Bi4999en – Structural Biology and Bioinformatics

Academic term: Autumn 2023

Course content:

1. **Introduction to the structure of macromolecules** – composition, methods for determination, application in biology, visualization.
2. **Structure of biomolecules** – different levels of structure of proteins and nucleic acids
3. **Bioinformatics databases and structure prediction** – sequence databases, structural databases, retrieval and evaluation of macromolecular structures
4. **Structural databases and models of structures** – structural databases, validation and methods for quality assessment, preparation of models.
5. **Stability and dynamics of macromolecules** – analysis of molecular dynamics and stability, prediction of stability, databases.
6. **Analysis of protein structures** – identification of important regions: binding/active sites, aggregation propensity, transport pathways, flexible regions, binding/catalytic amino acids.
7. **Protein-ligand complexes** – evaluation of complexes, analysis of interactions, druggability, databases, transport of small molecules.
8. **Macromolecular complexes and interactions** – protein-protein and protein-DNA complexes, analysis of interactions, databases.
9. **Engineering of protein structures** – effect of mutations on the protein structure, stability and function.
10. **Applications of structural biology and bioinformatics** – biological research, drug design, engineering of biocatalysts.

Detailed content

1. Introduction to the structure of macromolecules

- Course information
- Other courses from LL
- Motivation and applications of structural biology
- Structural biology: basics and historical perspective
- Structure visualization
- Energetics and molecular interactions
- Experimental methods for structure determination
- Basics of Bioinformatics: sequence, databases, homology modelling, machine learning, *ab initio*

2. Structure of biomolecules

- Proteins: primary to quaternary structures
- Calculation of secondary structures: DSSP method
- Protein motifs, domains and folds
- Nucleic acids: primary to higher structures
- Structural data formats: types of data format; PDB, mmCIF and PDBML
- Structural databases (list)

3. Bioinformatics databases and structure prediction

- Sequence-structure-function relationship (intro) [or refer to 1-4ry structures progression]
- Sequence databases
- Sequence alignments
- Sequence analysis (prediction of properties at sequence level (eg. solubility)
- Sequence-structure-function relationship
- Structure prediction from sequence

4. Structural databases and models of structures

- Structural databases
- Validation and quality assessment

5. Stability and dynamics of macromolecules

- Protein folding
- Protein stability, its prediction, databases
- Protein dynamics

6. Analysis of protein structures

- Solvent accessibility
- Solubility and aggregation
- Molecular interactions
- Functional sites
- Binding/catalytic amino acids
- Evolutionary conservation
- Transport pathways

7. Protein-ligand complexes

- Structure of complexes
- Databases of complexes
- Protein druggability

- Databases of small molecules
- Molecular docking
- Evaluation of complexes
- Transport of small molecules

8. Macromolecular complexes and interactions

- Evaluation of protein-protein and protein-DNA complexes
- Analysis of protein-protein interactions
- Databases

9. Engineering of protein structures

- Types of mutations
- Databases of mutations
- Effects of mutation on protein structure and function
- Prediction of mutation effects

10. Applications of structural biology and bioinformatics

- Biological research
- Drug design and development
- Design of biocatalysts

Literature

- **J. Gu & P. E. Bourne (2009), Structural Bioinformatics, Wiley-Blackwell,**
- **G. A. Petsko & D. Ringe (2004), Protein Structure and Function, New Science Press**
- Claverie, J-M., & Notredame, C. (2006), Bioinformatics for Dummies (2nd ed.) Wiley Publishing, Hoboken, p. 436
- Xiong, J. (2006) Essential Bioinformatics, Cambridge University Press, New York, p. 352.
- T. Schwede & M. C. Peitsch (2008), Computational Structural Biology: Methods and Applications, World Scientific Publishing Company
- A. Liljas, L. Liljas, J. Piskur, G. Lindblom, P. Nissen, M. Kjeldgaard (2009), Textbook Of Structural Biology, World Scientific Publishing Company

Evaluation methods

Multiple-choice test, multiple correct answers possible, 10 correct answers out of 25 needed to pass the exam

Evaluation grading

Grades are based on the number of correct answers as follows:

A: 22-25

B: 19-21

C: 16-18

D: 13-15

E: 10-12

F (fail): < 10