PODATKOVNE ZBIRKE

1. Internet

Nekateri strežniki, EBI, NCBI, KEGG, ExPASy

2. Podatkovne zbirke

Lastnosti: velikost, določenost, presežnost
Primarne, sekundarne; bibliografske
Podatkovne zbirke nukleotidnih zaporedij
Podatkovne zbirka proteinskih zaporedij
Podatkovna zbirka 3D struktur
Bibliografska informacija: PubMed, OMIM

STREŽNIKI Z BIOKEMIJSKO IN MOL BIOL INFORMACIJO

EBI	European Bioinformatics Institute
NCBI	The National Center for Biotechnology Information
ExPASy	Expert Protein Analysis System
KEGG	Kyoto Encyclopedia of Genes and Genomes

In še mnogi drugi!

NCBI- The National Center for Biotechnology Information

1988 Kot del National Library of Medicine

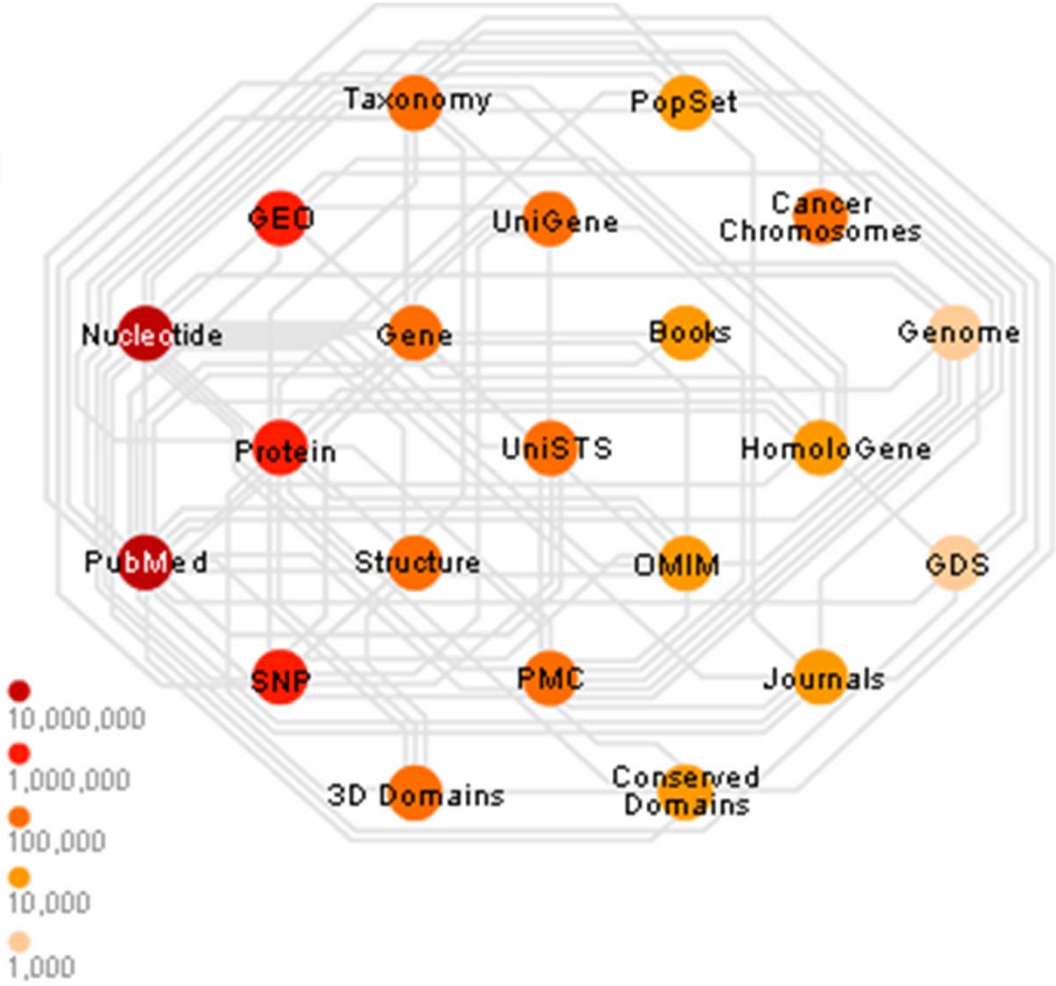
Namen: *razvoj novih informacijskih tehnologij, ki pomagajo razumeti molekularne in genetske procese*

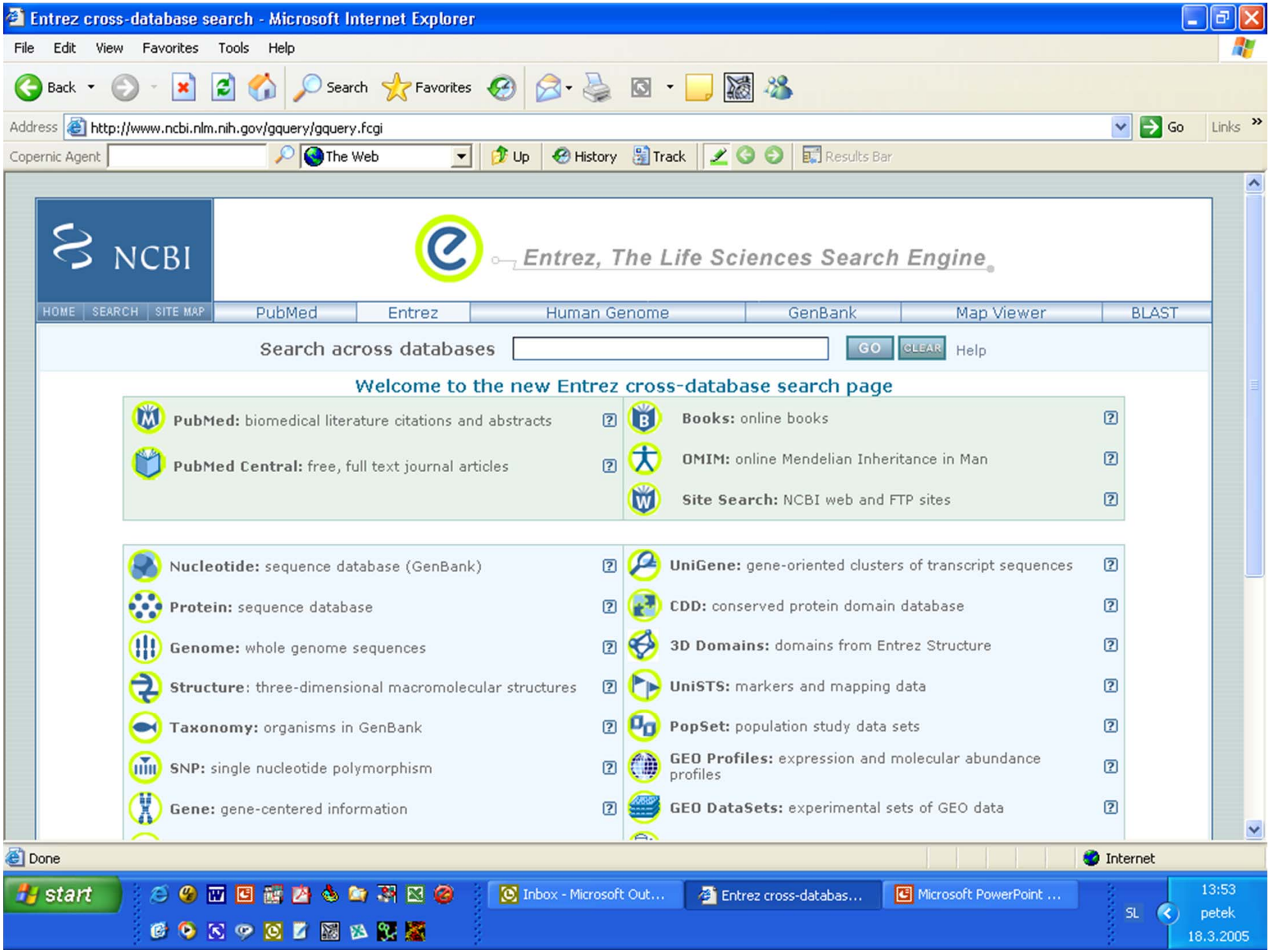
1992 Upravljanje z GenBank

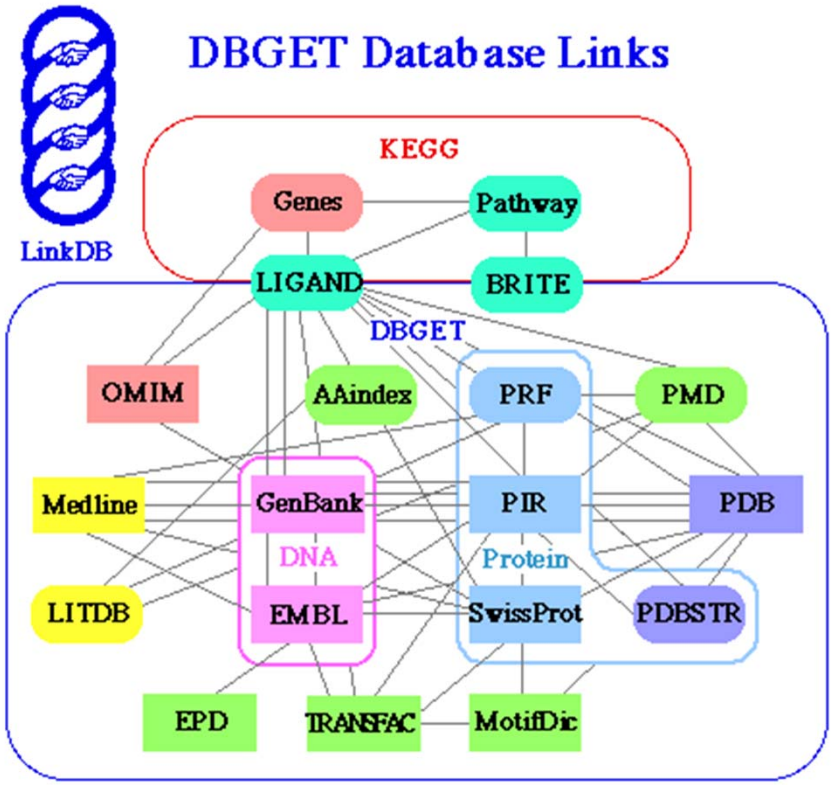
Entrez

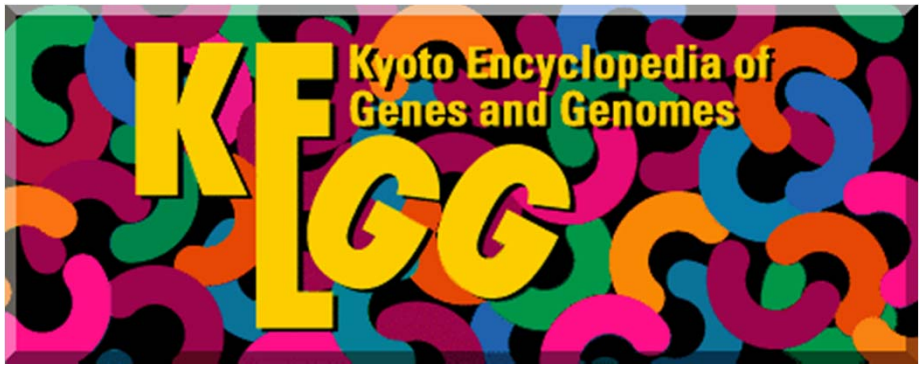
http://www.ncbi.nlm.nih.gov/Entr

Brskalnik za iskanje po bioloških podatkovnih zbirkah, ki jih ureja NCBI (proteinska zaporedja, nukleotidna zaporedja, gensko mapiranje, OMIM, 3D strukture iz PDB, PubMed)




Entrez cross-database search - Microsoft Internet Explorer
File Edit View Favorites Tools Help
Back Search Favorites
Address http://www.ncbi.nlm.nih.gov/gquery/gquery.fcgi
Go Links
Copernic Agent The Web Up History Track Results Bar
NCBI
Entrez, The Life Sciences Search Engine
HOME SEARCH SITE MAP
PubMed Entrez Human Genome GenBank Map Viewer BLAST
Search across databases
GO CLEAR Help
Welcome to the new Entrez cross-database search page
PubMed: biomedical literature citations and abstracts
PubMed Central: free, full text journal articles
Books: online books
OMIM: online Mendelian Inheritance in Man
Site Search: NCBI web and FTP sites
Nucleotide: sequence database (GenBank)
Protein: sequence database
Genome: whole genome sequences
Structure: three-dimensional macromolecular structures
Taxonomy: organisms in GenBank
SNP: single nucleotide polymorphism
Gene: gene-centered information
UniGene: gene-oriented clusters of transcript sequences
CDD: conserved protein domain database
3D Domains: domains from Entrez Structure
UniSTS: markers and mapping data
PopSet: population study data sets
GEO Profiles: expression and molecular abundance profiles
GEO DataSets: experimental sets of GEO data
Done
Internet
start
Inbox - Microsoft Out...
Entrez cross-databas...
Microsoft PowerPoint ...
SL
13:53
petek
18.3.2005





KEGG: Kyoto Encyclopedia of Genes and Genomes

Kyoto Encyclopedia of Genes and Genomes (KEGG) is an effort to computerize current knowledge of molecular and cellular biology in terms of the information pathways that consist of interacting molecules or genes and to provide links from the gene catalogs produced by genome sequencing projects. The KEGG project is undertaken in the Bioinformatics Center, Institute for Chemical Research, Kyoto University with supports from the Ministry of Education, Culture, Sports, Science and Technology and the Japan Society for the Promotion of Science.

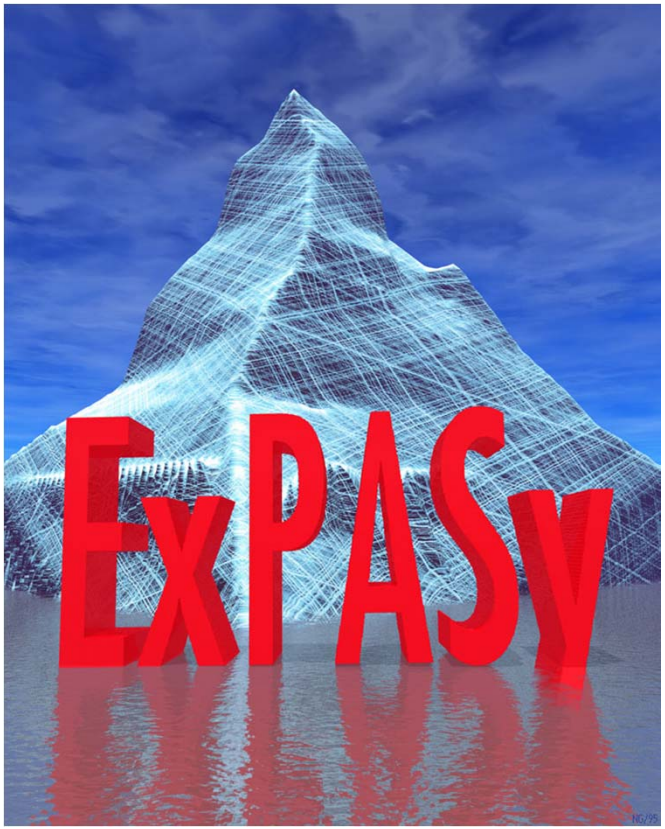
ExPASy Expert Protein Analysis System

http://www.expasy.org/
Swiss Institute of bioinformatics (SIB)

The ExPASy (**Ex**pert **P**rotein **A**nalysis **Sy**stem) proteomics server from the Swiss Institute of Bioinformatics (SIB) is dedicated to molecular biology with an emphasis on data relevant to **proteins.**

Podatkovne zbirke: **SwissProt /UniProt**
Swiss-Model
PROSITE

Programi: Orodja za proteomiko



1. VEEEEELIKOST PODATKOVNIH ZBIRK

Povezano z zajemanjem podatkov – kako težko je podatek dobiti.

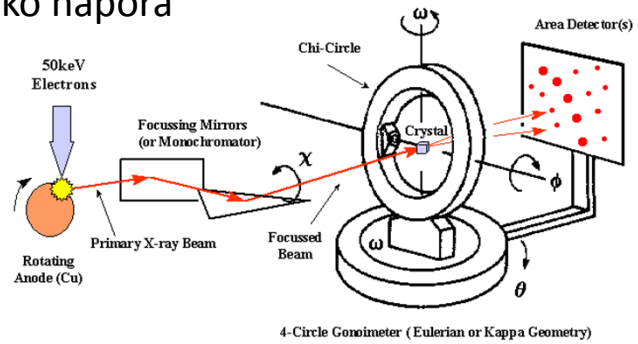
Podatkovne zbirke so lahko
VELIKE- npr. GeneBank; Največja podatkovna zbirka, nukleotidna zaporedja.
171.123.749 zaporedjih (februar 2014) iz **>165.000** organizmov

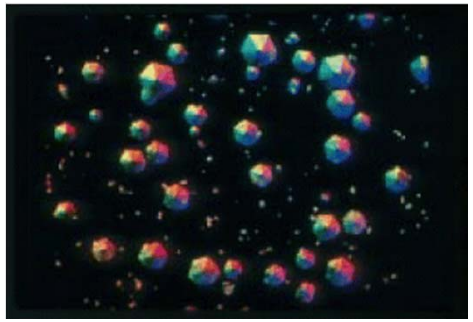
SREDNJE VELIKE- npr. UniProt. proteinska zaporedja.
542.503 zaporedij (februar 2014) iz različica **13.056** vrst

MAJHNE- npr. PDB. 3D strukture makromolekul.
76.349 struktur (februar 2014)

nukleotidna zaporedja možno dobiti sorazmerno enostavno

3D strukture je tudi možno dobiti, a z veliko napora





RAZKORAK MED ŠTEVILOM ZAPOREDIJ IN ŠTEVILOM 3D STRUKTUR

>170 000 000 GeneBank
>500 000 UniProt
>70 000 Protein Data Bank

Problemi pri pripravi vzorca (količina, izražanje), lastnostih (netopni, membranski), kristalizaciji

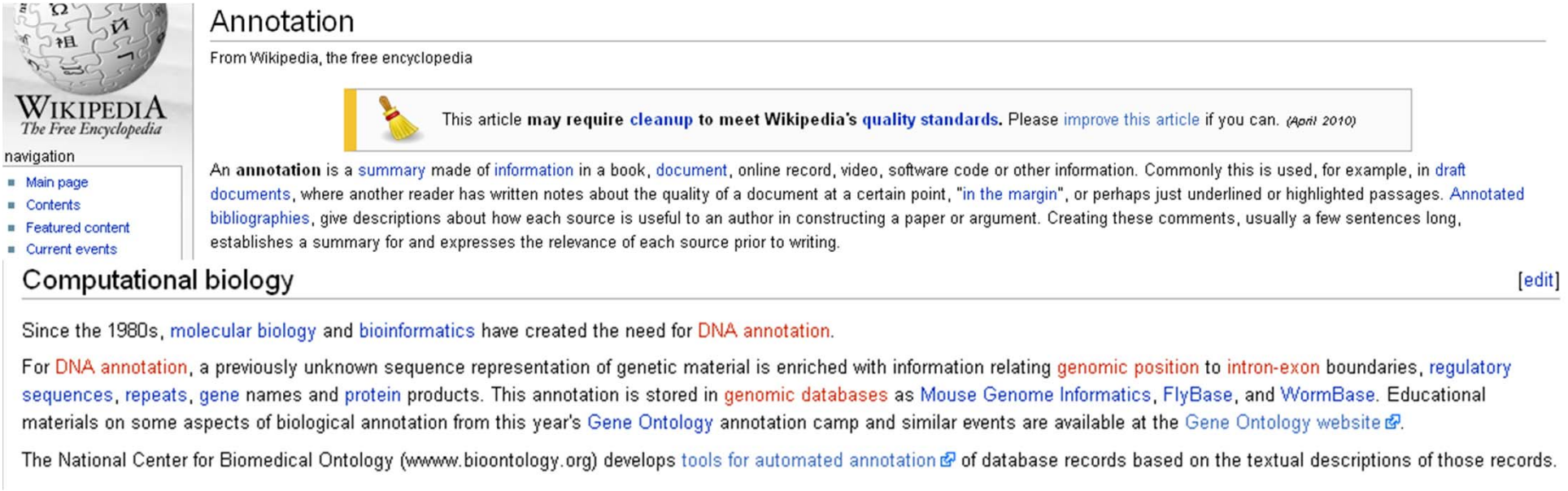
Npr. MsbA iz *E. coli* ABC transporter
>20 homologov iz 12 bakterijskih vrst izražajo
>20 detergentov z vsemi, skupaj 96 000 testov
35 kristalnih oblik
1 kristal, ki dobro sipa
....
1 SCIENCE članek
(Chang G and Roth CB (2001) Science 293, 1793-1800

2. Anotacija- določitev

Biološke, strukturne, funkcionalne, etc. lastnosti pripišemo biološkemu podatku, npr. zaporedju.

Podatkovne zbirke so lahko
DOBRO anotirane- npr. UniProt; kuratorji vpisujejo “na roke” različne podatke iz primarnih publikacij (glej naslednji slide). Zahteva veliko napora za urejanje. Zapisov navadno malo.

SLABO anotirane- npr. GeneBank; posledica avtomatskega vnašanja podatkov v podatkovne zbirke, količine podatkov. Manj napora za urejanje. Zapisov veliko.



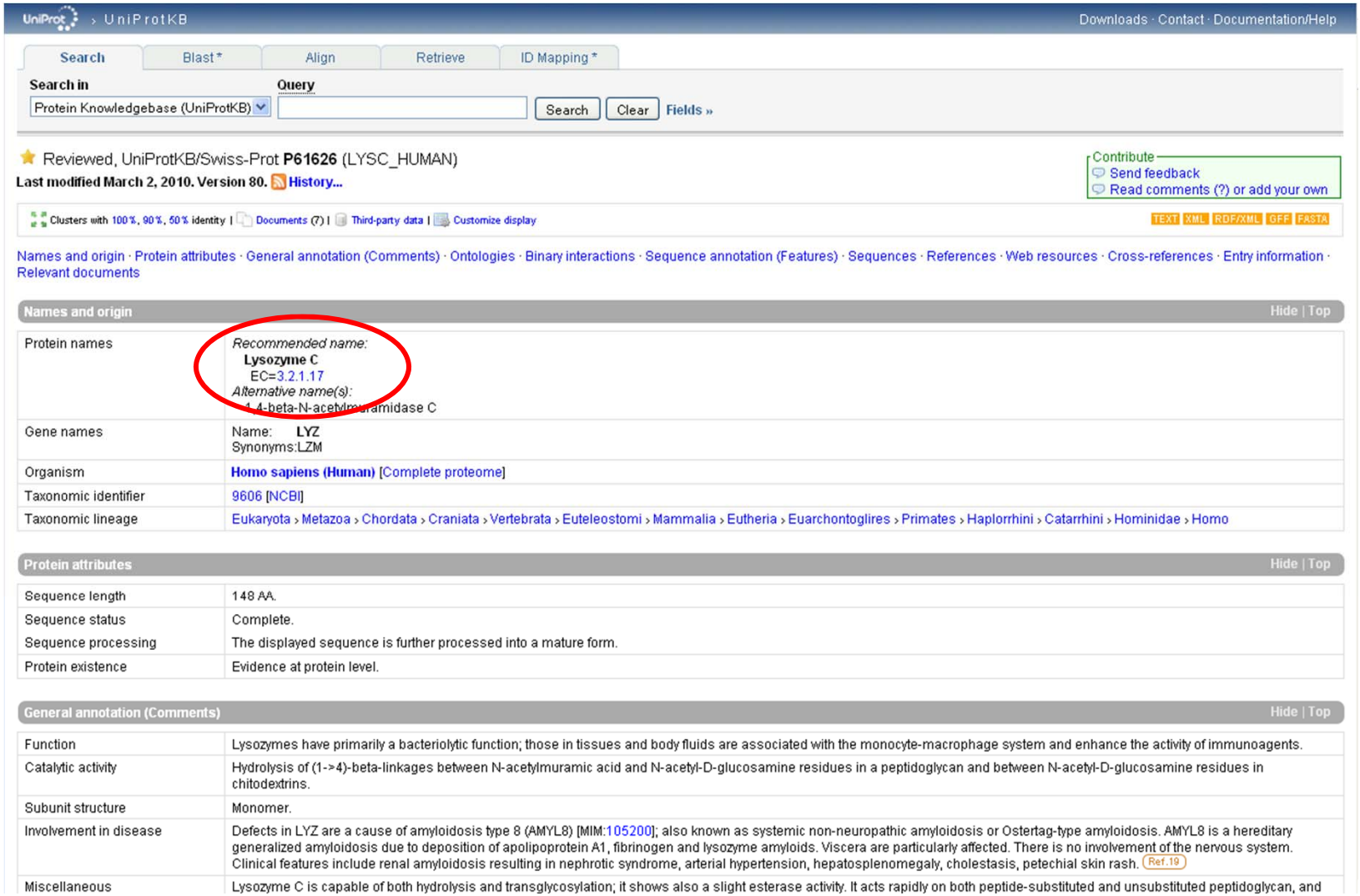
Core data

aminokislinsko zaporedje
ime proteina
taksonomski podatki
citati

Določitev (“annotation”)

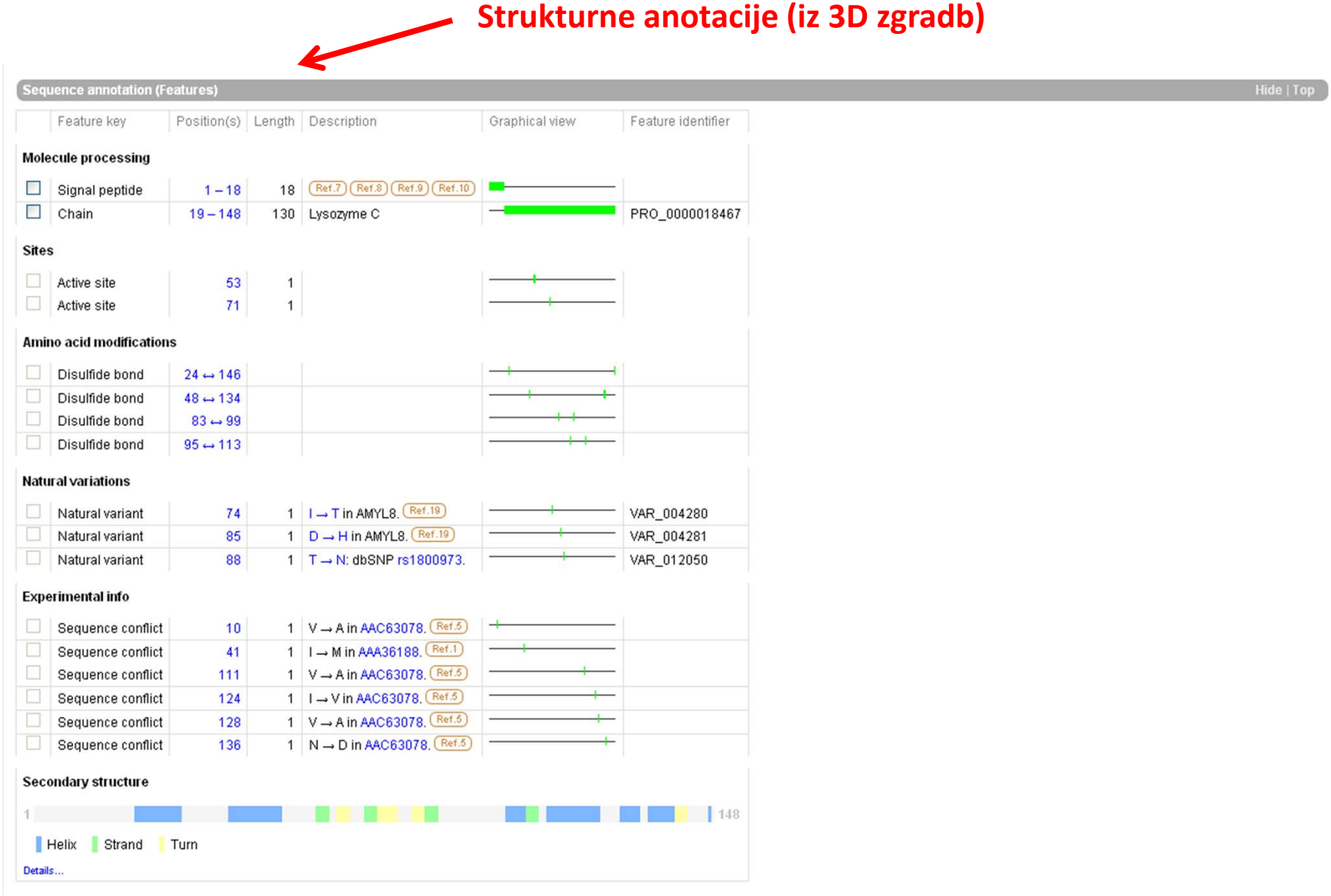
funkcija proteina
podatki o encimski aktivnosti (katalitska aktivnost, kofaktorji, metabolne poti...)
biološko pomembna mesta na molekuli (domene), posttranslacijske modifikacije
M določena z masno spektroskopijo
tkivno specifična izražanje
razvojno specifično izražanje
sekundarna struktura
kvartarna struktura
polimorfizmi
podobnost z drugimi proteini
uporaba v biotehnoloških procesih
napake (konflikti) v zaporedjih

Vpis “na roke” iz primarnih publikacij, preglednih člankov.
Pomoč zunanjih ekspertov za posamezne družine proteinov.


UniProt › UniProtKB
Downloads · Contact · Documentation/Help
Search
Blast *
Align
Retrieve
ID Mapping *
Search in
Protein Knowledgebase (UniProtKB)
Query
Search
Clear
Fields »
Reviewed, UniProtKB/Swiss-Prot P61626 (LYSC_HUMAN)
Last modified March 2, 2010. Version 80. History...
Contribute
Send feedback
Read comments (?) or add your own
Clusters with 100%, 90%, 50% identity | Documents (7) | Third-party data | Customize display
TEXT XML RDF/XML GFF FASTA
Names and origin · Protein attributes · General annotation (Comments) · Ontologies · Binary interactions · Sequence annotation (Features) · Sequences · References · Web resources · Cross-references · Entry information · Relevant documents
Names and origin
Hide | Top
Protein names
Recommended name:
Lysozyme C
EC=3.2.1.17
Alternative name(s):
1,4-beta-N-acetylmuramidase C
Gene names
Name: LYZ
Synonyms:LZM
Organism
Homo sapiens (Human) [Complete proteome]
Taxonomic identifier
9606 [NCBI]
Taxonomic lineage
Eukaryota › Metazoa › Chordata › Craniata › Vertebrata › Euteleostomi › Mammalia › Eutheria › Euarchontoglires › Primates › Haplorrhini › Catarrhini › Hominidae › Homo
Protein attributes
Hide | Top
Sequence length
148 AA.
Sequence status
Complete.
Sequence processing
The displayed sequence is further processed into a mature form.
Protein existence
Evidence at protein level.
General annotation (Comments)
Hide | Top
Function
Lysozymes have primarily a bacteriolytic function; those in tissues and body fluids are associated with the monocyte-macrophage system and enhance the activity of immunoagents.
Catalytic activity
Hydrolysis of (1->4)-beta-linkages between N-acetylmuramic acid and N-acetyl-D-glucosamine residues in a peptidoglycan and between N-acetyl-D-glucosamine residues in chitodextrins.
Subunit structure
Monomer.
Involvement in disease
Defects in LYZ are a cause of amyloidosis type 8 (AMYL8) [MIM:105200]; also known as systemic non-neuropathic amyloidosis or Ostertag-type amyloidosis. AMYL8 is a hereditary generalized amyloidosis due to deposition of apolipoprotein A1, fibrinogen and lysozyme amyloids. Viscera are particularly affected. There is no involvement of the nervous system. Clinical features include renal amyloidosis resulting in nephrotic syndrome, arterial hypertension, hepatosplenomegaly, cholestasis, petechial skin rash. Ref.19
Miscellaneous
Lysozyme C is capable of both hydrolysis and transglycosylation; it shows also a slight esterase activity. It acts rapidly on both peptide-substituted and unsubstituted peptidoglycan, and

Anotacije

Strukturne anotacije (iz 3D zgradb)



Sequence annotation (Features)

Hide | Top

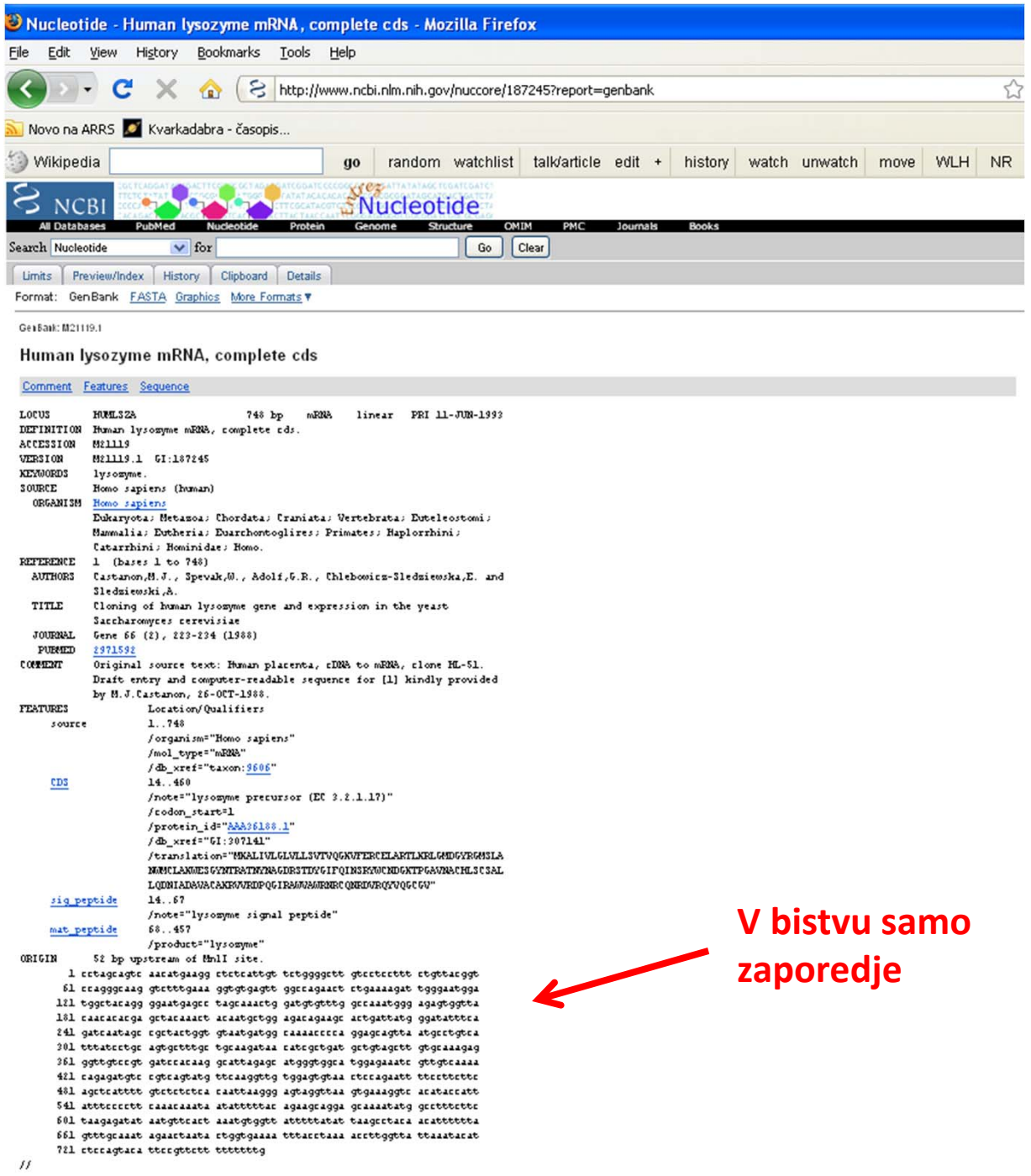
	Feature key	Position(s)	Length	Description	Graphical view	Feature identifier
Molecule processing						
☐	Signal peptide	1 – 18	18	Ref.7 Ref.8 Ref.9 Ref.10		
☐	Chain	19 – 148	130	Lysozyme C		PRO_0000018467
Sites						
☐	Active site	53	1			
☐	Active site	71	1			
Amino acid modifications						
☐	Disulfide bond	24 ↔ 146				
☐	Disulfide bond	48 ↔ 134				
☐	Disulfide bond	83 ↔ 99				
☐	Disulfide bond	95 ↔ 113				
Natural variations						
☐	Natural variant	74	1	I → T in AMYL8. Ref.19		VAR_004280
☐	Natural variant	85	1	D → H in AMYL8. Ref.19		VAR_004281
☐	Natural variant	88	1	T → N: dbSNP rs1800973.		VAR_012050
Experimental info						
☐	Sequence conflict	10	1	V → A in AAC63078. Ref.5		
☐	Sequence conflict	41	1	I → M in AAA36188. Ref.1		
☐	Sequence conflict	111	1	V → A in AAC63078. Ref.5		
☐	Sequence conflict	124	1	I → V in AAC63078. Ref.5		
☐	Sequence conflict	128	1	V → A in AAC63078. Ref.5		
☐	Sequence conflict	136	1	N → D in AAC63078. Ref.5		

Secondary structure

1 148

Helix Strand Turn

Details...



V bistvu samo zaporedje

3. Presežnost/nepresežnost (redundancy)

Podatkovne zbirke so lahko
PRESEŽNE- npr. GeneBank; vsebujejo več identičnih podatkov.

NEPRESEŽNE- npr. UniProt. Bolj pregledne. Lažje in hitrejše iskanje podatkov.

14. Homo sapiens lactotransferrin (LTF), mRNA
2,390 bp linear mRNA
NM_002343.2 GI:54607119

15. Homo sapiens arylsulfatase B (ARSB), transcript variant 1, mRNA
6,076 bp linear mRNA
NM_000046.3 GI:158634485

16. Human lysozyme mRNA, complete cds
1,483 bp linear mRNA
M19045.1 GI:187247

17. Human lysozyme mRNA, complete cds with an Alu repeat in the 3' flank
1,487 bp linear mRNA
J03801.1 GI:187243

V bistvu isto zaporedje

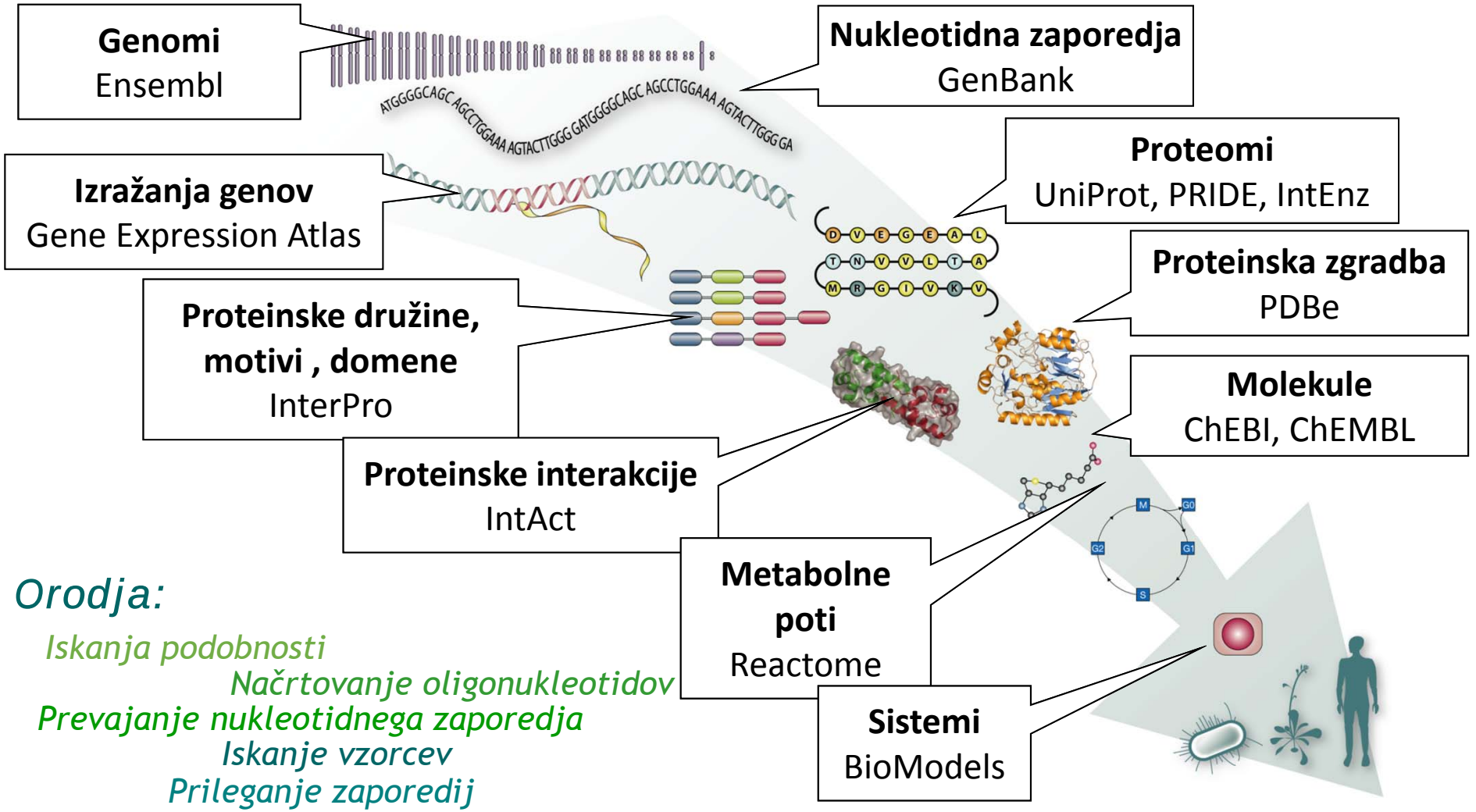
18. Homo sapiens alpha-lactalbumin (LALBA) mRNA, complete cds
701 bp linear mRNA
J00270.1 GI:186830

19. Homo sapiens lactalbumin, alpha-, mRNA (cDNA clone MGC:138521 IMAGE:8327784), complete cds
581 bp linear mRNA
BC112316.1 GI:85567732

20. Homo sapiens lysozyme precursor, mRNA, complete cds
456 bp linear mRNA
U25677.1 GI:847819

Podatkovne zbirke

od molekul do sistemov



Orodja:

Iskanja podobnosti

Načrtovanje oligonukleotidov

Prevajanje nukleotidnega zaporedja

Iskanje vzorcev

Prileganje zaporedij

Napoved genov

Napoved zgradbe

PODATKOVNE ZBIRKE

PRIMARNE ("archival", arhivske)
SEKUNDARNE ("curated", izpeljane)

				Podatkovna zbirka
	nukleotidno zaporedje	ATGGTGCACCTGAC TCCTGAGGAGAAG...	→	primarna GenBank, EMBL, DDBJ
primarna zgradba	proteinsko zaporedje	MVHLTPEEK...	→	primarna Swiss-Prot, PIR, MIPS
sekundarna zgradba	motiv	M-[VIL]-H-[VIL]- -[ST]-P-E2-K...	→	sekundarna Prosite, Profiles, Pfam, BLOCKS
terciarna, kvartarna zgradba	domena		→	strukturna PDB, SCOP, CATH

NUKLEOTIDNE PODATKOVNE ZBIRKE

Dnevna izmenjava zaporedij!

DDBJ *DNA Data Bank of Japan*
Zaporedja javno dostopnih virov in večjih genomskih projektov

EMBL
Podatkovna zbirka EBI. Vsebuje direktno vpisana zaporedja, rezultate določevanj zaporedij genomov, zaporedja iz literature in patentov.
Iskanje in primerjave zaporedij preko vmesnikov

GenBank
Zaporedja javno dostopnih virov in večjih genomskih projektov.
Dnevna izmenjava podatkov z DDBJ in EMBL.
Razdeljena na posamezne odseke (nivo organizmov, EST, PAT, STS, GSS, HTG).
157.943.793.171 baz v **171.123.749** zaporedjih (14. 2. 2014)
iz več kot **165 000** organizmov
Dostop preko Entreza (Medline ali BLAST)
dbEST podatkovna zbirka oznak izraženih zaporedij

Ostale specializirane podatkovne zbirke
GSDB (The Genome Sequence DataBase), SGD (*Saccharomyces* Genome Database), UniGene, TDB (TIGR podatkovna zbirka), ACeDB (A *C. elegans* DataBase)

STRUKTURA GenBank ZAPISA

GBFF- GenBank flat file — oblika zapisa v GenBank. Zapis, ki si ga izmenjujejo podatkovne zbirke.

Glava (*header*)
Lastnosti
Zaporedje

```
LOCUS       NM_000239               1487 bp    mRNA    linear   PRI 18-DEC-2001
DEFINITION  Homo sapiens lysozyme (renal amyloidosis) (LYZ), mRNA.
ACCESSION   NM_000239
VERSION     NM_000239.1  GI:4557893
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1487)
  AUTHORS   Reitamo,S., Klockars,M., Adinolfi,M. and Osserman,E.F.
  TITLE     Human lysozyme (origin and distribution in health and disease)
  JOURNAL   Ric Clin Lab 8 (4), 211-231 (1978)
  MEDLINE   79097291
   PUBMED   366724
```

Glava

```
LOCUS       NM_000239     1487 bp    mRNA    linear   PRI 18-DEC-2001
```

kratka oznaka zapisa
včasih ime lokusa
Npr. HUMHBB človeški
β-globinski lokus

dolžina
Manj kot 50 bp
ne sprejmejo, več
kot 350 kb tudi
ne

tip zaporedja
DNA, tRNA, rRNA,
mRNA, uRNA

Odsek GenBank

PRI	primati
ROD	glodalci
MAM	ostali sesalci
VRT	ostali vretenčarji
INV	nevretenčarji
PLN	rastline
BCT	bakterije
VRL	virusi
PHG	bakteriofag
SYN	sintetične
EST	oznaka izraženega zaporedja
PAT	patent
STS	sequence tagged sites
GSS	genome survey sequences
HTG	“high throughput” genomska zaporedja
HTC	nedokončane “high throughput” EST zap.

datum, ko je zapis
postal javen

```
DEFINITION  Homo sapiens lysozyme (renal amyloidosis) (LYZ), mRNA.
```
Biološki opis zaporedja (izpisan v FASTA formatu)

```
ACCESSION   NM_000239
```
Edinstvena koda, se ne spreminja, podana v publikacijah

```
VERSION     NM_000239.1  GI:4557893
```
Katera verzija zaporedja je. Se spreminja. GI (*geneInfo identifier)* edinstveno določena koda za zaporedje (enaka med različnimi podatkovnimi zbirkami). Tudi PID (*protein identifier*) v primeru prevedenih proteinskih zaporedij.

```
KEYWORDS    .

SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```
Izvor zaporedja.

```
REFERENCE   1  (bases 1 to 1487)
  AUTHORS   Reitamo,S., Klockars,M., Adinolfi,M. and Osserman,E.F.
  TITLE     Human lysozyme (origin and distribution in health and disease)
  JOURNAL   Ric Clin Lab 8 (4), 211-231 (1978)
  MEDLINE   79097291
   PUBMED   366724
```
Bibliografske enote povezane z zaporedjem (kdaj sklonirano, kdaj določena sturktura gena...)

```
NT_123456 constructed genomic contigs
NM_123456 mRNAs
NP_123456 proteins
NC_123456 chromosomes
```

```
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                     /db_xref="taxon:9606"
                     /chromosome="12"
                     /map="12q15"
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                     /cell_line="PMA treated U937"
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                     LQDNIADAVACAKRVVRDPQGIRAWVAWRNRCQNRDVRQYVQGCGV"
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                     /product="lysozyme"
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                     /note="lys; Region: C-type lysozyme/alpha-lactalbumin
                     family. Alpha-lactalbumin is the regulatory subunit of
                     lactose synthase"
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                     /note="LYZ1; Region: Alpha-lactalbumin / lysozyme C"
     variation       288
                     /allele="C"
                     /allele="A"
                     /db_xref="dbSNP:1800973"
     repeat_region   740..1054
                     /note="Alu repeat"
```

Lastnosti zaporedja.

Svojo lastno strukturo in povezave
z drugimi podatkovnimi zbirkami

Zaporedje

```
BASE COUNT      435 a    306 c    308 g    438 t
ORIGIN
        1 ctagcactct gacctagcag tcaacatgaa ggctctcatt gttctggggc ttgtcctcct
       61 ttctgttacg gtccagggca aggtctttga aaggtgtgag ttggccagaa ctctgaaaag
      121 attgggaatg gatggctaca ggggaatcag cctagcaaac tggatgtgtt tggccaaatg
      181 ggagagtggt tacaacacac gagctacaaa ctacaatgct ggagacagaa gcactgatta
      241 tgggatattt cagatcaata gccgctactg gtgtaatgat ggcaaaaccc caggagcagt
      301 taatgcctgt catttatcct gcagtgcttt gctgcaagat aacatcgctg atgctgtagc
      361 ttgtgcaaag agggttgtcc gtgatccaca aggcattaga gcatgggtgg catggagaaa
      421 tcgttgtcaa aacagagatg tccgtcagta tgttcaaggt tgtggagtgt aactccagaa
      481 ttttccttct tcagctcatt ttgtctctct cacattaagg gagtaggaat taagtgaaag
      541 gtcacactac cattatttcc ccttcaaaca aataatattt ttacagaagc aggagcaaaa
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     1081 ttgaatgata cgattatgcc caatattaag taaaaaatat aagaaaaggt tatcttaaat
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     1201 tccaaaaaca gtaaaaataa ccacttttg ttgggcaata tgaaattttt aaaggagtag
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```

http://www.expasy.uniprot.org/index.shtml

UniProt (Universal Protein Resource) is the world's most comprehensive catalog of information on proteins. It is a central repository of protein sequence and function created by joining the information contained in Swiss-Prot, TrEMBL, and PIR.

UniProt is comprised of three components, each optimized for different uses. The **UniProt Knowledgebase (UniProt)** is the central access point for extensive curated protein information, including function, classification, and cross-reference. The **UniProt Non-redundant Reference (UniRef)** databases combine closely related sequences into a single record to speed searches. The **UniProt Archive (UniParc)** is a comprehensive repository, reflecting the history of all protein sequences.

KAJ POTREBUJE NEKDO, KI SE UKVARJA S PROTEINI?

Kvalitetno podatkovno zbirko: nepresežno zbirko, čimboljša pokritost (izoforme, alternativno izrezovanje, variante pri boleznih.

Dobro identifikacijo proteinov: dobri označevalci, konsistentna nomenklatura.

Dobro določitev proteinov: podrobna informacija o proteinski funkciji, biološkem procesu, molekulskih interakcijah in udeležbi v različnih poteh in omrežjih. Reference na zunanje vire.

Swiss-Prot & TrEMBL PIR-PSD

UniProtKB/TrEMBL

Presežna zbirka, avtomatsko anotirana, nepregledana.

V UniProtKB/TrEMBL zapis predstavlja prevod enega ENA (nukleotidnega) zaporedja.

Več zapisov za isti protein je lahko rezultat:

- Napačnih napovedi genov
- Napak v zaporedjih (npr. premikov bralnega okvirja)
- Polimorfizmov
- Alternativnih startnih kodonov
- Izoform

ALI

- Ker so zaporedja vpisali različni raziskovalci

UniProtKB/Swiss-Prot

Nepresežna zbirka, zelo kvalitetna ročna anotacija, pregledana.

V UniProtKB/Swiss-Prot zapis predstavlja prevod enega proteina.

Vsa identična zaporedja so združena in dodatno analizirana s kuratorji, ki jim tudi pripišejo anotacije.

Zanesljivost zaporedij

1 Dokaz na nivoju proteina
2 Dokaz na nivoju transkripta
3 Določen na podlagi homologije
4 Napovedan
5 Negotov

UniProtKB/TrEMBL

Protein existence (PE):	entries	%
1: Evidence at protein level	12724	0.08%
2: Evidence at transcript level	534559	3.17%
3: Inferred from homology	3847758	22.79%
4: Predicted	12491797	73.97%
5: Uncertain	0	0.00%

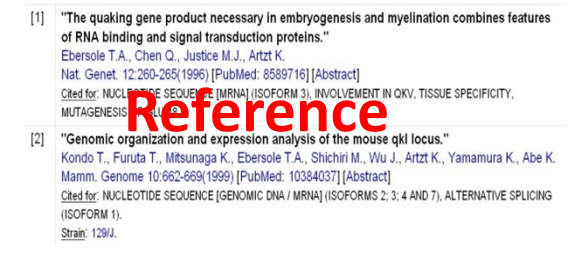
UniProtKB/Swiss-Prot

Protein existence (PE):	entries	%
1: Evidence at protein level	72765	13.7%
2: Evidence at transcript level	69863	13.1%
3: Inferred from homology	373177	70.1%
4: Predicted	14474	2.7%
5: Uncertain	1867	0.4%

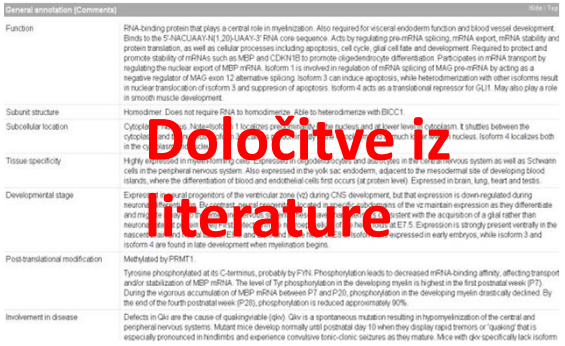
Anotirane proteine lahko uporabimo kot vodila za proteine, ki ji še niso podrobno študirali:

- 149 zapisov za ime „rhodopsin“ manualno anotiranih v UniProtKB/Swiss-Prot
- 7424 zapisov za ime „rhodopsin“ računalniško anotiranih v UniProtKB/TrEMBL

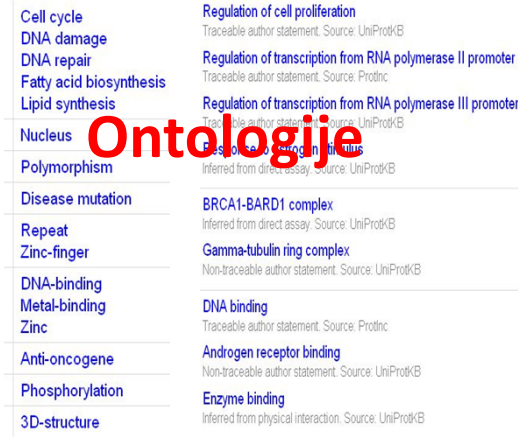
Informacije, ki jih dodajo UniProt/Swiss-Prot zapisu



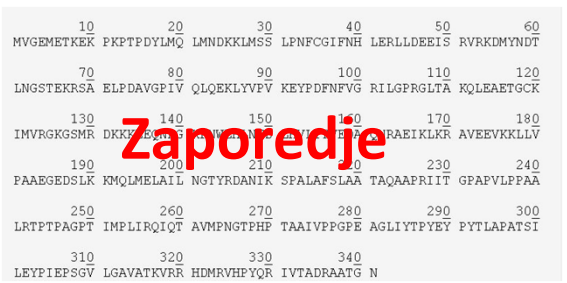
Reference



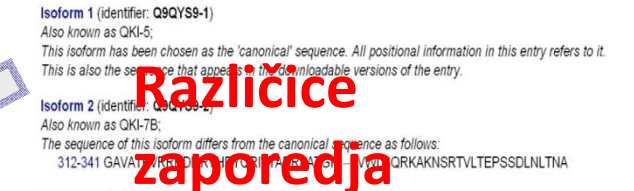
Določitve iz literature



Ontologije

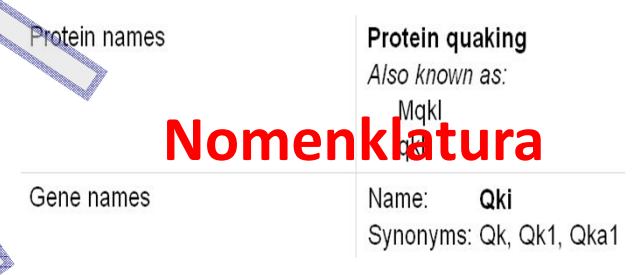


Zaporedje



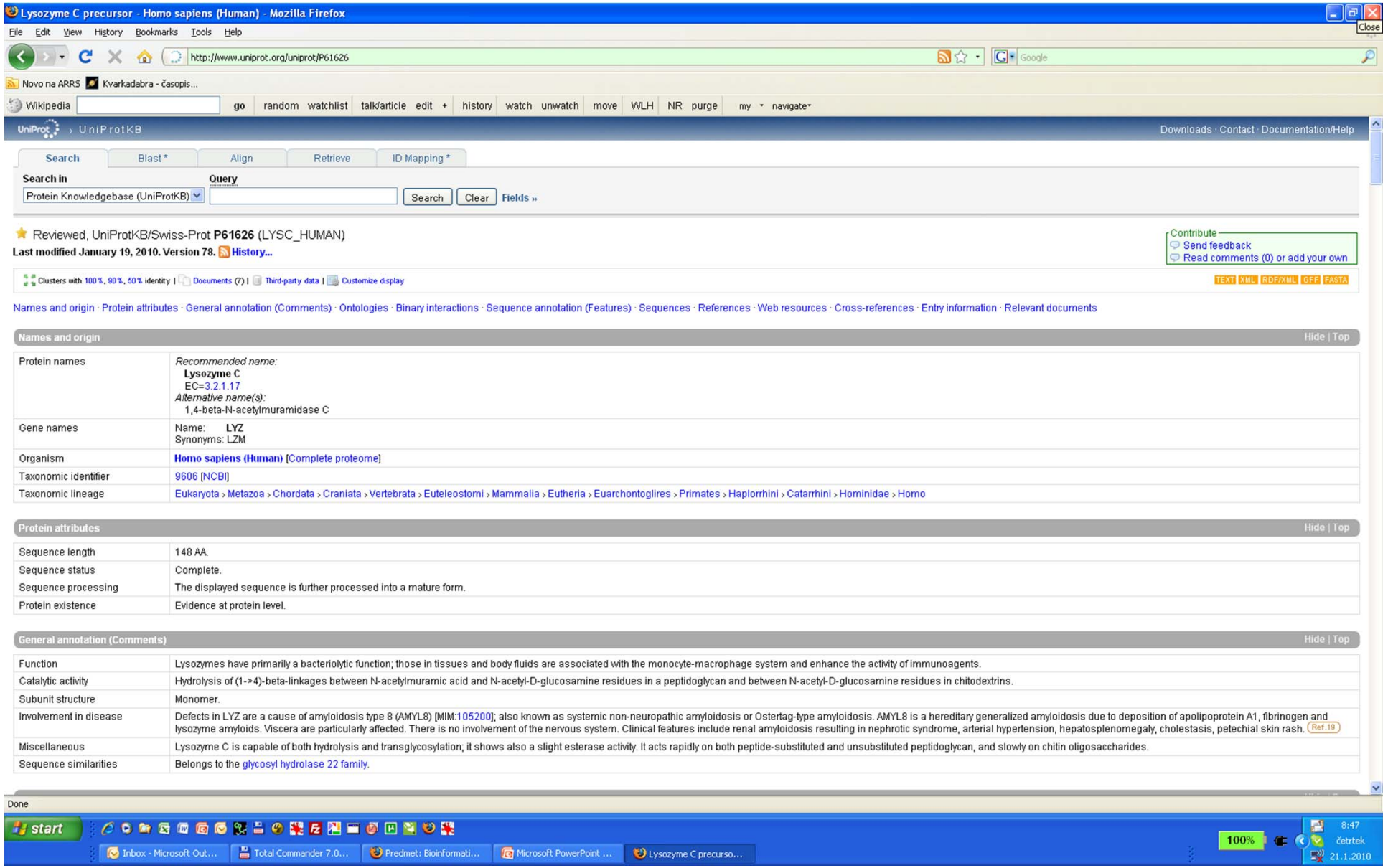
Različice zaporedja

KURATORJI



Nomenklatura

Lastnosti zaporedja


Lysozyme C precursor - Homo sapiens (Human) - Mozilla Firefox
File Edit View History Bookmarks Tools Help
http://www.uniprot.org/uniprot/P61626
Wikipedia go random watchlist talk/article edit + history watch unwatch move WLH NR purge my navigate
UniProt › UniProtKB
Downloads · Contact · Documentation/Help
Search Blast * Align Retrieve ID Mapping *
Search in
Protein Knowledgebase (UniProtKB)
Query
Search Clear Fields »
Reviewed, UniProtKB/Swiss-Prot P61626 (LYSC_HUMAN)
Last modified January 19, 2010. Version 78. History...
Contribute
Send feedback
Read comments (0) or add your own
Clusters with 100%, 90%, 50% identity | Documents (7) | Third-party data | Customize display
TEXT XML RDF/XML GFF FASTA
Names and origin · Protein attributes · General annotation (Comments) · Ontologies · Binary interactions · Sequence annotation (Features) · Sequences · References · Web resources · Cross-references · Entry information · Relevant documents
Names and origin
Hide | Top
Protein names
Recommended name:
Lysozyme C
EC=3.2.1.17
Alternative name(s):
1,4-beta-N-acetylmuramidase C
Gene names
Name: LYZ
Synonyms: LZM
Organism
Homo sapiens (Human) [Complete proteome]
Taxonomic identifier
9606 [NCBI]
Taxonomic lineage
Eukaryota › Metazoa › Chordata › Craniata › Vertebrata › Euteleostomi › Mammalia › Eutheria › Euarchontoglires › Primates › Haplorrhini › Catarrhini › Hominidae › Homo
Protein attributes
Hide | Top
Sequence length
148 AA.
Sequence status
Complete.
Sequence processing
The displayed sequence is further processed into a mature form.
Protein existence
Evidence at protein level.
General annotation (Comments)
Hide | Top
Function
Lysozymes have primarily a bacteriolytic function; those in tissues and body fluids are associated with the monocyte-macrophage system and enhance the activity of immunoagents.
Catalytic activity
Hydrolysis of (1->4)-beta-linkages between N-acetylmuramic acid and N-acetyl-D-glucosamine residues in a peptidoglycan and between N-acetyl-D-glucosamine residues in chitodextrins.
Subunit structure
Monomer.
Involvement in disease
Defects in LYZ are a cause of amyloidosis type 8 (AMYL8) [MIM:105200]; also known as systemic non-neuropathic amyloidosis or Ostertag-type amyloidosis. AMYL8 is a hereditary generalized amyloidosis due to deposition of apolipoprotein A1, fibrinogen and lysozyme amyloids. Viscera are particularly affected. There is no involvement of the nervous system. Clinical features include renal amyloidosis resulting in nephrotic syndrome, arterial hypertension, hepatosplenomegaly, cholestasis, petechial skin rash. Ref.19
Miscellaneous
Lysozyme C is capable of both hydrolysis and transglycosylation; it shows also a slight esterase activity. It acts rapidly on both peptide-substituted and unsubstituted peptidoglycan, and slowly on chitin oligosaccharides.
Sequence similarities
Belongs to the glycosyl hydrolase 22 family.
Done
start
Inbox - Microsoft Out...
Total Commander 7.0...
Predmet: Bioinformati...
Microsoft PowerPoint ...
Lysozyme C precurso...
100%
8:47
četrtek
21.1.2010

STRUKTURA SWISS-PROT ZAPISA

SWISS-PROT: P00695

NiceProt - a user-friendly view of this SWISS-PROT entry

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ID   LYC_HUMAN      STANDARD;      PRT;   148 AA.
AC   P00695; Q13170;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-OCT-1989 (Rel. 12, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Lysozyme C precursor (EC 3.2.1.17) (1,4-beta-N-acetylmuramidase C).
GN   LYZ OR LZM.
OS   Homo sapiens (Human),
OS   Pan troglodytes (Chimpanzee), and
OS   Pan paniscus (Pygmy chimpanzee) (Bonobo).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606, 9598, 9597;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   SPECIES=Human;
RX   MEDLINE=89325294; PubMed=2546758; [NCBI, ExPASy, EBI, Israel, Japan]
RA   Peters C.W.B., Kruse U., Pollwein R., Grzeschik K.H., Sippel A.E.;
RT   "The human lysozyme gene. Sequence organization and chromosomal
RT   localization.";
RL   Eur. J. Biochem. 182:507-516(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   SPECIES=Human;
RX   MEDLINE=89006264; PubMed=2971592; [NCBI, ExPASy, EBI, Israel, Japan]
RA   Peters C.W.B., Kruse U., Pollwein R., Grzeschik K.H., Sippel A.E.;
RT   "The human lysozyme gene. Sequence organization and chromosomal
RT   localization.";
RL   Eur. J. Biochem. 182:507-516(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   SPECIES=Human;
RX   MEDLINE=89006264; PubMed=2971592; [NCBI, ExPASy, EBI, Israel, Japan]
RA   Castanon M.J., Spevak W., Adolf G.R., Chlebowicz-Sledziewska E.,
RA   Sledziewski A.;
RT   "Cloning of human lysozyme gene and expression in the yeast
RT   Saccharomyces cerevisiae.";
RL   Gene 66:223-234(1988).
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PROTEIN_IZVOR	se lahko spreminjna
SwissProt koda	se ne spreminja
DT	datum vnosa
DE	opis proteina
GN	ime gena
OS	organizem
RN	bibliografski podatki

```
.....
CC   -!- FUNCTION: LYSOZYMES HAVE PRIMARILY BACTERIOLYTIC FUNCTION; THOSE
CC       IN TISSUES AND BODY FLUIDS ARE ASSOCIATED WITH THE MONOCYTE-
CC       MACROPHAGE SYSTEM AND ENHANCE THE ACTIVITY OF IMMUNOAGENTS.
CC   -!- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages between N-
CC       acetyl-D-glucosamine and N-acetylmuramic acid in peptidoglycan
CC       heteropolymers of the prokaryotes cell walls.
CC   -!- SUBUNIT: MONOMER.
CC   -!- DISEASE: DEFECTS IN LYZ CAN BE THE CAUSE OF HEREDITARY NON-
CC       NEUROPATHIC SYSTEMIC AMYLOIDOSIS (OSTERTAG-TYPE) (AMYLOIDOSIS
CC       VIII).
CC   -!- MISCELLANEOUS: LYSOZYME C IS CAPABLE OF BOTH HYDROLYSIS AND
CC       TRANSGLYCOSYLATION; IT SHOWS ALSO A SLIGHT ESTERASE ACTIVITY. IT
CC       ACTS RAPIDLY ON BOTH PEPTIDE-SUBSTITUTED AND UNSUBSTITUTED
CC       PEPTIDOGLYCAN &, SLOWLY, ON CHITIN OLIGOSACCHARIDES.
CC   -!- MISCELLANEOUS: THE LYSOZYMES ISOLATED FROM HUMAN MILK AND FROM THE
CC       URINE OF PATIENTS WITH CHRONIC LEUKEMIA ARE IDENTICAL.
CC   -!- SIMILARITY: BELONGS TO FAMILY 22 OF GLYCOSYL HYDROLASES.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; J03801; AAA59535.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
.....
DR   PIR; A00849; LZHU.
DR   PIR; S04938; S04938.
.....
DR   PDB; 1EQ5; 19-APR-00. [ExPASy / RCSB]
DR   PDB; 1EQE; 19-APR-00. [ExPASy / RCSB]
DR   CarbBank; CCSD:42661; -.
DR   MIM; 153450; -. [NCBI / EBI]
DR   GeneCards; LYZ.
DR   GeneLynx; LYZ.
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CC komentarji

DR zapis v drugih zbirkah

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FT   SIGNAL        1     18
FT   CHAIN        19    148       LYSOZYME C.
FT   DISULFID     24    146
FT   DISULFID     48    134
FT   DISULFID     83     99
FT   DISULFID     95    113
FT   ACT_SITE     53     53
FT   ACT_SITE     71     71
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FT                                /FTId=VAR_004280.
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FT   CONFLICT     41     41       I -> M (IN REF. 2).
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FT   HELIX        23     32
FT   TURN         33     34
FT   TURN         36     37
FT   STRAND       38     38
FT   TURN         39     40
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FT   TURN        119    119
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FT   TURN        143    145
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     TNYNAGDRST DYGIFQINSR YWCNDGKTPG AVNACHLSCS ALLQDNIADA VACAKRVVRD
     PQGIRAWVAW RNRCQNRDVR QYVQGCGV
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```

FT *feature table*
lastnosti proteina

SQ aminokislinsko zaporedje

OBLIKA ZAPISA

Računalnik vs človek

GBFF

ASN.1

FASTA(Pearson) najbolj enostaven zapis

```
>P00695
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VRQYVQGCGV

>gi|4557894|ref|NP_000230.1| lysozyme precursor [Homo sapiens]
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TDYGIFQINSRYWCNDGKTPGAVNACHLSCSALLQDNIADAVACAKRVVRDPQGIRAWVAWRNRCQNRD
VRQYVQGCGV

>gi|4557893|ref|NM_000239.1| Homo sapiens lysozyme (renal amyloidosis)
(LYZ), mRNA
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GTCCAGGGCAAGGTCTTTGAAAGGTGTGAGTTGGCCAGAACTCTGAAAAGATTGGGAATGGATGGCTACA
GGGGAATCAGCCTAGCAAACTGGATGTGTTTGGCCAAATGGGAGAGTGGTTACAACACACGAGCTACAAA
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GGCAAAACCCCAGGAGCAGTTAATGCCTGTCATTTATCCTGCAGTGCTTTGCTGCAAGATAACATCGCTG
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Brookhaven Protein Data Bank 1973

RCSB PDB : Structure Explorer - Microsoft Internet Explorer

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- Structure Analysis
- Help

Structure Summary Biology & Chemistry Materials & Methods Sequence Details Geometry

1J4N

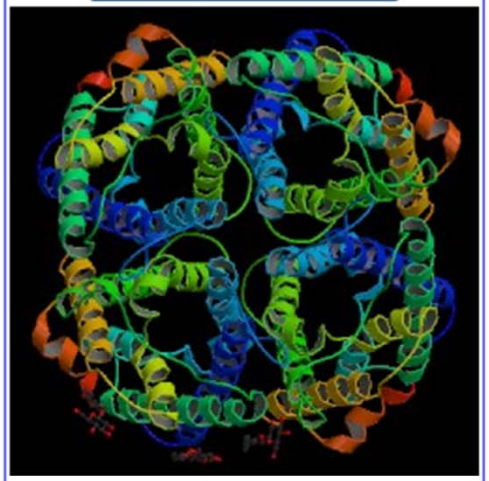
Title	Crystal Structure of the AQP1 water channel
Authors	Sui, H., Han, B.-G., Lee, J.K., Walian, P., Jap, B.K.
Primary Citation	**Sui, H., Han, B.G., Lee, J.K., Walian, P., Jap, B.K.** Structural basis of water-specific transport through the AQP1 water channel. *Nature v414 pp.872-878, 2001* [Abstract]
History	Deposition 2001-10-19 Release 2002-03-27
Experimental Method	Type x-ray diffraction Data N/A

Parameters	Resolution[Å]	R-Value	R-Free	Space Group
	2.20	0.266 (work)	0.308	I 4 2 2

Unit Cell						
Length [Å]	a	93.33	b	93.33	c	180.49
Angles [°]	alpha	90.00	beta	90.00	gamma	90.00

Images and Visualization

Biological Molecule



Display Options

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Jmol
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Protein Workshop
QuickPDB
All Images

Done

Internet

6. september 2006

start R SL 10:10

OSTALA BIOLOŠKA INFORMACIJA

OMIM, SPECIALIZIRANE PODATKOVNE ZBIRKE, SPLETNE STRANI RAZISKOVALCEV...

VIRI INFORMACIJ V SLOVENIJI

Izum, NUK, Lokalne knjižnice (CTK, IJS, biološka...)

PROGRAMI ZA ISKANJE IN UREJANJE REFERENC

TEKSTOVNE PODATKOVNE ZBIRKE (NCBI)

- **PubMed**

- **OMIM**
On-line Mendelian Inheritance in Man

Katalog človeških genov in bolezni s katerimi so povezani (=fenotipski dodatek človeškemu genomu).

Tekstovna informacija in reference, povezave na podatkovne zbirke znotraj NCBI in ostale.

Skupaj 19967 opisov (april 2010)

Iskanje s ključnimi besedami

- **BOOK-SHELF**

"on-line" knjig z vsebino mol biologije, biokemije, celične biologije... npr. Molecular Biology of the Cell (Alberts), Molecular Cell Biology (Lodish), Genomes (Brown), Biochemistry (Stryer)

- **PubMed Central**

Arhiv revij (>100) s področja naravoslovja v polnem tekstu!!!

NCBI- tekstovne podatkovne zbirke

- **PubMed**
- **OMIM**
- **BOOK-SHELF**
- **PubMed Central**

PubMed

Na NCBI. Prosto dostopna podatkovna zbirka.

http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=PubMed

Vsebuje citate iz MEDLINE in še dodatno informacijo
(nekatere druge revije, ki jih v MEDLINE ni)

MEDLINE: vsebuje bibliografsko informacijo 4300 revij iz 70 držav; vsebuje preko 11 mio citatov od 1960 naprej.
(OLDMEDLINE- 1958-1965)

PubMed Journal Browser*- informacija o revijah, iz katerih so članki v PubMed;* ***JournalLinkOutProvider****- povezave na spletne strani založnikov, ki imajo revije na spletu;* ***MeSH browser*** *(Medical Subject Heading)- pojmi, ki jih PubMed uporablja za indeksiranje člankov*

BOOK-SHELF

>50 “on-line” knjig z vsebino mol biologije, biokemije, celične biologije...

Iskanje gesel

Npr. Molecular Biology of the Cell (Alberts), Molecular Cell Biology (Lodish), Genomes (Brown), Biochemistry (Stryer)

PUB-MED CENTRAL

http://www.pubmedcentral.nih.gov/

Arhiv revij (>100) s področja naravoslovja v polnem tekstu!!!

Npr. EMBO J

Infection and Immunity

Journal of Bacteriology

The Plant Cell

Plant Physiology....

OMIM
Online Mendelian Inheritance in Man
Johns Hopkins University

OMIM

On-line Mendelian Inheritance in Man

http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=OMIM

Katalog človeških genov in bolezni s katerimi so povezani.
(=fenotipski dodatek človeškemu genomu)
Ureja dr. Victor A McKusick, John Hopkins University

Tekstovna informacija in reference, povezave na podatkovne zbirke znotraj NCBI in ostale.

Skupaj **22.236** opisov (februar 2014)

Iskanje s ključnimi besedami

Diseasome

Abstract

A network of disorders and disease genes linked by known disorder–gene associations offers a platform to explore in a single graph-theoretic framework all known phenotype and disease gene associations, indicating the common genetic origin of many diseases. Genes associated with similar disorders show both higher likelihood of physical interactions between their products and higher expression profiling similarity for their transcripts, supporting the existence of distinct disease-specific functional modules. We find that essential human genes are likely to encode hub proteins and are expressed widely in most tissues. This suggests that disease genes also would play a central role in the human interactome. In contrast, **we find that the vast majority of disease genes are nonessential and show no tendency to encode hub proteins, and their expression pattern indicates that they are localized in the functional periphery of the network.** A selection-based model explains the observed difference between essential and disease genes and **also suggests that diseases caused by somatic mutations should not be peripheral, a prediction we confirm for cancer genes.**

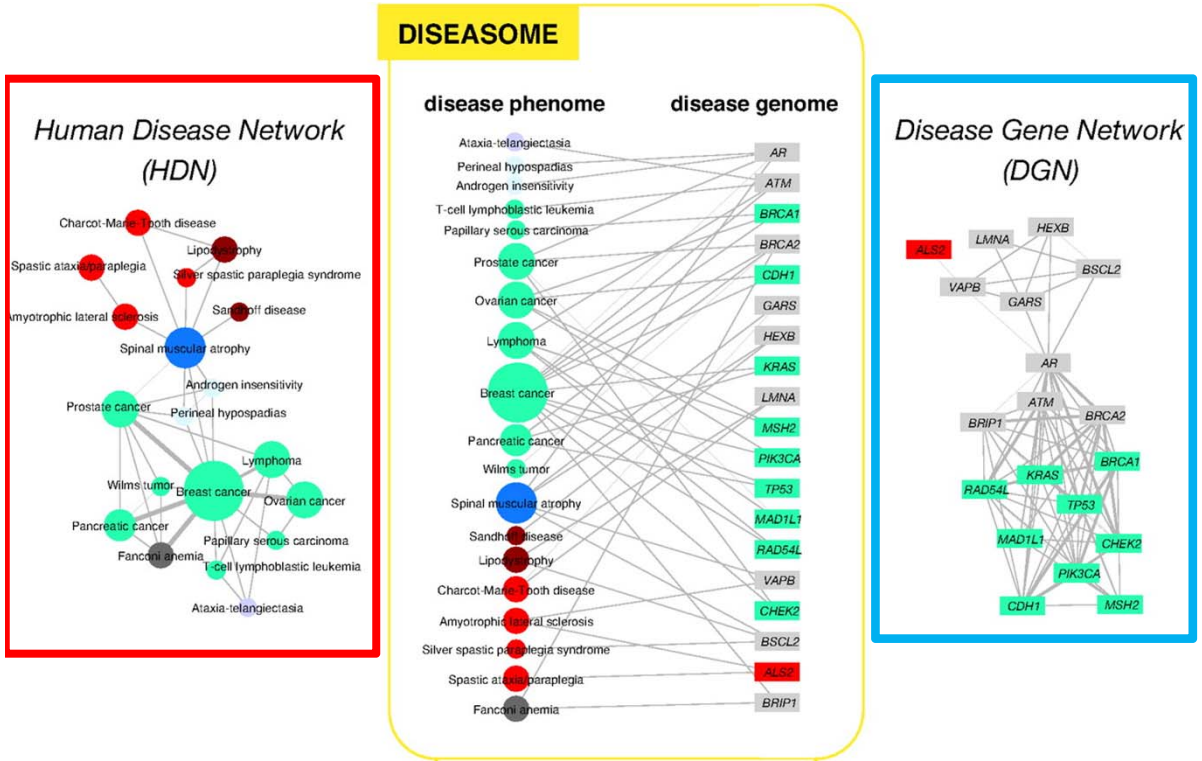
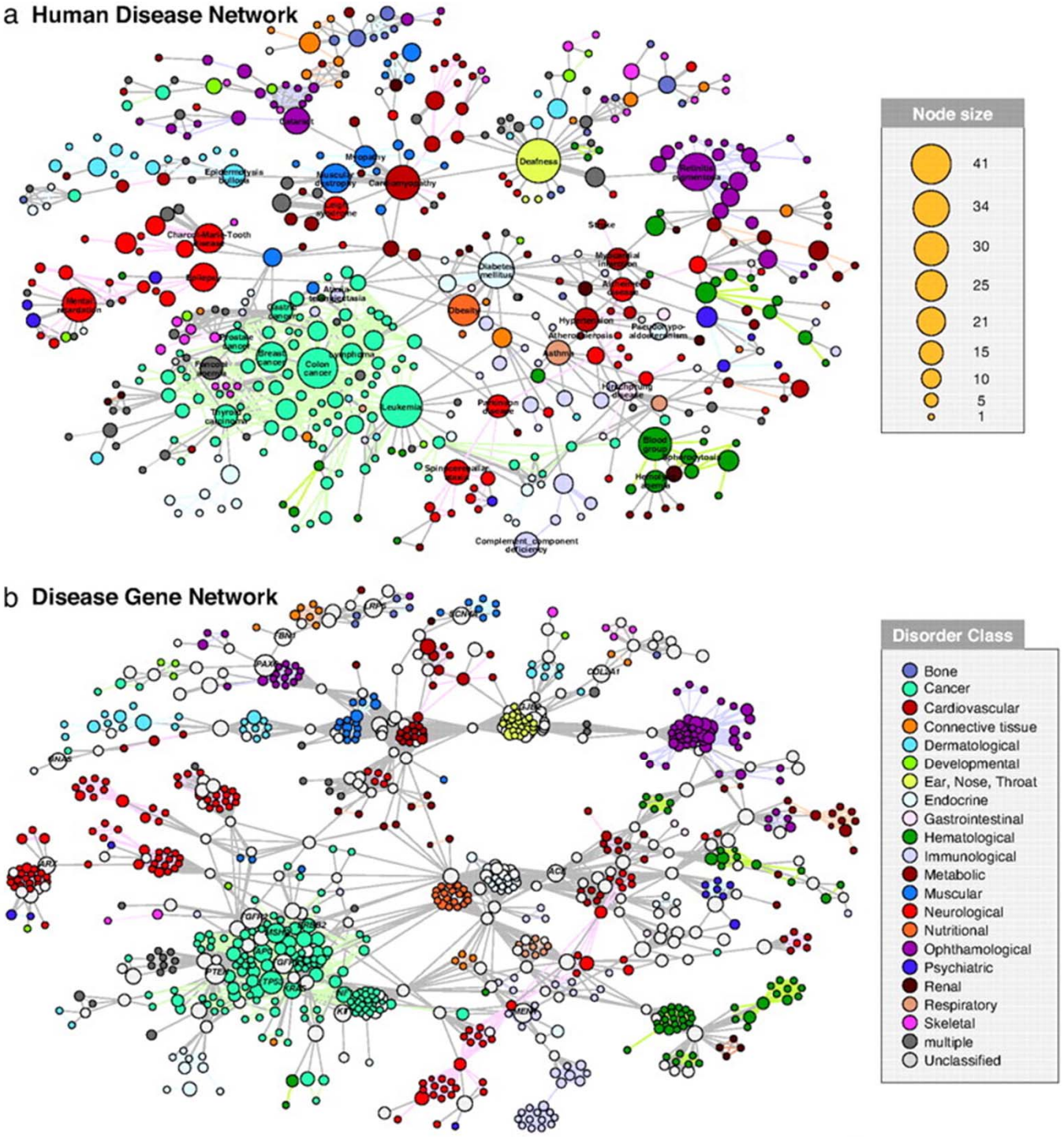


Fig. 1. Construction of the diseasome bipartite network. (*Center*) A small subset of OMIM-based disorder–disease gene associations (18), where circles and rectangles correspond to disorders and disease genes, respectively. A link is placed between a disorder and a disease gene if mutations in that gene lead to the specific disorder. The size of a circle is proportional to the number of genes participating in the corresponding disorder, and the color corresponds to the disorder class to which the disease belongs. (*Left*) The HDN projection of the diseasome bipartite graph**, in which two disorders are connected if there is a gene that is implicated in both. The width of a link is proportional to the number of genes that are implicated in both diseases.** For example, three genes are implicated in both breast cancer and prostate cancer, resulting in a link of weight three between them. (*Right*) The DGN projection **where two genes are connected if they are involved in the same disorder. The width of a link is proportional to the number of diseases with which the two genes are commonly associated**.

Goh KI et al. (2007) Human disease network. PNAS 104, 8685-8690.

Diseasome


a Human Disease Network
Node size
41
34
30
25
21
15
10
5
1
Deafness
Diabetes mellitus
Obesity
Colon cancer
Breast cancer
Leukemia
Asthma
Epilepsy
Charcot-Marie-Tooth disease
Mental retardation
Cardiomyopathy
Myopathy
Muscular dystrophy
Epidermolysis bullosa
Hypertension
Atherosclerosis
Pseudohypoaldosteronism
Prostate cancer
Pancreatic cancer
Thyroid carcinoma
Lymphoma
Ataxia-telangiectasia
Hearing disorder
Parkinson disease
Blood group
Complement component deficiency
b Disease Gene Network
Disorder Class
Bone
Cancer
Cardiovascular
Connective tissue
Dermatological
Developmental
Ear, Nose, Throat
Endocrine
Gastrointestinal
Hematological
Immunological
Metabolic
Muscular
Neurological
Nutritional
Ophthamological
Psychiatric
Renal
Respiratory
Skeletal
multiple
Unclassified

KAKO POISKATI INFORMACIJO?

Kaj potrebuješ (in a to res potrebuješ???)

INTERNET!!!!!!!!! vs Lokalne knjižnice

Splošni iskalniki (Google, Wikipedia) vs specializirani strežniki (Entrez)

- Pregledovanje kazal (TOC "Table of Contents"- online dostop po mailu).

  Večina revij ima na razpolago ta servis.

  Staro klasično prelistavanje revij!

- Iskanje člankov (specializirane podatkovne zbirke):

  prost dostop- npr. PubMed

  licenčne- npr. Science Direct (prost za uporabnike UL)

  odprt dostop- npr. PLOS Biology http://www.plosbiology.org

  Kazala vs polna besedila (pdf format)

- Ostala specializirana informacija, tekstovne podatkovne zbirke (npr. OMIM)

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IZUM- Inštitut informacijskih znanosti

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(CTK, IJS, na posameznih Oddelkih Biotehniške fakultete...)

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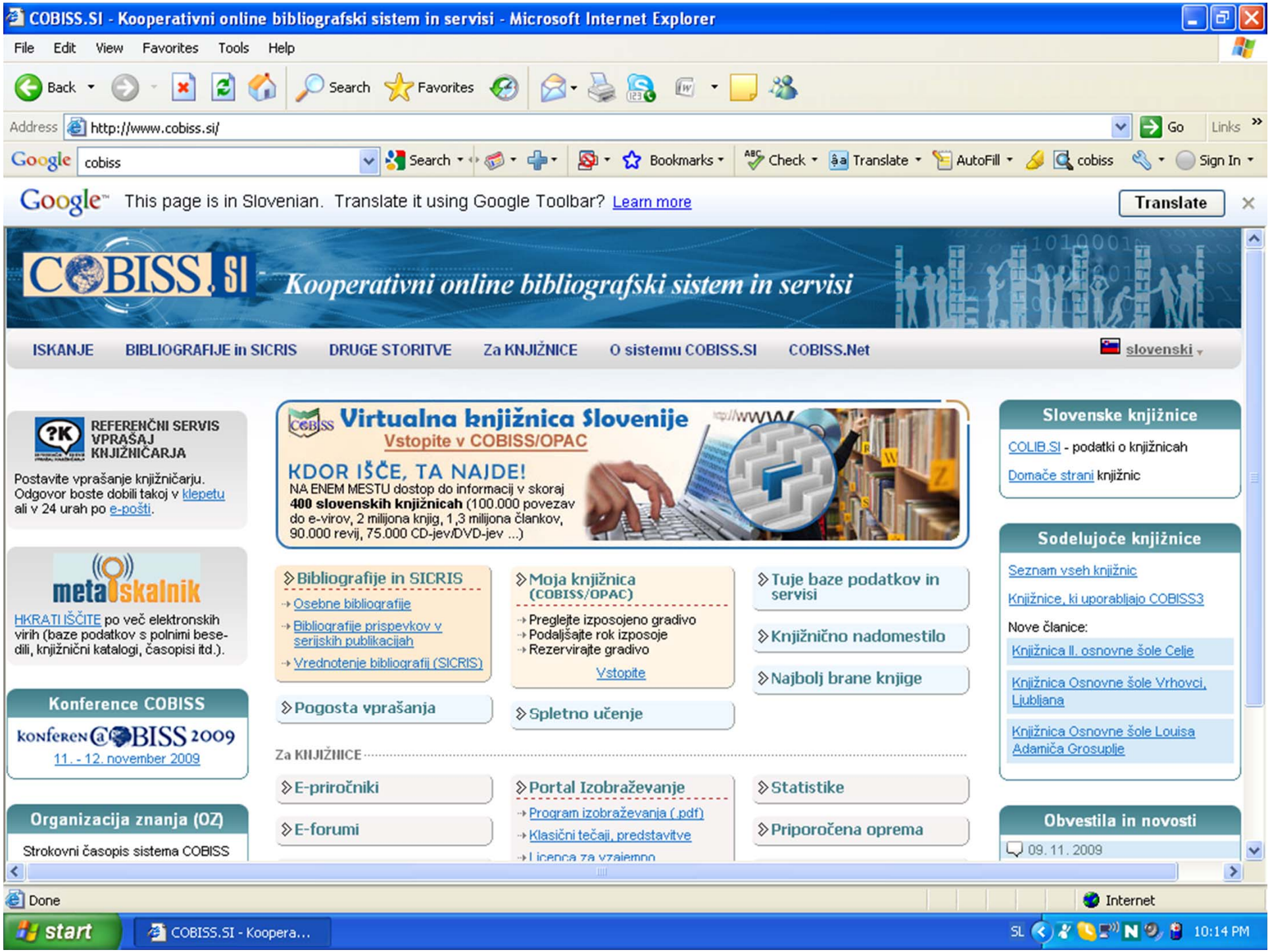
World's best Internet resource for Scientific, Technical and Medical Information. Using ScienceDirect you can access over 1,200 peer reviewed academic journals, search over 30 million abstracts from scientific articles and link out to articles from over 80 other publishers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CORES.SI - serijske publikacije: uredniki idr.

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ProQuest
EIFL Direct - EBSCOhost
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•Baza podatkov Journal Citation Reports
•Preko COBISSa dostop do nekaterih podatkovnih zbirk v tujini:
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EndNote

http://www.isiresearchsoft.com/en/enhome.htm

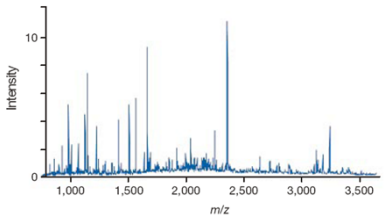
Reference Manager

http://www.refman.com/

- **Lastne podatkovne zbirke.**
- **Urejanje člankov in drugih bibliografskih podatkov.**
- **Iskanje (po interni bazi ali po internetu)**
- **Izmenjava z drugimi raziskovalci**
- **Priprava bibliografij v ustreznem formatu- zelo pomembno!!!!**
- **Navezava na programe in sisteme za pregledovanje povzetkov revij (npr. Reference Update)**

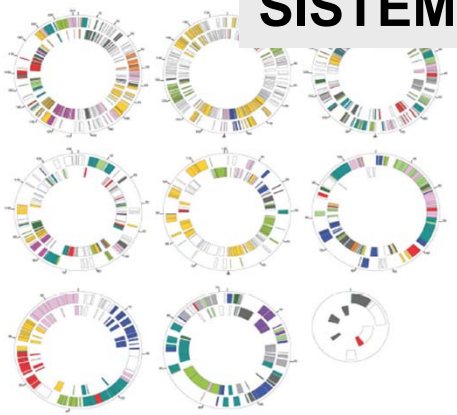
SISTEMSKA BIOLOGIJA

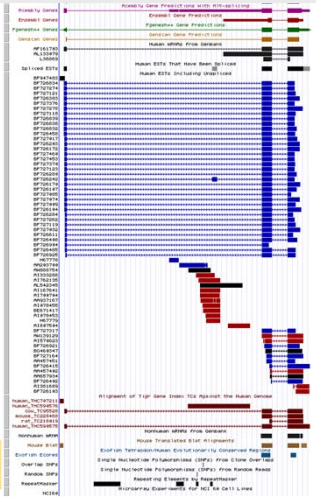
glikomika, lipidomika



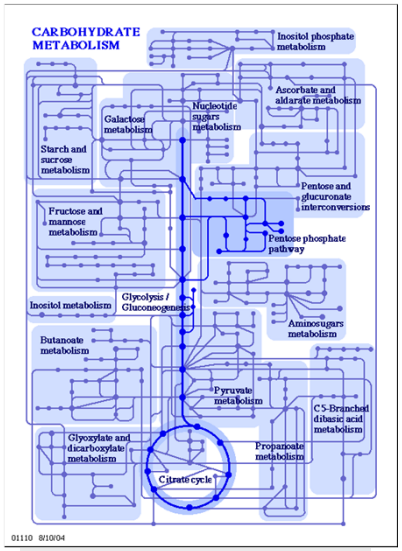
genomika

okoljska-
farmako-
primerjalna-
in silico predikcije

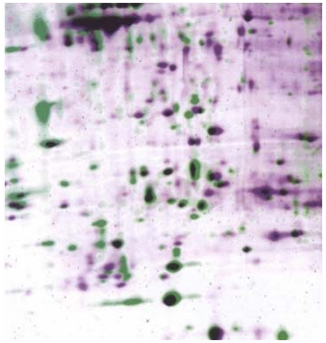


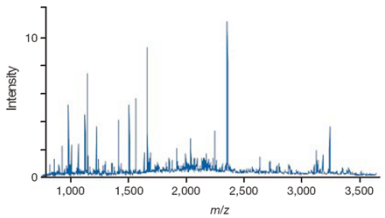


metabolomika

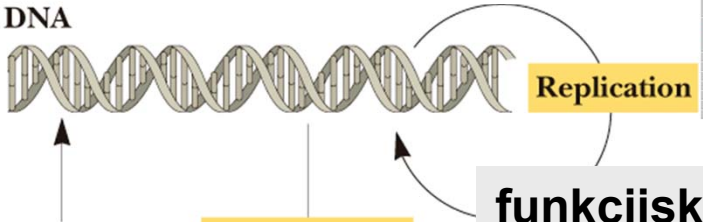


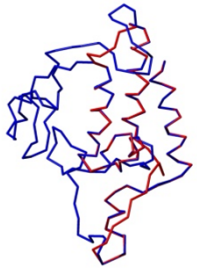
proteomika

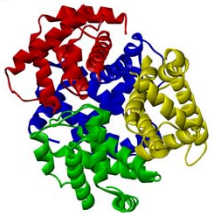


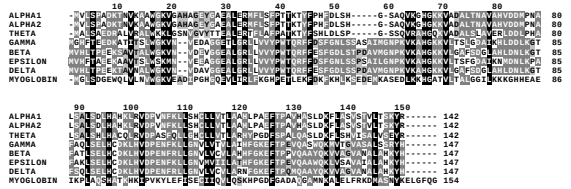


funkcijska genomika

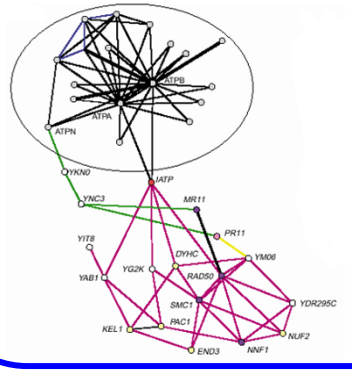






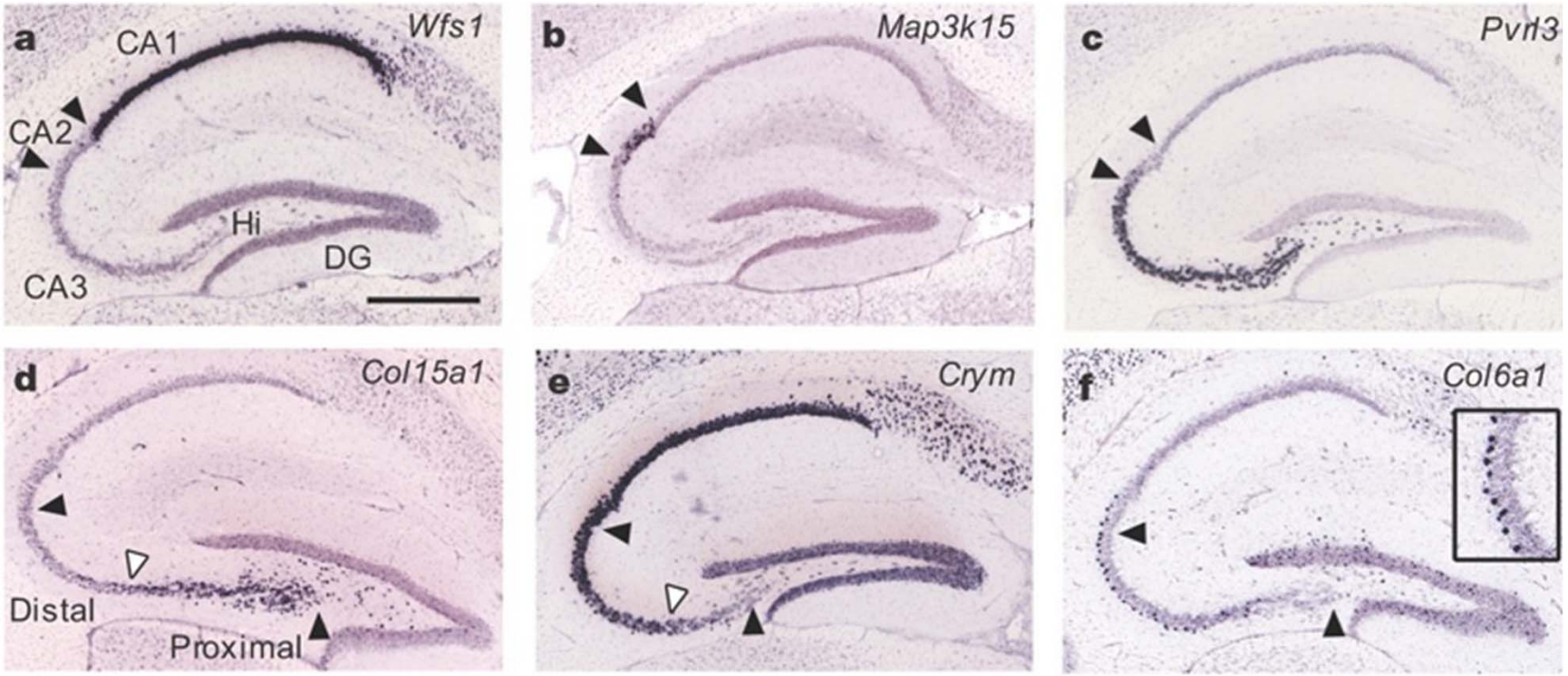


interaktomika

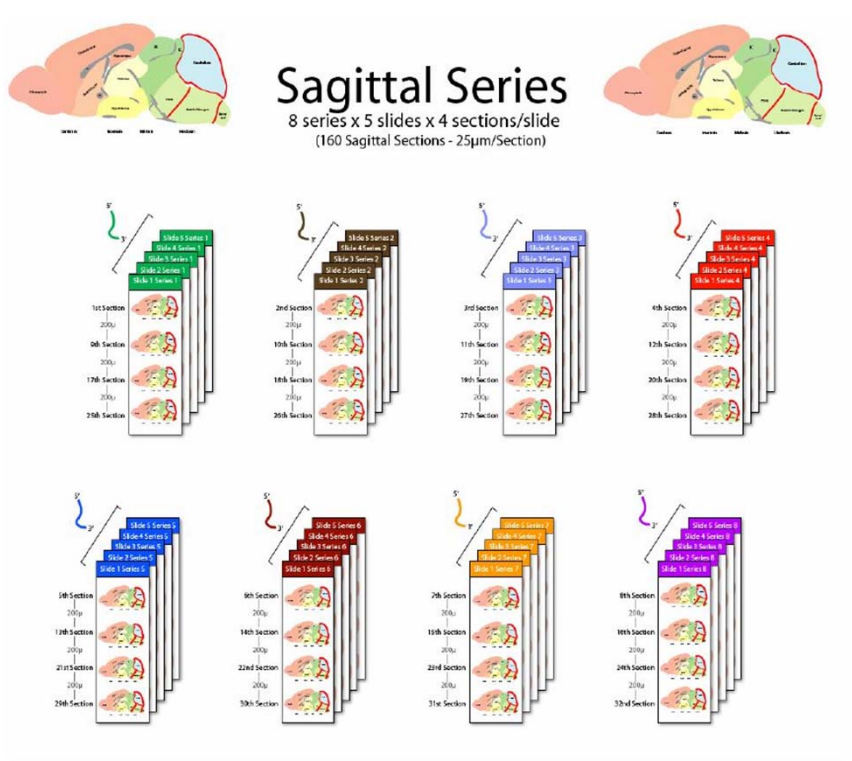


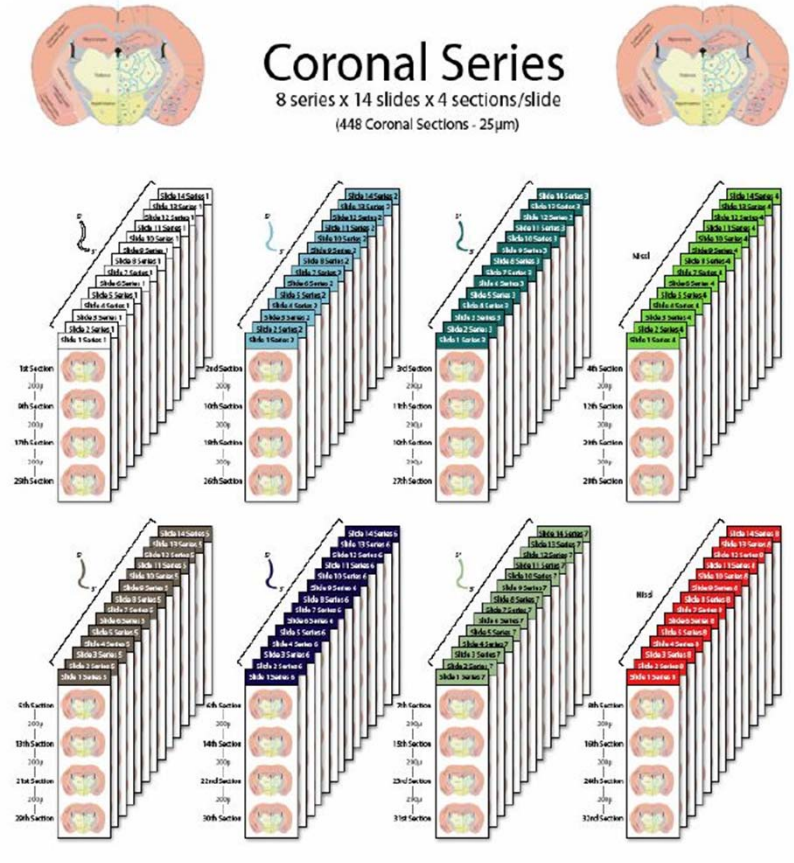
Genome-wide atlas of gene expression in the adult mouse brain

Lein ES et al. (2006) Nature 445(7124):168-176.



Serije stekelc





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- 10 stalno delujočih postaj za zajem slike (Image Capturing Systems, ICS)
  - Sestavljen iz mikroskopa, kamere, nalagalca stekelc, čitalca barkode in delovne postaje (računalnik z 2GB rama in 300 ali 400 GB trdim diskom)
  - Naloži stekelce
  - Poskenira barkodo in ustvari lokalno mapo za zbiranje slik
  - Z nekaj praznimi slikami preveri, če so barve pravilno kalibrirane
  - Locira posamezno rezino in pri različnih povečavah slika rezine, delček za delčkom
  - Slike naloži na ustreno lokacijo na mreži
  - Ko poslika vse štiri rezine na stekelcu, stekelce odloži v kaseto
  - Za eno stekelce porabi 15-20 minut

- **Ljudi potrebujejo le za dodajanje novih stekelc**

Rezultat

- 21500 genov
- Žrtvovanih več kot 6000 mišk
- 1000 stekelc oz. 4000 rezin možganov vsak dan
- 85 milijonov slik
- Povprečen dotok podatkov 1 TB (terabyte) /dan, skupno 600 TB
- Javno dostopno: http://www.brain-map.org