

# Computational tools for the analysis of time-resolved serial X-ray crystallography data

Transmembrane proteins, such as bacteriorhodopsin, cytochrome c oxidase, and photosynthetic reaction centers, use sunlight or chemical energy to power vital processes like ATP synthesis and photosynthesis. This energy drives conformational changes within these proteins, controlling the transport of molecules across the membrane. By using time-resolved serial crystallography and advanced numerical methods, we improve the confidence by which functionally important structural rearrangements are modeled and emphasise the value of systematic data treatment.



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