

Publication

A Medipix quantum area detector allows rotation electron diffraction data collection from submicrometre three-dimensional protein crystals

JournalArticle (Originalarbeit in einer wissenschaftlichen Zeitschrift)**ID** 4530970**Author(s)** Nederlof, Igor; van Genderen, Eric; Li, Yao-Wang; Abrahams, Jan Pieter**Author(s) at UniBasel** [Abrahams, Jan Pieter](#) ;**Year** 2013**Title** A Medipix quantum area detector allows rotation electron diffraction data collection from submicrometre three-dimensional protein crystals**Journal** Acta Crystallographica. Section D, Biological Crystallography**Volume** 69**Pages / Article-Number** 1223-1230**Mesh terms** Science & TechnologyLife Sciences & BiomedicinePhysical SciencesBiochemical Research MethodsBiochemistry & Molecular BiologyBiophysicsCrystallographyBiochemistry & Molecular Biology-BiophysicsCrystallography

When protein crystals are submicrometre-sized, X-ray radiation damage precludes conventional diffraction data collection. For crystals that are of the order of 100 nm in size, at best only single-shot diffraction patterns can be collected and rotation data collection has not been possible, irrespective of the diffraction technique used. Here, it is shown that at a very low electron dose (at most 0.1 e⁻/Å²), a Medipix2 quantum area detector is sufficiently sensitive to allow the collection of a 30-frame rotation series of 200 keV electron-diffraction data from a single similar to 100 nm thick protein crystal. A highly parallel 200 keV electron beam (λ = 0.025 Å) allowed observation of the curvature of the Ewald sphere at low resolution, indicating a combined mosaic spread/beam divergence of at most 0.4 degrees. This result shows that volumes of crystal with low mosaicity can be pinpointed in electron diffraction. It is also shown that strategies and data-analysis software (MOSFLM and SCALA) from X-ray protein crystallography can be used in principle for analysing electron-diffraction data from three-dimensional nanocrystals of proteins.

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