



European XFEL Science Seminar

Tuesday, 28th May 2019, 13:00

Campus Schenefeld, XHQ, room E1.173 (coffee & biscuits will be served at 12:30)

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15 years of single particle imaging at FELs

It has been predicted that the very intense pulses from an X-ray FEL contain enough power to produce an interpretable diffraction pattern from a single protein or virus. At the same time the very short pulse length can outrun the radiation damage and the scattered signal therefore represents the intact sample. This principle was demonstrated early at the first X-ray FELs but only for very large biological sample, such as whole cells. We are however now at a point where we expect to be able to collect the first data from single proteins very soon.

Taking single-particle imaging into the molecular region will potentially have large consequences for the ways that we study proteins. Proteins are dynamic molecules that gain their function by transitioning between different semi-stable conformations, but most of the information that we have on proteins is in the form of static structures. The time-scale for protein dynamics cover a very wide range and the faster processes are far too quick to be studied by most other methods such as CryoEM. X-ray free-electron lasers provide a unique opportunity to capture such fast dynamics by providing pulses whose length in time is similar to that of atomic vibrations. And by imaging particles one-at-a-time we can sort the data corresponding to different conformations after the experiment is done and thereby recover not a static structure but the full set of protein conformations.

In this talk I will outline the first 15 years of single-particle imaging at FELs based on my own perspective starting at early single-particle experiments at FLASH in 2007 and ending with my expectations for next couple of years. I will also describe the analysis methods required to bring out the most of the molecular data that will soon be produced here at the European XFEL.

Host: Johan Bielecki