

2021 – A Year of Patience

The emergence of the Coronavirus Delta variant and three major service disruptions are some of the hurdles we had to surmount this year. In spite of these challenges we rallied to reach three-quarters of the remaining full capacity. We are now looking forward to the forthcoming relocation of the Krios into the newly completed SupraFab building in 2022.

The prolonged winter closing and reduced access to the biochemical laboratories at FUB, both direct results of universal covid measures in place, severely affected sample submission by end-users. This coupled with a weeklong repair of the in-house cooling system significantly hampered our service delivery. Nonetheless, we rallied to 2904 hrs of measurements in 72 sessions only in the first half of the year.

In the second half of the year, we faced twin challenges. First, in July, an increase in sample drift indicated a serious problem at hand which ultimately led to the replacement of the sample holder a month later. Secondly, the microscope chiller broke in October further depriving us of another month of measurement time. Despite these setbacks we managed to rally to an even larger number of measurements hours as in 2020 thanks to a trouble free December.

At this place, we extend our deepest appreciation to Frank Hoffmann (TF) for excellent technical assistance in keeping the microscope off-times as short as possible. And the next effort is just around the corner: the relocation of the Titan Krios into the new SupraFAB building, where the microscope and the necessary preparation equipment will find their designated places alongside other scientific high-tech instrumentation.



The new SupraFAB building in Altensteinstraße 23a, 14195 Berlin, will shortly be dedicated to science high-tech instrumentation and laboratories. Foto: Boris Schade

Figures 2021

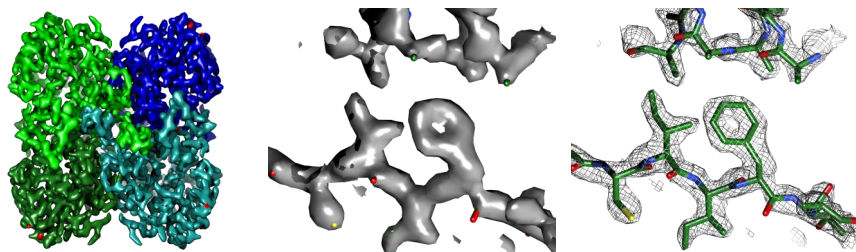
125 requests
138 sessions
4801.5 hrs beam-time (76% working load)
2440.5 hrs down-time
(1482 hrs out-of-service, 502.5 hrs maintenance and repair, 456 hrs winter closing)

SPA requests

SPA data collection can be requested by any of the applicants of the 91b proposal. We have implemented three services at fub.openiris.io to manage the beam times. In-depth instructions are provided on the FZEM's web-site at fzem.fu-berlin.de.

CryoEM analysis at sub 2 Å resolution

Still not self-evident, resolutions at or below 2 Å are within reach using our established pipeline from grid preparation to data analysis. In the past year, we thus managed to solve structures of small plant biocatalysts at a structural detail (figures below) even outperforming comparative crystallography studies (Chánique, A. *et al.*, 2021, [doi: 10.1002/cctc.202100110](https://doi.org/10.1002/cctc.202100110)). ☺



However, it is important to emphasize the criticality of high quality samples if you are interested in resolving alternative side chain conformations, single water molecules, or aromatic holes in your reconstructions.

Contact SPA data acquisition

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Publications

- Nikolay R., Hilal T., Schmidt S. *et al.* 2021, Snapshots of native pre-50S ribosomes reveal a biogenesis factor network and evolutionary specialization. #1*
Mol Cell **81**(6), 1200–1215.e9.
[doi:10.1016/j.molcel.2021.02.006](https://doi.org/10.1016/j.molcel.2021.02.006)
- Heyder N.A., Kleinau G., Speck D. *et al.* 2021, Structures of active melanocortin-4 receptor-Gs-protein complexes with NDP-α-MSH and setmelanotide. #2*
Cell Res **31**, 1176–1189.
[doi:10.1038/s41422-021-00569-8](https://doi.org/10.1038/s41422-021-00569-8)
- Dimos N., Helmer C.P.O., Wahl M.C. *et al.* 2022, CryoEM analysis of small plant biocatalysts at sub 2 Å resolution. #2*
Acta Cryst Sect D, **D78**, 113-123
[doi: 10.1107/S205979832101216X](https://doi.org/10.1107/S205979832101216X)
- Bergfort A., Preussner M., Kuropka B. *et al.*, A multi-factor trafficking site on the spliceosomal remodeling enzyme, BRR2, recruits C9ORF78 to regulate alternative splicing. #2*
Nat Commun, under revision
- Bergfort A., Hilal T., Kuropka B. *et al.*, The intrinsically disordered TSSC4 protein acts as a helicase inhibitor, placeholder and multi-interaction coordinator during snRNP assembly and recycling. #1*
Nucleic Acids Res, under revision

* number of SPA data sets (Krios) used in

FZEM

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SPA Team - SupraFAB

Benedikt Kirmayer (left), Dr. Tarek Hilal (middle), and Dr. Boris Schade (right).

