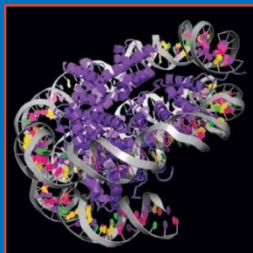


SAVE THE DATE

CALL FOR ABSTRACTS

## WORKSHOP



*New mass spectrometry approaches to study cancer genome functions and beyond...*

13 December 2018, Montpellier

### SPEAKERS



**Michiel VERMEULEN**, *Radboud Institute for Molecular Life Sciences, Nijmegen*  
“Deciphering chromatin biology using integrative omics approaches”

● **Jérôme DEJARDIN**  
*Institute of Human Genetics, Montpellier*



**Jérôme GOVIN**, *Institute for Advanced Biosciences, La Tronche*  
“Exploring the biology of histone variants with mass spectrometry”

● **Julien MARCOUX**  
*Institute of Pharmacology and Structural Biology Toulouse*



**Tony LY**, *Centre for Gene Regulation and Expression, University of Dundee*  
“Combining mass spectrometry with FACS for comprehensive proteomic and phosphoproteomic analysis of cell cycle transitions”

● **Anne-Aurélien RAYMOND**  
*INSERM U1053, Bordeaux Research In Translational Oncology*

● **Cyril RIBEYRE**  
*Institute of Human Genetics, Montpellier*

CALL FOR ABSTRACTS

CALL FOR ORAL COMMUNICATIONS - DEADLINE 29 OCTOBER 2018

Registration - free but mandatory: [WSTechnoMS2018.canceropole-gso.org](http://WSTechnoMS2018.canceropole-gso.org)

### OBJECTIVE

Mass-spectrometry (MS)-based proteomic analyses are essential approaches for studying genome function and cancer biology. It is now possible to analyse the biological impact of genetic aberrations in cancer on protein expression, and precisely quantify levels of individual proteins in all their different modified forms. By comparing healthy and diseased samples, MS analyses permit the identification and validation of diagnostic and prognostic biomarkers.

However, proteomics approaches are still technically demanding and involve numerous challenges. During this one-day meeting, renowned international experts in proteomics will share their experience, and ongoing projects within the GSO and SIRIC Montpellier Cancer will be presented and discussed. The meeting will be an opportunity to share know-how and tools for proteomics and other MS-based methods for structural and functional analysis of the genome, and beyond.

### VENUE

Conference Room, Institute of Cancer Research of Montpellier (IRCM)

