

Structurally denatured BSA using small-angle X-ray scattering

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We employed small-angle X-ray scattering (SAXS) to investigate the conformational transitions of bovine serum albumin (BSA) across a wide range of urea concentrations (0–8 M). By constructing three-dimensional (3D) ab initio models using GASBOR, we described the structural evolution of BSA from its native state to denatured and unfolded conformations. By integrating size exclusion chromatography and SAXS (SEC-SAXS), we accurately isolated elution profiles corresponding to monomeric BSA, even under conditions of conformational polydispersity at high urea concentrations (5–8 M). Detailed analysis yielded precise measurements of the radius of gyration (R_g) and maximum dimension (D_{max}) derived from the pair distance distribution function $P(r)$. Our results revealed that BSA maintains its native conformation at low urea concentrations (0–3 M), undergoes partial denaturation at 4 M urea, and fully unfolds at concentrations of 5–8 M. These findings offer valuable insights into the relationship between structural stability and protein function, contributing to a deeper understanding of protein folding and stability under denaturing conditions.

Paper submission Plan

Yes

Best Presentation

Yes

Contribution track

ICABU WG4. Applications of Particle Beams

Primary author: MALIKI, Siti Khadijah (Division of Advanced Nuclear Engineering (DANE), Pohang University of Science and Technology (POSTECH))

Co-authors: Mr KIM, Jun Ha (Pohang Accelerator Laboratory (PAL)); JIN, Kyeong Sik (Pohang Accelerator Laboratory (PAL), Division of Advanced Nuclear Engineering (DANE), Pohang University of Science and Technology (POSTECH)); Prof. CHUNG, Moses (Center for Accelerator Physics and Engineering (CAPH), Department of Physics and Division of Advanced Nuclear Engineering (DANE), Pohang University of Science and Technology (POSTECH))

Presenter: MALIKI, Siti Khadijah (Division of Advanced Nuclear Engineering (DANE), Pohang University of Science and Technology (POSTECH))

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