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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.

About these abstracts

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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.

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the foundation for structure-based drug discovery. However, despite extensive validation mechanisms, it is almost inevitable that among the ~215 000 entries, there will be some suboptimal or incorrect structure models. It is thus vital to apply careful verification procedures for those segments of the PDB that are of direct medicinal interest. We carried out such an analysis for crystallographic models of L-asparaginases, enzymes that include approved and candidate drugs for the treatment of leukemia. Our main focus was on the adherence of the atomic coordinates to the rules of stereochemistry and their agreement with the experimental electron density maps. We identified 189 asparaginase entries in the PDB and found that the majority of the deposits are without any serious errors, oversights, or misinterpretations. However, ~30 models posed various kinds of problems, from trivial but annoying inconsistent placement in the asymmetric unit, to misrepresentations of the solvent area, to inconsistencies between the deposited and published data, or the perpetual "to be published" declaration. Ultimately, and these were the most serious cases, we found crystal structures where parts of the protein were modeled without any support from the electron density or even in stark defiance against such evidence, or where – on the contrary – stretches of evident protein electron density were left unmodeled. In-between were very frequent cases of incorrect modeling of side chain rotamers, of impossible interatomic contacts, or misidentification of metal cations. We hope that the revised structures will help in search for improved L-asparaginase drugs.

P-01-007
A multiscale approach to study angiotensin-converting enzyme 2 (ACE2) and its peptide inhibitor DX600

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Most of the computational techniques employed in drug design have been originally introduced and optimized for the case of a small molecule interacting with a protein. As pharmaceutical research is gradually shifting its interest towards the use of short peptides instead of small molecules, the need to modify old methods or devise new ones is becoming more urgent. In this contribution, we show how a multiscale approach combining atomistic and coarse grained simulations is able to clarify the (as yet unresolved) molecular details of the interaction between ACE2, the membrane protein acting as a receptor for SARS-CoV-2 spike, and the peptide inhibitor of its enzymatic action called DX600. Apart from the intrinsic applicative interest of this complex, which is strong due to the roles played by ACE2 both in COVID-19 infection and in the function of the renin-angiotensin-aldosterone system, the strategy we adopted lends itself to be easily accommodated to the study of similar protein-peptide interactions.

P-01-008
Structural studies of the HOMER1 protein: combining experiments and modeling

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The postsynaptic density (PSD) is a protein rich network beneath the postsynaptic membrane. This network has a role in memory formation, learning processes. Alteration of the PSD has been linked to numerous neural disorders. HOMER1 is a major postsynaptic scaffold protein containing a long-coiled coil region attached to a globular EVH1 (Ena/VASP homology domain1) domain via a disordered linker. The EVH1 domain binds proline-rich regions on partner proteins such as the Shank family. Here we report the functional characterization and stucture investigation of the EVH1 domain and two of its mutants, M65I and S97L that have been observed in patients with autism spectrum disorder (ASD). We have determined the structure and dynamics of the wild-type domain by solution NMR spectroscopy. We characterized the partner binding of the wild-type and mutant domains. We have also performed multidimensional NMR and SAXS measurements, as well as molecular dynamics simulations to determine the structural effect of the mutations. Our results suggests that the mutations primarily affect the stability and partner binding affinity of the EVH1 domain. We also modeled the full-length tetrameric Homer1 protein by building theoretical structures of the coiled coil and disordered regions and assembling them with the experimentally determined EVH1 and tetramerization domains. Detailed analysis of the model allowed us to characterize the local stability and its changes along the coiled coil segment and estimating the distances that the full-length protein can bridge within the PSD network.

P-01-009
Deciphering lipid binding: unveiling novel interaction motifs in the C-terminal domain of *Schistosoma mansoni* septin10

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The interaction between phosphatidylinositols (PI) and proteins plays a crucial role in recruiting proteins to specific sites and inducing membrane deformation events. This process depends on the intrinsic properties of interacting proteins and their interactions with the lipid bilayer. Septins, ubiquitous cytoskeletal proteins found in animals and fungi, are associated with important cellular events involving membrane reshaping. Septins engage in