Advamced Cell Physiology

2 units (selection)

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Target⟩ This class is intended to demonstrate how to use capable molecular viewers (PyMol & Coot) for protein structure, which can be used for detailed analyses of protein 3D-structure.

Outline⟩ This class (portfolio) introduces how the programs (PyMol & Coot) can be used, and what their capabilities are.

Style⟩ Portfolio

Keyword⟩ *protein 3D-structure, protein data bank, PyMol, Coot*

Relational Lecture⟩ "**Biological macromolecular chemistry**"(0.5)

Requirement⟩ Students are required to bring note-type PC, if necessary (Windows is better).

Goal⟩
1. To understand protein coordinate file.
2. To understand operation of molecular viewers.

Schedule⟩
1. Protein Data Bank and coodinate file
2. Installation of the programs
3. Getting started with mouse controls
4. Getting started with commands
5. Comand syntax
6. Atom selection
7. Ray-tracing and stereo
8. Animation
9. Tutorial 1:basics
10. Tutorial 2:advanced techniques
11. Tutorial 3:example scripts
12. Exercise 1:editing of PDB file
13. Exercise 2:structural comparison
14. Exercise 3:DALI web server
15. Exercise 4: WHAT IF web server

Evaluation Criteria⟩ Drawing products with brief explanation (assignments count 100%)

Textbook⟩ To be introduced in the class

Reference⟩ To be introduced in the class

Contents⟩ http://cms.db.tokushima-u.ac.jp/cgi-bin/toURL?EID=216663

Student⟩ Able to be taken by only specified class(es)

Contact⟩
⇒ Administration Office(M703)

Note⟩
◇ When you take this class, it is necessary to do preparation for 2h and review for 2h everry 2h class for your understanding and taking credit.
◇ 成績評価に対する平常点と試験の比率は 50:50 とする．平常点には講義への参加状況，演習への回答及びレポートの提出状況と内容を含み，試験は中間テストと最終試験の成績を含む．