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“Cancer epigenetics: paradigms and drugs”

24 April 2012, 11:00 (*s.t.*)

Venue: Seminar Room, 2nd floor
Institute of Molecular Biology (IMB)
Johannes Gutenberg University Campus Mainz

All are welcome to attend

Abstract:

Cancer epigenetics: paradigms and drugs

Altered DNA methylation patterns represent one of the earliest and most consistent hallmarks of human cancers. Hypermethylation of tumor suppressor genes has been described in many tumors and represents an attractive target for cancer therapy. We are using array-based methylation profiling to examine the effects of various methylation inhibitors on human cancer cell lines. The results show non-random demethylation patterns and also identify cellular factors that are required for effective drug uptake. In parallel approaches, we are using whole-genome bisulfite sequencing to characterize the tumor methylome in mouse models. The results show widespread hypomethylation in large chromosomal regions and also suggest that the inhibition of DNA methyltransferases can further exacerbate cancer-specific epigenetic lesions. As such, novel approaches are required for the development of epigenetic drug candidates.