

Poster Session Tuesday

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| 26 | Huan Lan | Exchange catalysis by tapasin exploits conserved and allele-specific features of MHC-I molecules |
| 27 | Eric Lang | How can molecular modelling support de novo protein design, and vice versa? |
| 28 | Stefano Leoni | Advanced molecular dynamics simulations for drug discovery |
| 29 | Stephanie Linker | Polar/apolar interfaces modulate the conformational and kinetic behavior of cyclic peptides and catalyze their passive membrane permeability |
| 30 | Mohamed Marzouk Sobeh | Investigating the dissociation process and Binding energy of the DBD-p53/DNA complex by PaCS-MD and MSM |
| 31 | Samuel Musson | Deep learning protein conformational space with convolutions and latent interpolations |
| 32 | Daniel Nagel | MSMPathfinder: Finding Pathways of Markov State Models |
| 33 | Rainer Nikolay | Snapshots of native pre-50S ribosomes reveal a biogenesis factor network and evolutionary specialization |
| 34 | Jeffrey K. Noel | Quantification and demonstration of the constriction-by-ratchet mechanism in the dynamin molecular motor |
| 35 | Oscar Palomino Hernandez | On the impact of Tyr-39 for the structural features of α-synuclein and for the interaction with small molecules |
| 36 | Guillermo Pérez Hernández | mdciao: Analysis of molecular dynamics simulations using residue neighborhoods |

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| 37 | Matthias Post | Memory kernel estimation from constrained MD simulations |
| 38 | Victor Principe | Improving MM/PBSA binding affinity calculations using machine learning |
| 39 | Lluís Raich | Discovery of a hidden transient state in all bromodomain families |
| 40 | Tatiana Rosales | Understanding the implication of peptide register shifts in TCR cross-reactivity |
| 41 | Joseph Rudzinski | Automated identification of collective variables and metastable states from molecular dynamics data |
| 42 | Florian Seufert | Investigation of different protonation states on ADGRL1 flap dynamics |
| 43 | Jiale Shi | Novel elastic response in twist-bend nematic models |
| 44 | Kamolrat Somboon | Computational simulations reveal substrate translocation pathway through hydrophobic transporters |
| 45 | Marija Sorokina | Structural models of ACE2 with RBD of SARS-CoV-2 Spike protein |
| 46 | Rene Staritzbichler | SmoothT unbiased construction and visualization of transition pathways, linking monte carlo and molecular dynamics simulations |
| 47 | Matthias Stein | Accurate receptor-ligand binding free energies from fast QM conformational chemical space sampling |

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- 48 Hao Tian **Deciphering the allosteric process of the phaeodactylum tricornutum aureochrome 1a LOV domain**
- 49 Felix Wiggers **Diffusion of the disordered E-cadherin tail on β -catenin**
- 50 Romina Wild **Counter transport of potassium ions in the human serotonin transporter**
- 51 Jayasubba Reddy Yarava **Probing the site-specific backbone dynamics of YadA autotransporter in microcrystals and native membranes using solid-state NMR spectroscopy**