Martin Hirst

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Research Area
Dr. Hirst's research aims to further our understanding of the role of epigenetic dysfunction in cancer initiation and progression and to translate this knowledge into improved health outcomes for Canadians.
International efforts to characterize genetic lesions in cancer genomes have revealed recurrent mutations in epigenetic modifiers and in some cases these can represent the sole driver. Understanding the functional implications of these mutations, their contribution to abnormal cellular differentiation and how emerging epigenetic therapeutics may counteract their effects represent the next critical steps towards translating this knowledge. In this context, Dr. Hirst is studying cancers that harbor highly recurrent gain and loss of function mutations to epigenetic modifiers, such as acute myeloid leukemia, synovial sarcoma, malignant rhabdoid tumor. His research involves the development and application of molecular and computational tools to measure epigenetic features and drive new insights into normal and pathogenic epigenetic

regulatory control.
Follow Dr. Hirst on Twitter: https://twitter.com/hirst_lab

Selected Publications:

Visit Google Scholar for a complete list of publications.

Xiaoyang Lan, David J. Jörg, Florence M. G. Cavalli, Laura M. Richards, Long V. Nguyen, Robert J. Vanner, Paul Guilhamon, Lilian Lee, Michelle M. Kushida, Davide Pellacani, Nicole I. Park, Fiona J. Coutinho, Heather Whetstone, Hayden J. Selvadurai, Clare Che, Betty Luu, Annaick Carles, Michelle Moksa, Naghmeh Rastegar, Renee Head, Sonam Dolma, Panagiotis Prinos, Michael D. Cusimano, Sunit Das, Mark Bernstein, Cheryl H. Arrowsmith, Andrew J. Mungall, Richard A. Moore, Yussanne Ma, Marco Gallo, Mathieu Lupien, Trevor J. Pugh, Michael D. Taylor, Martin Hirst, Connie J. Eaves, Benjamin D. Simons & Peter B. Dirks. Fate mapping of human glioblastoma reveals an invariant stem cell hierarchy. Nature (2017)

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