**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