# *Séminaire externe*

## "Towards the identification of internal protein pathways: lessons from Olfactory Receptor models. "

The G-Coupled Protein Receptor family is one of the largest transmembrane protein fold involved in signal transduction. In order to recognize different ligands in various tissues, the evolution has selected a combinatorial number of amino acids specific to these effectors. Recent advances in crystallographic structures availability done by a large international coordination program[1] opens up the possibility to massively predict the GPCR structures using threading approaches with a high degree of confidence. As an introduction, an overview of the structural basis of signal transduction within GPCR structures will be presented. It will then be shown how these GPCR templates were assembled previously to produce models of a small subset of the GPCR rhodopsin family, the Olfactory Receptors[2]. Last, we shall focus on the possibility of detecting amino acids involved in energy acceptor-donor pairs upon ligand binding. The implications of these predictions for the PAPETS consortium will be discussed with the assembly.


1. Pieper, U. *et al.* Coordinating the impact of structural genomics on the human α-helical transmembrane proteome. *Nat. Struct. Mol. Biol.* **20,** 135–138 (2013).
2. Launay, G., Sanz, G., Pajot-Augy, E. & Gibrat, J.-F. Modeling of mammalian olfactory receptors and docking of odorants. *Biophys. Rev.* **4,** 255–269 (2012).



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Invité par Francesco Piazza

## Mardi 12 mai 2015 à 11h

Salle de conférence du CBM