

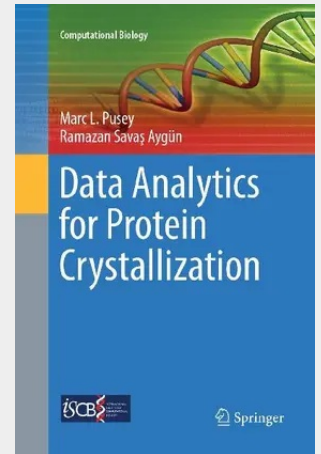
Data Analytics for Protein Crystallization

This unique text/reference presents an overview of the computational aspects of protein crystallization, describing how to build robotic high-throughput and crystallization analysis systems. The coverage encompasses the complete data analysis cycle, including the set-up of screens by analyzing prior crystallization trials, the classification of crystallization trial images by effective feature extraction, the analysis of crystal growth in time series images, the segmentation of crystal regions in images, the application of focal stacking methods for crystallization images, and the visualization of trials.

Topics and features: describes the fundamentals of protein crystallization, and the scoring and categorization of crystallization image trials; introduces a selection of computational methods for protein crystallization screening, and the hardware and software architecture for a basic high-throughput system; presents an overview of the image features used in protein crystallization classification, and a spatio-temporal analysis of protein crystal growth; examines focal stacking techniques to avoid blurred crystallization images, and different thresholding methods for binarization or segmentation; discusses visualization methods and software for protein crystallization analysis, and reviews alternative methods to X-ray diffraction for obtaining structural information; provides an overview of the current challenges and potential future trends in protein crystallization.

This interdisciplinary work serves as an essential reference on the computational and data analytics components of protein crystallization for the structural biology community, in addition to computer scientists wishing to enter the field of protein crystallization.

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