

Oral presentation**Protein serial electron diffraction for everyone****Gerhard Hofer***Stockholm University
gerhard.hofer@mmk.su.se*

Serial electron diffraction (SerialED) promises several advantages over traditional rotational data collection methods such as microED/3D ED. By distributing radiation over multiple crystals, SerialED achieves higher signal-to-noise ratios, which lead to higher resolution structures and significantly reduced radiation damage. This improvement is particularly beneficial for addressing site-specific questions such as small ligand binding, hydrogen positions, and charge states, which are often challenging to elucidate with conventional methods.

Here, we present our comprehensive pipeline for next generation SerialED. It provides a straightforward path to detailed protein-ligand structures with virtually no radiation damage. Our pipeline is designed to be user-friendly and only use widely available machines, making SerialED accessible to a broader range of researchers in the structural biology community. By also simplifying the setup and data processing steps, we aim to democratize the use of SerialED, enabling more laboratories to leverage this powerful technique for their research.