



**Molecular Biotechnology Programme**  
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Author	<b>Gösta Huldt</b>	
Title (English)	<b>X-ray diffraction imaging of single particles</b>	
Title (Swedish)		
Abstract	<p>Theory predicts that with a very short and intense X-ray pulse, a single diffraction image could be recorded from a large macromolecule, a virus, or a nanocluster of proteins without the need for a crystal. A three-dimensional data set could be obtained if images are collected from multiple copies of a reproducible sample. We outline a method for structure reconstruction from such a data set. A basic requirement is that the quality of the diffraction images is sufficient for their mutual orientations to be found. Averaging techniques can enhance the signal and extend the resolution in redundant data sets, provided that we are able to determine whether two noisy images present the same view of the sample or not. We present an analytical solution to this classification problem. The solution connects the achievable resolution to the particle size and to the number of incident photons.</p>	
Keywords	Diffraction imaging, single particle, X-ray free-electron laser, image processing	
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