

BIOCENTER OULU DOCTORAL PROGRAMME ADVANCED COURSE

Proteins and Peptides – *Properties, methods and applications*

Spring 2012

Place	Lectures: Linnanmaa Campus lecture halls (varies; see the map of the Linnanmaa campus at http://www oulu.fi/dokumentit/kartat/Linnanmaa_pohjapiirros.pdf) or Medical Campus lecture halls (F202 Dept of Pharmacology & Toxicology, or A101 Dept of Anatomy and Cell Biology). Discussion Groups: Dept of Biochemistry Meeting Room BK226 or BCO Meeting Room 487B, Kieppi Building, Aapistie 5A (Main Building of the Medical Campus).
Time	Tuesday afternoons at 14.15 (Exception: Monday, May 14 at 14.15). Discussion group sessions start about 10 minutes after the lecture has finished.
Study requirements	Validation for 2 ECTS Study Credits requires attending at least 8 lectures (involving suggested readings) and at least one discussion group.
Registration	Required for the study credit units only. Send e-mail to Ritva Saastamoinen by February 21, indicating your name, the suggested speaker for your discussion group, your Department and Principal Supervisor.
Transportation	There will be bus transportation between Linnanmaa and Kontinkangas. The bus leaves from in front of the Kieppi Building, Aapistie 5A at 13.55 pm (20 minutes before the scheduled beginning of the lecture) and returns after the lecture from Door J on the Linnanmaa campus back to the Kontinkangas campus (leaving, at 15.55 pm), or vice versa.
Information	Ritva Saastamoinen, tel. (08) 537 6102, e-mail: ritva.saastamoinen@oulu.fi and http://www.biocenter.oulu.fi/

PROGRAMME

Date	Place and host	Speaker	Title of the lecture
Feb 28	Kontinkangas Lecture hall A101 Host: Taina Pihlajaniemi	David Hulmes Institute of Protein Biology and Chemistry, Lyon, France	<i>Structural insights into the regulation of matrix assembly and associated tissue disorders</i>
March 13	Linnanmaa Lecture hall YB210 Host: Rik Wierenga	Jan Steyaert Structural Biology Brussels, Vrije Universiteit Brussel, Belgium	<i>Structural investigation of GPCR transmembrane signaling by use of Nanobodies</i>
March 27	Kontinkangas Lecture hall F202 Host: Karl-Heinz Herzig	Jürgen Eckel Paul-Langerhans-Group, German Diabetes Center, Duesseldorf, Germany	<i>Adipokines, myokines and the bi-directional fat – muscle crosstalk</i>
April 3	Kontinkangas Lecture hall F202 Host: Gonghong Wei	Jianmin Wu Cancer Bioinformatics, Cancer Research Program, Garvan Institute of Medical Research, Australia	<i>Understanding protein function through biological networks</i>
April 17	CANCELLED	Mauno Vihinen Department of Experimental Medical Science, Lund University, Sweden	<i>Effects of variations on protein structures and diseases</i>
April 24	Linnanmaa Lecture hall L10 Host: Lari Lehtiö	Bernhard Lüscher Institut für Biochemie und Molekularbiologie Universitätsklinikum RWTH, Aachen University, Germany	<i>Function and regulation of protein ADP-ribosylation</i>
May 8	Linnanmaa Lecture hall TA105 Host: Lloyd Ruddock	Robert Freedman School of Life Sciences, University of Warwick, UK	<i>How proteins form disulphide bonds (and how science has changed in the 50 years since the Anfinsen experiment)</i>
May 14 (Monday!)	Kontinkangas Lecture hall F202 Host: Seppo Vainio	Harald Mischak BHF Glasgow Cardiovascular Research Centre, University of Glasgow, UK, and Mosaiques diagnostics GmbH, Hannover, Germany	<i>Application of proteomics in clinical diagnosis and patient management: obstacles and solutions</i>
May 15	Linnanmaa Lecture hall YB210 Host: Petri Kursula	Anne Ulrich Karlsruhe Institute of Technology, Karlsruhe, Germany	<i>Structure and function of membrane-active peptides</i>
May 22	Linnanmaa Lecture hall YB210 Host: André Juffer	Mark Johnson Department of Biosciences, Biochemistry, Åbo Akademi University, Turku, Finland	<i>Seeking certainty from the modeling of proteins and their ligand complexes</i>
May 29	Linnanmaa Lecture hall YB210 Host: Ulrich Bergmann	Chuna Ram Choudhary Dept of Proteomics, NNF Center for Protein Research, Faculty of Health Sciences, University of Copenhagen, Denmark	<i>Decoding cell signaling networks using quantitative proteomics</i>