
FRANÇOIS FUKS

CV

PARTICIPANT AT:

CODING AND NON-CODING FUNCTIONS OF THE GENOME BARCELONA CONFERENCE ON EPIGENETICS AND CANCER



October, 29th-30th, 2015, Barcelona

François Fuks, Director of the Laboratory of Cancer Epigenetics at the Free University of Brussels, and “Senior Research Associate” of the Belgian “F.N.R.S.”, Brussels, Belgium

François Fuks performed his PhD thesis at the German Cancer Research Center (DKFZ) in Heidelberg, Germany. His project, conducted under the supervision of Prof. Jean Rommelaere concerned the regulation of the parvoviral early promoter activity. Next, François joined the laboratory of Prof. Tony Kouzarides at the Gurdon Institute, University of Cambridge, UK, where he initiated his work on the intimate link between DNA methylation and chromatin modifications. After his postdoctoral training, François established his own group at the Faculty of Medicine, Free University of Brussels. Currently, François is the Director of the Laboratory of Cancer Epigenetics at the Free University of Brussels, and is a “Senior Research Associate” of the Belgian “F.N.R.S.”. François received the EMBO Young Investigator Award and the Ithier Prize (Belgium) as well as the Lambertine-Lacroix Prize (Belgium).

B-DEBATE IS AN INITIATIVE OF:



FRANÇOIS FUKS

ABSTRACT

PARTICIPANT AT:

CODING AND NON-CODING FUNCTIONS OF THE GENOME BARCELONA CONFERENCE ON EPIGENETICS AND CANCER



October, 29th-30th, 2015, Barcelona

François Fuks, Director of the Laboratory of Cancer Epigenetics at the Free University of Brussels, and “Senior Research Associate” of the Belgian “F.N.R.S.”, Brussels, Belgium

DNA modifications: from Mechanisms to Genome-Wide Profiling in Cancers

The cancer epigenetic field has evolved from a gene-by-gene approach to more global epigenomic strategies, with far-reaching fundamental and clinical implications. Using genome-wide approaches, we have performed DNA methylation profiling in human breast tumor tissues. Results will be presented that highlight precise epigenetic portraits in breast cancers, uncovering a key contribution of the DNA methylome to the complexity of the disease. Besides DNA methylation, another DNA modification - DNA hydroxymethylation - has appeared on the scene, sparking great interest. Indeed, the TET family of enzymes (TET1, TET2 and TET3) are methyl dioxygenases that are known to convert 5-methylcytosine (5-mC) to 5-hydroxymethylcytosine (5-hmC), leading to changes in gene expression. The challenge is now to uncover the roles they play and how they relate to DNA demethylation. We will present our recent efforts to better understand the modes of regulation of TET enzymes and hydroxymethylation.

B-DEBATE IS AN INITIATIVE OF:

