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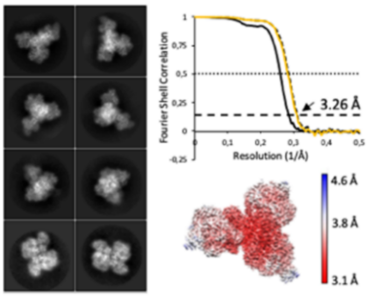
Elucidation of protein structure

Description



The team led by Petra Wendler, Professor of Biochemistry at the University of Potsdam, uses cryo-electron microscopy and single-particle analysis to investigate the structure and structural changes of molecular machines with the highest possible resolution. The structural data obtained by cryo-electron microscopy or X-ray crystallography are combined with results from mutation analyzes and biophysical experiments, such as dynamic light scattering, in order to find answers to various biological questions.

At the University of Potsdam, the group uses a 200 kV Talos F200C equipped with a Falcon III detector to screen and visualize proteins and colloidal samples. The 3D structure of protein complexes from 200 kDa molecular weight can be solved with this setup with a resolution of up to 4 Å.

Current research topics

- Import of peroxisomal proteins through the AAA + ATPases Pex1 and Pex6
    - Structure elucidation of the Pex1 / Pex6 complex
    - Structural studies of Zellweger mutations in Pex1 / Pex6
- Electron transfer in redox proteins
    - Structure elucidation of various redox proteins
    - Establishment of a protocol for the identification of charges by means of single particle analysis and cryoelectron microscopy
- Visualization of biopolymers that serve as a framework for (enzymatic) functions
- Structure elucidation of proteasomal precursor complexes

Scientific literature

Petrović, S., Wendler, P. (2021) A RADD approach to probing AAA+ protein function. Nat. Struct. Mol. Biol. 28, 329–330.

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Radon, C., Mittelstädt, G.…., Leimkühler, S. & Wendler, P. (2020) Cryo-EM structures reveal intricate Fe-S cluster arrangement and charging in Rhodobacter capsulatus formate dehydrogenase. Nat. Commun. 11, 1912.

Kölsch, A., Radon, C., Golub, M., Baumert, A., Bürger, J., …Wendler, P. (2020) The transient interaction between cytochrome c6 and photosystem I. Curr. Res. Struct. Biol. 2, 171-179.

Enenkel, C., Wendler, P. (2019) Nuclear Transport of Yeast Proteasomes. Front. Mol. Biosci. 6, 34.

Bhat, J. Y., G. Miličić, G. Thieulin-Pardo, A. Bracher, …P. Wendler, M. Hayer-Hartl (2017). Molecular Surgery: Enzyme Repair by the AAA+ Chaperone Rubisco Activase. Mol. Cell 5, 744-756.

Applications

- Life science research
- Medical analytics
- Medical therapy
- Drug design
- Drug stability

Keywords

- Cryo electron microscopy
- Dynamic light scattering
- Protein structure
- Protein stability

Interest in cooperation

- Research collaboration
- Contract research

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