Enzyme mechanisms at ultrahigh resolution
Physical distortions, bond elongations, low-barrier hydrogen bonds and carbenes.

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Although general principles of enzyme catalysis are fairly well understood nowadays, many important details of how exactly the substrate is bound and processed in an enzyme remain often invisible and as such elusive. In fortunate cases, structural analysis of enzymes can be accomplished at ultrahigh resolution (≤1 Å) thus making it possible to shed light on otherwise concealed fine-structural traits of bound substrates, intermediates, cofactors and protein groups. I will discuss structural studies of several enzymes using ultrahigh-resolution X-ray protein crystallography showcasing its potential as a tool in the elucidation of enzymatic mechanisms and in unveiling fundamental principles of enzyme catalysis. This includes the observation of seemingly hyper-reactive, physically distorted cofactors and intermediates with elongated scissile substrate bonds as well as the detection of carbenes and low-barrier hydrogen bonds and their role in catalysis and regulation.