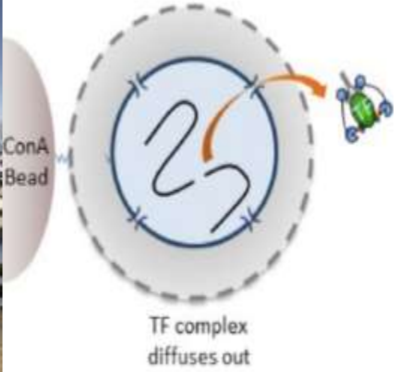
Mass General Brigham
Mass Eye and Ear

Schepens Eye Research Institute

The Technology Seminar Series Presents:

"*Profiling the epigenome with the enzyme-tethering methods CUT&RUN and CUT&Tag*"

Derek Janssens PhD.,
Postdoctoral Research
Fred Hutchinson Basic Sciences Division
Lab of Dr. Steven Henikoff



Thursday, April 17th, 2022
12:00 – 1:00 pm
Zoom Meeting

https://masseyeandear.zoom.us/j/583662273?pwd=TWJTUEV6ZTFUTzUzaWx5dXFmR2puQT09

Meeting ID: 583 662 273
Passcode: 248969

Summary of Dr. Janssens' talk:

Eukaryotic gene regulation is controlled by a myriad of DNA binding transcription factors and chromatin regulatory proteins. Until recently, our understanding of this process was largely reliant on the use of the chromatin immunoprecipitation followed by sequencing (ChIP-seq) method to profile the genome-wide association of a protein of interest with the chromatin. However, ChIP-seq is characterized by high background, driving up the cost of sequencing, and is prone to technical artifacts and limitations. To overcome these issues, we recently introduced two related methods called CUT&RUN and CUT&Tag. These methods use an antibody to direct either the proteinA-MNase or proteinA-Tn5 fusion protein to a chromatin-associated protein of interest in intact cells. The tethered MNase or Tn5 enzymes are then used to target the surrounding DNA for incorporation into a genome-wide sequencing library. These methods overcome many of the technical limitations of ChIP, and show exception signal-to-noise, driving down the cost of sequencing. In addition, CUT&Tag is compatible with the most widely used single-cell sequencing platforms. The high efficiency, low cost and ease of use of CUT&RUN and CUT&Tag make these methods ideal for profiling the occupancy of chromatin associated proteins genome-wide.

About Dr. Janssens:

Dr. Derek Janssens PhD is a postdoctoral researcher in the lab of Dr. Steven Henikoff in the Basic Sciences Division of the Fred Hutchinson Cancer Research Center. After completing his graduate thesis at the University of Michigan, Derek joined the Henikoff lab in 2017 and has been developing novel chromatin profiling tools to understand the epigenetic heterogeneity of cancer. Both the automated CUT&RUN and CUT&Tag platforms Derek developed are currently available as core services through the Fred Hutchinson Cancer Institute. More recently, Derek has been optimizing CUT&Tag for single cell applications and is working to increase the number of single cells profiled in each experiment, while minimizing the cost.