Základy genomiky

I. Úvod do bioinformatiky

Jan Hejátko

Masarykova univerzita, Laboratoř funkční genomiky a proteomiky
Laboratoř molekulární fyziologie rostlin

Základy genomiky I.

- Zdrojová literatura ke kapitole I:
  - Plant Functional Genomics, ed. Erich Grotewold, 2003, Humana Press, Totowa, New Jersey

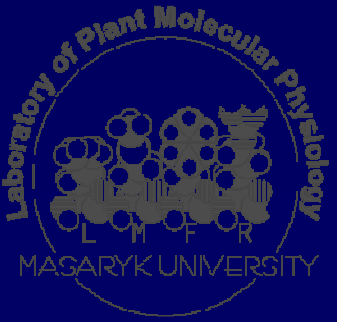
Základy genomiky I.

- Role BIOINFORMATIKY v současném pojetí FUNKČNÍ GENOMIKY
- Databáze
  - Spektrum „on-line“ zdrojů
  - PRIMÁRNÍ, SEKUNDÁRNÍ a STRUKTURÁLNÍ databáze
  - GENOMOVÉ zdroje
- Analytické nástroje
  - Vyhledávání homologií
  - Vyhledávání sekvenčních motivů, otevřených čtecích rámců, restrikčních míst….
  - Další www genomové nástroje

Základy genomiky I.

GENOMIKA-co to je?

- V širším pojetí-zkoumá **STRUKTURU** a **FUNKCI** genomů
  - Předpokladem je znalost genomu (sekvencí)- práce s databázemi
- V užším pojetí zkoumá FUNKCI jednotlivých genů - **FUNKČNÍ GENOMIKA**
  - používá zejména přístupy REVERZNÍ GENETIKY



GENOMIKA-co to je?

role BIOINFORMATIKY ve FUNKČNÍ GENOMICE

Přístupy „klasické“ genetiky

3 : 1

?

„Reverzně genetický“ přístup

5‘TTATATATATATATTAAAAAATAAAATA
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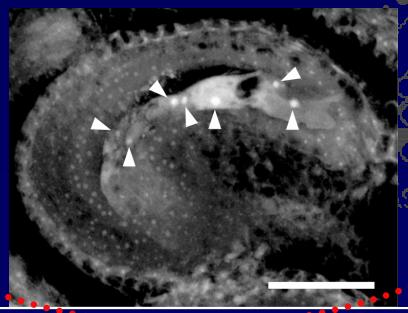
BIOINFORMATIKA

inzerční mutageneze

FUNKČNÍ GENOMIKA



Základy genomiky I.

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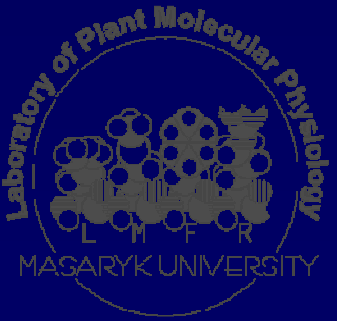
Databáze

Spektrum on-line zdrojů

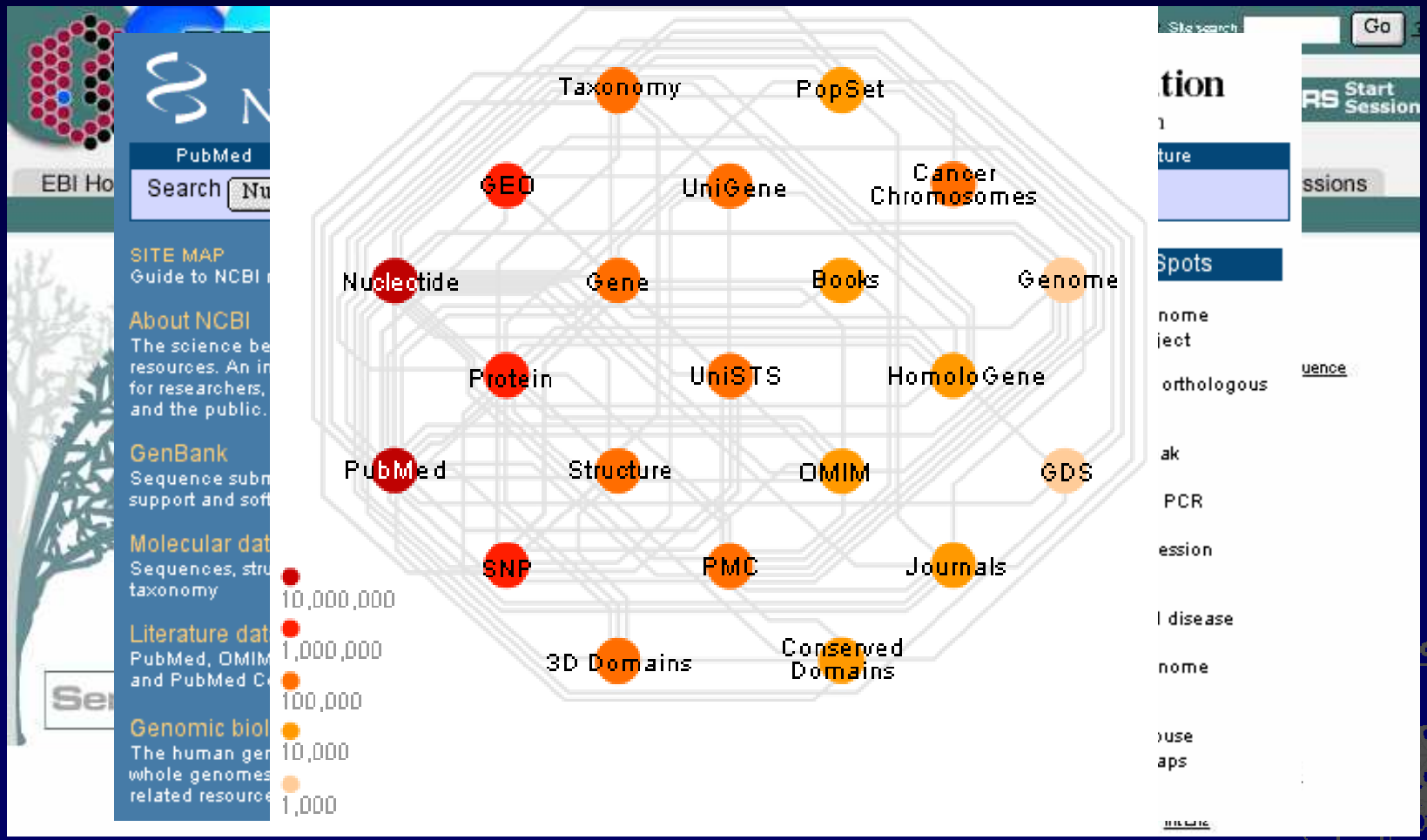
EMBnet National Nodes		
Vienna Biocenter	Austria	http://www.at.embnet.org/
BEN	Belgium	http://www.be.embnet.org/
BioBase	Denmark	http://biobase.dk/
CSC	Finland	http://www.fi.embnet.org/
INFOBIOGEN	France	http://www.infobiogen.fr/
GENIUSnet	Germany	http://genome.dkfz-heidelberg.de/biounit/
IMBB	Greece	http://www.imbb.forth.gr/
HEN	Hungary	http://www.hu.embnet.org/
INCBI	Ireland	http://acer.gen.tcd.ie/
INN	Israel	http://dapsas.weizmann.ac.il/bcd/inn.html
IEN-ADR	Italy	http://bio-www.ba.cnr.it:8000/BioWWW/Bio-WWW.htm
CAOS/CAMM	Netherlands	http://www.caos.kun.nl/
Bio	Norway	http://www.no.embnet.org/
IBB	Poland	http://www.ibb.waw.pl/
IGC	Portugal	http://www.igc.gulbenkian.pt/
GeneBee	Russia	http://www.genebee.msu.su/
CNB-CSIC	Spain	http://www.es.embnet.org/
BMC	Sweden	http://www.embnet.se/
SIB	Switzerland	http://www.ch.embnet.org/
SEQNET	UK	http://www.seqnet.dl.ac.uk/
EMBnet Specialist Nodes		
MIPS	Germany	http://www.mips.biochem.mpg.de/
ICGEB	Italy	http://www.icgeb.trieste.it/
Pharmacia Upjohn	Sweden	http://www.pnu.com/
F.Hoffmann-La Roche	Switzerland	http://www.roche.com/
EBI	UK	http://www.ebi.ac.uk/
HGMP-RC	UK	http://www.hgmp.mrc.ac.uk/
Sanger	UK	http://www.sanger.ac.uk/
UMBER	UK	http://www.bioinf.man.ac.uk/dbbrowser
EMBnet Associate Nodes		
IBBM	Argentina	http://sol.biol.unlp.edu.ar/embnet
ANGIS	Australia	http://www.angis.su.oz.au/
CBI	China	http://www.cbi.pku.edu.cn/
CIGB	Cuba	http://bio.cigb.edu.cu/
CDFD	India	http://salarjung.embnet.org.in/
SANBI	South Africa	http://www.sanbi.ac.za
USA Information Providers		
NCBI	USA	http://www.ncbi.nlm.nih.gov/
NLM	USA	http://www.nlm.nih.gov/
NIH	USA	http://www.nih.gov/



Databáze

Spektrum on-line zdrojů

- EBI http://www.ebi.ac.uk/services
- NCBI http://www.ncbi.nlm.nih.gov/



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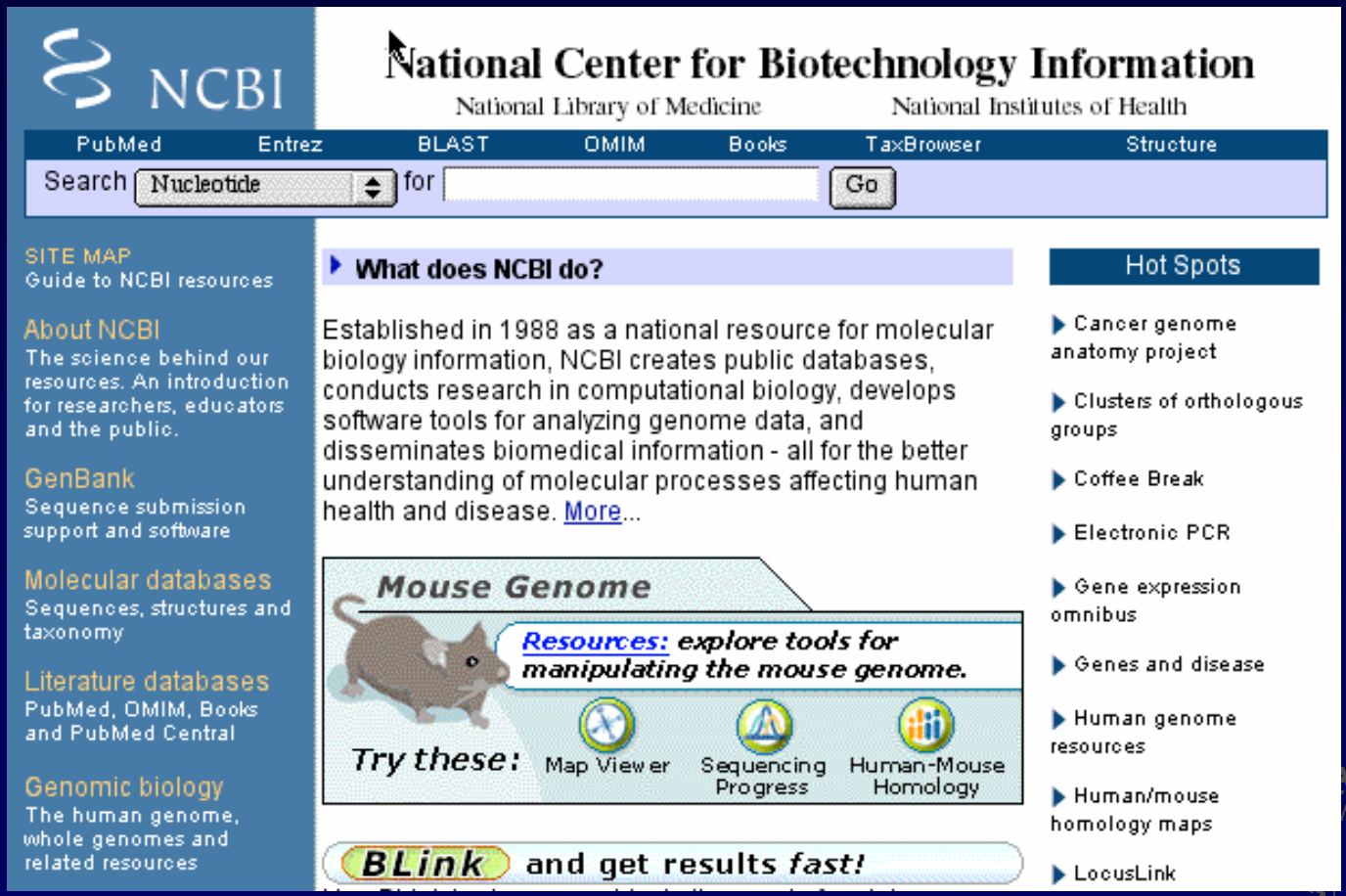
Primární databáze

- zahrnují soubory primárních dat – sekvencí DNA a proteinů
  - DNA sekvence:
    - EMBL, http://www.ebi.ac.uk/embl/
    - GenBank,http://www.ncbi.nih.gov/Genbank/GenbankSearch.html
    - DDBJ, http://www.ddbj.nig.ac.jp
  - Proteinové sekvence:
    - PIR, http://pir.georgetown.edu/
    - MIPS, http://www.mips.biochem.mpg.de
    - SWISS-PROT, http://www.expasy.org/sprot/

Primární databáze

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



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MAGARYK UNIVERSITY

Primární databáze

```
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      301 tctcatattg taagtgagag caatgctgct caactgctac gccagctaga agtgtctcta
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     1381 cgccttgagg cagttggtac acttgccggc ggaatagcac atgaatttaa taacattttg
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```
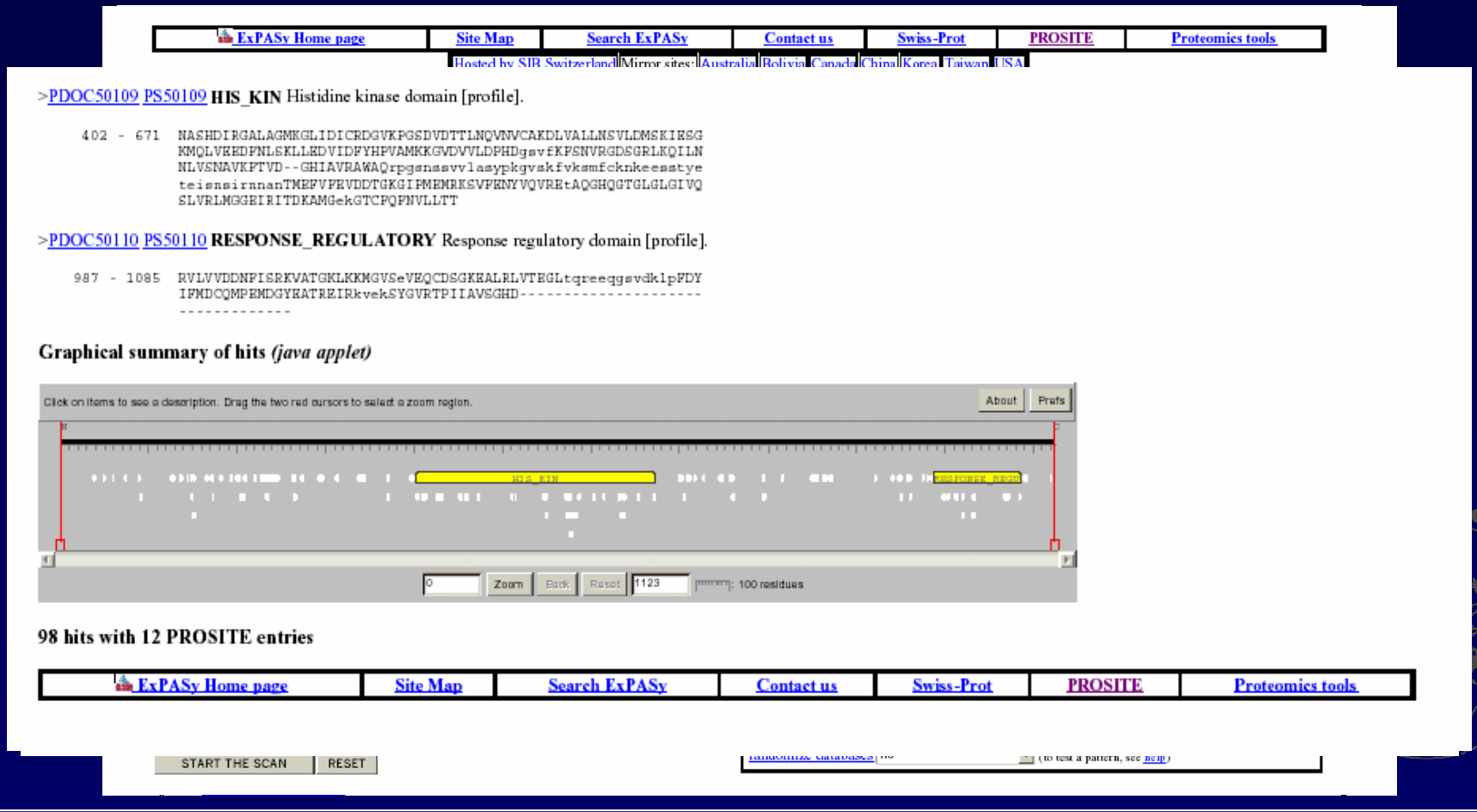
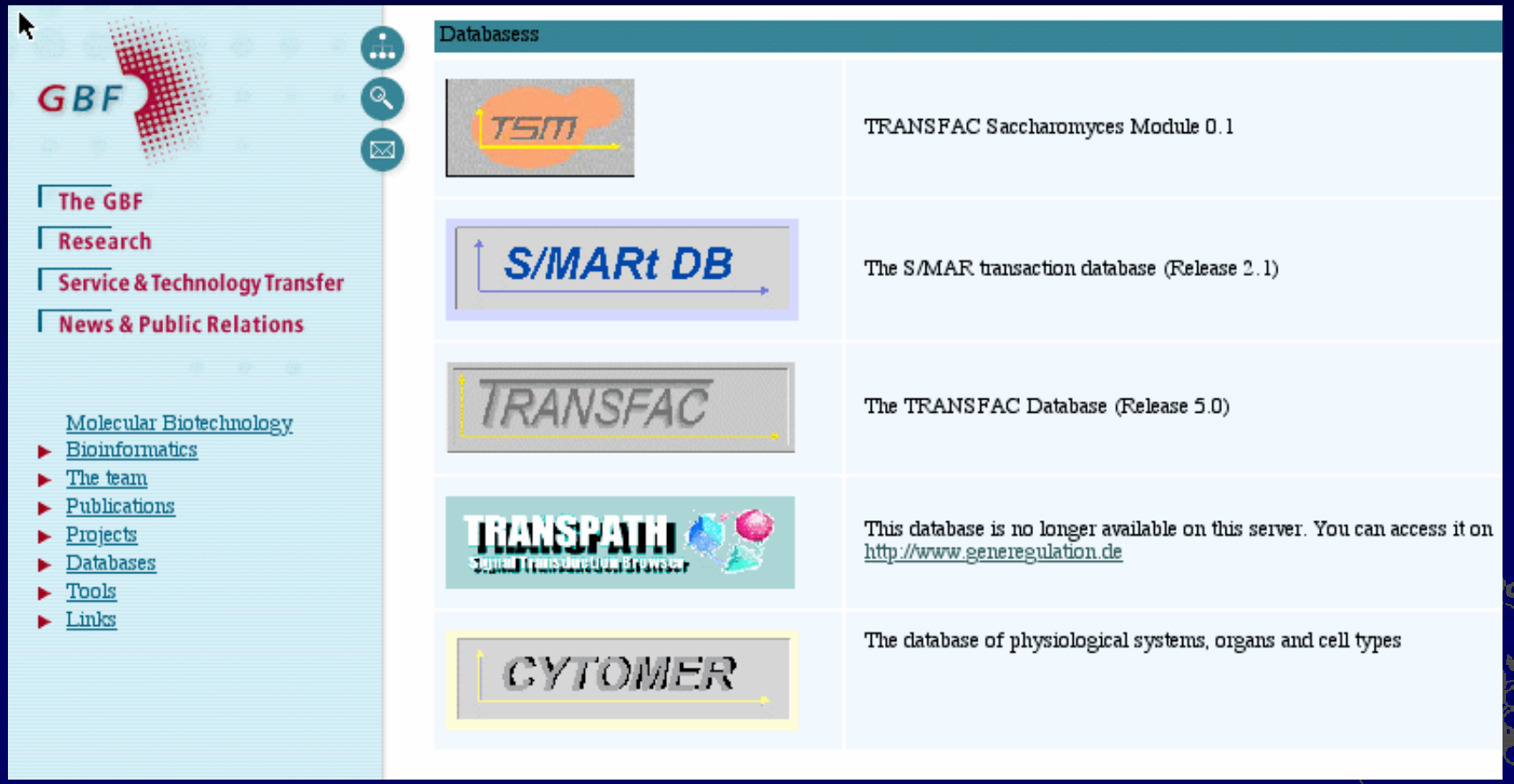

Proteinové sekundární databáze

- databáze funkčních nebo strukturálních ***motivů*** získaných srovnáváním primárních dat (sekvencí)
  - PROSITE, http://www.expasy.org/prosite/
  - DOMO, http://www.biochem.ucl.ac.uk/bsm/domo/
  - PRINTS, http://www.bioinf.man.ac.uk/dbbrowser/PRINTS/



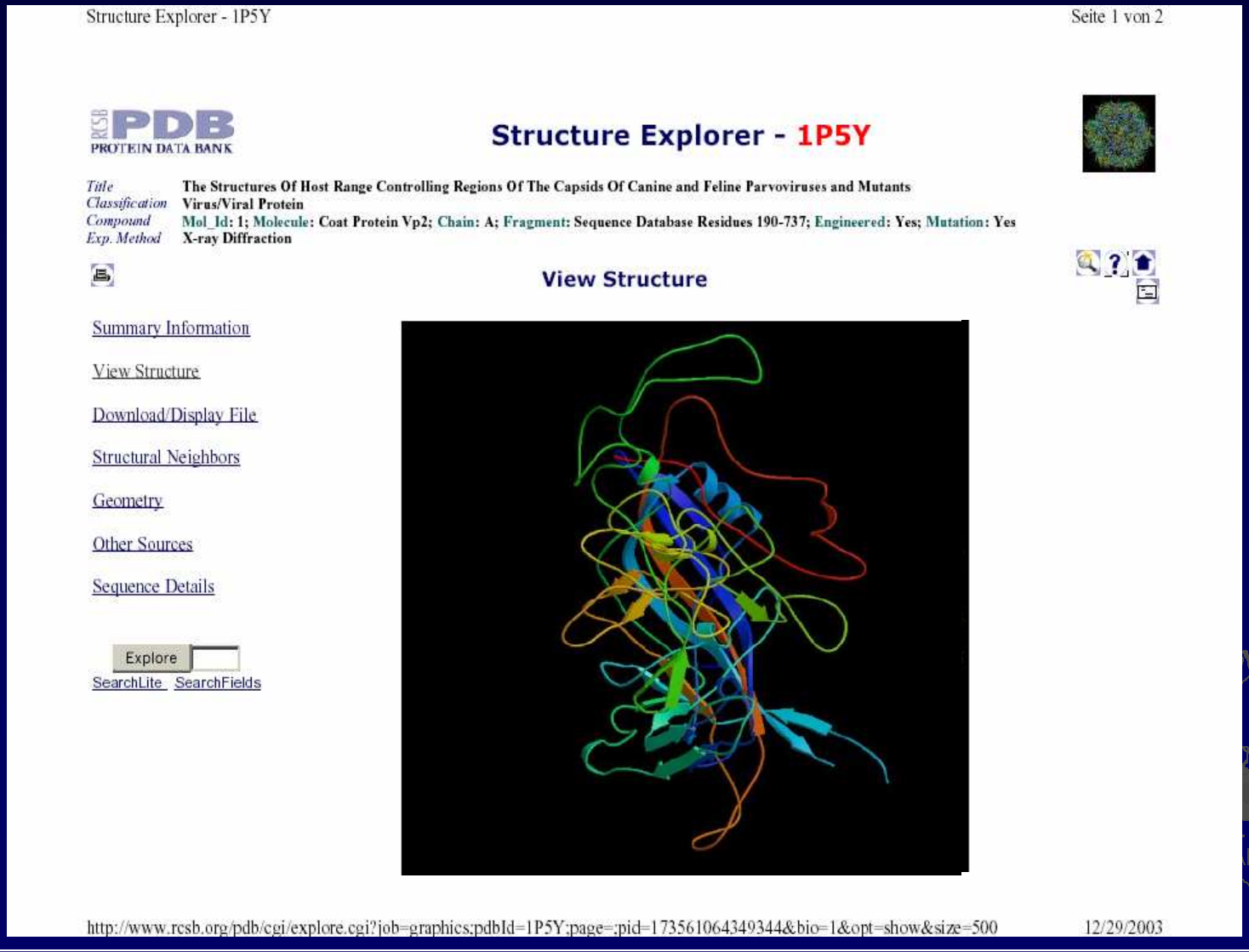
Sekundární databáze DNA

- TRANSFAC http://www.gene-regulation.com/



Strukturální databáze

- PDB http://www.rcsb.org/pdb/



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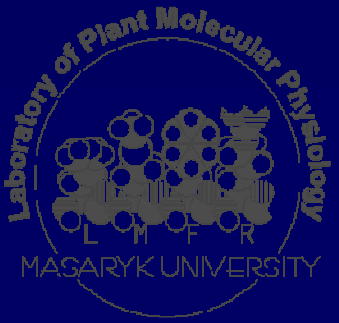
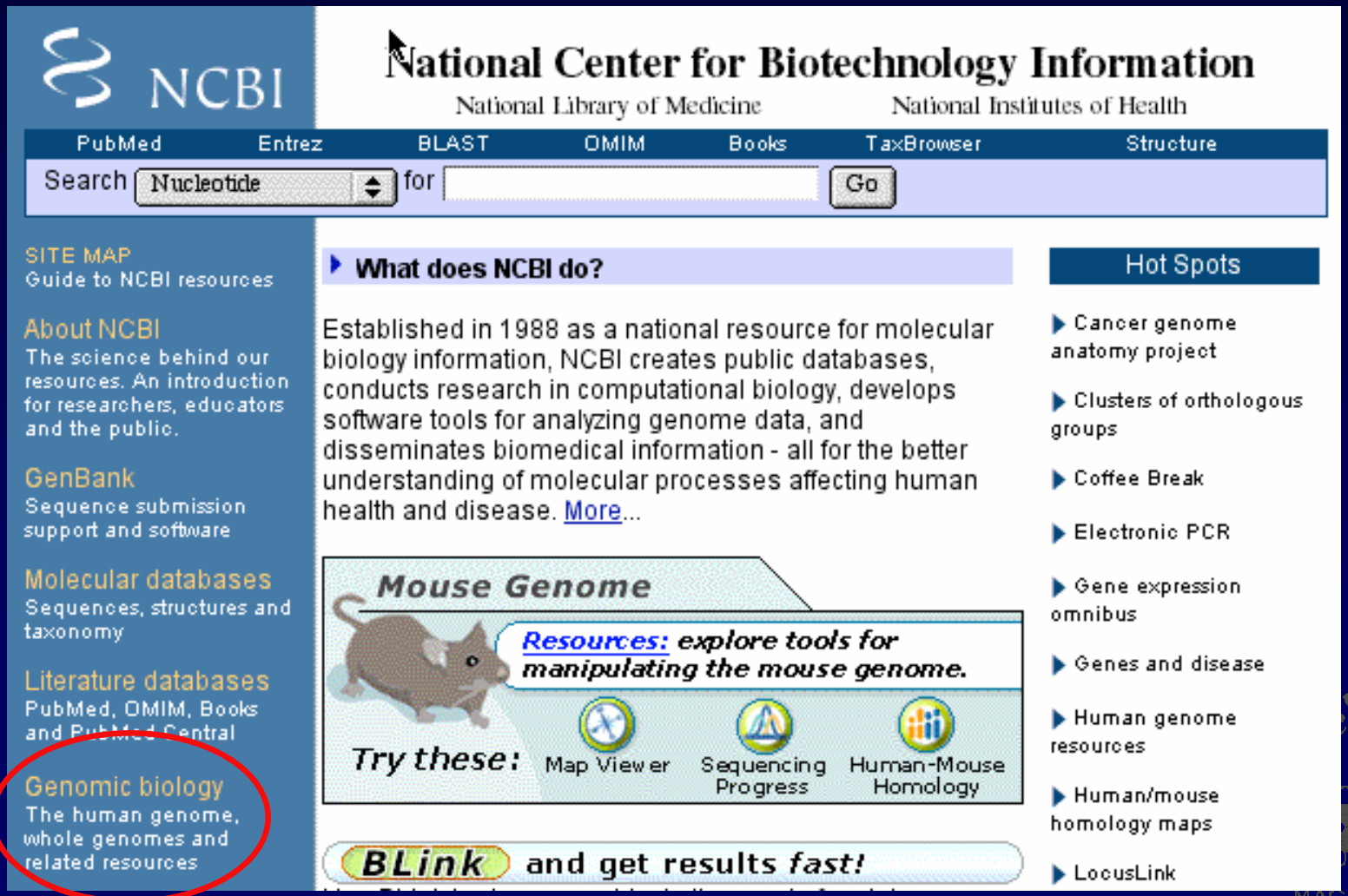
  - GENOMOVÉ zdroje



Primární data-genomové zdroje



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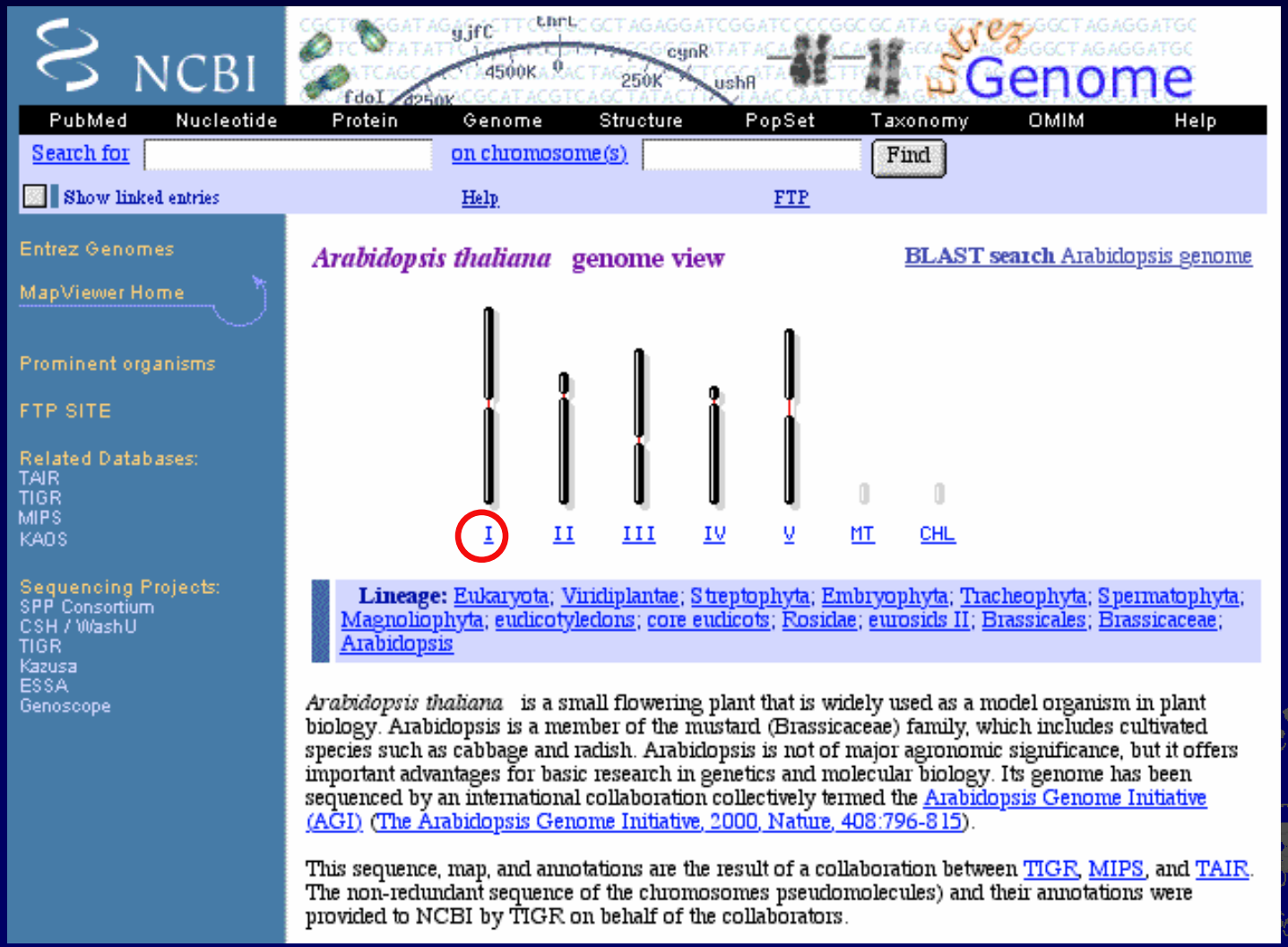

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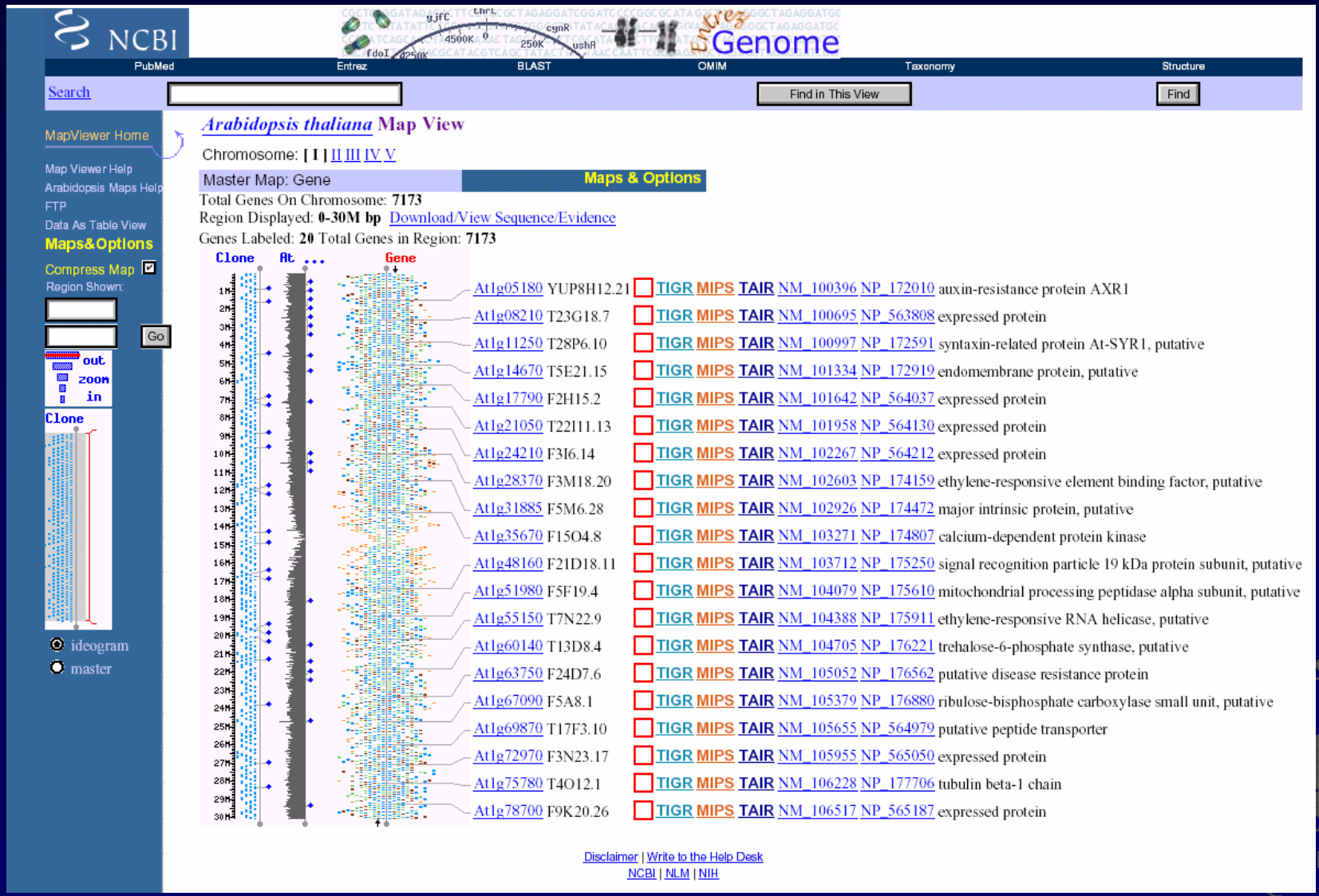

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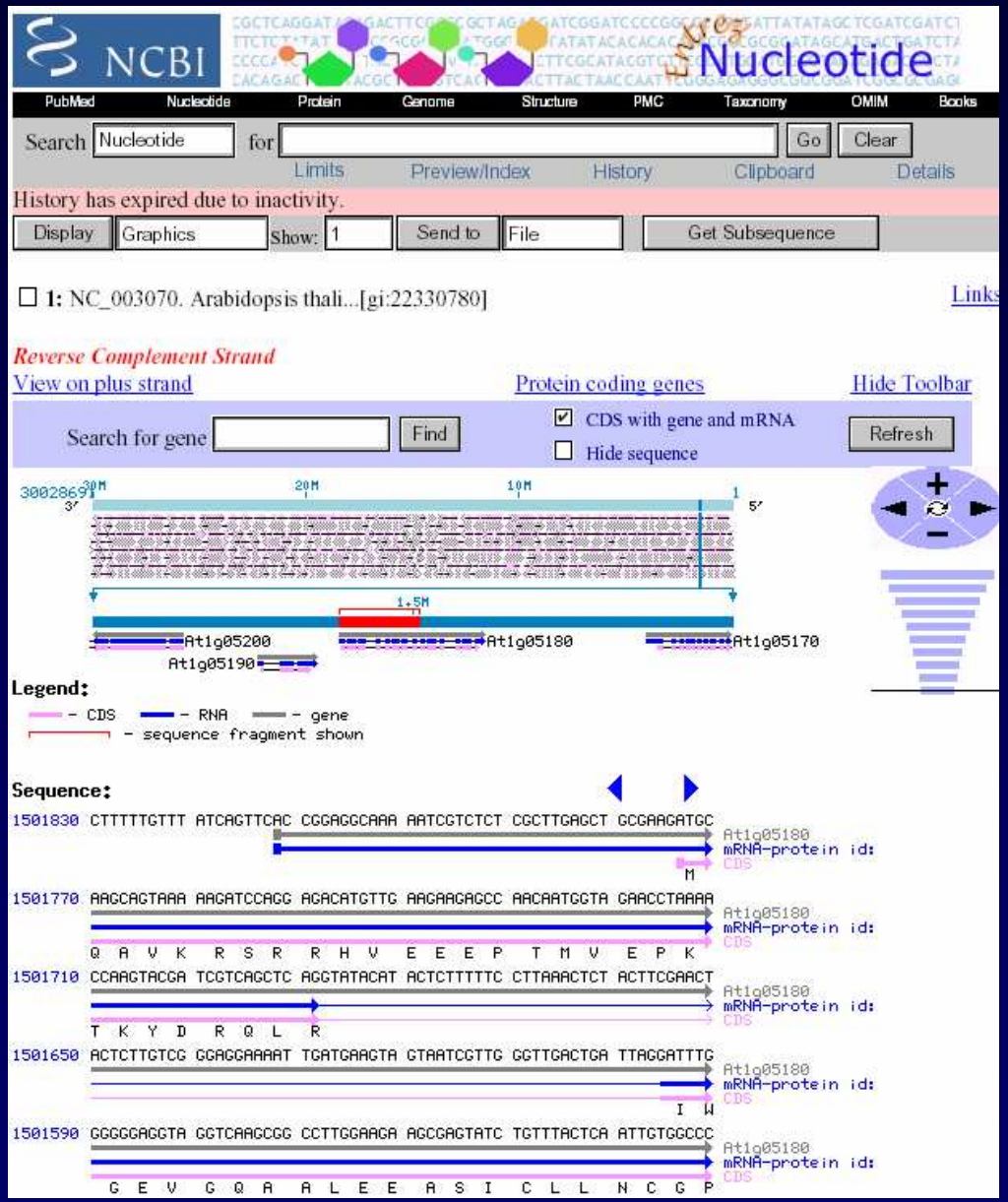

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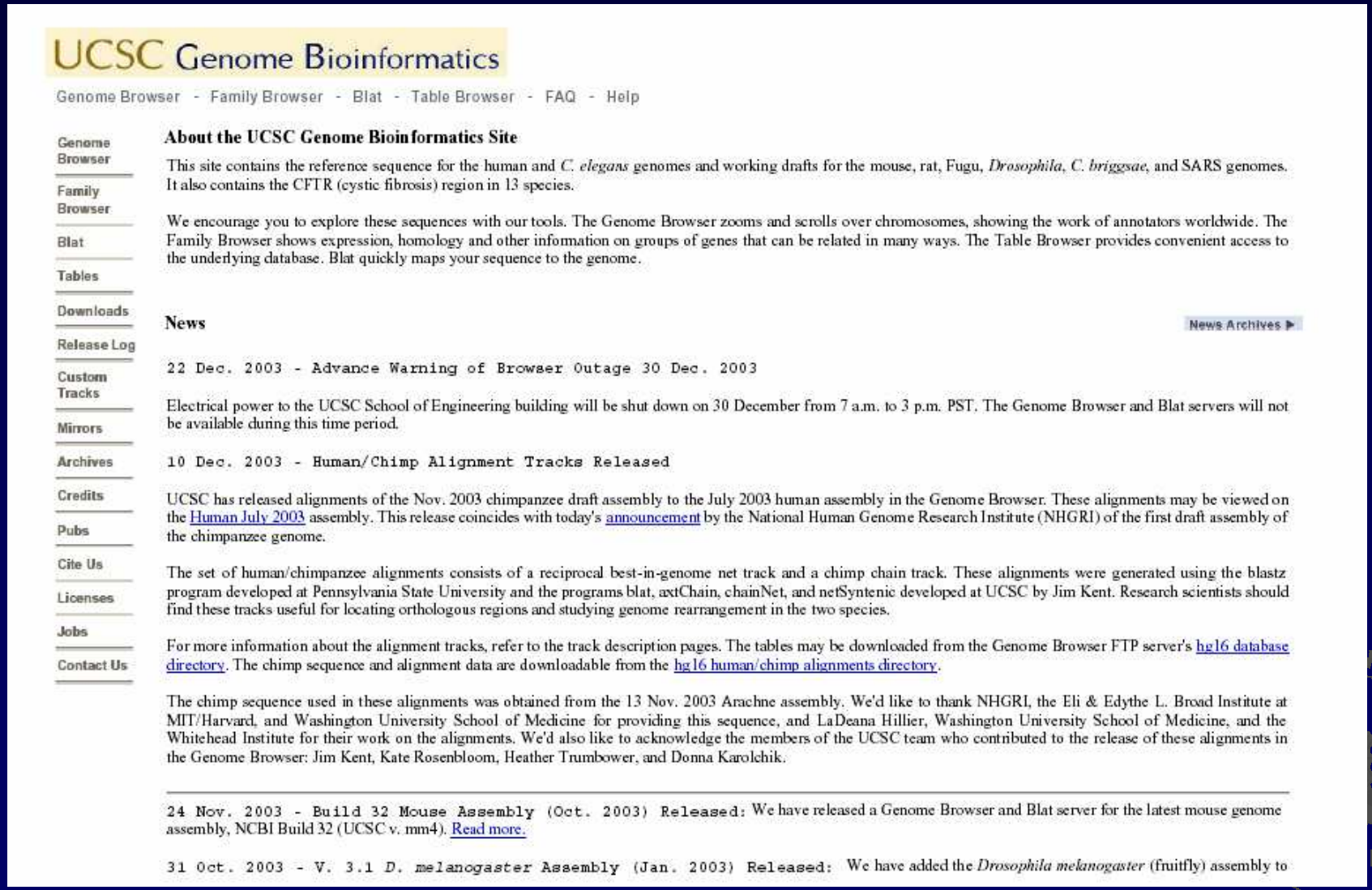
L M F R
MASARYK UNIVERSITY

Primární data-genomové zdroje

- Human Genome Browser http://genome.ucsc.edu/



UCSC Genome Bioinformatics

Genome Browser - Family Browser - Blat - Table Browser - FAQ - Help

Genome Browser
Family Browser
Blat
Tables
Downloads
Release Log
Custom Tracks
Mirrors
Archives
Credits
Pubs
Cite Us
Licenses
Jobs
Contact Us

About the UCSC Genome Bioinformatics Site

This site contains the reference sequence for the human and *C. elegans* genomes and working drafts for the mouse, rat, Fugu, *Drosophila*, *C. briggsae*, and SARS genomes. It also contains the CFTR (cystic fibrosis) region in 13 species.

We encourage you to explore these sequences with our tools. The Genome Browser zooms and scrolls over chromosomes, showing the work of annotators worldwide. The Family Browser shows expression, homology and other information on groups of genes that can be related in many ways. The Table Browser provides convenient access to the underlying database. Blat quickly maps your sequence to the genome.

News News Archives ▶

22 Dec. 2003 - Advance Warning of Browser Outage 30 Dec. 2003

Electrical power to the UCSC School of Engineering building will be shut down on 30 December from 7 a.m. to 3 p.m. PST. The Genome Browser and Blat servers will not be available during this time period.

10 Dec. 2003 - Human/Chimp Alignment Tracks Released

UCSC has released alignments of the Nov. 2003 chimpanzee draft assembly to the July 2003 human assembly in the Genome Browser. These alignments may be viewed on the Human July 2003 assembly. This release coincides with today's announcement by the National Human Genome Research Institute (NHGRI) of the first draft assembly of the chimpanzee genome.

The set of human/chimpanzee alignments consists of a reciprocal best-in-genome net track and a chimp chain track. These alignments were generated using the blastz program developed at Pennsylvania State University and the programs blat, axtChain, chainNet, and netSyntenic developed at UCSC by Jim Kent. Research scientists should find these tracks useful for locating orthologous regions and studying genome rearrangement in the two species.

For more information about the alignment tracks, refer to the track description pages. The tables may be downloaded from the Genome Browser FTP server's hg16 database directory. The chimp sequence and alignment data are downloadable from the hg16 human/chimp alignments directory.

The chimp sequence used in these alignments was obtained from the 13 Nov. 2003 Arachne assembly. We'd like to thank NHGRI, the Eli & Edythe L. Broad Institute at MIT/Harvard, and Washington University School of Medicine for providing this sequence, and LaDeana Hillier, Washington University School of Medicine, and the Whitehead Institute for their work on the alignments. We'd also like to acknowledge the members of the UCSC team who contributed to the release of these alignments in the Genome Browser: Jim Kent, Kate Rosenbloom, Heather Trumbower, and Donna Karolchik.

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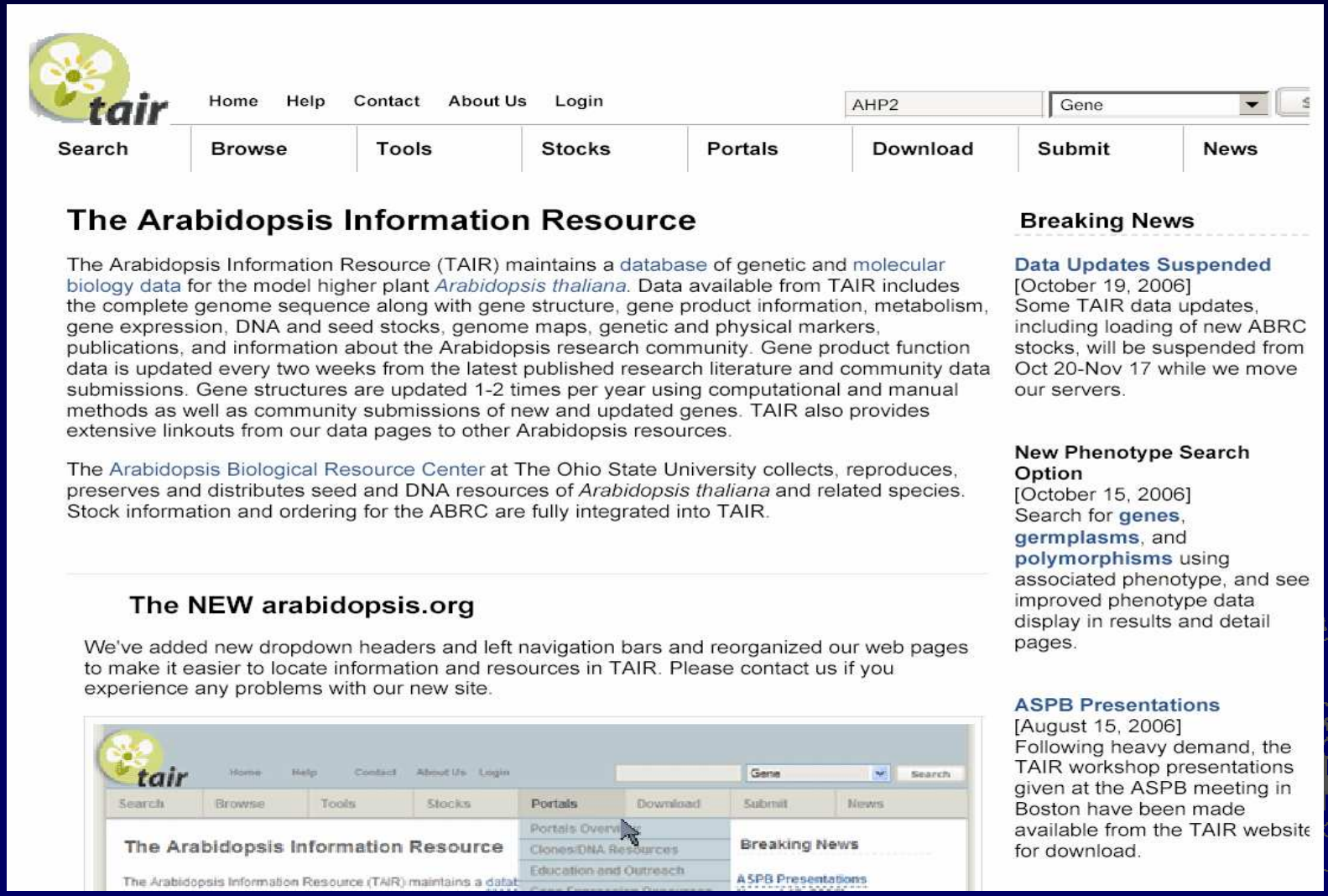
24 Nov. 2003 - Build 32 Mouse Assembly (Oct. 2003) Released: We have released a Genome Browser and Blat server for the latest mouse genome assembly, NCBI Build 32 (UCSC v. mm4). Read more.

31 Oct. 2003 - V. 3.1 *D. melanogaster* Assembly (Jan. 2003) Released: We have added the *Drosophila melanogaster* (fruitfly) assembly to

Primární data-genomové zdroje

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



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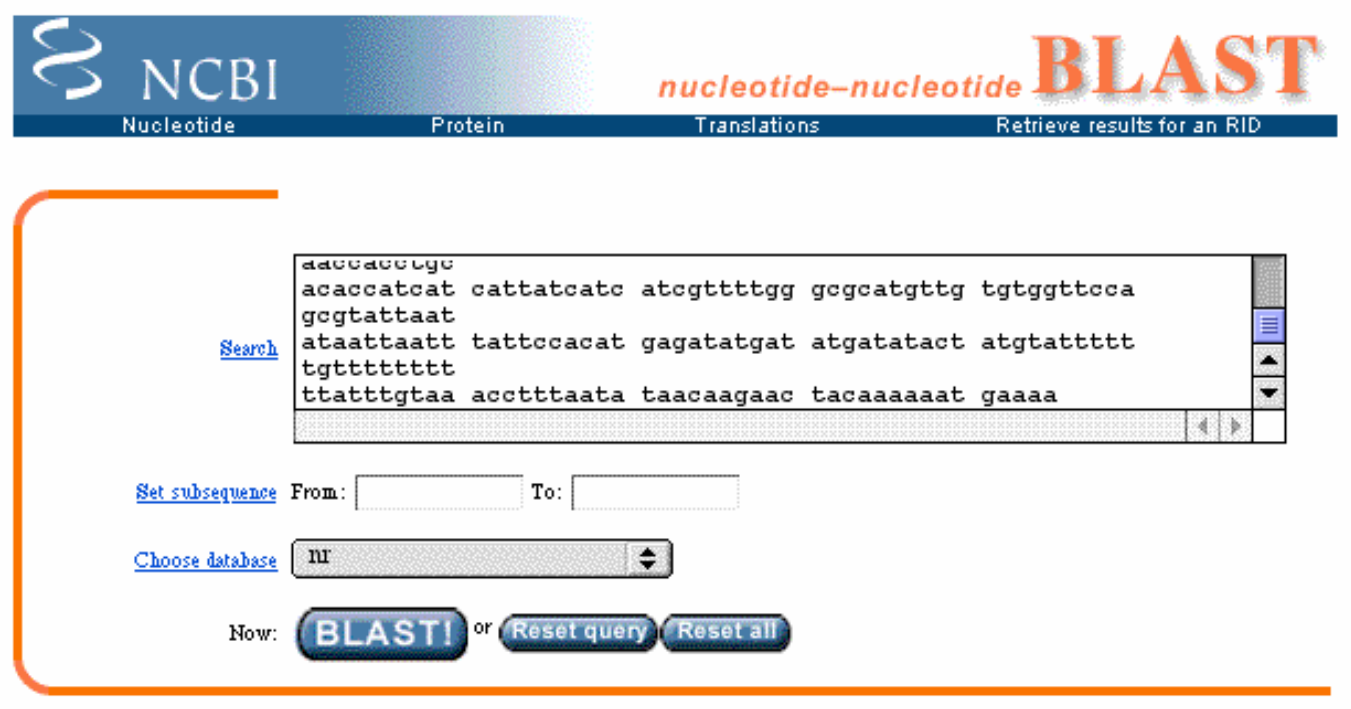
  - GENOMOVÉ zdroje
- Analytické nástroje
  - Vyhledávání homologií

Analytické nástroje

- BLAST http://ncbi.nlm.nih.gov/BLAST/



Podstata algoritmu BLAST
(**B**asic **L**ocal **A**lignment **S**earch **T**ool)

- Velikost vyhledávacího slova (word size): 7 - 15 bazí
  - Primární podobnosti (seed matches)
  - Rozšiřování oblasti homologie doprava i doleva
- Hodnocení homologie pomocí matice PAM (Point Accepted Mutation) nebo BLOSUM (BLOcks Substitution Matrix)
- Zobrazení výsledků

MRKE
MRKE
MRKY
MRAK

Matrice PAM 250

	C	S	T	P	A	G	N	D	E	Q	H	R	K	M	I	L	V	F	Y	W
C	12																			
S	0	2																		
T	-2	1	3																	
P	-3	1	0	6																
A	-2	1	1	1	2															
G	-3	1	0	-1	1	5														
N	-4	1	0	-1	0	0	2													
D	-5	0	0	-1	0	1	2	4												
E	-5	0	0	-1	0	0	1	3	4											
Q	-5	-1	-1	0	0	-1	1	2	2	4										
H	-3	-1	-1	0	-1	-2	2	1	1	3	6									
R	-4	0	-1	0	-2	-3	0	-1	-1	1	2	6								
K	-5	0	0	-1	-1	-2	1	0	0	1	0	3	5							
M	-5	-2	-1	-2	-1	-3	-2	-3	-2	-1	-2	0	0	6						
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L	-6	-3	-2	-3	-2	-4	-3	-4	-3	-2	-2	-3	-3	4	2	6				
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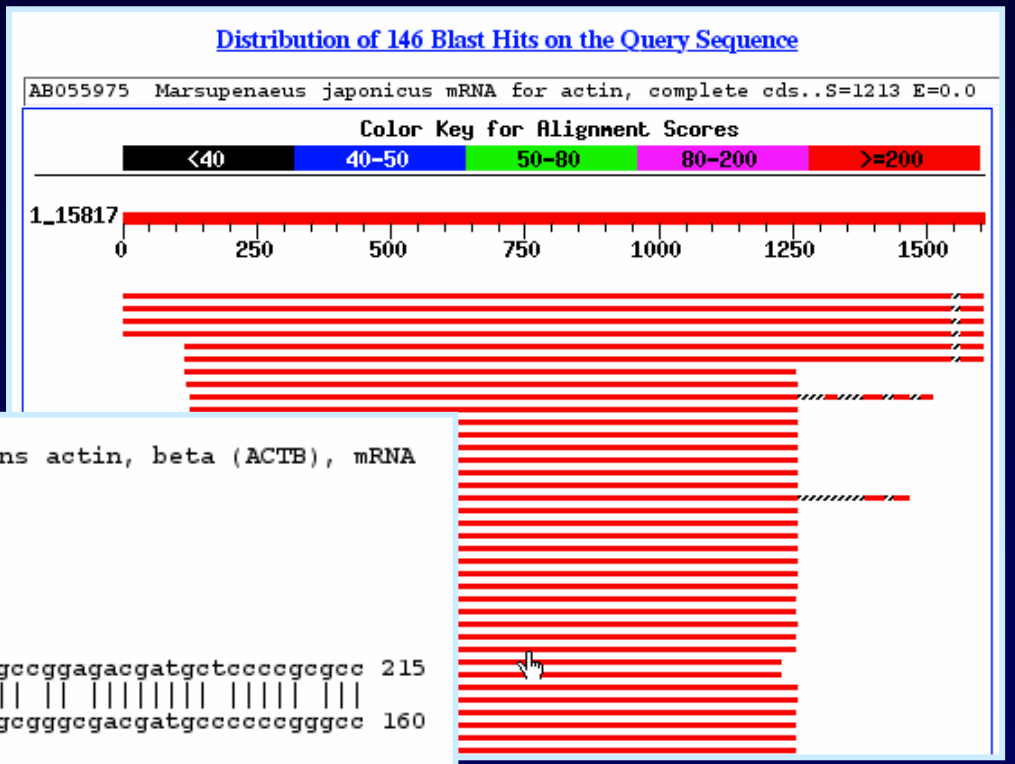
Analytické nástroje



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Strand = Plus / Plus

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Základy genomiky I.

- Role BIOINFORMATIKY v současném pojetí FUNKČNÍ GENOMIKY
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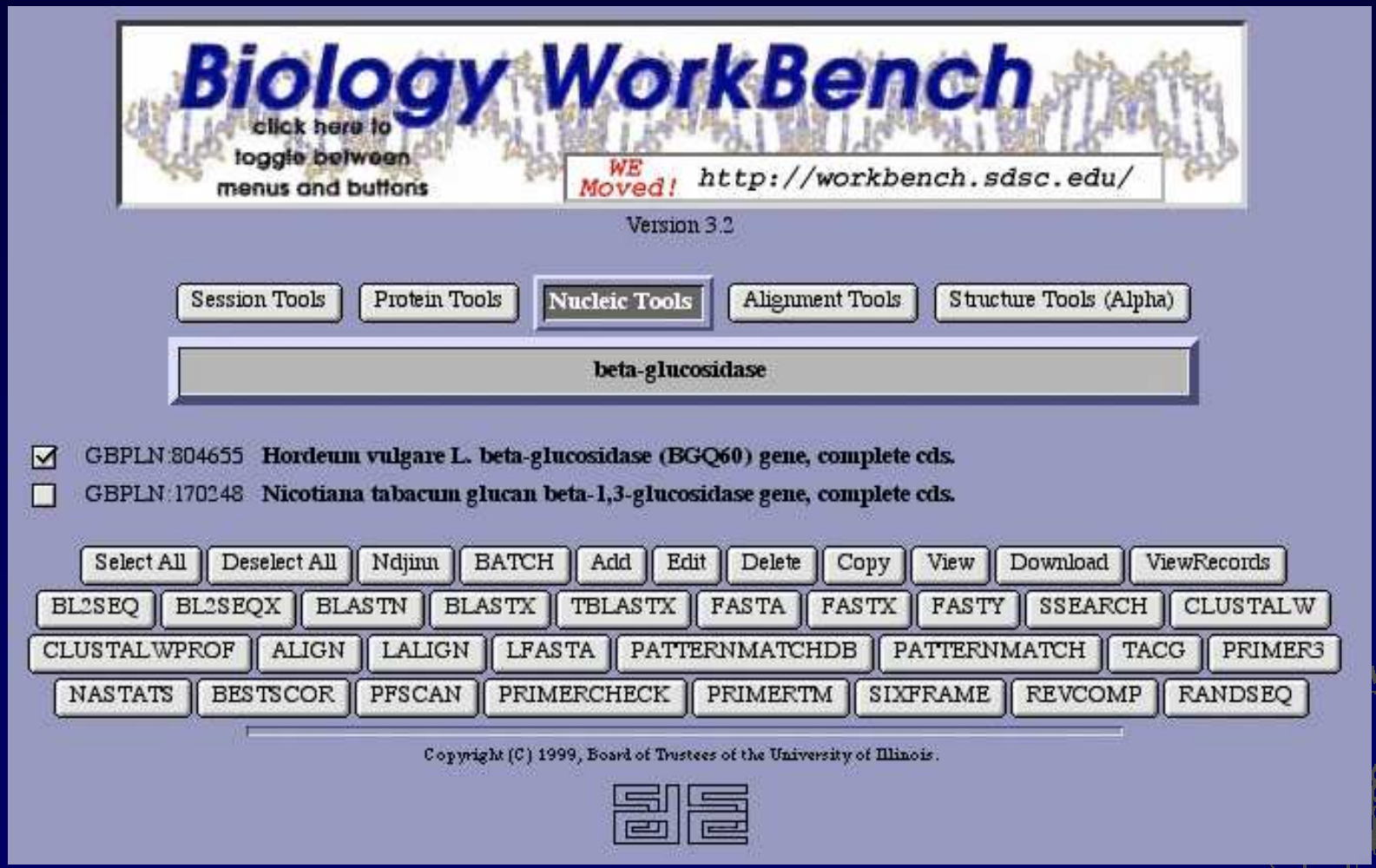
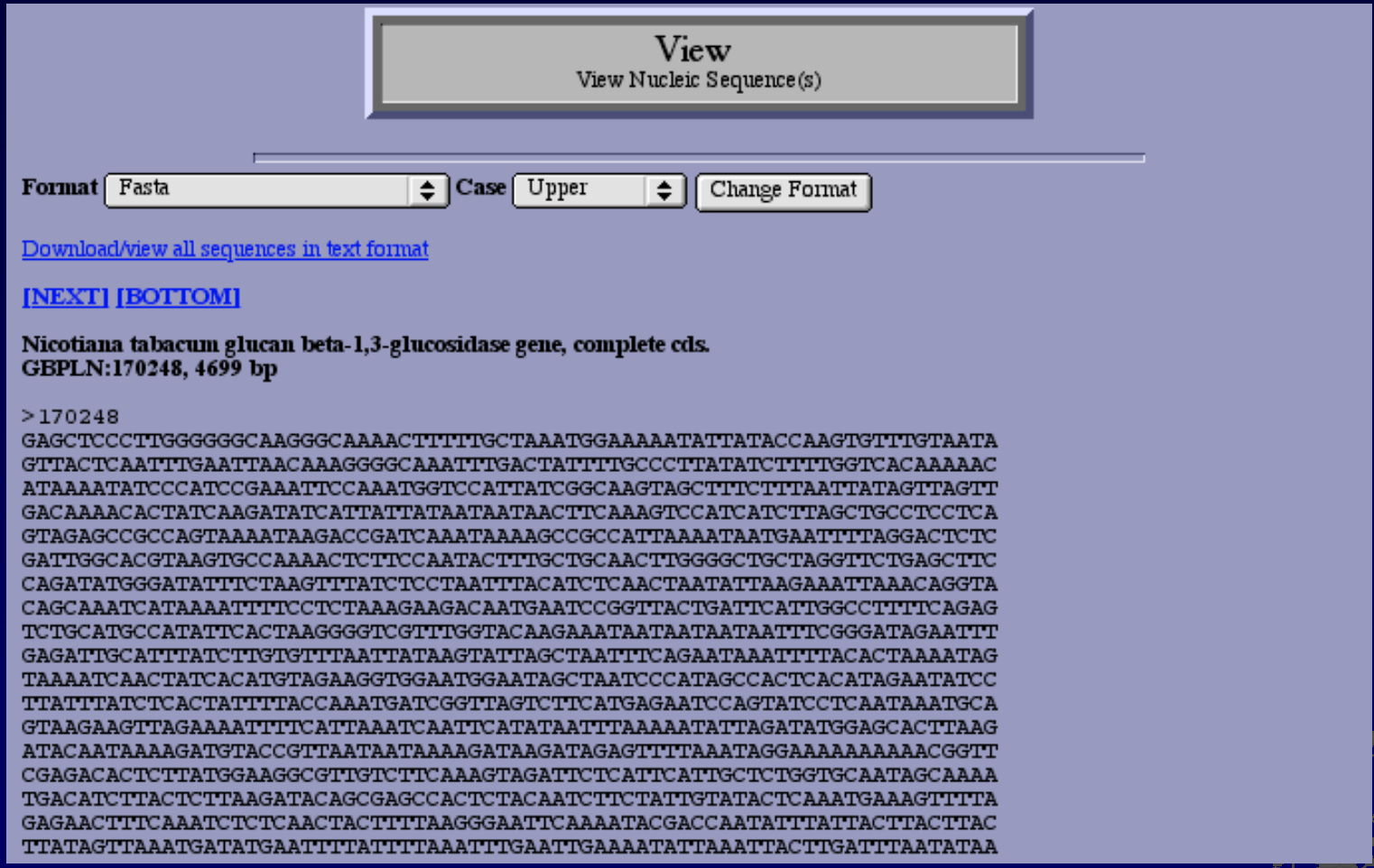
  - Vyhledávání sekvenčních motivů, otevřených čtecích rámců, restrikčních míst….

Analytické nástroje

- http://workbench.sdsc.edu/



Analytické nástroje



View
View Nucleic Sequence(s)

Format Fasta Case Upper Change Format

Download/view all sequences in text format

[NEXT] [BOTTOM]

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Analytické nástroje

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1 match was found

Matches are indicated in blue

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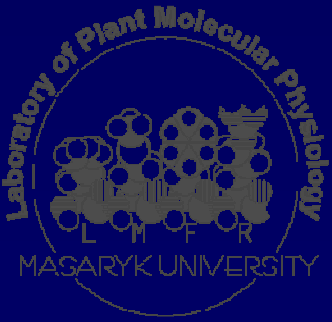
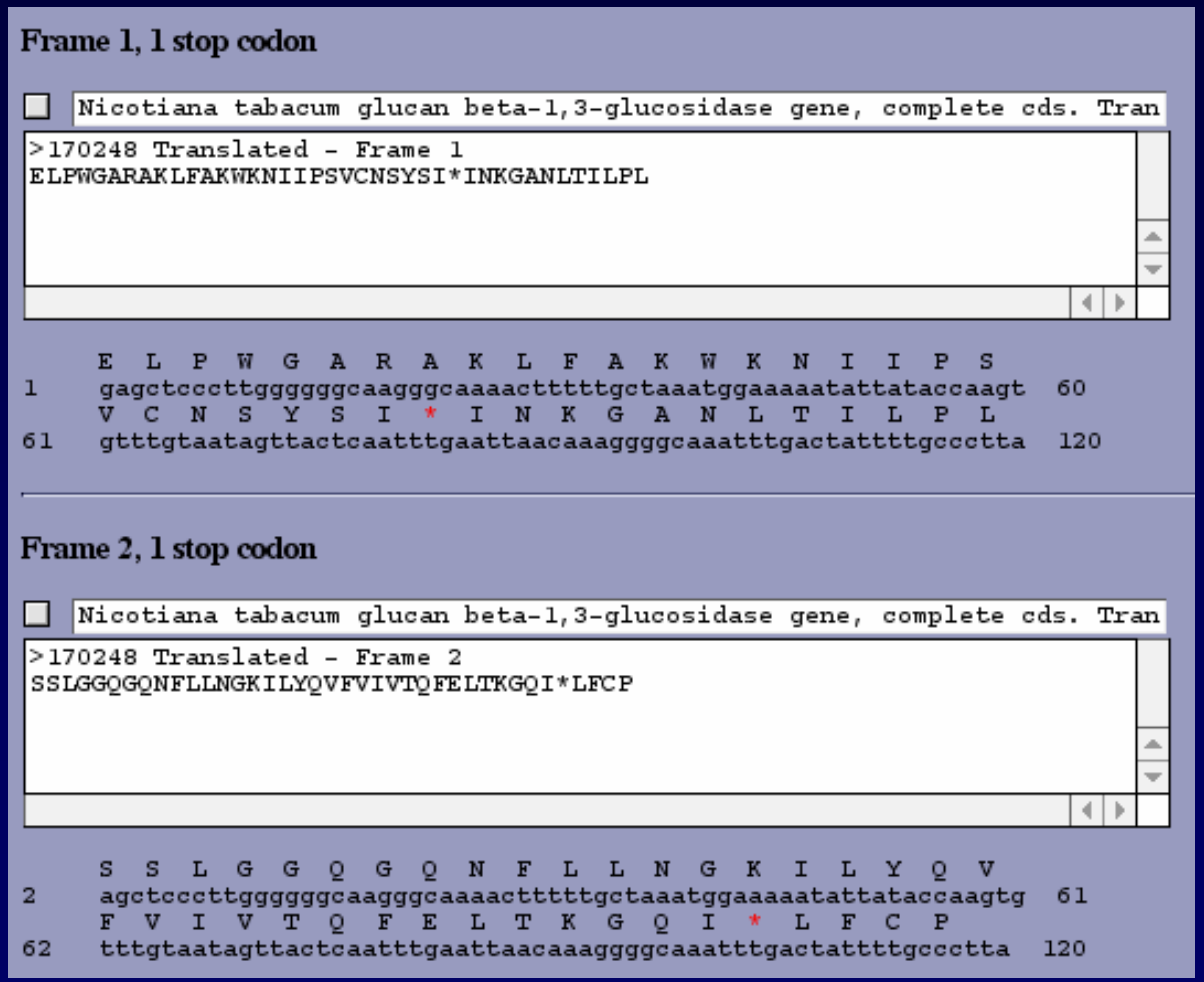


Analytické nástroje



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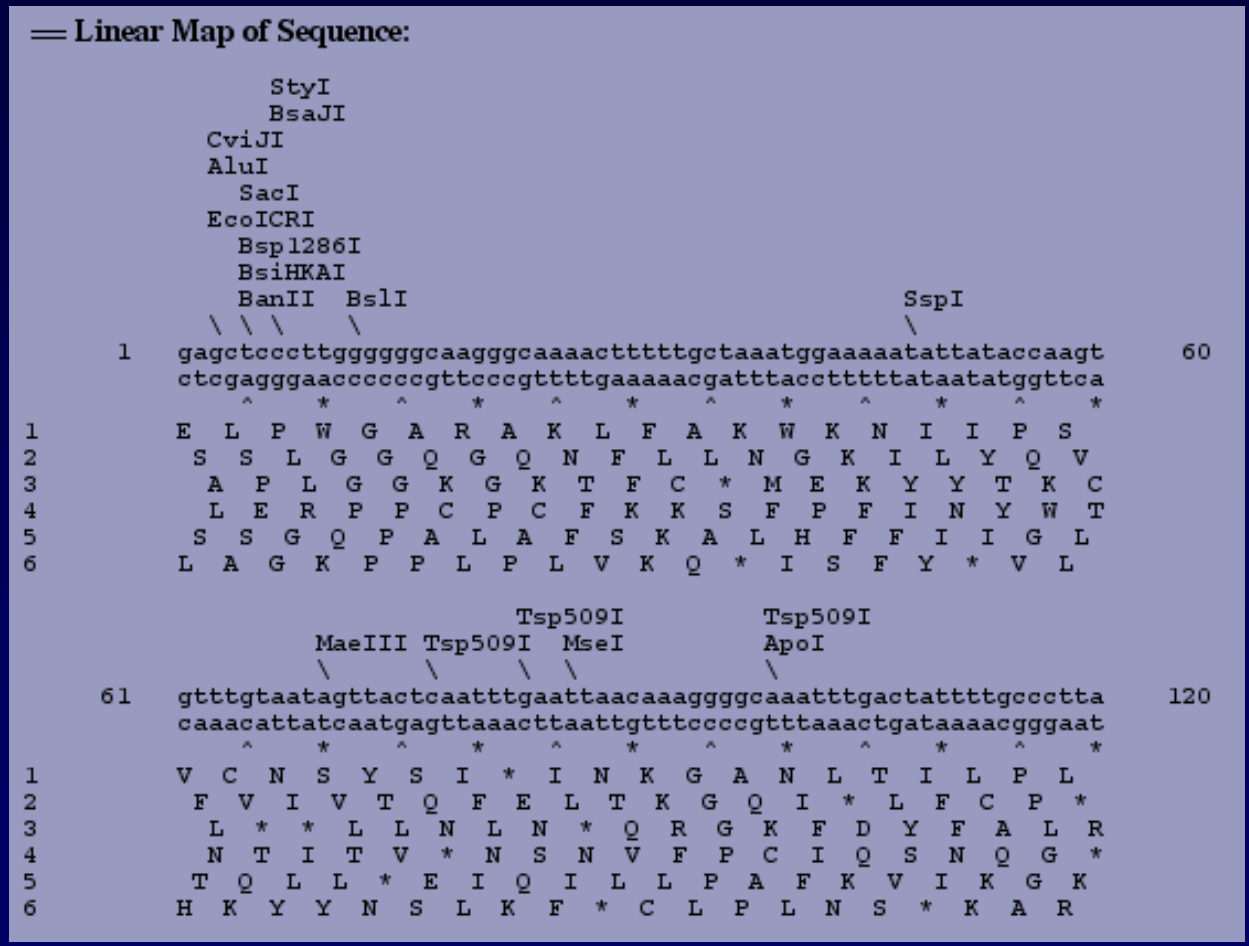
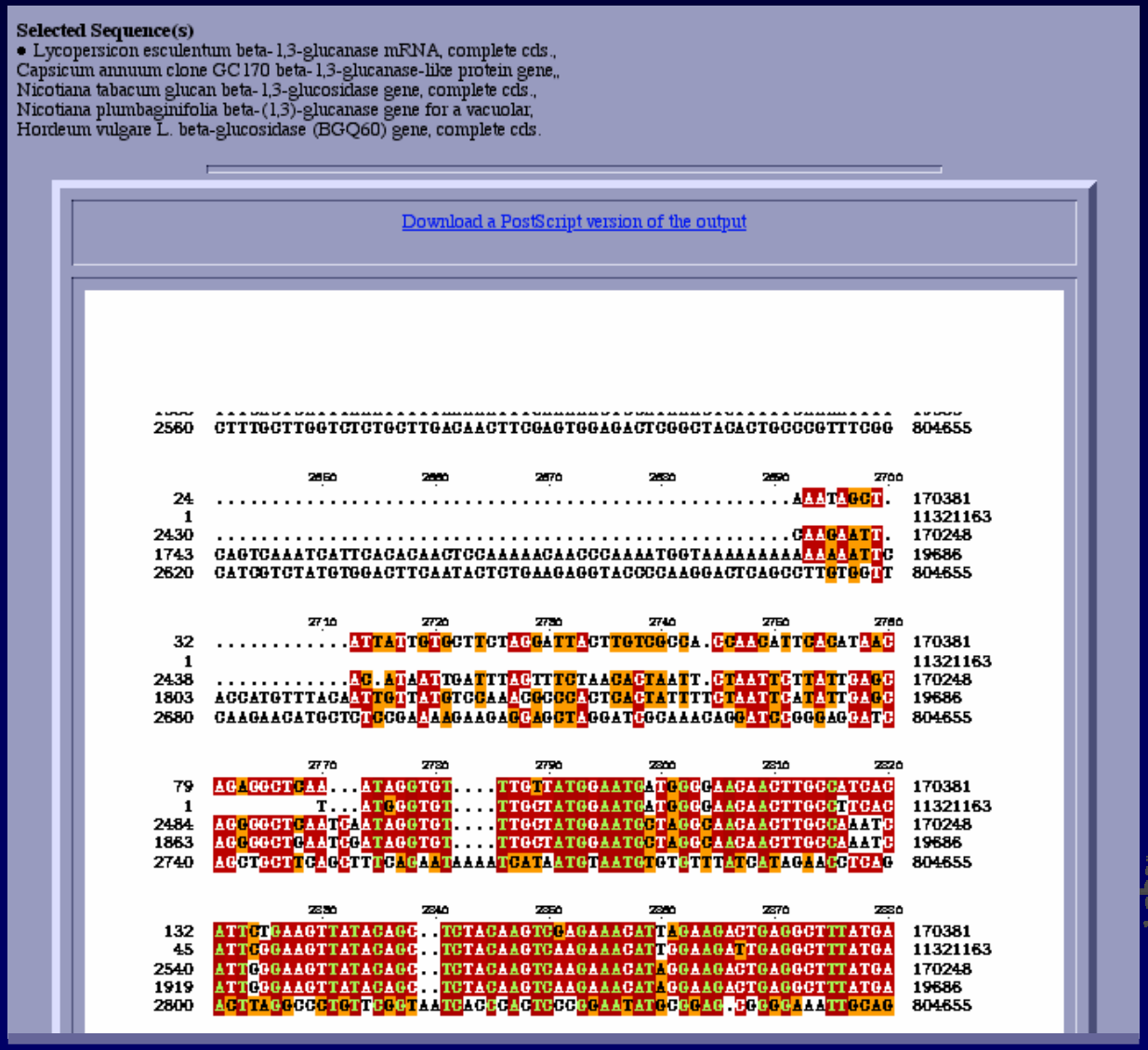


Analytické nástroje



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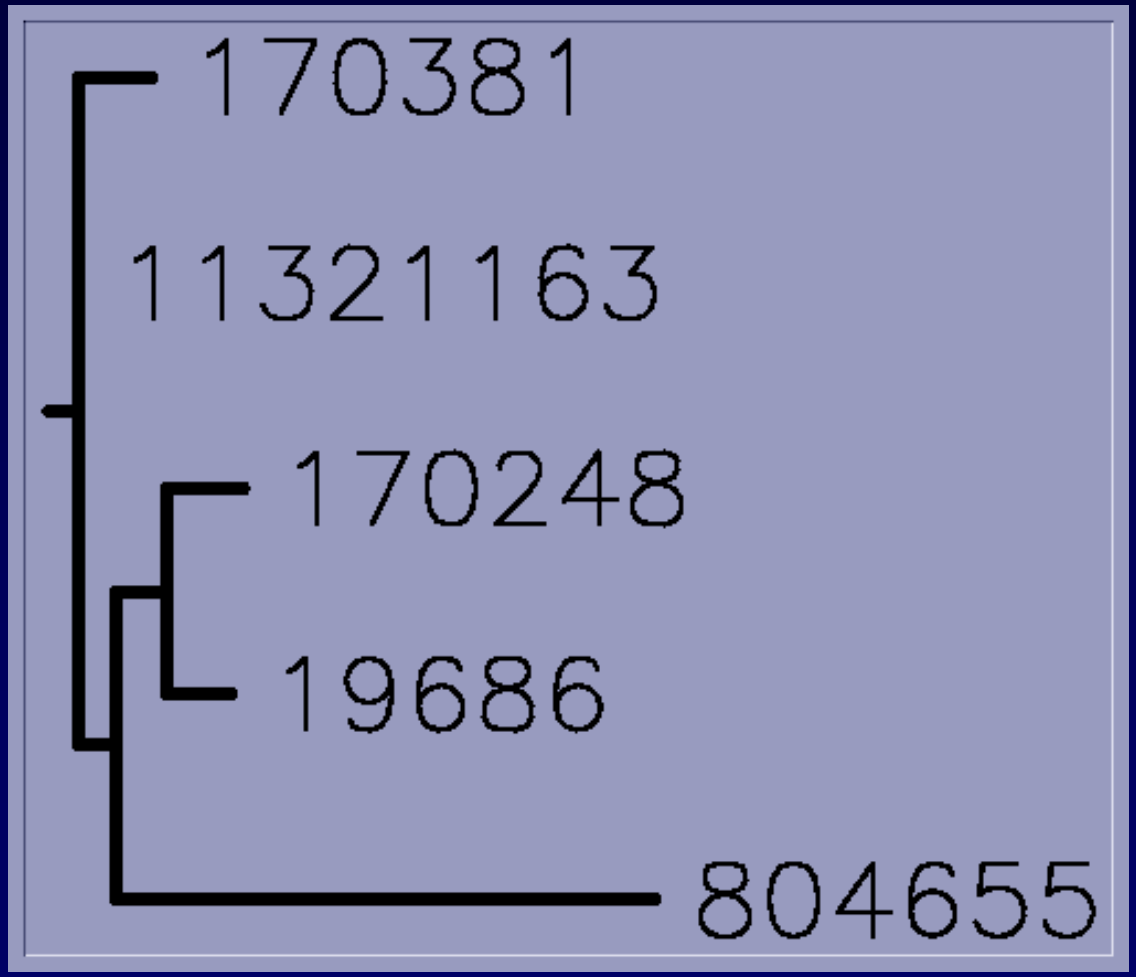
Analytické nástroje



Analytické nástroje

- VPCR http://elanor.sci.muni.cz/LMFR/vpcr/

Analytické nástroje

Základy genomiky I.

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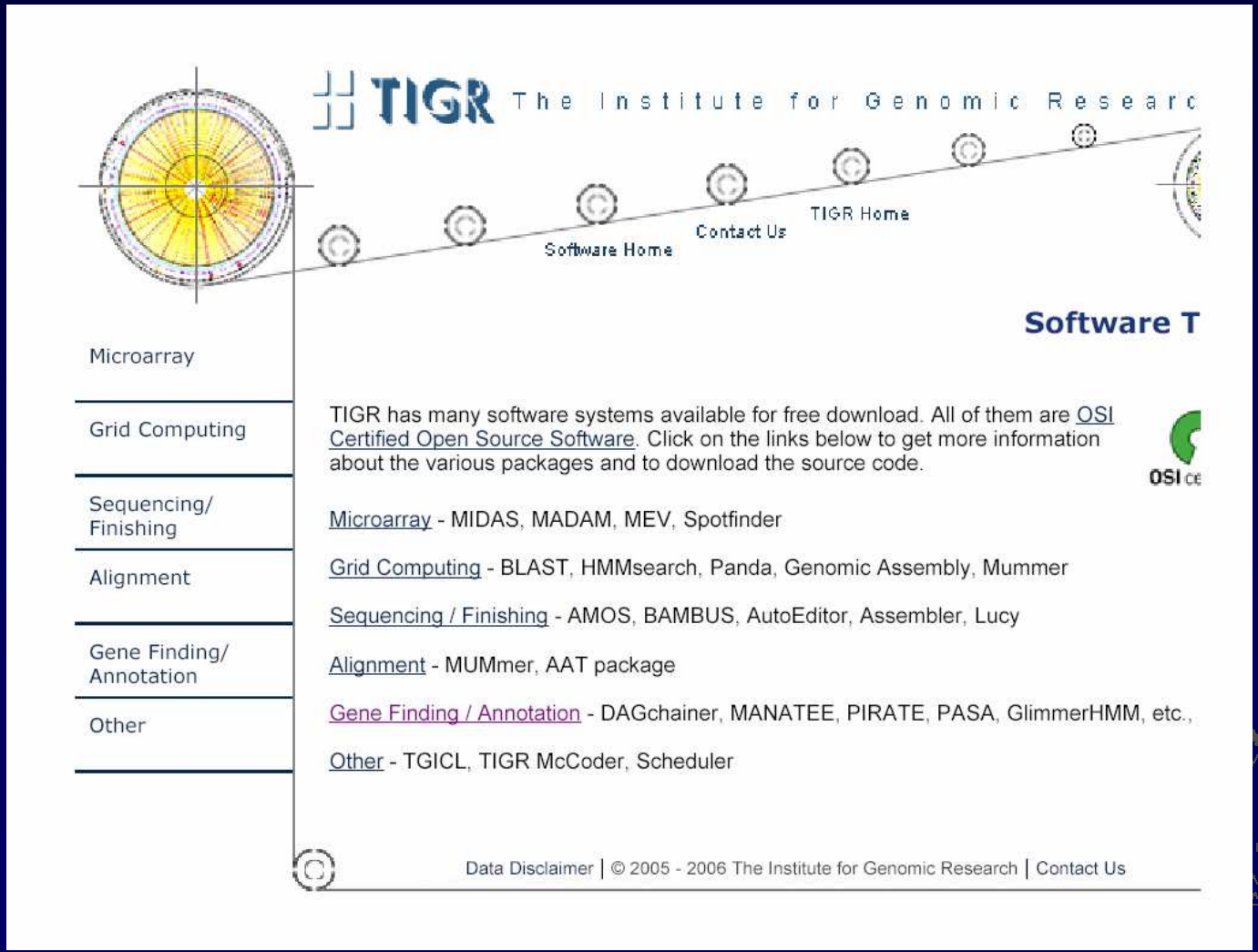
  - Další www genomové nástroje

www analytické nástroje

- TIGR (The Institute for Genomic Research, http://www.tigr.org/software/)



Základy genomiky I.
shrnutí

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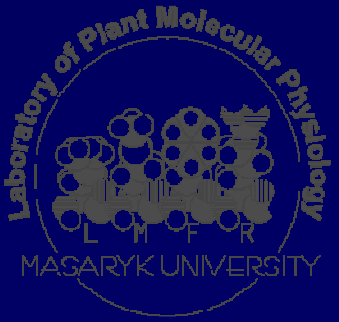
Základy genomiky I.

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