

Structural Studies of Proteins From the Proteome Project

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Abstract No. Gold1558

Beamline(s) X25

Introduction: The proteome project (<http://proteome.bnl.gov/>) is a consortium working on a wide variety of *Saccharomyces cerevisiae* proteins expressed in *E. coli*. Two of them are P79, the NAD-dependent 5,10-methylenetetrahydrofolate dehydrogenase, and P107, a protein with glutaredoxin activity. Both have been overexpressed, purified and crystallised using our standard protocols.

Methods and Materials: The proteins were cloned into pET vectors, expressed in 1 l growths and purified by ion exchange gel filtration. Crystallization conditions were initially found using Hampton Research PEG/ion and crystal screen cryo screens.

Results: None of the crystals tested on the beamline diffracted beyond 4 Å resolution. We were therefore able to say definitely that the crystals were proteins, but no usable data were collected.

Conclusions: Further crystallization trials are being undertaken.

Acknowledgments: Office of Biological Research, Department of Energy and Academy of Finland.