Abstract Example

Coherent X-ray diffraction imaging of malaria parasite-infected erythrocytes

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Non-crystallographic methods for imaging cellular architecture and, ultimately macromolecular complexes and individual proteins, particularly membrane proteins, within a cellular environment, is a "holy grail" of cell and molecular biology.

We are developing methods to use X-ray coherent diffractive imaging (CDI) to obtain information about the architecture of cells and biological macromolecules. Soft X-rays have wavelengths of about 1-10 nm allowing imaging of cellular and intracellular structures at high spatial resolution. CDI is a method of lensless imaging that can be applied to any individual finite object. A diffraction pattern from a single biological structure is recorded and an iterative Fourier transform between real space and reciprocal space is used to reconstruct information about the architecture and chemical composition of the sample to high resolution. In contrast to X-ray crystallography, CDI does not require crystallization of the sample and therefore does not benefit from the amplification effect of the repeated crystal unit cell. Highly intense and coherent X-rays are needed to obtain sufficient signal to noise.

Our test system for cellular imaging is the malaria parasite-infected erythrocyte. The parasite establishes a system of membranes within the host cell cytosol and induces changes in the host cell membrane. Because of the limitations of the available techniques, there is on-going debate regarding the origin and organization of the different membranous structures in the host cell cytoplasm.

Glutaraldehyde-fixed, dehydrated infected erythrocyte samples were labelled with different metals or left unstained and imaged at the Advanced Photon Source, Chicago. The diffraction signal from 400 data collections (1.5 keV, 8.2 ^{o}A) was integrated. The phase and intensity profiles of the cells were successfully reconstructed revealing the major features of the cells. The data suggest that the ultimate goal of obtaining 3D structural information from non-crystaline biological samples at a resolution of 10-40 nm is achievable.