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Benjamin Werth
Sr. Science Editor - Chemistry | Biochemistry
JoVE

Dear Dr. Benjamin Werth,

Thank you very much for the invitation to publish in JoVE. In 2016/2017/2018/2019 we have worked together on the manuscripts "Online Size-exclusion and Ion-exchange Chromatography on a SAXS Beamline", "Structure Solution of the Fluorescent Protein Cerulean Using MeshAndCollect" and "Fully Autonomous Characterization and Data Collection from Crystals of Biological Macromolecules" and due to our good experiences with JoVE we would be happy to publishing in your journal, again.

We would like to propose a manuscript describing a project of high interest to the structural biology and general biology community, using top notch innovative new techniques. We describe the data collection and analysis of difficult samples using Bio-Small Angle X-ray Scattering using a combination of deconvolution of the curves and data analysis. We are using the program/interface Scatter, which is commonly used by SAXS specialist and non-specialists to analyse and interpret their SAXS data. Until now, there is only an online tutorial but no publication about the program nor how to use or cite it in the literature. We would like to change this and would like to submit to you our manuscript "Analysis of SEC-SAXS data via deconvolution".

I am looking forward to hearing from you at your earliest convenience

Stephanie Hutin