Protein polycrystallography and laboratory diffractometer data

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The capability of modern powder diffractometers to provide a reasonable data form protein samples have been shown on HE lysozyme. Data was good enough for indexing, space group determination and even Rietveld refinement was reasonable. Although a bit longer measurement time than on a beam-line was required, no disturbing radiation decay was detected. In order to further investigate the capability of standard laboratory system, Br derivative of insulin has been prepared and measured at a room temperature. The obtained data were also of indexing quality. The data and refinement attempts will be shown.