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POSTERS

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Abstracts submitted to the 48th FEBS Congress from 29th June to 3rd July 2024 and accepted by the Congress Scientific Committee are published in this Supplement of *FEBS Open Bio*. Late-breaking abstracts are not included in this supplement. The abstracts are available as three PDF files: Talks (Plenary Lectures, Symposia and Speed Talks), Posters and Posters Annex.

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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.

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interaction between residues D928 and R975, which played a pivotal role in stabilizing the N-terminal domain and restricting its mobility in simulations. Thereby, our analysis highlighted the significance of residue R975 in this critical intramolecular interaction, shedding light on a possible pathogenicity mechanism of the R795W variant. This variant, lacking a basic amino acid in the insert region, failed to maintain a compact structure akin to WT MVt. Overall, our results underscore the essential role of electrostatic interactions in the metavinculin-specific insert for conformational dynamics, emphasizing the utility of all-atom MD simulations in understanding the structural impact of missense variants.

P-01-015
Architectural role of the CTCF-CHD8 complex in shaping and organising the human genome

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The higher-order genome organization is intricately associated to gene expression and vice versa. Accordingly, disorders affecting spatial genome architecture and functional organization often result in genomic instability, a leading cause of cancer and several neurodevelopmental disorders. Specific "architectural" protein complexes shape the three-dimensional structure of the genome, which is packaged into a tight protein-DNA complex named chromatin. The fundamental functional unit of chromatin is the nucleosome, formed by 150 base pairs of DNA wrapped around a histone octamer. The mechanisms by how the chromatin is dynamically arranged and how DNA–protein interactions play a crucial role in this process remain poorly understood. The highly conserved zinc finger protein CCCTC-binding factor (CTCF) is one of the core genome architecture proteins and acts as a transcription regulator. CTCF regulates long-range chromatin loops and contributes to the establishment of topological-associating domains. Chromatin remodeling protein chromodomain helicase DNA binding protein 8 (CHD8) has been shown to colocalize extensively with CTCF at CTCF binding sites near chromatin loop anchors. Recent studies highlight the importance of the crosstalk between these CTCF and chromatin remodellers to establish specific chromatin structures, affecting genome architecture and function, but the mechanisms underlying this process are severely ill-defined. The proposed project aims at filling this gap by exploiting a multidisciplinary approach, involving biochemistry, biophysics (Single-molecule Optical tweezers), and structural biology (XL-MS and cryo-EM) to characterize the structural and functional role of the CTCF-CHD8 complex. Specifically, the main objective is to understand at the molecular level how CTCF and CHD8 interact and to study the function of this complex by cryo-electron microscopy in the context of chromatin to probe its role in genomic functional and spatial organization.

P-01-016
Structural studies of *Caenorhabditis* elegans septins through CryoEM

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Septins are highly conserved GTP-binding proteins that form filaments *in vivo* through repeating heterooligomers, in which the subunits alternate G and NC interfaces. *Caenorhabditis elegans*, an important animal model, has two septins named UNC-59 and UNC-61, that assemble into a tetramer. It is proposed that this tetramer is formed via a homodimeric G interface between two subunits of UNC-61 and a heterodimeric NC interface, with UNC-59's G domain exposed to the media [John CM et al. (2007) EMBO J., 3296-3307]. This organization is unlike other organisms, that usually present an exposed NC interface. To confirm the subunit organization, proteins were expressed in *E. coli Rosetta* and purified by affinity and size exclusion chromatography, then submitted to SEC-MALS, circular dichroism (CD) and nucleotide content experiments, and cryogenic electron microscopy (CryoEM) single particle analysis to obtain a 3D structure of the tetramer. UNC-59 and UNC-61 were purified as a tetramer, and nucleotide content analysis indicated GDP bound to both subunits. CD analysis for secondary structure confirmed proteins were properly folded. The tetramers were used for CryoEM grid preparation, and initial data collection has indicated a preferred orientation of the proteins on the grid, which has held back data processing. However, 2D classification in this orientation allowed visualization of the interfaces and visualization of the septins' C-domains, long coiled-coils formed at the NC interfaces that are not usually observed due to their high flexibility. The position of the interfaces is congruent with the proposed model of subunit organization, but the position of each septin subunit is still unclear without high-resolution data. Therefore, with further optimization of CryoEM grid preparation to obtain a 3D structure of the *C. elegans* septin tetramer, this study will contribute to understanding the structure of this unusual septin organization.

P-01-017
Elucidating structural dynamics of peroxisomal matrix protein import complex

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Peroxisomes are crucial organelles involved in cellular metabolic process. Defects in the normal functioning of these organelles may lead to various peroxisome biogenesis disorders (PBDs). There are peroxisomal membrane proteins and receptor proteins (peroxins) responsible for maintaining the influx of peroxisomal proteins from cytosol. Pex5 is a receptor protein that recognizes peroxisomal signals on cargo proteins and interacts with peroxisomal membrane proteins Pex14 to facilitate the transport of cargo proteins. In the present study the structural characterization and interaction dynamics between cargo protein, Pex5 receptor and Pex14 proteins were explored by the Cryo-EM analysis. Further the mutations were introduced in the interacting sites and their effect on binding affinity is measured by biophysical