CG920 Genomics

Lesson 1

Introduction into Bioinformatics

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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

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

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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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

GENOMICS – What is it?

The role of BIOINFORMATICS in FUNCTIONAL GENOMICS

Forward („classical“) Genetics Approaches

3 : 1

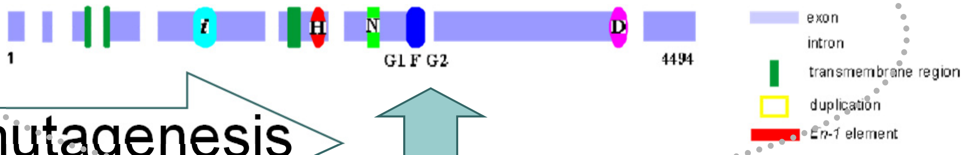
?

Reverse Genetics Approaches

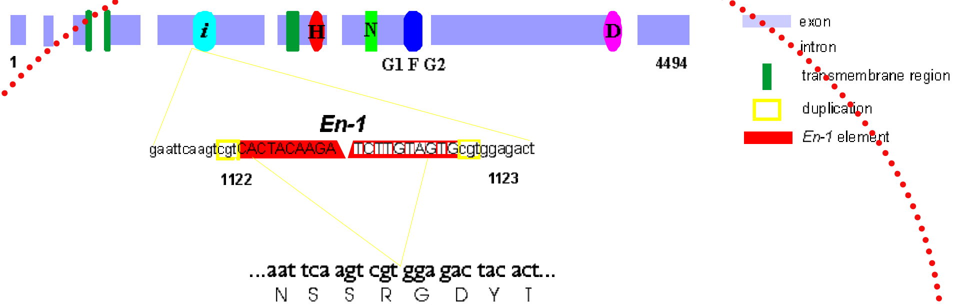
5‘TTATATATATATATTAAAAAATAAAATAAAA GAACAAAAAAGAAAATAAAATA….3‘

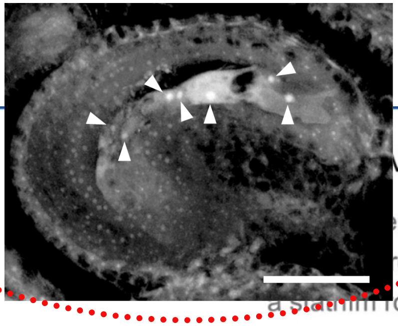
BIOINFORMATICS

Insertional mutagenesis



FUNCTIONAL GENOMICS





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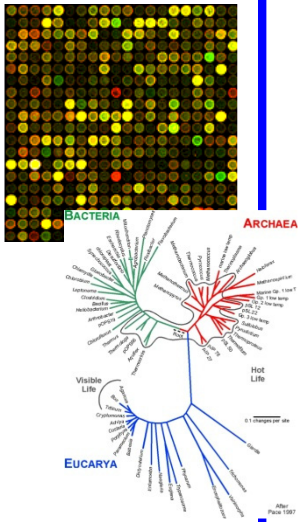
- Role of BIOINFORMATICS in FUNCTIONAL GENOMICS

Bioinformatics



- **Definiction 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.**

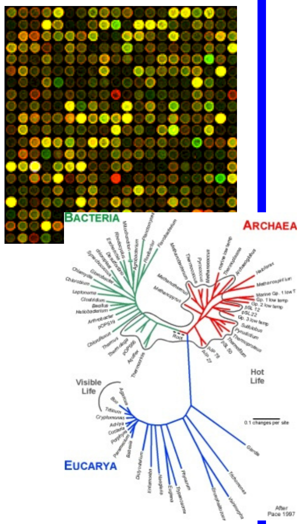
What is bioinformatics?

- **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

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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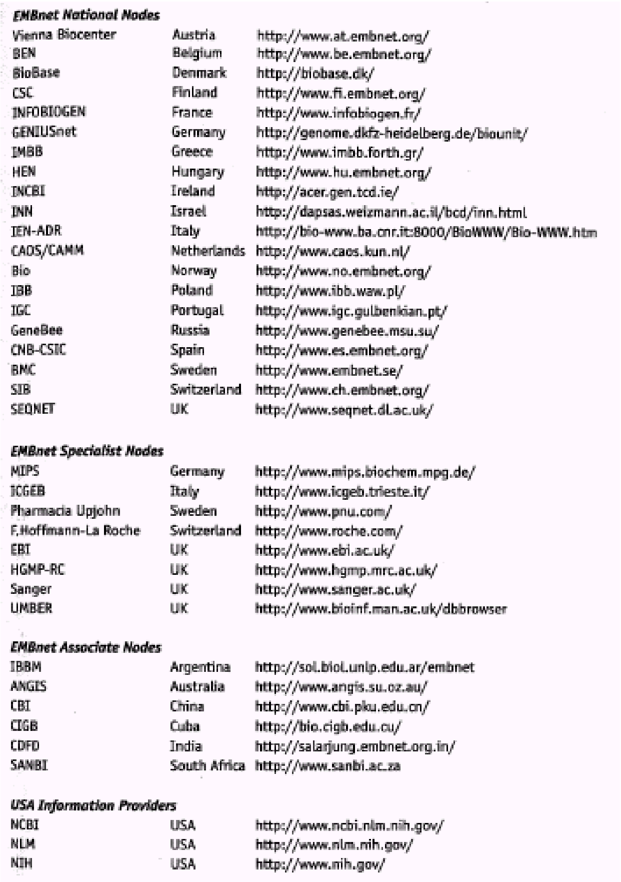
Spectre of on-line Resources



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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/
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F.Hoffmann-La Roche	Switzerland	http://www.roche.com/
EBI	UK	http://www.ebi.ac.uk/
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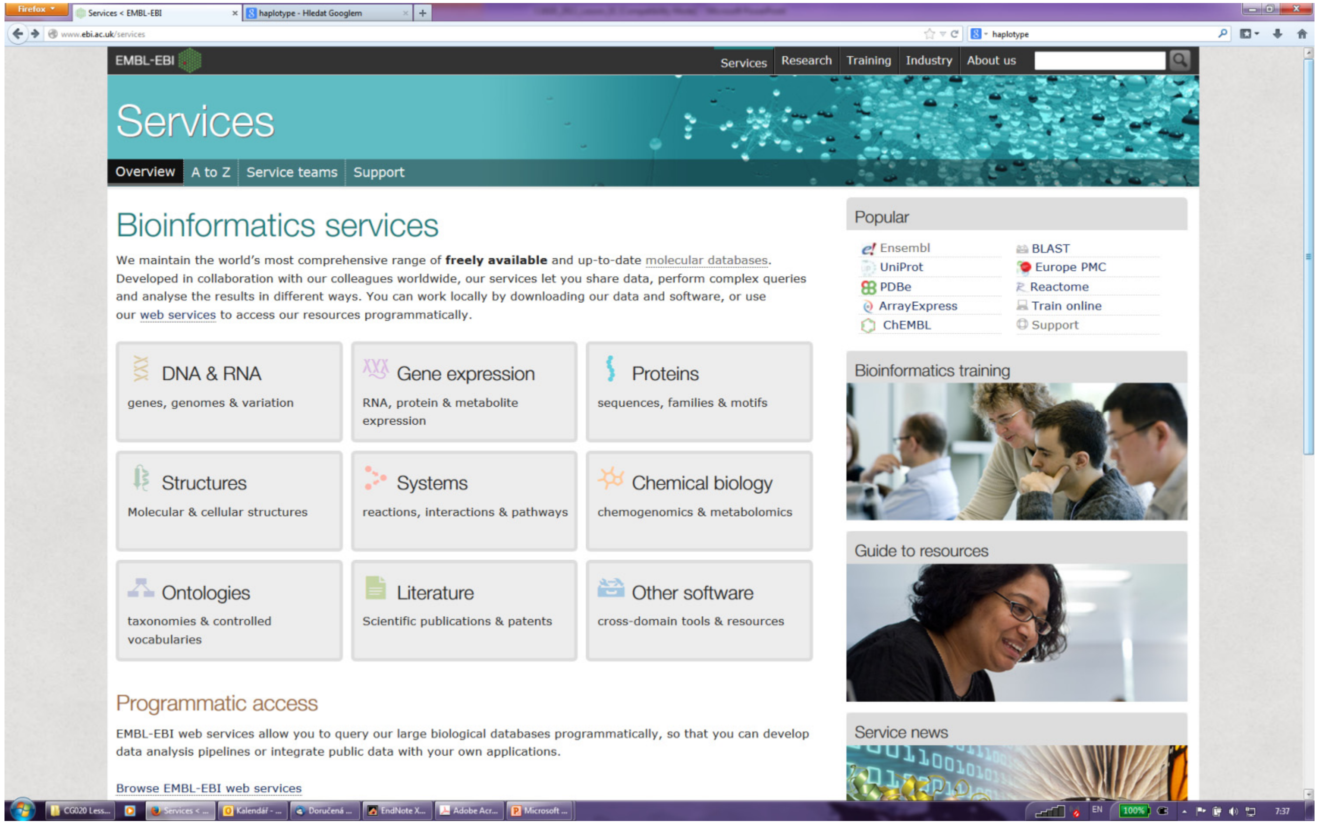
Sanger	UK	http://www.sanger.ac.uk/
UMBER	UK	http://www.bioinf.man.ac.uk/dbbrowser
EMBnet Associate Nodes		
IBBM	Argentina	http://sol.biol.unlp.edu.ar/embnet
ANGIS	Australia	http://www.angis.su.oz.au/
CBI	China	http://www.cbi.pku.edu.cn/
CIGB	Cuba	http://bio.cigb.edu.cu/
CDFD	India	http://salarjung.embnet.org.in/
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/

Spectre of on-line Resources

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



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Bioinformatics services

We maintain the world's most comprehensive range of **freely available** and up-to-date molecular databases. Developed in collaboration with our colleagues worldwide, our services let you share data, perform complex queries and analyse the results in different ways. You can work locally by downloading our data and software, or use our web services to access our resources programmatically.

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genes, genomes & variation

Gene expression
RNA, protein & metabolite expression

Proteins
sequences, families & motifs

Structures
Molecular & cellular structures

Systems
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Scientific publications & patents

Other software
cross-domain tools & resources

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EMBL-EBI web services allow you to query our large biological databases programmatically, so that you can develop data analysis pipelines or integrate public data with your own applications.

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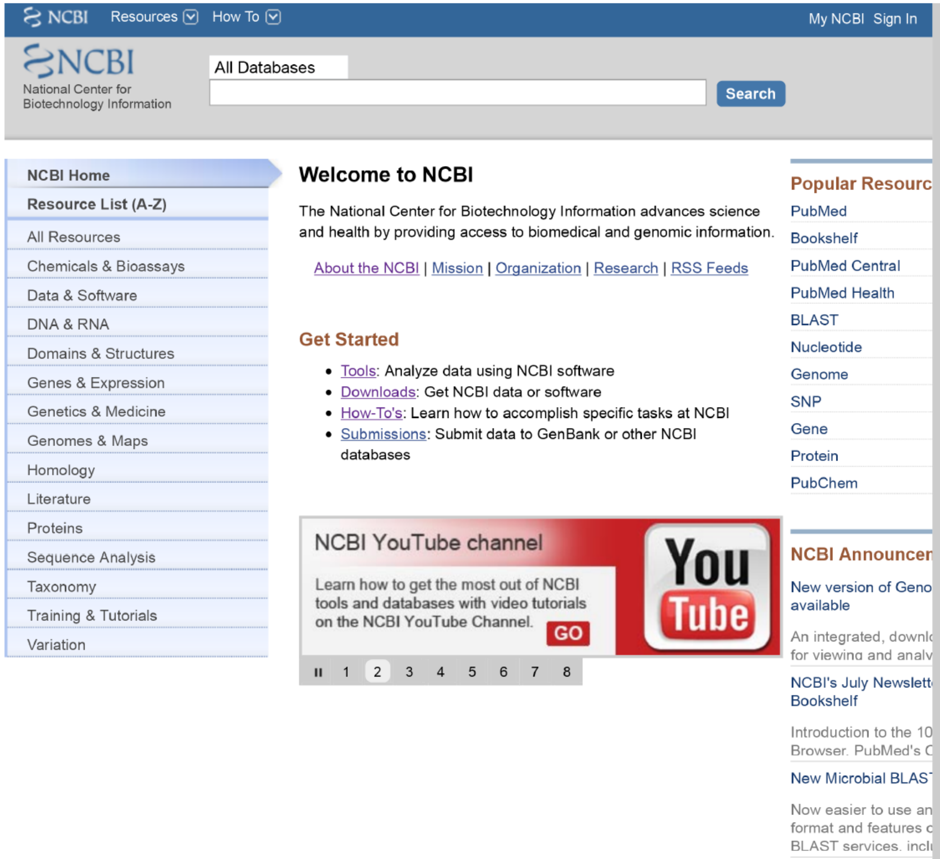
Spectre of on-line Resources

- NCBI http://www.ncbi.nlm.nih.gov/



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Homology

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Sequence Analysis

Taxonomy

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Variation

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Gene

Protein

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New version of Geno available

An integrated, downl for viewing and analy

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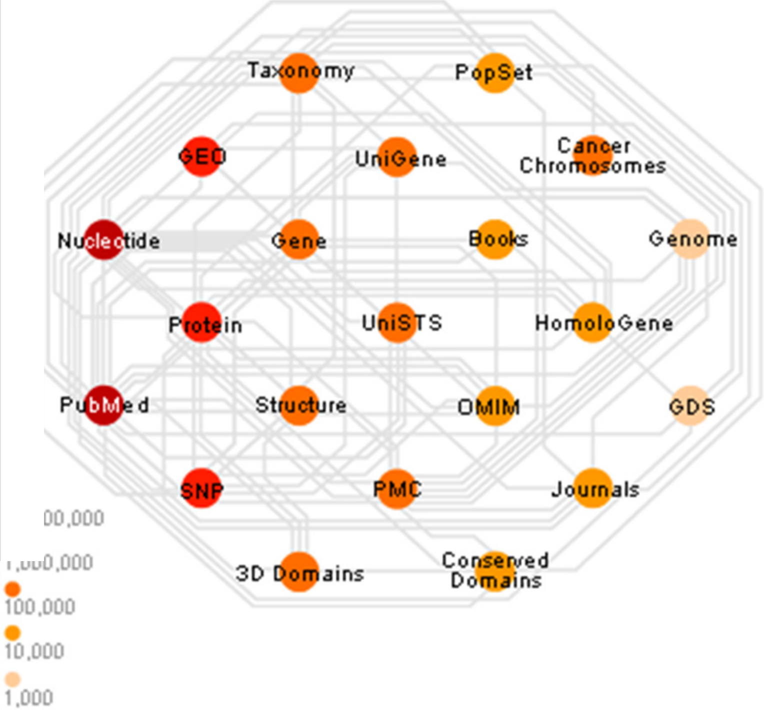
New Microbial BLAS

Now easier to use an format and features c BLAST services. inclu



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  - PRIMARY, SECONDARY and STRUCURAL databases

INVESTICE DO ROZVOJE VZDĚLÁVÁNÍ

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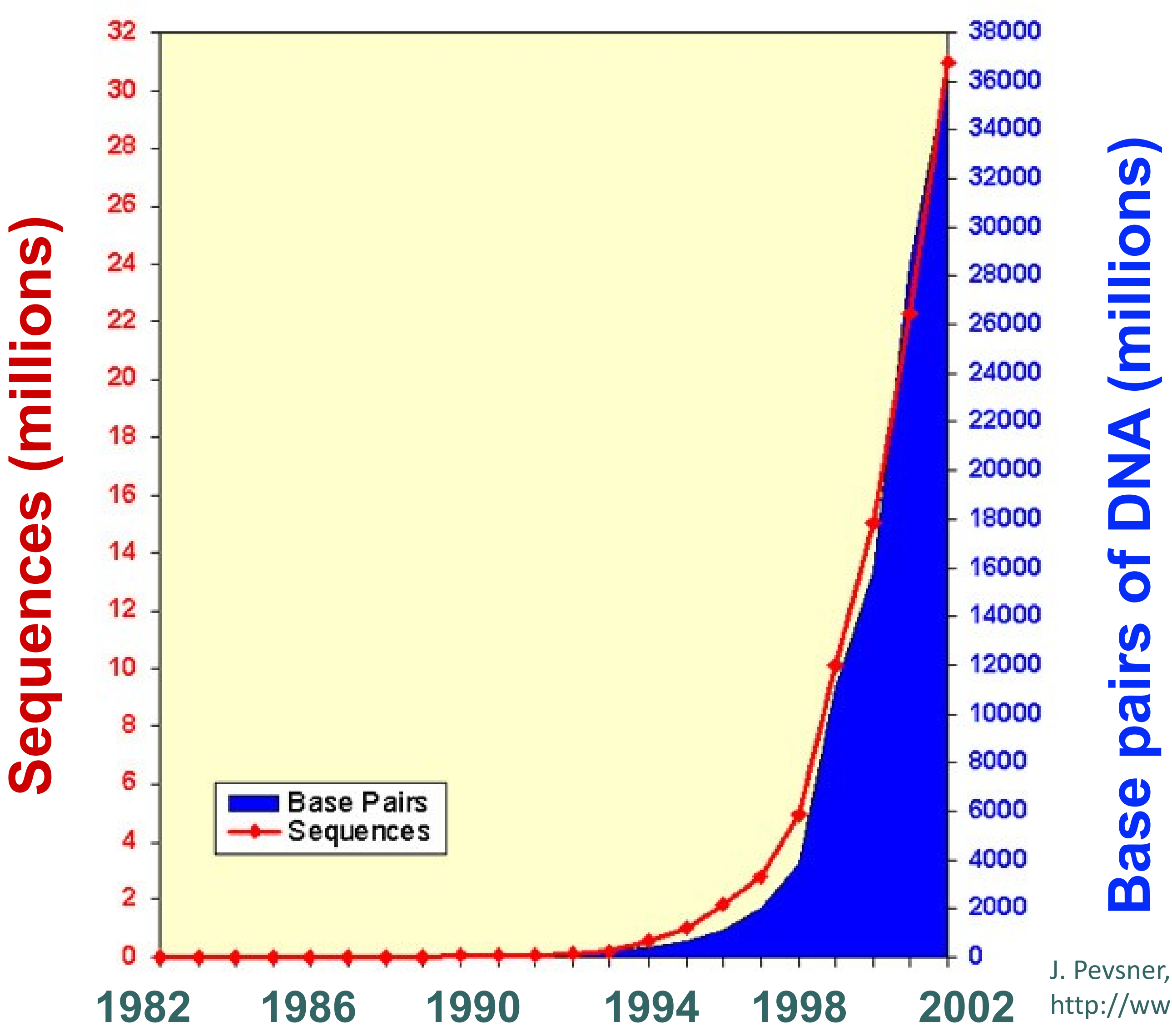
Primary Databases

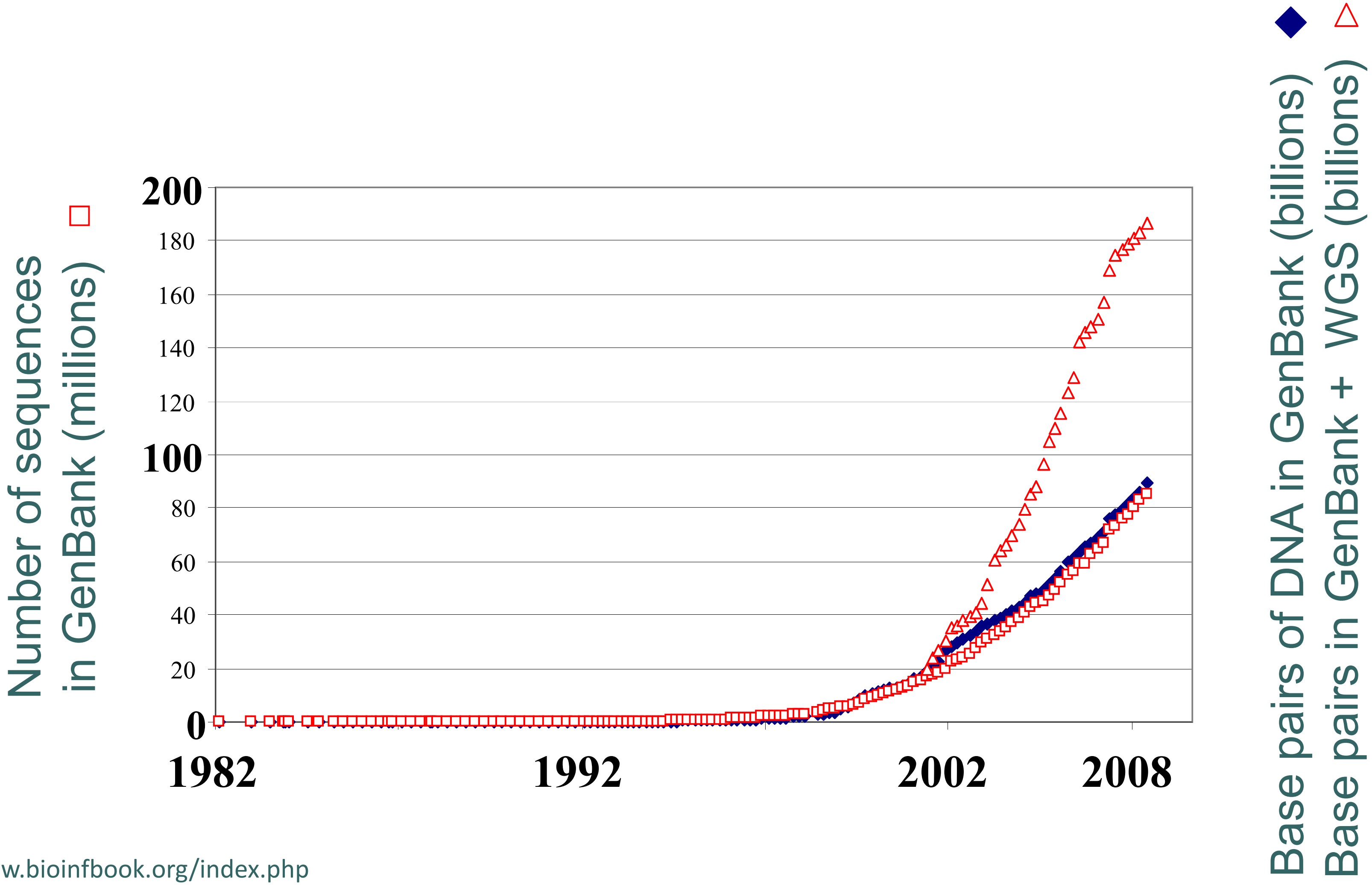
- Include primary datasets – DNA and Protein sequences
  - Sequences in databases of „The Big Three“:
    - EMBL
      - http://www.ebi.ac.uk/embl/
    - GenBank,
      - http://www.ncbi.nih.gov/Genbank/GenbankSearch.html
    - DDBJ,
      - http://www.ddbj.nig.ac.jp
  - Daily mutual exchange and backup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

Growth of GenBank



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

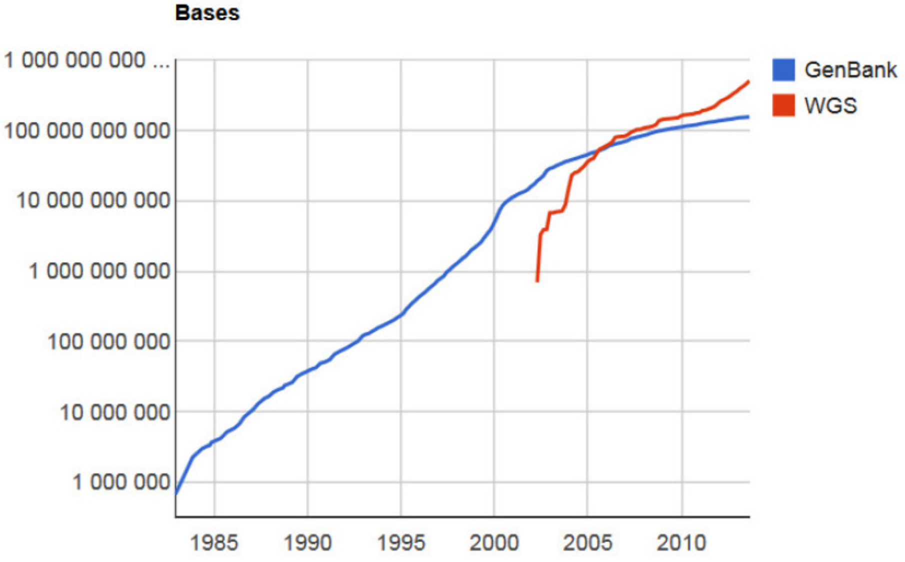
Growth of GenBank + Whole Genome Shotgun (1982-November 2008): we reached 0.2 terabases

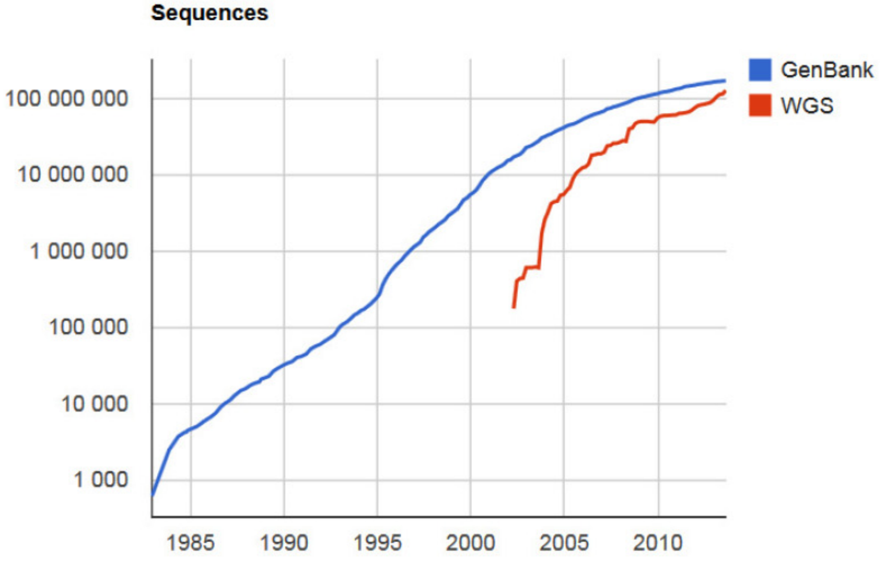


J. Pevsner,
http://www.bioinfbook.org/index.php

Growth of GenBank

Feb 15 2013





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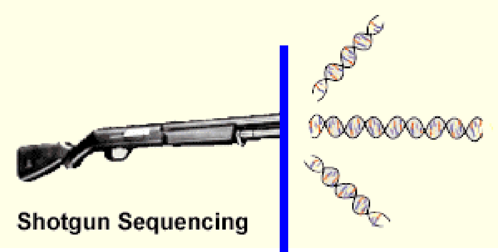
WGS



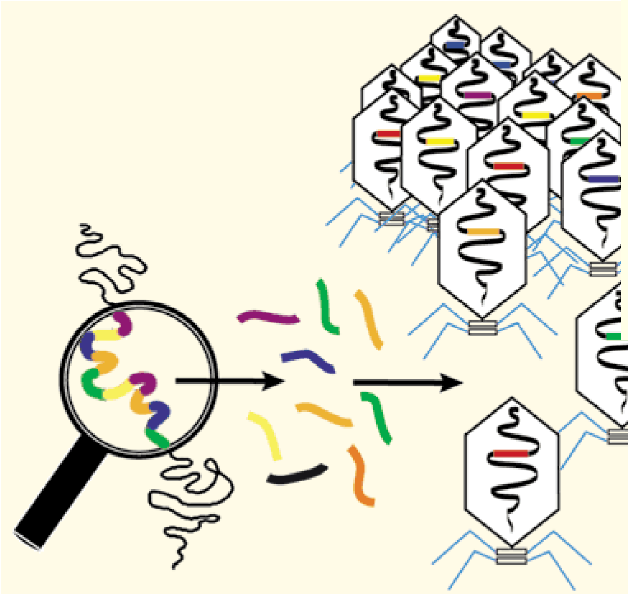


Fig 1: Genomic DNA is fragmented, ligated into viral DNA and packaged into viral particles to create a library

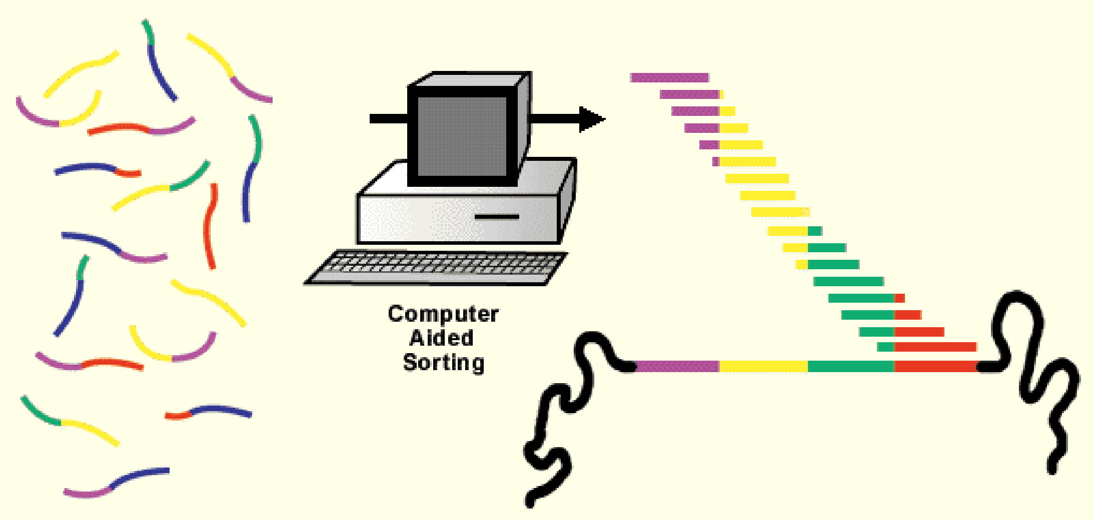
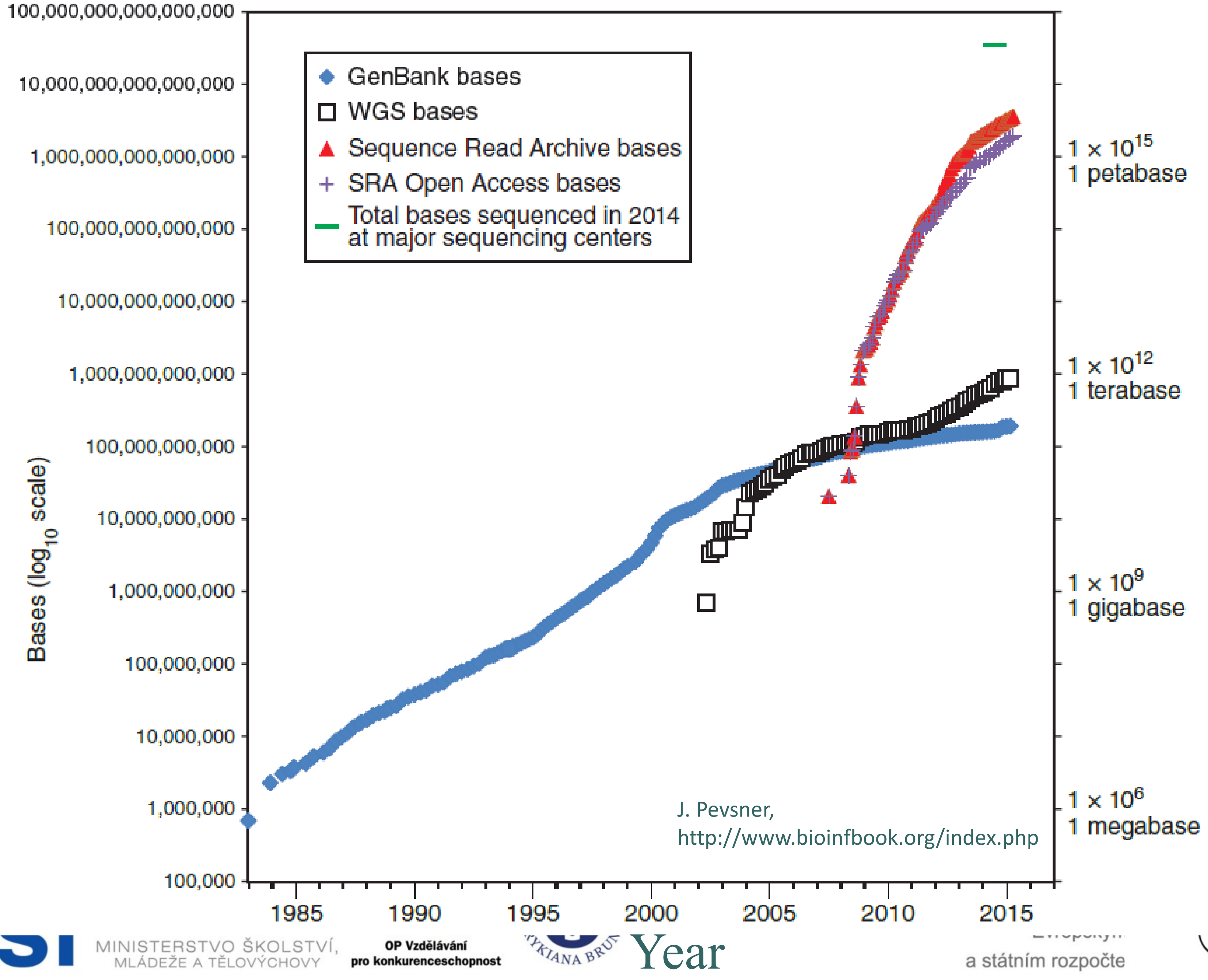


Fig 2: Short fragments of DNA sequence are ordered by overlapping data to recreate the whole genome sequence

Interactive concepts in biochemistry, Rodney Boyer, Wiley, 2002, http://www.wiley.com//college/boyer/0470003790/

Growth of DNA Sequence in Repositories



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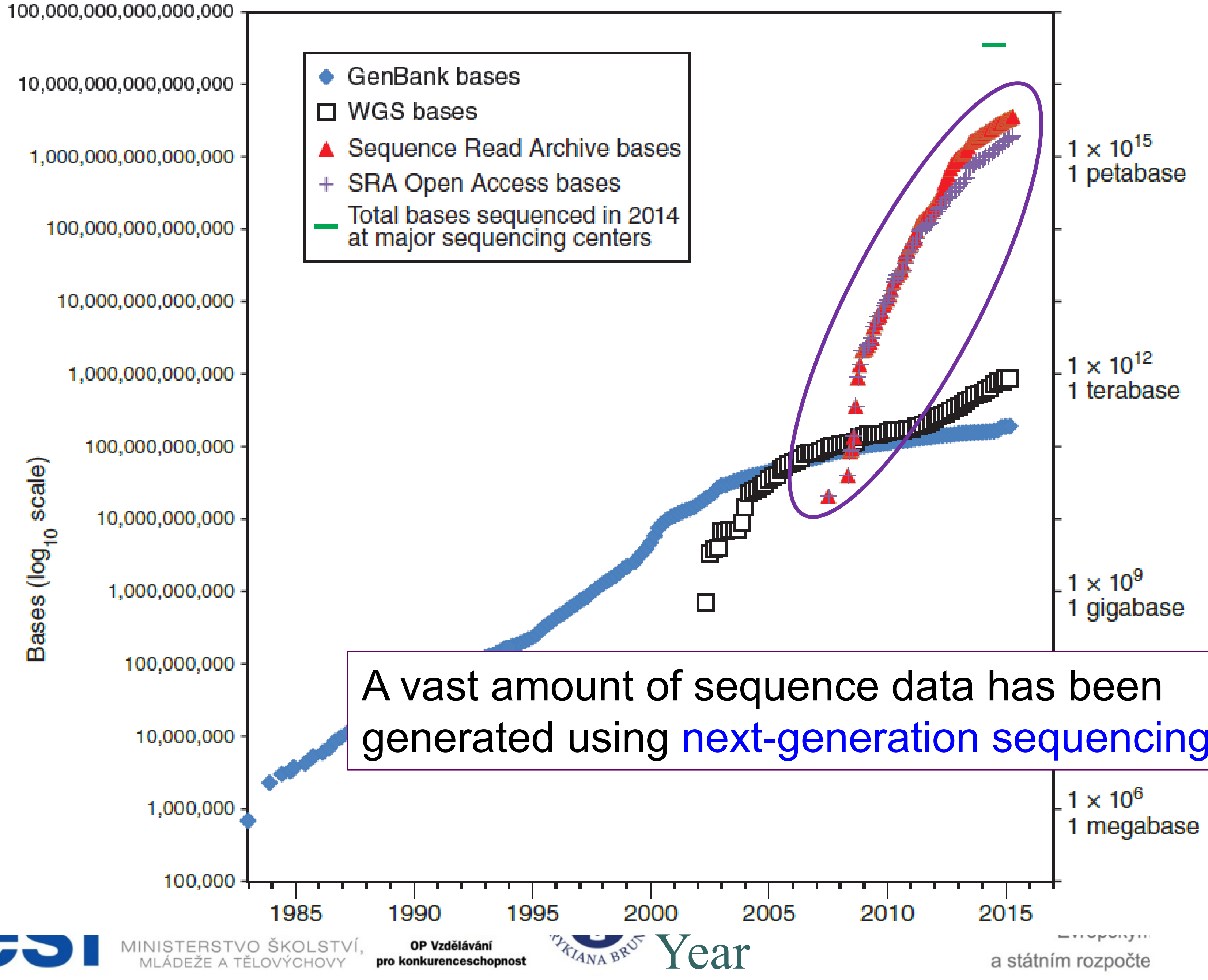
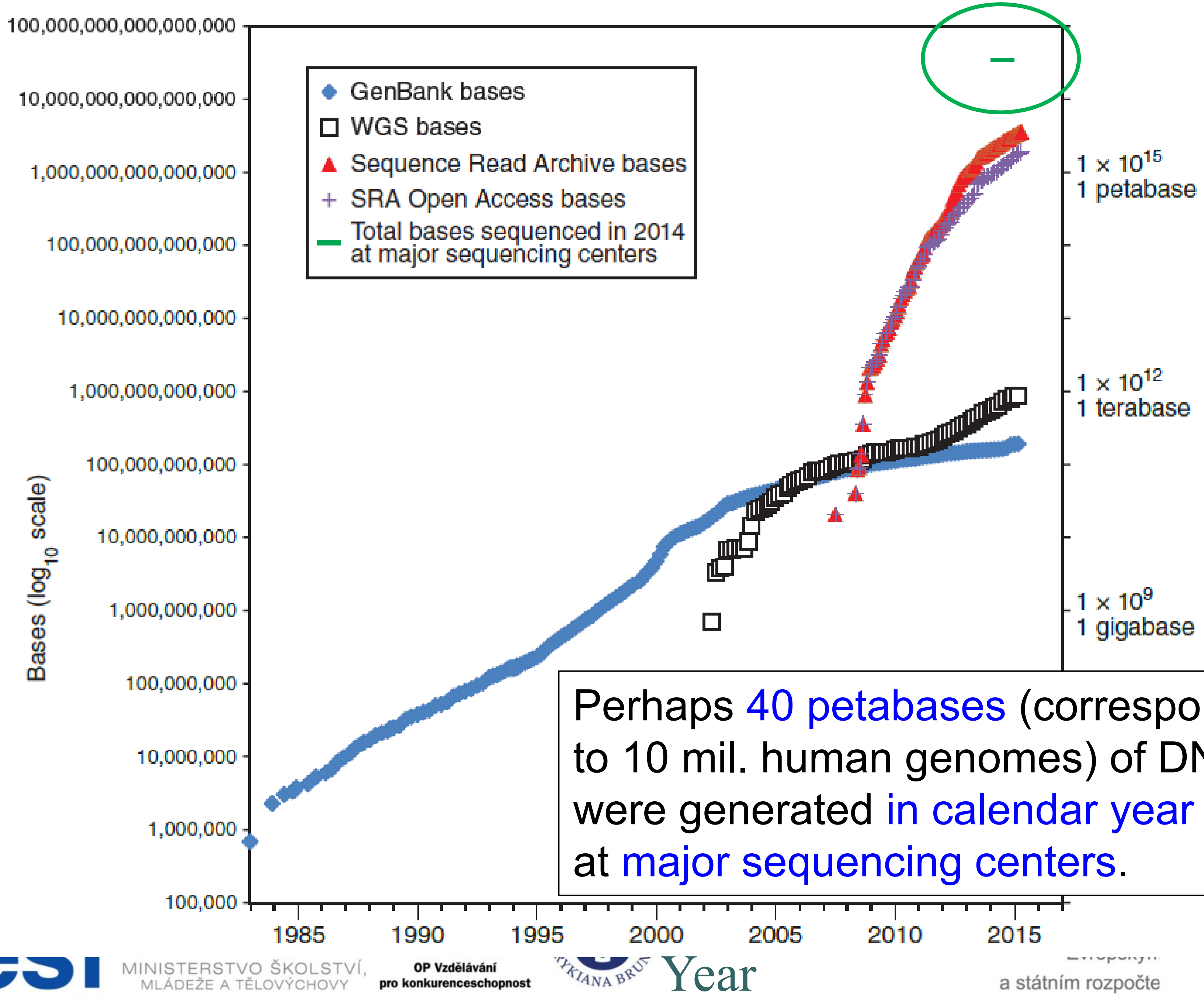
Growth of DNA Sequence in Repositories



A vast amount of sequence data has been generated using next-generation sequencing.

B&FG 3e
Fig. 2-3
Page 22

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.

B&FG 3e
Fig. 2-3
Page 22

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/

Primary Databases

- Types of sequences in primary databases
  - ☐ Standard nucleotide sequences acquired by high quality sequencing
  - ☐ **ESTs** (**E**xpressed **S**equence **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 orginal authors)

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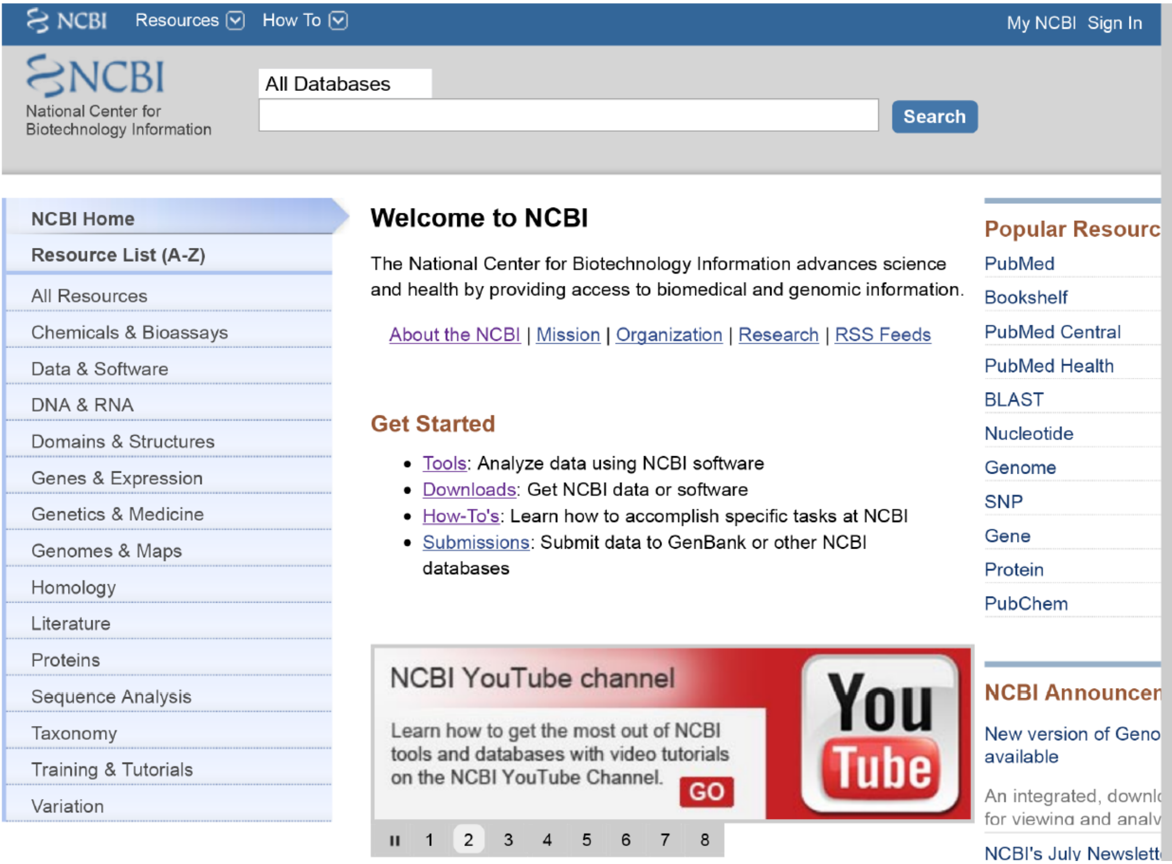
Primary Databases

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



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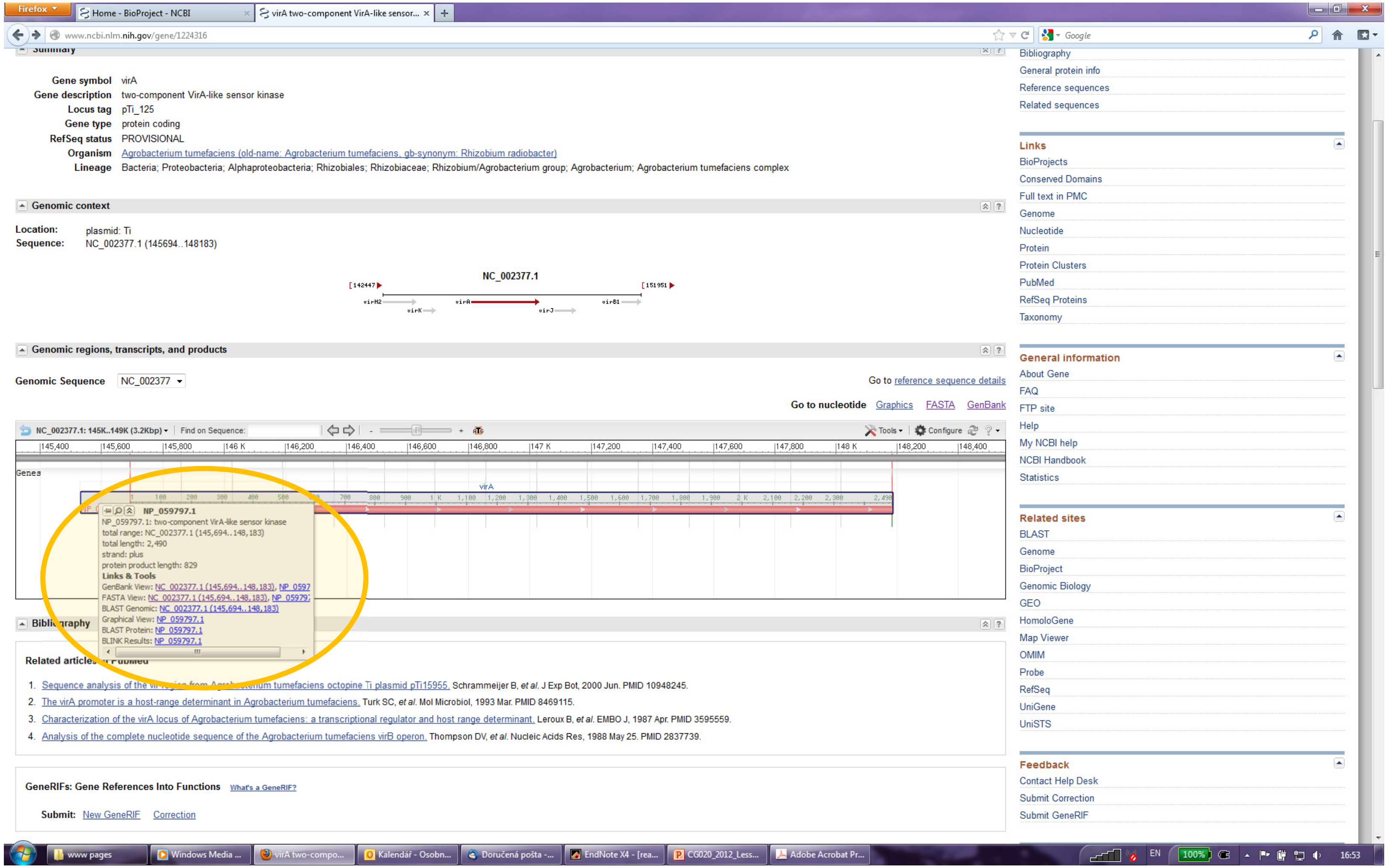
Primary Databases



Gene symbol virA
Gene description two-component VirA-like sensor kinase
Locus tag pTi_125
Gene type protein coding
RefSeq status PROVISIONAL
Organism Agrobacterium tumefaciens (old-name: Agrobacterium tumefaciens, gb-synonym: Rhizobium radiobacter)
Lineage Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium; Agrobacterium tumefaciens complex

Genomic context

Location: plasmid: Ti
Sequence: NC_002377.1 (145694..148183)

Genomic regions, transcripts, and products

Genomic Sequence NC_002377

Go to reference sequence details

Go to nucleotide Graphics FASTA GenBank

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_0597
FASTA View: NC_002377.1 (145,694..148,183), NP_05979
BLAST Genomic: NC_002377.1 (145,694..148,183)
Graphical View: NP_059797.1
BLAST Protein: NP_059797.1
BLINK Results: NP_059797.1

Bibli[illegible]graphy

Related articles [illegible] PubMed

1. Sequence analysis of the vi[illegible] from Agro[illegible]ium tumefaciens octopine Ti plasmid pTi15955. Schrammeijer B, *et al.* J Exp Bot, 2000 Jun. PMID 10948245.
2. The virA promoter is a host-range determinant in Agrobacterium tumefaciens. Turk SC, *et al.* Mol Microbiol, 1993 Mar. PMID 8469115.
3. Characterization of the virA locus of Agrobacterium tumefaciens: a transcriptional regulator and host range determinant. Leroux B, *et al.* EMBO J, 1987 Apr. PMID 3595559.
4. Analysis of the complete nucleotide sequence of the Agrobacterium tumefaciens virB operon. Thompson DV, *et al.* Nucleic Acids Res, 1988 May 25. PMID 2837739.

GeneRIFs: Gene References Into Functions What's a GeneRIF?

Submit: New GeneRIF Correction

Bibliography
General protein info
Reference sequences
Related sequences

Links
BioProjects
Conserved Domains
Full text in PMC
Genome
Nucleotide
Protein
Protein Clusters
PubMed
RefSeq Proteins
Taxonomy

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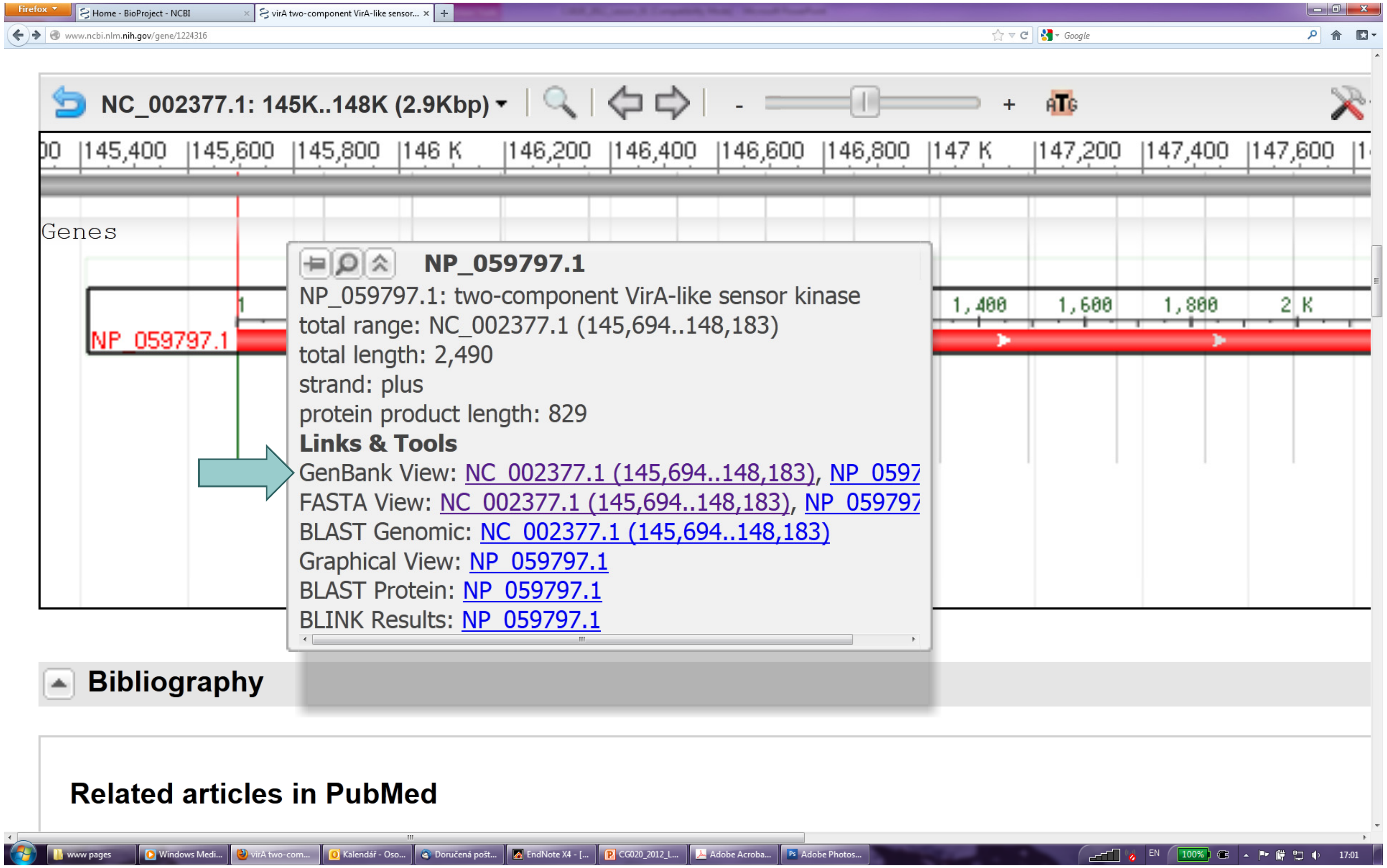
Primary Databases



NP_059797.1

NP_059797.1: two-component VirA-like sensor kinase
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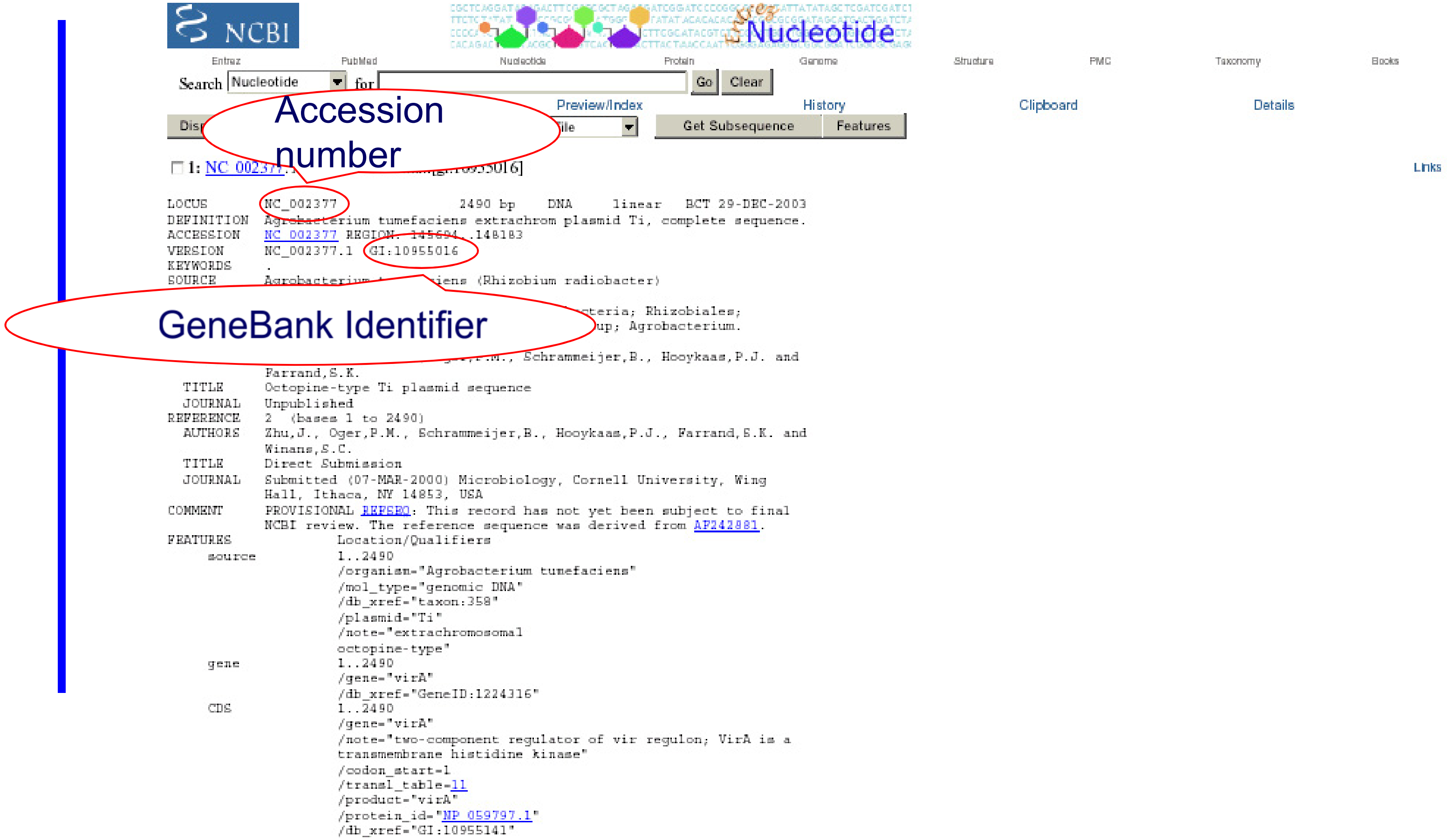
protein product length: 829

Links & Tools

GenBank View: NC_002377.1 (145,694..148,183), NP_0597
FASTA View: NC_002377.1 (145,694..148,183), NP_059797
BLAST Genomic: NC_002377.1 (145,694..148,183)
Graphical View: NP_059797.1
BLAST Protein: NP_059797.1
BLINK Results: NP_059797.1

Primary Databases



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☐ 1: NC_002377.                [gi:10955016]

LOCUS       NC_002377               2490 bp    DNA     linear   BCT 29-DEC-2003
DEFINITION  Agrobacterium tumefaciens extrachrom plasmid Ti, complete sequence.
ACCESSION   NC_002377 REGION: 145694..148183
VERSION     NC_002377.1  GI:10955016
KEYWORDS    .
SOURCE      Agrobacterium        iens (Rhizobium radiobacter)
                                    teria; Rhizobiales;
                                    up; Agrobacterium.

                            P.M., Schrammeijer,B., Hooykaas,P.J. and
            Farrand,S.K.
  TITLE     Octopine-type Ti plasmid sequence
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2490)
  AUTHORS   Zhu,J., Oger,P.M., Schrammeijer,B., Hooykaas,P.J., Farrand,S.K. and
            Winans,S.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-MAR-2000) Microbiology, Cornell University, Wing
            Hall, Ithaca, NY 14853, USA
COMMENT     PROVISIONAL REFSEQ: This record has not yet been subject to final
            NCBI review. The reference sequence was derived from AF242881.
FEATURES             Location/Qualifiers
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                     /plasmid="Ti"
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                     /note="two-component regulator of vir regulon; VirA is a
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Primary Databases

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                     TQAILSQLRSINADSASLQRDVLRAHTGTVANYRPIISRLGALRKNLEDLKQLFRQSH
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                     SSGDRAMLIIDQILTLSRKQERMIKPFSVSELVTEIAPLLRMALPPNIELSFRFDQMQ
                     SVIEGSPLELQQVLINICKNASQAMTANGQIDIIISQAFLPVKKILAHGVMPPGDYVL
                     LSISDNGGGIPEAVLPHIFEPFFTTRARNGGTGLGLASVHGHISAFAGYIDVSSTVGH
                     GTRFDIYLPPSSKEPVNPDSFFGRNKAPRGNGEIVALVEPDDLLREAYEDKIAALGYE
                     PVGFRTFNEIRDWISKGNEADLVMVDQASLPEDQSPNSVDLVLKTASIIIGGNDLKMT
                     LSREDVTRDLYLPKPISSRTMAHAILTKIKT"
ORIGIN
        1 atgaacggaa gatattcacc gacgcggcag gattttaaga caggcgcgaa gccttggtct
       61 atattggccc ttatcgttgc tgcaatgatt ttcgcgttca tggcggttgc gtcctggcag
      121 gacaatgcga ctacccaggc aatcctcagc caactacgat cgattaacgc cgacagcgcc
      181 tcactgcagc gcgatgtact ccgcgctcac acgggcaccg tggcgaacta ccgccccatt
      241 atctccaggc tgggagctct gcggaagaat ctggaagatt tgaagcaatt atttagacaa
      301 tctcatattg taagtgagag caatgctgct caactgctac gccagctaga agtgtctcta
      361 aattcggctg acgcggcggt cgccgccttt ggtgcgcaaa atgtacgcct gcaagattcg
      421 ctggccagtt tcactcgtgc tttgagcagt cttccaggaa aagcctcaac cgatcagact
      481 ttagaaaaac caacagaatt ggctagcatg atgctccaat ttcttcggca accaagcccg
      541 gctatttcat tcgagatcag ccttgaacta gagaggctcc aaaaacaacg cggtcttgat
      601 gaagctcccg tgcgcatact tgcacgtgaa ggtcccatta tcttatcgct tttgccacag
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      781 tttcttgggt ccgcttcagt gggtctttgc ctctacatca tcaccttagt ctataggcta
      841 cgcaaaaaaa ccgattggtt agcgcggcgt ttagattacg aagagctaat caaagagatc
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      961 attcagcgct tctttgatgc cgatacgtgc gcgttagctc tagtggacca tgaccgtaga
     1021 tgggctgtcg aaacattcgg tgcgaaacac ccaaaacctg tgtgggacga cagcgtgcta
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     1261 ccttgccaag gcgaaattca gcttcttgaa ctcgccaccg cctgcctctg tcactatatc
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     1501 cgaagatata ttgactatat catttcgtca ggcgacagag ccatgctcat tatcgatcag
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     1621 gtgaccgaaa tcgctccctt gctacgtatg gctcttccgc caaacatcga gcttagtttc
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     1801 atcagccaag ctttttttacc agttaagaaa attctggcgc atggtgttat gccacctggc
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     2341 ttagtgctca agaccgcctc catcatcatt ggcggaaatg atctcaaaat gaccctttca
```

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

NCBI's important RefSeq project:
best representative sequences

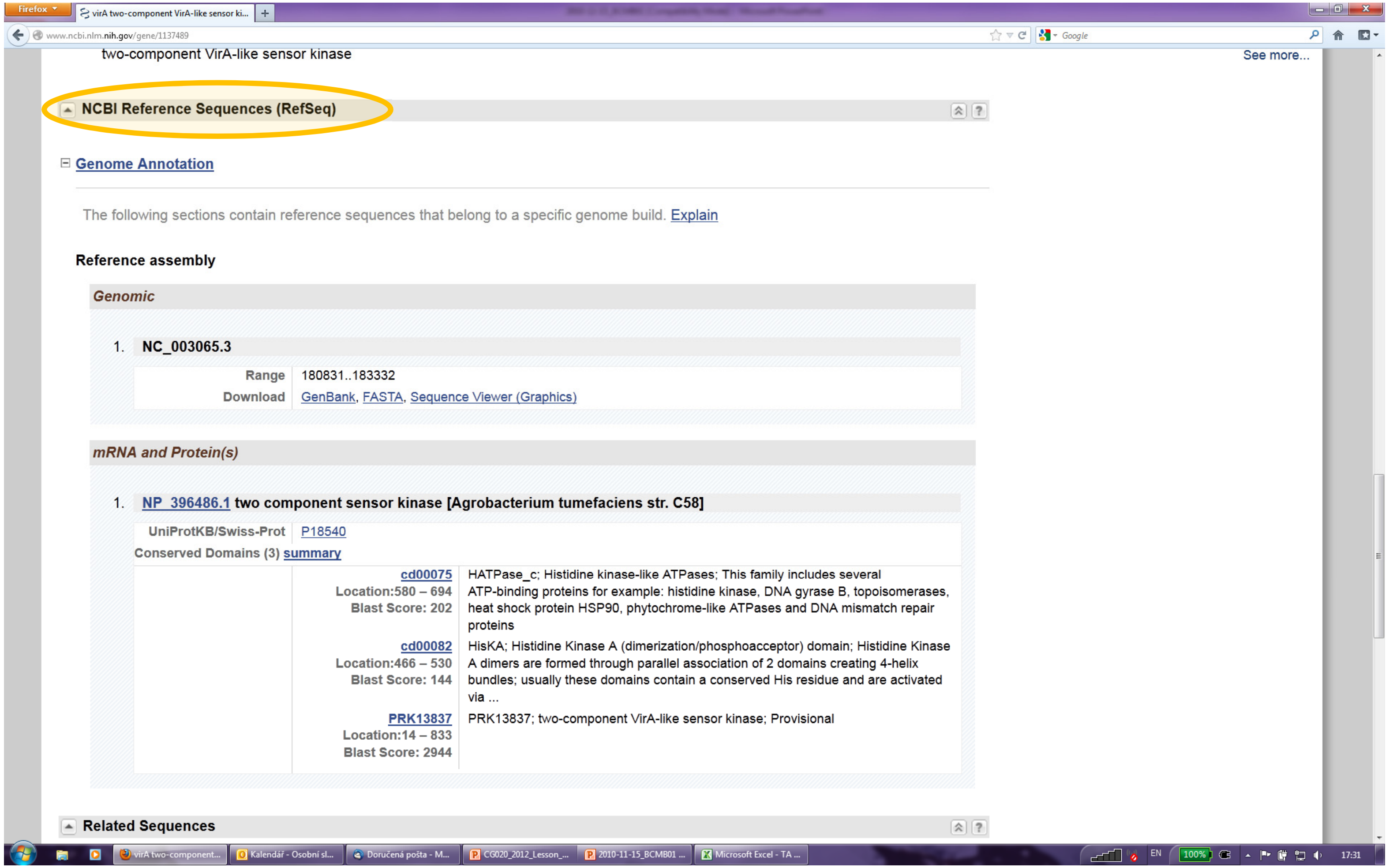
RefSeq (accessible via the main page of NCBI) provides an expertly curated accession number that corresponds to the most stable, agreed-upon "reference" version of a sequence.

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

RefSeq



two-component VirA-like sensor kinase

See more...

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	180831..183332
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	P18540

Conserved Domains (3) summary

cd00075 **Location:580 – 694** **Blast Score: 202**	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 **Location:466 – 530** **Blast Score: 144**	HisKA; Histidine Kinase A (dimerization/phosphoacceptor) 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 ...
PRK13837 **Location:14 – 833** **Blast Score: 2944**	PRK13837; two-component VirA-like sensor kinase; Provisional

Related Sequences

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

Accession	Molecule	Method	Note
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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http://www.bioinfbook.org/index.php

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Tato prezentace je spolufinancována
Evropským sociálním fondem
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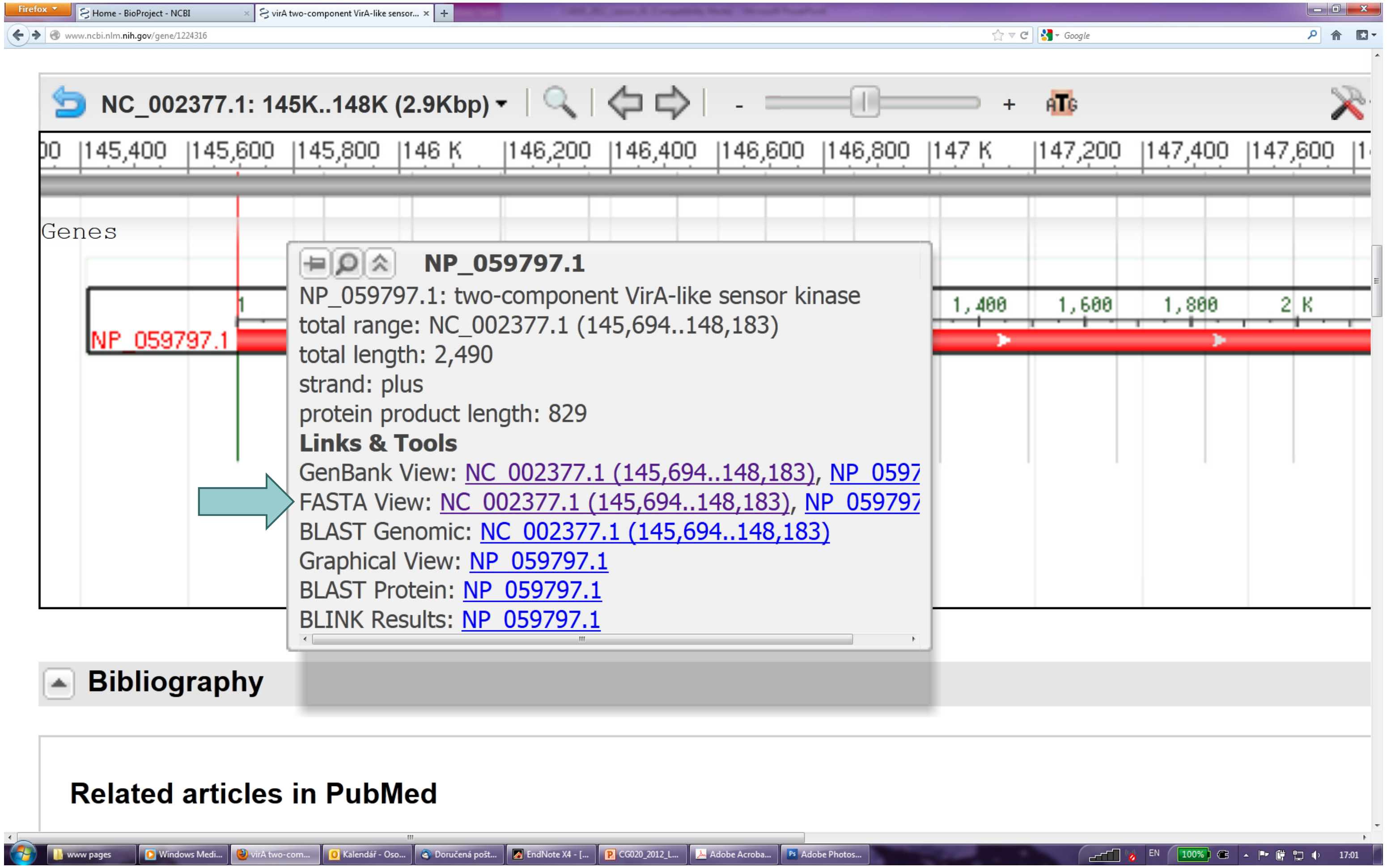
Primary Databases



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

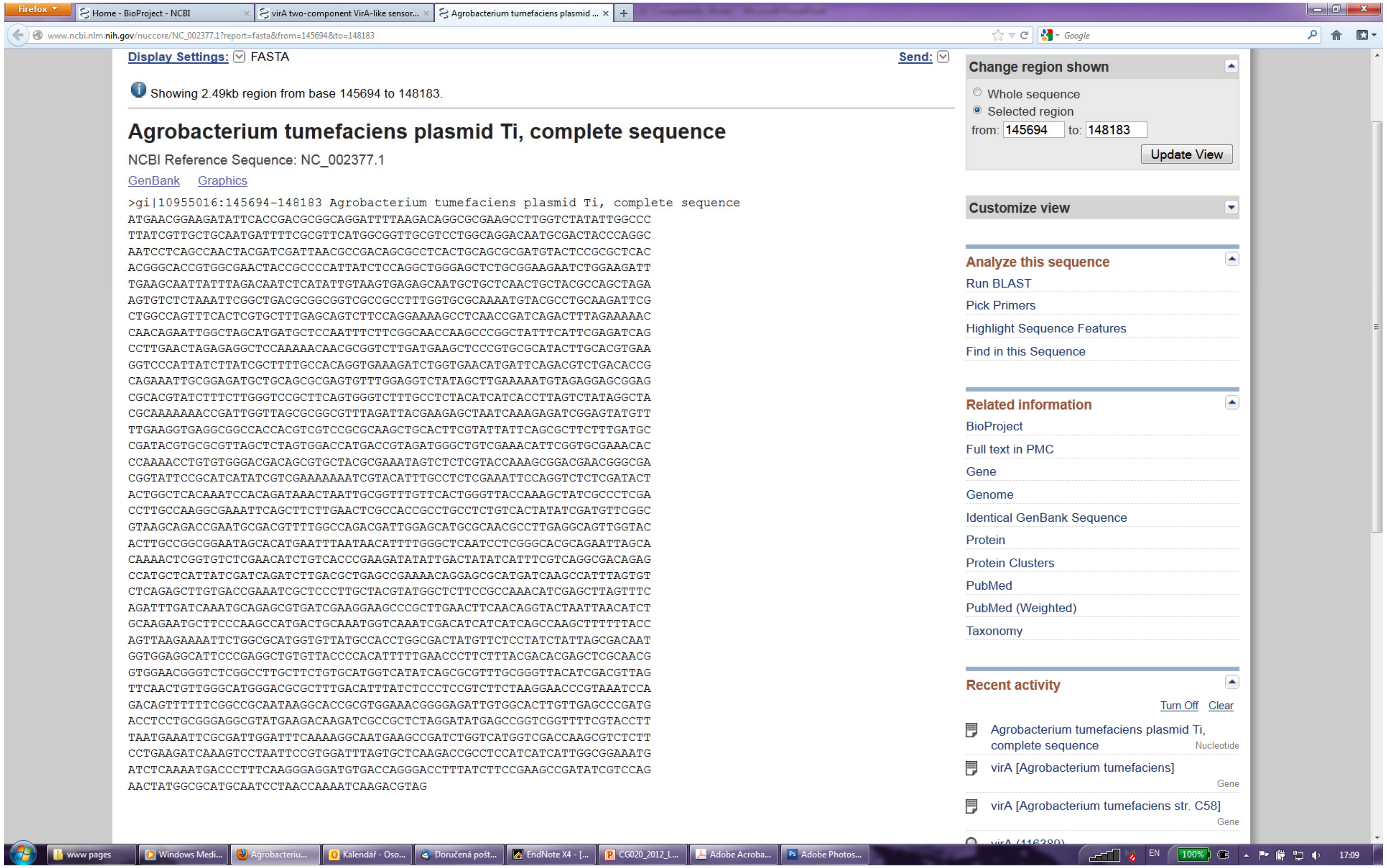
Links & Tools

GenBank View: NC_002377.1 (145,694..148,183), NP_0597
FASTA View: NC_002377.1 (145,694..148,183), NP_059797
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

Primary Databases



Display Settings: FASTA

Showing 2.49kb region from base 145694 to 148183.

Agrobacterium tumefaciens plasmid Ti, complete sequence

NCBI Reference Sequence: NC_002377.1

GenBank Graphics

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>gi|10955016:145694-148183 Agrobacterium tumefaciens plasmid Ti, complete sequence
ATGAACGGAAGATATTCACCGACGCGGCAGGATTTTAAGACAGGCGCGAAGCCTTGGTCTATATTGGCCC
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ACGGGCACCGTGGCGAACTACCGCCCCATTATCTCCAGGCTGGGAGCTCTGCGGAAGAATCTGGAAGATT
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CCTGAAGATCAAAGTCCTAATTCCGTGGATTTAGTGCTCAAGACCGCCTCCATCATCATTGGCGGAAATG
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AACTATGGCGCATGCAATCCTAACCAAAATCAAGACGTAG
```

Change region shown

○ Whole sequence
● Selected region
from: 145694 to: 148183

Customize view

Analyze this sequence

Run BLAST
Pick Primers
Highlight Sequence Features
Find in this Sequence

Related information

BioProject
Full text in PMC
Gene
Genome
Identical GenBank Sequence
Protein
Protein Clusters
PubMed
PubMed (Weighted)
Taxonomy

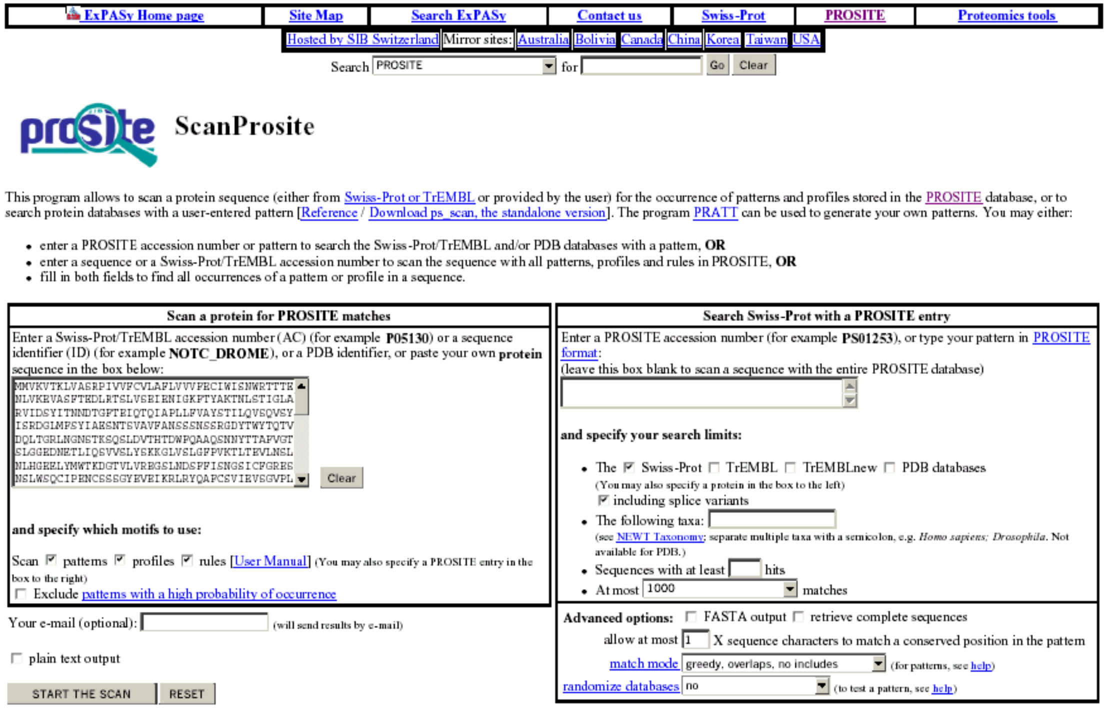
Recent activity

Turn Off Clear

Agrobacterium tumefaciens plasmid Ti, complete sequence Nucleotide
virA [Agrobacterium tumefaciens] Gene
virA [Agrobacterium tumefaciens str. C58] Gene

Secondary Databases

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

Enter a Swiss-Prot/TrEMBL accession number (AC) (for example **P05130**) or a sequence identifier (ID) (for example **NOTC_DROME**), or a PDB identifier, or paste your own **protein** sequence in the box below:

```
MMVKVTKLVASRPIVVFCVLAFLVVVFECIWISNWRTTTE
NLVKEVASFTEDLRTSLVSEIENIGKFTYAKTNLSTIGLA
RVIDSYITNNDTGFTEIQTQIAPLLFVAYSTILQVSQVSY
ISRDGLMFSYIAESNTSVAVFANSSSNSSRGDYTWYTQTV
DQLTGRLNGNSTKSQSLDVTHTDWFQAAQSNNYTTAFVGT
SLGGEDNETLIQSVVSLYSKKGLVSLGFPVKTLTEVLNSL
NLHGEELYMWTKDGTVLVREGSLNDSFFISNGSICFGRES
NSLWSQCIPENCSSSGYEVEIKRLRYQAFCSVIEVSGVPL
```

and specify which motifs to use:

Scan ☑ patterns ☑ profiles ☑ rules [User Manual] (You may also specify a PROSITE entry in the box to the right)

☐ Exclude patterns with a high probability of occurrence

Your e-mail (optional): (will send results by e-mail)

☐ plain text output

Search Swiss-Prot with a PROSITE entry

Enter a PROSITE accession number (for example **PS01253**), or type your pattern in PROSITE format:
(leave this box blank to scan a sequence with the entire PROSITE database)

and specify your search limits:

- The ☑ Swiss-Prot ☐ TrEMBL ☐ TrEMBLnew ☐ PDB databases
  (You may also specify a protein in the box to the left)
  ☑ including splice variants
- The following taxa:
  (see NEWT Taxonomy; separate multiple taxa with a semicolon, e.g. *Homo sapiens; Drosophila*. Not available for PDB.)
- Sequences with at least hits
- At most 1000 matches

Advanced options: ☐ FASTA output ☐ retrieve complete sequences

allow at most 1 X sequence characters to match a conserved position in the pattern

match mode greedy, overlaps, no includes (for patterns, see help)

randomize databases no (to test a pattern, see help)

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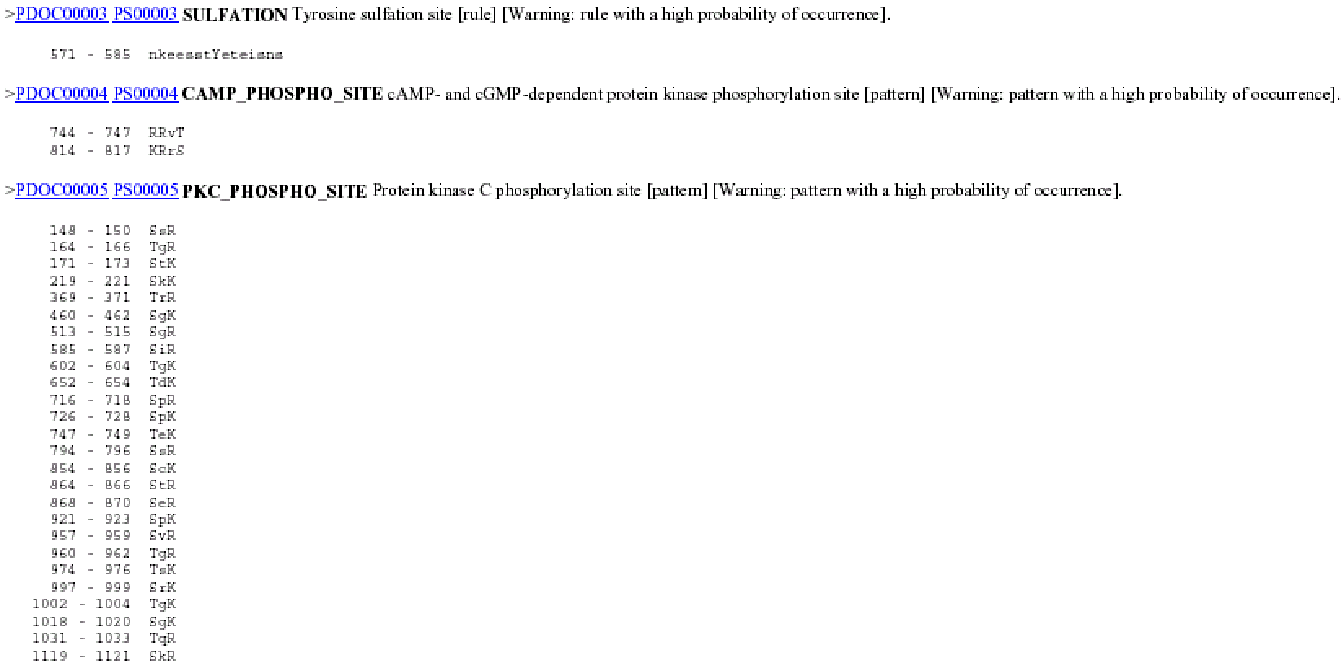

>PDOC00003 PS00003 **SULFATION** Tyrosine sulfation site [rule] [Warning: rule with a high probability of occurrence].

```
     571 - 585  nkeesstYeteisns
```

>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  KRrS
```

>PDOC00005 PS00005 **PKC_PHOSPHO_SITE** Protein kinase C phosphorylation site [pattern] [Warning: pattern with a high probability of occurrence].

```
     148 - 150  SsR
     164 - 166  TgR
     171 - 173  StK
     219 - 221  SkK
     369 - 371  TrR
     460 - 462  SgK
     513 - 515  SgR
     585 - 587  SiR
     602 - 604  TgK
     652 - 654  TdK
     716 - 718  SpR
     726 - 728  SpK
     747 - 749  TeK
     794 - 796  SsR
     854 - 856  ScK
     864 - 866  StR
     868 - 870  SeR
     921 - 923  SpK
     957 - 959  SvR
     960 - 962  TgR
     974 - 976  TsK
     997 - 999  SrK
    1002 - 1004  TgK
    1018 - 1020  SgK
    1031 - 1033  TqR
    1119 - 1121  SkR
```

Secondary Databases

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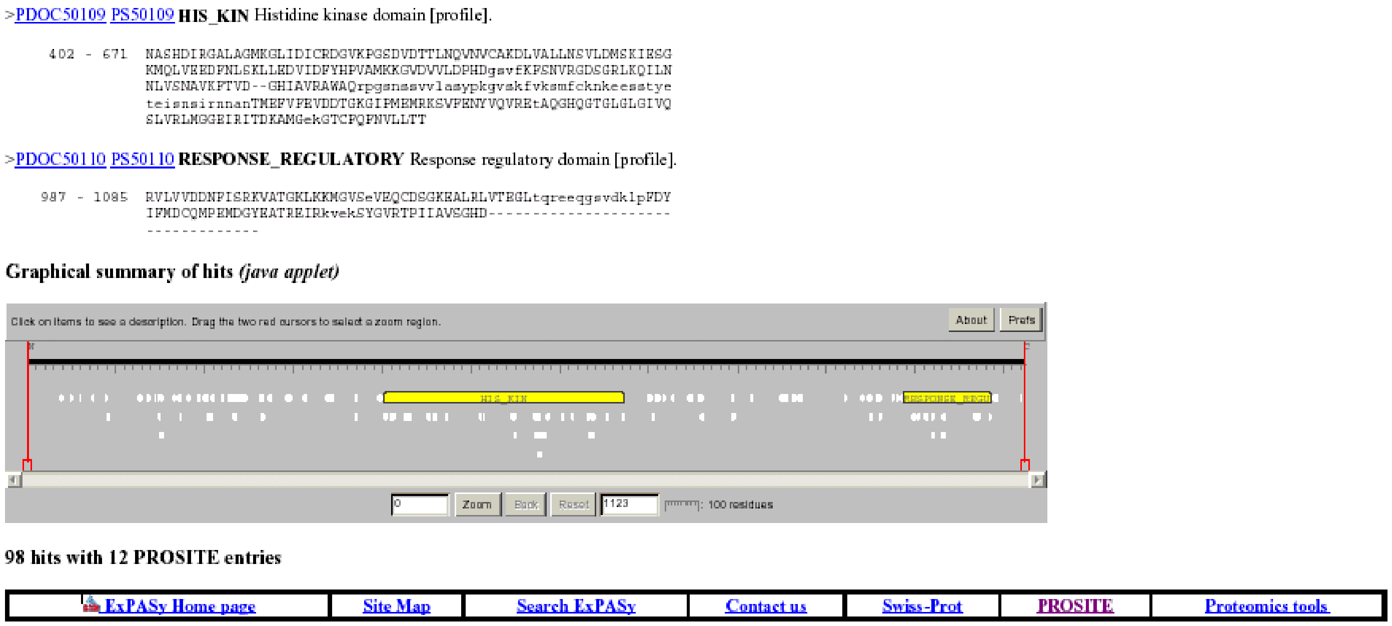

>PDOC50109 PS50109 **HIS_KIN** Histidine kinase domain [profile].

```
402 - 671  NASHDIRGALAGMKGLIDICRDGVKPGSDVDTTLNQVNVCAKDLVALLNSVLDMSKIESG
           KMQLVEEDFNLSKLLEDVIDFYHPVAMKKGVDVVLDPHDgsvfKFSNVRGDSGRLKQILN
           NLVSNAVKFTVD--GHIAVRAWAQrpgsnssvvlasypkgvskfvksmfcknkeesstye
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           SLVRLMGGEIRITDKAMGekGTCFQFNVLLTT
```

>PDOC50110 PS50110 **RESPONSE_REGULATORY** Response regulatory domain [profile].

```
987 - 1085  RVLVVDDNPISRKVATGKLKKMGVSeVEQCDSGKEALRLVTEGLtqreeqgsvdklpFDY
            IFMDCQMPEMDGYEATREIRkvekSYGVRTPIIAVSGHD---------------------
            -------------
```

Graphical summary of hits ***(java applet)***

Click on items to see a description. Drag the two red cursors to select a zoom region.

98 hits with 12 PROSITE entries

Secondary Databases

- Databases of **functional** or **structural *motifs***, acquired by primary data (sequences) comparison

☐ PRINTS, http://www.bioinf.man.ac.uk/dbbrowser/PRINTS/

PRINTS is a compendium 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 *SWISS-PROT/TrEMBL* composite. Usually the motifs do not overlap, but are separated 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. **References**

New:

- SPRINT - *Search PRINTS-S (relational PRINTS)*
- prePRINTS - *Search PRINTS' automatic supplement*
- InterPro - *Search the integrated InterPro family database*

Direct PRINTS access:

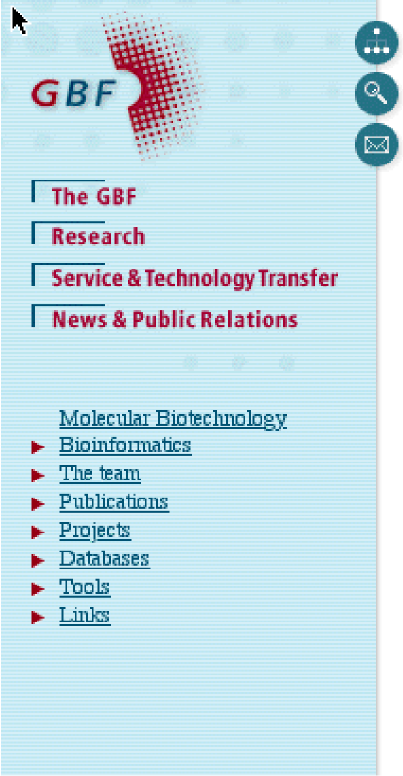
- By accession number
- By PRINTS code
- By database code
- By text
- By sequence
- By title
- By number of motifs
- By author
- By query language

PRINTS search:

- Search PRINTS with NEW FingerPRINTScan
- FPScan
- GRAPHScan
- MULScan
- FingerPRINTScan binaries and source are available: contact scordis@bioinf.man.ac.uk

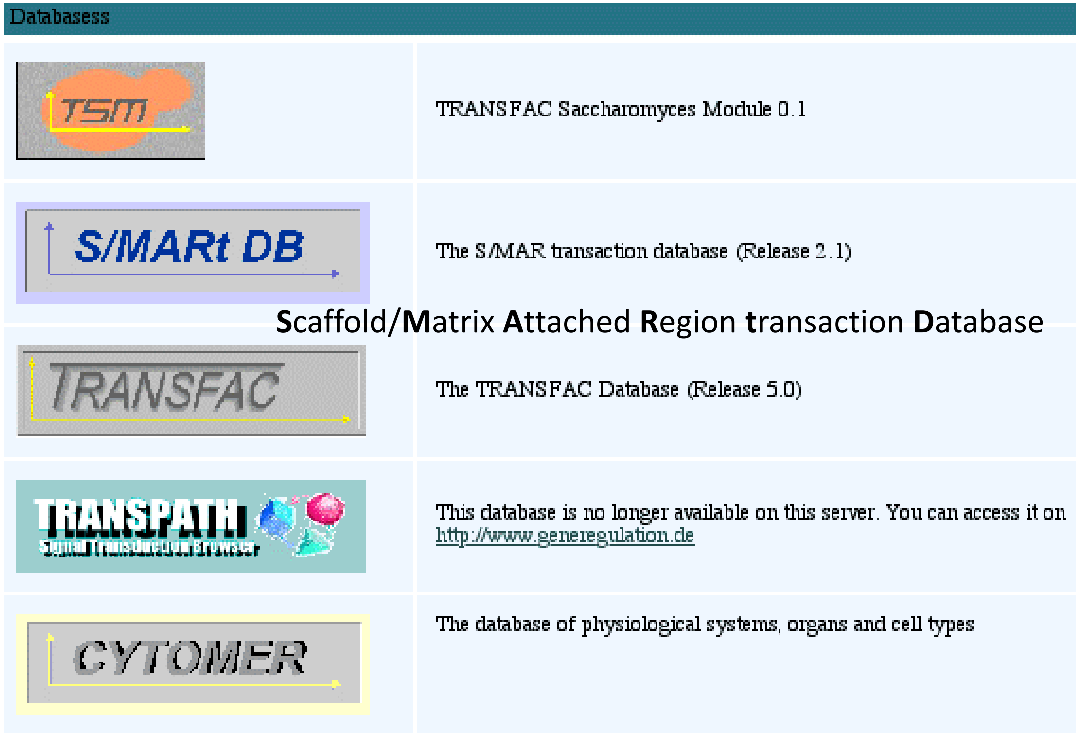
Secondary Databases

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



The GBF
Research
Service & Technology Transfer
News & Public Relations

Molecular Biotechnology
- Bioinformatics
- The team
- Publications
- Projects
- Databases
- Tools
- Links



Databasess	
TSM	TRANSFAC Saccharomyces Module 0.1
S/MARt DB	The S/MAR transaction database (Release 2.1)
TRANSFAC	The TRANSFAC Database (Release 5.0)
TRANSPATH	This database is no longer available on this server. You can access it on http://www.generegulation.de
CYTOMER	The database of physiological systems, organs and cell types

Scaffold/**M**atrix **A**ttached **R**egion **t**ransaction **D**atabase

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Structural Databases

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

DEPOSIT data
DOWNLOAD files
browse LINKS
BETA TEST new features
BETA mmCIF files

Current Holdings

19623 Structures
Last Update: 30-Dec-2002
PDB Statistics

Molecule of the Month: Cytochrome c

The Protein Data Bank (PDB) is operated by Rutgers, The State University of New Jersey; the San Diego Supercomputer Center at the University of California, San Diego; and the National Institute of Standards and Technology -- three members of the Research Collaboratory for Structural Bioinformatics (RCSB). The PDB is supported by funds from the National Science Foundation, the Department of Energy, and two units of the National Institutes of Health: the

PROTEIN DATA BANK

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Welcome to the PDB, the single worldwide repository for the processing and distribution of 3-D biological macromolecular structure data.

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Find a structure

☐ query by PDB id only ☐ match exact word
☐ remove sequence homologues

SearchLite keyword search form with examples
SearchFields customizable search form
Status Search find entries awaiting release

News   Complete News Newsletter   pdb-l Archive Subscribe

23-Dec-2002
Happy Holidays from the PDB! The PDB staff wish to extend our best wishes to the community for a happy holiday season and a wonderful new year!

PDB Mirrors

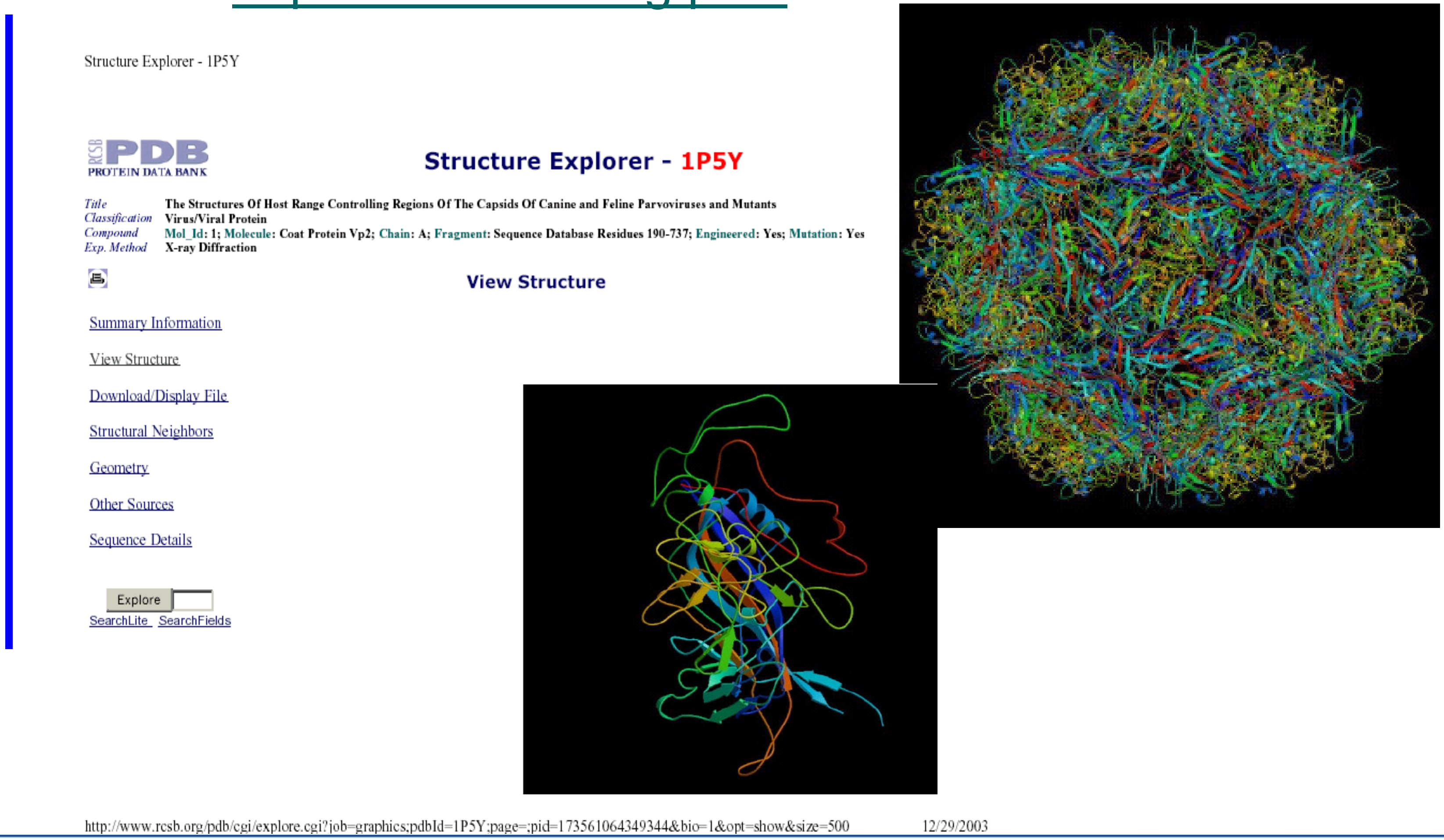
Please bookmark a mirror site

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
Max Delbrück Center for Molecular Medicine, Germany

OTHER SITES

Structural Databases

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



Structure Explorer - 1P5Y

Structure Explorer - 1P5Y

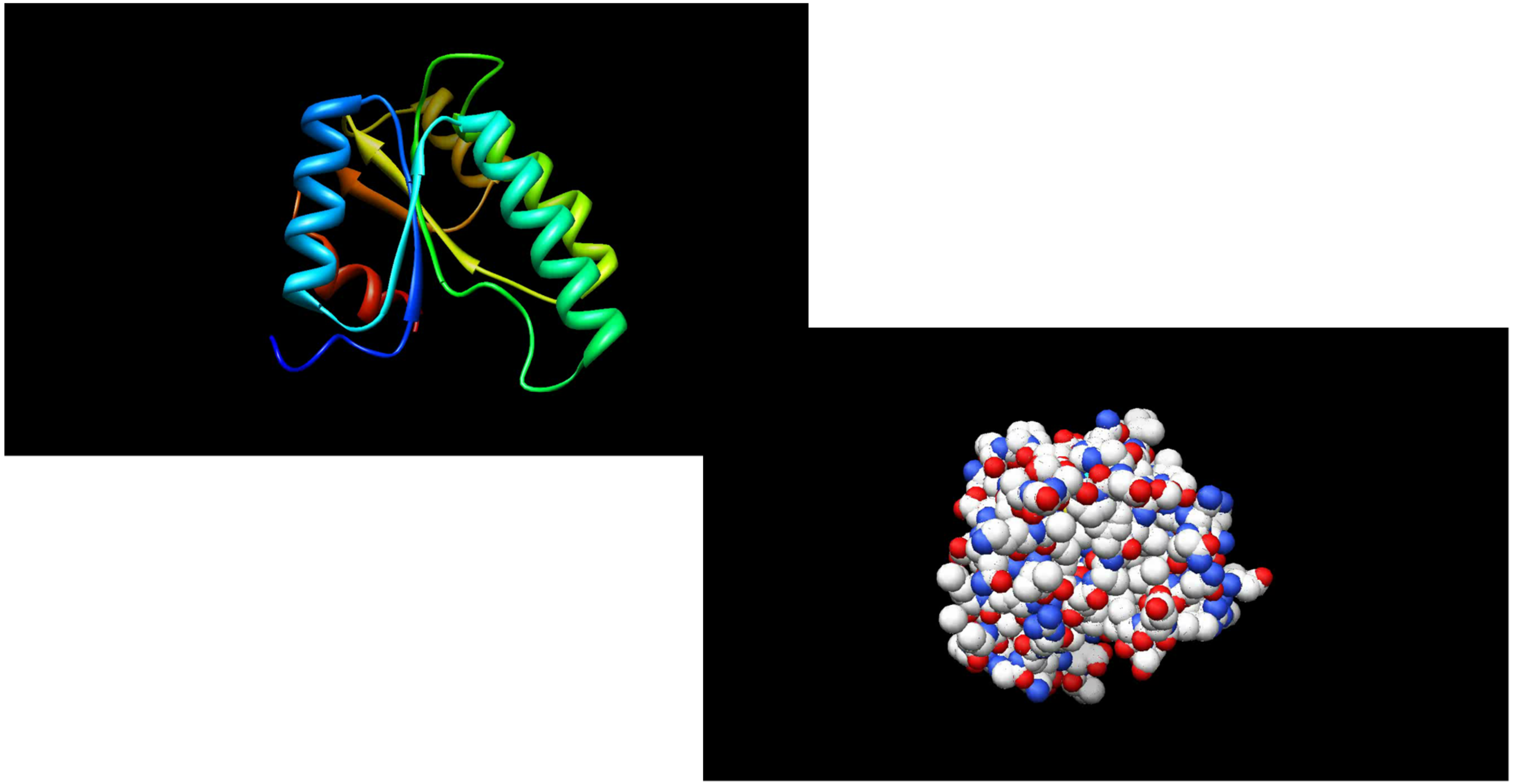
Title	**The Structures Of Host Range Controlling Regions Of The Capsids Of Canine and Feline Parvoviruses and Mutants**
Classification	**Virus/Viral Protein**
Compound	**Mol_Id: 1; Molecule: Coat Protein Vp2; Chain: A; Fragment: Sequence Database Residues 190-737; Engineered: Yes; Mutation: Yes**
Exp. Method	**X-ray Diffraction**

View Structure

http://www.rcsb.org/pdb/cgi/explore.cgi?job=graphics;pdbId=1P5Y;page=;pid=173561064349344&bio=1&opt=show&size=500 12/29/2003

Structural Databases

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



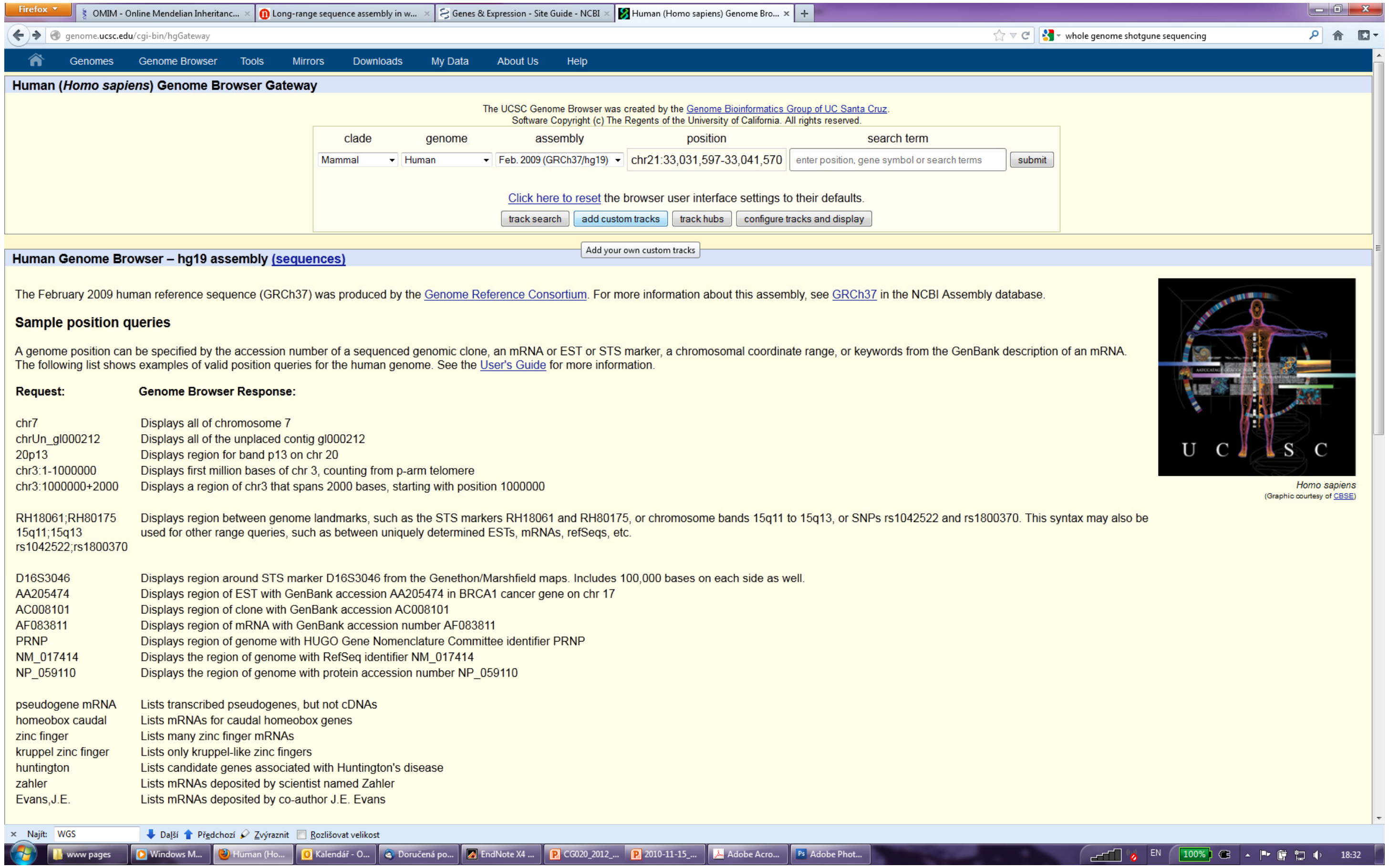
Pekárová et al., *Plant Journal* (2011)

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

Genome Resources

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



Human (*Homo sapiens*) Genome Browser Gateway

The UCSC Genome Browser was created by the Genome Bioinformatics Group of UC Santa Cruz.
Software Copyright (c) The Regents of the University of California. All rights reserved.

clade	genome	assembly	position	search term	
Mammal	Human	Feb. 2009 (GRCh37/hg19)	chr21:33,031,597-33,041,570	enter position, gene symbol or search terms	submit

Click here to reset the browser user interface settings to their defaults.

Human Genome Browser – hg19 assembly (sequences)

The February 2009 human reference sequence (GRCh37) was produced by the Genome Reference Consortium. For more information about this assembly, see GRCh37 in the NCBI Assembly database.

Sample position queries

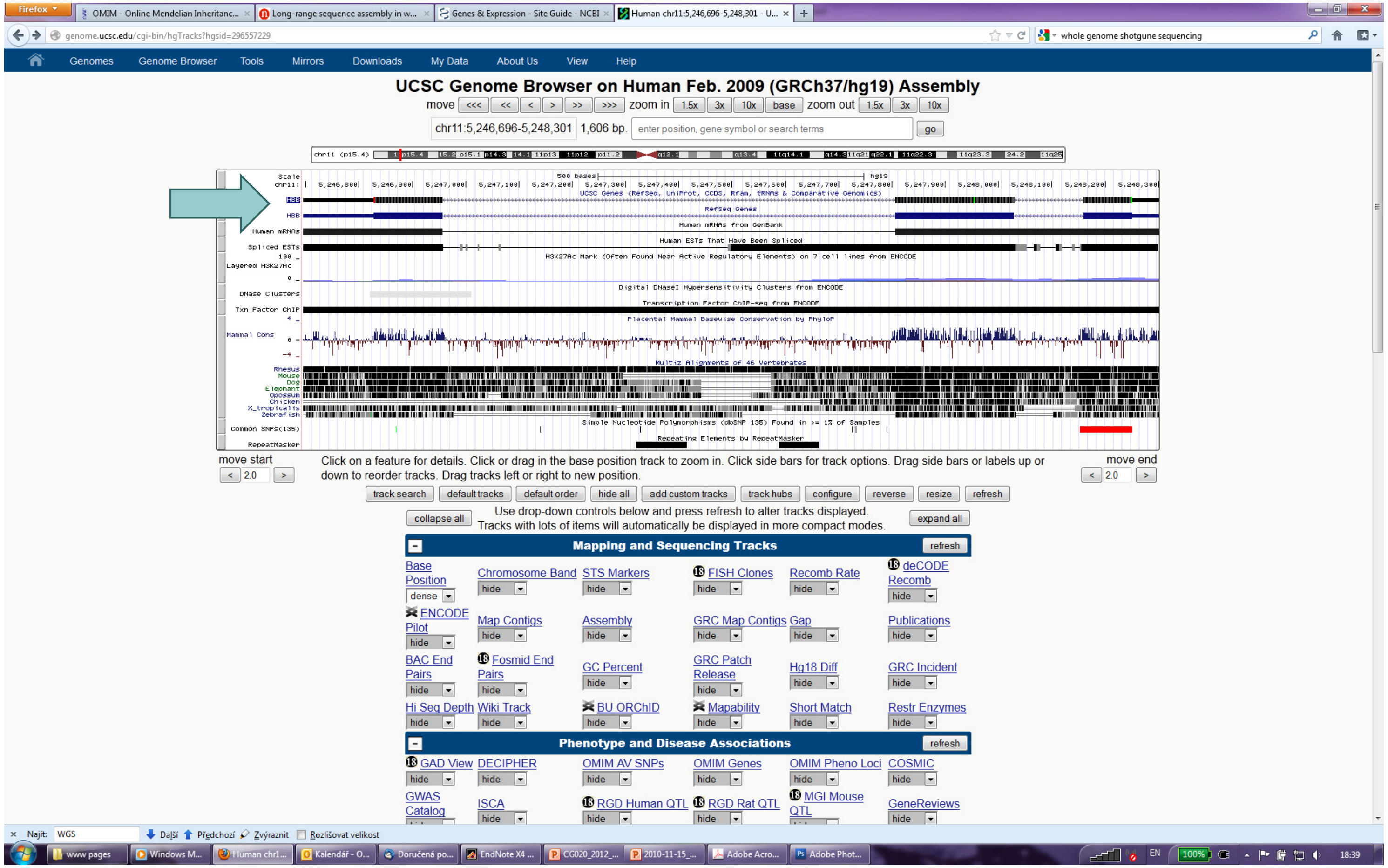
A genome position can be specified by the accession number of a sequenced genomic clone, an mRNA or EST or STS marker, a chromosomal coordinate range, or keywords from the GenBank description of an mRNA. The following list shows examples of valid position queries for the human genome. See the User's Guide for more information.

Request:	Genome Browser Response:
chr7	Displays all of chromosome 7
chrUn_gl000212	Displays all of the unplaced contig gl000212
20p13	Displays region for band p13 on chr 20
chr3:1-1000000	Displays first million bases of chr 3, counting from p-arm telomere
chr3:1000000+2000	Displays a region of chr3 that spans 2000 bases, starting with position 1000000
RH18061;RH80175 15q11;15q13 rs1042522;rs1800370	Displays region between genome landmarks, such as the STS markers RH18061 and RH80175, or chromosome bands 15q11 to 15q13, or SNPs rs1042522 and rs1800370. This syntax may also be used for other range queries, such as between uniquely determined ESTs, mRNAs, refSeqs, etc.
D16S3046	Displays region around STS marker D16S3046 from the Genethon/Marshfield maps. Includes 100,000 bases on each side as well.
AA205474	Displays region of EST with GenBank accession AA205474 in BRCA1 cancer gene on chr 17
AC008101	Displays region of clone with GenBank accession AC008101
AF083811	Displays region of mRNA with GenBank accession number AF083811
PRNP	Displays region of genome with HUGO Gene Nomenclature Committee identifier PRNP
NM_017414	Displays the region of genome with RefSeq identifier NM_017414
NP_059110	Displays the region of genome with protein accession number NP_059110
pseudogene mRNA	Lists transcribed pseudogenes, but not cDNAs
homeobox caudal	Lists mRNAs for caudal homeobox genes
zinc finger	Lists many zinc finger mRNAs
kruppel zinc finger	Lists only kruppel-like zinc fingers
huntington	Lists candidate genes associated with Huntington's disease
zahler	Lists mRNAs deposited by scientist named Zahler
Evans,J.E.	Lists mRNAs deposited by co-author J.E. Evans

Homo sapiens
(Graphic courtesy of CBSE)

Genome Resources

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



UCSC Genome Browser on Human Feb. 2009 (GRCh37/hg19) Assembly

chr11:5,246,696-5,248,301 1,606 bp.

Click on a feature for details. Click or drag in the base position track to zoom in. Click side bars for track options. Drag side bars or labels up or down to reorder tracks. Drag tracks left or right to new position.

Use drop-down controls below and press refresh to alter tracks displayed.
Tracks with lots of items will automatically be displayed in more compact modes.

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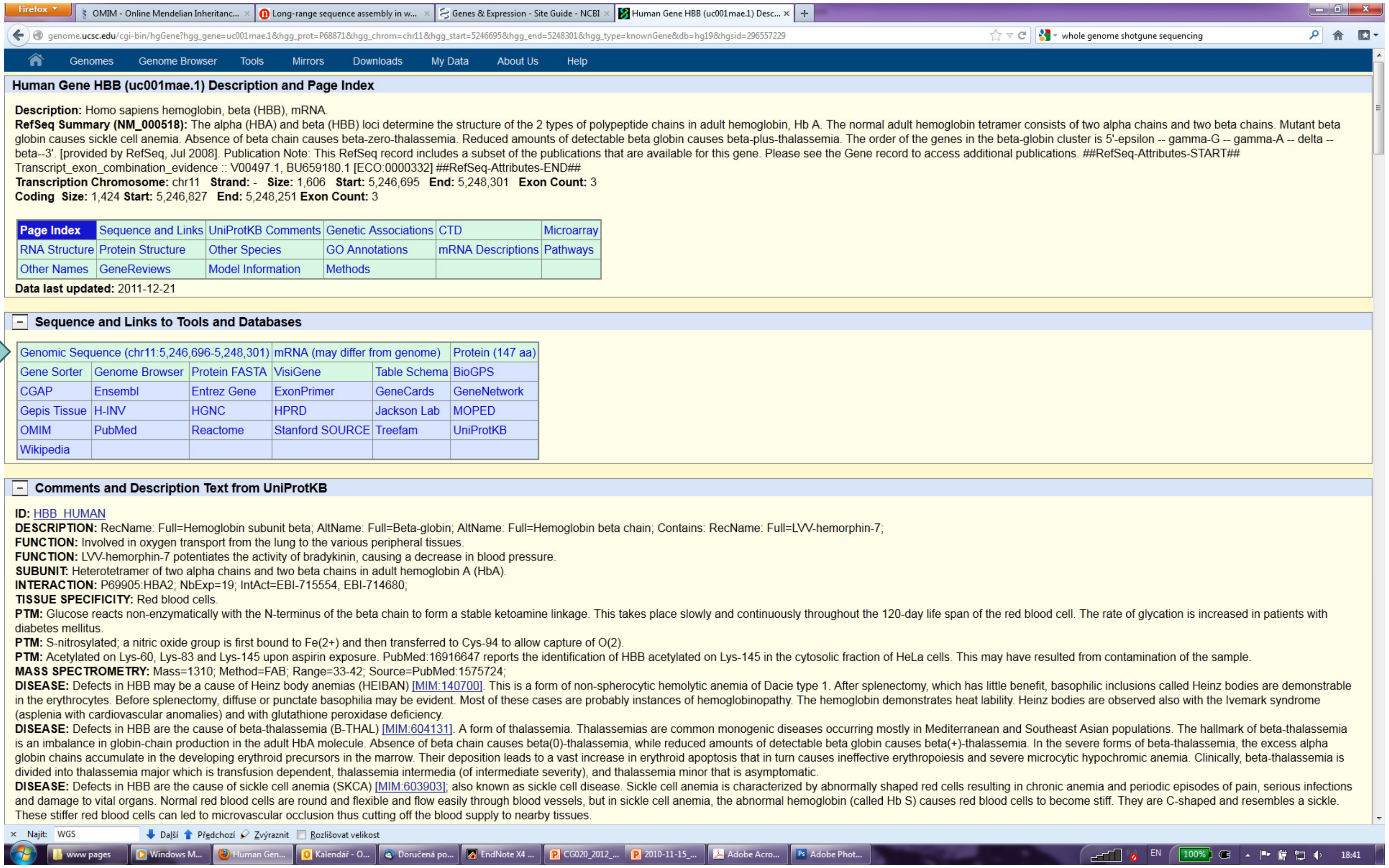

Human Gene HBB (uc001mae.1) Description and Page Index

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, Hb A. 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-G -- gamma-A -- delta -- beta--3'. [provided by RefSeq, Jul 2008]. 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-START## Transcript_exon_combination_evidence :: V00497.1, BU659180.1 [ECO:0000332] ##RefSeq-Attributes-END##
Transcription Chromosome: chr11 **Strand:** - **Size:** 1,606 **Start:** 5,246,695 **End:** 5,248,301 **Exon Count:** 3
Coding Size: 1,424 **Start:** 5,246,827 **End:** 5,248,251 **Exon Count:** 3

Page Index	Sequence and Links	UniProtKB Comments	Genetic Associations	CTD	Microarray
RNA Structure	Protein Structure	Other Species	GO Annotations	mRNA Descriptions	Pathways
Other Names	GeneReviews	Model Information	Methods		

Data last updated: 2011-12-21

Sequence and Links to Tools and Databases

Genomic Sequence (chr11:5,246,696-5,248,301)		mRNA (may differ from genome)		Protein (147 aa)
Gene Sorter	Genome Browser	Protein FASTA	VisiGene	Table Schema	BioGPS
CGAP	Ensembl	Entrez Gene	ExonPrimer	GeneCards	GeneNetwork
Gepis Tissue	H-INV	HGNC	HPRD	Jackson Lab	MOPED
OMIM	PubMed	Reactome	Stanford SOURCE	Treefam	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=LVV-hemorphin-7;
FUNCTION: Involved in oxygen transport from the lung to the various peripheral tissues.
FUNCTION: LVV-hemorphin-7 potentiates the activity of bradykinin, causing a decrease in blood pressure.
SUBUNIT: Heterotetramer of two alpha chains and two beta chains in adult hemoglobin A (HbA).
INTERACTION: P69905:HBA2; NbExp=19; IntAct=EBI-715554, EBI-714680;
TISSUE SPECIFICITY: Red blood cells.
PTM: Glucose reacts non-enzymatically with the N-terminus of the beta chain to form a stable ketoamine linkage. This takes place slowly and continuously throughout the 120-day life span of the red blood cell. The rate of glycation is increased in patients with diabetes mellitus.
PTM: S-nitrosylated; a nitric oxide group is first bound to Fe(2+) and then transferred to Cys-94 to allow capture of O(2).
PTM: Acetylated on Lys-60, Lys-83 and Lys-145 upon aspirin exposure. PubMed:16916647 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=1310; Method=FAB; Range=33-42; Source=PubMed:1575724;
DISEASE: Defects in HBB may be a cause of Heinz body anemias (HEIBAN) [MIM:140700]. This is a form of non-spherocytic hemolytic anemia of Dacie type 1. After splenectomy, which has little benefit, basophilic inclusions called Heinz bodies are demonstrable in the erythrocytes. Before splenectomy, diffuse or punctate basophilia may be evident. Most of these cases are probably instances of hemoglobinopathy. The hemoglobin demonstrates heat lability. Heinz bodies are observed also with the Ivemark syndrome (asplenia with cardiovascular anomalies) and with glutathione peroxidase deficiency.
DISEASE: Defects in HBB are the cause of beta-thalassemia (B-THAL) [MIM:604131]. 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 (SKCA) [MIM: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 stiffer red blood cells can led to microvascular occlusion thus cutting off the blood supply to nearby tissues.

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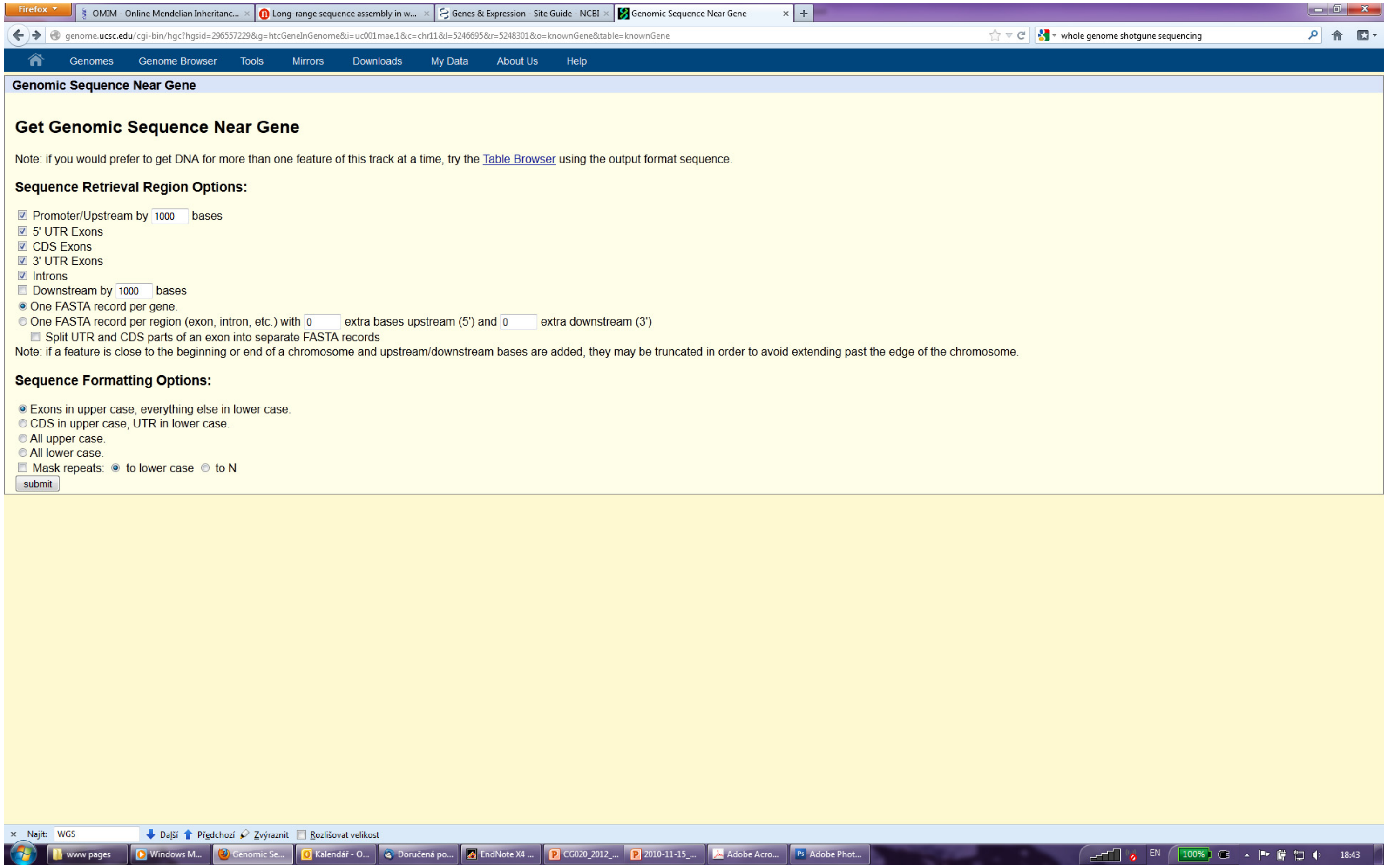
a státním rozpočtem České republiky

Genome Resources

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



Genomic Sequence Near Gene

Get Genomic Sequence Near Gene

Note: if you would prefer to get DNA for more than one feature of this track at a time, try the Table Browser using the output format sequence.

Sequence Retrieval Region Options:

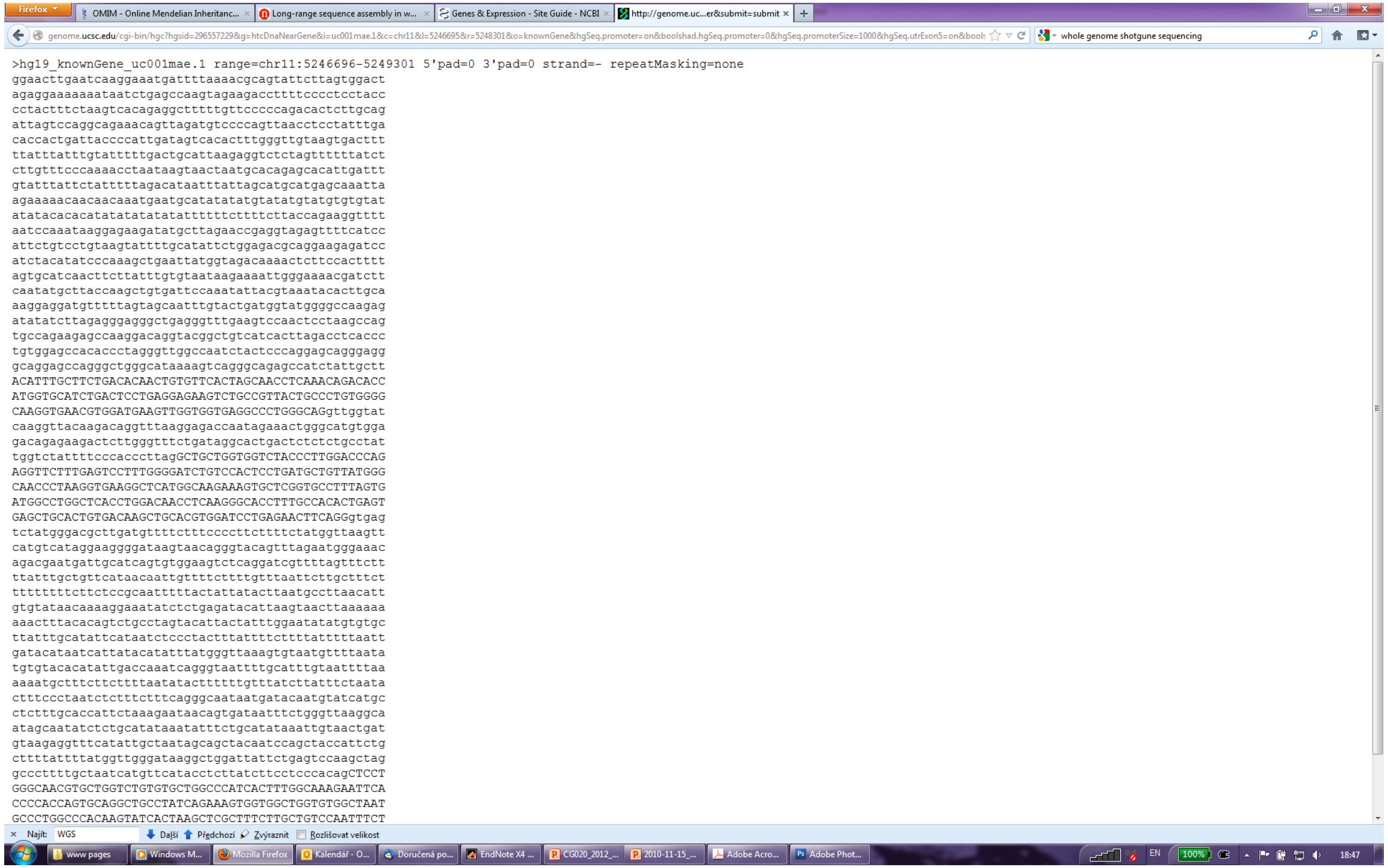
☑ Promoter/Upstream by 1000 bases
☑ 5' UTR Exons
☑ CDS Exons
☑ 3' UTR Exons
☑ Introns
☐ Downstream by 1000 bases
● One FASTA record per gene.
○ One FASTA record per region (exon, intron, etc.) with 0 extra bases upstream (5') and 0 extra downstream (3')
☐ Split UTR and CDS parts of an exon into separate FASTA records
Note: if a feature is close to the beginning or end of a chromosome and upstream/downstream bases are added, they may be truncated in order to avoid extending past the edge of the chromosome.

Sequence Formatting Options:

● Exons in upper case, everything else in lower case.
○ CDS in upper case, UTR in lower case.
○ All upper case.
○ All lower case.
☐ Mask repeats: ● to lower case ○ to N
submit

Genome Resources

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



```
>hg19_knownGene_uc001mae.1 range=chr11:5246696-5249301 5'pad=0 3'pad=0 strand=- repeatMasking=none
ggaacttgaatcaaggaaatgattttaaaacgcagtattcttagtggact
agaggaaaaaaataatctgagccaagtagaagaccttttcccctcctacc
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GCCCTGGCCCACAAGTATCACTAAGCTCGCTTTCTTGCTGTCCAATTTCT
```

Genome Resources

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

The Arabidopsis Information Resource

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.

TAIR is located at the Carnegie Institution for Science Department of Plant Biology and funded by the National Science Foundation with additional support from TAIR sponsors.

Updates on TAIR funding are available **here**.

Click here

to try our new online submission form

and submit the molecular function (e.g. *protein kinase*), biological process (e.g. *seed development*), localization (e.g. *plasma membrane*) or interacting partner of your favorite gene

Breaking News

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2012 MASC Report Now Available
[July 11, 2012]
Please check out the **latest report** from the Multinational Arabidopsis Steering Committee.

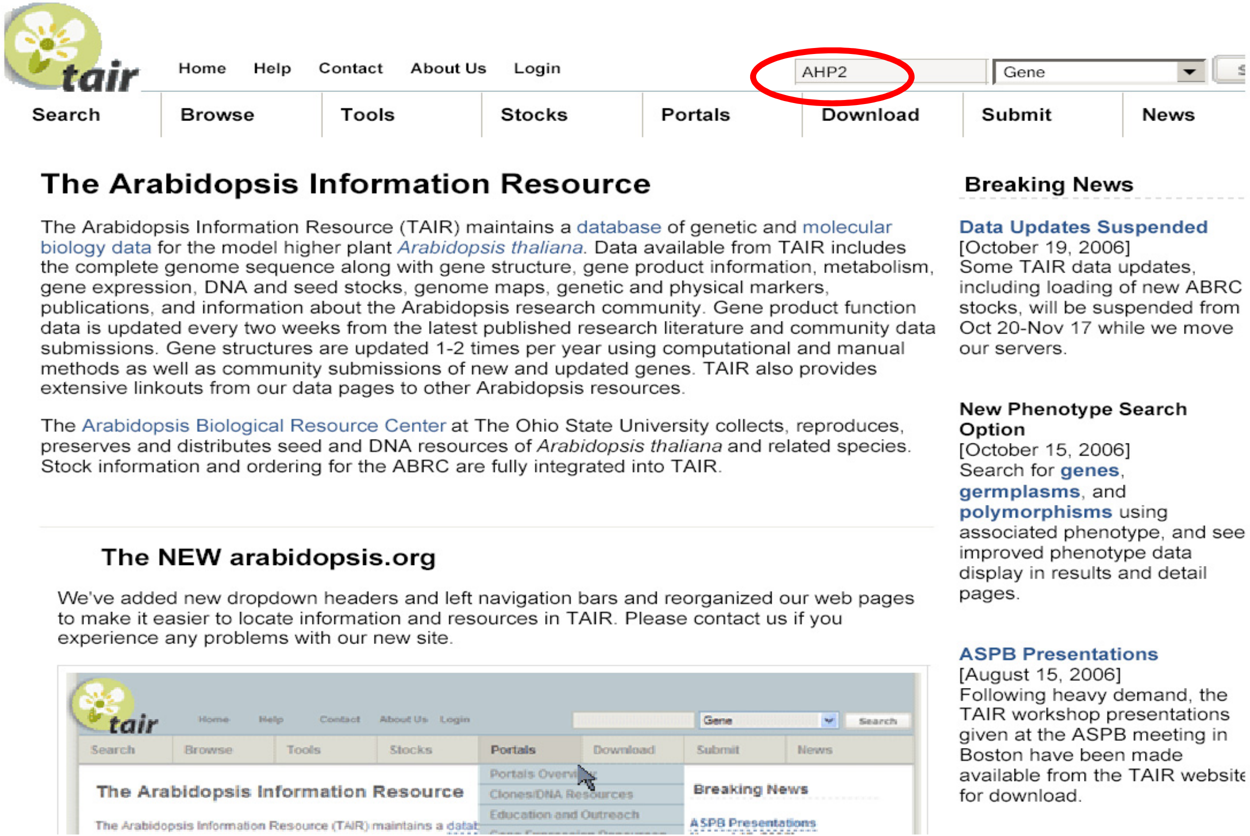
New Protein Chip and Cell Cultures at ABRC
[May 9, 2012]
A new protein chip (**AtProteinChip 2**) developed by **M. Snyder and S.P. Dinesh-Kumar**, is now available. Cell line PSB-D (**CCL84840**), donated by Geert De Jaeger and derived from MM2d developed by M. Menges and J. Murray, is also available. These stocks can be found using the **ABRC catalog**.

Share Your Education Resources [February 1, 2012]
Do you teach an undergraduate Lab using Arabidopsis? Can you imagine your research project on Arabidopsis illustrating an important scientific concept? Contribute to moving Arabidopsis from the bench to the classroom!

GO Annotations At TAIR
[January 25, 2012]

Genome Resources

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



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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.

Outline

- Syllabus Of The Course
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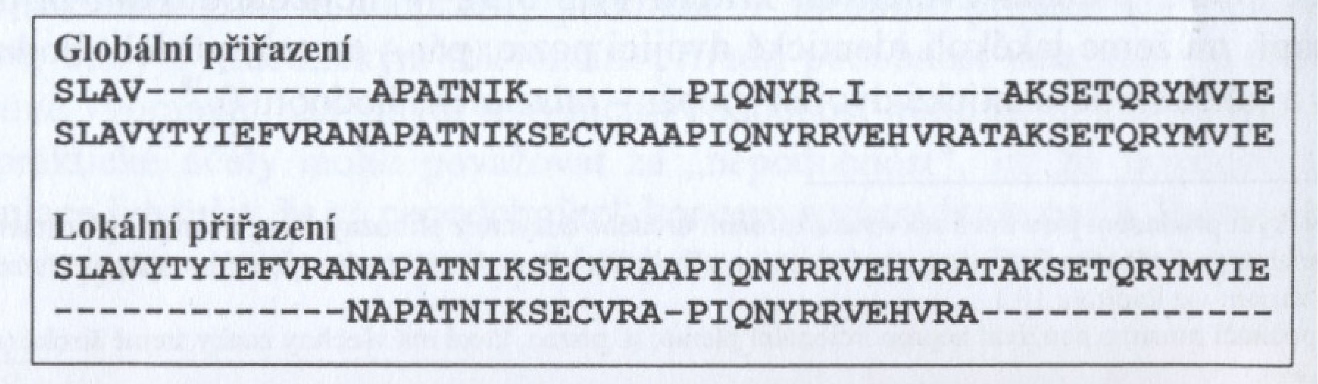
- Databases
    - Spectre Of „On-line“ Resources
    - PRIMARY, SECONDARY And STRUCURAL Databases
    - GENOME Resources
- Analytical Tools
    - Homology Searching

Analytical Tools

- ☐ **Global** versus **Local** alignment



Globální přiřazení

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

Lokální přiřazení

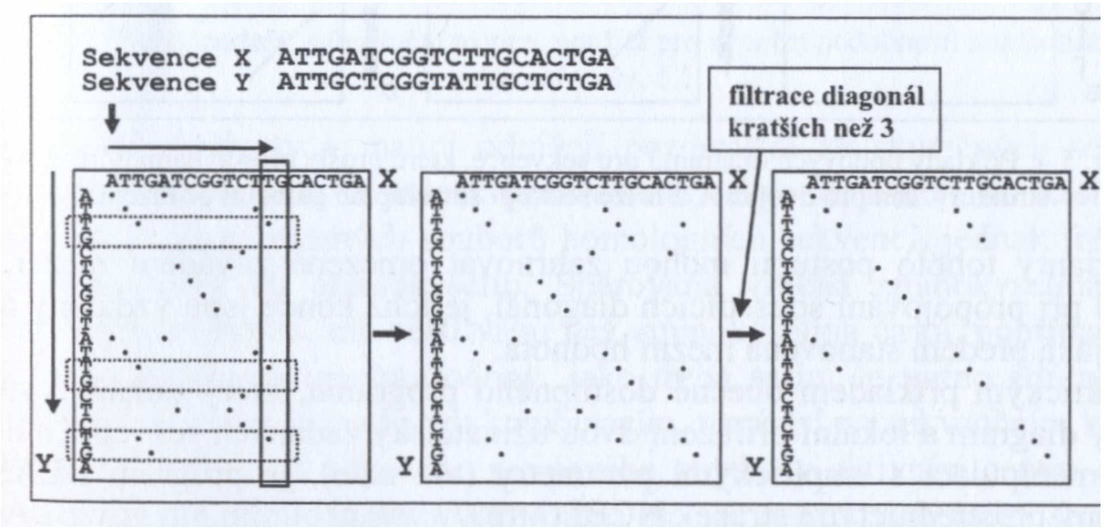
```
SLAVYTYIEFVRANAPATNIKSECVRAAPIQNYRRVEHVRATAKSETQRYMVIE
-------------NAPATNIKSECVRA-PIQNYRRVEHVRA-------------
```

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

Analytical Tools

- Choosing the right type of alignment using dotplot

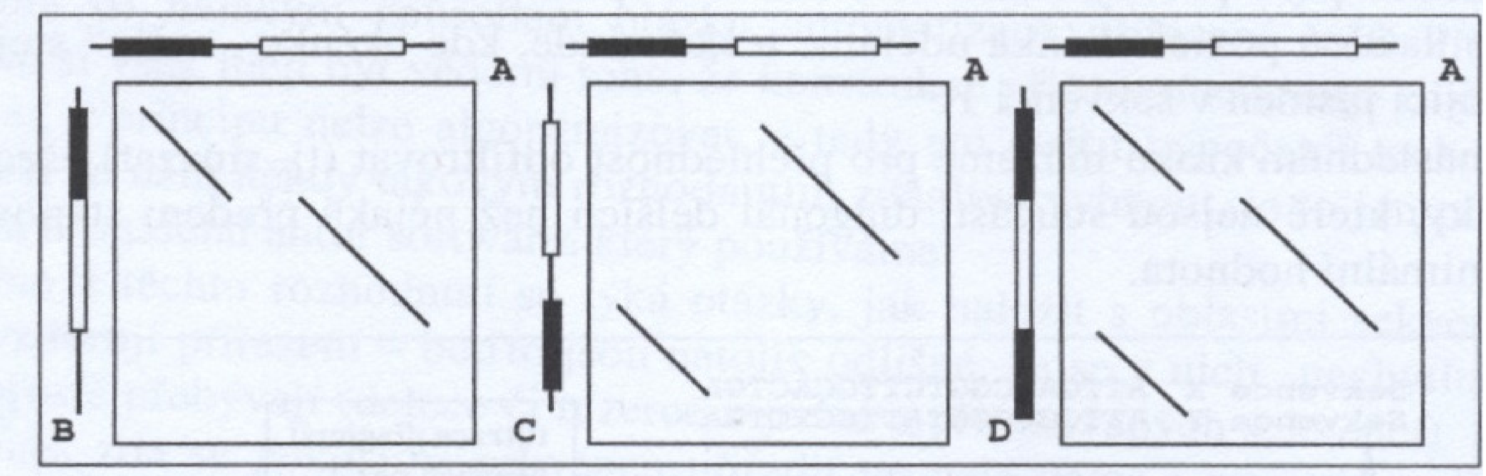


Cvrčková, Úvod do praktické bioinformatiky

- 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 treshold

Analytical Tools

- Examples of sequence alignment using dotplot

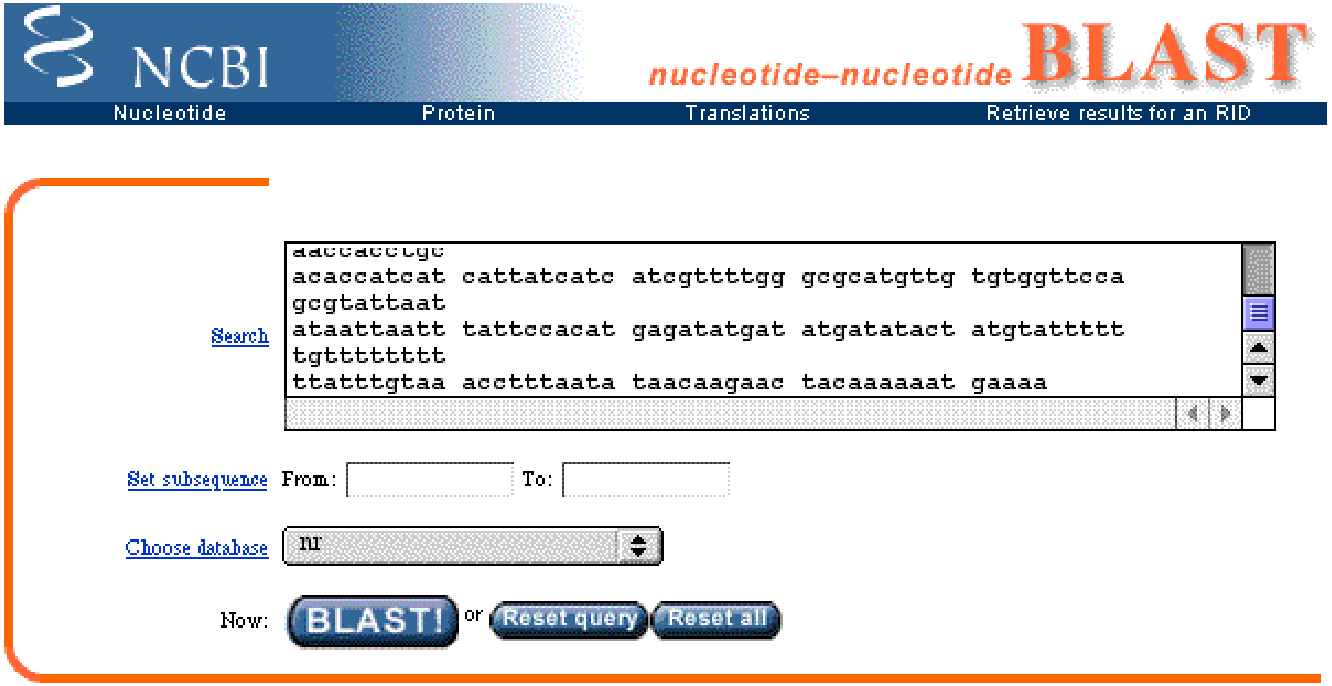


Cvrčková, Úvod do praktické bioinformatiky

- **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 neccessary to do a local alignment
- Dotplot can be obtained using BLAST2 (see further in the presentation)

Analytical Tools

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



```
acaccatcat cattatcatc atcgttttgg gcgcatgttg tgtggttcca
gcgtattaat
ataattaatt tattccacat gagatatgat atgatatact atgtattttt
tgtttttttt
ttatttgtaa acctttaata taacaagaac tacaaaaaat gaaaa
```

From: To:

Choose database: nr

Now: BLAST! or Reset query Reset all

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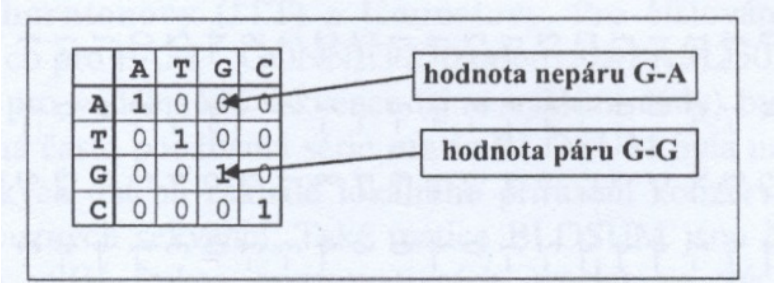
BLAST

Basic **L**ocal **A**lignment **S**earch **T**ool

- Word size: 10-11 bp or 2-3 aa
    - Primary similarities (seed matches)
    - Expanding the homology regions to the left and to the right
- Scoring the homology with matrices PAM (Point Accepted Mutation) or BLOSUM (BLOcks Substitution Matrix)
- Showing the results

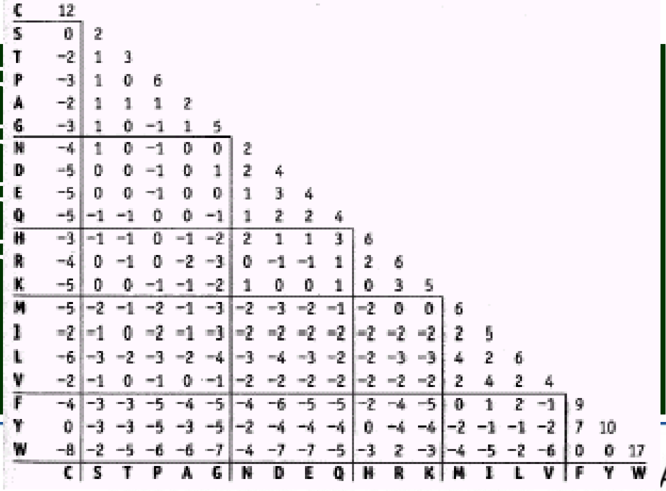


	A	T	G	C
A	1	0	0	0
T	0	1	0	0
G	0	0	1	0
C	0	0	0	1

Cvrčková, Úvod do praktické bioinformatiky

MF
MF
MF
MF

Matice PAM 250



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						
I	−2	−1	0	−2	−1	−3	−2	−2	−2	−2	−2	−2	−2	2	5					
L	−6	−3	−2	−3	−2	−4	−3	−4	−3	−2	−2	−3	−3	4	2	6				
V	−2	−1	0	−1	0	−1	−2	−2	−2	−2	−2	−2	−2	2	4	2	4			
F	−4	−3	−3	−5	−4	−5	−4	−6	−5	−5	−2	−4	−5	0	1	2	−1	9		
Y	0	−3	−3	−5	−3	−5	−2	−4	−4	−4	0	−4	−4	−2	−1	−1	−2	7	10	
W	−8	−2	−5	−6	−6	−7	−4	−7	−7	−5	−3	2	−3	−4	−5	−2	−6	0	0	17
	C	S	T	P	A	G	N	D	E	Q	H	R	K	M	I	L	V	F	Y	W

BLAST

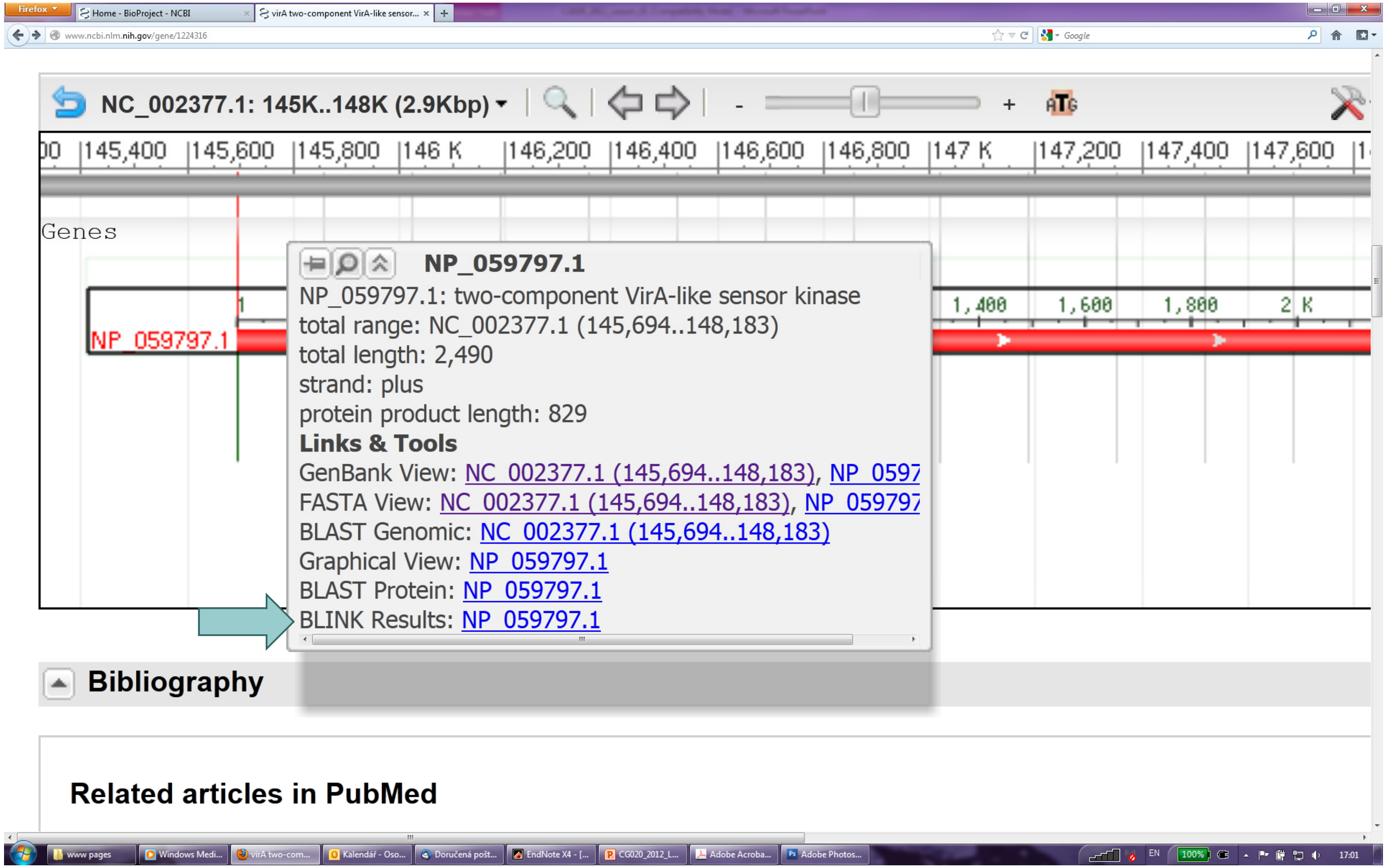
Basic **L**ocal **A**lignment **S**earch **T**ool

E= expectancy value

```
☐ >gi|5016088|ref|NM_001101.2|                        actin, beta (ACTB), mRNA
          Length = 1793

 Score = 1110 bits (560), Expect = 0.0
 Identities = 965/1100 (87%)
 Strand = Plus / Plus


Query: 156  gtcgacaacggctctggcatgtgcaaggccggatttgccggagacgatgctccccgcgcc 215
            |||||||||||||| ||||||||||||||||| || || || |||||||| ||||| |||
Sbjct: 101  gtcgacaacggctccggcatgtgcaaggccggcttcgcgggcgacgatgccccccgggcc 160


Query: 216  gtcttcccatcgattgtgggacgtccccgtcaccagggtgtgatggtcggcatgggccag 275
            |||||||| || || ||||| || ||| | |||||||| |||||||| |||||||| |||
Sbjct: 161  gtcttcccctccatcgtggggcgccccaggcaccagggcgtgatggtgggcatgggtcag 220


Query: 276  aaggactcgtacgtgggtgatgaggcgcagagcaagcgtggtatcctcaccctgaagtac 335
            ||||| || || ||||| || ||||| ||||||||| | || ||||||||||||||||||
Sbjct: 221  aaggattcctatgtgggcgacgaggcccagagcaagagaggcatcctcaccctgaagtac 280


Query: 336  cccattgagcacggtatcgtgaccaactgggacgatatggagaagatctggcaccacacc 395
            ||||| |||||||| ||||| |||||||||||||| |||||||| |||||||||||||||
Sbjct: 281  cccatcgagcacggcatcgtcaccaactgggacgacatggagaaaatctggcaccacacc 340
```

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

Primary Databases



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

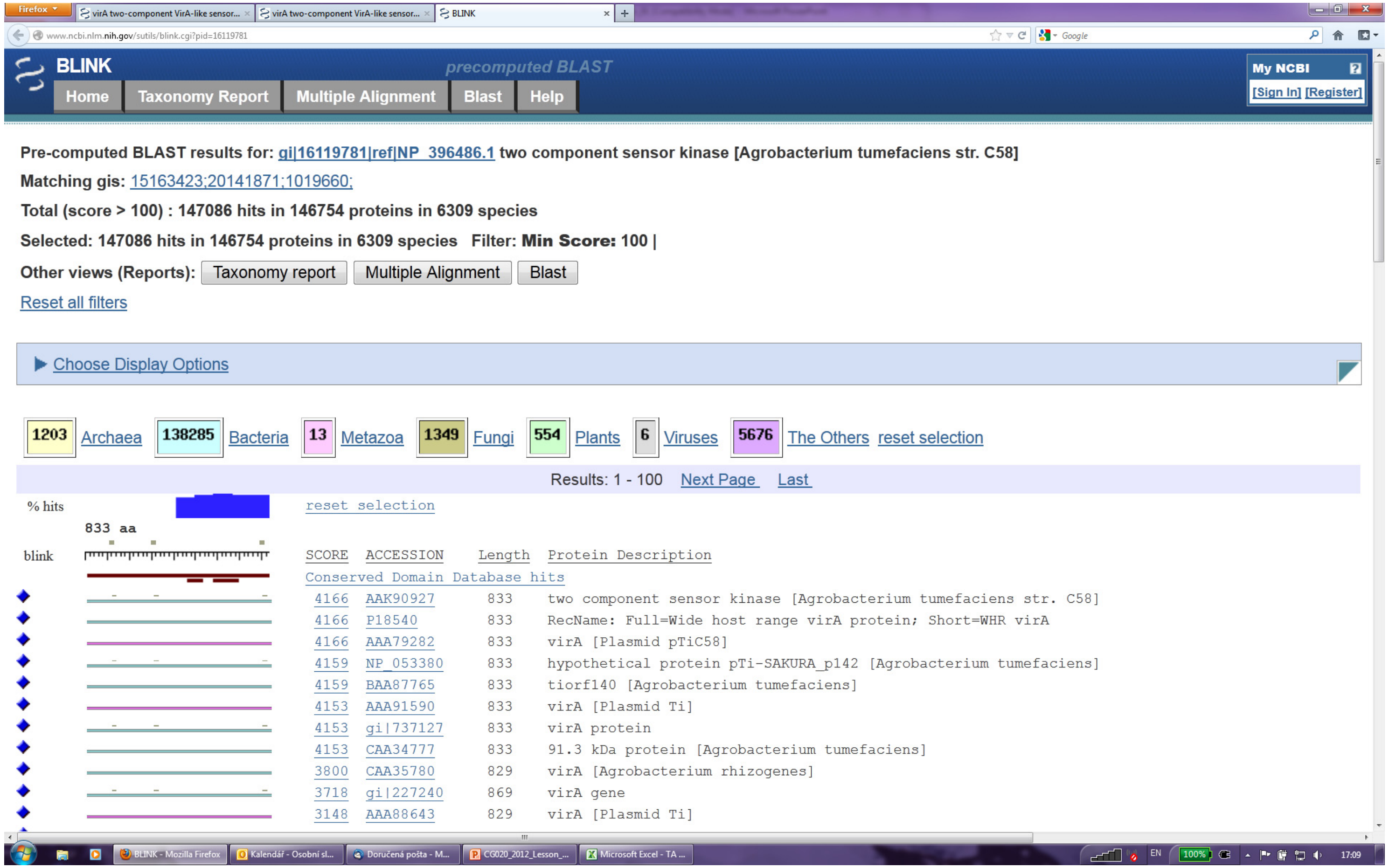
Links & Tools

GenBank View: NC_002377.1 (145,694..148,183), NP_0597
FASTA View: NC_002377.1 (145,694..148,183), NP_059797
BLAST Genomic: NC_002377.1 (145,694..148,183)
Graphical View: NP_059797.1
BLAST Protein: NP_059797.1
BLINK Results: NP_059797.1

Related articles in PubMed

BLAST

Basic **L**ocal **A**lignment **S**earch **T**ool



Pre-computed BLAST results for: gi|16119781|ref|NP_396486.1 two component sensor kinase [Agrobacterium tumefaciens str. C58]

Matching gis: 15163423;20141871;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 | 138285 Bacteria | 13 Metazoa | 1349 Fungi | 554 Plants | 6 Viruses | 5676 The Others | reset selection

Results: 1 - 100 Next Page Last

% hits

reset selection

833 aa

blink

Conserved Domain Database hits

SCORE	ACCESSION	Length	Protein Description
4166	AAK90927	833	two component sensor kinase [Agrobacterium tumefaciens str. C58]
4166	P18540	833	RecName: Full=Wide host range virA protein; Short=WHR virA
4166	AAA79282	833	virA [Plasmid pTiC58]
4159	NP_053380	833	hypothetical protein pTi-SAKURA_p142 [Agrobacterium tumefaciens]
4159	BAA87765	833	tiorf140 [Agrobacterium tumefaciens]
4153	AAA91590	833	virA [Plasmid Ti]
4153	gi|737127	833	virA protein
4153	CAA34777	833	91.3 kDa protein [Agrobacterium tumefaciens]
3800	CAA35780	829	virA [Agrobacterium rhizogenes]
3718	gi|227240	869	virA gene
3148	AAA88643	829	virA [Plasmid Ti]

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.

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.

BLAST

Specialized Versions

- ☐ Currently there exist a lot of specialized versions of BLAST

  - **PSI-BLAST** (**P**osition-**S**pecific **I**terated Blast)
    - 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 (Position Specific Substitution Matrix)
    - 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.

BLAST

Specialized Versions

- Currently there exists a lot of specialized versions of BLAST

  - **PHI-BLAST** (**P**attern-**H**it **I**nitiated 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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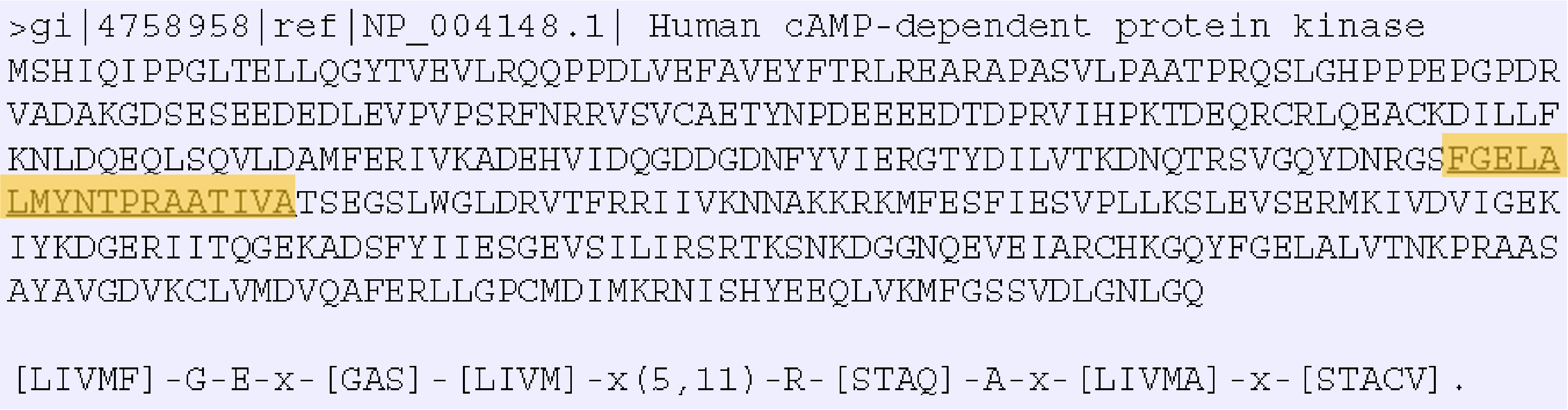
BLAST

Specialized Versions

- Example of search by PHI-BLAST



```
>gi|4758958|ref|NP_004148.1| Human cAMP-dependent protein kinase
MSHIQIPPGLTELLQGYTVEVLRQQPPDLVEFAVEYFTRLREARAPASVLPAATPRQSLGHPPPEPGPDR
VADAKGDSESEEDEDLEVPVPSRFNRRVSVCAETYNPDEEEEDTDPRVIHPKTDEQRCRLQEACKDILLF
KNLDQEQLSQVLDAMFERIVKADEHVIDQGDDGDNFYVIERGTYDILVTKDNQTRSVGQYDNRGSFGELA
LMYNTPRAATIVATSEGSLWGLDRVTFRRIIVKNNAKKRKMFESFIESVPLLKSLEVSERMKIVDVIGEK
IYKDGERIITQGEKADSFYIIESGEVSILIRSRTKSNKDGGNQEVEIARCHKGQYFGELALVTNKPRAAS
AYAVGDVKCLVMDVQAFERLLGPCMDIMKRNISHYEEQLVKMFGSSVDLGNLGQ

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

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…

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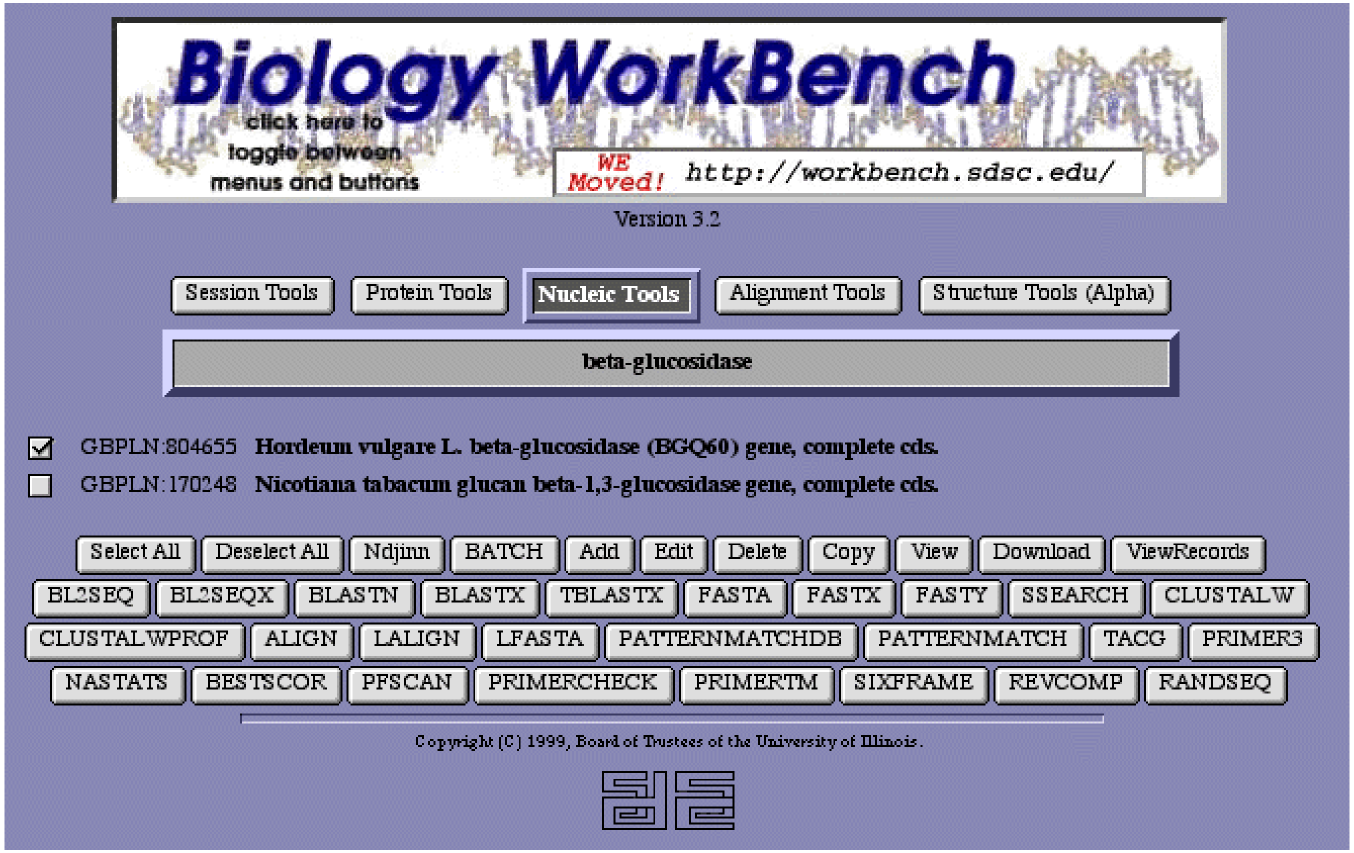
Analytical Tools

- http://workbench.sdsc.edu/



☑ GBPLN:804655 **Hordeum vulgare L. beta-glucosidase (BGQ60) gene, complete cds.**

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

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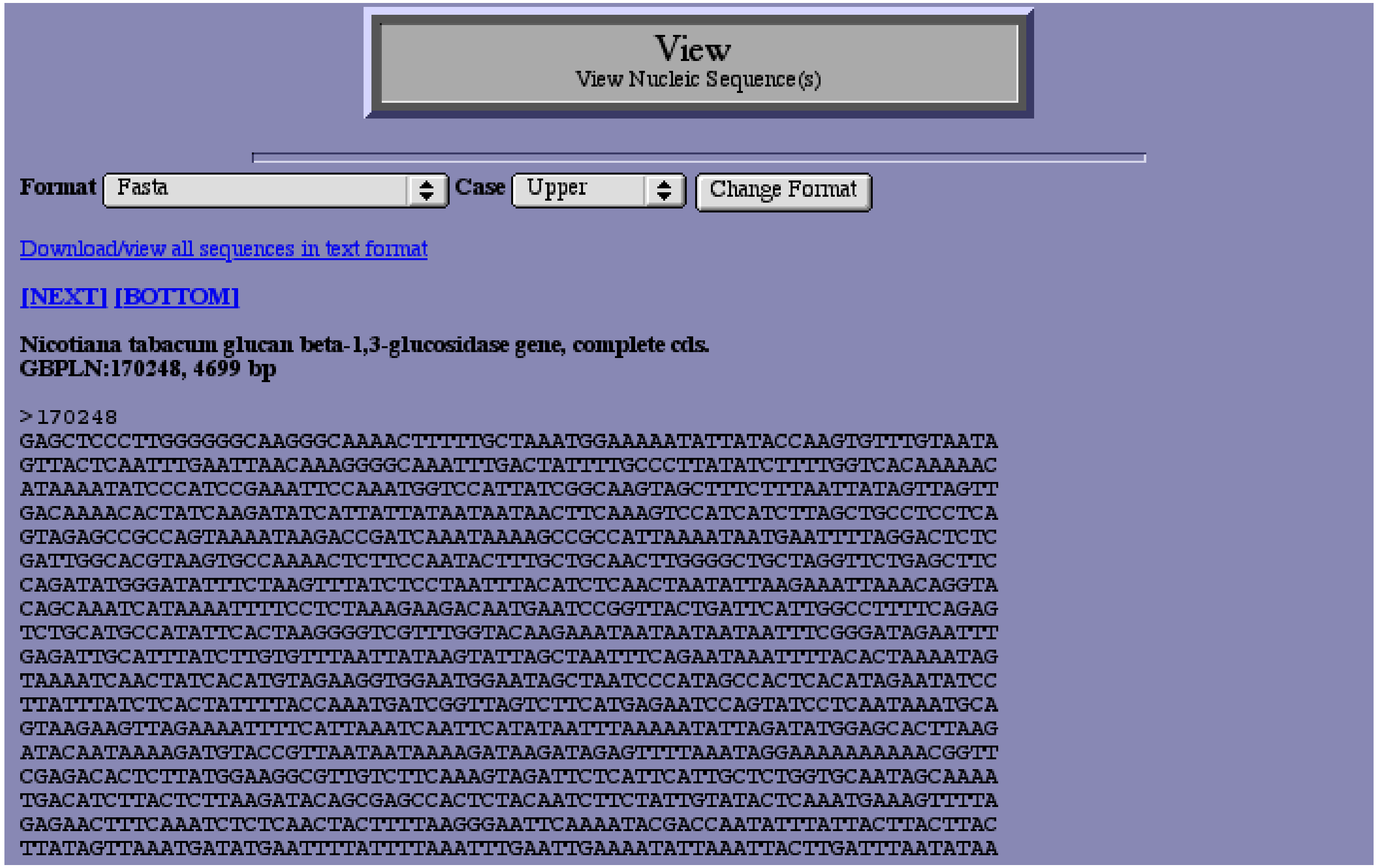
Analytical Tools

- http://workbench.sdsc.edu/



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

```
>170248
GAGCTCCCTTGGGGGGCAAGGGCAAAACTTTTTGCTAAATGGAAAAATATTATACCAAGTGTTTGTAATA
GTTACTCAATTTGAATTAACAAAGGGGCAAATTTGACTATTTTGCCCTTATATCTTTTGGTCACAAAAAC
ATAAAATATCCCATCCGAAATTCCAAATGGTCCATTATCGGCAAGTAGCTTTCTTTAATTATAGTTAGTT
GACAAAACACTATCAAGATATCATTATTATAATAATAACTTCAAAGTCCATCATCTTAGCTGCCTCCTCA
GTAGAGCCGCCAGTAAAATAAGACCGATCAAATAAAAGCCGCCATTAAAATAATGAATTTTAGGACTCTC
GATTGGCACGTAAGTGCCAAAACTCTTCCAATACTTTGCTGCAACTTGGGGCTGCTAGGTTCTGAGCTTC
CAGATATGGGATATTTCTAAGTTTATCTCCTAATTTACATCTCAACTAATATTAAGAAATTAAACAGGTA
CAGCAAATCATAAAATTTTCCTCTAAAGAAGACAATGAATCCGGTTACTGATTCATTGGCCTTTTCAGAG
TCTGCATGCCATATTCACTAAGGGGTCGTTTGGTACAAGAAATAATAATAATAATTTCGGGATAGAATTT
GAGATTGCATTTATCTTGTGTTTAATTATAAGTATTAGCTAATTTCAGAATAAATTTTACACTAAAATAG
TAAAATCAACTATCACATGTAGAAGGTGGAATGGAATAGCTAATCCCATAGCCACTCACATAGAATATCC
TTATTTATCTCACTATTTTACCAAATGATCGGTTAGTCTTCATGAGAATCCAGTATCCTCAATAAATGCA
GTAAGAAGTTAGAAAATTTTCATTAAATCAATTCATATAATTTAAAAATATTAGATATGGAGCACTTAAG
ATACAATAAAAGATGTACCGTTAATAATAAAAGATAAGATAGAGTTTTAAATAGGAAAAAAAAAAACGGTT
CGAGACACTCTTATGGAAGGCGTTGTCTTCAAAGTAGATTCTCATTCATTGCTCTGGTGCAATAGCAAAA
TGACATCTTACTCTTAAGATACAGCGAGCCACTCTACAATCTTCTATTGTATACTCAAATGAAAGTTTTA
GAGAACTTTCAAATCTCTCAACTACTTTTAAGGGAATTCAAAATACGACCAATATTTATTACTTACTTAC
TTATAGTTAAATGATATGAATTTTATTTTAAATTTGAATTGAAAATATTAAATTACTTGATTTAATATAA
```

Analytical Tools

- http://workbench.sdsc.edu/

Regex pattern:

`ctt.{1,32}ctt`

0 sequences were searched

1 match was found

Matches are indicated in blue

```
>170248
GAGCTCCCTTGGGGGGCAAGGGCAAAACTTTTTGCTAAATGGAAAAATATTATACCAAGTGTTTGTAATA
GTTACTCAATTTGAATTAACAAAGGGGCAAATTTGACTATTTTGCCCTTATATCTTTTGGTCACAAAAAC
ATAAAATATCCCATCCGAAATTCCAAATGGTCCATTATCGGCAAGTAGCTTTCTTTAATTATAGTTAGTT
GACAAAACACTATCAAGATATCATTATTATAATAATAACTTCAAAGTCCATCATCTTAGCTGCCTCCTCA
GTAGAGCCGCCAGTAAAATAAGACCGATCAAATAAAAGCCGCCATTAAAATAATGAATTTTAGGACTCTC
GATTGGCACGTAAGTGCCAAAACTCTTCCAATACTTTGCTGCAACTTGGGGCTGCTAGGTTCTGAGCTTC
CAGATATGGGATATTTCTAAGTTTATCTCCTAATTTACATCTCAACTAATATTAAGAAATTAAACAGGTA
CAGCAAATCATAAAATTTTCCTCTAAAGAAGACAATGAATCCGGTTACTGATTCATTGGCCTTTTCAGAG
TCTGCATGCCATATTCACTAAGGGGTCGTTTGGTACAAGAAATAATAATAATAATTTCGGGATAGAATTT
GAGATTGCATTTATCTTGTGTTTAATTATAAGTATTAGCTAATTTCAGAATAAATTTTACACTAAAATAG
TAAAATCAACTATCACATGTAGAAGGTGGAATGGAATAGCTAATCCCATAGCCACTCACATAGAATATCC
TTATTTATCTCACTATTTTACCAAATGATCGGTTAGTCTTCATGAGAATCCAGTATCCTCAATAAATGCA
GTAAGAAGTTAGAAAATTTTCATTAAATCAATTCATATAATTTAAAAATATTAGATATGGAGCACTTAAG
ATACAATAAAAGATGTACCGTTAATAATAAAAGATAAGATAGAGTTTTAAATAGGAAAAAAAAAACGGTT
CGAGACACTCTTATGGAAGGCGTTGTCTTCAAAGTAGATTCTCATTCATTGCTCTGGTGCAATAGCAAAA
TGACATCTTACTCTTAAGATACAGCGAGCCACTCTACAATCTTCTATTGTATACTCAAATGAAAGTTTTA
GAGAACTTTCAAATCTCTCAACTACTTTTAAGGGAATTCAAAATACGACCAATATTTATTACTTACTTAC
TTATAGTTAAATGATATGAATTTTATTTTAAATTTGAATTGAAAATATTAAATTACTTGATTTAATATAA
ACAATAGATATCGCTAAGTATTTACCACAAACATGGAGATACTACAGAAGATTTTATTATTTGTAACGAT
GATTAAGCAGCTATTCATCTGGTTGTGCAGGATGAAAGAAAGTAACTAGCTATAATTTCTTTTGTAAAGT
```

Analytical Tools

- http://workbench.sdsc.edu/

Frame 1, 1 stop codon

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

```
>170248 Translated - Frame 1
ELPWGARAKLFAKWKNIIPSVCNSYSI*INKGANLTILPL
```

```
     E  L  P  W  G  A  R  A  K  L  F  A  K  W  K  N  I  I  P  S
1    gagctcccttgggggcaagggcaaaacttttgctaaatggaaaaatattataccaagt  60
     V  C  N  S  Y  S  I  *  I  N  K  G  A  N  L  T  I  L  P  L
61   gtttgtaatagttactcaatttgaattaacaaaggggcaaatttgactattttgccctta  120
```

Frame 2, 1 stop codon

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

```
>170248 Translated - Frame 2
SSLGGQGQNFLLNGKILYQVFVIVTQFELTKGQI*LFCP
```

```
     S  S  L  G  G  Q  G  Q  N  F  L  L  N  G  K  I  L  Y  Q  V
2    agctcccttgggggcaagggcaaaacttttgctaaatggaaaaatattataccaagtg  61
     F  V  I  V  T  Q  F  E  L  T  K  G  Q  I  *  L  F  C  P
62   tttgtaatagttactcaatttgaattaacaaaggggcaaatttgactattttgccctta  120
```

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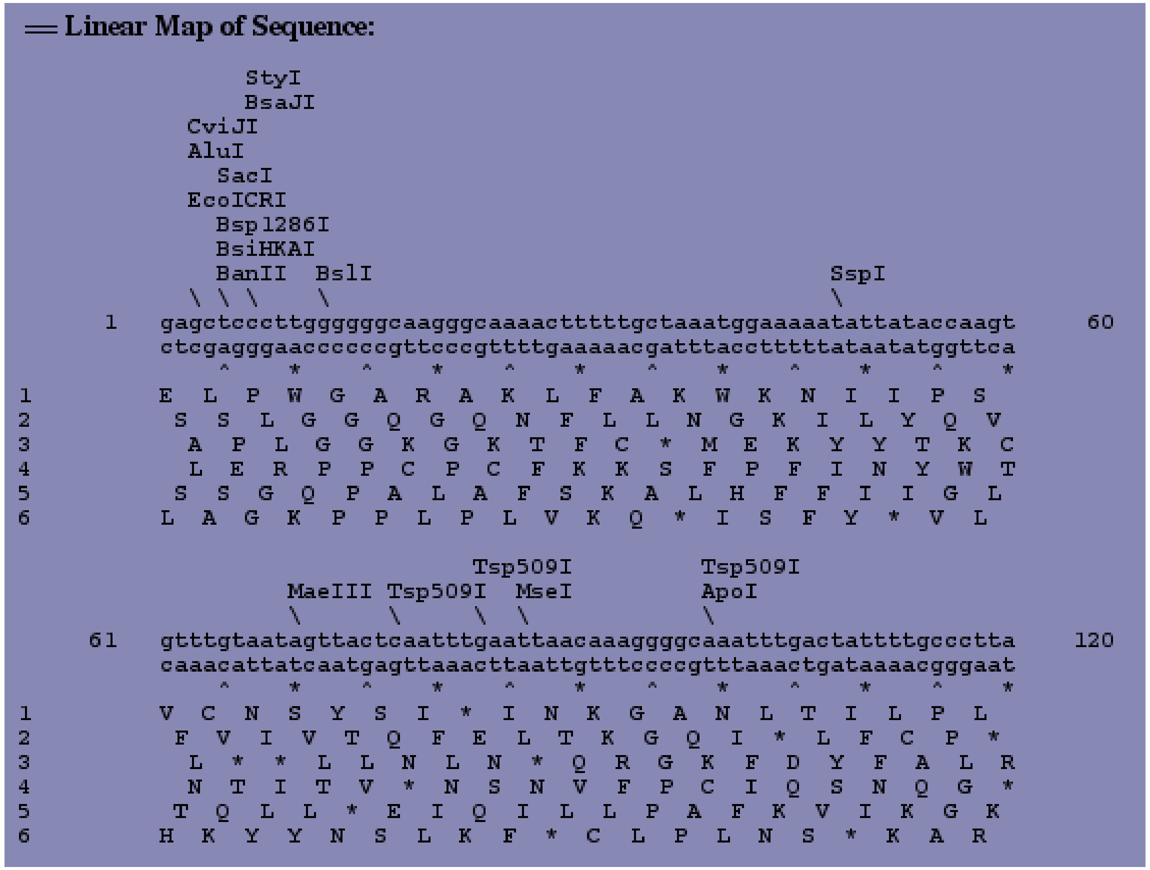
Analytical Tools

- http://workbench.sdsc.edu/

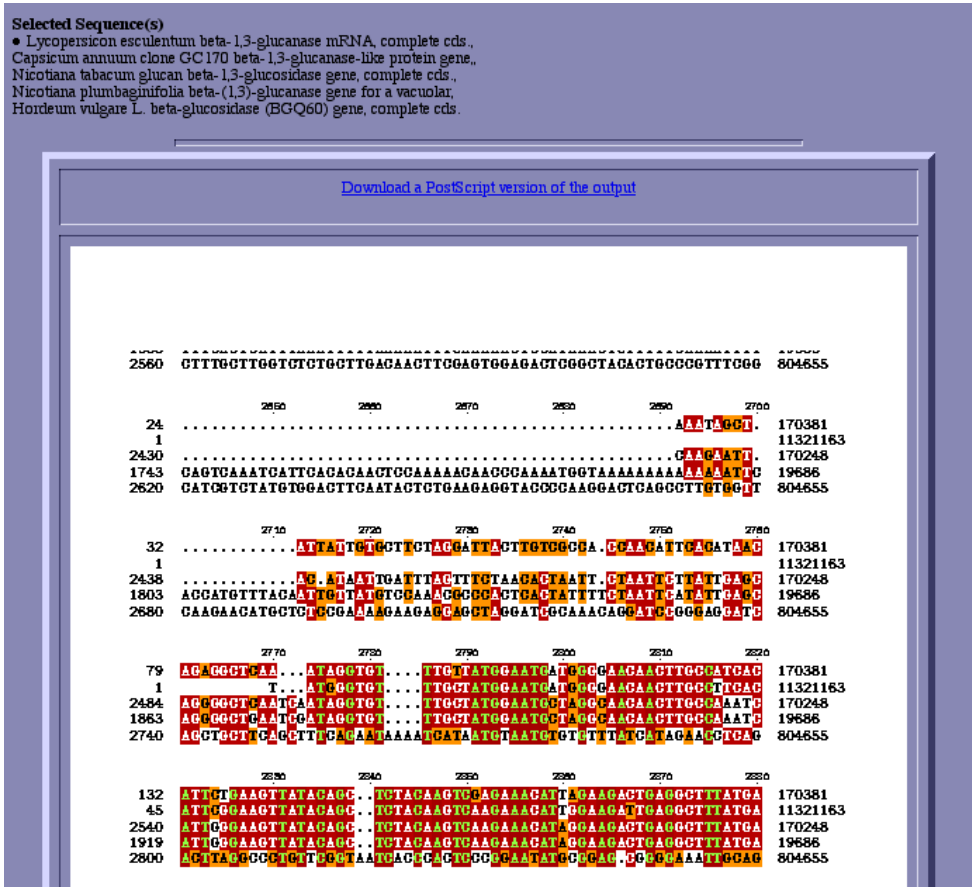


Linear Map of Sequence:

```
                StyI
                BsaJI
            CviJI
            AluI
              SacI
            EcoICRI
              Bsp1286I
              BsiHKAI
              BanII  BslI                                SspI
            \ \ \    \                                   \
      1   gagctcccttggggggcaagggcaaaactttttgctaaatggaaaaatattataccaagt     60
          ctcgagggaaccccccgttcccgttttgaaaaacgatttacctttttataatatggttca
              ^    *    ^    *    ^    *    ^    *    ^    *    ^    *
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  P  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         Tsp509I
                   MaeIII Tsp509I  MseI         ApoI
                   \      \     \  \            \
     61   gtttgtaatagttactcaatttgaattaacaaaggggcaaatttgactattttgccctta    120
          caaacattatcaatgagttaaacttaattgtttccccgtttaaactgataaaacgggaat
              ^    *    ^    *    ^    *    ^    *    ^    *    ^    *
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
```

Analytical Tools

- http://workbench.sdsc.edu/



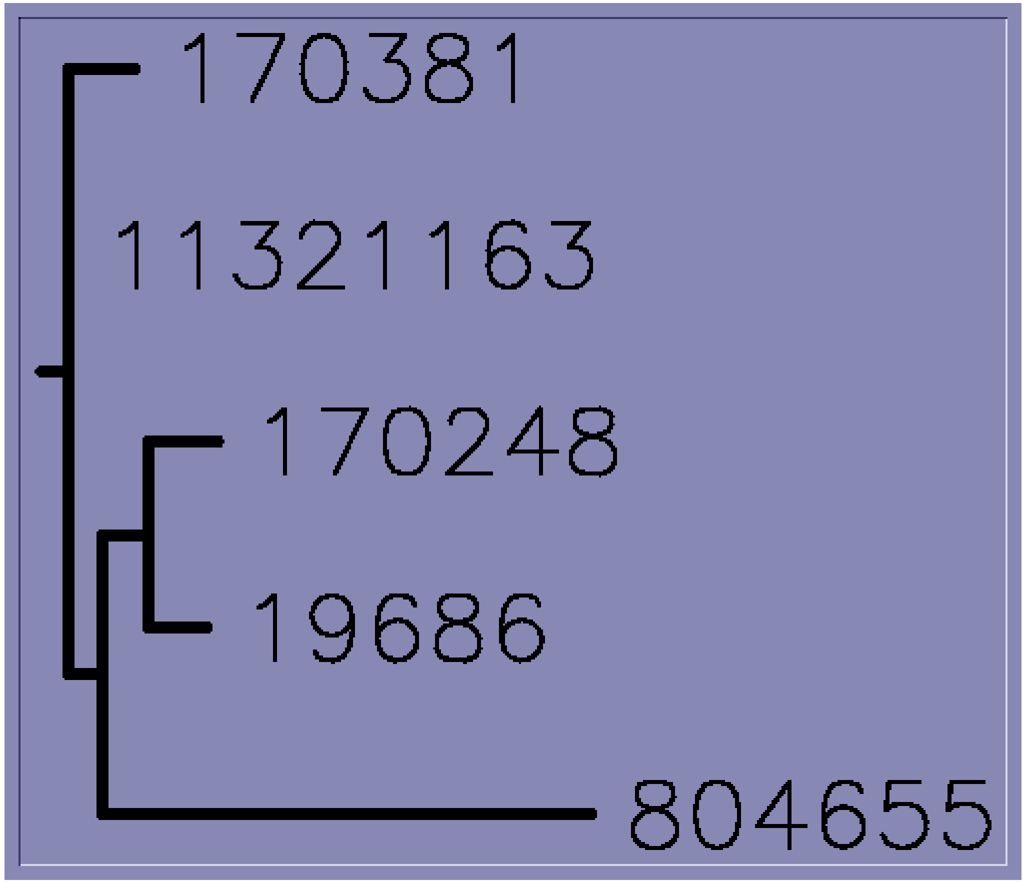
Selected Sequence(s)

- Lycopersicon esculentum beta-1,3-glucanase mRNA, complete cds., Capsicum annuum clone GC170 beta-1,3-glucanase-like protein gene,, Nicotiana tabacum glucan beta-1,3-glucosidase gene, complete cds., Nicotiana plumbaginifolia beta-(1,3)-glucanase gene for a vacuolar, Hordeum vulgare L. beta-glucosidase (BGQ60) gene, complete cds.

```
2560  CTTTGCTTGGTCTCTGCTTGACAACTTCGAGTGGAGACTCGGCTACACTGCCCGTTTCGG  804655

                2650      2660      2670      2680      2690      2700
  24  ...................................................AAATAGCT.  170381
   1                                                                11321163
2430  ...................................................CAAGAATT.  170248
1743  CAGTCAAATCATTCACACAACTCCAAAAACAACCCAAAATGGTAAAAAAAAAAAAAATTC  19686
2620  CATCGTCTATGTGGACTTCAATACTCTGAAGAGGTACCCCAAGGACTCAGCCTTGTGGTT  804655

                2710      2720      2730      2740      2750      2760
  32  ............ATTATTGTGCTTCTACGATTACTTGTCGCCA.CCAACATTCACATAAC  170381
   1                                                                11321163
2438  ............AC.ATAATTGATTTACTTTCTAACACTAATT.CTAATTCTTATTGAGC  170248
1803  ACCATGTTTACAATTGTTATGTCCAAACGCCCACTCACTATTTTCTAATTCATATTGAGC  19686
2680  CAAGAACATGCTCTCCGAAAAGAAGAGCAGCTAGGATCGCAAACAGGATCCGGGAGGATC  804655

                2770      2780      2790      2800      2810      2820
  79  AGAGGCTCAA...ATAGGTGT....TTGTTATGGAATGATGGGGAACAACTTGCCATCAC  170381
   1           T...ATGGGTGT....TTGCTATGGAATGATGGGGAACAACTTGCCTTCAC  11321163
2484  AGGGGCTCAATCAATAGGTGT....TTGCTATGGAATGCTAGGCAACAACTTGCCAAATC  170248
1863  AGGGGCTGAATCGATAGGTGT....TTGCTATGGAATGCTAGGCAACAACTTGCCAAATC  19686
2740  AGCTGCTTCAGCTTTCACAATAAAATCATAATGTAATGTGTCTTTATCATAGAACCTCAG  804655

                2830      2840      2850      2860      2870      2880
 132  ATTCTGAAGTTATACAGC..TCTACAAGTCGAGAAACATTAGAAGACTGAGGCTTTATGA  170381
  45  ATTCGGAAGTTATACAGC..TCTACAAGTCAAGAAACATTGGAAGATTGAGGCTTTATGA  11321163
2540  ATTGGGAAGTTATACAGC..TCTACAAGTCAAGAAACATAGGAAGACTGAGGCTTTATGA  170248
1919  ATTGGGAAGTTATACAGC..TCTACAAGTCAAGAAACATAGGAAGACTGAGGCTTTATGA  19686
2800  ACTTAGGCCCTGTTCGGTAATCACCACTCCCGGAATATGCCGAC.CGGGCAAATTGCAG  804655
```

Analytical Tools

- http://workbench.sdsc.edu/



Analytical Tools

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

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 inability 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

Analytical Tools

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

```
619 NC_003076.1 2254473 2253854
```

```
Read 2 primers, 18 matches and 1 amplicons. TEMP=50oC
PCR limited by Taq in cycle 19
0:1e-06 619 NC_003076.1 2254473 2253854 1 2
```

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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

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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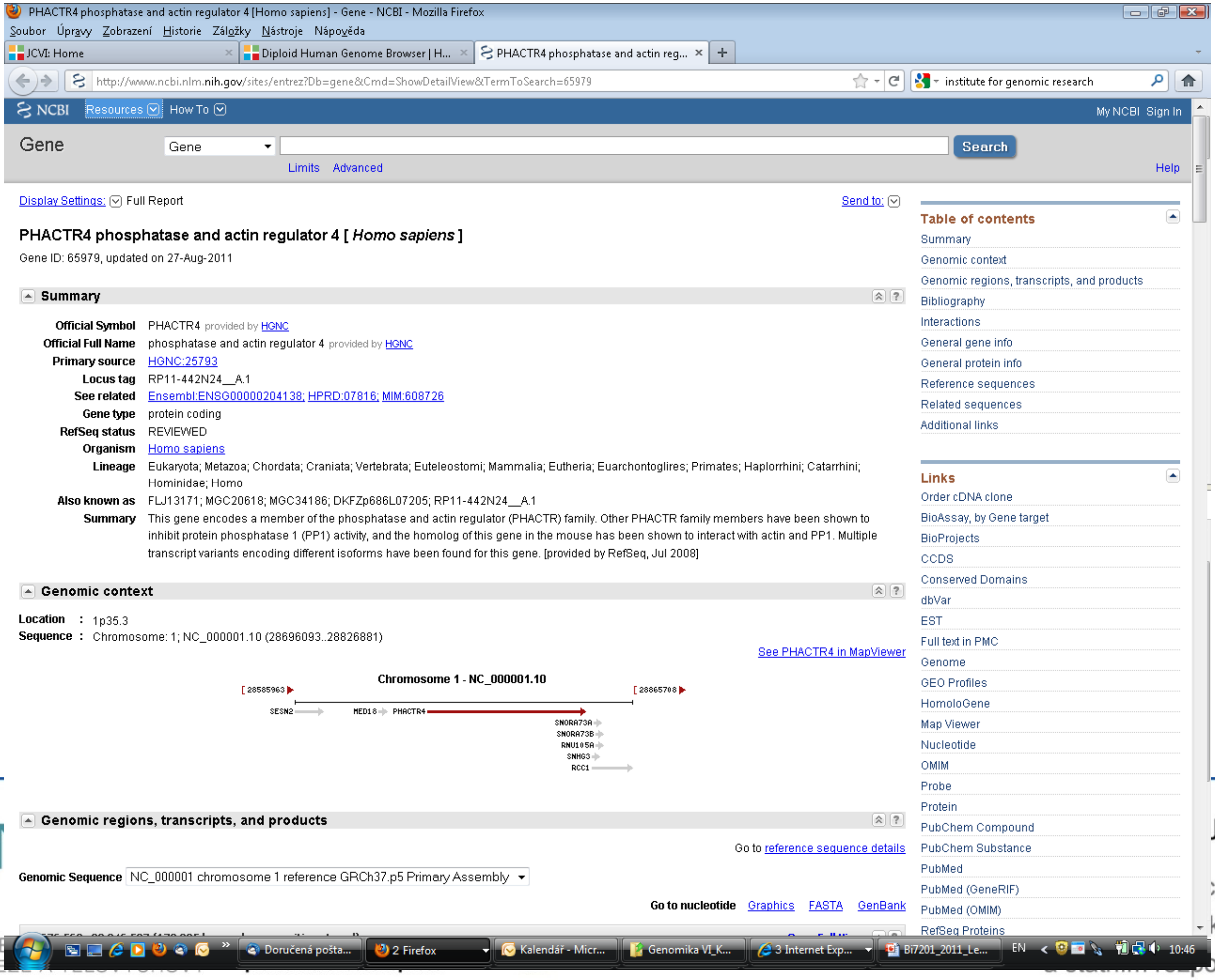
Other On-Line Genome Resources

- **TIGR** (**T**he **I**nstitute for **G**enomic **R**esearch, http://www.tigr.org/software/)
  - Recently part of the J. Craig Venter Institute



PHACTR4 phosphatase and actin regulator 4 [*Homo sapiens*]

Gene ID: 65979, updated on 27-Aug-2011

Summary

Official Symbol	PHACTR4 provided by HGNC
Official Full Name	phosphatase and actin regulator 4 provided by HGNC
Primary source	HGNC:25793
Locus tag	RP11-442N24__A.1
See related	Ensembl:ENSG00000204138; HPRD:07816; MIM:608726
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Homo sapiens
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo
Also known as	FLJ13171; MGC20618; MGC34186; DKFZp686L07205; RP11-442N24__A.1
Summary	This gene encodes a member of the phosphatase and actin regulator (PHACTR) family. Other PHACTR family members have been shown to inhibit protein phosphatase 1 (PP1) activity, and the homolog of this gene in the mouse has been shown to interact with actin and PP1. Multiple transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Jul 2008]

Genomic context

Location : 1p35.3
Sequence : Chromosome: 1; NC_000001.10 (28696093..28826881)

See PHACTR4 in MapViewer

Genomic regions, transcripts, and products

Go to reference sequence details

Genomic Sequence NC_000001 chromosome 1 reference GRCh37.p5 Primary Assembly

Go to nucleotide Graphics FASTA GenBank

Table of contents

- Summary
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- Genomic regions, transcripts, and products
- Bibliography
- Interactions
- General gene info
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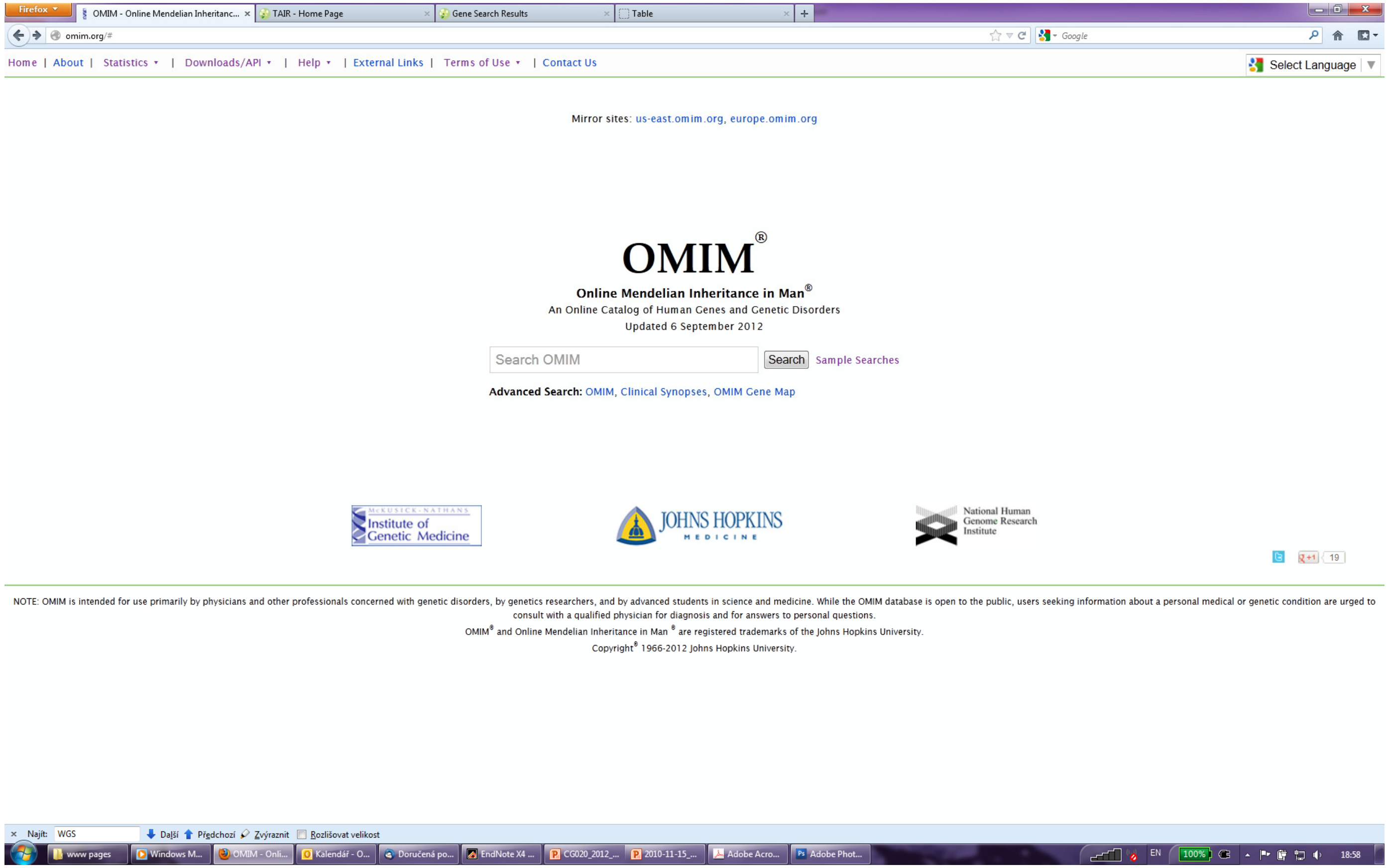
- Additional links

Links

- Order cDNA clone
- BioAssay, by Gene target
- BioProjects
- CCDS
- Conserved Domains
- dbVar
- EST
- Full text in PMC
- Genome
- GEO Profiles
- HomoloGene
- Map Viewer
- Nucleotide
- OMIM
- Probe
- Protein
- PubChem Compound
- PubChem Substance
- PubMed
- PubMed (GeneRIF)
- PubMed (OMIM)
- RefSeq Proteins

Other On-Line Genome Resources

- **O**nline **M**endelian **I**nheritance in **M**an (**OMIM**)



Mirror sites: us-east.omim.org, europe.omim.org

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NOTE: OMIM is intended for use primarily by physicians and other professionals concerned with genetic disorders, by genetics researchers, and by advanced students in science and medicine. While the OMIM database is open to the public, users seeking information about a personal medical or genetic condition are urged to consult with a qualified physician for diagnosis and for answers to personal questions.

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Discussion