

Stereozobrazování molekul

C9531 - Seminář k přednášce Strukturní biochemie

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24. září 2024

Úvodní slovo

Požadavky k udělení zápočtu

- nutno napsat **4 průběžné testy** (každý minimálně na 60 %)
- neúspěšný test lze opakovat na konci semestru
- úspěšné složení testů je potřebné pro udělení zápočtu, vstupenka na ústní zkoušku k C9530

Úvodní slovo

Datum	Náplň cvičení
25.9./27.9.	3D zobrazování molekul, stereozobrazování
2.10./4.10.	Určování torzních úhlů - peptidy, Ramachandranův diagram
9.10./11.10.	Určování torzních úhlů - nukleotidy, struktura sacharidů
16.10./18.10.	Průběžný test 1: torzní úhly peptidů a nukleotidů
23.10./25.10.	Sekvenace
30.10./1.11.	Optické metody
6.11./8.11.	Průběžný test 2: sekvenace, optické metody
13.11./15.11.	Rentgenová krystalografie
20.11./22.11.	Rentgenová krystalografie
27.11./29.11.	Průběžný test 3: Rentgenová krystalografie
4.12./6.12.	Nukleární magnetická rezonance
11.12./13.12.	Nukleární magnetická rezonance
18.12./20.12.	Průběžný test 4: Nukleární magnetická rezonance

Stereozobrazování

- zobrazení pohledu levého a pravého oka vedle sebe
- otočené o cca 5° kolem vertikální osy
- zaostřuje se mimo rovinu, ze dvou obrázků vzniknou čtyři
- prostřední dva se složí v pseudo-3D obraz

Varianty stereozobrazování

wall-eyed:

- oči zaostřují za rovinou obrázku
- vyžaduje přesnou vzdálenost mezi obrázky
- častější při zobrazení na papíře
- levé oko se dívá na levý obrázek, pravé na pravý
- **pomůcka: zaostřit na vzdálený bod (cca 3 metry)**

Varianty stereozobrazování

cross-eyed:

- oči zaostřují před rovinou obrázku
- vzdálenost mezi obrázky není tak důležitá
- častější při zobrazení na monitorech
- levé oko se dívá na pravý obrázek, pravé na levý
- **pomůcka: zaostřit na bližší předmět, např. tužku**

PDB databáze: stereo zobrazení (cross-eyed)

<https://www.rcsb.org/>

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1,068,577 Computed Structure Models (CSM)

3D Structures 14-3-3 Include CSM Search

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PDB-101 PDB EMDB/Europe NAKB PDB-Dev

New: More Computed Structure Models (CSM) available [Learn more](#)

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- Experimentally-determined 3D structures from the Protein Data Bank (PDB) archive
- Computed Structure Models (CSM) from AlphaFold DB and ModelArchive

These data can be explored in context of external annotations providing a structural view of biology.

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SEARCH API
DATA API

September Molecule of the Month

Histone Deacetylases

Latest Entries *As of Jul, Sep, 22 2023*

Features & Highlights

News

Publications

BAXE
Small molecule stabilizer for ERalpha and 4A_2-3.1 (PDB: 1Y04)

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Learn about Leveraging RCSB PDB APIs for Bioinformatics Analyses and Machine Learning. Part 1 will introduce the Data and Search APIs. Part 2 will offer hands-on exercises.

Coming Soon: PDB Entries with Novel Ligands Distributed Only in PDBx/mmCIF and PDBML File Formats
PDB will run out of 3-character CCD IDs before the end of 2023. Afterwards, PDB entries with novel ligands will not be

Poster Prize Awarded at ACA 2023
Congratulations to Alexander Paredes for *Biophysical characterization of the Pseudomonas aeruginosa BqsA/BqsS two-component system*
= 09/19/2023

September 19: DNS name changes for PDB archive downloads from RCSB PDB
Programmatic users (ftp, rsync or https) should update scripts
= 09/15/2023

PDB databáze: stereo zobrazení (cross-eyed)

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Return Structures grouped by No Grouping Include Computed Structure Models (CSM) Count Clear Search

Search Summary This query matches 1,718 Structures.

Refinements Structure Determination Methodology experimental (1,718)

Scientific Name of Source Organism

- Homo sapiens (1,325)
- Mus musculus (279)
- synthetic construct (91)
- Dictyostelium discoideum (47)
- Hepatitis C virus isolate HC-J4 (44)
- Rattus norvegicus (39)
- Influenza A virus (12)
- Nicotiana glauca (12)
- Pseudomonas horreola (11)
- Pseudomonas aeruginosa (11)
- [More...](#)

Taxonomy

- Eukaryota (1,649)
- Riboviria (129)
- other sequences (91)
- Bacteria (30)
- Microsporidia (8)
- Viridivirales (3)
- unclassified sequences (2)
- Archaea (1)
- Duplodictyonia (1)

Experimental Method

- X-RAY DIFFRACTION (1,618)
- SOLUTION NMR (52)
- ELECTRON MICROSCOPY (48)

Polymer Entity Type

- Protein (1,718)
- DNA (92)
- RNA (6)

Refinement Resolution (Å)

- 0.5 - 1.0 (1)
- 1.0 - 1.3 (213)

1 to 25 of 1,718 Structures Page 1 of 69 25 Sort by Score

2NDM crystal structure of *Cryptosporidium parvum* 14-3-3 protein in complex with peptide
Dong, A., Lew, J., Wasney, G., Ren, H., Lin, L., Hassanat, A., Qiu, W., Zhao, Y., Doyle, D., Voth, A., Koziaradzki, I., Edwards, A.M., Arrowsmith, C.H., Weigek, J., Arrowsmith, C.H., Edwards, A.M., Bochkarev, A., Hul, R., Brok, S., Structural Genomics Consortium (SGC)
(2011) PLoS One 6: e14827-e14827
Released 2008-11-07
Method X-RAY DIFFRACTION 2.52 Å
Organisms *Cryptosporidium parvum*
Macromolecule 14-3-3 domain containing protein (protein)
CONSENSUS PEPTIDE FOR 14-3-3 PROTEINS (protein)

3EFZ Crystal Structure of a 14-3-3 protein from cryptosporidium parvum (cgd1_2980)
Wernimont, A.K., Dong, A., Qiu, W., Lew, J., Wasney, G.A., Vedadi, M., Koziaradzki, I., Zhao, Y., Ren, H., Alam, Z., Lin, Y.H., Sundstrom, M., Weigek, J., Arrowsmith, C.H., Edwards, A.M., Bochkarev, A., Hul, R., Brok, S., Structural Genomics Consortium (SGC)
(2011) PLoS One 6: e14827-e14827
Released 2008-09-23
Method X-RAY DIFFRACTION 2.08 Å
Organisms *Cryptosporidium parvum* Iowa II
Macromolecule 14-3-3 protein (protein)
Unique Ligands EDO

1O9C Structural view of a fungal toxin acting on a 14-3-3 regulatory complex
Wurtele, M., Jelic-Ottmann, C., Wittlinger, A., Oecking, C.
(2003) EMBO J 22: 987
Released 2003-03-06
Method X-RAY DIFFRACTION 2.6 Å
Organisms *Nicotiana glauca*
Macromolecule 14-3-3-LIKE PROTEIN C (protein)
Unique Ligands CL, FLC

<https://www.rcsb.org/structure/2NDM>

PDB databáze: stereo zobrazení (cross-eyed)

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3D Structures [Enter search term(s), Entry ID(s), or sequence] Include CSM Help

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f t v

Structure Summary 3D View Annotations Experiment Sequence Genome Versions

Biological Assembly 1

2NPM

crystal structure of *Cryptosporidium parvum* 14-3-3 protein in complex with peptide

PDB DOI: <https://doi.org/10.2210/pdb/2NPM/pdb>

Classification: PROTEIN BINDING
Organism(s): *Cryptosporidium parvum*
Expression System: *Escherichia coli*
Mutation(s): No

Deposited: 2006-10-27 **Released:** 2006-11-07
Deposition Author(s): Dong, A., Lew, J., Wasney, G., Ren, H., Lin, L., Hassanali, A., Qiu, W., Zhao, Y., Doyle, D., Vedadi, M., Koeieradzki, I., Edwards, A.M., Arowsmith, C.H., Weigelt, J., Sundstrom, M., Bochkarev, A., Hui, R., Broks, S., Structural Genomics Consortium (SGC)

Experimental Data Snapshot
Method: X-RAY DIFFRACTION
Resolution: 2.52 Å
R-Value Free: 0.275
R-Value Work: 0.221
R-Value Observed: 0.222

wwPDB Validation

Metric	Percentile Ranks	Value
B-factor		6.292
Chlorides		5
Ramachandran outliers		6
Sidechain outliers		7.33
RSRZ outliers		4.15

This is version 1.5 of the entry. See complete [history](#).

Literature [Download Primary Citation](#)

Characterization of 14-3-3 proteins from *Cryptosporidium parvum*.
[Broks, S.J., Wernimont, A.K., Dong, A., Wasney, G.A., Lin, Y.H., Lew, J., Vedadi, M., Lee, W.H., Hui, R.](#) (2011) *PLoS One* 6: e14827-e14827

3D View | Structure | 3D View | Electron Density Visualization Report

Global Symmetry: Cyclic - C2 (3D View)
Global Stoichiometry: Hetero 4-mer - A2B2

Pseudo Symmetry: Asymmetric - C1
Pseudo Stoichiometry: Hetero 4-mer - A2B1C1

Find Similar Assemblies

Biological assembly 1 assigned by authors and generated by PISA (software)

Macromolecule Content

- Total Structure Weight: 61.02 kDa
- Atom Count: 3,756
- Modelled Residue Count: 484
- Unmodelled Residue Count: 532

<https://www.rcsb.org/3d-view/2NPM/>

PDB databáze: stereo zobrazení (cross-eyed)

Sequence of 2NP1 | cryst... | Chan | 1: 14-3-3 dom... | A

```
GI1LPTD772 DFLRITKDDHGLSDSNAERVYIMELAGLADSTYSDMAYTNDVYRQDQIIGKLTYSRHLIYVAYENYGGKSSHWI11LIVGKQKSHSMAIDASKNPK  
YASVVAASVYICMIDILM171 181 191 201 211 221 231 241 251 261 271 281 291 301 311 321 331 341 351 361 371 381 391 401 411 421 431 441 451 461 471 481 491 501 511 521 531 541 551 561 571 581 591 601 611 621 631 641 651 661 671 681 691 701 711 721 731 741 751 761 771 781 791 801 811 821 831 841 851 861 871 881 891 901 911 921 931 941 951 961 971 981 991 1001  
SAFENMATEIQLKLEEDCYKSTLIMQLLQKLLTMTA:
```

Structure

2NP1 | crystal structure of Cryptos...
Type Assembly
Asm Id 1: Author And Software...
Dynamic Bonds x Off
Nothing Focused

Measurements
Structure Motif Search

Components 2NP1

Presets + Add
Polymer Carbon
Non-standard Ball & Stick
Water Ball & Stick
Unit Cell P 41 21 2

Density
Quality Assessment
Assembly Symmetry
Export Models
Export Animation
Export Geometry

Settings / Controls Info

Animate	Off
Camera	Perspective
Background	---
Occlusion	✓ On
Shadow	x Off
Outline	x Off
Fog	✓ On
Clipping	58
Layout	1 of 1

Moving in 3D
Mouse & Key Controls

Select a different viewer Mol* (VMDGL)

PDB databáze: stereo zobrazení (cross-eyed)

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Sequence of 2ZNP | crystal... Chain 1: 14-3-3 dom... A

GLLPDCHT...
YKSFVKAET...
EAFEMATE...

Structure
2ZNP | crystal structure of Cryptos...
Type Assembly
Asm Id 1: Author And Software...
Dynamic Bonds X Off
Nothing Focused
Measurements
Structure Motif Search
Components 2ZNP
Preset + Add
Polymer Carbon
Non-standard Ball & Stick
Water Ball & Stick
Unit Cell P 41 21 2
Density
Quality Assessment
Assembly Symmetry
Export Models
Export Animation
Export Geometry

Settings / Controls Info
Animate Off
Camera Perspective
Axes On
Stereo X Off
Field of View 45
Background
Occlusion On
Shadow X Off
Outline X Off
Fog On
Clipping 58
Layout 1 of 1

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Help

Sequence of 2NPM | cryst... Chain 1: 14-3-3 dom... A

```
GLLPDPTDQDLKLTNHSVGLGSHNAGEVYVMAKLAGLQARVYDGNFVREYVFAQ...ELTVSRNLGVAFFKRWGQRSGNII...LGVGKPKHSNADGASNKQK  
YRQVFAEDFVYKMLLILNLRKLLKPTVYDQVYVYFVYKQVYRVTYDSEYDQDQSDAGLAKATKATVVAQDGLPDSHGLGLAIDVYVYVYI...LREPRKATIMAK  
EAFDVAIEGLQKLEDECYKSTLNLKLLKQKTLAKA
```

Structure

2NPM | crystal structure of Cryoprot...
Type Assembly
Asm Id 1: Author And Software...
Dynamic Bonds X Off
Nothing Focused
Measurements
Structure Motif Search
Components 2NPM
Preset + Add
Polymer Cartoon
Non-standard Ball & Stick
Water Ball & Stick
Unit Cell P 41 21 2
Density
Quality Assessment
Assembly Symmetry
Export Models
Export Animation
Export Geometry

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