



POSTERS

Nr	Name and affiliation	Poster title
1	Alain André, <i>Aarhus University</i>	Biosynthesis within bio-inspired engineered artificial condensates
2	Anamika Biswas, <i>University of Copenhagen</i>	Competitive displacement of lipoprotein lipase is orchestrated by a conserved acidic cluster in GPIHBP1
3	Ankush Garg, <i>Aarhus University</i>	Biomolecular condensates exclude oxygen via enhanced protein density
4	Annette Nielsen, <i>University of Copenhagen</i>	From Alanine Scanning to High-Throughput DMS: Characterizing ArcCA's Low-Affinity Ligand Binding
5	Anni Kumari, <i>University of Copenhagen</i>	ANGPTL3/8 is an atypical unfoldase that regulates intravascular lipolysis by catalyzing LPL inhibition
6	Arriën Symon Rauh, <i>University of Copenhagen</i>	Probing the Interactions in Biomolecular Condensates using Simulations of Double Mutant Cycles
7	Azad Farzadfard, <i>Technical university of Denmark</i>	The amplification of alpha-synuclein amyloid fibrils is suppressed under fully quiescent conditions
8	Beenish Sadaqat, <i>Lund university</i>	Expression, characterization, and substrate specificity of GH36 β -galactosidase from <i>Roseburia hominis</i>
9	Bram Mylemans, <i>University of Bristol</i>	De novo design of minimal proteins for targeted protein degradation
10	Celia Fricke, <i>DTU</i>	Thermodynamic stability of alpha-synuclein fibrils as a determinant of disaggregation by chaperones
11	Daria Gusew, <i>University of Copenhagen</i>	Combining NMR spectroscopy and Molecular Dynamics simulations to study conformational dynamics of proteins and protein-ligand interactions
12	Emil Thomasen, <i>University of Copenhagen</i>	Interdomain interactions in the nuclear receptor PPAR γ from an integrative ensemble model
13	Eva Smorodina, <i>University of Oslo</i>	Structural modeling of antibody variant epitope specificity with complimentary experimental and computational techniques
14	Fabian Hecker, <i>DTU Health Tech</i>	Hyperpolarized water via UV-generated radicals to study the hydration of proteins
15	Fan Cao, <i>University of Copenhagen</i>	A coarse-grained model for disordered and multi-domain proteins
16	Francisca Pinheiro, <i>Aarhus University</i>	Targeting peptide drugs based on the activity state of synapses
17	Frederik Theisen, <i>Institut de Biologie Structurale</i>	The Dual Identity of Proline: Exploring the Effects of Proline Isomerization in IDP Interactions
18	Freia Buus, <i>University of Copenhagen</i>	Phase-Separation of Two Highly Charged Disordered Proteins at the Residue Level Explored by NMR Spectroscopy
19	Giulio Tesei, <i>University of Copenhagen</i>	Conformational ensembles of the human intrinsically disordered proteome
21	Ida Kjærsgaard Grene, <i>Aarhus university</i>	De-novo protein design for neuroscience: Homology and specificity



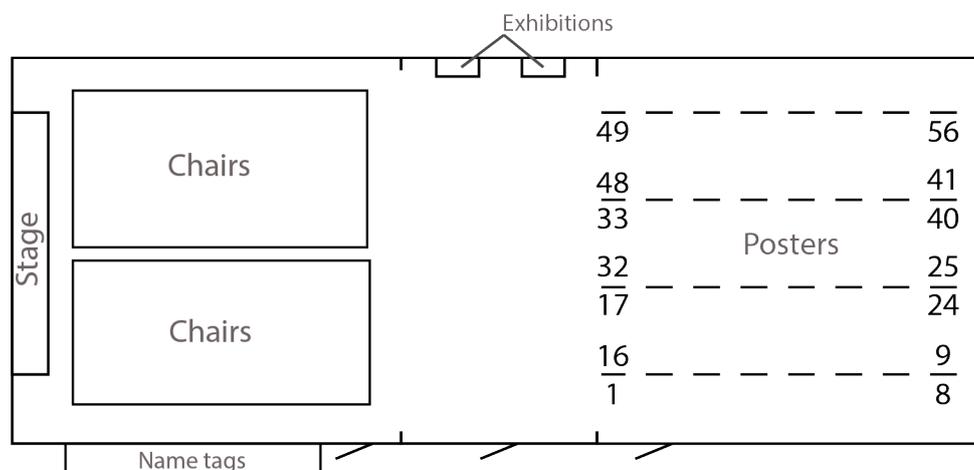
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22	Ida Marie Vedel, <i>Leibniz-Forschungsinstitut für Molekulare Pharmakologie</i>	Unveiling the competitive interactions of Dab2 and Eps15 during initiation of clathrin mediated endocytosis
23	Jan Nowak, <i>Aarhus University</i>	Fast Track to Functional Binders: Screening De Novo Proteins with FIDA
20	Jens Nicolai Decker, <i>University of Copenhagen</i>	Pioneer factor Sox2 modulates nucleosome architecture
24	Jesper Elmsted Dreier, <i>University of Copenhagen</i>	Small molecule mediated inhibition of α -synuclein amyloid fibril formation
25	Jing Zhao, <i>University of Copenhagen</i>	Discovery of de novo molecular glues
26	Joel J. Chubb, <i>University of Bristol</i>	: RASSCoL: Simplifying Computational Design of Small-Molecule Binding Pockets
27	Joseph Rogers, <i>University of Copenhagen</i>	De novo peptides and proteins to modulate protein disorder
28	Julian Beck, <i>University of Bayreuth</i>	Scaffolding a Kemp Eliminase Activity into an idealized de novo TIM barrel
29	Karolina Krzesińska, <i>DCI, DTU</i>	MAVISp: A Modular Structure-Based Framework for Protein Variant Effects
30	Kristine Degn, <i>DTU & Danish Cancer Institute</i>	Unraveling Compensation in Cancer: A Novel Approach to Identifying Pathogenic and Rescue Mutations through a XGBoost Algorithm with p53 as a Model Protein
31	Kristoffer Johansson, <i>University of Copenhagen</i>	Global Analysis of Multi-Mutants to Improve Protein Function and Stability
32	Lars Santema, <i>Rijksuniversiteit of Groningen</i>	Discovery by cell-free protein synthesis and biochemical characterization of thermostable glycerol oxidases
33	Luis I. Gutierrez-Rus, <i>University of Bristol</i>	Combining rational and computational design for de novo metalloenzymes
34	Maria Correia, <i>Aarhus University</i>	Mechanism of consecutive multisite phosphorylation
35	Matteo Cagiada, <i>University of Copenhagen / University of Oxford</i>	Predicting absolute protein folding stability using generative models
36	Mette Rønne, <i>DTU</i>	Carbohydrate-binding module regulation of enzymatic transglycosylation
37	Milena Lalic, <i>University of Copenhagen</i>	Interdomain Interaction Through Structural Disorder in Nuclear Receptors
38	Nadja Joachim, <i>University of Copenhagen</i>	Phosphorous recovery using optimised phosphate binding proteins
39	Nancy Forde, <i>University of Copenhagen</i>	Repurposing non-motor proteins to make novel molecular motors
40	Nicolas Sebastian Gonzalez Foutel,	Effect of protein condensates on kinase signaling



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<i>Aarhus University.</i>		
41	Nina Louise Jacobsen, <i>University of Copenhagen</i>	Calmodulin regulates the signaling pathways of the Interleukin-4 Receptor
42	Oriana Sacco, <i>DTU Bioengineering</i>	Biochemical characterization of a novel archaeal 4- α -glucanotransferase from <i>Pyrobaculum arsenaticum</i> : Insights into disproportionation and cyclization activity
43	Poul Thrane, <i>Roskilde University</i>	A Michaelis-Menten model for heterogeneous enzyme kinetics on a rugged energy landscape
44	Rasmus Krogh Norrild, <i>DTU</i>	Large-scale quantification of protein and RNA energetic contributions to biomolecular condensation
45	Samuel Peña Díaz, <i>Aarhus University</i>	Alternative protein-based strategies for plastic degradation
46	Simina Cuciurean, <i>University of Copenhagen</i>	Transient helicity in the intrinsically disordered protein ACTR measured by hydrogen exchange
50	Sören von Bülow, <i>University of Copenhagen</i>	Prediction of phase separation propensities of disordered proteins from sequence
47	Soumik Ray, <i>DTU</i>	Divergent effects of pathological alpha-synuclein mutations on phase separation
48	Steffie Elkjær, <i>University of Copenhagen</i>	How do intrinsically disordered transcription factors compete for the same hub?
49	Stephanie Heusser, <i>University of Copenhagen</i>	Understanding Desensitization Mechanisms in Acid-Sensing Ion Channels Through Protein Modifications
51	Thea Klarsø Schulze, <i>University of Copenhagen</i>	Predicting residue-level free energies of hydrogen exchange from structure
52	Vili, <i>Aarhus University</i>	Targeted Design of Protein Binders to Probe Receptor Signaling in Neuronal Connectivity and Memory
53	Yu Wang, <i>DTU Bioengineering</i>	Comparative Study of Three Starch Branching Enzymes Identifies Effective Enzyme Tools for Granular Starch Modification



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