OMICS International
conferenceseries.com

8th Euro Global Summit on
Cancer Therapy
November 03-05, 2015 Valencia, Spain

Systematic identification and characterization of the methyl proteome for cancer intervention

Shawn S C Li
Western University, Canada

Methylation of Lys and Arg residues has emerged as a prevalent post-translational modification (PTM) occurring on numerous non-histone proteins, drastically extending its role beyond the known histone code. We have developed an approach that combines mass spectrometry with peptide arrays and bioinformatics to systematically identify protein methylation and quantify dynamic changes in the methylome associated with tumorigenesis or drug resistance. Our studies not only led to the identification of numerous novel methylation sites, but also generated new insights into how protein methylation regulates cellular functions such as DNA damage repair, apoptosis and drug resistance. With recent advances in mass spectrometry, the stage is now set to decode the methyl proteome and to elucidate, systematically, the mechanisms of interplay between histone and non-histone methylation and between methylation and other types of PTM for cancer diagnosis and intervention.

Biography

Dr. Shawn Li is Professor of Biochemistry at Western University and Canada Research Chair in Functional Genomics and Cellular Proteomics. The Li lab employs an integral approach that combines proteomic tools such as mass spectrometry and peptide and protein arrays with molecular and cellular methods to identify protein post-translational modifications (PTM) and to characterize their roles in cell proliferation, differentiation, migration, apoptosis and the DNA damage response.

sli@uwo.ca

Notes: