Structural enzymology using neutron crystallography and small angle scattering

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Sensitivity to hydrogen/deuterium and lack of observable radiation damage makes cold neutrons an ideal probe for structural studies of enzymes. Neutron protein crystallography is a powerful tool for investigating protein chemistry because it directly locates hydrogen atom positions in a protein structure. The visibility of hydrogen and deuterium atoms arises from the strong interaction of neutrons with the nuclei of these isotopes. Small-angle scattering (SAS) provides low resolution information on protein dimensions, described by the radius of gyration (Rg) and maximum dimension (Dmax). Combined with deuterium labeling and contrast variation techniques, small angle neutron scattering (SANS), further allows the structural investigation individual components within protein-protein complexes. The biochemical insight gained from the neutron crystallographic structures of H-Ras, Cholesterol Oxidase and a lytic polysaccharide monooxygenase (LPMO) will be reviewed. Application of SANS to investigate the electron transfer between LPMO and its redox partner cellobiose dehydrogenase will be discussed.