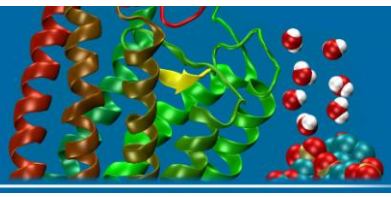
Structural Biology *of* Membrane Proteins



E-bulletin of Marie-Curie Integrated Training Network - SBMPs

March 2010

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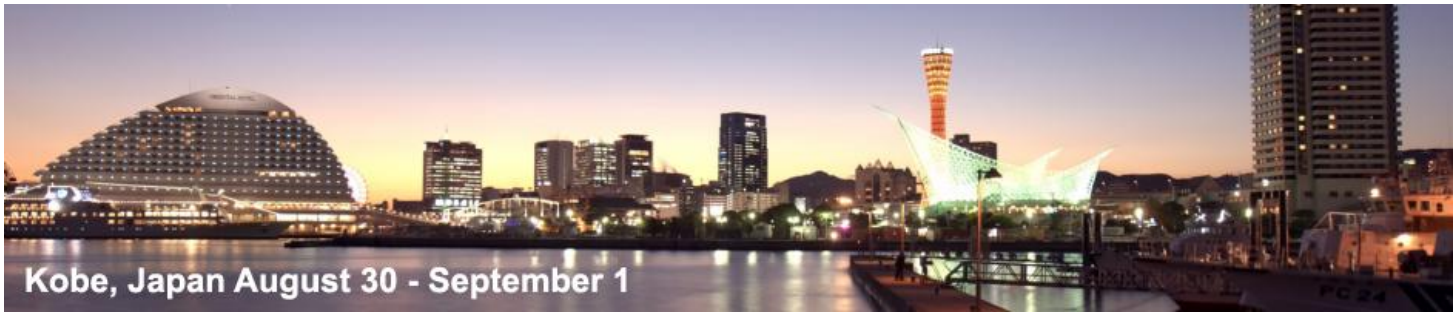
Conferences and workshops related to membrane proteins in 2010:

NEUROINFORMATICS 2010

Aug 30 – Sep 1, 2010 / Kobe, Japan

http://www.neuroinformatics2010.org/



Neuroinformatics 2010 in Kobe will be the 3rd Congress organized by INCF; previous Congresses were held in Stockholm, Sweden and Pilsen, Czech Republic. Both events attracted well over 200 attendees of diverse backgrounds but common questions.

INCF is an international organization devoted to advancing the field of neuroinformatics. The annual INCF Congress provides a meeting place for researchers in this emerging field. **Some lectures related to membrane proteins**:
Philip Biggin - Classification, structure and function of neural membrane proteins,
Nicolas Le Novère - Describing the whole life-cycle of modelling in neuroscience,
Slawomir Filipek - Ligand binding and action of microswitches in G protein coupled receptors.

Workshop1: How to describe a model: description language solutions and challenges
Workshop2: Synaptoprojectomes: Assembling, using and sharing dense cellular micromaps of brains
Workshop3: Neuroinformatics of BMI: decoding and control of neural codes
Workshop4: Molecular mechanisms of neural signaling

Each workshop will typically feature three 25-minute lectures and a panel discussion. In addition, there may be spotlight presentations of selected poster or demo abstracts. The lectures will address a common theme to be subsequently discussed by the panel, which

will include the workshop speakers and additional invited persons. Audience members are encouraged to participate in the discussion!

Modeling and Design of Molecular Materials 2010

July 4 - 8, 2010 / Wroclaw, Poland

http://mdmm.pl/2010/

Modeling and Design of Molecular Materials is a biannual conference devoted to presenting contemporary computational methods along with their applications in molecular modeling, molecular material design, bioinformatics and related fields. Participation of experimentalists interested in application molecular modeling techniques is encouraged. Planned sessions include:

- advances in computational methods
- progress in bioinformatics
- interactions in molecular materials and crystal structure prediction
- biopolymer structure prediction
- rational drug design
- modeling chemical reaction mechanisms
- catalyst and biocatalyst design
- modeling materials for photonics and electronics
- modeling biomaterials

Membrane Transport Proteins

August 15 – 20, 2010 / Biddeford, ME, USA

http://www.grc.org/

The Gordon Research Conference (GRC) on Membrane Transport Proteins will be held for the 7th time and continue to bring together researchers from many different areas in the field of membrane transport. It is a major goal of the conference to bring together people who do not normally interact and to ensure participation of as many students, post docs and young investigators as possible. To reinforce the international aspect of the conference it has been decided to alternate between European and US venues. This time the conference returns to University of New England, which is situated on the beautiful coast of southern Maine. The conference sessions will cover a spectrum of different membrane transport proteins including ion pumps, ABC transporters, ion coupled transporters, vesicular transporters, aquaporins and ion channels. Specifically, the talks will describe the most recent developments in our understanding of membrane transport protein structure and mechanisms as well as the newest insights into the role of genetic variation in transporters for disease development, the molecular pharmacology and physiology of transport proteins, the use of computational and systems biology approaches in transporter research, the cellular mechanisms regulating transporter activity and the physiological and patophysiological function of transporters in the brain.

EMBO Practical Course

Computational aspects of protein structure determination and analysis: from data to structure to function

September 6-10, 2010 / EMBL-EBI, Hinxton, Cambridge, UK

http://www.ebi.ac.uk/training/handson/course_100906_structures.html

The course will teach computational aspects of protein structure determination, validation and analysis. It will cover the background of X-ray crystallography, Nuclear Magnetic Resonance Spectroscopy, Electron Microscopy and Small-angle X-ray scattering (SAXS) and provide hands-on experience in building a model from X-ray diffraction data, comparing and integrating different types of structural data, and the differences in interpretation. Subsequent days will teach the students to critically examine and validate data from the Protein Data Bank and use a variety of analysis tools to identify similarities that can help identify function. The course will also provide an introductory session to homology modelling for use with proteins less amenable to structure determination. Finally, the importance of protein structure to drug development will be illustrated with a day focussing on protein interactions, small molecules, chemoinformatics and docking.

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The information about new **conferences**, **courses** and **workshops** related to membrane proteins as well as some important news related to **SBMPs** (including meetings, publications etc) please send to:

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