University of Warsaw
Faculty of Mathematics, Informatics and Mechanics

Uniwersytet Warszawski

Architecture of large projects in bioinformatics (ADP)

Lecture 02

Łukasz P. Kozłowski

lukaskoz@mimuw.edu.pl

Warsaw, 2024

1. Data formats in bioinformatics

2. Popular software libraries (BioPerl, BioPython)

3. Most important bioinformatics databases (UniProt, PDB, RefSeq, GenBank, ENA, InterPro, etc.)

4. Software licensing for scientific purposes. Free-software licensing. Patents.

5. Generic model Organism database (GMOD) project - assumptions, history and usage

6. Genome browsers, problem description and state of the solutions

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The essay: mini-review about specific bioinformatics topic

Exemplary subjects
Review about available software for:
– Structural biology (proteins, RNA, drugs)
– Phylogenetics
– NGS
– Chemoinformatics
– Data warehouse in bioinformatics (e.g. Biomart)
– Genomics (e.g. chip-seq)
– Machine learning (clustering, classification, deep learning, etc.)
– Image processing from microscopes/scanners etc.
– own suggestions ...?

You had 1 week to decide/find the subject.

Please send your proposition to ***lukaskoz@mimuw.edu.pl*** *with the email subject* ***ADP24_essay_Surname_Name***

Popular software libraries

Perl → BioPerl

Popular software libraries

Perl → BioPerl

Php → BioPHP

Popular software libraries

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Java → BioJava

Popular software libraries

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Popular software libraries

Python → BioPython, but also Cogent3, bioconda

Frequently solving bioinformatic problem also means that you will use some custom, small libraries (often with multiple bugs)

Popular software libraries

Python → BioPython, but also pyCogent, bioconda

Frequently solving bioinformatic problem also means that you will use some custom, small libraries (often with multiple bugs)

For statistics and machine learning:

LIBSVM

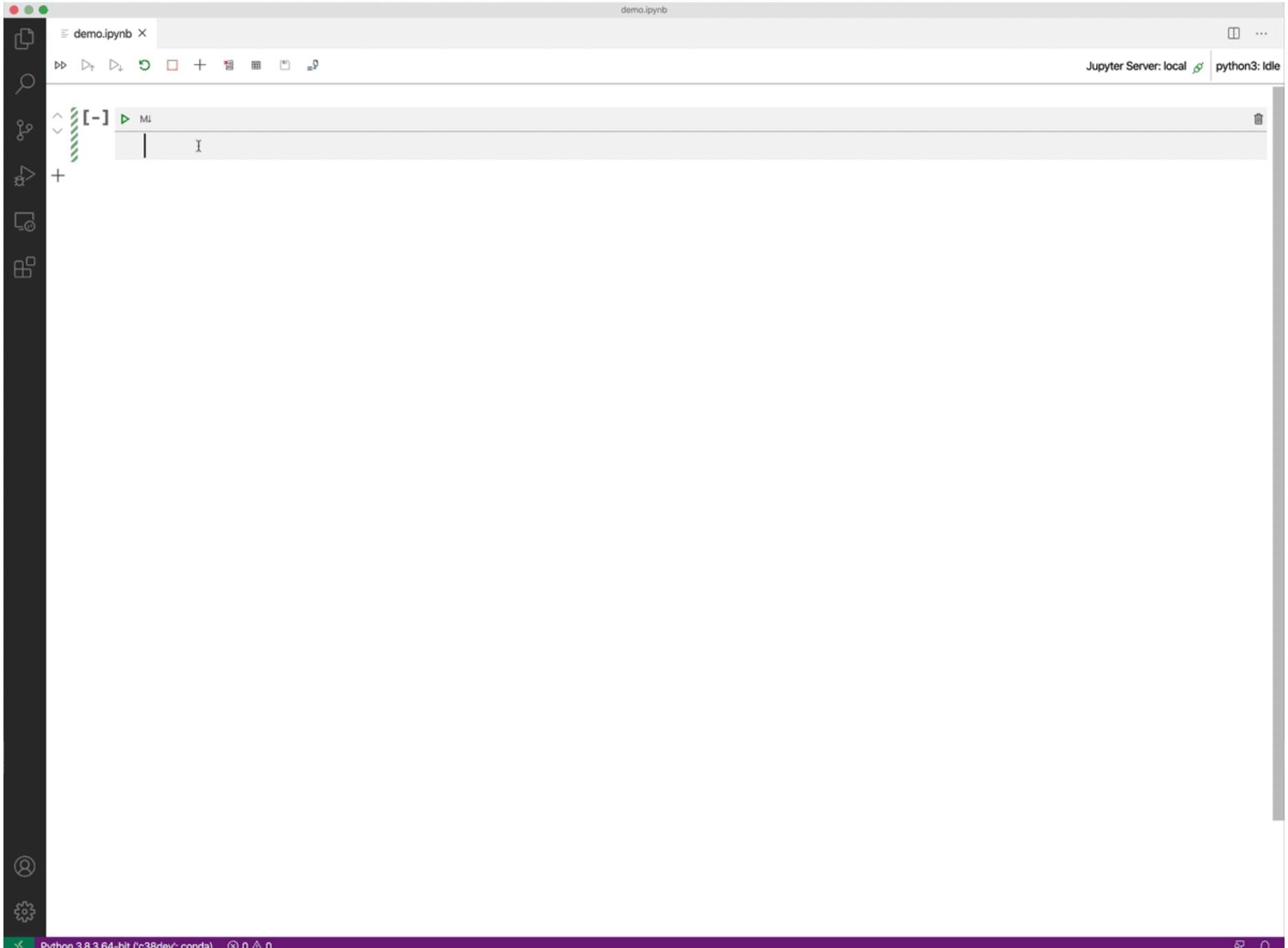
Popular software libraries

Popular software libraries

Popular software libraries

Cogent3 (as an alternative to biopython)

Popular software libraries



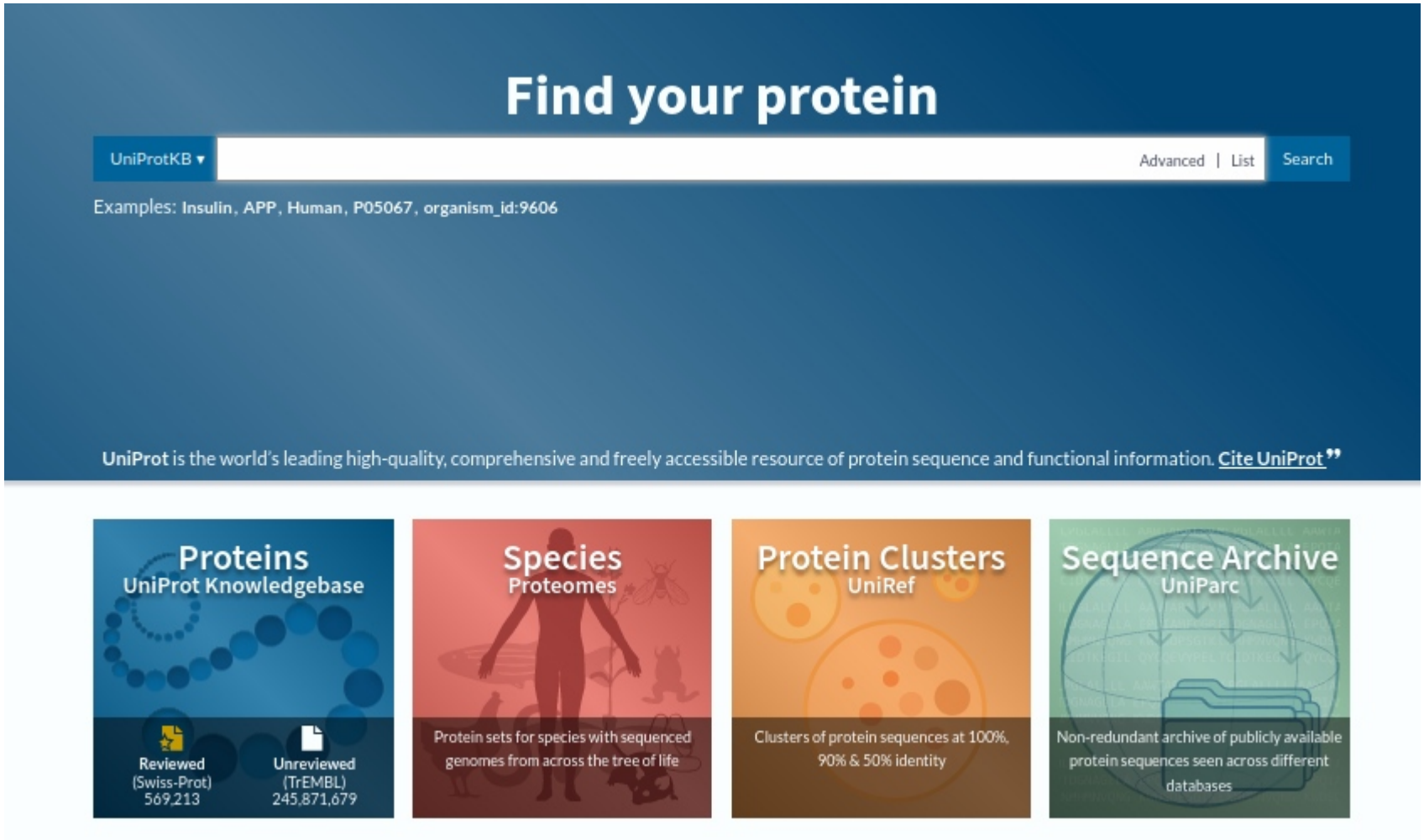
Most important bioinformatics databases

Most important bioinformatics databases

UniProt

> 230M

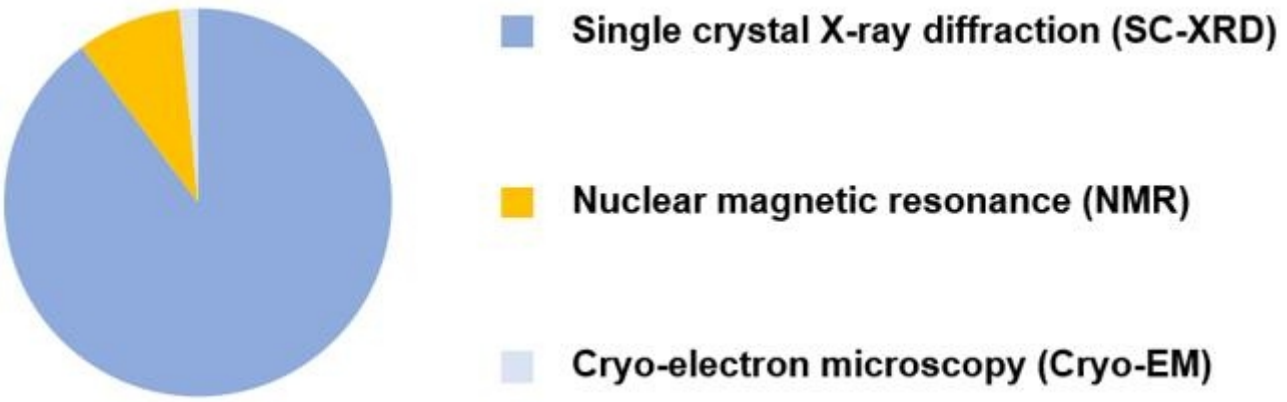
https://www.uniprot.org



Most important bioinformatics databases

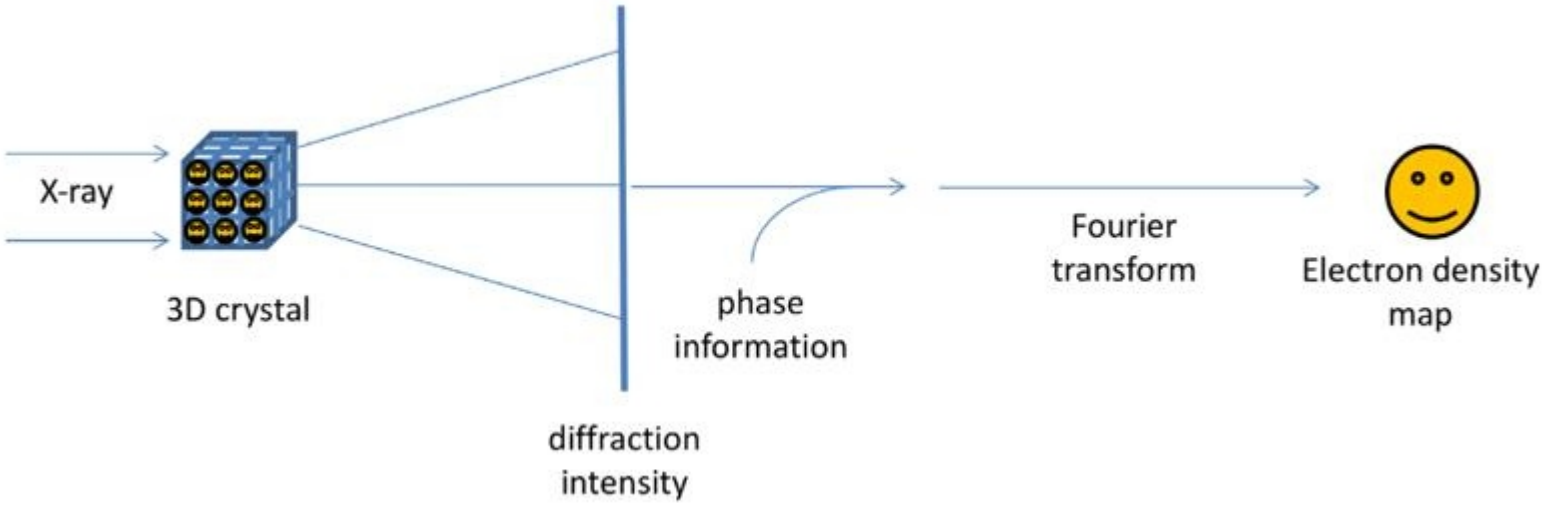
Most important bioinformatics databases

RCSB PDB
PROTEIN DATA BANK



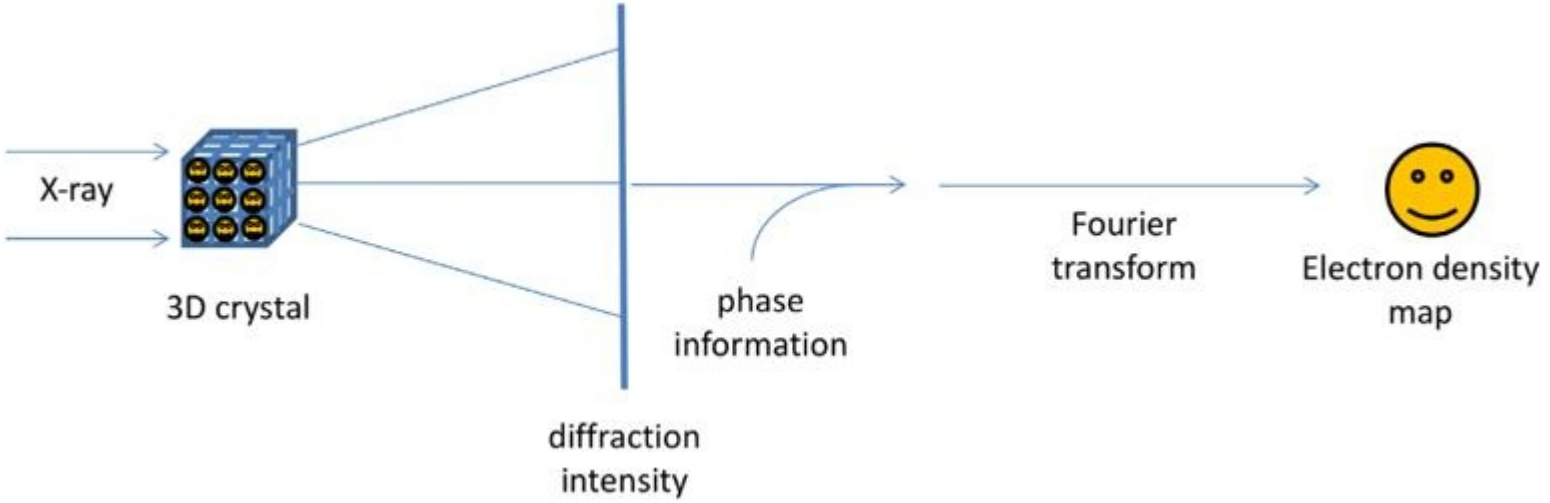
X-ray diffraction

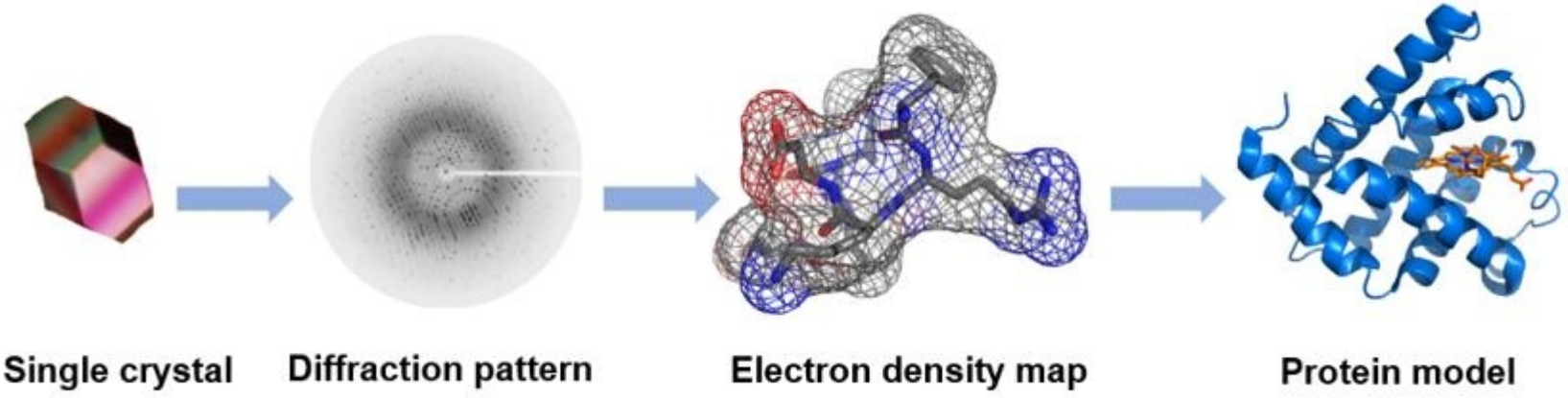
ADP



https://www.creative-biostructure.com/comparison-of-crystallography-nmr-and-em_6.htm

X-ray diffraction





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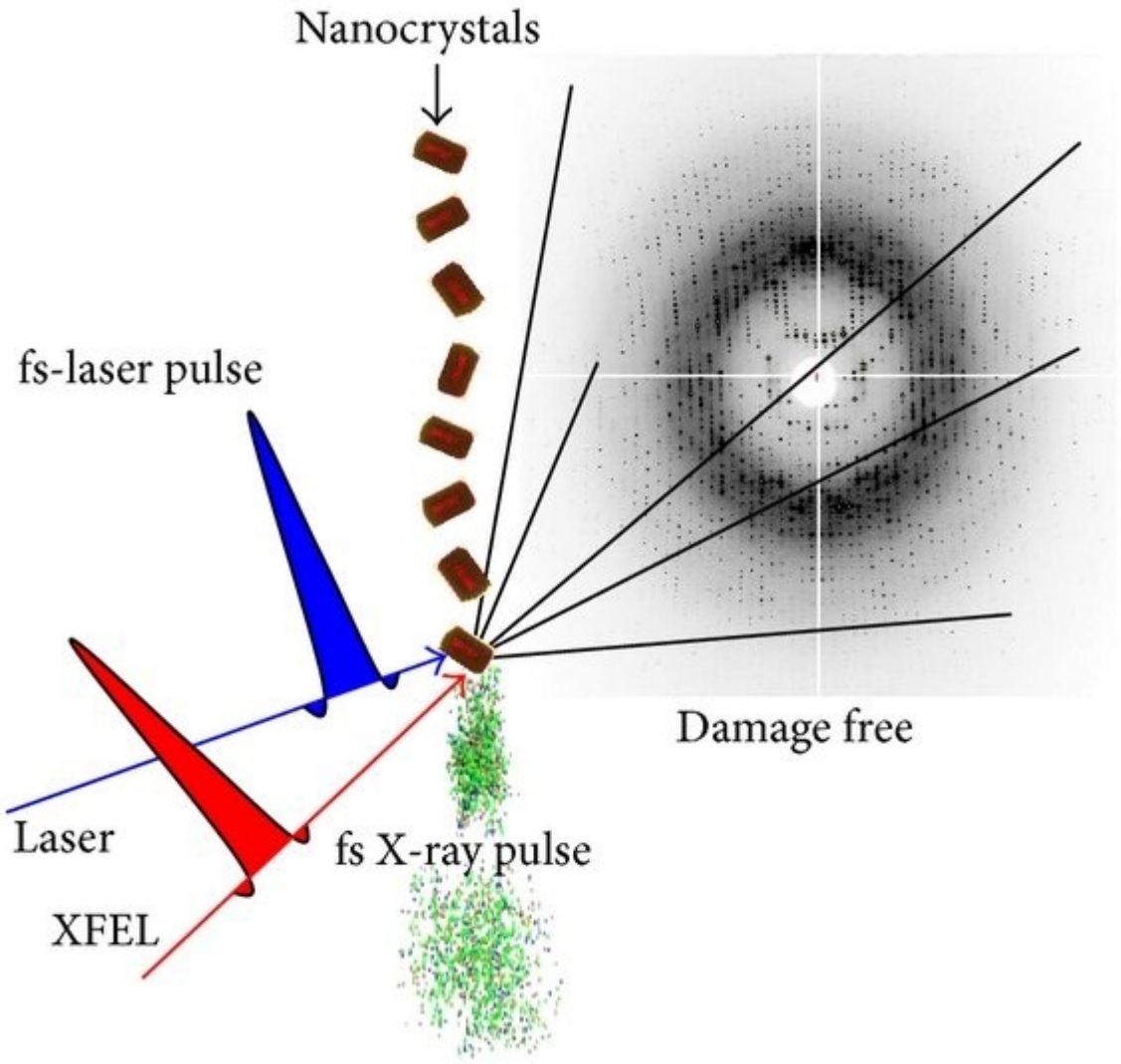
XFEL - X-ray free electron lasers

ADP



For more watch: https://www.youtube.com/watch?v=-VMDytbTbNw

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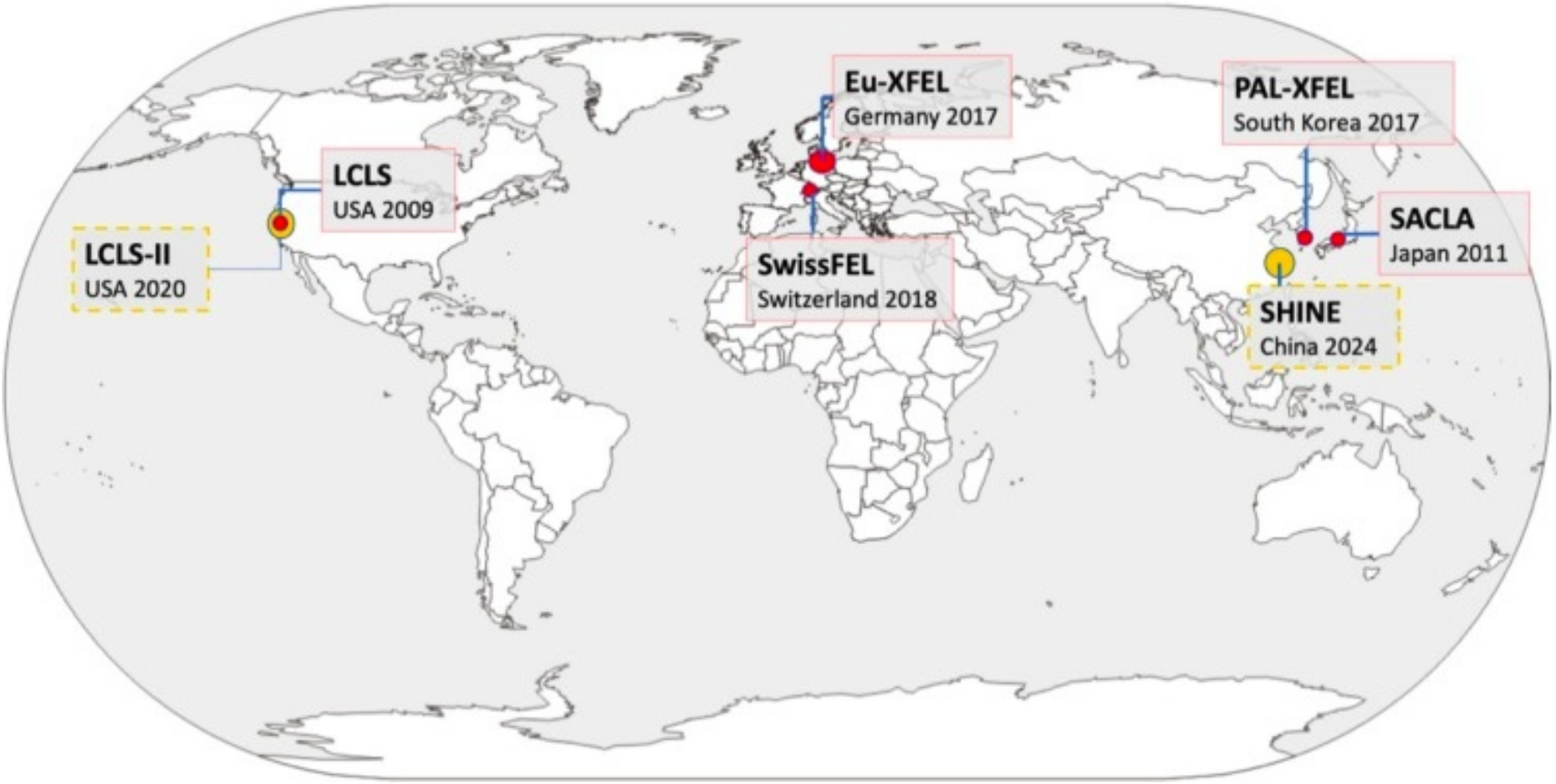
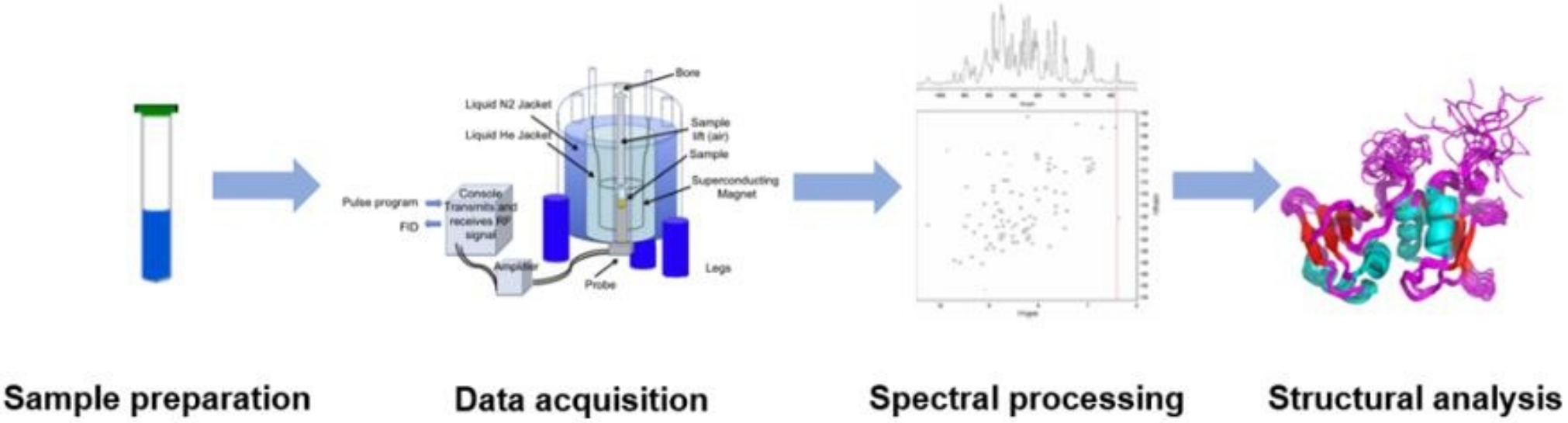


Nuclear Magnetic Resonance (NMR)

ADP



Sample preparation | Data acquisition | Spectral processing | Structural analysis

https://www.creative-biostructure.com/comparison-of-crystallography-nmr-and-em_6.htm

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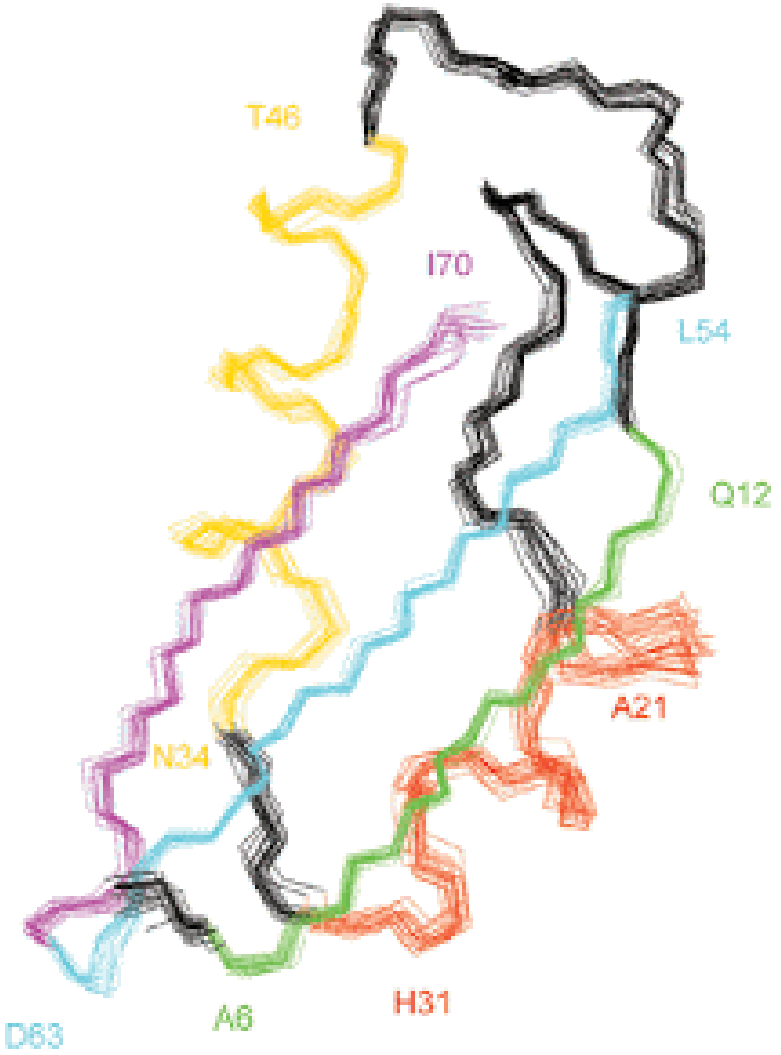
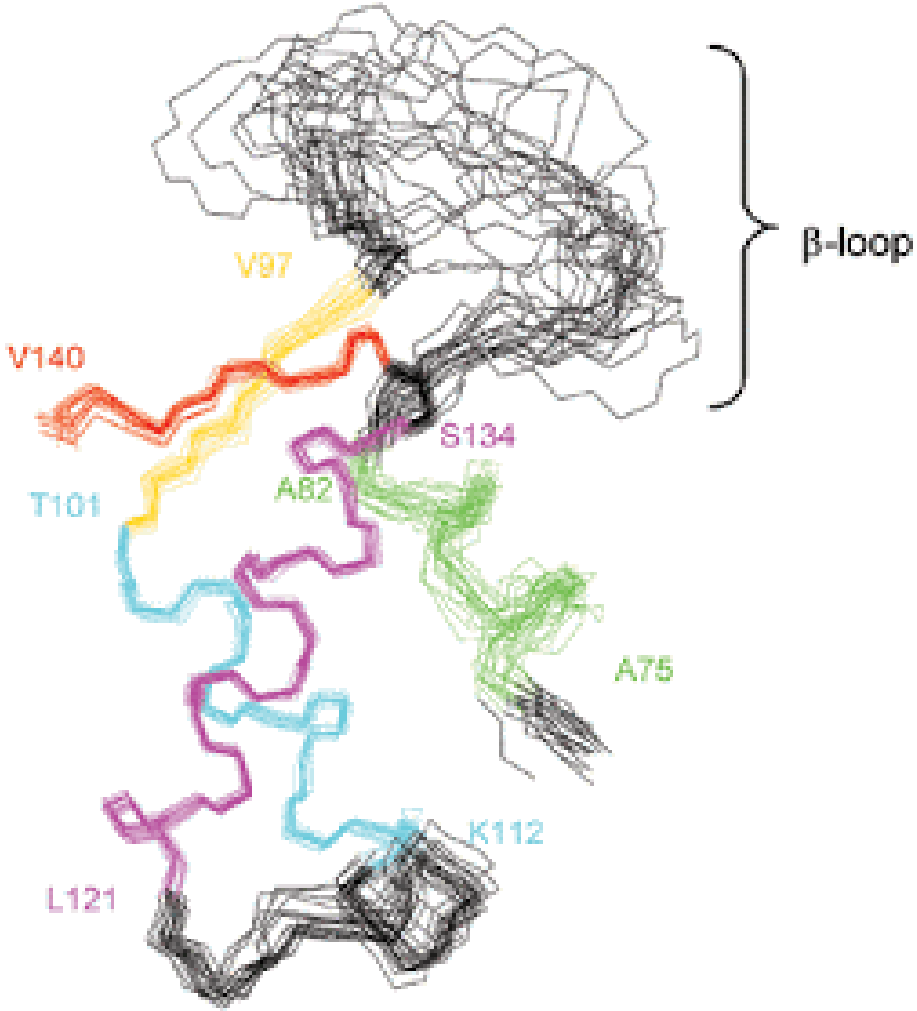
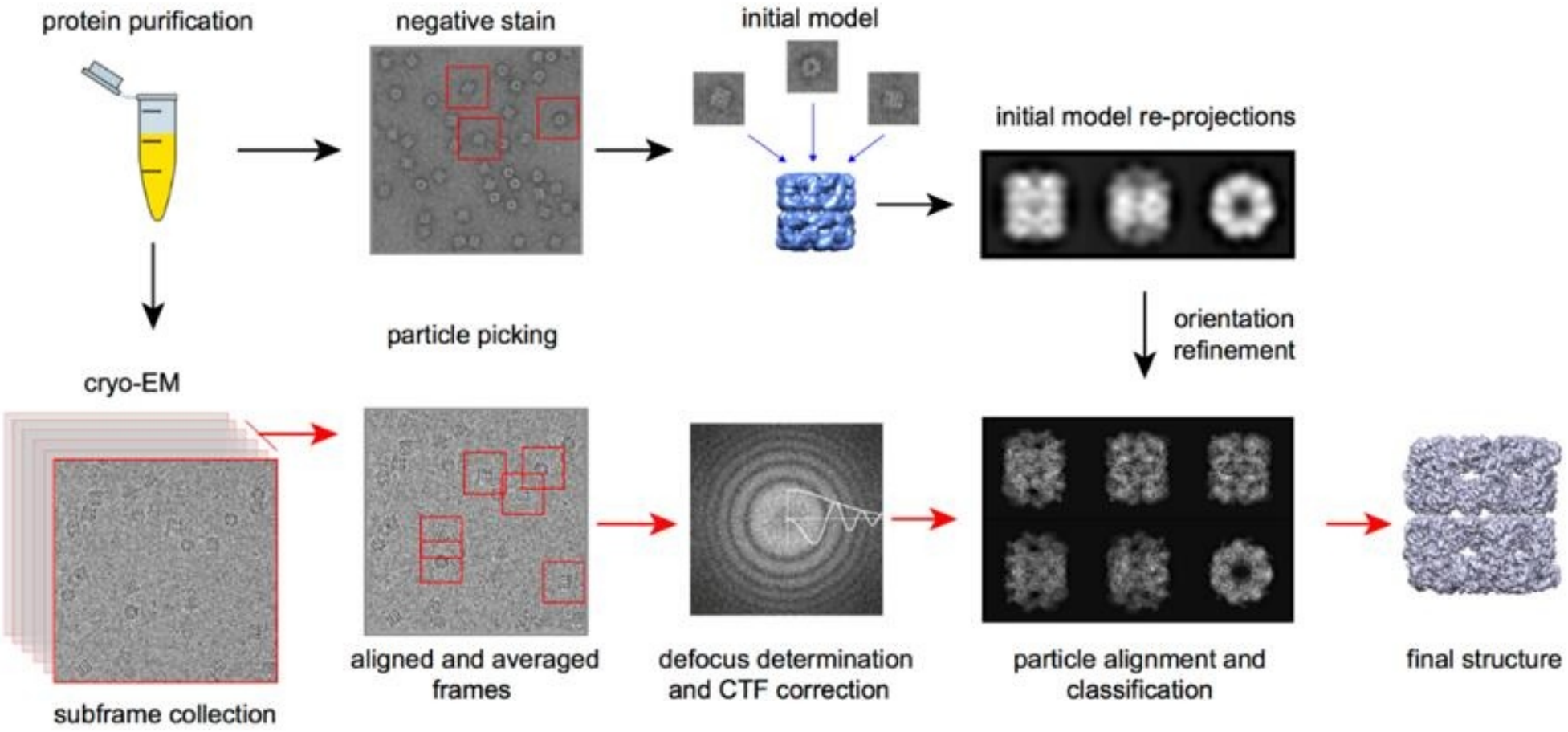


L11 N-Terminus (5-70)



L11 C-Terminus (75-140)

http://schwalbe.org.chemie.uni-frankfurt.de/node/684



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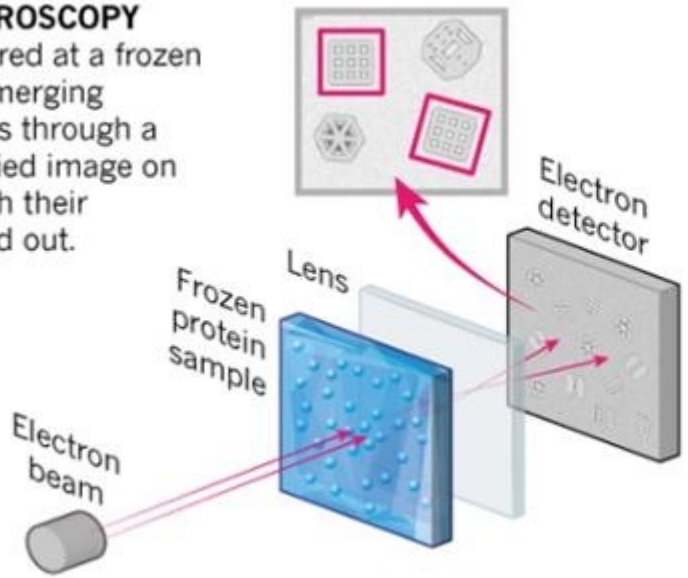
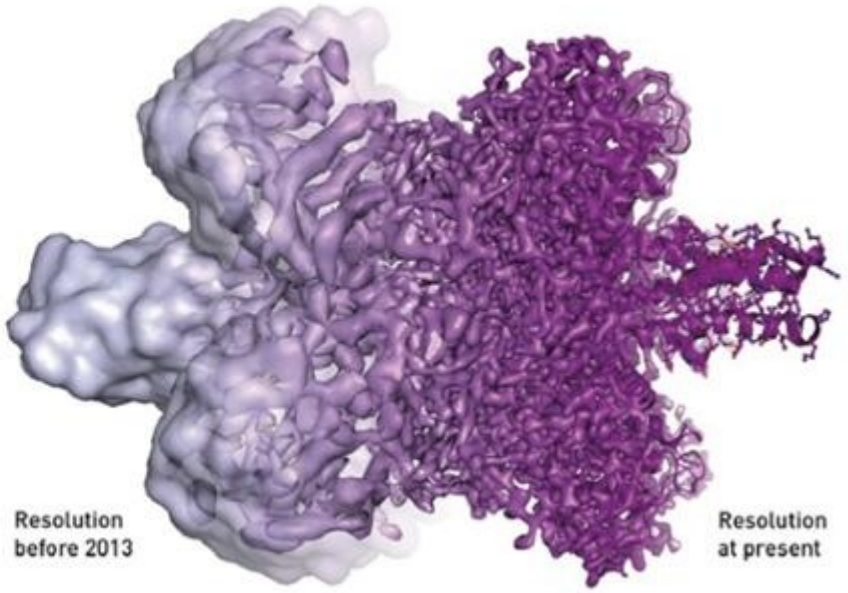
Cryo-EM

ADP

CRYO-ELECTRON MICROSCOPY
A beam of electron is fired at a frozen protein solution. The emerging scattered electrons pass through a lens to create a magnified image on the detector, from which their structure can be worked out.





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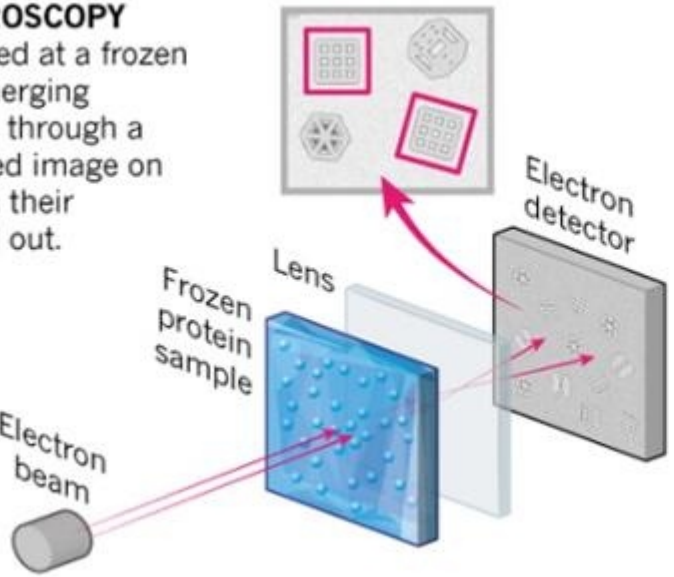

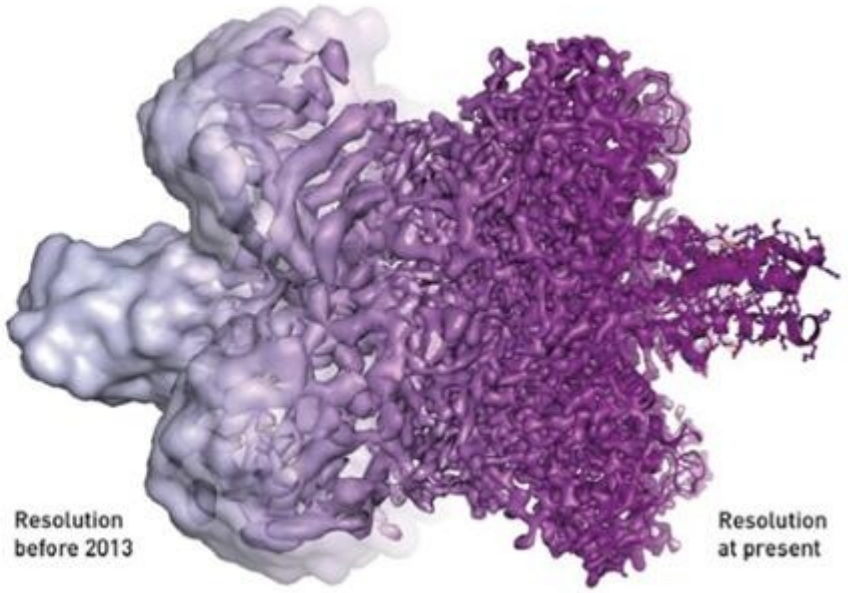

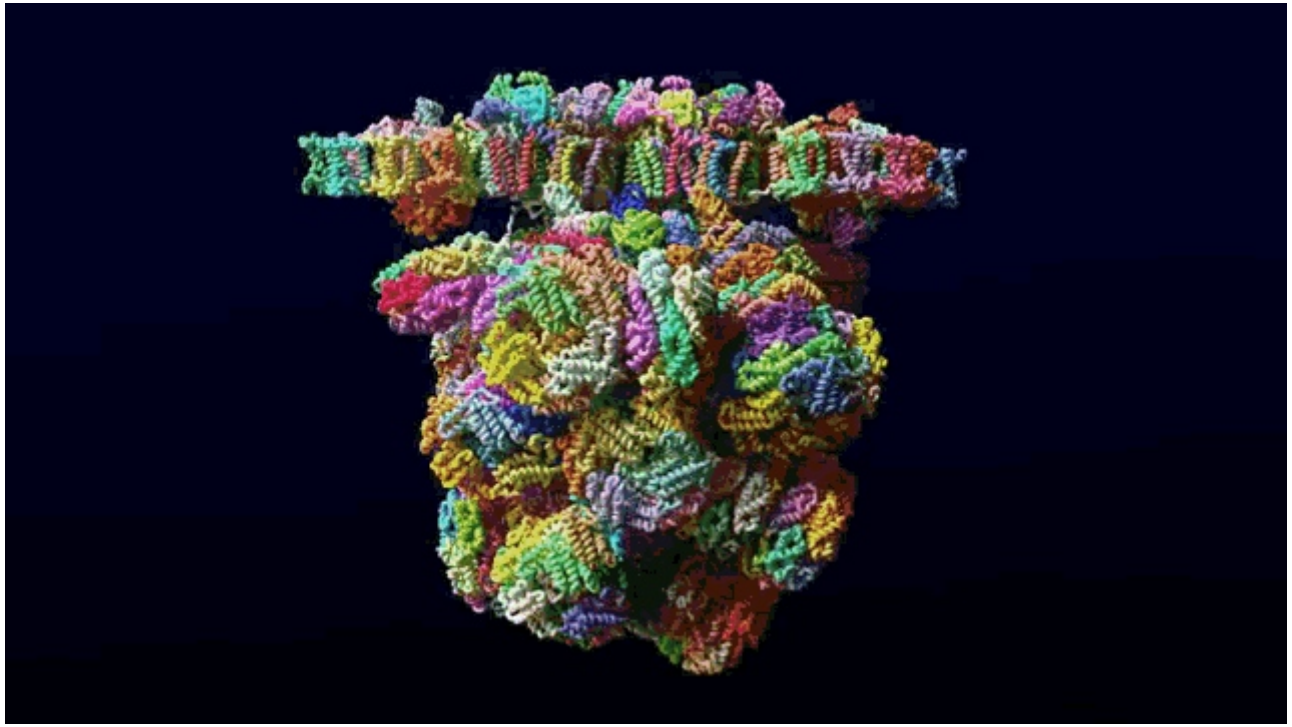

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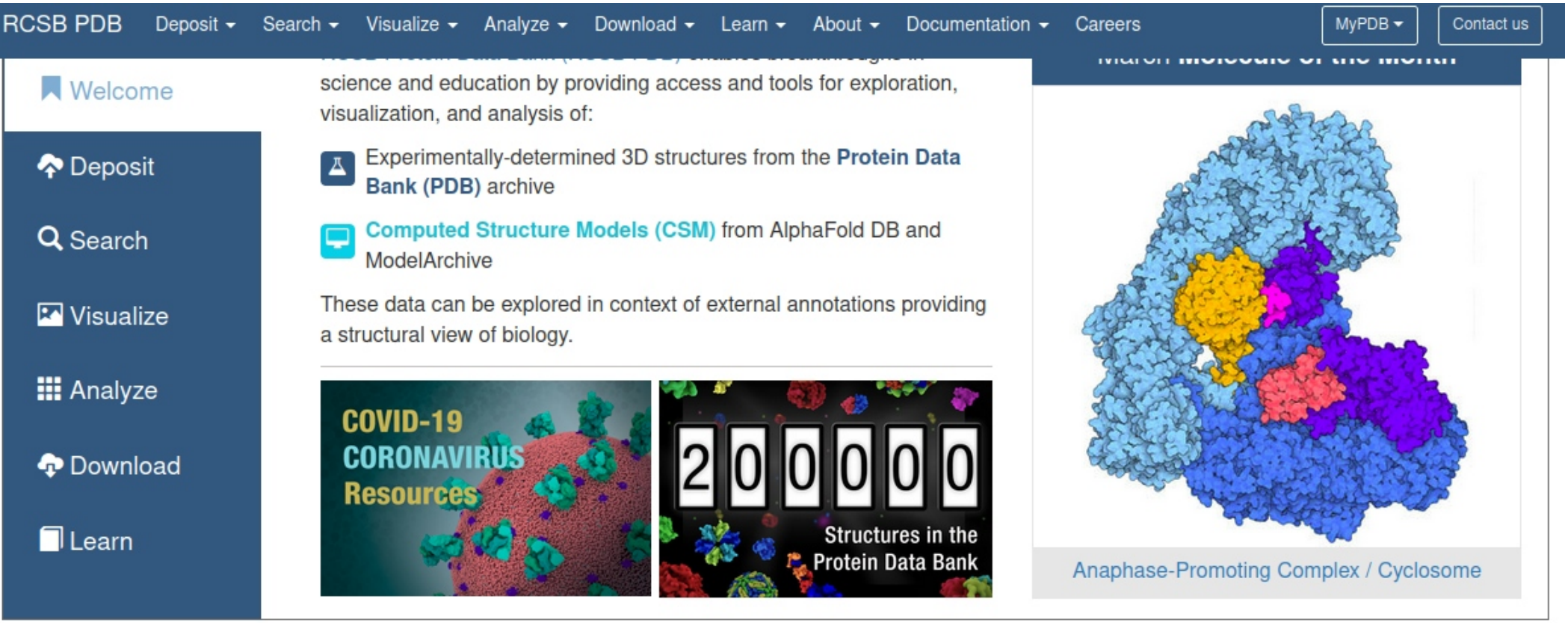
Most important bioinformatics databases

ADP

RCSB PDB
PROTEIN DATA BANK

https://www.rcsb.org/



Most important bioinformatics databases

ALPHA FOLD

PROTEIN STRUCTURE

DATABASE

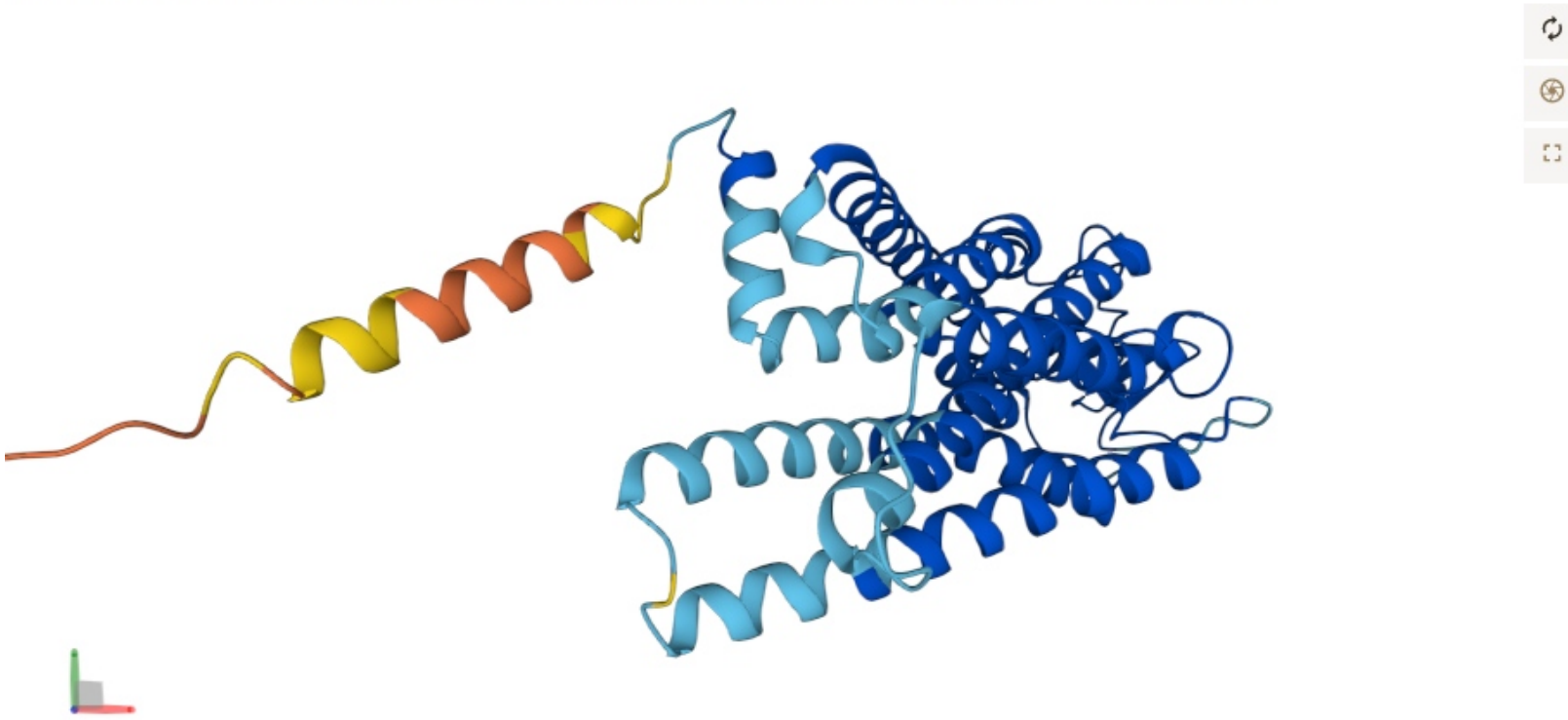
DeepMind

214M

25TB

Sequence of AF-P35359-F1 Chain 1: Rhodopsin A

```
MNGTEGPAFYVPMSNATGVVRSPYEYPQYYLVAPWAYGLLAAYMFFLIITGFPVNFLTLYVTIEHKKLRTPLNYILLNLAIADLFMVFGGFTTTMYTSLHGYFVFGRLGCNLEGFFATLGGEMGLW
SLVVLAIERWMVVCKPVSNFRFGENHAIMGVAFTWVMACSCAVPPLVGWSRYIPEGMQCSCGVDYYTRTPGVNNESFVIYMFIVHFFIPLIVIFFCYGRLVCTVKEAAAQQQESETTQRAEREVTR
MVIIMVIAFLICWLPYAGVAWYIFTHQGSEFGPVFMTLPAFFAKTSAVYNPCIYICMNKQFRHCMITTLCCGKNPFEEEEGASTTASKTEASSVSSSSVSPA
```



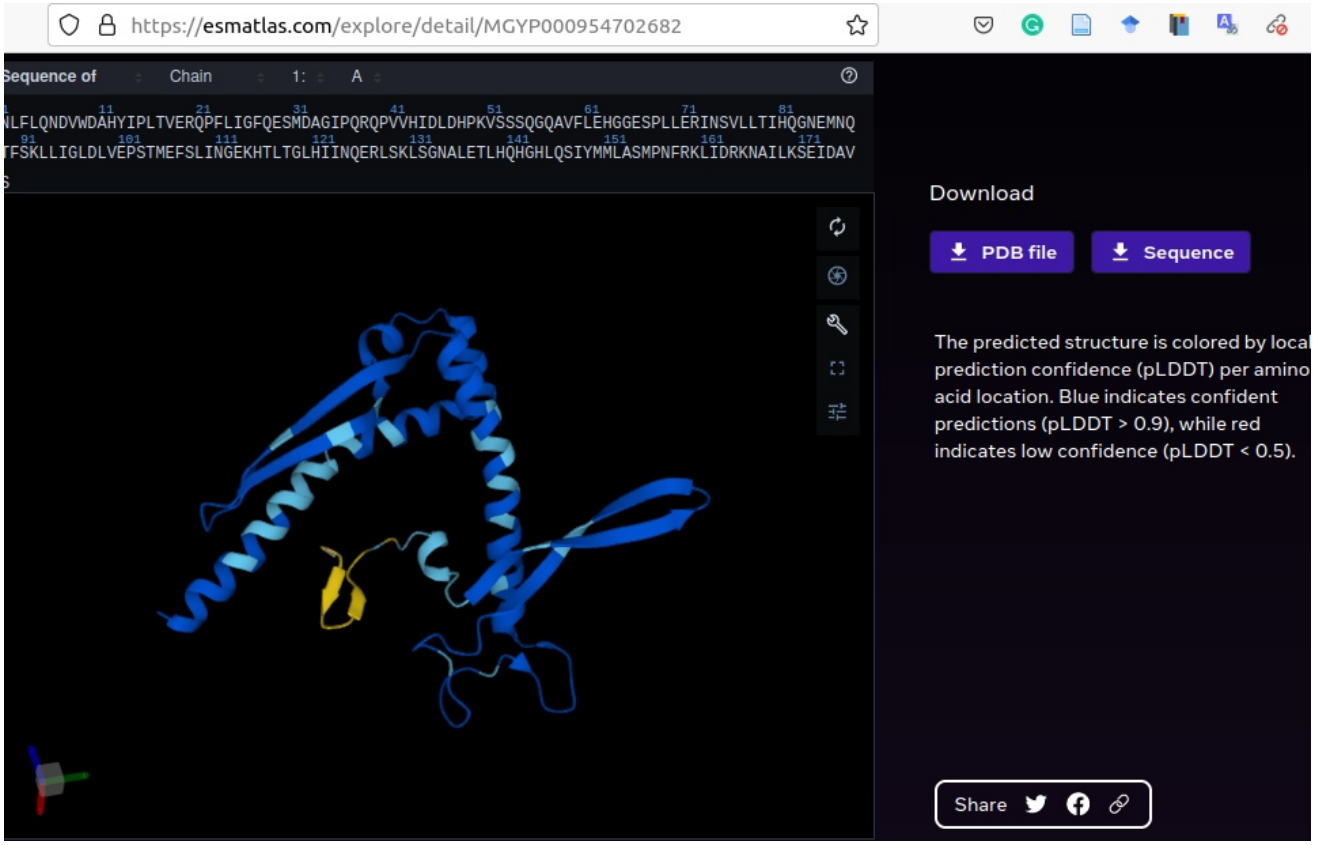
https://alphafold.ebi.ac.uk/entry/P35359

Most important bioinformatics databases

ESM Atlas
Metagenomics
Protein Dataset

Meta AI

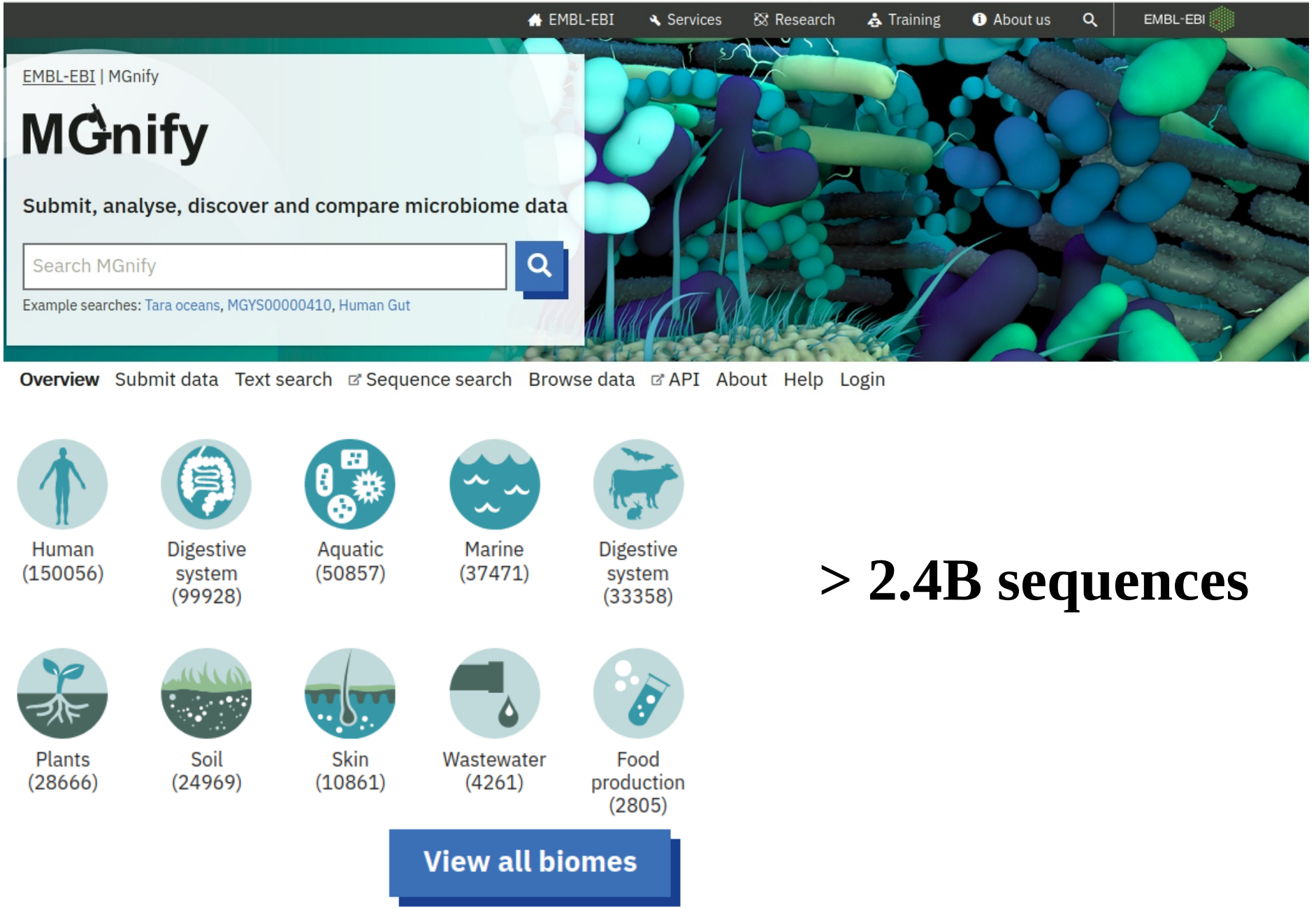
617M sequences & 15TB data



https://esmatlas.com/

Most important bioinformatics databases

ADP

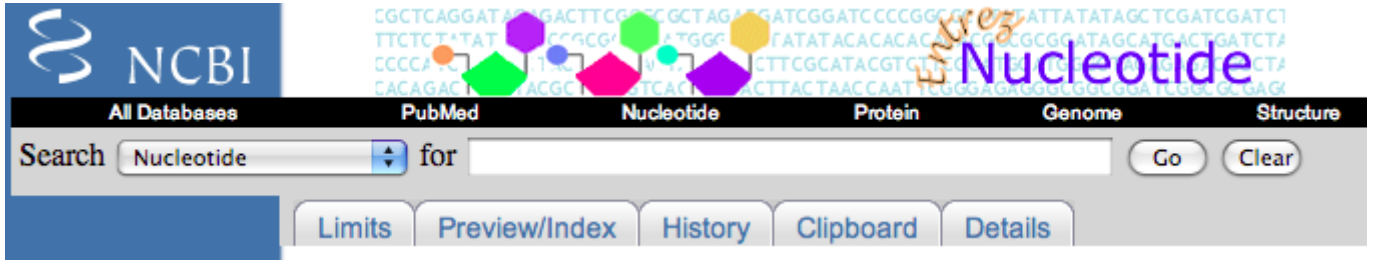


> 2.4B sequences

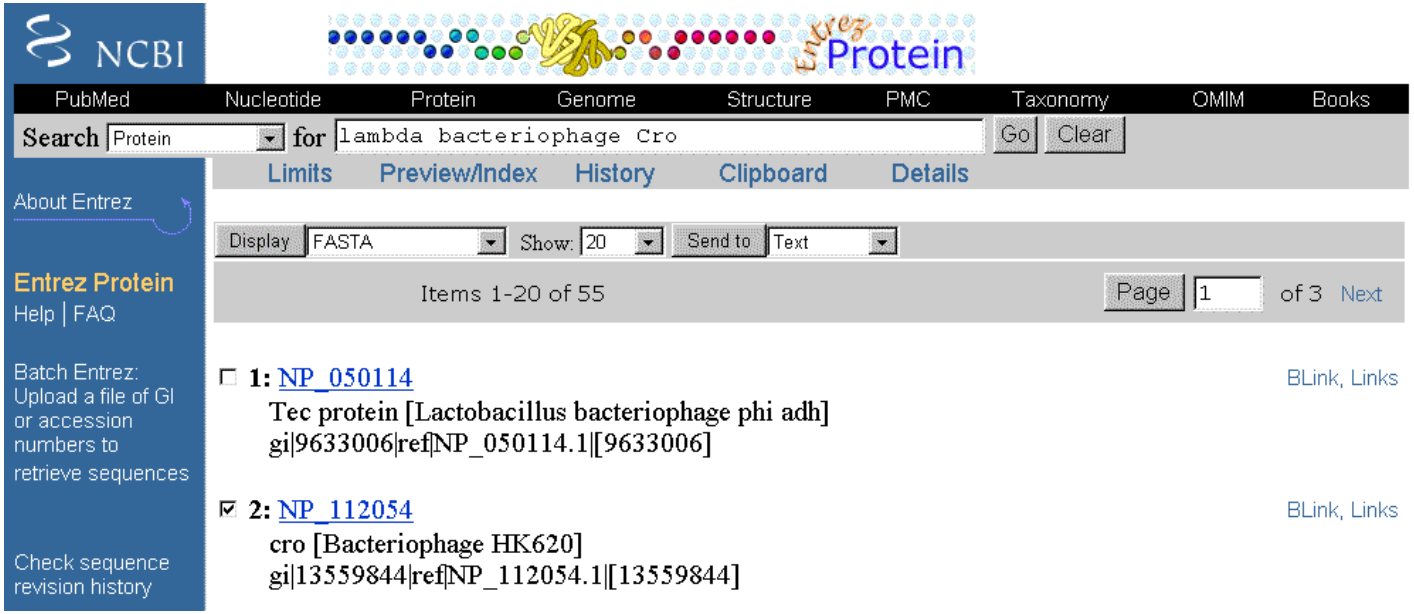
https://www.ebi.ac.uk/metagenomics/

Most important bioinformatics databases

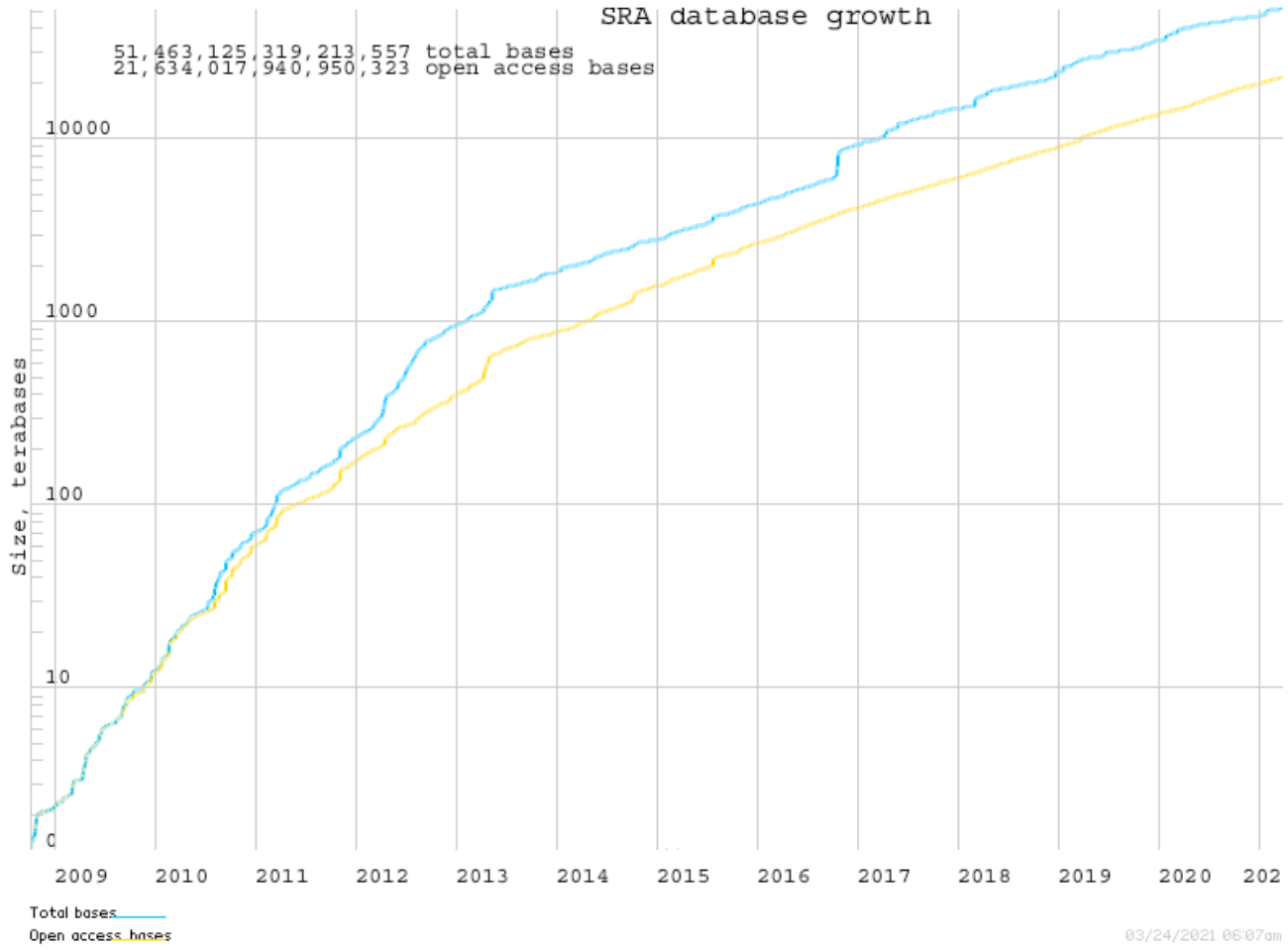
GenBank



GenPept



Sequence Read Archive (SRA)



Sequence Read Archive (SRA)

Sequence Read Archive (SRA) stores raw sequence data from "next-generation" sequencing technologies including Illumina, 454, IonTorrent, Complete Genomics, PacBio and OxfordNanopores

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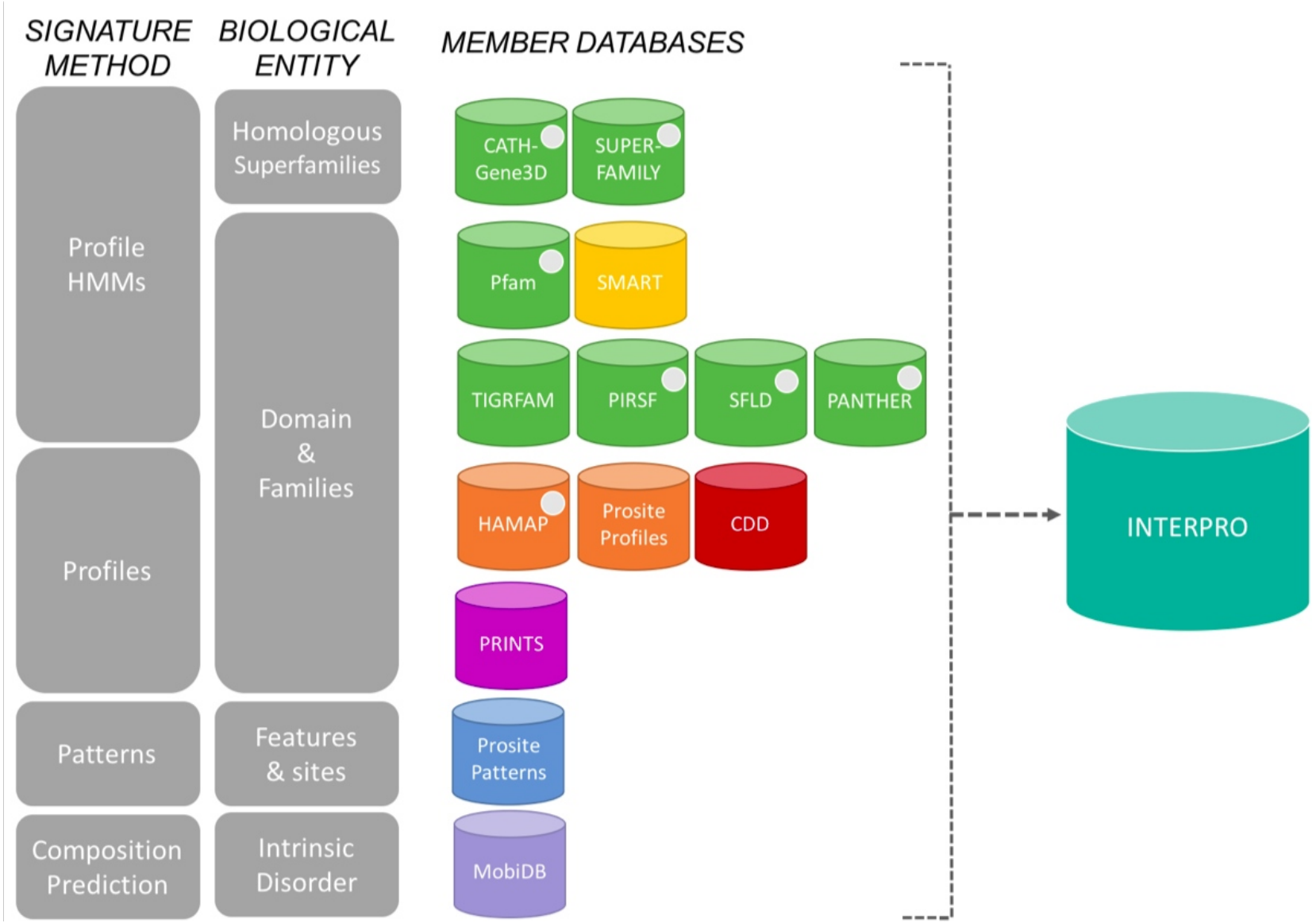
SRA = NGS data

InterPro

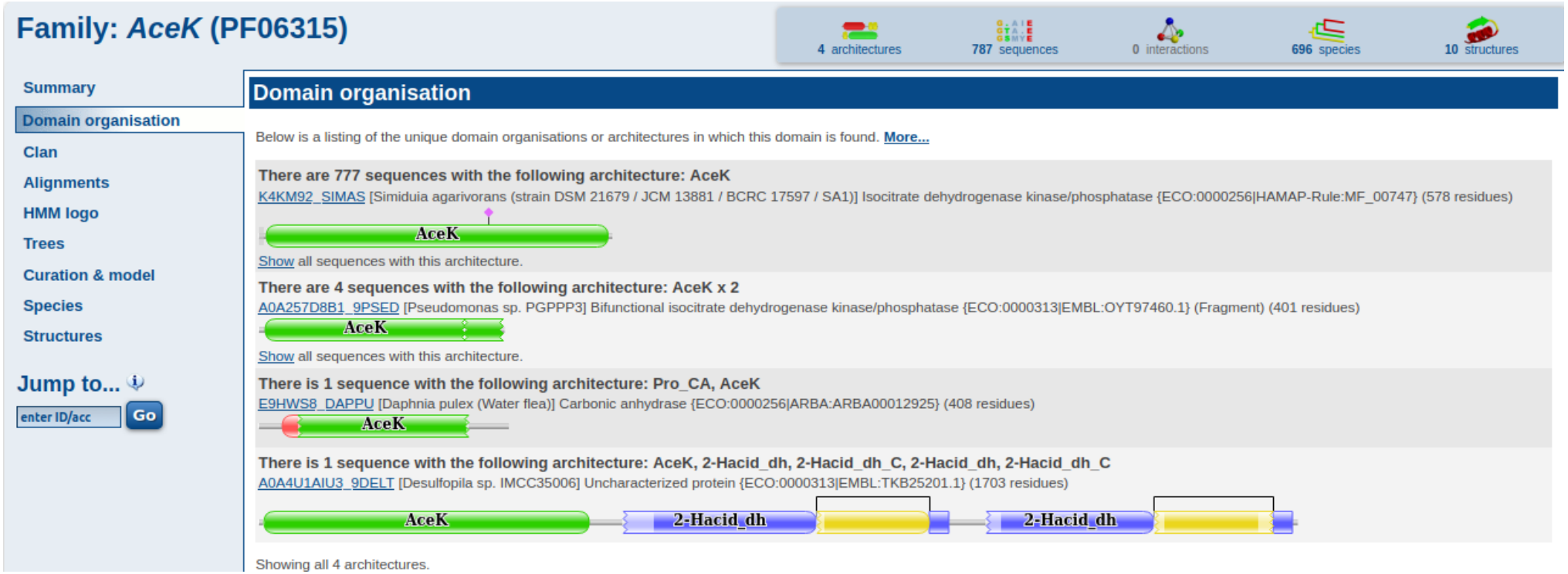

SIGNATURE METHOD
BIOLOGICAL ENTITY
MEMBER DATABASES
Profile HMMs
Profiles
Patterns
Composition Prediction
Homologous Superfamilies
Domain & Families
Features & sites
Intrinsic Disorder
CATH-Gene3D
SUPER-FAMILY
Pfam
SMART
TIGRFAM
PIRSF
SFLD
PANTHER
HAMAP
Prosite Profiles
CDD
PRINTS
Prosite Patterns
MobiDB
INTERPRO

Most important bioinformatics databases

ADP

Pfam

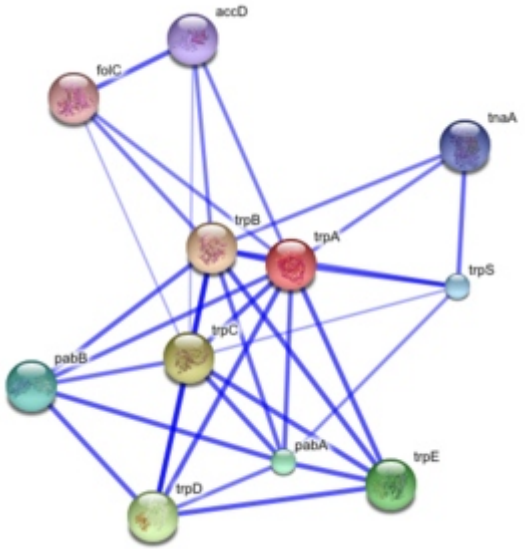
Rfam



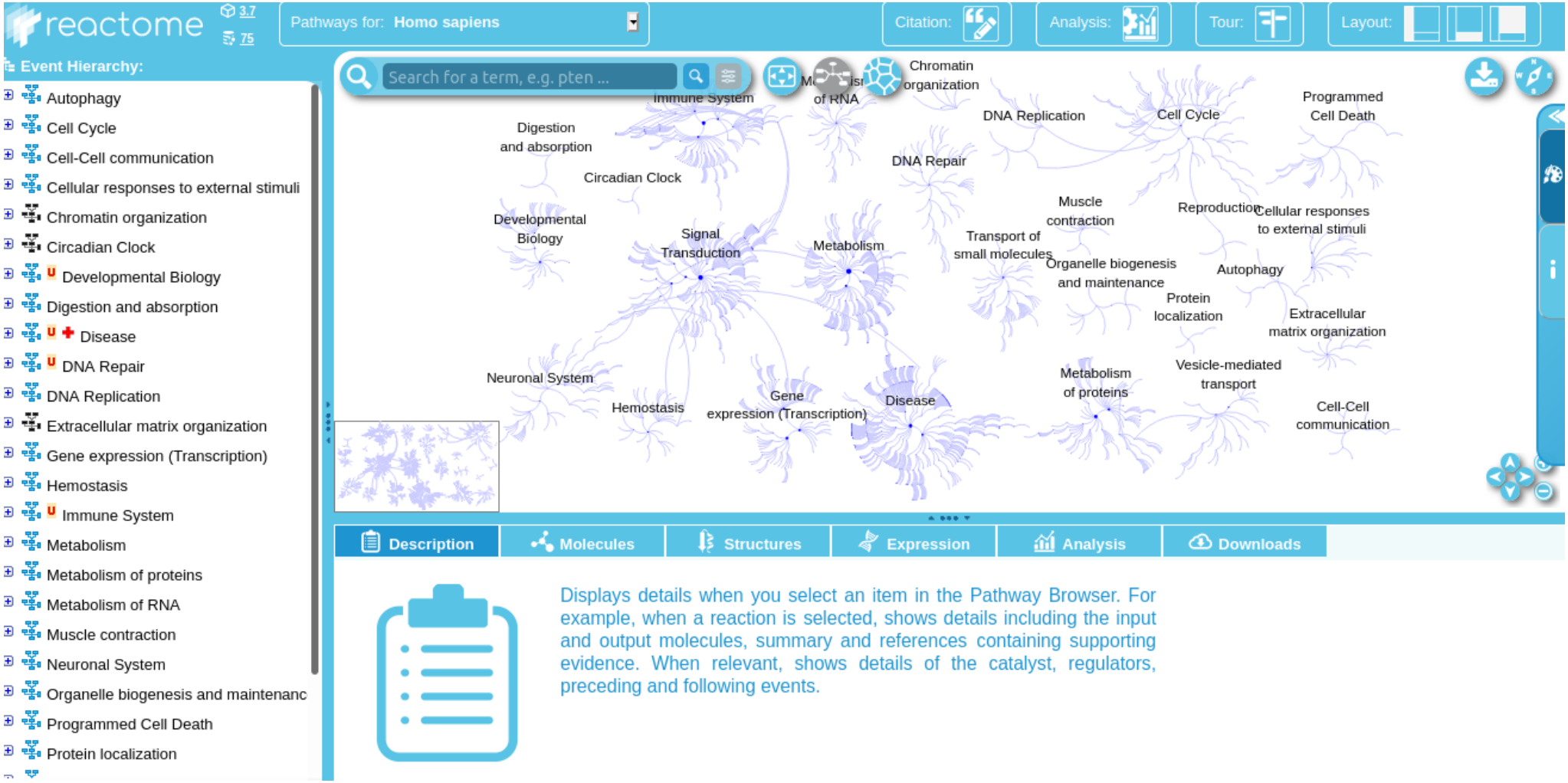
Most important bioinformatics databases

ADP

STRING



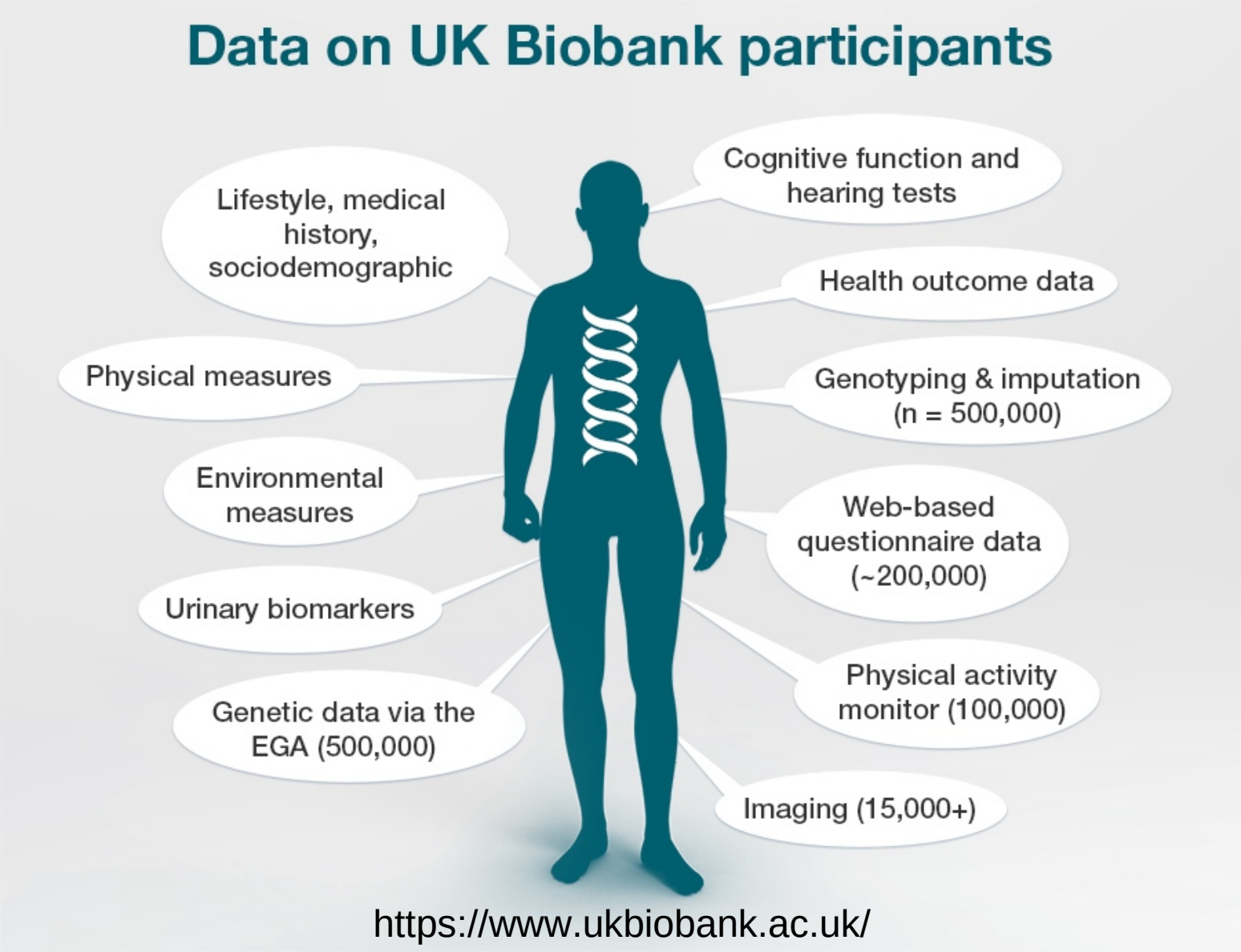
Reactome – biological pathways



Most important bioinformatics databases

biobank uk

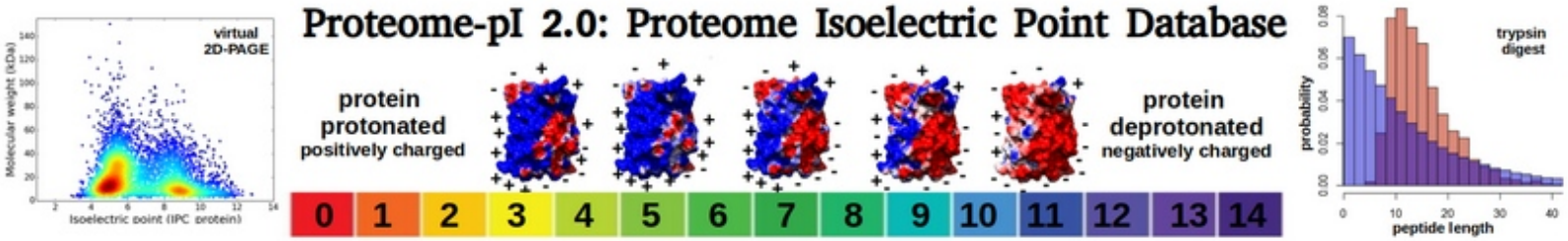
Enabling scientific discoveries that improve human health



https://www.ukbiobank.ac.uk/

Proteome-pI 2.0

NARODOWE CENTRUM NAUKI
Opus



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Database of **pre-computed** isoelectric points and molecular weights for proteins and digest peptides from model organism proteomes (20,115 species)

The goals of the database include making statistical comparisons of the various prediction methods (21 algorithms implemented) as well as facilitating the biological investigation of protein isoelectric point space. The isoelectric point, the pH at which a particular molecule carries no net electrical charge, is an important parameter for many analytical biochemistry and proteomics techniques, especially for 2D gel electrophoresis (2D-PAGE), capillary isoelectric focusing (cIEF), liquid chromatography–mass spectrometry (LC-MS) and X-ray protein crystallography

2D plots of predicted molecular weight and isoelectric point can be useful for initial identification of proteins in the sample and limiting the complexity of the further analysis

Protease digests (peptides with molecular weight and isoelectric point) can be useful for bottom-up proteomics MS analysis

61,329,034 protein sequences from **20,115** proteomes with isoelectric point predicted using **21** algorithms

5.38 Billion dissociation constant (pKa) predictions for proteins

Proteomes *in silico* digested with the five most frequently used proteases (Trypsin, Chymotrypsin, Trypsin+LysC, LysN, ArgC)
In total, **9.58 Billion** peptides

isoelectricpointdb2.mimuw.edu.pl

Kozlowski LP. Proteome-pI 2.0: Proteome Isoelectric Point Database Update. NAR 2022 50 (D1), D1535-D1540

Proteome-pI 2.0

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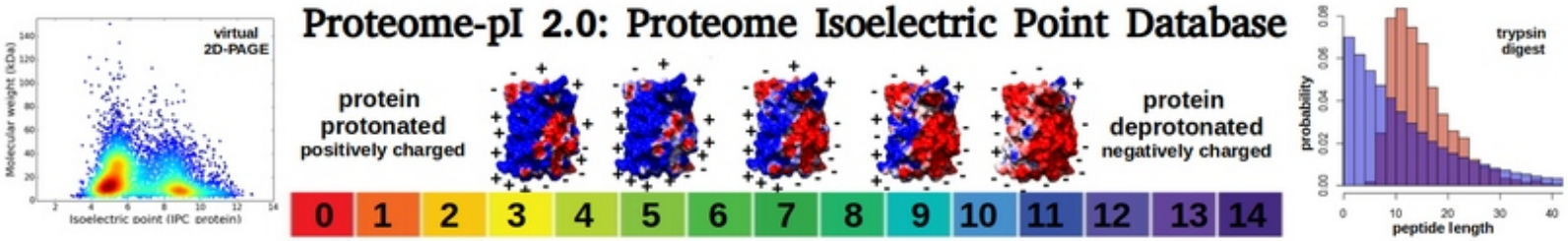
Opus



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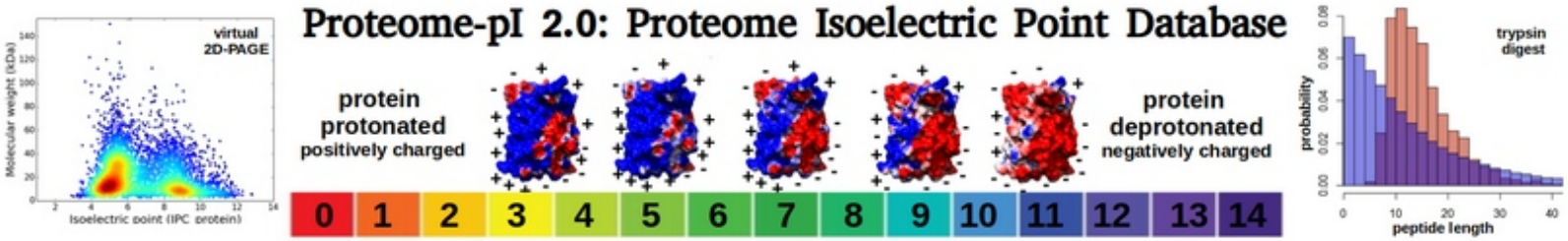
isoelectricpointdb2.mimuw.edu.pl

Kozlowski LP. Proteome-pI 2.0: Proteome Isoelectric Point Database Update. NAR 2022 50 (D1), D1535-D1540

Proteome-pI 2.0

NARODOWE CENTRUM NAUKI
Opus



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Proteome-pI 2.0

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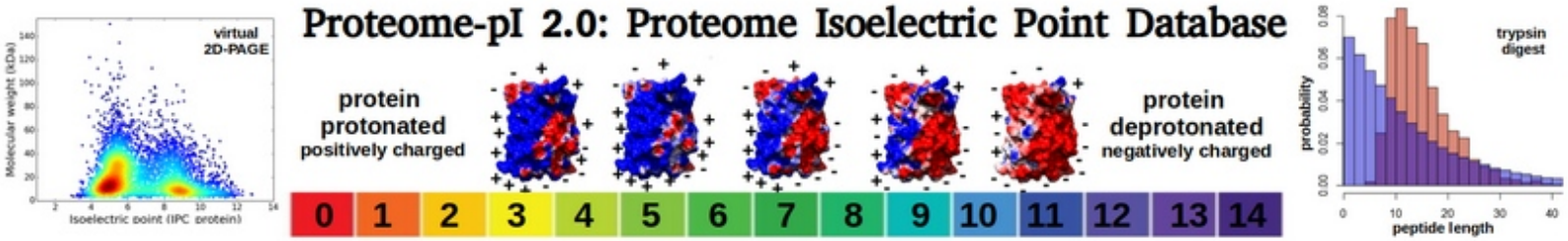

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Database of **pre-computed** isoelectric points and molecular weights for proteins and digest peptides from model organism proteomes (20,115 species)

The goals of the database include making statistical comparisons of the various prediction methods (21 algorithms implemented) as well as facilitating the biological investigation of protein isoelectric point space. The isoelectric point, the pH at which a particular molecule carries no net electrical charge, is an important parameter for many analytical biochemistry and proteomics techniques, especially for 2D gel electrophoresis (2D-PAGE), capillary isoelectric focusing (cIEF), liquid chromatography–mass spectrometry (LC-MS) and X-ray protein crystallography

2D plots of predicted molecular weight and isoelectric point can be useful for initial identification of proteins in the sample and limiting the complexity of the further analysis

Protease digests (peptides with molecular weight and isoelectric point) can be useful for bottom-up proteomics MS analysis

61,329,034 protein sequences from **20,115** proteomes with isoelectric point predicted using **21** algorithms

5.38 Billion dissociation constant (pKa) predictions for proteins

Proteomes *in silico* digested with the five most frequently used proteases (Trypsin, Chymotrypsin, Trypsin+LysC, LysN, ArgC)
In total, **9.58 Billion** peptides

isoelectricpointdb2.mimuw.edu.pl

Kozlowski LP. Proteome-pI 2.0: Proteome Isoelectric Point Database Update. NAR 2022 50 (D1), D1535-D1540

Proteome-pI 2.0

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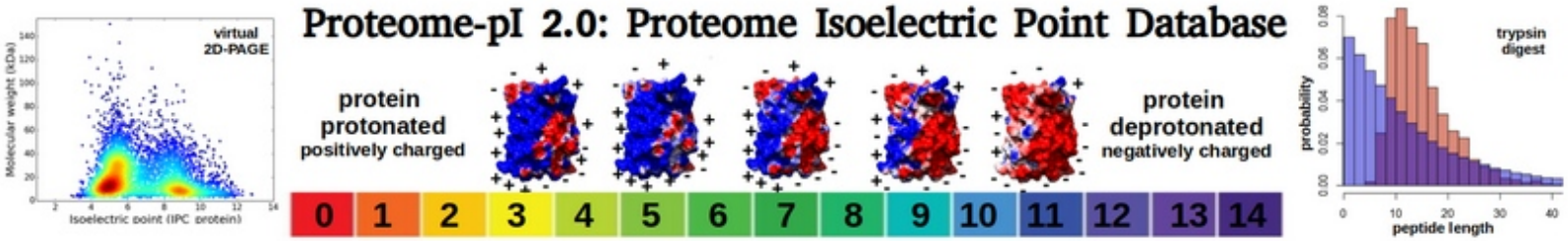

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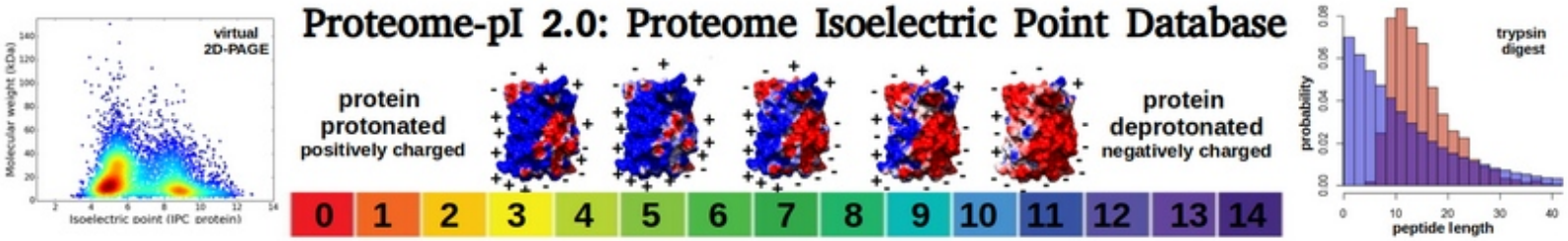

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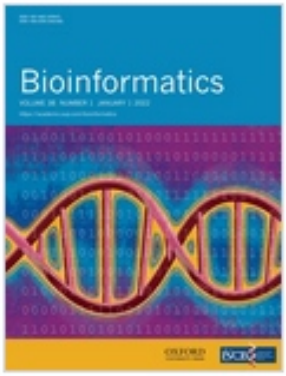

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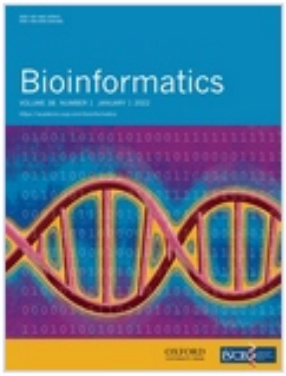

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pKPDB is a database of over 12 M theoretical pKa values calculated over 120k protein structures deposited in the Protein Data Bank

PypKa (structure based method) with ~0.9 RMSD accuracy

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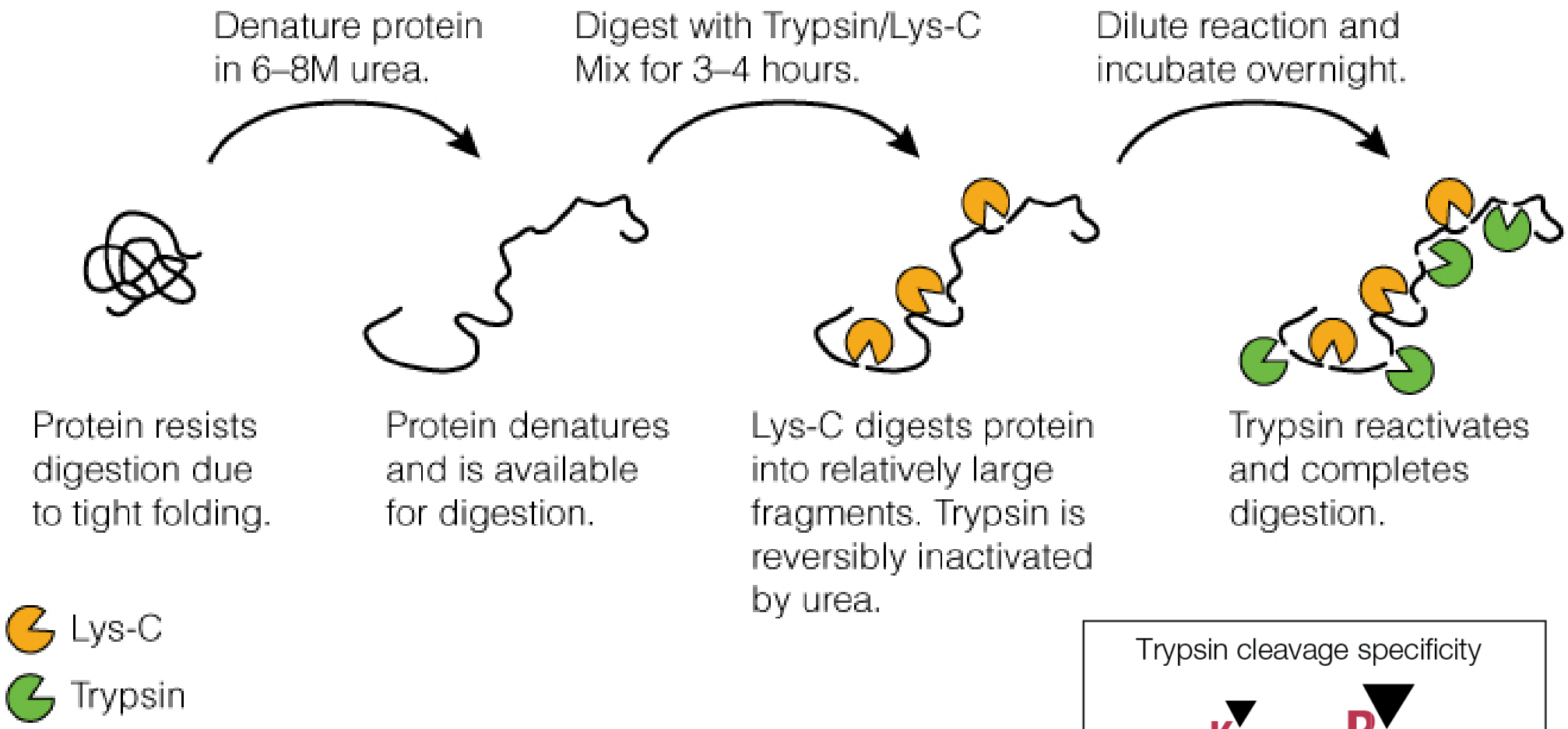

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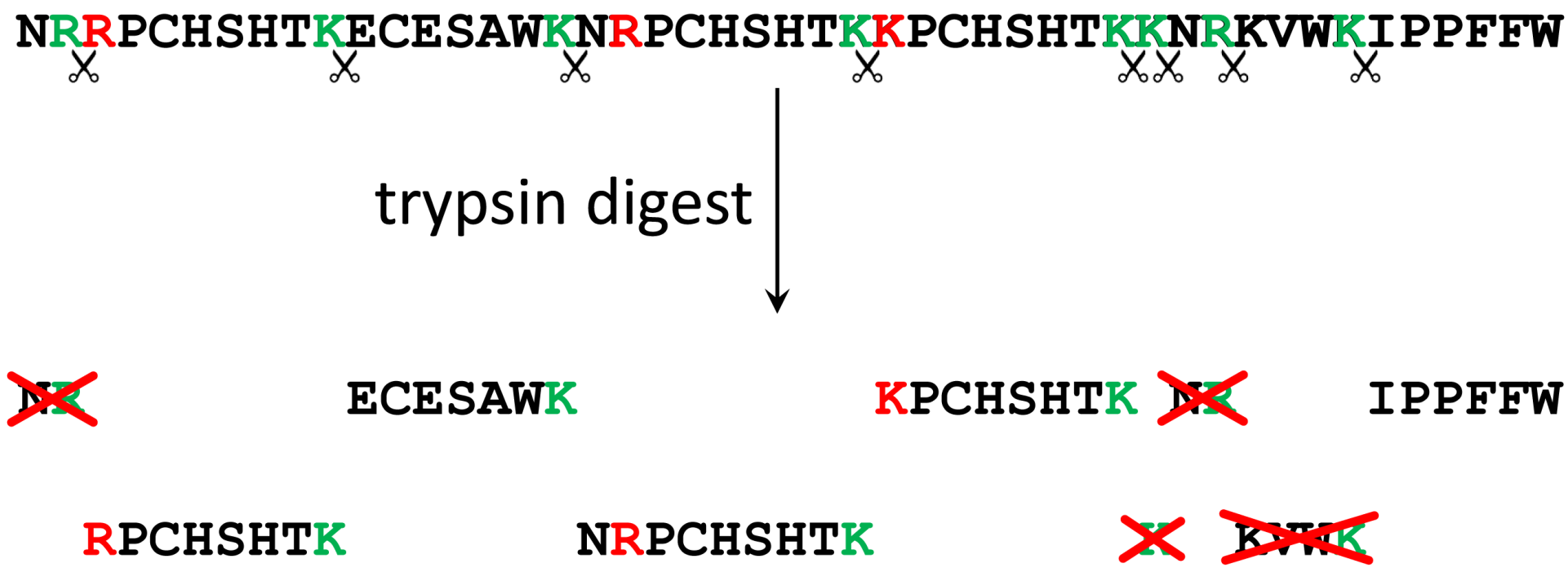

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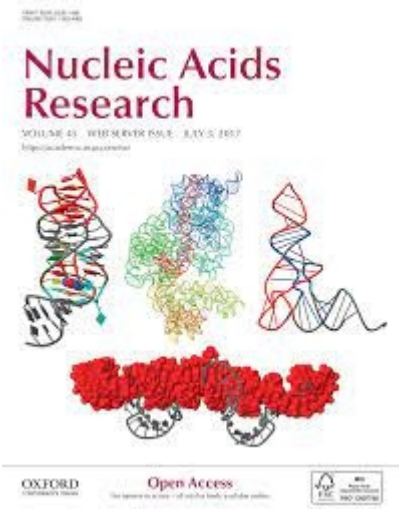

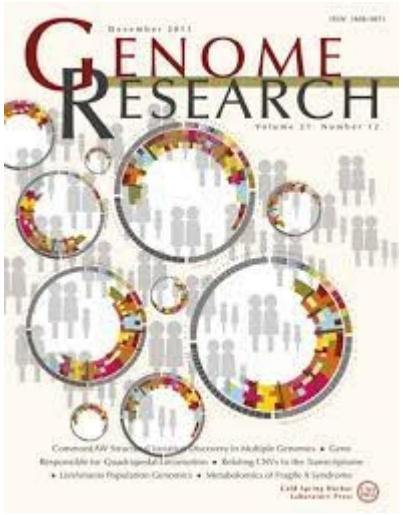

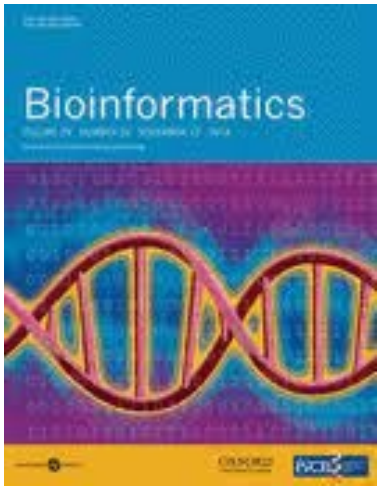

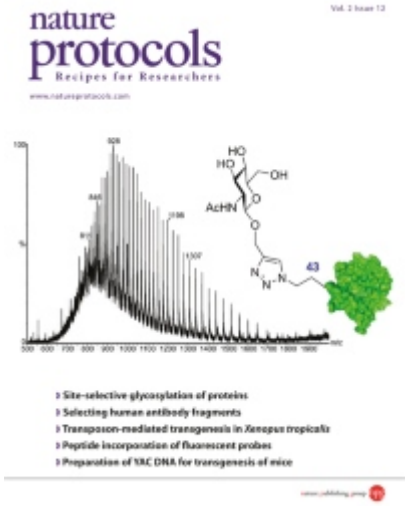

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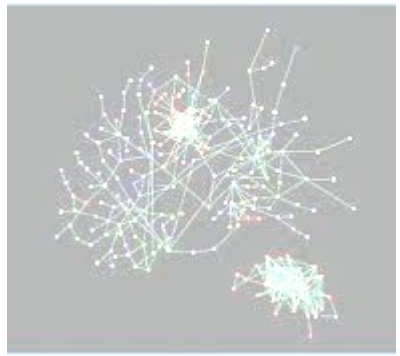

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