



中国科学院上海巴斯德研究所  
INSTITUT PASTEUR OF SHANGHAI  
CHINESE ACADEMY OF SCIENCES



# *Seminar*

## **Chromatin-encoded memory of transcriptional programs inferred from cell clones: novel views from single cell omics**



**[Speaker]** Dr. Olivier CUVIER

**[Time]** 10:00-11:30 AM , October 17, 2017

**[Host]** Prof. Lubin Jiang & Nicolas GILBERT

**[Venue]** A0201, Life Science Research Building

### **[Speaker introduction]**

05/1995-07/2000, **Ph.D.** University of Geneva, Switzerland.

08/2000-03/2003, **Post-Doc.** Cold Spring Harbor Laboratory (CSHL), NY, USA.

05/2003-12/2008, **Researcher.** Institute of Human Genetics, Montpellier, France.

07/2009- now, **Research Director.** Center of Integrative Biology, Toulouse, France.

### **[Abstract]**

We will present our genome-wide analyses illustrating how long-range contacts in chromosomes, as detected from hidden information in ChIP-Seq, support the role of functional long-range contacts in regulating gene expression including of oncogenes, as confirmed through analysis of looping by Hi-C data along with further development of computational methods to probe long-range contact maps at a high resolution ( $< 500$  bp). Furthermore, we will present recently published data together with unpublished stuffs highlighting a role of histone lysine-methyl transferases (KMTs) together with additional chromatin factors in regulating the inherited transmission of gene expression states, as inferred from single cell omics. We shall show the mechanisms of protection of active genes including oncogenes that are protected from heterochromatin-mediated gene silencing, at genome-wide levels. In particular, our data support the view that KMTs contribute to cell identity by protecting genes from stochastic changes in expression, thereby maintaining transcriptional programs through cell divisions.