s1.m8.p20 **Crystal structure of two isolectins from the fungus *Coprinus cinereus*: a model for studying evolutionary pathways.** María F. López-Lucendo,[a] Hans-Joachim Gabius[b] and Antonio Romero[a], [a]*Departamento de Estructura y Función de Proteínas, Centro de Investigaciones Biológicas - CSIC, C/ Velázquez 144, Madrid, 28006, Spain,* [b] *Institut für Physiologische Chemie, Tierärztliche Fakultät, Ludwig-Maximilians-Universität München, Veterinärstr. 13, D-80539 München, Germany. E-mail: maria.f@cib.csic.es*

Keywords: Galectins; X-ray structure; *Coprinus cinereus*

The emerging importance of glycans of cellular glycoconjugates to serve as hardware in biological information storage and transfer, reflected by coining the term *sugar code*, engenders increasing interest to study the molecular details of protein-carbohydrate interactions [1]. In addition to insights into the fundamental mechanisms of this type of intermolecular recognition the structural study of carbohydrate-binding proteins, especially lectins, is helpful in at least two further aspects, i.e. to provide input for the design of custom-made pharmaceuticals targeting clinically relevant lectins and to define structural traits to track down evolutionary pathways and basic structure-function relationships [2]. Consequently, structural analysis especially of distant members in a family, here lectins involved in cell adhesion and growth regulation in animals, i. e. galectins, is required. For this purpose, recent work has been focused on the first galectins known from outside the animal kingdom. These are two isolectins from the basidiomycete *Coprinus cinereus* (inky cap mushroom), termed Cgl-1 and -2 [3]. The occurrence of the fungal galectins implies that all eukaryotes have inherited some galectin gene(s) from a common ancestor. The structure of Cgl-1 and Cgl-2 were resolved by x-ray crystallography and the data sets were collected to 1.85 and 1.6 Å resolution respectively.

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s1.m8.p21 **Cubic Lipid Phase Crystallization of Membrane Proteins.** Hartmut Luecke, *University of California, Irvine, CA, 92697-3900, USA, E-mail: hudel@uci.edu*

Keywords: Membrane; Protein

Cubic Lipid Phase (CLP): The CLP method for membrane protein crystallization has been refined to allow large-scale screening of various membrane proteins. The various parameters (CLP lipid, water content, bilayer lipid additive, pH, ionic strength, precipitating agent etc.) can be varied. Three distinct seven-transmembrane proteins where crystallized and their structures determined.

Bacteriorhodopsin (BR): High-resolution maps from X-ray diffraction of bacteriorhodopsin crystal obtained in CLP and some of its photointermediates have yielded insights to how the isomerization of the bound retinal drives ion transport. Although some important mechanistic details are still undecided, the events of the photochemical cycle are now understood to reflect changes in specific hydrogen bonds of protein groups and bound water molecules in response to motions of the retinal chain. A nearly complete lipid bilayer is also present in the x-ray model.

Sensory Rhodopsin (SR): Atomic resolution structures of a phototaxis receptor in haloarchaea, the first sensory member of the widespread microbial rhodopsin family, have yielded insights into spectral tuning and the interaction face with its membrane-embedded transducer. Spectral differences between the sensory rhodopsin and light-driven proton pump bacteriorhodopsin depend largely on the repositioning of a conserved arginine residue in the chromophore-binding pocket. Information from the structures combined with biophysical and biochemical analysis have established a model for receptor activation and signal relay involving light-induced helix tilting in the receptor transmitted to the transducer by lateral transmembrane helix-helix interactions.

Anabaena SR (ASR): Most recently, the structure of a sensory rhodopsin from the cyanobacterium *Anabaena* has been determined to 1.9 Å resolution. This represents the first bacterial rhodopsin structure. In comparison to the archaeal rhodopsins BR and SR there are many striking rearrangements and shifts in hydrogen bonding patterns on both the extracelullar and the cytoplasmic half of the receptor. Also, the cytoplasmic face, which is thought to interact with the soluble transducer, is structurally well-defined and very different from that of the archaeal rhodopsins. The structure of the soluble transducer of this photoreceptor has also been determined.