Lecture 1

Introduction to bioinformatics
- Basic definitions
- Scope of the course

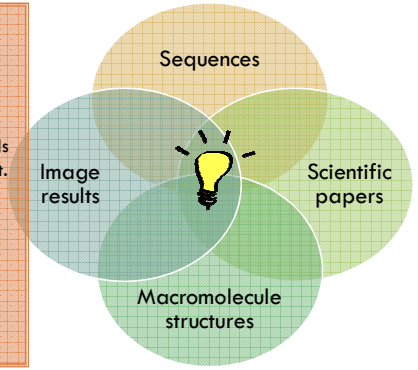
Internet bio-data resources
- NCBI
- EBI
- ExPASy
- Sanger Institute
- KEGG
- BRENDA

What does „data" mean in Bio-sciences?

We need to have an easy access to all existing information in our research field.

Amount of information extends traditional means of sharing it.

Hopefully bioinformatics analysis will enable us to discover the most reliable „truths" (the ones which are in accordance with all/the most of existing data).

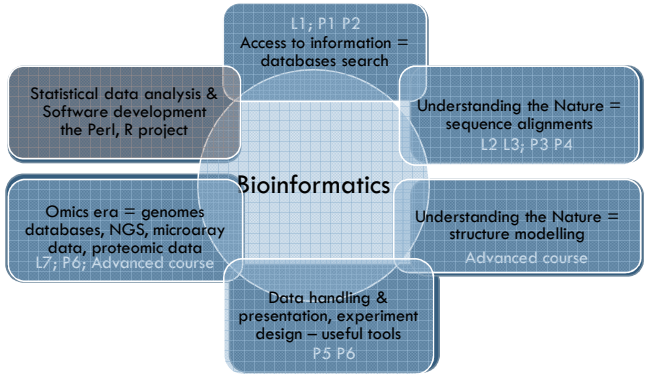


Definitions

According to National Institutes of Health (NIH):

- „**BIOINFORMATICS** is:
  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, analyze, or visualize such data**"
- „COMPUTATIONAL BIOLOGY is:
  the development and application of data-analytical and theoretical methods, mathematical modeling and computational simulation techniques to the study of biological, behavioral, and social systems".

Bioinformatics course



Scope of the Bioinformatics course

LECTURES (15 hours)
Dr Katarzyna Kubiak
Tue 12:15-14:00

PRACTICALS (30 hours)
MSc Natalia Kwiatos
Mon 8:30 – 11:00
Wed 11:15-14:00

- ECTS 2 credits
- Last lecture (25.Nov): **TEST**

Final mark up to 4.5 = sum of test & practical results

- 5 – after oral questioning

- **START: 6th of October**
- 6 individual exercises
- Small project in pairs finished with presentation

The course website

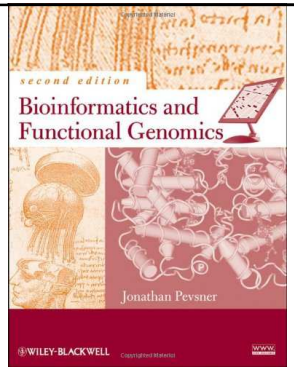
http://bioinformatics.p.lodz.pl

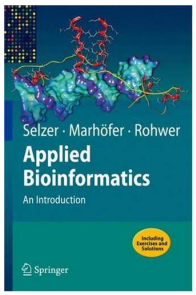
- *Timetable with lectures/laboratoty topics*
- Weekly updated downloads:
  - Whole lectures & printouts
- Useful links
- Now available: lectures from the last academic year

Passwords:

L1 INTRO; L2 DATA; L3 BLAST; L4 MULTI; L5 PROT; L6 GENE

All software used during this course is free available online





Textbooks in English (available at my office: room9, BiNoZ ground floor)

The course has no required textbook.

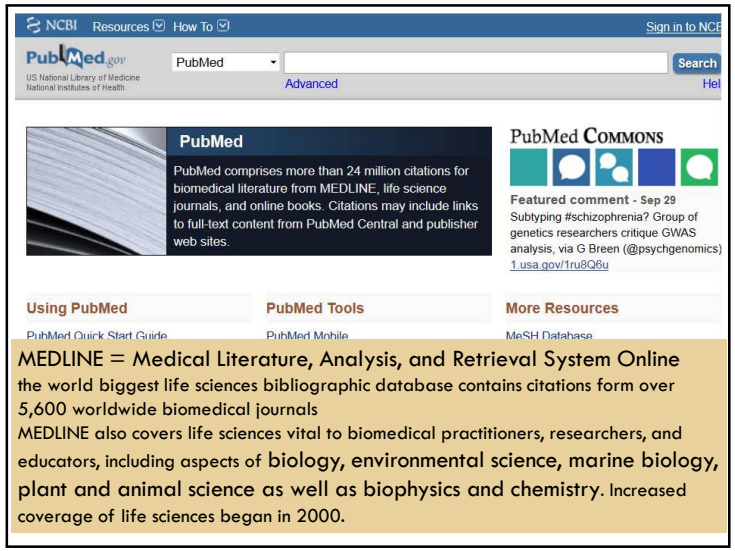
The lectures in this course correspond to a few chapters of Jonathan Pevsner *Bioinformatics and Functional genomics*, Wiley-Blackwell, 2009. Author's lectures and additional documents are there available on the publisher website (http://www.bioinfbook.org/)

Common websites with access to data and tools

NCBI - National Center for Biotechnology Information (USA)
- GenBank; RefSeq, PubMed; OMIM
- BLAST

EBI – European Bioinformatics Institute
- ENA; UniProt; ArrayExpress;
- Euro PubMed;

ExPASy - Expert Protein Analysis System
- UniProt; prosite; 2D-page results
- Great source of protein & proteomic **tools** (e.g. SWISS Model)

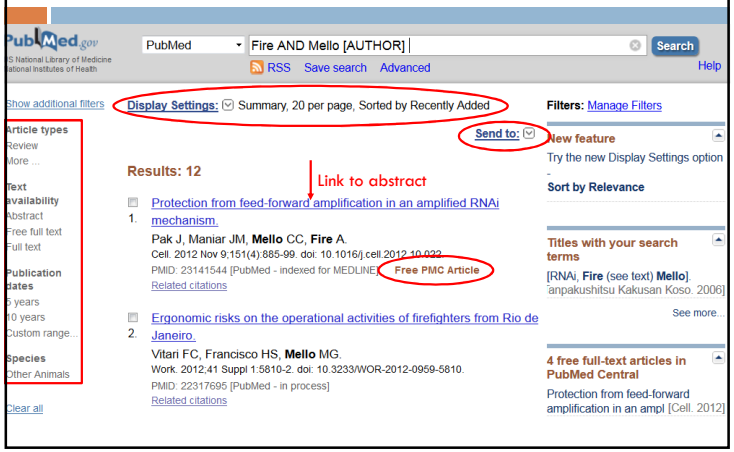


MEDLINE = Medical Literature, Analysis, and Retrieval System Online

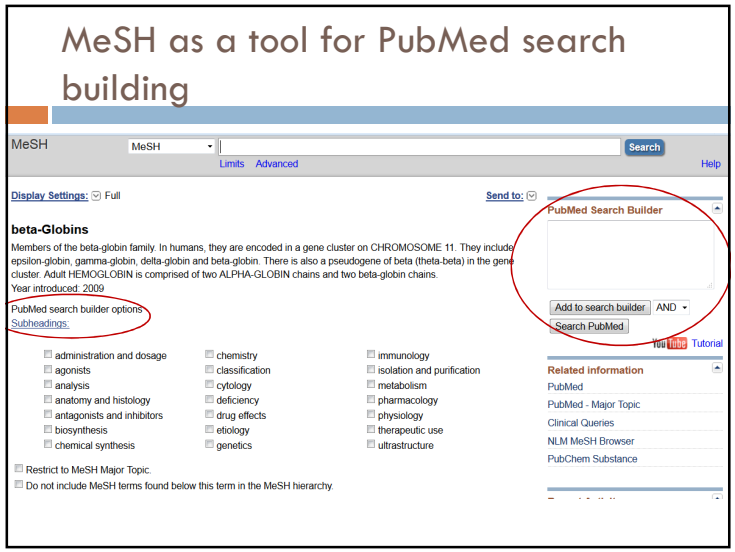
the world biggest life sciences bibliographic database contains citations form over 5,600 worldwide biomedical journals

MEDLINE also covers life sciences vital to biomedical practitioners, researchers, and educators, including aspects of biology, environmental science, marine biology, plant and animal science as well as biophysics and chemistry. Increased coverage of life sciences began in 2000.

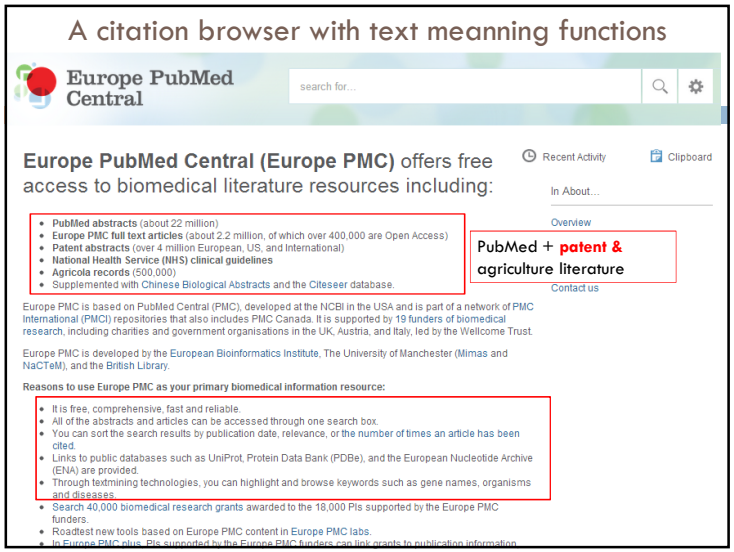
PubMed list of results

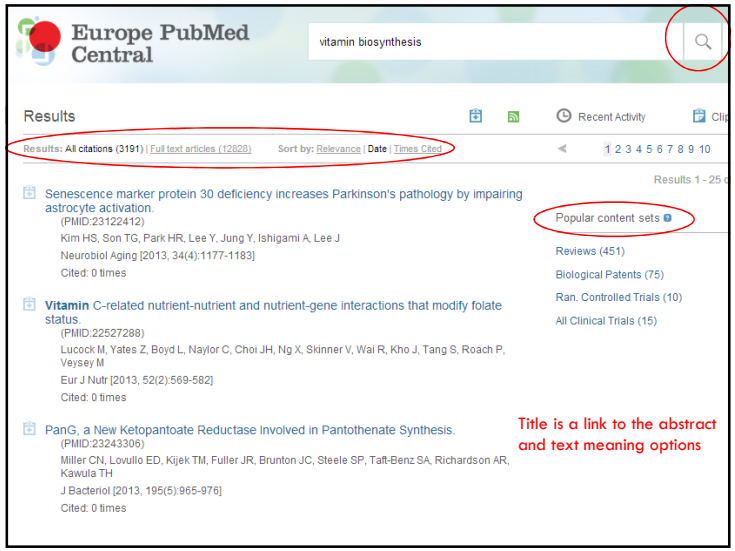


MeSH as a tool for PubMed search building



A citation browser with text meanning functions

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Senescence marker protein 30 deficiency increases Parkinson's pathology by impairing astrocyte activation.
(PMID:23122412)
Kim HS, Son TG, Park HR, Lee Y, Jung Y, Ishigami A, Lee J
Neurobiol Aging [2013, 34(4):1177-1183]
Cited: 0 times
Vitamin C-related nutrient-nutrient and nutrient-gene interactions that modify folate status.
(PMID:22527288)
Lucock M, Yates Z, Boyd L, Naylor C, Choi JH, Ng X, Skinner V, Wai R, Kho J, Tang S, Roach P, Veysey M
Eur J Nutr [2013, 52(2):569-582]
Cited: 0 times
PanG, a New Ketopantoate Reductase Involved in Pantothenate Synthesis.
(PMID:23243306)
Miller CN, Lovullo ED, Kijek TM, Fuller JR, Brunton JC, Steele SP, Taft-Benz SA, Richardson AR, Kawula TH
J Bacteriol [2013, 195(5):965-976]
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Miller CN, Lovullo ED, Kijek TM, Fuller JR, Brunton JC, Steele SP, Taft-Benz SA, Richardson AR, Kawula TH
Department of Microbiology and Immunology, School of Medicine, University of North Carolina, Chapel Hill, North Carolina, USA.
Journal of Bacteriology [2013, 195(5):965-976]
Type: Journal Article
DOI: 10.1128/JB.01740-12
Abstract
Highlight Terms
Gene Ontology(2)
Diseases(1)
Genes/Proteins(2)
Species(15)
Chemicals(4)
Pantothenate, commonly referred to as vitamin B(5), is an essential molecule in the metabolism of living organisms and forms the core of coenzyme A. Unlike humans, some bacteria and plants are capable of de novo biosynthesis of pantothenate, making this pathway a potential target for drug development. Francisella tularensis subsp. tularensis Schu S4 is a zoonotic bacterial pathogen that is able to synthesize pantothenate but is lacking the known ketopantoate reductase (KPR) genes, panE and ilvC, found in the canonical Escherichia coli pathway. Described herein is a gene encoding a novel KPR, for which we propose the name panG (FTT1388), which is conserved in all sequenced Francisella species and is the sole KPR in Schu S4. Homologs of this KPR are present in other pathogenic bacteria such as Enterococcus faecalis, Coxiella burnetii, and Clostridium difficile. Both the homologous gene from E. faecalis V583 (EF1861) and E. coli panE functionally complemented Francisella novicida lacking any KPR. Furthermore, panG from F. novicida can complement an E. coli KPR double mutant. A Schu S4 ΔpanG strain is a pantothenate auxotroph and was genetically and chemically complemented with panG in trans or with the addition of pantoiactone. There was no virulence defect in the Schu S4 ΔpanG strain compared to the wild type in a mouse model of pneumonic tularemia. In summary, we characterized the pantothenate pathway in Francisella novicida and F. tularensis and identified an unknown and previously uncharacterized KPR that can convert 2-dehydropantoate to pantoate. PanG.
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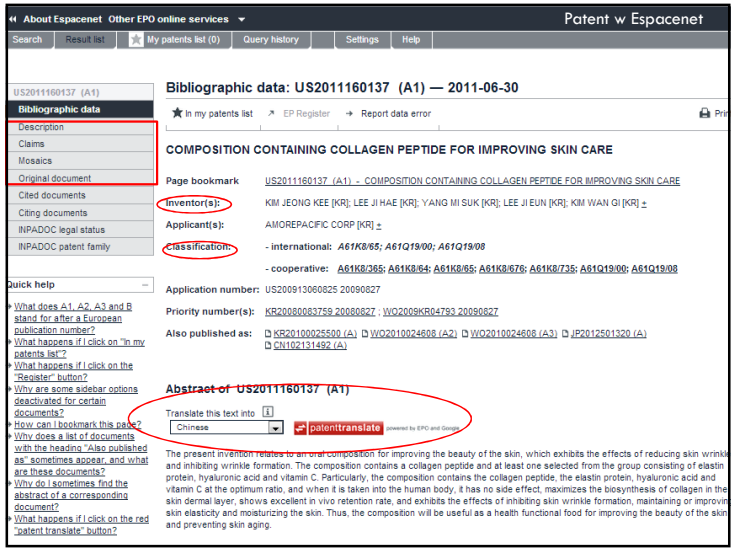
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US2011160137 (A1) - COMPOSITION CONTAINING COLLAGEN PEPTIDE FOR IMPROVING SKIN CARE
Inventor(s):
KIM JEONG KEE [KR]; LEE JI HAE [KR]; YANG MI SUK [KR]; LEE JI EUN [KR]; KIM WAN GI [KR]
Applicant(s):
AMOREPACIFIC CORP [KR]
Classification:
- international: A61K8/65; A61Q19/00; A61Q19/08
- cooperative: A61K8/365; A61K8/64; A61K8/65; A61K8/676; A61K8/735; A61Q19/00; A61Q19/08
Application number: US20091060825 20090827
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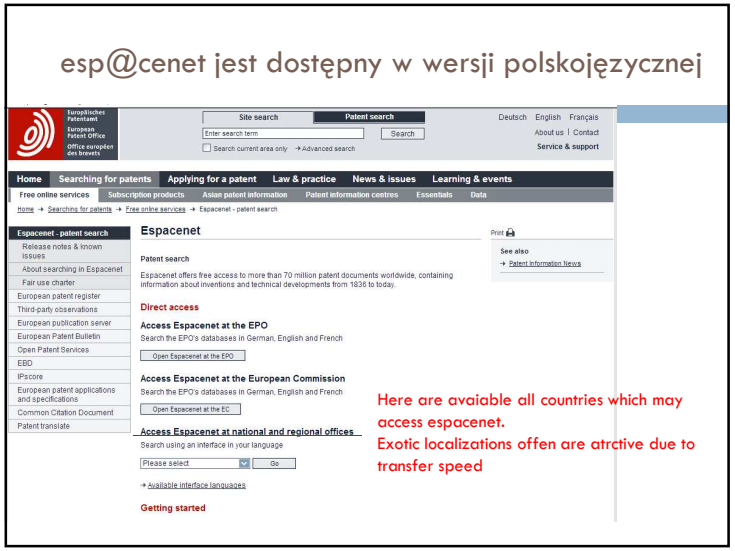
KR20100025500 (A)
WO2010024608 (A2)
WO2010024608 (A3)
JP2012501320 (A)
CN102131492 (A)
Abstract of US2011160137 (A1)
Translate this text into
Chinese
patenttranslate
The present invention relates to an oral composition for improving the beauty of the skin, which exhibits the effects of reducing skin wrinkle and inhibiting wrinkle formation. The composition contains a collagen peptide and at least one selected from the group consisting of elastin protein, hyaluronic acid and vitamin C. Particularly, the composition contains the collagen peptide, the elastin protein, hyaluronic acid and vitamin C at the optimum ratio, and when it is taken into the human body, it has no side effect, maximizes the biosynthesis of collagen in the skin dermal layer, shows excellent in vivo retention rate, and exhibits the effects of inhibiting skin wrinkle formation, maintaining or improving skin elasticity and moisturizing the skin. Thus, the composition will be useful as a health functional food for improving the beauty of the skin and preventing skin aging.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Exotic localizations offen are atrctive due to transfer speed

Biotechnology = subclass C12

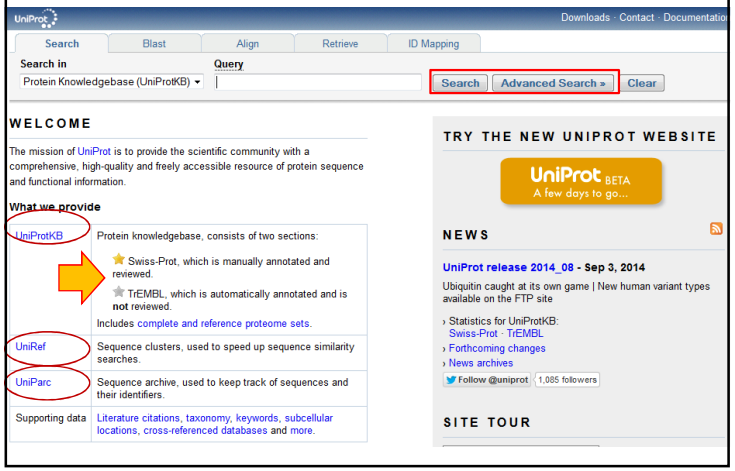
ExPASy: proteomic server → bioinformatics resource

UniProt

UniProt is the most comprehensive, centralized protein sequence catalog, it consists of 3 databases:

- **Swiss-Prot** best-annotated protein database at Swiss Institute of Bioinformatics
- **The Translated EMBL** (TrEMBL) Nucleotide Sequence Database Library provides automated annotations of proteins not in Swiss-Prot
- **PIR** (Protein Information Resource) Protein Sequence Database curated by experts from Georgetown University

SIB EMBL-EBI PIR



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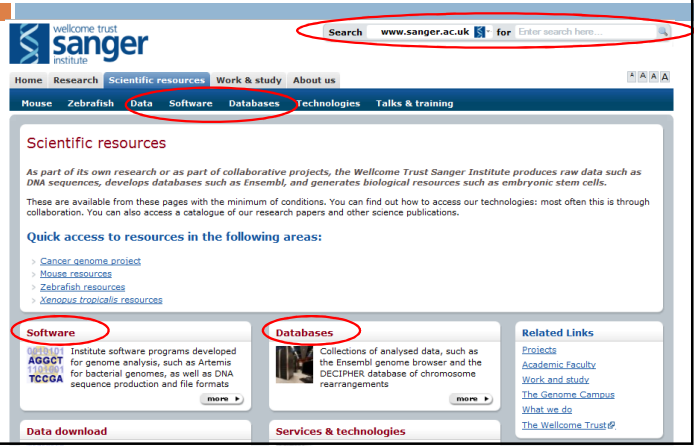
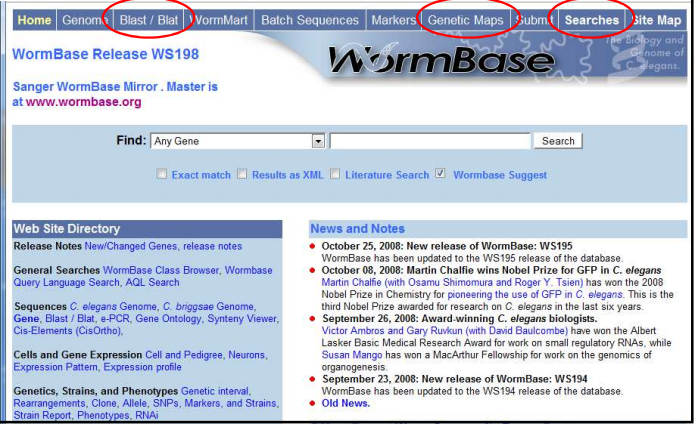
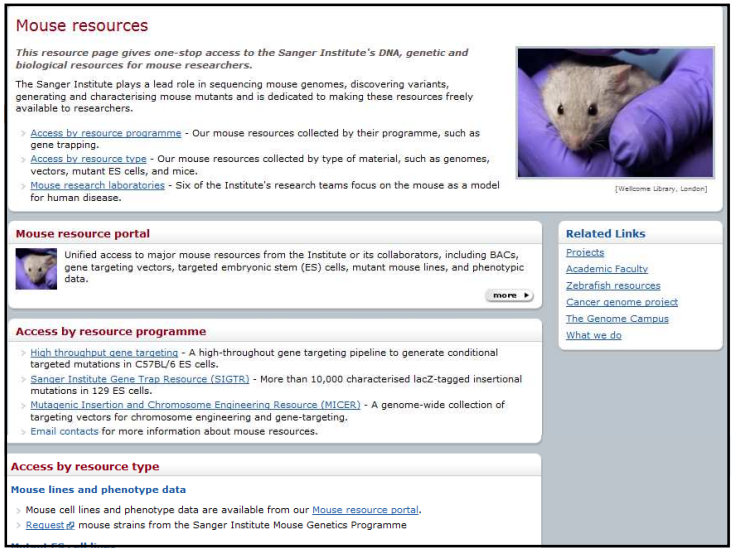


Model organisms

- BACTERIA: *Escherichia coli* K-12
  4.6 Mb genome sequenced in 1997
- YEAST: *Saccharomyces cerevisiae* (12.5 Mb)
  First Eukaryotic genome sequenced (in1996)
- PLANT: *Arabidopsis thaliana* (125 Mb)
  First plant (second Eukaryotic) genome sequenced in 2000
- FRUITFLY: *Drosophila melanogaster* (137 Mb)
  model for genetics; sequencing finished in 2000
- NEMATODE: *Caenorhabditis elegans* (100.2 Mb)
  first multicellular animal sequenced (in 1998), exacly 595 somatic cells, transparent body
- FISH: *Danio rerio* (1.8Gb !)
  short generation time, large amount of progeny, well annotated genes
- MAMMAL: *Mus musculus* sequenced in 2002 (3 Gb)
  Rodents diverged from primetes ~80MYA and share most genes with humans

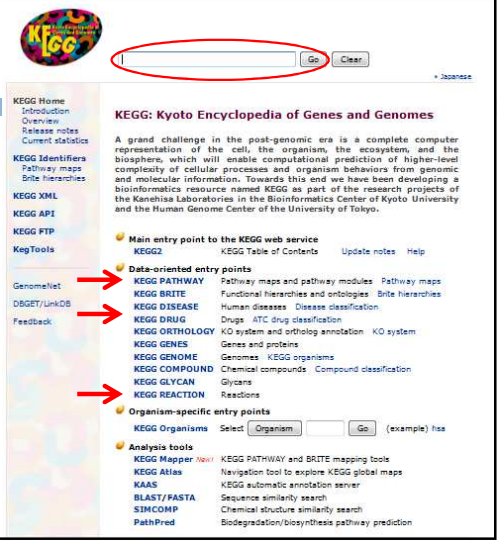
Example of model organism webpage



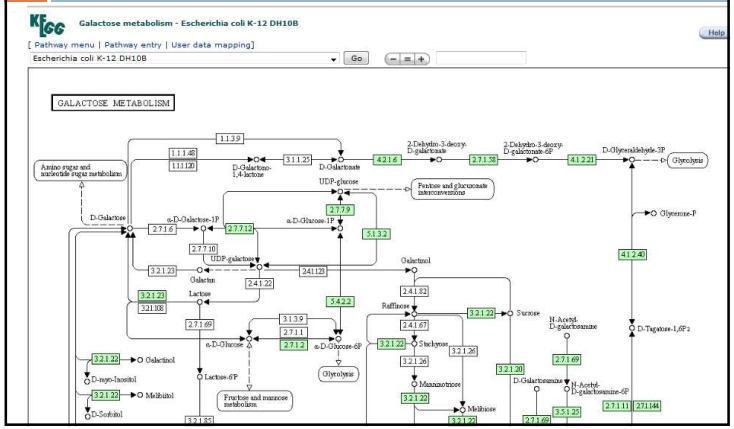


KEGG

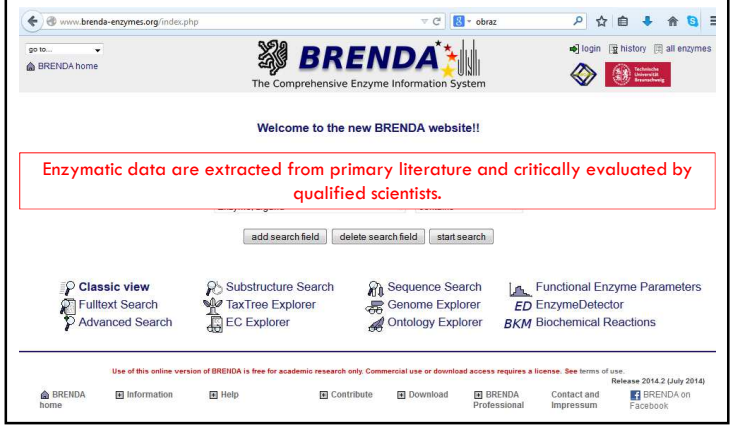
- **K**yoto **E**ncyclopedia of **G**enes and **G**enomes
- Extremely useful for methabolic pathways – focused searches



Green boxes = enzymes active in selected organism



BRENDA at the Institute of Biochemistry and Bioinformatics at the Technical University of Braunschweig, Germany



Take-home messages

- Bioinformatics help scientists to understand their laboratory results and to keep their research up to date
- Biological data is collected in databases, most of them are freely available online
- Data in bioinformatics may be: scientific publications, sequences & structures of macromolecules, organism – focused information, metabolic pathways etc…
- There are bioinformatics websites enabling the access to all these kinds of information (such as NCBI, EBI and ExPASy)