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3D reconstruction from 2D crystal image and diffraction data

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Author(s) Schenk, Andreas D; Castaño-Díez, Daniel; Gipson, Bryant; Arheit, Marcel; Zeng, Xiangyan; Stahlberg, Henning

Author(s) at UniBasel [Stahlberg, Henning](#) ; [Castano Diez, Daniel](#) ; [Gipson, Bryant](#) ; [Arheit, Marcel](#) ;

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Electron crystallography of 2D protein crystals can determine the structure of membrane embedded proteins at high resolution. Images or electron diffraction patterns are recorded with the electron microscope of the frozen hydrated samples, and the 3D structure of the proteins is then determined by computer data processing. Here we introduce the image-processing algorithms for crystallographic Fourier space based methods using the Medical Research Council (MRC) programs, and illustrate the usage of the software packages 2dx, XDP, and IPLT.

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