

Publication

2dx_merge : data management and merging for 2D crystal images

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Author(s) Gipson, Bryant; Zeng, Xiangyan; Stahlberg, Henning

Author(s) at UniBasel [Stahlberg, Henning](#) ;

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Electron crystallography of membrane proteins determines the structure of membrane-reconstituted and two-dimensionally (2D) crystallized membrane proteins by low-dose imaging with the transmission electron microscope, and computer image processing. We have previously presented the software system 2dx, for user-friendly image processing of 2D crystal images. Its central component 2dx_image is based on the MRC program suite, and allows the optionally fully automatic processing of one 2D crystal image. We present here the program 2dx_merge, which assists the user in the management of a 2D crystal image processing project, and facilitates the merging of the data from multiple images. The merged dataset can be used as a reference to re-process all images, which usually improves the resolution of the final reconstruction. Image processing and merging can be applied iteratively, until convergence is reached. 2dx is available under the GNU General Public License at <http://2dx.org>.

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