Protein crystallography analysis and \textit{ab initio} structure determination with the new series of diffractometers from Rigaku Oxford Diffraction, the \textit{XtaLAB Synergy.}

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In the course of the past two years, activities at Rigaku Oxford Diffraction have given birth to a new series of single crystal X-ray diffractometers, the \textit{XtaLAB Synergy}. As its name indicates, the \textit{XtaLAB Synergy} combines the best of Rigaku and Oxford Diffraction in terms of hardware components, software programs and years of experience and savoir-faire in X-Ray crystallography on small molecule and protein compounds in the home lab.

Combining high X-Ray flux, multiple radiation wavelengths, very high data collection speed and proven easy-of-use of the control program CrysAlis$^\text{Pro}$, the \textit{XtaLAB Synergy} has been designed both for small molecule and protein work and features:

- A standardized and compact design that accommodates a rotating anode, a single wavelength or dual wavelength microfocus sealed tube X-Ray source without any change in its design.
- For the sealed tube version, a NEW PhotonJet-S series of microfocus sources available in Cu, Mo and Ag wavelengths that, combined to new optics, provide a significant increase of X-ray photons at the sample over previous generations of sealed tube microfocus sources.
- A completely redesigned kappa goniometer that allows for very fast data collection speed (10\textdegree/second), symmetrical 2\theta positioning and omega collection scans in either direction.
- New hybrid photon counting detector from ROD, the HyPix-6000HE, featuring 100 \mu m pixel size and a high frame rate of 100 Hz for very fast data collection.
- For protein work, the ability to decrease the beam divergence via a computer-controlled slit, allowing for reflection resolution along longer unit cell axes.

In this work, we focus on the usage of the \textit{XtaLAB Synergy} for protein work and show how reflections along the long unit cell axis of thaumatin (~150 \AA) and catalase (~230 \AA) can be resolved, leading to structure solution for thaumatin by sulfur-SAD phasing and for catalase by molecular replacement at short detector distances.