A brief introduction to new developments for the *ab initio* structure prediction of proteins based on AI-methodology

Dr. Till Rudack, Prof. Dr. Eckhard Hofmann

This year saw a breakthrough in the accuracy of *ab initio* generated protein models, with impact for most groups working in protein research. In the seminar we will give a quick info about the current state:

- Background to protein structure modelling
  - Situation „pre AlphaFold“
- New developments and the impact on protein research

ZOOM: Meeting ID: 65625842795, Passcode: 254757

Participants:
Students and Researchers of the RUB involved in protein research and interested in protein structures. The seminar will be recorded for offline viewing.

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