

# Minutes PSF MX User Meeting on ZOOM 2026-06-04

Time: 4 pm Thursday 4 June 2026

Zoom: <https://ki-se.zoom.us/j/2552303941>

Participants: Martin Moche, Joanna Zawacka

## §1 INFO: Next PSF MX User Meeting

16:00 on Thursday 27 Aug 2026.

## §2 INFO: Experimentalist assignment procedures for BioMAX

To avoid BAG member friction, below is a reminder on how we assign experimentalists.

- The goal of "**§3 DECISION: Assign experimentalists**" below is to allocate experimentalists.
- Meeting participants are responsible for sharing the available beamtime, and determining who will start, share dewar shipping etc.
- Individuals absent from the meeting may receive beamtime as a courtesy from the assigned experimentalists in b) who reserve the right to refuse others from joining.

## §3 DECISION: Assign experimentalists

Light source	Beamline	Date	Duration	Start	Experimentalists
MAX IV	BioMAX	2026-06-10	8 hours	16:00	None => Cancel

Table 1. See also <http://ki.se/en/mbb/psf-mx>.

Please share sample information (UniprotID, heavy atoms, expression host) and approximate number of crystals asap after meeting.

## §4 INFO: Combining AlphaFold with SAXS for partially or intrinsically disordered proteins

Welcome to join "*Combining AlphaFold with SAXS for partially or intrinsically disordered proteins*" seminar by Doctor Mattia Rocco, retired from IRCCS Polyclinic Hospital San Martino, Genova, Italy.

We start **15:00, Friday 21 August 2026, in room "Nils Ringertz", Biomedicum, Solnavägen 9.**

AI tools like AlphaFold (AF) are transforming structural biology. However, they still struggle with intrinsically disordered regions, flexible linker-connected domains, and conformational changes driven by environmental conditions—limitations that are difficult to resolve computationally alone.

A recent method combines predicted or experimentally determined protein domains with flexible linkers to generate model ensembles refined against small-angle X-ray scattering (SAXS) data [Brookes et al., 2023].

This approach is now available through the public web platform SAXS-A-FOLD

(<https://saxsafold.genapp.rocks>).

The case of a supposedly fully intrinsically disordered protein will be shown, manuscript in submission right now."

We catch Mattia "on the fly" on his travel towards [AUC 2026](#) in Uppsala 24-28 August, where Mattia together with Emre Brookes, will lead two workshops, one on the US-SOMO hydrodynamics module, and the second on SAXS-A-FOLD, please register and participate in [AUC 2026](#).

## §5 INFO: PSF in iLab - [https://karolinska.corefacilities.org/service\\_center/show\\_external/3663](https://karolinska.corefacilities.org/service_center/show_external/3663)

- ✓ Please register your research group, students, postdocs, and project numbers in iLab.
- ✓ Visit <https://staff.ki.se/research-support/research-data-management/ilab> for guidance.
- ✓ Ask [cfm-support@ki.se](mailto:cfm-support@ki.se) for help.