



POSTERS

Nr	Name and affiliation	Poster title
1	Alain André, <i>Aarhus University</i>	Biosynthesis within bio-inspired engineered artificial condensates
2	Anna Toft Sakamoto, <i>Aarhus University</i>	Investigating the structure and function of cable bacteria truncated hemoglobins
3	Beatriz Piniello, <i>Uni. of Cph.</i>	Computational modeling of N-glycosylation mechanisms
4	Bram Mylemans, <i>Uni. of Cph.</i>	De novo designed bifunctional proteins for targeted protein degradation
5	Celia Fricke, <i>DTU</i>	Thermodynamic Stability Modulates Chaperone-Mediated Disaggregation of α -Synuclein Fibrils
6	Christa Kanstrup, <i>Uni. of Cph.</i>	Cytoplasmic IDRs as Regulators of Plant POT Activity
7	Christian Kofoed, <i>Uni. of Cph.</i>	Programming Protein Function via Cell Surface Induced Proximity
8	Daniel Saar, <i>Linderstrøm-Lang Centre</i>	The Subtle Art of Nuclear Receptor Modulation Captured by NMR: MTMR7 as a Non-Canonical PPAR γ Modulator with Potentially Low Affinity
9	Danielle Swingle, <i>Linderstrøm-Lang Centre</i>	Chirality in complexes and condensates
10	Darian Yang, <i>Uni. of Cph.</i>	Driving MD Simulations with Dynamic Experimental Data: Adaptive Refinement of Conformational Ensembles
11	Emil G P V Stender, <i>Fidabio</i>	RAPID KD SCREENING WITH A SINGLE MEASUREMENT USING FLOW INDUCED DISPERSION ANALYSIS
12	Emilie Johansen, <i>Uni. of Cph.</i>	Enhanced resistant starch - Starch with improved performance during digestion
13	Eric Beyerle, <i>Uni. of Cph.</i>	Machine Learning Ligand Binding Pathways
14	Fan Cao, <i>Linderstrøm-Lang Centre</i>	A coarse-grained model for disordered and multi-domain proteins
15	Federica Saraceno, <i>DTU</i>	Characterising the phase separation and aggregation behaviour of the C-terminal LCD of TDP-43
16	Frederik Oskar Graversgaard Henriksen, <i>Aarhus University</i>	Antitoxin CrlA of the CrlTA toxin-antitoxin system mediates defence against T5-like phages
17	Georgia Nasi, <i>DTU</i>	Amyloid fibril formation from rapeseed proteins through mild processing
18	Holly McKenzie, <i>University of Bristol</i>	Blended Domains: A Design Strategy for Constructing Ligand-Responsive Coiled-coil Proteins
19	Hossein Mohammad-Beigi, <i>DTU</i>	Taylor Dispersion Analysis of Micellization (TDAM) Reveals Distinct Assembly and Dissociation Pathways of α -, β -, and κ -Casein Micelles
20	Ida Marie Vedel, <i>Linderstrøm-Lang Centre</i>	Multivalent and competitive interactions between Disabled-2 and Eps15 lead to co-phase separation



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21	Ida Sjøgaard, <i>Uni. of Cph.</i>	Regulation of the stress responsive transcription factor DREB2A through formation of a ternary complex between the repressor RCD1 and the MED25 subunit
22	Isabell Lindahl, <i>Uni. of Cph., NBI</i>	Who induces what? Exploring Membrane Curvature Generation and Sensing of Mitochondrial Membrane Proteins using Coarse-Grained MD
23	Jacob Aunstrup Larsen, <i>DTU</i>	Solubility profiling of Peptides with minimal sample consumption
24	Jeppe Kari, <i>Roskilde University</i>	A Michaelis-Menten model for heterogeneous substrates: An Energy Distribution Approach
25	Jiayu Jiang, <i>DTU</i>	Enhanced Thermostability and Catalytic Efficiency of Hyaluronidase through Computational-aided Rational Design
26	Josefine Lorentzen, <i>Aarhus University</i>	Structural Insights into Chromatin Recognition and Repair
27	Ketty Tamburrini, <i>Linderstrøm-Lang Centre</i>	Deciphering the Disordered Interaction of Prothymosin α with S100A13
28	Kristoffer Johansson, <i>Linderstrøm-Lang Centre</i>	Global Analysis of Multi-Mutants to Improve Protein Function and Stability
29	kyriakos tsatsis, <i>DTU</i>	Exploring domain nesting in carbohydrate-active enzymes
30	Lea Strother, <i>DTU</i>	Semi-rational engineering of a thermophilic amidase for CO ₂ desorption in carbon capture processes
31	Louise Laursen, <i>BRIC/Finsenlab</i>	A PROSS-designed lipoprotein lipase displays enhanced thermal stability and native regulation mechanism
32	Luis I Gutierrez Rus, <i>NNF Center for Protein Design</i>	Expanding all-alpha-helical protein space through rational computational design
33	Maria Haugaard Bohl Andersen, <i>DTU</i>	Two mutations convert the first T-antigen specific sialidase into a trans-sialidase
34	Markéta Linhartová, <i>Aarhus University</i>	CooJ -The first nickel-binding protein purified from cable bacteria
35	Mathias Jensen, <i>DTU</i>	Dynamic recognition of multiple H- and Lewis antigens by an Akkermansia muciniphila alpha-1,2-fucosidase
36	Maxime Naudé, <i>Uni. of Cph.</i>	Layers of α -helical barrels for the control of excitons leading to transport of energy
37	Mette Errebo Rønne, <i>DTU</i>	Carbohydrate-binding module regulation of enzymatic transglycosylation
38	Nadja Joachim, <i>Uni. of Cph.</i>	Phosphorous recovery using optimised phosphate binding proteins
39	Nicole Galenkamp, <i>Lund University</i>	Cooperative Protein Binding on simple and complex membranes
40	Nina Jacobsen, <i>Linderstrøm-Lang Centre</i>	Calmodulin regulates the signaling pathways of the Interleukin-4 Receptor



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41	Oline Kirstine Nyhegn-Eriksen, <i>Uni. of Cph.</i>	Understanding the Role of Disorder in Organellar Na ⁺ /H ⁺ Exchangers
42	Onur Kirtel, <i>DTU</i>	Evolving polyextremophilic amidases for enzymatic CO ₂ scrubbing
43	Peter Røgen, <i>DTU</i>	Sequence-Similar Protein Domain Pairs With Structural or Topological Dissimilarity
44	Ryan Cantwell Chater, <i>Uni. of Cph.</i>	Leveraging cryo-EM to design allosteric inhibitors of GlyT2 that alleviate neuropathic pain without on-target side effects
45	Selene Forget, <i>Uni. of Cph.</i>	FreeQuantum: Bridging Quantum Computing and Machine Learning for Accurate Biomolecular Binding Free Energy Predictions
46	Vili Lampinen, <i>Aarhus University</i>	Design of protein binders to Probe Neurotrophin Signaling in Neuronal Connectivity and Memory
47	Westley Pawloski, <i>Lund University</i>	Evaluating the use of lanthanide containing dendrimers for solvent paramagnetic relaxation enhancement NMR spectroscopy
48	William Pallisgaard Olsen, <i>NNF Center for Biosustainability</i>	Enzymatic Detoxification of Deoxynivalenol (DON) for Low-Impact Agriculture
49	Ying Xia, <i>Uni. of Cph.</i>	Heterogeneous sampled subgraph neural networks with knowledge distillation to enhance double-blind compound-protein interaction prediction