

Streamlining data collection and analysis for cryo-EM based structure determination

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Abstract

The shared Novartis and FMI electron microscopy center has been operational for five years. During that time, the process from biological sample to final protein model has been greatly improved, enabling the EM center to support drug discovery projects of previously intractable targets in an accelerated timeline. An essential corner stone of that development was the creation of a robust and streamlined screening, data collection and analysis workflow. In this context, I will discuss some challenges and strategies employed to streamline the single-particle cryo-EM pipeline that underpins the cryo-EM structure determination efforts at Novartis and present the CryoFLARE software [1] we use for live analysis of all collected data.