UCLouvain

wsbim2115
2024

Protein structure / Function relationships

4.00 credits	30.0 h	Q1

Teacher(s)	Bertrand Luc ;Bommer Guido (coordinator) ;Collet Jean-François ;Laloux Géraldine ;
Language :	English
Place of the course	Bruxelles Woluwe
Prerequisites	Good background in chemistry, physics and biochemistry. Basic computer skills (including use of search engines and data base searching).
Main themes	Methods of expression, purification an in vitro renaturation of proteins (5h) Protein sequencing (2h) Bioinformatic analysis of proteins (homology searches, alignments, phylogenetic studies, motif and domain searching, structure modelling) (10h) Structure determination by NMR, crystal structures by X-ray diffraction in relation to function (3h) Enzymology (thermodynamics, pre- and steady state kinetics, calculation of kinetic parameters, ligand binding and allosteric enzymes, site-directed mutagenesis, theory of metabolic control) (10 h)

Learning outcomes	**At the end of this learning unit, the student is able to :**
	
	1 To provide Masters students in Biomedical Sciences with the necessary competence to study:
	     - techniques of overexpression/purification and structural analysis of proteins
	     - structure-function relationships in proteins
	     - physiological roles of enzymes

Evaluation methods	Written exam of 6 questions with at least one question from each lecturer. The exam questions will be in English but the students are free to answer either in French or in English. The final mark is the arithmetic mean if the marks for the 6 questions. A final mark between 9/20 et 10/20 is not automatically rounded up to 10/20. There are no negative points or weighting according to the questions and chapters of the subject. However, when a student has a mark between 9/20 and 10/20 after correction, the lecturers review together the exam copy to decide whether the mark should be rounded down or up according to the overall evaluation of the copy. The evaluation covers the whole course content.
Teaching methods	Formal lectures plus a "workshop" on bioinformatic analysis. The teaching will be conducted face-to-face or at distance according to health restrictions.
Content	The aim is to teach to masters students in biomedical sciences (SBIM Master) techniques of enzymology and metabolic control analysis, purification, sequencing, structure determination and bioinformatic analysis of proteins. Content: - Expression, purification and renaturation of proteins *in vitro* (6h) - Techniques for determining the 3D structures of proteins (3h) - Analysis of protein-protein interactions (3h) - Protein sequencing and mass spectrometry (3h) - Bioinformatic analysis of proteins (3h) - What governs the native structure of proteins (3h) - Thermodynamic of enzymes and metabolic pathways (3h) - Kinetics and mechanisms of enzymes (6h)
Inline resources	There is no formal syllabus ! PDF versions of slides presented in the course, which cover the subject in a comprehensive way, will be made available on MoodleUCL (https://moodleucl.uclouvain.be/). In addition, a tablet will be used to explain certain aspects of the course. The "Tablet" PDF versions of the PowerPoint files will also be made available to students via MoodleUCL.
Bibliography	Les étudiants sont encouragés à lire des revues dans la littérature ! The students are encouraged to do background reading, for example by consulting numerous comprehensive reviews on the subject matter of the course available in the literature (for example via Pub Med).
Other infos	Teaching of the course material will be in English and the Power Point files will be mostly in English.

Faculty or entity in charge	SBIM

Programmes containing this learning unit (UE)				
Program title	Acronym	Credits	Prerequisite	Learning outcomes
Master [120] in Biomedicine	SBIM2M	4		🔍
Master [60] in Biomedicine	SBIM2M1	3		🔍