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## Room-temperature X-ray fragment screening with serial crystallography

X-ray crystallography is a cornerstone technique in providing essential information in the process of structure-based drug development. The instrument HiPhaX at PETRA III is dedicated to 'High-throughput Pharmaceutical X-ray screening' in an early stage of drug development aiming at a high degree of automatization. It offers a temperature- and humidity-controlled sample chamber for serial and single crystal data collection. Typically, X-ray diffraction data collection in drug development is conducted at cryogenic temperatures to mitigate radiation damage effects. Cryogenic temperatures can however introduce artifacts and influence both the protein conformation and protein-ligand interactions. We performed serial fixed-target room-temperature fragment screening at HiPhaX and systematically compared it to conventional single crystal data collection at cryogenic temperature. The protein target is the Fosfomycin-resistance protein A from *Klebsiella pneumoniae* (FosAKP), an enzyme involved in antibiotic resistance and a highly relevant drug target accordingly.

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