

**Mercredi 6 Décembre 2023 à 11h**

**Ecole Polytechnique**  
*Amphithéâtre Curie, Ecole Polytechnique*

Attention : jour inhabituel

**Martin WEIK**

*Institut de Biologie Structurale, Grenoble*

## ***Watching proteins at work by kinetic X-ray crystallography***

Kinetic X-ray crystallography permits the structural characterization of macromolecular conformational changes along a reaction pathway at the atomic level of spatial resolution. After triggering the biological reaction within a macromolecular crystal, functionally relevant conformational changes are either arrested by flash-cooling the crystal, allowing characterization of the structure by conventional cryo-crystallography (intermediate trapping), or followed in real time by time-resolved crystallography at room temperature. The temporal resolution of the latter is limited to 100 ps if carried out in the form of Laue crystallography at synchrotrons. The advent of X-ray free electron lasers (XFELs) has pushed the resolution to the sub-ps regime, allowing ultrafast changes to be studied by time-resolved serial femtosecond crystallography. After reviewing the current status of the field, we will illustrate the time-resolved crystallography approach with the study of photoisomerization of the chromophore in a reversibly photoswitchable fluorescent protein. We will indicate how information on ultrafast structural dynamics can be used to rationally modify photoswitchable fluorescent proteins for applications in biological imaging.