

LIFE SCIENCES

seminar series

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High-resolution Structure Determination of Dynamic Macromolecular Complexes by Cryo-EM

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Thursday, 16:00

Seminar room 132, pavilion A11
University campus Bohunice

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Single particle cryo-EM is a powerful method to determine the high-resolution structures of protein complexes due to recent improvements in electron microscopic instrumentation and data processing. Structures can be determined without the need for crystallization at resolution levels that very often allow atomic model building. We use the method to determine the structure of large macromolecular complexes such as the ribosome, spliceosome and proteasome and we develop biochemical and computational tools to further improve the analysis of the dynamic behavior of these complexes during their reaction cycles. Using cryo-EM therefore allows us to get an understanding of their dynamics behavior at near-atomic resolution which provides valuable information to understand their functional modes of action.