ESRF	**Experiment title:** FRANKFURT BAG: Strictosidine Synthase	**Experiment number**: MX-135
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Report:

The first attempt to obtain phases for Strictosidine Synthase was performed with crystals labeled with selenium at the two methionines in the sequence of this protein. Using the unit-cell size (a=b=150.8, c=121.7, γ=120˚) and the molecular weight (35kDa) of Strictosidine Synthase, it can be expected to find 3 protein molecules per asymmetric unit. A self-rotation search for a non-crystallographic 3-fold symmetry gave only a peak at the orientation of the crystallographic axes, while the search for a 2-fold non-crystallographic axis showed a peak in the a,b-plane, 12˚ off the diagonal. The energy scan of Se-labeled Strictosidine Synthase exhibited a pronounced absorption edge for Selenium with a peak at 12663eV (f'=-8.2 and f''=5.1) and an inflection point at 12661eV (f'=-9.7 and f''=3.6). Data were collected at peak and inflection point wavelengths (0.97911 and 0.97926Å) and a remote wavelength at 0.97625Å (12700eV). The data were processed with XDS and hereafter feed into the structure solution program SOLVE. The best solution found contained only two Se positions, while 4 or 6 positions have been expected from the above considerations. This solution resulted in a figure of merit of only 0.29, much too low for reliable phases. Other species contain 2 or 4 additional methionine residues in their sequence. We therefore expect improvement from Se-edge MAD experiments with mutants containing more methionines.