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Some questions can only be answered by time: how time-resolved crystallography reshapes structural biology

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Cryo-crystallography was the driving force of structural biology, literally deciphering the structures of life. The integrated knowledge has informed powerful machine learning technologies to not only solve the folding problem but to imagine new proteins, some of which are even functional. However, protein function is often dominated by small kinetic barriers that are not easily predicted. Time-resolved crystallography has set out to answer new questions about protein function and to resolve atomic motion on the femtosecond scale and kinetic intermediates ranging from femtoseconds to seconds - hopefully culminating in the ability to design molecular machines one day. The talk aims to embed some of our research into this greater context.

Presenter: WEINERT, Tobias (Paul Scherrer Institute)

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