**Preliminar Diffraction Study of the Full-lengh Protein Hexokinase 2 of *Saccharomyces cerevisiae***

Laura Roces[a], Pilar Herrero[b], Fernando Moreno[b], Santiago García-Granda[a], [a]*Departmento de Química Física y Analítica.* [b]*Departamento de Bioquímica y Biología Molecular, Universidad de Oviedo. Spain.* E-mail: lrf@fq.uniovi.es

Hexokinase 2 (Hxk2) is, with the protein Mig1, the mayor mediator of glucose repression in *Saccharomyces cerevisiae*. It has been recently reported that both proteins interact to generate a repressor complex located in the nucleus of *S. cerevisiae* during growth in glucose medium [1]. The Lys6-Met15 decapeptide of Hxk2 was found to be necessary for interaction with the Mig1 protein.

The crystal structure of a fragment of Hxk2 containing residues 18-486 is deposited in the Protein Data Bank [2], though there is no structural information about the first 17 residues of the N terminus, where the Hxk2 decapeptide interacting with Mig1 protein is contained. Moreover, it is in this N terminus where the specific regulatory capacity of *S. cerevsiae* hexokinase 2 resides. The aim will be to define the three-dimension full-lengh protein Hxk2 fold, in order to get new hits and be able to explain the formation of the repression complex.

We report here the crystallization of the full-lengh protein Hxk2 using the microbath under oil method and the preliminar diffraction patterns obteined. The *S. cerevisiae* Hxk2 crystals have an hexagonal plate shape (different from the elongated bipyramidal shape reported for the Hxk2 fragment). The crystal dimensions are about 0.2 x 0.2 x 0.05 mm.

[1] Ahuatzi D., Herrero P., de la Cera T., Moreno F., *J. Biol. Chem.*, 2004, **279**, 14440. [2] Kuser P.R., Krauchenco S., Auntenes O.A.C., Polikarpov I., *J. Biol. Chem.,*. 2000, **275**, 20814.

**Keywords: crystallization, protein folding, regulation**