Poster Sessions

Table of Contents

Poster Session 1

Sunday 5 July & Monday 6 July
08:30–19:30, Foyer Convention Center

56 Gen EX S1, Chromatin Structure and Epigenetic Modifications and Maintenance of the Genome

70 Gen EX S2, Turning Signals into Messages – the Complexity of Gene Regulation

89 Gen EX S3, Translational Control and Protein Turnover

107 Mem Biol S1, Autophagy and Degradation

110 Mem Biol S3, Redox-Regulation of Biological Activities

129 Chem Biol S1, Probing Cellular Function with Small Molecules

158 Chem Biol S2, Targeted Cancer Therapy

160 Chem Biol S4, RNA-Based Disease Mechanism and Therapy

166 Mol Neu S1, Neuronal Ion Channels and their Role in Disease

168 Mol Neu S2, Mechanisms of Nervous System Development and Regeneration

172 Mol Neu S3, Degeneration and Ageing of the Nervous System

184 Sys Biol S2, Molecular Clocks

187 Sys Biol S3, Comprehensive Models of Metabolism and Signaling

198 Struct Biol S1, Mechanisms of Membrane Transport

205 Struct Biol S2, Channels and Transporters

206 Struct Biol S3, Protein-Mediated Membrane Deformation and Penetration

Poster Session 2

Tuesday 7 July & Wednesday 8 July
08:30–19:30, Foyer Convention Center

209 Gen Ex S4, RNA Processing and Modifications

215 Gen Ex S5, Non-Coding RNAs in Gene Regulation

220 Mem Biol S4, Extrinsc and intrinsic regulation of cellular growth control

228 Mem Biol S5, Lipid Signaling & Dynamics

240 Chem Biol S2, Targeted Cancer Therapy

247 Chem Biol S3, Functional Glycobiology – from Mechanism to Disease

281 Chem Biol S5, Signal Transduction in Tumor Development, Differentiation and Immune Escape

293 Mol Neu S4, Molecular Architecture and Assembly of the Synapse

297 Mol Neu S5, Control of Neuronal Function by Regulating Protein Homeostasis

302 Sys Biol S1, Interspecies Communications

304 Sys Biol S4, Functional Networks Regulating Cellular Stress Response and Ageing

315 Sys Biol S5, Systems Biology in Stem Cells

316 Struct Biol S2, Channels and Transporters

324 Struct Biol S4, Monitoring Protein Conformational Dynamics and Movement

329 Struct Biol S5, Advances in Structural Biology – from Subcellular to Molecular Resolution

353 FEBS Education Session

380 Late-breaking abstracts

Each poster has been given a unique number and the first part of the poster number relates to the session in which the poster was presented. Gen EX S1 = P02; Gen EX S2 = P03; Gen EX S3 = P04; Gen EX S4 = P06; Mem Biol S1 = P08; Mem Biol S2 = P09; Mem Biol S3 = P10; Mem Biol S4 = P11; Mem Biol S5 = P12; Chem Biol S1 = P14; Chem Biol S2 = P15; Chem Biol S3 = P16; Chem Biol S4 = P17; Chem Biol S5 = P18; Mol Neu S1 = P20; Mol Neu S2 = P21; Mol Neu S3 = P22; Mol Neu S4 = P23; Mol Neu S5 = P24; Sys Biol S1 = P26; Sys Biol S2 = P27; Sys Biol S3 = P28; Sys Biol S4 = P29; Sys Biol S5 = P30; Struct Biol S1 = P32; Struct Biol S2 = P33; Struct Biol S3 = P34; Struct Biol S4 = P35; Struct Biol S5 = P36; FEBS Education Session = P38; Late-breaking abstracts = LB.
high activity in a variety of different conditions, whereas enterobacterial MraY homologues from numerous pathogens were inhibited by detergents and high quality protein samples could only be produced in presence of specific compounds. The complete biosynthetic pathway starting from UDP-N-acetylgalcosamine precursor to lipid II formation could be reconstituted with cell-free expressed proteins and will provide the basis for developing new drug screening platforms in defined environments.

P32-016
Structural investigation into the comprehensive mechanism of concentrative nucleoside transport
Z. Hao1,2, A. Lesiuk1, R. Kolodziejczyk1, J. D. Young3, S. A. Baldwin4, V. L. G. Postis3, A. Goldman1, M. Bartlam6, Y. Wang2
1Faculty of Biomedical Sciences, University of Leeds, Leeds, UK, 2College of Environmental Science and Engineering, Nankai University, Tianjin, China, 3Department of Physiology, University of Alberta, Edmonton, Canada, 4State Key Laboratory of Medicinal Chemical Biology, Nankai University, Tianjin, China

Nucleoside transporters (NTs) are very important in humans, and play vital roles in nucleic acid synthesis, energy metabolism and a host of physiological processes involving regulation of intra- and extra-cellular concentrations of purine and pyrimidine (deoxy) nucleosides. Furthermore, it possesses a wide range of potential applications in the development of drugs, especially for antiviral and anticancer drugs. To date, two main families of membrane nucleoside transporters have been identified in mammalian cells, including the concentrative nucleoside transporter (CNT) and the equilibrative nucleoside transporter (ENT) families. In the former family, concentrative transport of nucleosides is energized by transmembrane sodium and/or proton gradients, whereas in the latter bidirectional nucleoside transport is driven solely by the concentration gradient of the nucleosides across the membrane. However, our understanding of the molecular mechanisms of nucleoside transport remains limited. The only known structure of a CNT is VcCNT from Vibrio cholera in an inward-facing and partially occluded conformation. At present, we are attempting to resolve the nucleoside transport mechanism by capturing and analyzing the different conformations likely to be involved in the translocation cycles of different bacterial CNTs. Meanwhile, by comparing sodium-driven transporters such as VcCNT and homologous proton-driven transporters such as NupC from Escherichia coli, we aim to illustrate the basis for the differing cation selectivities of CNTs. This work should help to elucidate the molecular mechanisms of concentrative nucleoside transport by a structural approach, not only in the bacterial transporters but also in their physiologically and medically important counterparts in humans.

P32-017
MacAB efflux system of Serratia marcescens as a potential protective system against oxidative stress
T. V. Shirshikova1, L. Y. Matrosova2, I. V. Khilyas2, M. R. Sharipova2, L. M. Bogomolnaya2
1Institute of Fundamental Medicine and Biology, Kazan Volga region Federal University, Kazan, Russian Federation, 2Kazan (Volga region) Federal University, Kazan, Russian Federation

Bacterial resistance to antibiotics is one of the major problems in the world. The most important in the appearance of bacterial antibiotic resistance is understanding and investigation of its molecular mechanisms. Bacteria genus of Serratia is opportunistic and antibiotic resistance pathogens with increased clinical significance. Efflux systems of Serratia marcescens involved in an excretion of a wide range of antibiotics. Analysis of genome sequence of S. marcescens allowed discovering a new ABC-type efflux system. This system has a high homology to MacAB system of E. coli. Special characteristic of MacAB efflux system of S. marcescens consists in defending against reactive oxygen species (ROS) addition to participating in antibiotics excretion. Goal of this research was an investigation of resistance of wild type (w.t.) and mutant ΔmacAB (m.t.) S. marcescens to ROS. Resistance of both strains to hydrogen peroxide (HP) was explored. HP presence in the medium led to m.t. cell death and w.t. viability. Co-cultivation of both strains resulted in the emergence of resistance of m.t. to HP. W.t. supernatant provided a clear protective effect for m.t. in the presence of HP. Thermostability and sensitivity to proteinase K treatment of w.t. supernatant metabolites allowed suggesting that protective compounds have a protein essence. Thus, macAB efflux system of S. marcescens plays a crucial role in a cell defense against ROS and its absence prevent to extracellular protective metabolites formation. This work was funded by the subsidy of the Russian Government to support the Program of Competitive Growth of Kazan Federal University.

P32-018
Acetazolamide, an inhibitor of carbonic anhydrase, suppresses photophosphorylation and stimulates light-induced ATP hydrolysis in isolated spinach chloroplast
O. K. Zolotarova, A. V. Semenikhin, E. B. Onoiko
Membranology & Phytochemistry, M.G.Kholodny Botany Institute, Kyiv, Ukraine

The chloroplast CF1/CF0·ATPase synthase is located in energy-transducing thylakoid membranes of chloroplasts where it catalyzes light-induced ATP synthesis and ΔH+ generating ATP hydrolysis. It has a membrane sector (CFo) attached to a membrane trisic oligomeric complex (CF1), that contains the catalytic sites for ATP synthesis and hydrolysis and noncatalytic (regulatory) sites. The noncatalytic sites can bind some oxyanions (bicarbonate, sulfite, borate etc.), activating CF1·ATPase. We have shown recently (Semenikhin & Zolotarova, 2014) that both CF1·CF0 complex and its isolated catalytic part, factor CF1, are able to accelerate the process of interconversion of carbonic acid forms: CO2 + H2O → H+ + HCO3−, ie to exhibit carbonic anhydrase activity. The aim of the present work is studying the effect of acetazolamide, an inhibitor of carbonic anhydrase, on the rate of photophosphorylation and the light-induced ATP hydrolysis in isolated spinach chloroplasts. The rate of ATP synthesis was determined by hexokinase method in chloroplast suspension illuminated for 2 min in the presence of electron acceptors. The amount of ATP was determined enzymatically using glucose-6-phosphate dehydrogenase and NADP. Formed in the reaction NADPH was measured by fluorescent method. The amount of Pi released in ATPase reaction of thylakoids was determined by colorimetric method after illumination of the chloroplast suspension for 2-5 min. The data show that acetazolamide inhibits light-induced synthesis and stimulates ATP hydrolysis suggesting participation of carbonic anhydrase activity in transmembrane proton transfer coupled with ATPsynthesis/hydrolysis in thylakoid membrane of chloroplasts.