

Program

Monday, 26 April 2021

08:30 – 09:00	Technical check	
09:00 – 09:30	Christian Freund Frank Noé Stefan Jorda	Welcome About the Wilhelm and Else-Heraeus Foundation
<i>Session I:</i>	<u><i>NMR methods for probing dynamics</i></u>	
09:30 – 10:15	Christian Freund	Dynamic aspects of antigen presentation by MHC class II molecules
10:15 – 11:00	Michael Sattler	Combining NMR and integrative structural biology to study dynamics and allostery in protein complexes
11:00 – 11:45	Birthe B. Kragelund	Dynamic complexes of intrinsically disordered proteins by NMR spectroscopy
11:45 – 12:30	<i>LUNCH BREAK</i>	
12:30-13:30	<u><i>Cultural Event: Virtual Tour in Museum Barberini</i></u>	
13:30-14:00	<i>COFFEE BREAK</i>	
14:00 – 16:00	Poster session I	
16:00 – 16:30	<i>COFFEE BREAK</i>	

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16:30 – 17:15	Nikolaos Sgourakis	Dynamics of MHC-I molecules in the antigen processing and presentation pathway
17:15 – 18:00	Lewis E Kay	The important role of dynamics in the function and misfunction of molecular machines
18:00 – 18:45	Julie D. Forman-Kay	NMR insights into phase separation of a CAPRIN1 intrinsically disordered protein region
18:45 – 19:30	Roundtable discussion I: Perspectives of NMR	

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Session II: Molecular dynamics simulation and free energy landscapes

09:00 – 09:45	Cecilia Clementi	Designing molecular models by machine learning and experimental data
09:45 – 10:30	Carlo Camilloni	Modelling biomolecules structure and dynamics by combining small-angle X-ray scattering and computer simulations
10:30 – 11:00	<i>COFFEE BREAK</i>	
11:00 – 11:45	De Fabritiis	Neural networks potentials for molecular simulations
11:45 – 12:30	Frank Noé	Exploring protein dynamics with Markov modeling and deep learning
12:30 – 13:30	<i>LUNCH BREAK</i>	
13:30 – 14:30	<u>Cultural event: Virtual Musical Performance</u>	
14:30 – 16:00	Poster session II	
16:00 – 16:30	<i>COFFEE BREAK</i>	

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16:30 – 17:15	Kresten Lindorff-Larsen	Biophysical experiments and biomolecular simulations: A perfect match?
17:15 – 18:00	Bert de Groot	The molecular dynamics of potassium channel gating
18:00 – 18:45	Rommie Amaro	A glycan gate controls the opening of the SARS-CoV-2 spike protein
18:45 – 19:30	Roundtable discussion II: Future aspects of theoretical approaches	

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Session III: Structure and dynamics of macromolecular systems

09:00 – 09:45	Oliver Daumke	The mechanism of dynamin in membrane constriction - From static snapshots to a dynamic model
09:45– 10:30	Christian Spahn	A cold look at the formation and activation of the bacterial large ribosomal subunit
10:30 – 11:00	<i>COFFEE BREAK</i>	
11:00 – 11:45	Ben Schuler	Probing the dynamics and interaction mechanisms of disordered proteins with single-molecule spectroscopy
11:45 – 12:30	Enrica Bordignon	Probing conformational heterogeneity of ABC transporters in vitro and in cells via EPR
12:30 –13:30	<i>LUNCH BREAK</i>	
13:30 – 14:15	Markus Wahl	RNA polymerase dynamics during transcription termination and anti-termination
14:15 – 15:00	Alke Meents	Fixed target serial crystallography for studying protein dynamics
15:00 –15:45	4 best poster presentations	
15:45 –16:15	<i>COFFEE BREAK</i>	

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16:15 – 17:00	Brian Baker	Dynamic allostery in class I major histocompatibility complex proteins
17:00 – 17:45	Stefan Raunser	Bringing life into frozen proteins to elucidate molecular mechanisms
17:45 – 18:30	Roundtable discussion III: Towards cellular structural biology	
18:30	Christian Freund Frank Noé	Final remarks

End of the Symposium