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The Biochemistry Global Summit

25th IUBMB Congress, 46th FEBS Congress, 15th PABMB Congress

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Abstracts submitted to The Biochemistry Global Summit (25th IUBMB Congress, 46th FEBS Congress and 15th PABMB Congress) from 9th to 14th July 2022 and accepted by the Congress Organizing Committee are published in this Supplement of *FEBS Open Bio*. Late-breaking abstracts are not included in this supplement. The abstracts are available as two PDF files: Talks (Plenary Lectures, Symposia and FEBS Special Sessions) and Posters.

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FEBS openbio

Volume 12 Supplement 1 July 2022

POSTERS

Table of Contents

POSTERS – RESEARCH

69 Cancer and metastasis
118 Neurodegeneration and regeneration
137 Diabetes and obesity
146 Cardiovascular diseases
153 Ageing
156 Host–pathogen interactions
167 Looking for new antibiotics
175 Molecular evolution
177 Microbial metabolism
185 Human microbiome
186 Cell division and cell cycle regulation
187 Apoptosis
191 Molecular immunology
201 Cell signalling
222 Proteins
267 Lipids
271 Saccharides
272 DNA and RNA
287 Metabolism and metabolic regulation
302 Food and nutrition in biochemistry
309 Sensors and nanotechnology
315 Synthetic biology
316 Genomics
321 Proteomics
324 Systems biology
326 Atomic and molecular imaging
327 Cellular imaging
328 Quantitative analysis of bioimages

POSTERS – EDUCATION

329 Undergraduate teaching/Learning
334 Postgraduate teaching/learning
335 Faculty development

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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 (see p.68 for key).

P-01.1 Cancer and metastasis
P-01.2 Neurodegeneration and regeneration
P-01.3 Diabetes and obesity
P-01.4 Cardiovascular diseases
P-01.5 Ageing
P-02.1 Host–pathogen interactions
P-02.2 Looking for new antibiotics
P-02.3 Molecular evolution
P-02.4 Microbial metabolism
P-02.5 Human microbiome
P-03.1 Cell division and cell cycle regulation
P-03.2 Apoptosis
P-03.3 Molecular immunology
P-03.4 Cell signalling
P-04.1 Proteins
P-04.2 Lipids
P-04.3 Saccharides
P-04.4 DNA and RNA
P-04.5 Metabolism and metabolic regulation
P-05.1 Food and nutrition in biochemistry
P-05.2 Sensors and nanotechnology
P-05.3 Synthetic biology
P-06.1 Genomics
P-06.2 Proteomics
P-06.3 Systems biology
P-07.1 Atomic and molecular imaging
P-07.2 Cellular imaging
P-07.3 Quantitative analysis of bioimages
P-E-01 Undergraduate teaching/Learning
P-E-02 Postgraduate teaching/learning
P-E-03.01 Faculty development

biological effect of SETD3 activity so far. However, SETD3 was also postulated to play a role in the regulation of processes that are not directly related to actin homeostasis such as response to hypoxic conditions, and enterovirus pathogenesis. Several studies showed that human SETD3 physically interacts with ≈100 different intracellular proteins, implying that some of these interactors may actually be its protein substrates. The identification of those proteins might help to fully disclose the biological importance of SETD3 and was the objective of this investigation. Three different human SETD3-knockout cell lines (HAP1, HeLa, HEK293T) were generated employing CRISPR/Cas9 method and used as a source of SETD3 substrates in fluorography experiments. The SETD3-dependent methylation of proteins present in cell lysates was performed with [3H]SAM or [2H]SAM. Labeled proteins were separated by SDS-PAGE, soaked in a fluorographic reagent and enclosed in a hypercassette for 1 month at -70°C, and developed. Pieces of the dried SDS-PAGE gel containing labeled proteins were cut out, digested with trypsin and analyzed by hybrid mass spectrometry (Q-TOF). Fluorography revealed the presence of six protein bands that were labeled by SETD3. The Q-TOF analysis of these bands identified quinone oxidoreductase and glyoxalase domain containing protein 4 as potential novel substrates for SETD3 in human cells. They will be further investigated to verify their physiological importance. Acknowledgements: This work was funded by the Opus 14 grant (UMO-2017/27/B/NZ1/00161) from the National Science Centre, Poland.

P-04.1-096

Aspects of septin polymerization influenced by the presence of the Borg3 protein

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Septins are characterized by binding guanine nucleotides and forming heterocomplexes that can associate into filaments that, in turn, can form higher-order structures such as bundles and rings. These structures are considered the biologically active form of septins and, thus, it is crucial to understand how and under what conditions this process occurs. Families that regulate this process have been highlighted in the literature, among them the BORG's protein family has been described as a possible regulator of septin cytoskeleton formation and its architecture. In this work, we studied the influence of the C-terminal region of the proteins SEPT2, SEPT6 and SEPT7 on the formation of septin filaments, varying the ionic strength of the medium, the protein concentration and the presence of the region predicted to interact with septins of the Borg3 protein, called the BD3 motif. The polymerization assays were carried out *in vitro* under the desired conditions and then the samples were adsorbed onto glow-discharged ultrathin carbon film supported by lacey carbon on a copper grid (Ted Pella) and the contrast was carried out using 2% of uranyl phosphate. Images were obtained by transmission electron microscopy. Our results suggested that the ionic strength and the concentration of proteins are relevant factors for the formation of filaments and that, although the C-terminal regions of all proteins play a stabilizing role, only the C-terminus of SEPT2 is crucial for this process. The BD3 motif of the Borg3 protein, in turn, was able to induce the polymerization of septins under different conditions from those observed for septins alone, suggesting this to be potentially a key regulatory protein in this process. It was also demonstrated that the BD3 region is only able to recognize septin hexamers and assist in their polymerization when the C-termini of SEPT6 and SEPT7 are present.

P-04.1-097

Biochemical investigation of anti-CRISPR AcrIE4-F7 reveals a common inhibition strategy against divergent CRISPR-Cas types

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To defend invasions of bacteriophages and foreign plasmids, bacteria and archaea employ the clustered regularly interspaced short palindromic repeats (CRISPR)-CRISPR-associated (Cas) systems. In turn, bacteriophages have evolved anti-CRISPR (Acr) proteins to neutralize the CRISPR-mediated immunity. AcrIE4-F7 is a fused Acr protein of AcrIE4 and AcrIF7 that inactivate type I-E and I-F CRISPR-Cas systems, respectively. Here, we report the NMR structure of AcrIE4-F7 and its target Cas components. The N-terminal AcrIE4 domain adopts a novel α-helical fold and binds to the PAM-interacting residues in the type I-E Cas8e subunit. The C-terminal AcrIF7 resembles the αβ fold of the native AcrIF7 that targets the PAM recognition site in the type I-F Cas8f subunit. Conserved negatively-charged residues in each Acr domain are essential for interaction with their respective Cas8 target components. Our study demonstrates that PAM recognition sites are the primary targets of AcrIE4-F7 to counter type I-E and I-F CRISPR-Cas systems, highlighting a common inhibition mechanism against divergent CRISPR-Cas types. Previously published in: Hong S., Lee G. et al (2022) Nucleic Acids Res 50(4), 2363-2376. *The authors marked with an asterisk equally contributed to the work.

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Characterization of CPRs derived from hot pepper (*Capsicum annuum* L. cv. Bukang) and tomato (*Solanum lycopersicum* cv. Micro-Tom)

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Cytochrome P450s (CYP) play important roles in development and defense system in plant. CYPs perform their functions by NADPH-cytochrome P450 reductase (CPR) enzyme, which transfers electrons from NADPH to cytochrome P450. There are two CPR genes in the hot pepper (*Capsicum annuum* L. *cv. Bukang*) and tomato (*Solanum lycopersicum*. cv. Micro-Tom) genome each, which are *Ca*, *SlCPR1* and *-CPR2*. The *CPRs* expression levels were measured by quantitative real-time PCR in various development stages and stress conditions (jasmonic acid, salicylic acid, drought treatments). The *CaCPR1* expression level was gradually increased during fruit ripening. The *CaCPR2* gene was constitutively expressed in all the tested tissues but the expression