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POSTERS

Table of Contents

Monday 11 September

104 Synthetic Biology
108 DNA Damage and Repair
118 Proteomic Approaches in Cell Biology
120 Molecular Basis of Diseases
150 Signaling Across Membranes: Receptors, Channels and Transporters
165 CRISPR and RNA Processing and Regulation
174 Mechanisms for Protein Homeostasis
177 Organelle Biogenesis and Dynamics
179 Integrated Structural Biology for Innovative Translational Research
180 Education, Training, and Career Planning in Molecular Life Sciences

Tuesday 12 September

180 Protein Dynamics and Interactions
205 Molecular Machines in Action
211 Protein Folding and Misfolding
218 Chromatin Structure and Epigenetic Modifications
228 Redox Regulation of Biological Activities
234 Systems Biology
241 Molecular Neuroscience

Wednesday 13 September

254 Cancer Biology
293 Translational Control and mRNA Localization
297 Protein Degradation
305 Autophagy
307 Structural Computational Biology
320 The Structural Organization of the Cell

Thursday 14 September

321 Intrinsically Disordered Proteins
322 Medicinal Chemistry
345 The Human Microbiome
347 Metabolism and Signaling
373 Miscellaneous

Abstracts submitted for the main call for abstracts to the 42nd FEBS Congress (Jerusalem, Israel; September 10–14, 2017) and accepted by the Congress Organizing Committee, as well as abstracts from invited speakers for the event, are published in this Supplement to *The FEBS Journal*. Late-breaking abstracts are not included in this supplement.

About these abstracts

Abstracts submitted to the Congress are **not peer-reviewed**. In addition, abstracts are published as submitted and are **not copyedited** prior to publication.

We are unable to make **corrections of any kind** to the abstracts once they are published.

Indexing

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* Each poster has been given a unique number beginning with the letter P; the next part relates to the session in which the poster will be presented.

1.1	Synthetic Biology
1.2	DNA Damage and Repair
1.3	Protein Dynamics and Interactions
1.4	Proteomic Approaches in Cell Biology
1.5	Molecular Basis of Diseases
2.1	Signaling Across Membranes: Receptors, Channels and Transporters
2.2	CRISPR and RNA Processing and Regulation
2.3	Mechanisms for Protein Homeostasis
2.4	Organelle Biogenesis and Dynamics
2.5	Integrated Structural Biology for Innovative Translational Research
3.1.A	Molecular Machines in Action
3.1.B	Protein Folding and Misfolding
3.2	Chromatin Structure and Epigenetic Modifications
3.3.A	Redox Regulation of Biological Activities
3.3.B	Systems Biology
3.4	Molecular Neuroscience
4.1	Cancer Biology
4.2	Translational Control and mRNA Localization
4.3.A	Protein Degradation
4.3.B	Autophagy
4.4.A	Structural Computational Biology
4.4.B	The Structural Organization of the Cell
5.1	Intrinsically Disordered Proteins
5.2	Medicinal Chemistry
5.3	The Human Microbiome
5.4	Metabolism and Signaling
Edu	Education, Training, and Career Planning in Molecular Life Sciences
Mis	Miscellaneous

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biological processes. Hence in the present study, two dimensional gel based proteomic profiling followed by mass-spectrometric identification of differentially expressed proteins of bacterial pathogens grown in the absence and presence of anti-infectives were done to shed more light on molecular mechanisms and identification of promising druggable targets. Vanillic acid was found to attenuate the QS and biofilm formation in *Serratia marcescens* by down-regulating the proteins involved in surface layer formation, fatty acid biosynthesis and amino acid metabolism. Furthermore, proteomic analysis revealed the ability of L-Ascorbyl 2, 6-dipalmitate to down-regulate the expression of intracellular peptidases in methicillin-resistant *Staphylococcus aureus* to attenuate the pathogenicity and biofilm formation and not by directly affecting the QS signalling process. Hence, it is advocated that studying the responses of bacterial pathogens to anti-infective agents would pave the way for identification of novel molecular mechanism(s) and hidden protein target(s). Further, this target protein(s) and pathways could be useful in designing/screening of novel anti-QS and antibiofilm agents to combat the QS and biofilm mediated infectious diseases.

P.1.4-005
The combination of Surface Acoustic Wave technique with mass spectrometry provides a novel tool to study metabolic pathways

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Surface Acoustic Wave (SAW) technique has emerged as a powerful tool to study a wide range of affinity biomolecular interactions at near physiological conditions, ranging from protein-protein to protein-peptide or protein-DNA interactions. Its combination with proteomic approaches allows the direct characterization of proteins in biological samples, providing new tools to analyse interacting proteins related to the same metabolic pathways.

In the current work, this combination was selected to study the pathway of epithelial growth factor (EGF) protein and its receptor (EGFR). It has been reported that overexpression of EGFR is related with inflammation diseases and cancer. Briefly, the growth factor EGF was immobilized on a chip surface of a SAW biosensor. Samples of prostate homogenates of 12-week old rats with aged-related hyperplasia, were injected and passed through the chip surface. Affinity binding phenomena of prostatic homogenate proteins with the immobilized EGF protein and also with its receptor were first measured via the SAW biosensor. Interacting proteins were then eluted from the chip surface and submitted to a classical bottom-up proteomic analysis (enzymatic digestion and nanoliquid chromatography coupled to tandem mass spectrometry of the peptide mixture). Not only EGFR, which is a member of the Erbb family, but also Erbb2, Erbb3 and Erbb4 were found. Moreover, other proteins described as interactors of EGFR such as hornerin, clatherin, myosin or filaggrin were detected.

The eluted proteins were related with EGF and EGFR metabolic pathway. All of them have been previously reported to play crucial roles in inflammation diseases, cancer proliferation and metastasis when they are overexpressed in cells.

Our results point out that the combination of the SAW technique with mass spectrometry is a valuable novel tool to deeply study metabolic pathways.

P.1.4-006
SDS-PAGE analysis of heat shock proteins of *Enterococcus faecalis* and *Enterococcus faecium* isolates from urine and feces samples

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In this study, the synthesis of heat shock proteins (HSP) was investigated in enterococci isolated from urine and stool samples of humans. For this purpose, a total of 30 *E. faecalis* isolates, 20 (62.5%) from 32 urine and 10 (16.6%) from 60 stool samples were identified by multiplex PCR technique. A total of 30 *E. faecium* isolates were identified as 8 (4.5%) from 177 urine and 22 (47.8%) from 46 stool samples. In protein band analysis performed on SDS-PAGE; *E. faecalis* and *E. faecium* reference strains were subjected to different heat treatments at various application times for preliminary testing to determine optimal temperatures and application times for HSP synthesis. According to the treatment of *E. faecalis* reference strain with 42°C and 45°C temperatures for 30 min. separately, new and different protein molecules as 38, 68 and 120 kDa molecular weight, were determined respectively. After treatment of *E. faecium* reference strain at 42°C and 52°C temperatures for 30 min. respectively, it synthesized new and different protein molecules at 67, 73, 80 and 120 kDa molecular weight at both heat treatments. Protein molecules of 38 (3.3%), 43 (50%) and 120 (80%) kDa were detected at 42°C in 30 *E. faecalis* isolates. Same protein molecules were also observed at 45°C. While only 3 *E. faecium* isolates synthesized 120 kDa protein at 30 min with 42°C treatment, 38, 43, 56 and 120 kDa protein molecules were observed at 52°C.

P.1.4-007
Separation and fractionation of peptide mixtures in proteomic analysis using simple capillary gradient chromatographic setup

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Separation and (pre-)fractionation of a complex peptide mixtures, glycopeptides and glycans using a comprehensive, fast and straightforward chromatographic system in a microliters volumes is demonstrated. The introduced chromatographic system consists of a capillary column, a microsyringe, a steel weight, a holder, a laboratory stand and either a MALDI target or tubes for collecting eluate fractions and the handling does not require special

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