POLITECHNIKA GDAŃSKA

DOCTORAL SCHOOL AT GDAŃSK UNIVERSITY OF TECHNOLOGY

Course: Advances in Biotechnology: Protein Folding and Assembly

Teaching hours: 15 h

Prerequisites: The course is primarily open to all PhD students at Gdansk University of Technology.

This course is compulsory for PhD students assigned to Chemical Sciences discipline - Biotechnology area tracks at Doctoral School at Gdańsk University of Technology

Course outline

Content

This module is all about getting the student to be prepared to understand basic principals and current advances in protein folding process. The sessions provide essential information that you require to know at molecular, genetic and biochemical level various components that drive in vivo protein folding. The course is designed to deliver to students knowledge on chaperones, folding catalysts, proteases and protein aggregation and disaggregation process. Throughout the course the students should gain skills to proteostasis process and involvement in improving protein solubility and human diseases.

General topics coverage:

1. Classical concept of protein folding (the Anfinsen postulate and the Levinthal paradox).
2. Protein folding models, the energy landscape and the folding funnel.
3. Protein misfolding, unfolding and aggregation.
4. Molecular chaperones and catalysts of protein folding.
5. Hsp70/Hsp40 molecular chaperone system and Hsp60/Hsp10 chaperonin system.
6. Disulfide bond formation proteins.
7. Peptidyl-prolyl *cis/trans* isomerases.
8. Heat shock response.
9. Proteases that remove unfolded or aggregated proteins.
10. Pathways for protein disaggregation.
11. Regulation of protein folding.
12. Assembly of proteins.
13. Prions – infectious agents composed of protein in a misfolded form.

14. Diseases cause by protein misfolding or aggregation (for example Parkinson's, Huntington's, Alzheimer's diseases, cataract, sickle cell disease, cystic fibrosis).
15. Protein folding: a perspective for biology, medicine and biotechnology, protein engineering and design.

Teaching mode

There will be 15 hours of lectures to be completed during the first and/or second semesters of PhD programme. The teaching method is basically discussing protein folding machinery combined with recent publications elucidating protein folding process. During the course students will be asked to discuss new publications that will be provided during lectures. The course is entirely delivered in English.

Examination

A wide range of formative feedback from your tutor, questions and practical individual and group exercises will be used by tutors to aid learning as will exercises to encourage the researchers' abilities in critical and reflective learning. The exact nature of these assessment devices will be at the discretion of the tutor. The PhD students will be required to demonstrate their skills, knowledge and understanding of protein folding and assembly during written examination.

Fundamental readings:

1. Thomas E. Creighton "Protein Folding" textbook
2. Labbadia, J. and Morimoto, R.I. The biology of proteostasis in aging and disease. 2015, *Annu. Rev. Biochem.* 84, 435-465.
3. Raina, S. and Missiakas, D. Making and breaking disulfide bonds. 1997, *Annu. Rev. Microbiol.* 51, 179-202.
4. Saibil, H. Chaperone machines for protein folding, unfolding and disaggregation. 2013, *Nat. Rev. Mol. Cell Biol.* 14, 630-642.
5. Fersht, A.R. From the first protein structures to our current knowledge of protein folding: delights and scepticisms. 2008, *Nat. Rev. Mol. Cell Biol.* 9, 650-654.
6. Kim, Y.E., Hipp, M.S., Bracher, A., Hayer-Hartl, M. and Hartl, FU. Molecular chaperone functions in protein folding and proteostasis. 2013, *Annu. Rev. Biochem.* 82, 323-355.