UCLouvain

wsbim2115
2020

Protein structure / Function relationships

Due to the COVID-19 crisis, the information below is subject to change, in particular that concerning the teaching mode (presential, distance or in a comodal or hybrid format).

4 credits	30.0 h	Q1

Teacher(s)	Bertrand Luc ;Collet Jean-François ;Gatto Laurent ;Laloux Géraldine ;Rider Mark (coordinator) ;
Language :	English
Place of the course	Bruxelles Woluwe
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)
Aims	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 - - - - *The contribution of this Teaching Unit to the development and command of the skills and learning outcomes of the programme(s) can be accessed at the end of this sheet, in the section entitled "Programmes/courses offering this Teaching Unit".*
Evaluation methods	**Due to the COVID-19 crisis, the information in this section is particularly likely to change.** 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. There are no negative points or ponderation according to the questions and course content. However, when a student has a mark between 9/20 et 10/20 after correction, the lecturers re-examine all the points to decide if the mark should be rounded up or down. If the answers are insufficient (for example failure of more than half of the questions), the final mark will be rounded down to 9/20.
Teaching methods	**Due to the COVID-19 crisis, the information in this section is particularly likely to change.** 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) Protein sequencing (3h) Bioinformatic analysis of proteins (3h) Techniques for determining the 3D structures of proteins (3h) Analysis of protein-protein interactions (3h) Kinetics and mechanisms of enzymes, cooperativity, structure-fuction relationships, epresentation of protein structures, metabolic control analysis (12h)
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	Aims
Master [120] in Biomedicine	SBIM2M	4		🔍
Master [60] in Biomedicine	SBIM2M1	3		🔍