

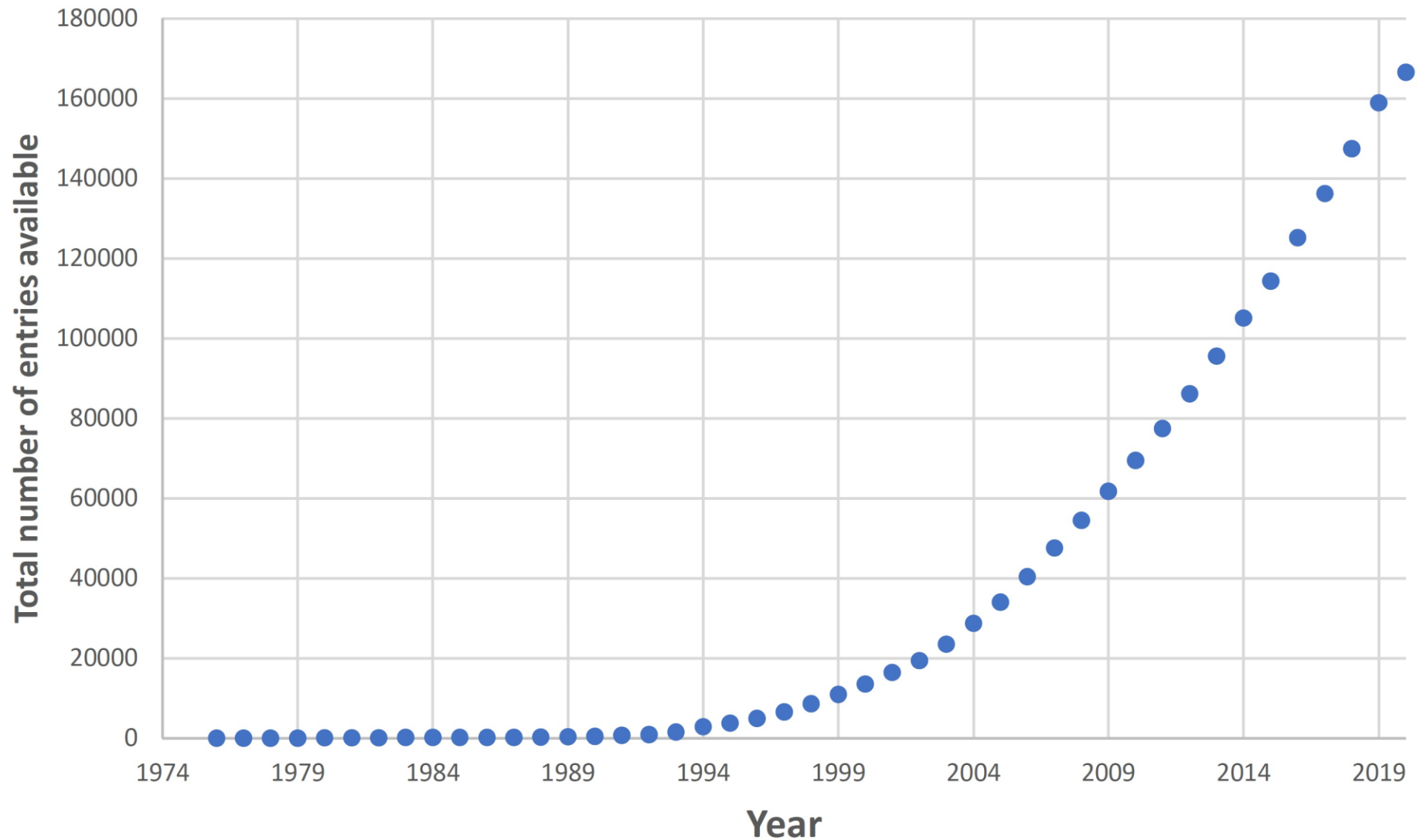
Secondary structure diagrams of proteins, protein families and ligands

Radka Svobodová

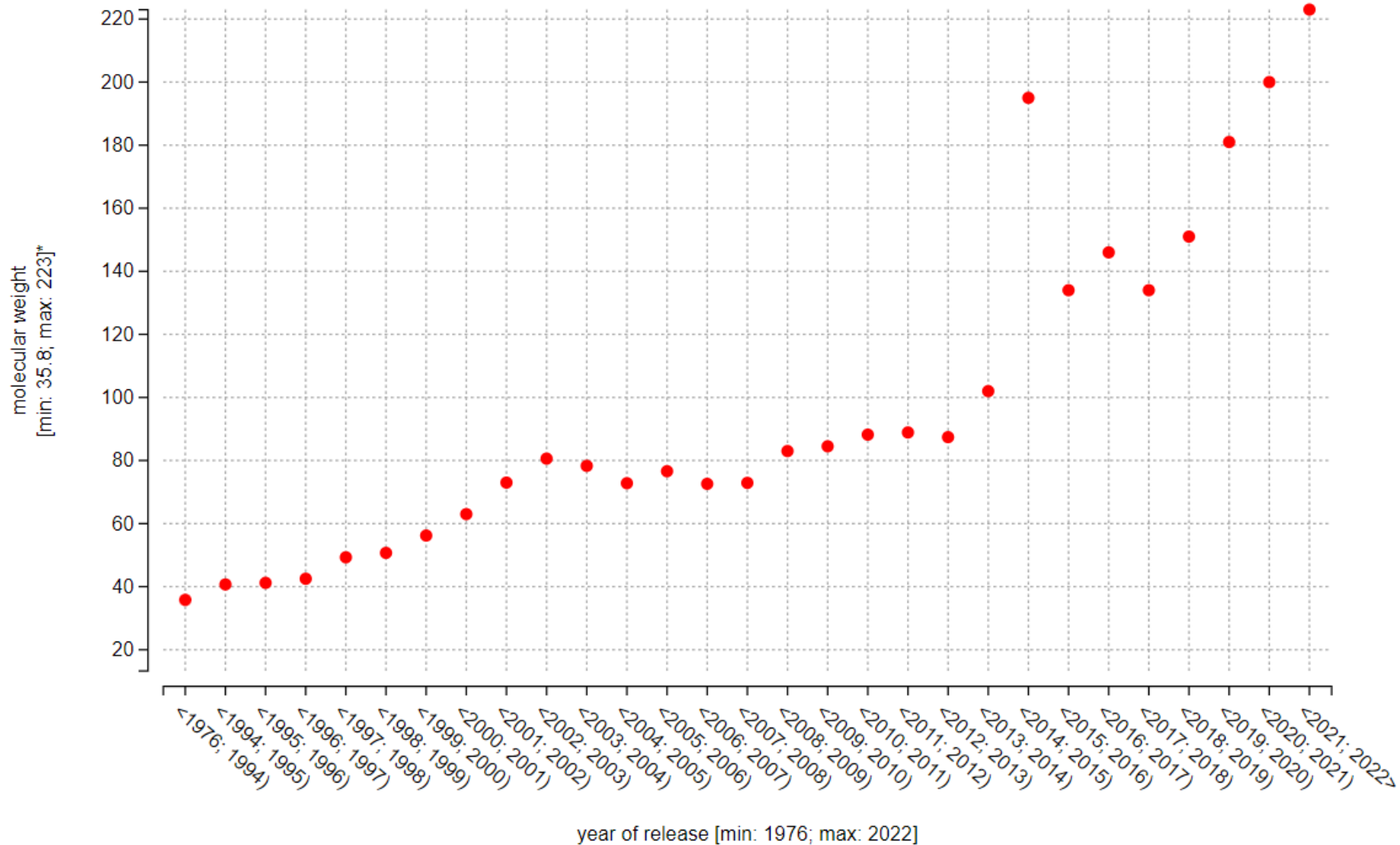
NCBR, CEITEC
MASARYK UNIVERSITY



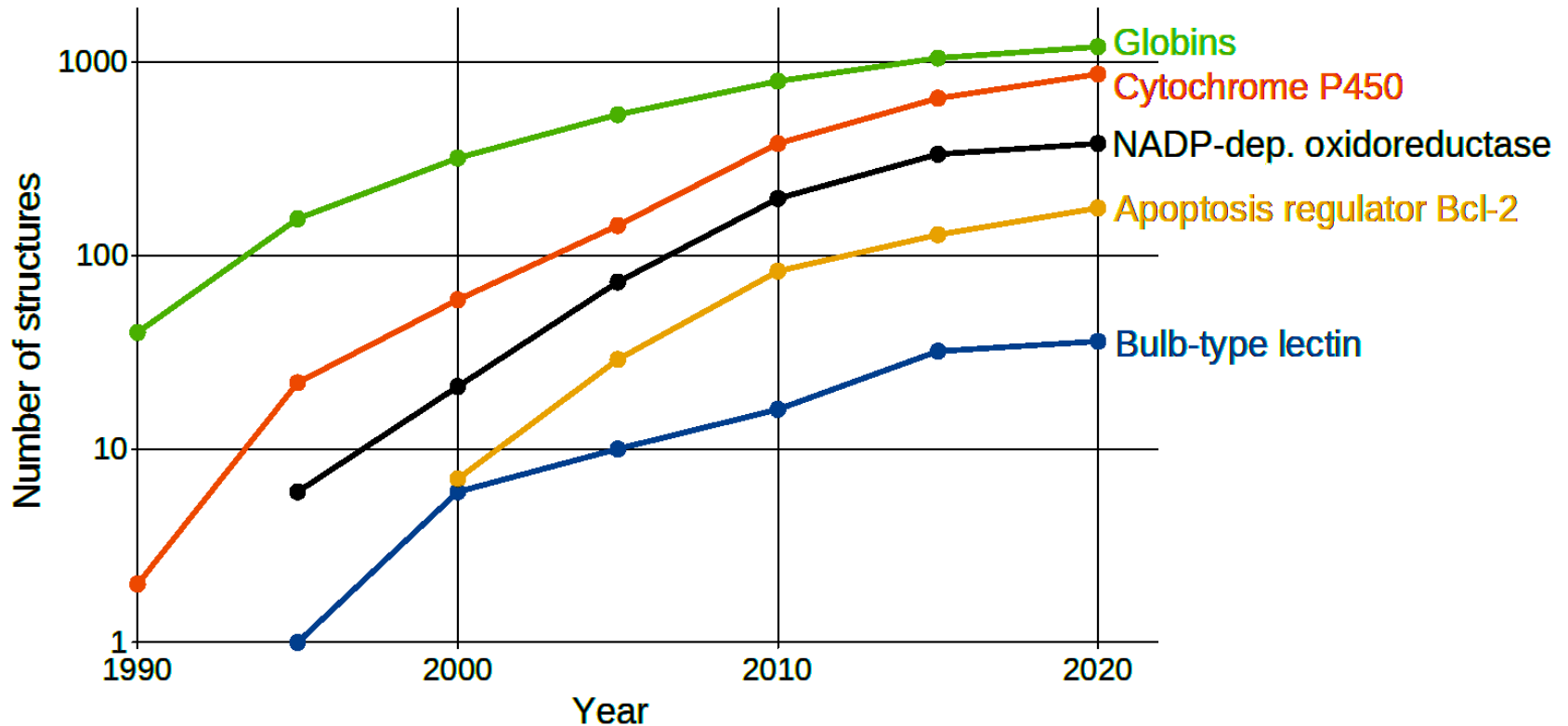
Current trends: Number of available structures grows



Current trends: Size of deposited structures also grows



Current trends: Protein families are getting bigger



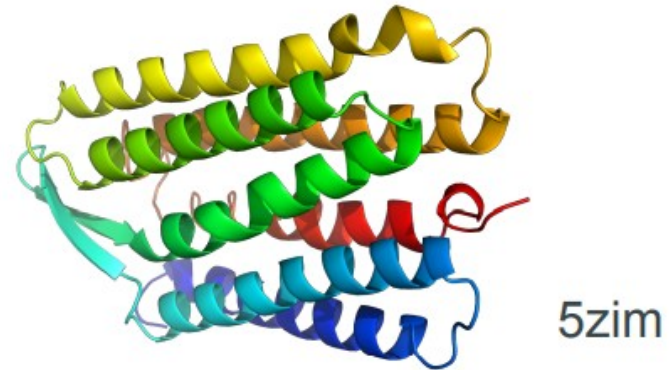
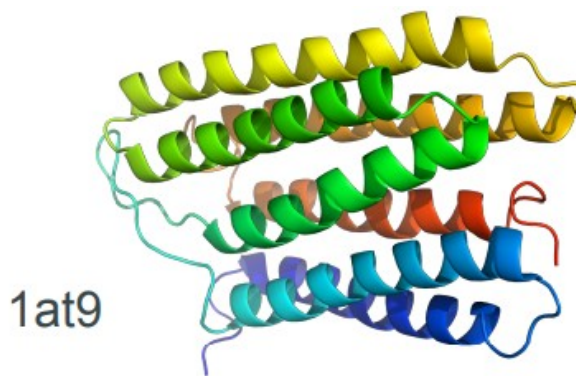
Analysis of individual structure



Analysis of a whole family

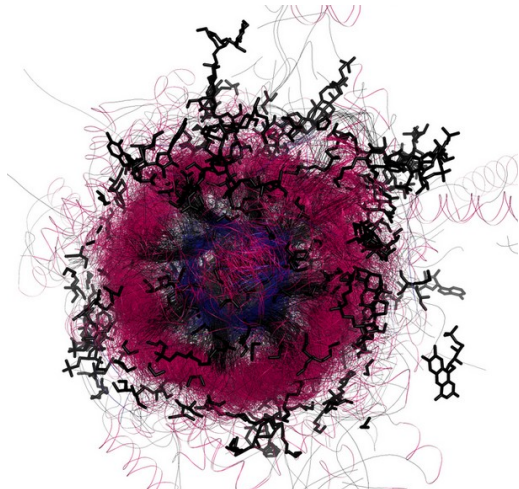
Protein family structures and their analysis

- Comparison of protein family members
 - Different species
 - Different substituents
 - Mutations
 - Active and inactive forms
- Firm (conserved) and flexible regions
- Binding of ligands



Protein family structures and their analysis

How to do it?



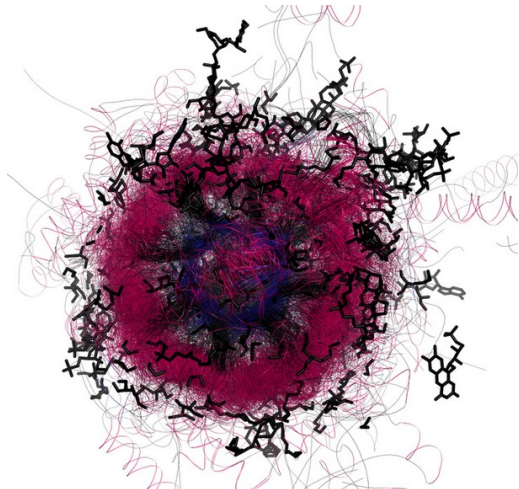
Aldolase class I
(protein family 3.20.20.70)



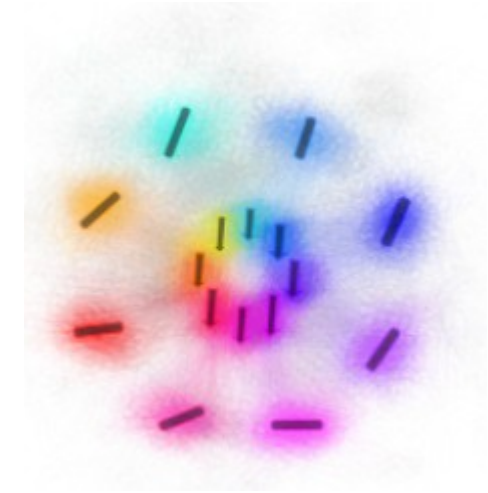
Cytochrome P450
(protein family 1.10.630.10)

Protein family structures and their analysis

How to do it?



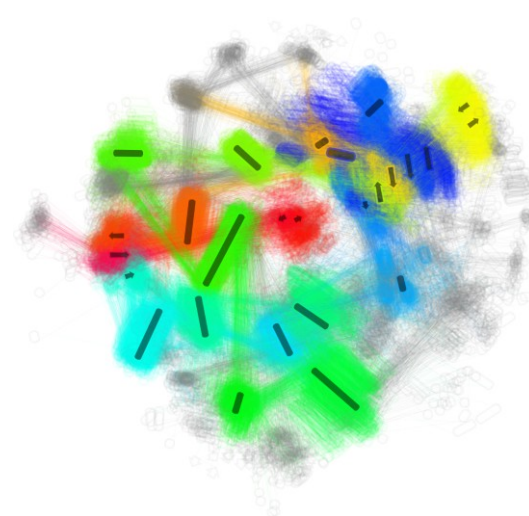
Aldolase class I
(protein family 3.20.20.70)



Insight into protein family:
Secondary structure
2D diagrams



Cytochrome P450
(protein family 1.10.630.10)



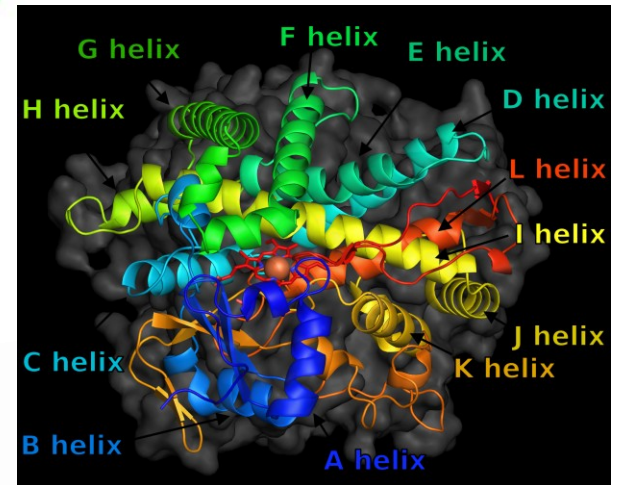
Protein family structures and their analysis

Secondary structure utilization – necessary steps

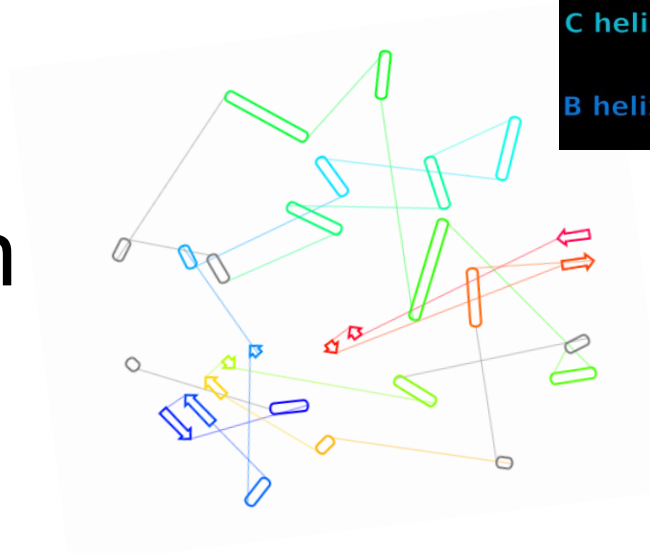
- Detection



- Annotation

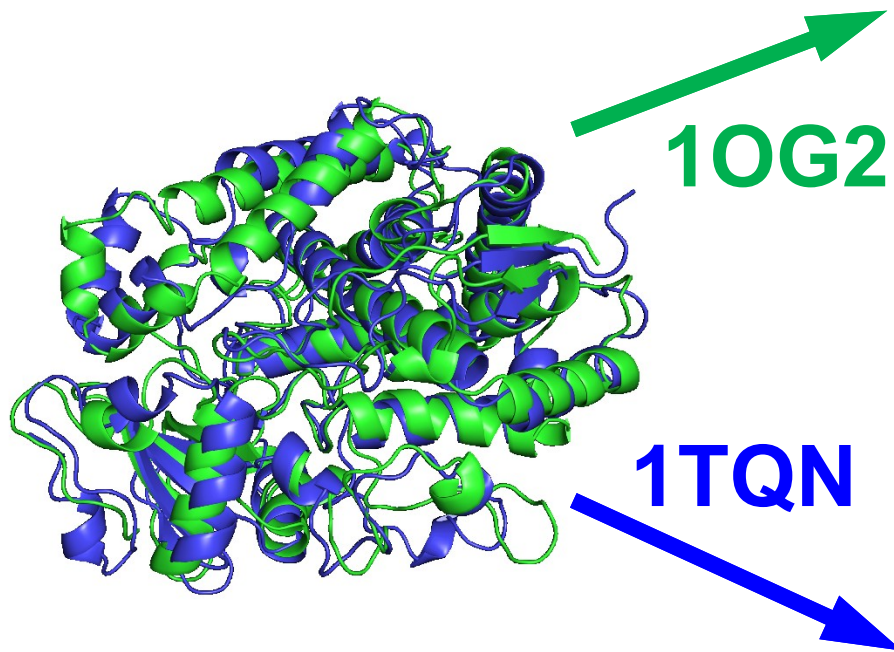


- Visualization



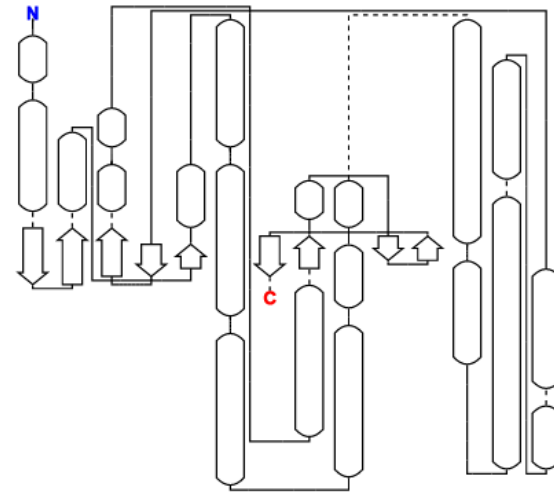
Visualization of secondary structure in 2D: Solved in past? Not for protein families!

ISSUE 1: Similar proteins have
different 2D diagrams

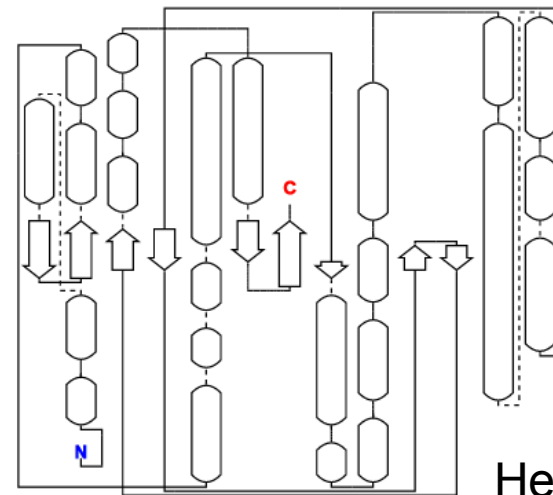


1OG2

1TQN



RMSD: 2.295 Å



Hera, PDBe

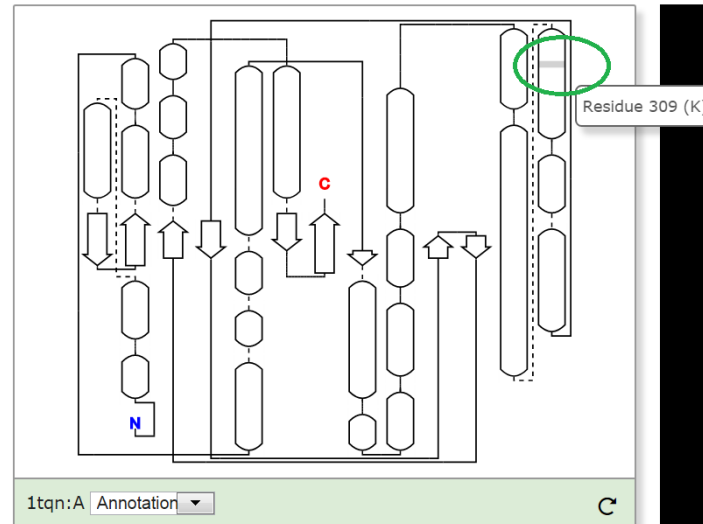
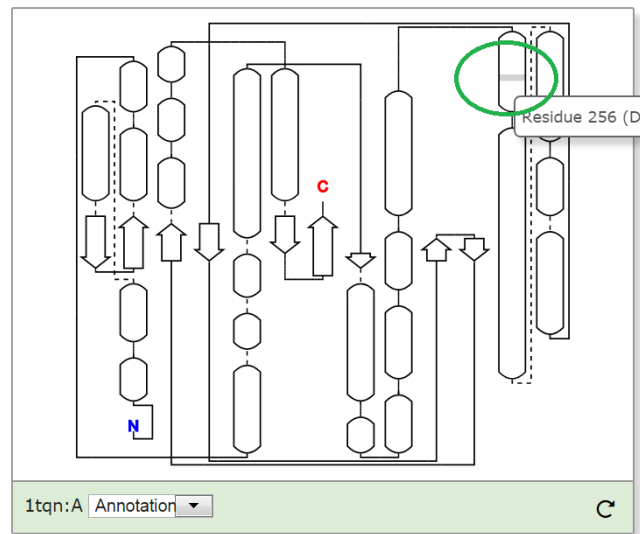
Visualization of secondary structure in 2D: Solved in past? Not for protein families!

ISSUE 2:

Secondary structure elements close in 2D diagrams are far in reality

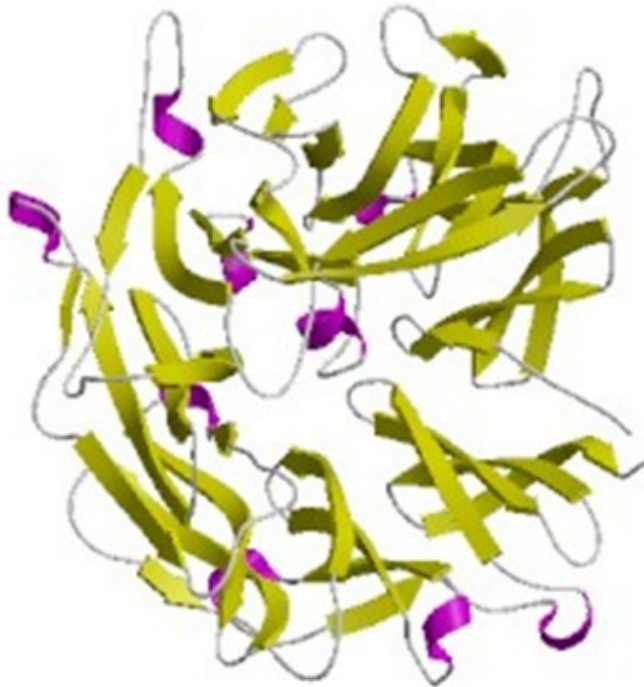
1TQN

Hera,
PDBe

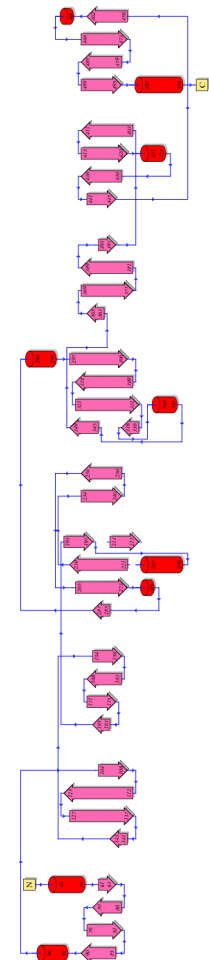


Visualization of secondary structure in 2D: Solved in past?

ISSUE 3: 2D diagrams does not reflect
a shape of a protein



1ORW



HERA

Protein family based 2D diagrams

How to get them?

Input:



Step 1: Detection & annotation

- Find secondary structure elements (SSE)
- Annotate them

Step 2: Statistics

- Average length of SSE
- Average occurrence of SSE

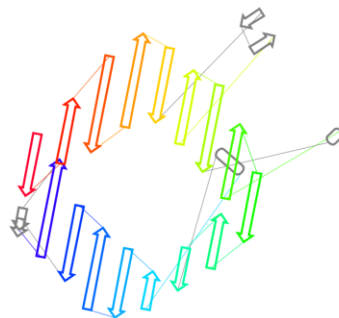
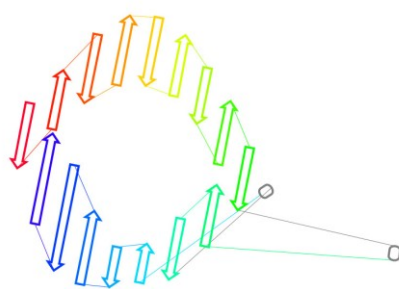
Protein family based 2D diagrams

How to get them?

Step 3: Construct the 2D diagram

- Group all β -strands into sheets
- Divide the **helices and sheets into primary** (common for most of the domains) **and secondary** (the remaining ones).
- **Place all primary** helices and sheets into the 2D diagram.
- **Adjust the angles** of the primary helices and sheets.
- **Add all secondary** helices and sheets into the 2D diagram.
- **Adjust the angles** of the secondary helices and sheets.

Step 4: Draw the 2D diagrams



Protein family 2D diagrams

2DProts database

<https://2dprots.ncbr.muni.cz>

2DProts

Custom entry

User manual

Description of methods

e.g., 1r9nA01, 1r9n, 2.140.10.

Search 2DProts

2DProts

Database of 2D diagrams of domain secondary structures

Examples

Click headings below to expand:



Porin (protein family 2.40.160.10)

Protein family 2D diagrams

2DProts database

2DProts

Custom entry

User manual

Description of methods

e.g., 1r9nA01, 1r9n, 2.140.10.3

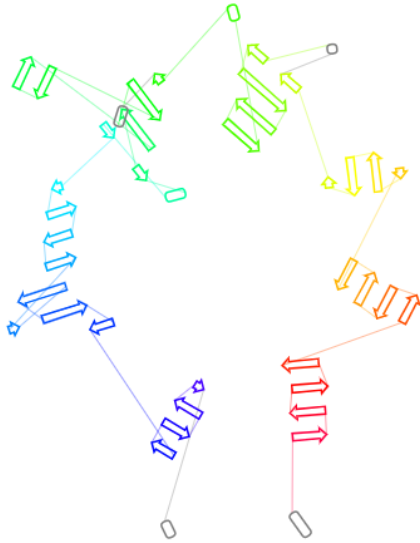
Search 2DProts

Domain 1j2eA01

2D domain diagram

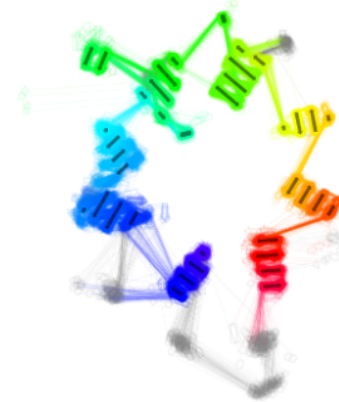
No ligands

With ligands



« no prev. | [1j2eB01](#) »

Member of
family:
[2.140.10.30](#)



Part of protein:
[1j2e](#)

Protein family 2D diagrams

2DProts database

Family 2.140.10.30

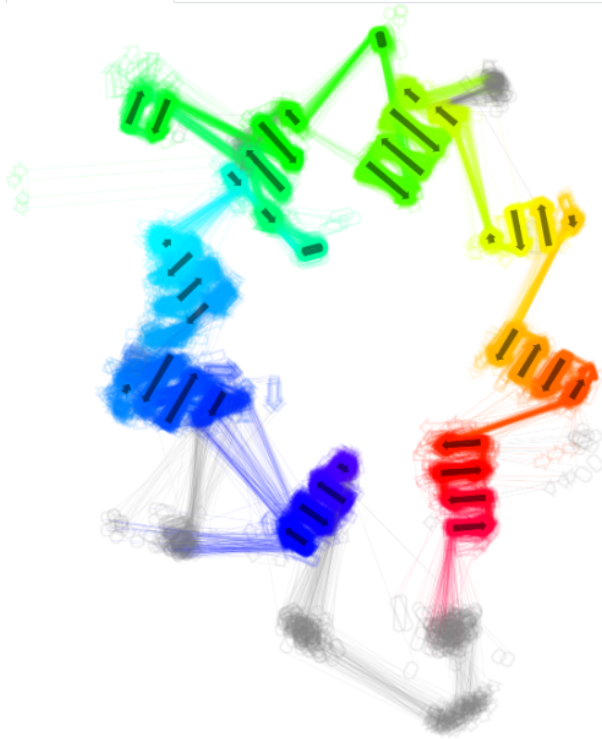
2D multi diagram

No ligands

With ligands

No ligands, opaque

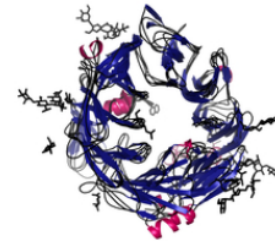
No ligands, opaque, no averages



Multi image for 2.140.10.30 ([svg source](#))

[« 2.140.10.20](#) | [2.150.10.10 »](#)

3D model ([CATH](#))

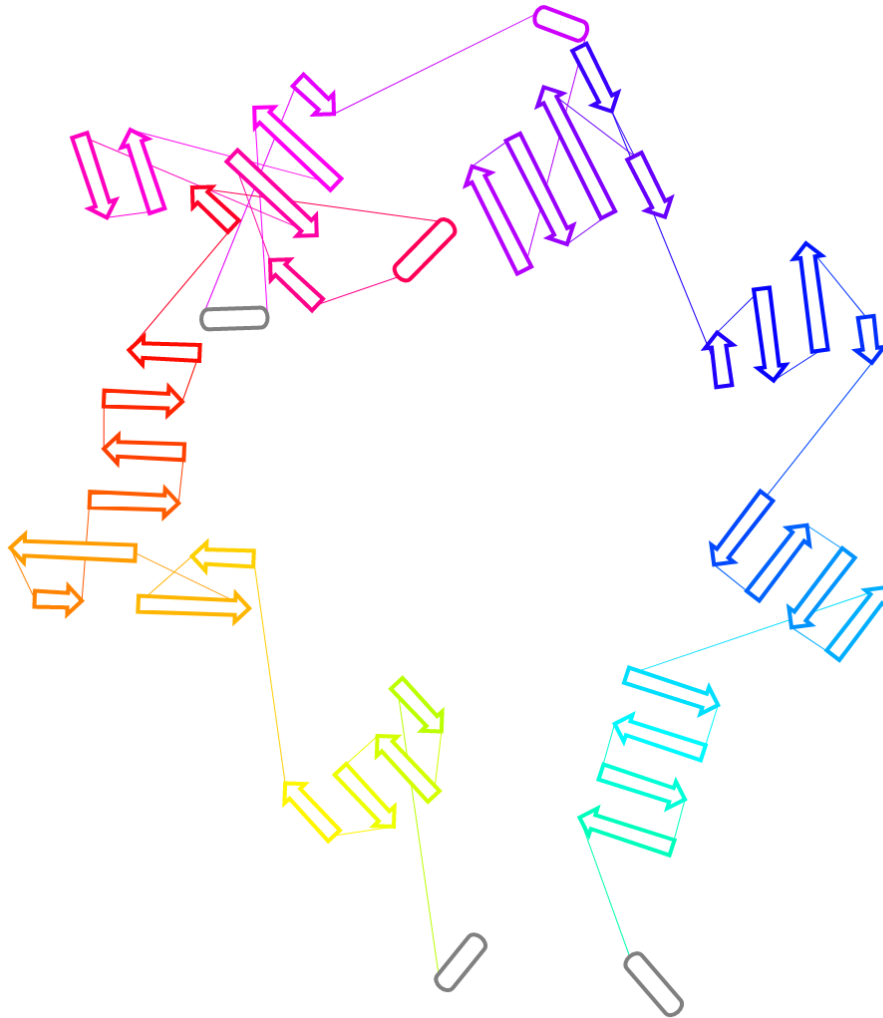


Domains (325)

- [1j2eA01](#)
- [1j2eB01](#)
- [1n1mA02](#)
- [1n1mB01](#)
- [1nu6A01](#)
- [1nu6B01](#)
- [1nu8A01](#)
- [1nu8B01](#)
- [1orvA01](#)

2DProts outputs

2D diagram of a protein domain



2DProts outputs: Multiple 2D diagram of protein domains in a family



With opacity



No opacity

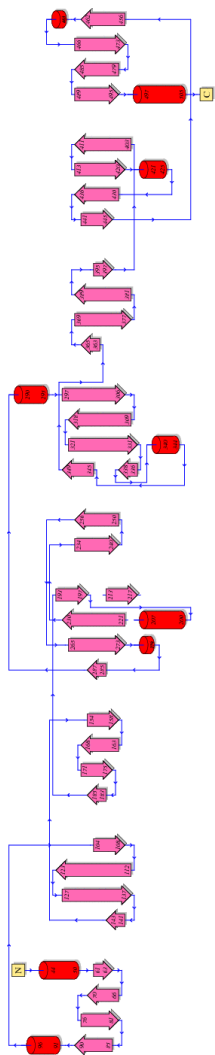
Superfamily: Dipeptidylpeptidase IV (2.140.10.30)

PROTEIN

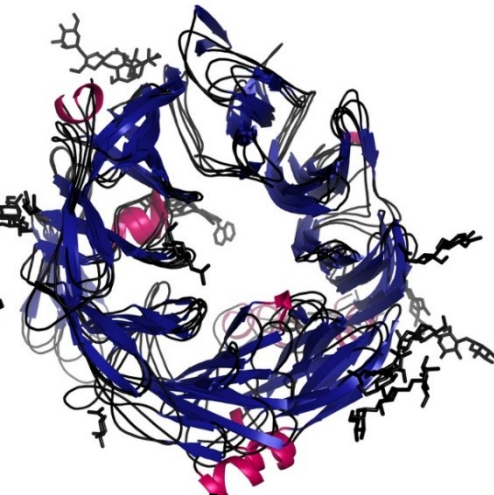
PROTEIN FAMILY

Current solution

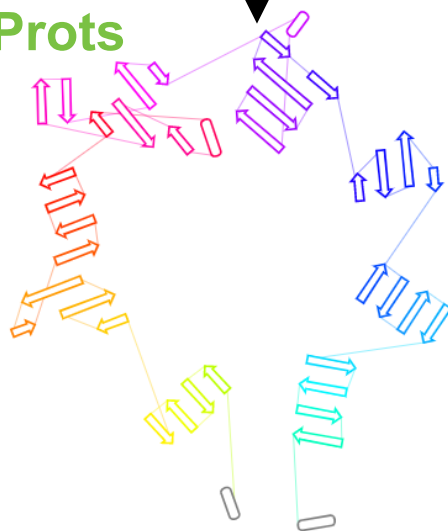
HERA



CATH



2DProts



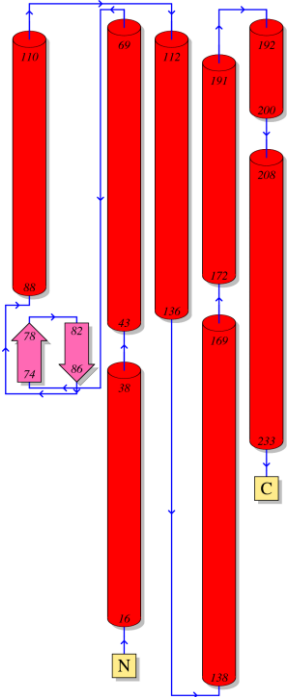
Superfamily: Rhodopsin 7-helix transmembrane proteins

PROTEIN (1.20.1070.10)

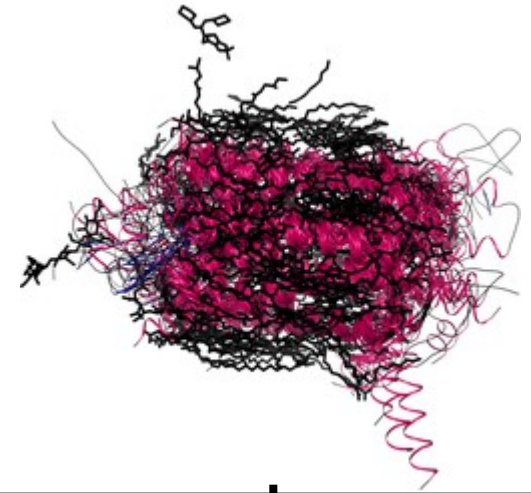
PROTEIN FAMILY

Current solution

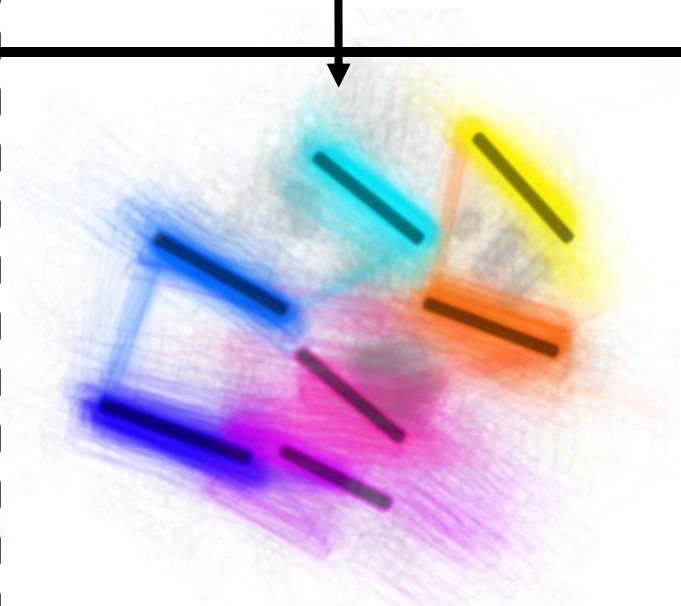
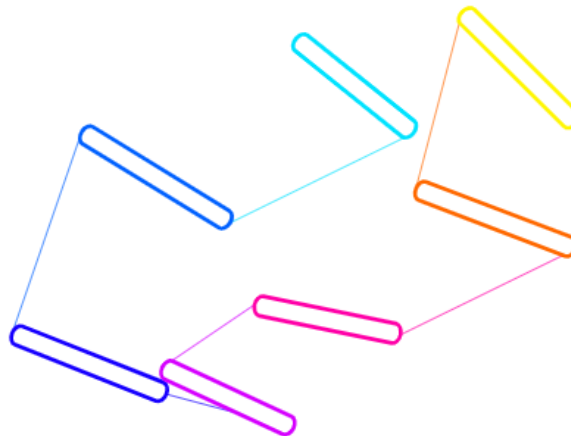
HERA



CATH



2DProts



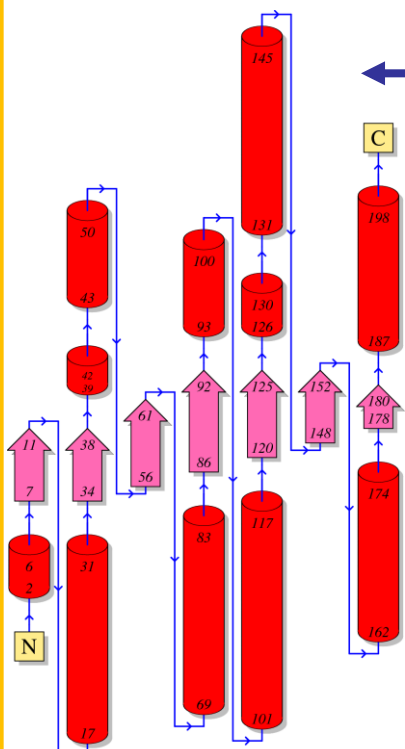
Superfamily: Aldolase class I (3.20.20.70)

PROTEIN

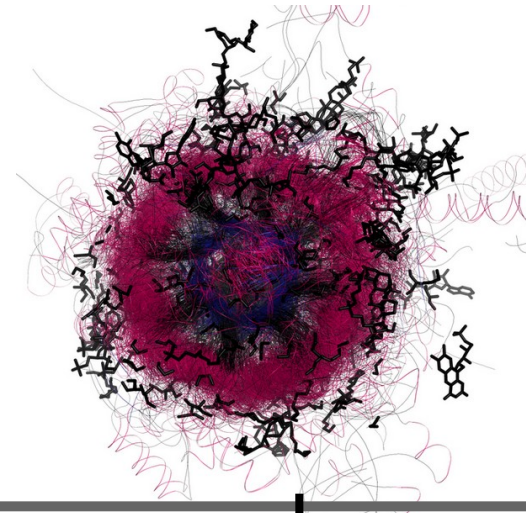
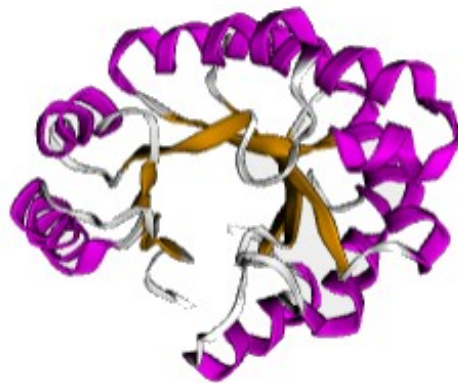
PROTEIN FAMILY

Current solution

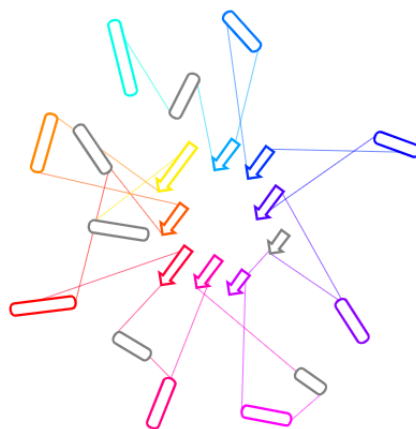
HERA



CATH



2DProts



2DProts integration to CATH

The screenshot shows the CATH database interface for Superfamily 1.10.60.10. The page title is "CATH Superfamily 1.10.60.10" with a subtitle "Iron dependent repressor, metal binding and dimerisation domain". A search bar and navigation menu are at the top. The main content area features a "SUPERFAMILY LINKS" sidebar with options like "Summary", "Superfamily Superposition", "Classification / Domains", "Functional Families", and "Structural Neighbourhood". The "Functional Families" section includes an overview and a diagram showing structural clusters (SC.1) and their functional families: Diphtheria t Transcriptio, Transcriptio, Iron (Metal), and Manganese. The main content area has tabs for "SS", "Alignbow", "2DProts", and "2DProts". A "Visit 2DProts (1.10.60.10)" button is visible. The central image is a 3D superposition of protein structures, with a blue box at the bottom stating: "These superposition figures provide an indication of the relative distance and position of secondary structure elements within CATH superfamilies. Image are generated by the 2DProts database".

CATH Superfamily 1.10.60.10

Iron dependent repressor, metal binding and dimerisation domain

Home / Superfamily 1.10.60.10

SUPERFAMILY LINKS

- Summary
- Superfamily Superposition**
- Classification / Domains
- Functional Families
- Structural Neighbourhood

Functional Families

Overview of the Structural Clusters (SC) and Functional Families within this CATH Superfamily. Clusters with a representative structure are represented by a filled circle.

- SC.1
- Diphtheria t Transcriptio
- Transcriptio
- Iron (Metal)
- Manganese

SS Alignbow 2DProts 2DProts

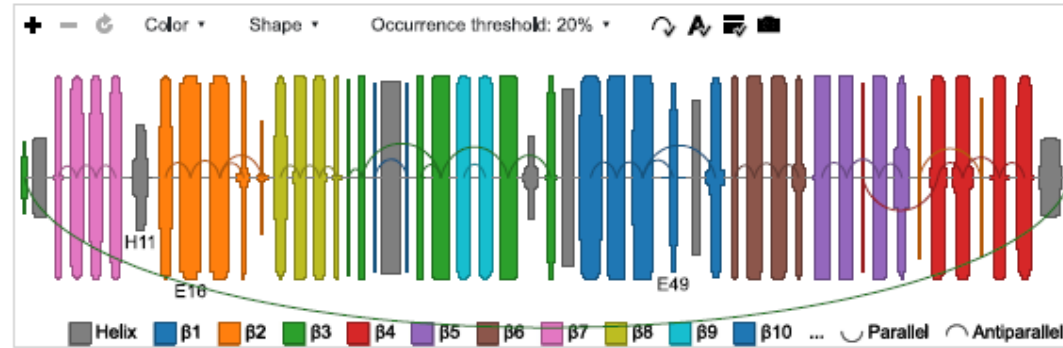
Visit 2DProts (1.10.60.10)

These superposition figures provide an indication of the relative distance and position of secondary structure elements within CATH superfamilies. Image are generated by the 2DProts database

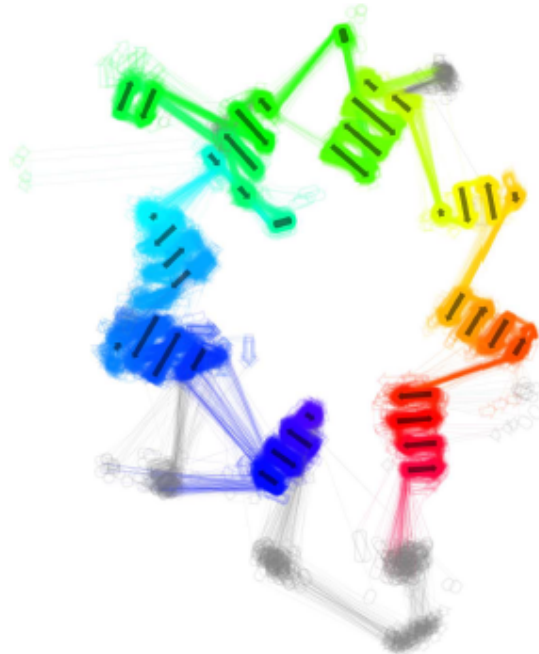
2DProts integration into OverProt

<https://overprot.ncbr.muni.cz>

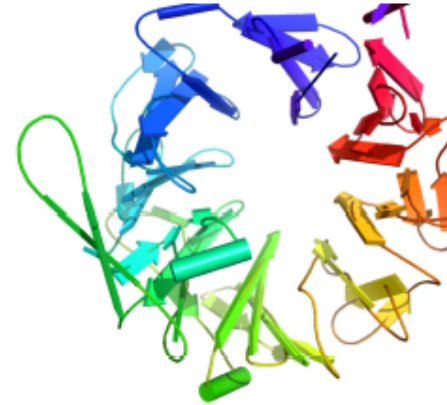
Family: 2.140.10.30 *Dipeptidylpeptidase IV, N-terminal domain*



2D view (2DProts)



3D view (MAPSCI + OverProt)



2DProts integration into OverProt

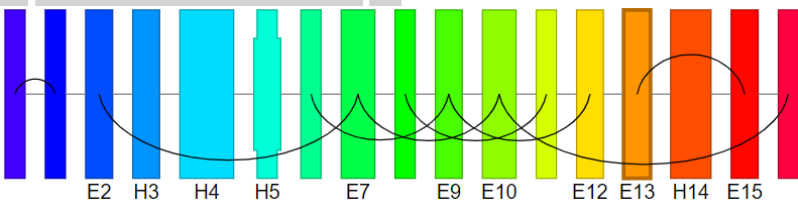
<https://overprot.ncbr.muni.cz>

Integrated Viewer

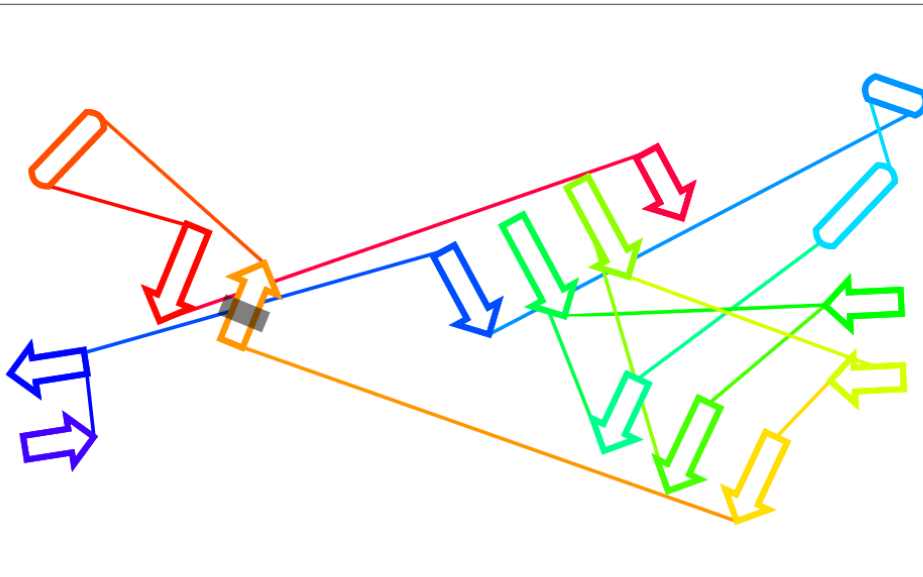
Current family (CATH): 2.160.10.30
Current domain: 3ogzA02

Protein family (CATH): 2.160.10.30
Protein domain: 3ogzA02 Submit

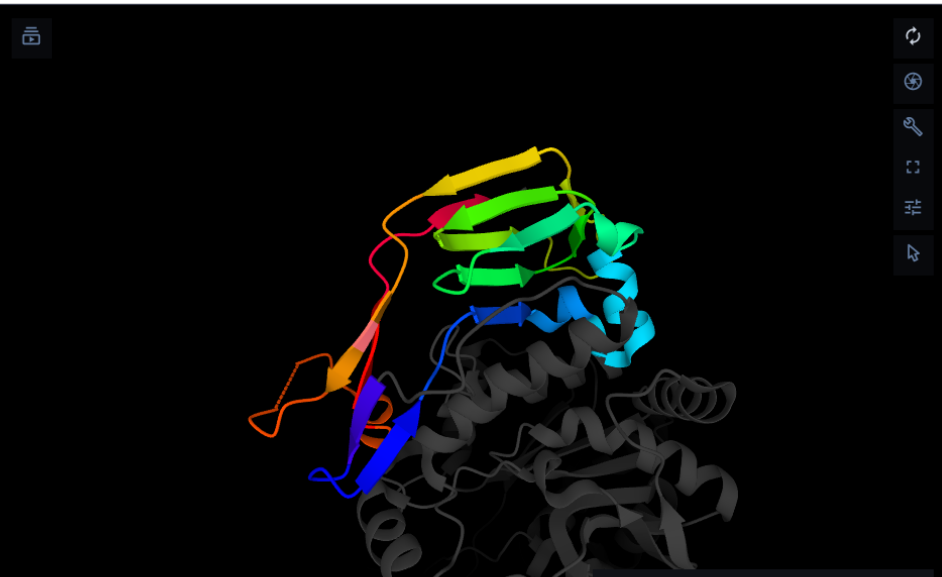
+ - ↺ Color ▾ Shape ▾ Beta-connectivity ▾ Occurrence threshold: 25% ▾ 📷



E2 H3 H4 H5 E7 E9 E10 E12 E13 H14 E15



3ogz | Entity 1 | Chain A Annotation ▾



UDP-sugar pyrophosphorylase
3OGZ | Model 1 | Instance_1_555 | A | VAL 575

Publications

Sillitoe I, ..., Berka K, Hutařová Vařeková I, Svobodová R., et al. (2021). *CATH: increased structural coverage of functional space*. **Nucleic Acids Research**, 49(D1), D266-D273.

Hutařová Vařeková, I., Hutař, J., Midlik, A., Horský, V., Hladká, E., Svobodová, R., & Berka, K. (2021). *2DProts: database of family-wide protein secondary structure diagrams*. **Bioinformatics**, 37(23), 4599-4601.

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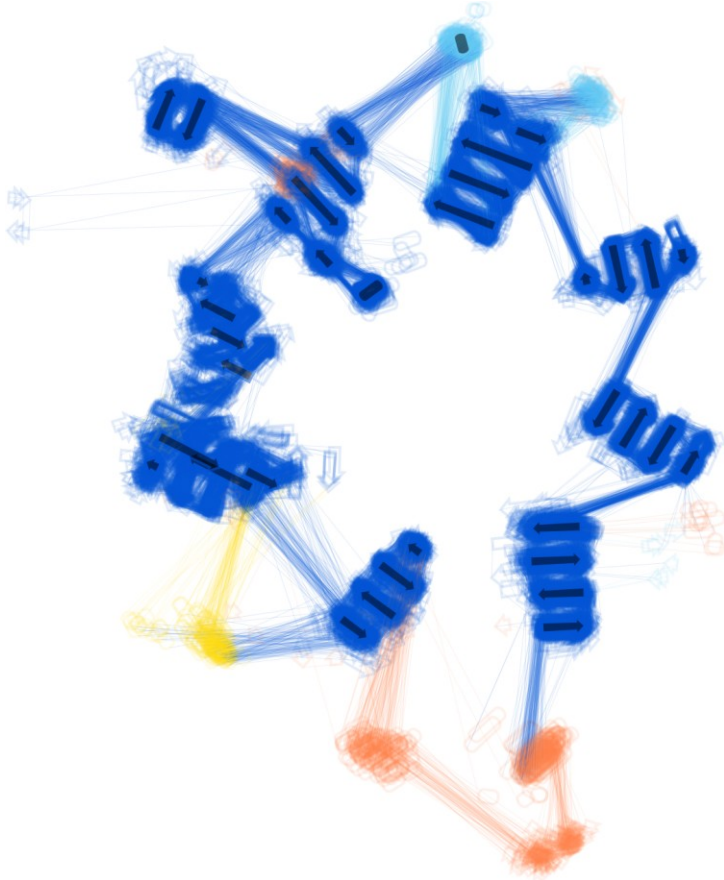
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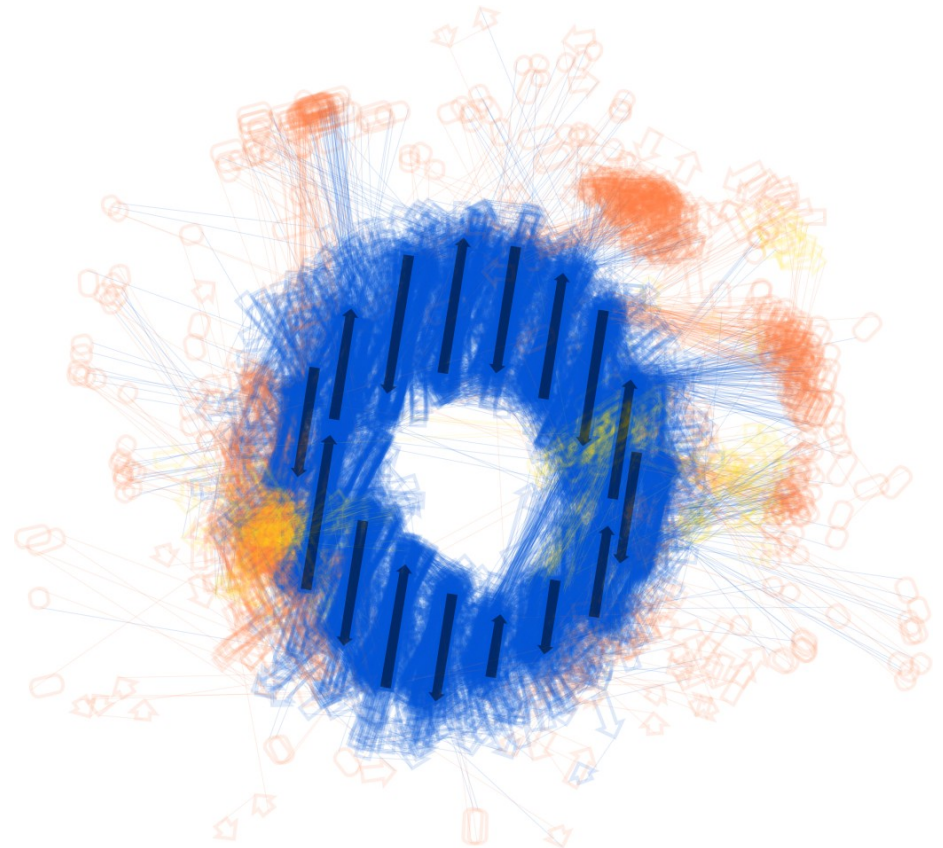


2DProts: Coloring by structure properties

Example: Occurrence of secondary structures

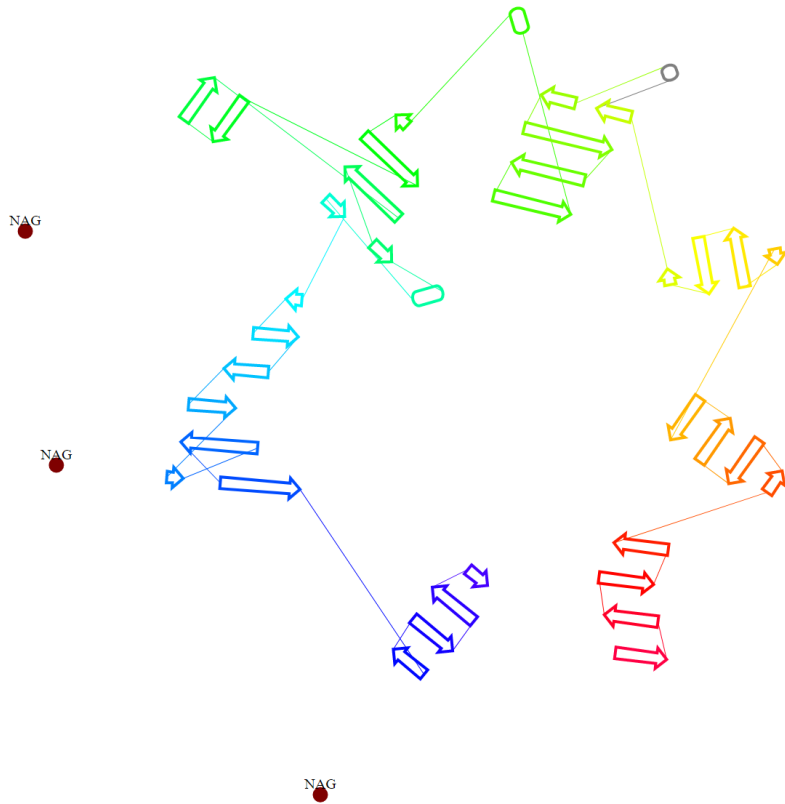


**Cytochrome reductase,
Family 2.140.10.30**

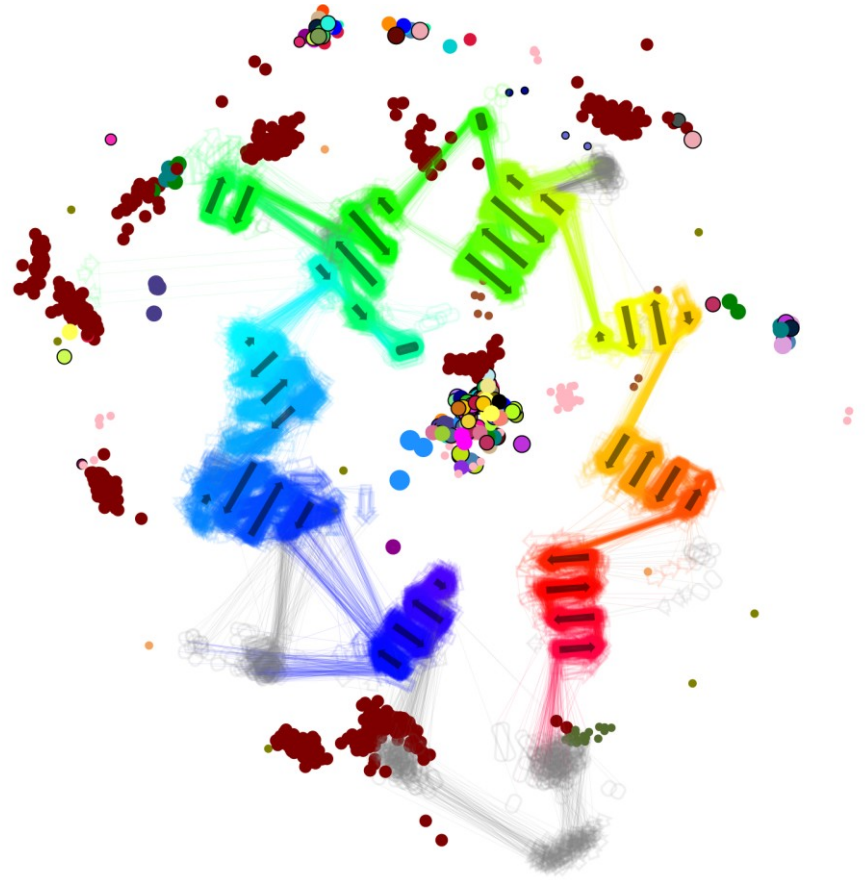


**Porin
Family 2.40.160.10**

2DProts: Integration of ligands



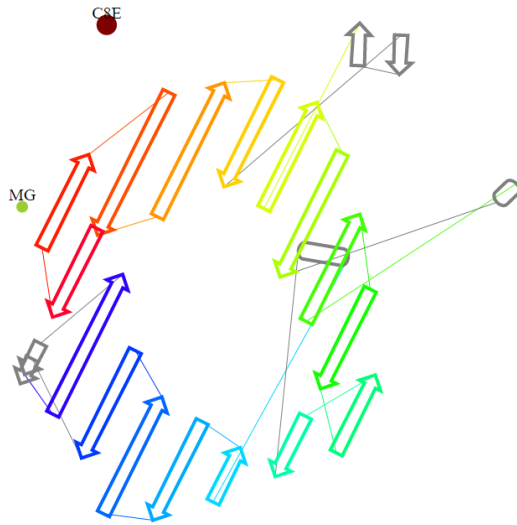
**PDB ID 2bgn,
domain A00**



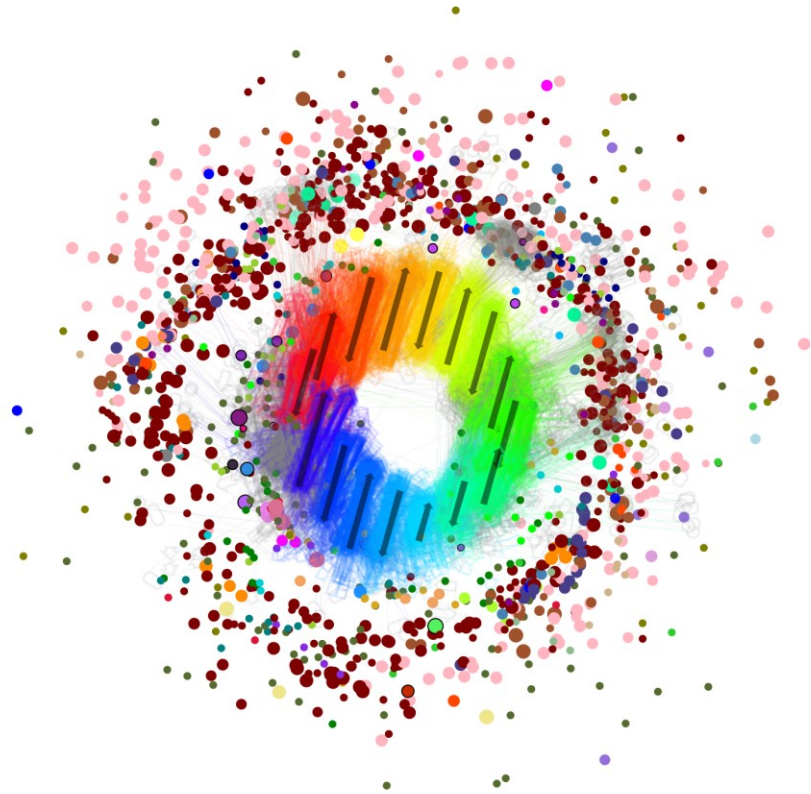
Cytochrome reductase, family 2.140.10.30

● ...NAG (742 pcs)	● ...SY1 (8 pcs)	● ...T22 (4 pcs)	● ...RUF (4 pcs)	● ...P2Y (4 pcs)	● ...0WG (4 pcs)	● ...10T (4 pcs)	● ...B2Q (2 pcs)
● ...S04 (56 pcs)	● ...SC3 (8 pcs)	● ...6RL (4 pcs)	● ...B2Y (4 pcs)	● ...8O3 (4 pcs)	● ...0QG (4 pcs)	● ...008 (4 pcs)	● ...P54 (2 pcs)
● ...NA (20 pcs)	● ...6Z8 (8 pcs)	● ...8OL (4 pcs)	● ...7AC (4 pcs)	● ...BPR (4 pcs)	● ...AES (4 pcs)	● ...01T (4 pcs)	● ...677 (2 pcs)
● ...HG (10 pcs)	● ...XIH (5 pcs)	● ...8VU (4 pcs)	● ...LF7 (4 pcs)	● ...007 (4 pcs)	● ...13Z (4 pcs)	● ...LUI (4 pcs)	● ...277 (2 pcs)
● ...EDO (9 pcs)	● ...715 (4 pcs)	● ...RUM (4 pcs)	● ...PHI (4 pcs)	● ...PEG (4 pcs)	● ...9K4 (4 pcs)	● ...75L (2 pcs)	● ...D3C (2 pcs)

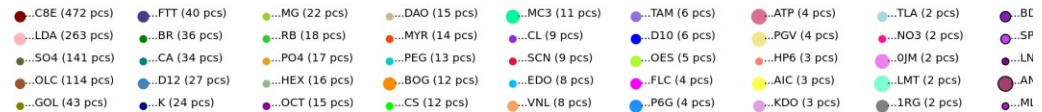
2DProts: Integration of ligands



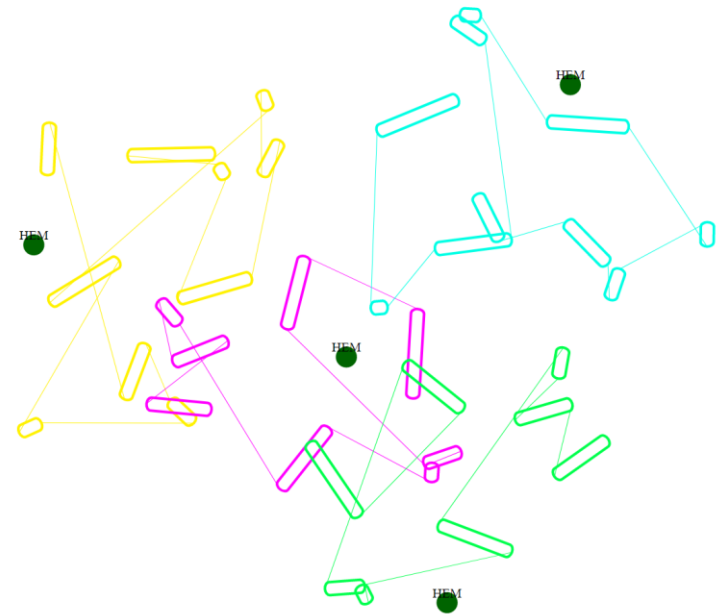
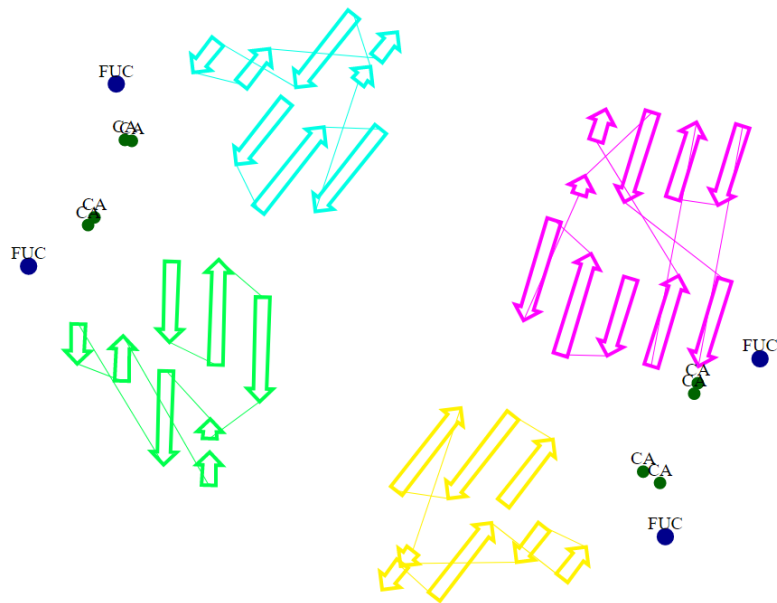
OMP Porin
PDB ID 2zfg,
domain A00



Porin, Family 2.40.160.10



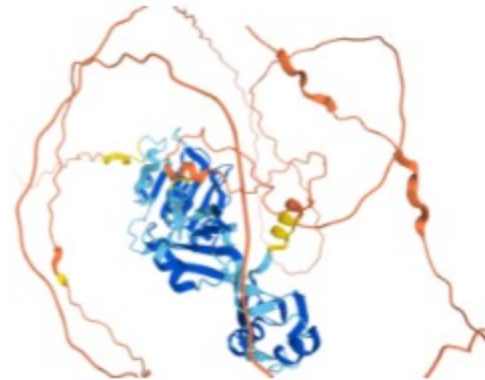
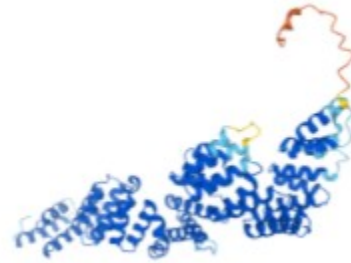
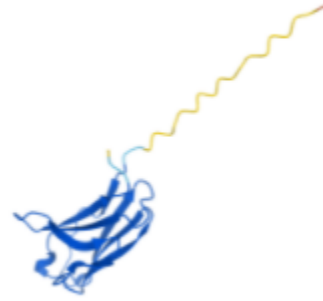
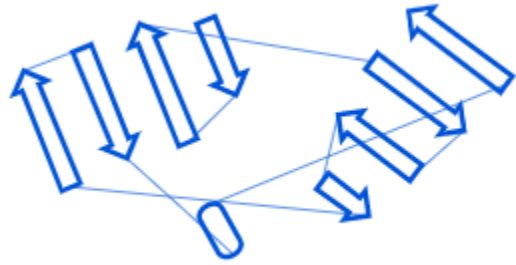
2DProts: 2D diagrams for proteins



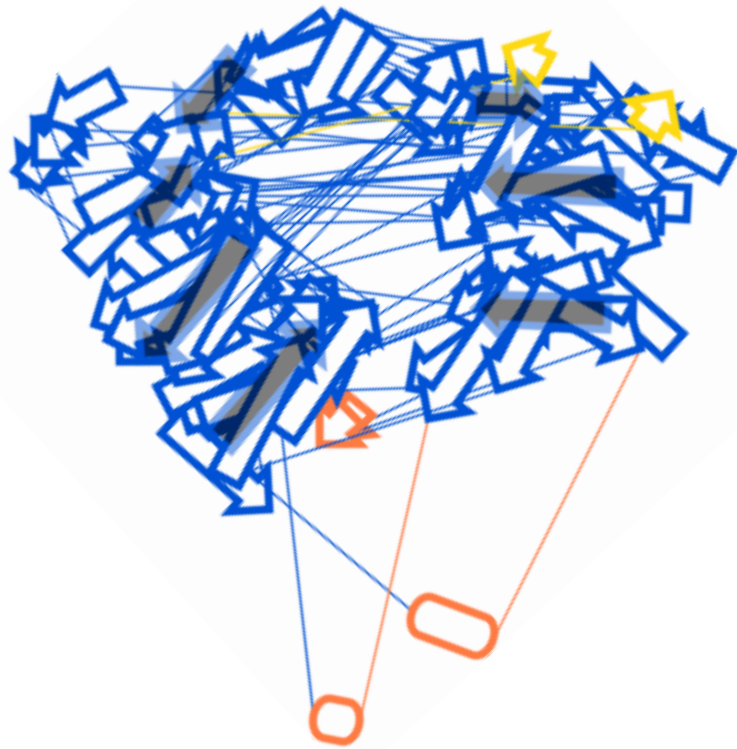
**Pseudomonas
aeruginosa lectin II
PDB ID 1gzt**

**Hemoglobine
PDB ID 1v4w**

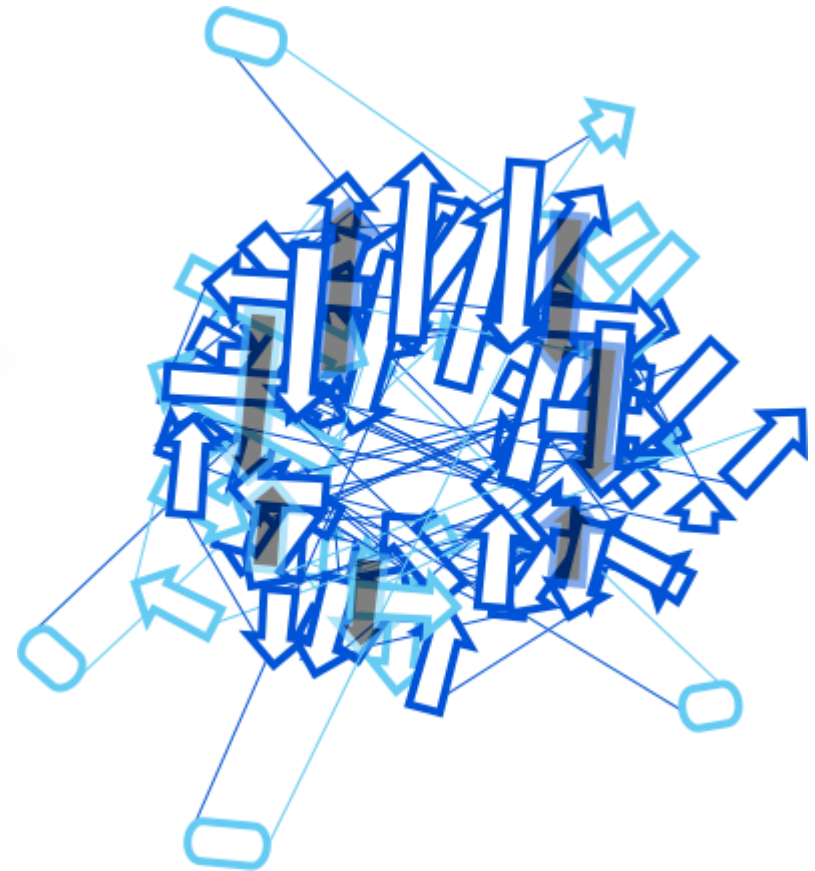
2DProts: Integration of AlphaFoldDB



2DProts: Integration of AlphaFoldDB



**Structures
from PDB**



**Structures from
AlphaFoldDB**

**E. coli PapC protein, C-terminal domain
Family 2.60.40.2070**