IMBG 2011

Institute of Molecular Biology and Genetics Conference for Young Scientists

Invited Speakers:

Prof. Jurgen Hescheler,

Director of the Institute of Neurophysiology at the University of Cologne, Cologne, Germany

Prof. Hescheler, President of the German Society of Stem Cell Research, Director of the Institute of Neurophysiology at the University of Cologne, has been working with mouse embryonic stem cells for over 14 years. Beginning with studies on cellular signal transduction, he has defined many important basic aspects both for fundamental research and for clinical applications. Prof. Hescheler was the first to perform electrophysiological experiments on stem cells and is a pioneer in establishing stem cell research for application in transplantation medicine.

Deadline for abstract submission is May 31, 2011

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Young Researchers' Council of IMBG

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Invited Speakers:

Dr. Pontus Aspenström,

Karolinska Institute, Stockholm, Sweden

The work of Pontus Aspenström's group is aimed to elucidate the Rho-dependent signaling mechanisms in health and disease. Researchers from Aspenström's group have characterised the little known members of the Rho GTPases and evaluated their impact on the organisation of the actin filament system. Currently, we want to identify the mechanism that determines the signaling specificity of the Rho GTPases and we have focused on the cellular roles of the atypical Rho GTPases (RhoBTB, RhoH, Rnd1-3, Chp and Wrch-1).

Recently group members identified a new family of Ras-like proteins, the Miro GTPases. These proteins bind mitochondria and link them to the kinesin motor proteins. This way, Miro functions as a regulator of mitochondrial transport along microtubules. We want to examine the potential involvement of Miro GTPases in diseases caused by deregulated mitochondrial function.

Group is also studying regulators and effectors of Rho GTPases, since many of them have profound effects on the cytoskeletal organisation. We are particularly interested in proteins that can function as links actin regulation and membrane dynamics. We have a specific interest in F-BAR domain-containing proteins (such as CIP4 and Toca-1) and WASP-interacting proteins (such as WIP and WIRE). Our goal is to identify how signalling involving Rho GTPases contribute to processes such as cell migration, cell growth and tumour progression.

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Invited Speakers:

Prof. Valentin Vlassov,

RAS Academician, SB RAS Institute of Chemical Biology and Fundamental Medicine, Novosibirsk, Russian Federation

Projects:

- Development of tools for protein structure prediction. We develop software for protein structure prediction from sequence. The pipeline of methods developed in our laboratory, which includes the fold recognition metaserver, modeling tools, and model quality assessment tools is available via the GeneSilico TOOLKIT.
- Development of tools for modeling and analysis of RNA and RNP 3D structures. We develop software for both comparative and de novo modeling of RNA and for prediction of RNA-ligand interactions. Our "flagship" method is ModeRNA, software for comparative modeling of RNA 3D structures.
- Development of databases of nucleic acid metabolism. First, we developed and maintain the MODOMICS database of systems biology of posttrascriptional RNA modification. Currently, we are developing databases of DNA repair pathways, and RNA processing pathways.
- RNA modification enzymes. We predict (using bioinformatics) and characterize experimentally novel RNA modification enzymes, in particular RNA methyltransferases.
- Nucleases. We predict (using bioinformatics) and characterize experimentally novel RNAses and DNases, and we use protein engineering techniques to obtain enzymes with new functions, e.g. restriction enzymes with new substrate specificities.

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Invited Speakers:

Dr. Marta Miaczynska,

International Institute of Molecular and Cell Biology, Warsaw, Poland

Dr. Miaczynska is chief of the Laboratory of Cell Biology at the International Institute of Molecular and Cell Biology in Warsaw, Poland. She received her Ph.D. in genetics in 1997 from Vienna University and went on to do postdoctoral work in Germany at the European Molecular Biology Laboratory in Heidelberg and at the Max Planck Institute for Molecular Cell Biology and Genetics in Dresden. She has received fellowships from the Human Frontier Science Program Organization, the Federation of European Biochemical Societies, the Max Planck Society, and L'Oréal Polska. In 2005 she was awarded a Wellcome Trust Senior Research Fellowship in basic biomedical science.

Marta Miaczynska is interested in the integration of endocytic membrane transport with intracellular signal transduction. The aim of her laboratory is to elucidate the molecular mechanisms by which endocytic transport regulates signal transmission and affects final signaling output. The specific projects developed by the Laboratory of Cell Biology follow two general lines of investigation, with the aim of clarifying the following:

1. The role of endosomal compartments in trafficking and signaling of growth factors.
2. The involvement of endocytic proteins in the regulation of gene expression in the nucleus.

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Invited Speakers:

Prof. Vladislav Verkhusha,

Albert Einstein College, New York, USA

The long-term goal of Vladislav Verkhusha's laboratory is development of a collection of chromophore containing molecular nano-tools based on fluorescent proteins, which could be employed for analysis, manipulation or modification of biochemical processes in living cells, tissues and organisms with light photons. Cloning of homologs of a green fluorescent protein (GFP), which emit not only green but also yellow, red and far-red fluorescence, provided a powerful boost for labeling and detection technologies due to availability of colors and biochemical features never before encountered in GFP variants. In the lab headed by Vladislav Verkhusha three types of protein labels to be applied in biomedical research are developed: photoactivatable fluorescent proteins (PAFPs), which are originally dark or fluoresce at one wavelength but become fluorescent at different wavelength upon irradiation with a distinct light, monomeric Fluorescent Timers (FTs) that change fluorescent color with time, and enhanced far-red fluorescent proteins (RFPs) with improved photostability for a deep-tissue imaging.

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Invited Speakers:

Prof. Ivan Gout,

University College London, London, UK

Ivan Gout obtained MD in Surgery at Lviv Medical University (Ukraine) in 1983 and PhD at the Institute of Experimental Oncology, National Academy of Sciences of Ukraine in 1987. Since 1989, he worked at the Ludwig Institute for Cancer Research in University College of London studying signal transduction pathways in cancer. Since 2003, Ivan Gout is a Professor of Cancer Biochemistry in Research Department of Structural and Molecular Biology. Since 1998, Professor Gout has also managed a laboratory (jointly with Professor Valeriy Filonenko) at the Institute of Molecular Biology and Genetics in Kyiv, Ukraine, which is affiliated to the Ludwig Institute for Cancer Research through the Kerr Programme.

Ivan Gout research interests lie in the regulation of cell growth and metabolism in normal and cancer cells. The work of his group focuses mainly on: a) elucidation of cell growth, metabolism and proliferation via the mTOR/S6K pathway; b) the role of Coenzyme A and its derivatives in cellular metabolism and gene expression. In collaboration with academic and industrial partners, Ivan Gout and his colleagues pursue the development of novel diagnostic and therapeutic approaches for cancer.

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Invited Speakers:

Dr. Janusz Bujnicki,

Laboratory of Bioinformatics and Protein Engineering, International Institute of Molecular and Cell Biology, Warsaw, Poland

The laboratory of Dr. Bujnicki is multidisciplinary and comprises three sections, devoted to: development of bioinformatic methods and databases, application of computational tools to study particular macromolecules, and experimental research on protein-nucleic acid interactions. In the past, the group of Dr. Bujnicki has developed software tools for protein structure prediction, including the GeneSilico meta-server for protein 3D structure prediction, and TOOLKIT, a set of online tools for generation, validation and experimental probing of structural models. On the RNA side, the first database of RNA modification pathways MODOMICS was developed. Currently the group of Dr. Bujnicki is involved in modeling studies on a number of proteins important for splicing regulation, and works on developing new tools for structure prediction of RNA and protein-RNA complexes.

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Invited Speakers:

Dr. Vladimir Kashuba,

Karolinska Institute, Stockholm, Sweden

Molecular mapping of the human chromosome 3 and isolation of candidate tumour suppressor or genes whose loss may contribute to the genesis of kidney and lung carcinomas and other solid tumours. Identification of human chromosome 3-specific tumor suppressor candidate genes whose loss contribute to the genesis of kidney, lung and other major epithelial cancers. We have performed careful deletion mapping of human chromosome 3 to localize tumor suppressor genes (TSG) involved in major human malignancies. Methylation studies including NotI clone microarrays were also used. We have shown that chr. 3 contains many TSGs including classical and haploinsufficient. Some of these TSGs are cancer-specific and other are multiple TSGs involved in different tumors. We have also shown that several chr.3-specific oncogenes are involved in carcinogenesis and therefore more correct will be to speak about chr.3-specific cancer-causing genes (CCG). Our data suggest that two the most important TSGs are located in 3p21.3 centromeric (LUCA) and telomeric (AP20) regions. Very high rates of allelic losses (>90%) were demonstrated here for lung, kidney, breast, cervical, other epithelial cancers. Moreover, we have found that both regions are hot spots for homozygous deletions in all mentioned above cancers. Methylation studies samples showed that many genes in these regions are inactivated by methylation in tumors. Altogether 53 genes were mapped to LUCA and AP20 regions. Development of epithelial cancers is a result of interaction of several chr. 3-specific TSGs that are inactivated by different mechanisms. It is still obscure how many of them are located on chr.3 and which of the numerous candidate TSGs are the key players. To overcome these problems we have developed new approaches for the identification of TSGs.

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