

Recent progress on the *D. radiodurans* structural genomics project

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Over the past ten years an increasing number of genomes from very diverse organisms (bacteria, fungi, plants, insects, mammals etc.) have been sequenced. The macromolecular crystallography group at ESRF has decided to focus its interest on a bacteria, named *Deinococcus radiodurans*, which displays an extreme resistance to γ -radiation and for which the genome was recently sequenced. The project involves multiple steps: cloning of the genes of interest, production of the corresponding proteins in a soluble form and finally structural and/or functional characterisation of these proteins. The information obtained will shed light on both the cellular roles of the individual proteins and on the outstanding resistance mechanism of *D. radiodurans*. An overview of the current status of the project will be presented followed by a more detailed description of one of these targets, MTHase. MTHase (maltooligosyltrehalose trehalohydrolase) is involved in the synthesis of trehalose from maltooligosaccharides. Trehalose (α -D-glucopyranosyl-1,1- α -D-glucopyranose) is a non-reducing diglucoside found in various organisms that serves not only as a carbohydrate reserve, but also as an agent that protects against a variety of physical and chemical stresses. The crystal structure of MTHase from *D. radiodurans* was solved at 1.1Å resolution in its apo-form and subsequently at 1.2 and 1.5Å resolution in complex with maltose and trehalose respectively. These structures reveal the conformational changes and essential residues involved in trapping sugars in the substrate binding cleft.