Warning: rule with a high probability of occurrence].
573 - 585 skneaatTet.e1aae

>PDOC00004 PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site [pattern] [Warning: pattern with a high probability of occurrence].
744 - 747 RRvT
814 - 817 RRzG

>PDOC00005 PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site [pattern] [Warning: pattern with a high probability of occurrence].
148 - 150 EeR
164 - 166 TgR
172 - 173 EeK
219 - 221 EeK
369 - 371 TgR
460 - 462 EeK
513 - 516 EeR
585 - 587 EeR
602 - 604 TgR
610 - 604 TgR
716 - 718 EeR
726 - 728 EeK
747 - 749 TgR
794 - 796 EeR
854 - 856 EeK
884 - 886 EeR
884 - 870 EeR
921 - 923 EeR
957 - 959 EeR
960 - 962 TgR
974 - 976 TgR
997 - 999 EeK
1002 - 1004 TgR
1018 - 1020 EeK
1031 - 1033 TgR
1119 - 1121 EeR
```



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- Databases of **functional** or **structural motifs**, acquired by **primary data** (sequences) **comparison**
- PRINTS, <http://www.bioinf.man.ac.uk/dbbrowser/PRINTS/>



PRINTS is a compilation of protein fingerprints. A fingerprint is a group of conserved motifs used to characterise a protein family; its diagnostic power is refined by iterative scanning of a PRINTS/PF/FAM/STR comparison. Usually the motifs do not overlap, but are scattered along a sequence, though they may be contiguous in 3D space. Fingerprints can encode protein folds and functionalities more flexibly and powerfully than can single motifs, full diagnostic potency deriving from the mutual context provided by motif neighbours. [Reference](#)

New:

- [SPRINT](#) - Search PRINTS-3 evolutionary PRINTS
- [comPRINTS](#) - Search PRINTS automatic map/cluster
- [similarity](#) - Search the integrated InterPro family database

Direct PRINTS access:

- [By accession number](#)
- [By PRINTS code](#)
- [By FASTA code](#)
- [By ID](#)
- [By name](#)
- [By number of motifs](#)
- [By domain](#)
- [By other language](#)

PRINTS search:

- Search PRINTS with **NEW FingerPRINTScan**
- [FPScan](#)
- [U.F.PINScan](#)
- [MULScan](#)
- FingerPRINTScan binaries and source are available: patrick.scofield@bioinf.man.ac.uk

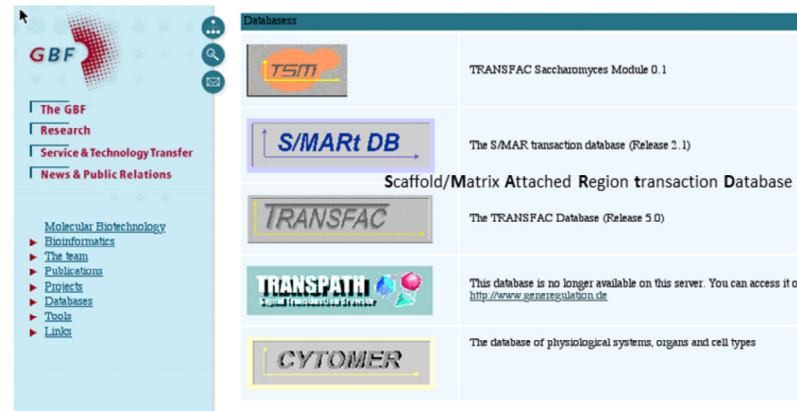


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Secondary Databases

- o TRANSFAC <http://www.gene-regulation.com/>



The screenshot shows the TRANSFAC website interface. On the left is a navigation menu for GBF (German Biotechnology Foundation) with categories like Research, Service & Technology Transfer, and News & Public Relations. The main content area is titled 'Databases' and lists several databases:

Database Name	Description
TSM	TRANSFAC Saccharomyces Module 0.1
S/MARt DB	The S/MAR transaction database (Release 2.1) Scaffold/Matrix Attached Region transaction Database
TRANSFAC	The TRANSFAC Database (Release 5.0)
TRANSPATI	This database is no longer available on this server. You can access it on http://www.gene-regulation.de
CYTOMER	The database of physiological systems, organs and cell types



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S/MARt DB (scaffold/matrix attached region transaction database). This database collects information about S/MARs and the nuclear matrix proteins that are supposed to be involved in the interaction of these elements with the nuclear matrix. <http://transfac.gbf.de/SMARTDB/index.html>

Structural Databases

- o PDB <http://www.rcsb.org/pdb/>

The screenshot shows the PDB website interface. At the top, it says "PROTEIN DATA BANK" with the RCSB logo and navigation links for Home, Contact, and Help. A welcome message states: "Welcome to the PDB, the single worldwide repository for the processing and distribution of 3-D biological macromolecular structure data." Below this are navigation links for "ABOUT PDB", "DATA UNIFORMITY", "RECENT FEATURES", "USER GUIDES", "FILE FORMATS", "EDUCATION", "STRUCTURAL GENOMICS", "PUBLICATIONS", and "SOFTWARE".

On the left side, there are links for "DEPOSIT data", "DOWNLOAD files", "Browse LINKS", "BETA TEST new features", and "BETA release files". Below these are "Current Holdings" statistics: "19623 Structures", "Last Update: 30-Dec-2002", and "PDB Statistics". A "Molecule of the Month" section features a 3D protein structure and the name "Cytochrome c".

The main content area includes a "Search the Archive" section with a search box, a "Find a structure" button, and checkboxes for "query by PDB id only", "match exact word", and "remove sequence homologues". There are also links for "SearchLite" and "Status Search".

On the right side, there is a "PDB Mirrors" section listing various international mirrors such as "San Diego Supercomputer Center", "Rutgers University", "National Institute of Standards and Technology", "Cambridge Crystallographic Data Centre, UK", "National University of Singapore", "Osaka University, Japan", "Universidade Federal de Minas Gerais, Brazil", and "Max Delbrück Center for Molecular Medicine, Germany".

At the bottom of the page, there is a "News" section dated "23-Dec-2002" with a "Happy Holidays from the PDB!" message. A small image of a Christmas tree is visible next to the text.




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Structural Databases

- o PDB <http://www.rcsb.org/pdb/>

Structure Explorer - 1PSY

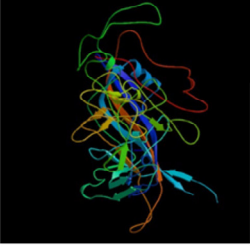
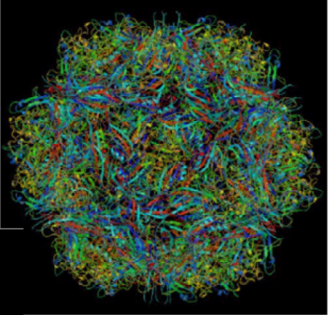
 **Structure Explorer - 1PSY**

Title: The Structure Of Hot Range Controlling Region Of The Capsid Of Canine and Feline Parvovirus and Mutants
Classification: Virus/Viral Protein
Compound: Mol. Id. 1; Molecule: Coat Protein Yp2; Chain: A; Fragment: Sequence Database Residues 190-231; Engineering: Yes; Mutation: Yes
Exp. Method: X-ray Diffraction

 **View Structure**

Summary Information
[View Structure](#)
[Download Display File](#)
[Structural Neighbors](#)
[Geometry](#)
[Other Sources](#)
[Sequence Details](#)

[Search by](#) [Search by](#)



<http://www.rcsb.org/pdb/cgi/structure.cgi?job=graphics&pdb=1PSY&page=pdb-173561064329344&bio=1&opt=show&size=500> 12/20/2003

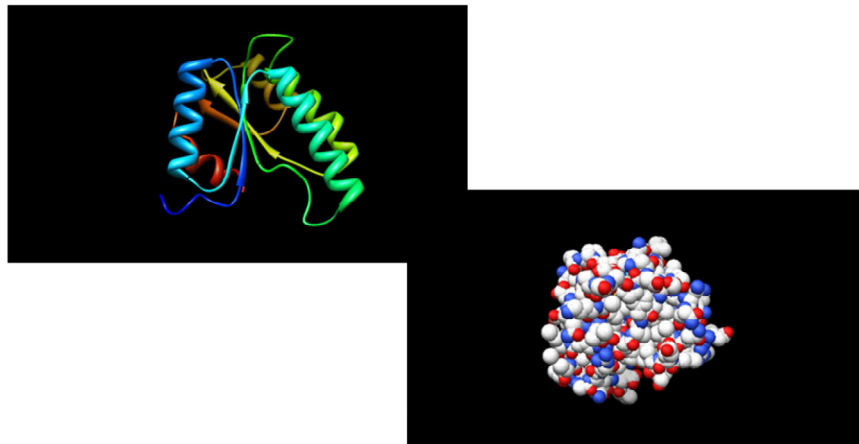


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Structural Databases

- o PDB <http://www.rcsb.org/pdb/>



Pekárová et al., *Plant Journal* (2011)



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Outline

- Syllabus Of The Course
- Definition Of Genomics
- Role Of Bioinformatics In Functional Genomics
- Databases
 - Spectre of „on-line“ Resources
 - PRIMARY, SECONDARY And STRUCURAL Databases
 - **GENOME Resources**



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Genome Resources

Human Genome Browser <http://genome.ucsc.edu/cgi-bin/hgGateway>

The screenshot shows the Human Genome Browser interface. At the top, there's a search bar with fields for 'clade', 'genome', 'assembly', and 'position'. Below this, there's a section titled 'Human Genome Browser - hg19 assembly (sequences)'. It includes a 'Sample position queries' section with a table of requests and their corresponding descriptions.

Request:	Genome Browser Response:
chr7	Displays all of chromosome 7
chr7p_g000212	Displays all of the unpaired contig g000212
20p13	Displays region for band p13 on chr 20
08S1.1000000	Displays first million bases of chr 1, counting from p-arm telomere
chr3:100000-2000	Displays a region of chr3 that spans 2000 bases, starting with position 100000
RH1801:R80175 15q11-15q13 rs154252/rs1600376	Displays region between genome landmarks, such as the STS markers RH1801 and R80175, or chromosome bands 15q11 to 15q13, or SNPs rs154252 and rs1600376. This syntax may also be used for other range queries, such as between unpaired contigs, ESTs, mRNAs, refSeq, etc.
D18S3046	Displays region around STS marker D18S3046 from the Genethon/Manfield maps. Includes 100,000 bases on each side as well.
AQ20414	Displays region of EST with GenBank accession AQ20414 on BRCA1 cancer gene on chr 17
AC081011	Displays region of clone with GenBank accession AC081011
AF382811	Displays region of mRNA with GenBank accession number AF382811
FRNP	Displays region of genome with HUGO Gene Nomenclature Committee identifier FRNP
NM_017414	Displays the region of genome with RefSeq identifier NM_017414
NP_056160	Displays the region of genome with protein accession number NP_056160
pseudogene mRNA	Lists transcribed pseudogenes, but not cDNAs
novelncs csnidat	Lists mRNAs for novel noncoding genes
zinc_finger	Lists many zinc finger mRNAs
knapped_zinc_finger	Lists only knapped-like zinc fingers
huntington	Lists candidate genes associated with Huntington's disease
zeller	Lists mRNAs deposited by scientist named Zeller
Evans, J E	Lists mRNAs deposited by co-author J E. Evans

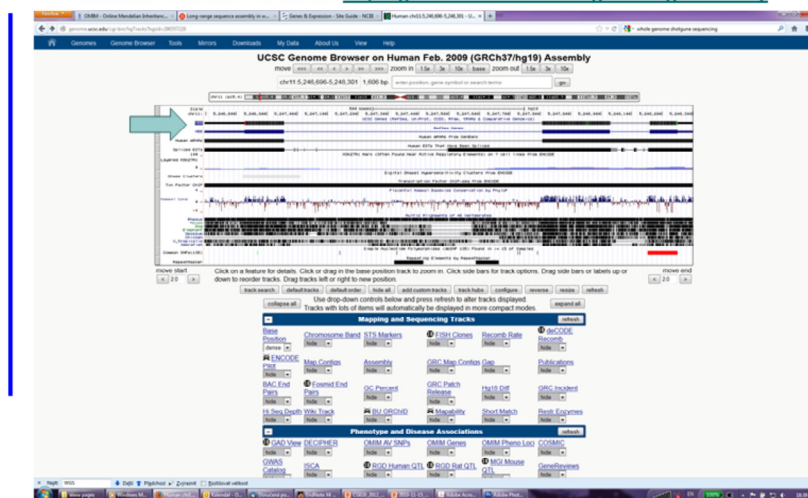


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Genome Resources

□ Human Genome Browser <http://genome.ucsc.edu/cgi-bin/hgGateway>



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Genome Resources

Human Genome Browser <http://genome.ucsc.edu/cgi-bin/hgGateway>

Human Gene HBB (uc001mae.1) Description and Page Index

Description: Homo sapiens hemoglobin, beta (HBB), mRNA.
RefSeq Summary (NM_000518): The alpha (HBA) and beta (HBB) loci determine the structure of the 2 types of polypeptide chains in adult hemoglobin, HbA. The normal adult hemoglobin tetramer consists of two alpha chains and two beta chains. Mutant beta globin causes sickle cell anemia. Absence of beta chain causes beta-zero-thalassemia. Reduced amounts of detectable beta globin causes beta-plus-thalassemia. The order of the genes in the beta-globin cluster is 5'-epsilon - gamma A - delta - beta 2 - beta 1 (provided by RefSeq, Jul 2005). Publication Note: This RefSeq record includes a subset of the publications that are available for this gene. Please see the Gene record to access additional publications. [RefSeq Attributes STATED](#)
Transcript Structure: [Transcript](#) [mRNA](#) [CDS](#) [UTR](#)
Transcription Chromosome: chr11 **Strand:** - **Size:** 1,656 **Start:** 5,245,501 **End:** 5,245,501 **Exon Count:** 3
Coding Size: 1,011 **Start:** 5,245,527 **End:** 5,245,531 **Exon Count:** 3

Page Index: [Sequence and Links](#) [UniProtKB](#) [Comments](#) [Genetic](#) [Associations](#) [CTD](#) [Microarray](#)
[RNA Structure](#) [Protein Structure](#) [Other Species](#) [GO Annotations](#) [miRNA Descriptions](#) [Pathways](#)
[Other Names](#) [GeneReviews](#) [Model Information](#) [Methods](#)

Data last updated: 2011-12-21

Sequence and Links to Tools and Databases

Genomic Sequence (chr11:5,245,501-5,245,501)	mRNA (may differ from genome)	(Protein 147 aa)				
Gene Name	Gene Browser	Protein FASTA	UniProt	Table	Sequence	RefSeq
CSAP	Ensembl	Ensembl Gene	Ensembl Protein	GeneCards	GeneNetwork	
Craps Tissue (HMM)	NCIC	HEP2	Jackson Lab	NCBI		
OMIM	PubMed	Reaction	Standard SOURCE	TrEMBL	UniProtKB	
Wikipedia						

Comments and Description Text from UniProtKB

ID: HBB [HUMAN]
DESCRIPTION: RecName: Full-Hemoglobin subunit beta; AltName: Full-beta-globin; AltName: Full-Hemoglobin beta chain; Contains: RecName: Full-LV-hemophorin 7.
FUNCTION: Involved in oxygen transport from the lung to the various peripheral tissues.
FUNCTION: LVV hemophorin 7 potentiates the activity of bradykinin, causing a decrease in blood pressure.
SUBUNIT: Heterodimer of two alpha-chains and two beta-chains in adult hemoglobin A (HbA).
INTERACTION: P19665 (HBA2_NBEExp-19, HBA3-EB:715554, EBI-714690).
TISSUE SPECIFICITY: Red blood cells.
PTM: Glycosylated non-covalently with the N-terminus of the beta chain to form a stable ketosamine linkage. This takes place slowly and continuously throughout the 120-day life span of the red blood cell. The rate of glycosylation is increased in patients with sickle cell anemia.
PTM: N-glycosylated, a nitric oxide group is first bound to Fe(2+) and then transferred to Cys-64 to allow capture of O(2).
PTM: N-glycosylated on Lys-60, Lys-61 and Lys-145-glycylglycyl residues. PubMed|Hirose et al. reports the identification of HBB acetylated on Lys-145 in the cytosolic fraction of HeLa cells. This may have resulted from contamination of the sample.
MASS SPECTROMETRY: Mass (110) (Method: FAB): Range: 33-42. Source: PubMed|1537274.
DISEASE: Defects in HBB may be a cause of Hereditary spherocytosis (HESAN) (OMIM 181033). This is a form of non-spherocytic hemolytic anemia of Dacie type 1. After splenectomy, which has little benefit, spherocytic inclusions called Heinz bodies are demonstrable in the erythrocytes. Before splenectomy, spherocytosis or paroxysmal nocturnal hemoglobinuria may be evident. Most of these cases are probably instances of hemoglobinopathy. The hemoglobin demonstrates great stability. Heinz bodies are observed also with the hemark syndrome (paroxysmal nocturnal hemoglobinuria) and with galactose permease deficiency.
DISEASE: Defects in HBB are the cause of beta-thalassemia (B-THAL) (OMIM 101113). A form of thalassemia. Thalassemias are common monogenic diseases occurring mostly in Mediterranean and Southeast Asian populations. The hallmark of beta-thalassemia is an imbalance in globin-chain production in the adult HbA molecule. Absence of beta chain causes beta(0)-thalassemia, while reduced amounts of detectable beta globin causes beta(+)-thalassemia. In the severe forms of beta-thalassemia, the excess alpha globin chains accumulate in the developing erythroid precursors in the marrow. Their deposition leads to a vast increase in erythroid apoptosis that in turn causes ineffective erythropoiesis and severe microcytic hypochromic anemia. Clinically, beta-thalassemia is divided into thalassemia major which is transfusion dependent, thalassemia intermedia (of intermediate severity), and thalassemia minor that is asymptomatic.
DISEASE: Defects in HBB are the cause of sickle cell anemia (SCA) (OMIM 603903), also known as sickle cell disease. Sickle cell anemia is characterized by abnormally shaped red cells resulting in chronic anemia and periodic episodes of pain, serious infections and damage to vital organs. Normal red blood cells are round and flexible and flow easily through blood vessels, but in sickle cell anemia, the abnormal hemoglobin (called Hb S) causes red blood cells to become stiff. They are C-shaped and resembles a sickle. These stiff red blood cells can lead to microvascular occlusions thus cutting off the blood supply to nearby tissues.

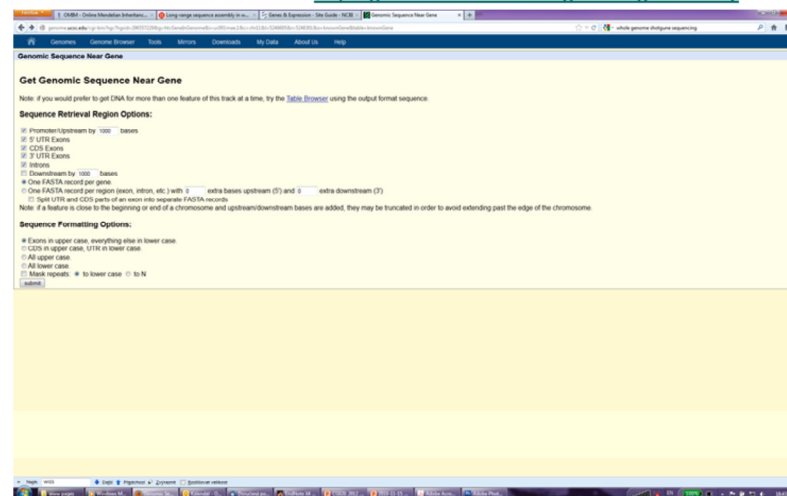


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Genome Resources

Human Genome Browser <http://genome.ucsc.edu/cgi-bin/hgGateway>



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Genome Resources

□ The Arabidopsis Information Resource (TAIR) <http://www.arabidopsis.org>



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Genome Resources

- TAIR, The Arabidopsis Information Resource, <http://www.arabidopsis.org>

The Arabidopsis Information Resource (TAIR) maintains a database of genetic and molecular biology data for the model higher plant *Arabidopsis thaliana*. Data available from TAIR includes the complete genome sequence along with gene structure, gene product information, metabolism, gene expression, DNA and seed stocks, genome maps, genetic and physical markers, publications, and information about the Arabidopsis research community. Gene product function data is updated every two weeks from the latest published research literature and community data submissions. Gene structures are updated 1-2 times per year using computational and manual methods as well as community submissions of new and updated genes. TAIR also provides extensive linkouts from our data pages to other Arabidopsis resources.

The Arabidopsis Biological Resource Center at The Ohio State University collects, reproduces, preserves and distributes seed and DNA resources of *Arabidopsis thaliana* and related species. Stock information and ordering for the ABRC are fully integrated into TAIR.

The NEW arabidopsis.org

We've added new dropdown headers and left navigation bars and reorganized our web pages to make it easier to locate information and resources in TAIR. Please contact us if you experience any problems with our new site.

Breaking News

Data Updates Suspended
[October 19, 2006]
Some TAIR data updates, including loading of new ABRC stocks, will be suspended from Oct 20-Nov 17 while we move our servers.

New Phenotype Search Option
[October 15, 2006]
Search for genes, germplasms, and polymorphisms using associated phenotype, and see improved phenotype data display in results and detail pages.

ASPB Presentations
[August 15, 2006]
Following heavy demand, the TAIR workshop presentations given at the ASPB meeting in Boston have been made available from the TAIR website for download.



INVESTICE DO ROZVOJE VZDĚLÁVÁNÍ

Tato prezentace je spolufinancována
Evropským sociálním fondem
a státním rozpočtem České republiky

Outline

- Syllabus Of The Course
- Definition Of Genomics
- Role Of Bioinformatics In Functional Genomics
- Databases
 - Spectre Of „On-line“ Resources
 - PRIMARY, SECONDARY And STRUCURAL Databases
 - GENOME Resources
- Analytical Tools
 - Homology Searching



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Analytical Tools

□ Global versus Local alignment

Globální přiřazení

```
SLAV-----APATNIK-----PIQNYR-I-----AKSETQRYMVIE  
SLAVYTYIEFVRANAPATNIKSECVRAAPIQNYRRVEHVRATAKSETQRYMVIE
```

Lokální přiřazení

```
SLAVYTYIEFVRANAPATNIKSECVRAAPIQNYRRVEHVRATAKSETQRYMVIE  
-----NAPATNIKSECVRA-PIQNYRRVEHVRA-----
```

Cvrčková, Úvod do praktické bioinformatiky

- **Global Alignment:** only for sequences, which are **similar** and of a **similar length** (BUT can insert spaces into one or both sequences)
- **Global Alignment** is used mainly in case of **multiple alignment** (CLUSTALW, further in the presentation)
- **Local Alignment** provides identification and comparison even in case of alignment of **regions of sequences with high similarity**, e.g. even in case of **change of order of protein domains** during evolution

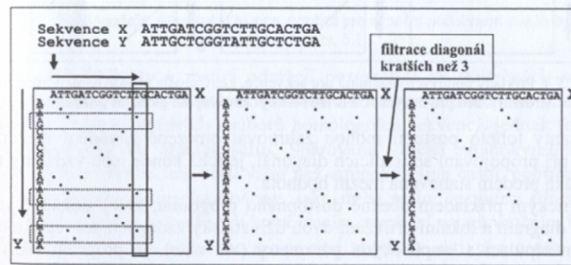


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Analytical Tools

- Choosing the right type of alignment using dotplot



Cvrčková, Úvod do praktické bioinformatiky

- Plotting the sequences against each other (x and y axis)
- Identification of identity in „dot“ of specific size (e.g. 2 bp)
- Filtering the diagonals of lengths lower than a threshold

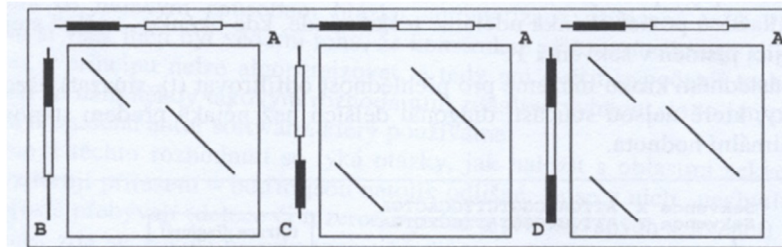


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Analytical Tools

□ Examples of sequence alignment using dotplot



Cvrčková, Úvod do praktické bioinformatiky

- **Global Alignment:** possible **only** for **sequences A and B**
- The rest of the sequences underwent change of order of protein domains and therefore it is necessary to do a local alignment
- Dotplot can be obtained using **BLAST2** (see further in the presentation)



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Analytical Tools

- o BLAST <http://ncbi.nlm.nih.gov/BLAST/>

NCBI *nucleotide-nucleotide* **BLAST**
Nucleotide Protein Translations Retrieve results for an RID

[Search](#)

```
aacccacccggaacaccatcatcattatcaccatc atcgcttttgg ggcgatgttg tctgggttcca  
gcygtattaat  
ataattaatt tattccacat gagatgatgat atgatataact atgtattttt  
tttttttttt  
ttattttgtaa acotttaata taacaagaac tacaaaaaat gaaaa
```

[Set subsequence](#) From: To:

[Choose database](#)

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

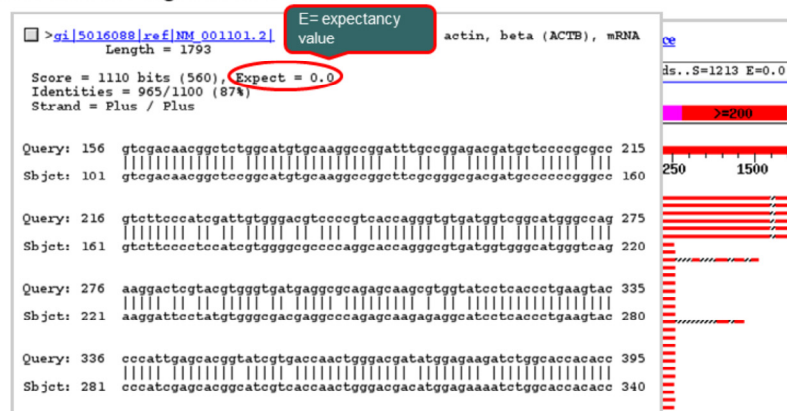


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BLAST

Basic Local Alignment Search Tool



- „expectancy value“ provides the number of expected sequence number with the same or higher similarity when searching in the database consisting of randomly assembled sequences
- the results shows fraction of identical and in case of proteins also similar sequence positions and/or inserted spaces



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Primary Databases

NC_002377.1: 145K..148K (2.9Kbp)

Genes

NP_059797.1

NP_059797.1: two-component VirA-like sensor kinase
total range: NC_002377.1 (145,694..148,183)
total length: 2,490
strand: plus
protein product length: 829

Links & Tools

GenBank View: [NC_002377.1 \(145,694..148,183\)](#), [NP_059797.1 \(145,694..148,183\)](#)
FASTA View: [NC_002377.1 \(145,694..148,183\)](#), [NP_059797.1 \(145,694..148,183\)](#)
BLAST Genomic: [NC_002377.1 \(145,694..148,183\)](#)
Graphical View: [NP_059797.1](#)
BLAST Protein: [NP_059797.1](#)
BLINK Results: [NP_059797.1](#)

Bibliography

Related articles in PubMed



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BLINK is a link to the pre-computed BLAST search results for the respective sequence (see the next slide).

BLAST

Basic Local Alignment Search Tool

Pre-computed BLAST results for: [a16119781rvf/NP_396485.1](#) two component sensor kinase [Agrobacterium tumefaciens str. C58]
 Matching gis: [15163423.20141874-1019660](#)
 Total (score > 100) : 147086 hits in 146754 proteins in 6309 species
 Selected: 147086 hits in 146754 proteins in 6309 species Filter: Min Score: 100 |
 Other views (Reports): [Taxonomy report](#) | [Multiple Alignment](#) | [Blast](#)
[Reset all filters](#)

Choose Display Options

1203 Archaea 138295 Bacteria 13 Metazoa 1349 Fungi 554 Plants 6 Viruses 5676 The Others [reset selection](#)

Results: 1 - 100 [Next Page](#) [Last](#)

% hits	Score	Accession	Length	Protein Description
833 aa				
4166	AM99527	833	two component sensor kinase [Agrobacterium tumefaciens str. C58]	
4166	P18540	833	ProName: Full-Wide host range virA protein Short-WDR virA	
4166	AAA79262	833	virA [Plasmid pTIC58]	
4159	NP_053300	833	hypothetical protein pT1-GAMMA_p142 [Agrobacterium tumefaciens]	
4159	AAA07765	833	tiorf140 [Agrobacterium tumefaciens]	
4153	AAA91590	833	virA [Plasmid Ti]	
4153	g11737127	833	virA protein	
4153	CAA34777	833	91.3 kDa protein [Agrobacterium tumefaciens]	
3800	CAA33380	829	virA [Agrobacterium rhizogenes]	
3718	g11227240	849	virA gene	
3348	AAA88643	829	virA [Plasmid Ti]	



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BLAST

Specialized Versions

- Currently there exists a lot of specialized versions of BLAST
 - Searching according to source (organism) of sequences, e.g. known genomes of microorganisms
 - **BLASTP**
 - Given the **protein query**, it returns the most similar protein sequences from the **protein database**.
 - **BLASTN**
 - Given the **DNA query**, it returns the most similar DNA sequences from the **DNA database**.
 - Other variants, e.g. **MEGABLAST**, for identification of identical or **very similar sequences** (searches **long similar regions** of nucleotide sequences)
 - **BLASTX**
 - Compares the all possible **six-frame translation products** of a **nucleotide query sequence** (both strands) against a **protein sequence database**.



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BLAST

Specialized Versions

- Currently there exists a lot of specialized versions of BLAST
 - **TBLASTN**
 - Compares a **protein query** against the **all six reading frames** of a **nucleotide sequence database**.
 - **TBLASTX**
 - Translates the **query nucleotide sequence** in **all six possible frames** and compares it against the **six-frame translations** of a **nucleotide sequence database**.



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BLAST

Specialized Versions

- Currently there exist a lot of **specialized versions** of **BLAST**
 - **PSI-BLAST** (**P**osition-**S**pecific **I**terated **B**last)
 - **First step: standard BLAST**, during which PSI-BLAST identifies a **list of similar sequences** with **E value better than minimal value** (standard = 0,005)
 - For every alignment, PSI-BLAST creates so-called **PSSM** (**P**osition **S**pecific **S**ubstitution **M**atrix)
 - **PSSM** takes into account **relative frequency of specific aminoacid residue in a specific position** within sequences identified as similar in first step, which can mean functional conservation.



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BLAST

Specialized Versions

- Currently there exists a lot of specialized versions of BLAST
 - **PHI-BLAST (Pattern-Hit Initiated BLAST)**
 - For identification of **specific sequence**, e.g. motif (pattern) in sequence of similar protein sequences
 - Sequence of motif must be inserted using **special syntax**:
 - [LVIMF] means either Leu, Val, Ile, Met or Phe
 - - is spacer (means nothing)
 - x(5) means 5 positions in which any residue is allowed
 - x(3, 5) means 3 to 5 positions where any residue is allowed



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BLAST

Specialized Versions

□ Example of search by PHI-BLAST

```
>gi|4758958|ref|NP_004148.1| Human cAMP-dependent protein kinase  
MSHIQIPPGLELLQGYTVEVLRQQPPDLVEFAVEYFTRLREARAPASVLPAAATPRQSLGHPPPPEPGPDR  
VADAKGDSSESEDEDELEVVPVPSRFNRRVSVCAETYNPDEBBEDTDPRVIHPKTDEQRCRLQBEACKDILLF  
KNLDQEQLSQVLDAMFERIVKADHEVIDQGDDGDNFYVIERGTYDILVTKDNQTRSVGQYDNRGSFGELA  
LMYNTPRAAITVATSEGLWGLDRVTFRRIIVKNNAKRRKMFESFIESVPLLSLEVSRMKIVDVIGEK  
IYKDGERRIITQGEKADSFYIIBSGEVSILIRSRTKSNKDGNGQBEVEIARCHKGQYFGBLALVINKPRAAS  
AYAVGDVKCLVMDVQAFERLLGPCMDIMKRNI SHYBQLVKMFGSSVDLGNLGQ
```

```
[LIVMF] -G-B-x- [GAS] - [LIVM] -x(5,11) -R- [STAQ] -A-x- [LIVMA] -x- [STACV] .
```



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 - GENOME Resources
- Analytical Tools
 - Homologies Searching
 - Searching Of Sequence Motifs, Open Reading Frames, Restriction Sites...



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Analytical Tools

- o <http://workbench.sdsc.edu/>

Biology WorkBench
click here to toggle between menus and buttons
NE Moved! <http://workbench.sdsc.edu/>
Version 3.2

Session Tools Protein Tools **Nucleic Tools** Alignment Tools Structure Tools (Alpha)

beta-glucosidase

GBPLN:804655 Hordeum vulgare L. beta-glucosidase (BGQ60) gene, complete cds.
 GBPLN:170248 Nicotiana tabacum glucan beta-1,3-glucosidase gene, complete cds.

Select All Deselect All Nbjinn BATCH Add Edit Delete Copy View Download ViewRecords

BLSEQ BLSEQX BLASTN BLASTX TBLASTX FASTA FASTX FASTY SSEARCH CLUSTALW
CLUSTALWPROF ALIGN LALIGN LFASTA PATTERNMATCHDB PATTERNMATCH TACG PRIMER3
NASTATS BESTSCOR PFSCAN PRIMERCHECK PRIMER3M SIXFRAME REVCOMP RANDSEQ

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SE



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Analytical Tools

- o <http://workbench.sdsc.edu/>

View
View Nucleic Sequence(s)

Format: Fasta Case: Upper Change Format

[Download/View all sequences in text format](#)

[\[NEXT\]](#) [\[BOTTOM\]](#)

Nicotiana tabacum glucan beta-1,3-glucosidase gene, complete cds.
GBPLN:170248, 4699 bp

> 170248
GAGCTCCCTTGGGGGGCAAGGGCAAAAACCTTTTGGCTAAATGGAAAAATATATACC AAGTGTGTTGTAATA
GTTACTCAATTTGAATTAACAAGGGGCAAAATTTGACTATTTTGGCCCTTATATCTTTTGGTCACA AAAAC
ATAAAATATCCCATCCGAAATTCCAAATGGTCCATTATCGGCAAGTAGCTTCTTTAATTTAGTTAGTT
GACAAAACACTATCAAGATATCATTAATTAATAATAAATCTCAAGTCCATCATCTTAGCTGCTCCTCA
GTTAGAGCCCGAGTAAATAGACCGATCAATAAAGCCCGCATTAATAATAGAAATTTAGGACTCTC
GATTTGGACGTAACTCCAAAACCTTTCCAAATCTTTTCCCAAGCTTTGGGGCTCCAGGTTCTAGCTTC
CAGATATGGGATATTTCTAGTTTATCTCTTAATTTACATCTCAACTAATATTAAGAAATTAACAGGTA
CAGCAATCATAAAATTTCTCTTAAGAAAGCAATGAATCCGGTTACTGATTCATTGGCCTTTTCAGAG
TCATGATCCCATATTCCTAAGGGGTCGTTTGGTACAGAAATTAATAATAATTTGGGATAGAAATTT
GAGATTCATTTATCTTTGTTTAAATTAAGATTTAGCTAATTCAGAAATTAATTTGCTTAAATATAG
TAAATCACTTTCACATGTAGAAAGTGAATGGATAGCTAATCCCATAGCCACTCACTAGATATTC
TTAATTTATCTACATTTTACCAAATGATCGTTAGTCTTCATAGAGATCCAGTATCTCAATAAATGCA
GTAGAAAGTTAGAAAATTTCTAATTAATCAATTCATATAATTTAAAATATTAGATATGGAGCACTTAG
ATACATAAAGATGTACCGTTAATAATAAAGATAAGATAGATTTTAAATAGGAAAAAAAACGGTT
CGAGACTCTTTATGGGAAGGGGTGCTCTCAAGTAGATTCATTCATTTGCTCTGGTGCANTAGCAAAA
TACACTTTGCTCTTAGATTCAGCCGAGCCACTTCATCTCTTATTTATCTCAAAATGAAGTTTTA
GGAACCTTCAAACTTCAACTACTTTTAAAGGAAATTCAAAATACGACCAATTTATTTACTTACTAC
TTATAGTTAAATGATATGAATTTTAAATTTGAATTTGAAAATATTAATTTACTTGATTTAATATA



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Regex pattern:

ott. {1, 32}ott

0 sequences were searched

1 match was found

Matches are indicated in blue

```
>170248
GAGCTCCCTTGGGGGGCAAGGGCAAACCTTTGGCTAAATGGAAAAATATATACCAAGTGTGTAATA
GTIATCAATTTGAAMTAACAAAGGGGCAAAATTTGACTATTTTGGCCCTTATATCTTTTGGTCACAAAAAC
ATAAAATATCCCATCCGAATTCGAATGGTCCATATCGGCAAGTAGCTTTCTTTTAAITTAGTITAGTT
GACAAACCTATCCAGATATCTATTATTAATTAATTAATTTCAAGGGTCTCTTTAGTCCCTCTCA
GTAGAGCCGCCAGTAAATAGACCGATCAANTAAAGCCGCCATTAATAATGAATTTTGGACTCTC
GATGGCACGTAAAGTCCAAAACCTCTCCAAATCTTGGCTGCAACTTGGGGCTGTAGGTTCTGAGCTTC
CAGATATGGGATATCTAAGTTTATCTCCTAATTCATCTCAACTAATTAAGAAATTAACAGGTA
CAGCAAKTATAAAATTTCTCTAAAGAGACAAATCCGGTTACTATTCATGSSCTTTCTAGAG
TCTGATGCCATATTCACDAAGGGGCTGTTGGTACAAGAAATAATAATAATTTCCGGATAGAAATTT
TAAATCAACTATACATGTAGAGGTGGAATGGAATAGTAATCCCATAGCCACTCACATAGAAATCC
TATTTATCTCACTATTTTACCAAATGATCGGTTAGTCTCATAGAAATCCAGTATCCCAATTAATGCA
GTAGAAATTTAGAAATTTTCAATTAATCAATTCATTAATTTTAAAAATTTAGATTTGGACACTTAG
ATACAATAAAGATGTACCGTAAATAAAGATAGATAGAGTTTAAATAGGAAAAAAAACCGGTT
CGAGACACTTTATGGAGGGCTTGTCTCAAGGTAGATCTCATTCATTTGCTCTGGTCAATAGCAAAA
TGACATTTACTCTTAGATACAGCGACCTCTACAACTTCTATTTGTAATCTAAATGAAAGTTTAA
GAGAACTTAAATCTTCACTAGCTTTTAGGGAAATCAAAATACGACCAATTTATTAATTTACTTAC
TTATGTTAAATGATAGAAATTTATTTAAATTTGAAATGAAATTTAAATTTAGATTTAATATAA
ACAATAGATATCGCTAAGTATTTACCACAACATGGAGATACACAGAAGATTTATTTATTTGTAACGAT
GATTAAGCAGCTATTCATCTGGTTGTGCAAGGATGAAGAAAGTAACAGCTATTAATTTCTTTGTAAGT
```



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Analytical Tools

- o <http://workbench.sdsc.edu/>

Frame 1, 1 stop codon

Nicotiana tabacum glucan beta-1,3-glucosidase gene, complete cds. Tran

>170248 Translated - Frame 1
ELPWGARA K L FAKWKNI I P S V C N S Y S I * I N K G A N L T I L P L

E L P W G A R A K L F A K W K N I I P S
1 g a g c t c c o t t g g g g c a a g g g c a a a a c t t t t g c t a a t g g a a a a t a t t a t a c c a a g t 60
V C N S Y S I * I N K G A N L T I L P L
61 g t t t g t a a t a g t t a c t c a a t t t g a a t t a a c a a a g g g c a a a t t g a c t a t t t t g c c o t t a 120

Frame 2, 1 stop codon

Nicotiana tabacum glucan beta-1,3-glucosidase gene, complete cds. Tran

>170248 Translated - Frame 2
S S L G G Q Q N F L L N G K I L Y Q V F E L T R G Q I * L F C P

S S L G G Q Q N F L L N G K I L Y Q V
2 a g c t c c o t t g g g g c a a g g g c a a a a c t t t t g c t a a t g g a a a a t a t t a t a c c a a g t 61
F V I V T O F E L T K G O I * L F C P
62 t t t g t a a t a g t t a c t c a a t t t g a a t t a a c a a a g g g c a a a t t g a c t a t t t t g c c o t t a 120



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Analytical Tools

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```
== Linear Map of Sequence:

      SbyI
      BsaJI
      CviJI
      AluI
      SacI
      EcoICRI
      Bsp1286I
      BsiHKAI
      BanII  BslI
      \ \ \ \ \
1 gagctcccttgggggcaagggaacaaacttttgcataatgaaaaatattataccaagt 60
ctcgagggaacccccctccgctttgaaaaagattaccttttataataggttca
      * * * * *
1 E L P W G A R A K L F A K W K N I I P S
2 S S L G G Q G Q N F L L N G K I L Y Q V
3 A P L G G K G K T F C * M E K Y Y T K C
4 L E R P P C P C F K K S F F F I N Y W T
5 S S G Q P A L A F S K A L H F F I I G L
6 L A G K P P L P L V K Q * I S F Y * V L

      Tsp509I
      MaeIII Tsp509I  MseI
      \ \ \ \ \
61 gtttgaatgcttactcaattgaattaacaaagggaacaaattgactattttgcocctta 120
caaacattatcaatgagttaaacttaattgtttccccgttaaacgtataaacggggaat
      * * * * *
1 V C N S Y S I * I N K G A N L T I L P L
2 F V I V T Q F E L T K G Q I * L F C P *
3 L * * L L N L N * Q R G K F D Y F A L R
4 N T I T V * N S N V F P C I Q S N Q G *
5 T Q L L * E I Q I L L P A F K V I K G K
6 H K Y Y N S L K F * C L P L N S * K A R
```

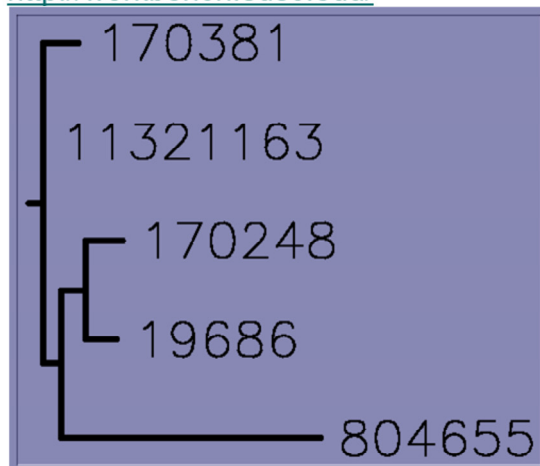


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Analytical Tools

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Analytical Tools

- VPCR <http://grup.cribi.unipd.it/cgi-bin/mateo/vpcr2.cgi>

SEARCH  ABOUT DOWNLOAD LINKS

VPCR 2.0 (WWW interface) - Please, enter nucleotide primer sequences (IUB codes allowed for degenerate primers). VPCR 2.0 searches the specified database for matches to the primers. If matches are found within 10000 bases, a PCR simulation model predicts amplification. Calculated PCR products are displayed within a minute.

NOTE: Abilities of VPCR 2.0 are still limited by BLAST capabilities and settings, as well as instability of our current software to deal with more than a couple thousand matches per primer. For example, using primers shorter or roughly equal to our 11-base word size misses most matches. Primers with overrepresented sequences cause problems as well. We are now busy solving most of these problems, please, be patient. If you have a minute, please, let us know what kind of expectations you have for VPCR 2.0 etc. Currently, this address is for testing VPCR 2.0, stable features will be installed on [VPCR 2.0 Homepage](#).

Search using: BLAST in the database for: M. musculus

Primer 1
Primer 2
Primer 3
Primer 4
Primer 5
Primer 6
Primer 7
Primer 8

Annealing temperature: 50

Do PCR! 



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Analytical Tools

- VPCR <http://grup.cribi.unipd.it/cgi-bin/mateo/vpccr2.cgi>



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Outline

- Syllabus Of The Course
- Definition Of Genomics
- Role Of Bioinformatics In Functional Genomics
- Databases
 - Spectre Of „On-line“ Resources
 - PRIMARY, SECONDARY And STRUCURAL Databases
 - GENOME Resources
- Analytical Tools
 - Homologies Searching
 - Searching Of Sequence Motifs, Open Reading Frames, Restriction Sites...
 - Other On-line Genome Tools



MINISTERSTVO ŠKOLSTVÍ,
MLÁDEŽE A TĚLOVÝCHOVY



OP Vzdělávání
pro konkurenceschopnost



INVESTICE DO ROZVOJE VZDĚLÁVÁNÍ

Tato prezentace je spolufinancována
Evropským sociálním fondem
a státním rozpočtem České republiky

Other On-Line Genome Resources

- TIGR (The Institute for Genomic Research, <http://www.tigr.org/software/>)
 - Recently part of the J. Craig Venter Institute

The screenshot displays the NCBI Gene database entry for PHACTR4. The main heading is "PHACTR4 phosphatase and actin regulator 4 [Homo sapiens]". Below this, the "Summary" section provides key information: Official Symbol (PHACTR4), Official Full Name (phosphatase and actin regulator 4), Location (11q25.3), Gene type (protein-coding), RefSeq status (REVIEWED), Organism (Homo sapiens), and a detailed "Summary" paragraph describing the gene's function and its relationship to the PP1 family. The "Genomic context" section shows the gene's location on Chromosome 1, NC_000011.10, with a diagram of the chromosome and a zoomed-in view of the gene structure. The "Genomic regions, transcripts, and products" section lists various genomic features and provides links to reference sequence details and the nucleotide sequence.



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řídí Ministerstvo školství, mládeže a tělovýchovy
Česka

Other On-Line Genome Resources

- Online Mendelian Inheritance in Man (OMIM)



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Discussion



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