

# JOURNÉES CAMPUS D'ILLKIRCH 2010

*3 et 4 mai 2010*

organisées par

l'Institut de génétique et de biologie moléculaire et cellulaire (IGBMC)  
le Laboratoire de biophotonique et de pharmacologie (LBP)  
le Laboratoire de conception et application de molécules bioactives (LCAMB)  
le Laboratoire d'innovation thérapeutique (LIT)  
l'Institut de recherche de l'École de biotechnologie de Strasbourg (IREBS)

## RÉSUMÉS DES CONFÉRENCES

### Abstracts of plenary lectures

**lundi 3 mai 2010**

Grand Amphithéâtre  
Pôle API – École Supérieure de Biotechnologie de Strasbourg  
Boulevard Sébastien Brant - Illkirch

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# **New tools for imaging and modulation of intracellular signaling networks**

par le Dr Carsten SCHULTZ

*Interdisciplinary Group Leader and Senior Scientist  
Chemical cell biology Group, EMBL Heidelberg*

Models derived from Systems Biology describe the complex molecular networks in cells in a holistic way, giving rise to the hope that new possibilities arise for a more efficient drug development and improved predictions of drug side effects. A concise modelling requires experimental evaluation of model structures and ideally of predictions provided by the model. Therefore we are interested to develop new methods to image and modulate intracellular events. In particular, we focus on methods for dissecting signaling events by switching on proteins in the absence of membrane receptor activation.

In this lecture, a variety of methods to detect signaling events in living cells as well as new methods to activate enzymes by small molecules will be presented. This includes synthetic membrane-permeant second messenger molecules such as phosphoinositides and protein constructs that are rapidly activated by chemical dimerizers such as rapamycin and its analogues. While these new tools helped to reveal surprising new findings in receptor endocytosis, endosomal fusion, and calcium signal generation, the methods are also employed to validate a new model, called DynaCellNet, of G-protein-coupled receptor signaling featuring 45 elements and 290 molecular interactions. The model has predictive power and recently led to the discovery of a novel feedback loop in the regulation of intracellular calcium transients in our lab.

# **High throughput sequencing: a wealth of applications**

par le Dr Philippe GLASER

*Directeur de la Génopole Institut Pasteur  
Laboratoire d'Évolution et génomique bactériennes, Institut Pasteur de Paris*

We are facing a dramatic increase in the speed of DNA sequencing. During the two last years, sequencers have multiplied their capacity by one hundred, reaching more than 300 billion bases in ten days, thereby making possible the sequencing of a human genome in less than two weeks for less than 10000 Euros. Not only the speed of sequencing has increased but also its accuracy, allowing the detection of a few polymorphisms between two almost identical genomes.

These technological developments have a profound impact on almost every field in biology. In ecology, it's used to analyze life diversity and to characterize microbial communities through their metagenomes. It's also a powerful tool to study evolution, either by sampling organisms with differential adaptations or under laboratory conditions. The possibility to sequence hundreds of genomes provides new opportunities in genetics and in population and quantitative genetics. It becomes the most straightforward method to associate phenotype to genotype, in particular for medical applications. In addition to genomics, high throughput sequencing has revolutionized the functional analysis of the genome to map and quantify RNA, to discover small and non-coding RNAs and for epigenetic studies by genome wide analyses of methylation or histone modification.

In this lecture I will present various biological questions addressed by high throughput sequencing in the study of microorganisms.

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