ESRF	**Experiment title:** Complexes of ***E.coli*** ribonucleotide reductase	**Experiment number:** LS497
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Report:

Data was collected on Salmonella Typhimurium nrdE Rl Riboncleotide reductase (RNR). The crystals were small (0.05*0.04*0.03 mm') spacegroup C2221 with cell dimensions 135 135 292 Å. These crystals initially diffracted to 3.2 Å but rapidly decayed to 4Å. A 85% complete data to 4Å could be collected on 3 crystals. The structure could be solved by Molecular Replacement (AMORE) using the class la RlA RNR as a search model. The asymmetric unit contains 2 nrdE molecules.

RNR class 1 is composed of two homodimeric proteins denoted Rl and R2. The class 1 can be divided into two subgroups class la and class lb. The Rl and R2 from class la has been previously structurally determined (Uhlin & Eklund, 1994 and Nordlund et al 1990 respectively). The nrdE protein belongs to class lb of RNR and corresponds to Rl. The class la is regulated with two allosteric effector sites while the class lb only uses one. The structure of class lb reveals that the domain responsible for the second allosteric regulation is drastically changed and no allosteric site is present.

The nrdE protein forms a much more stable complex with the nrdF protein (R2 in classlb) than in tested class la enzymes. It is therefore a suitable target for crystallization attempts of the first complete RlR2 RNR structure.

We plan to use the structure of nrdE together with the structure of nrdF (Eriksson, M.unpublished result) for molecular replacement in solving the first tetramer ($\alpha_2\beta_2$) structure of RNR.

The evaluation of nrdE and experiments to obtain tetramer crystals are in progress.