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Profiling epigenomic landscapes and gene regulatory networks**Johanna K Samuelsson**
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Chromatin immunoprecipitation followed by next generation sequencing (ChIP-Seq) and other genome wide technologies have been integral in advancing our understanding of how epigenetic phenomena are regulated and how they affect gene expression. However, as we ask more complex questions the limitations of traditional genome-scale approaches have motivated researchers to develop new and improved methodologies for the characterization of the epigenomic landscape. This presentation will cover some of the progress that we and others have made in advancing the traditional ChIP-based assays and will include a new ChIP-Seq spike-in method for improved normalization and quantitation, a unique engineered DNA-binding molecule-mediated ChIP technology using the CRISPR system for dissecting the chromatin structure of your genomic regions of interest, and the development of a novel transposase based ChIP assay in which each antibody is conjugated to a barcoded transposome enabling the investigation of multiple targets within the same sample. These advanced technologies can be applied in new fields and diverse models to gain a deeper understanding of the complex regulatory mechanisms governing our genomes.