



**Principal Investigator Candidate
Seminar Series
For Molecular, Cell and Systems Biology**

Dr. Carl de Boer

Broad Institute
Cambridge, MA, USA

Title:

**Deciphering cis-regulatory logic to understand
disease-associated regulatory variation**

**Thursday, January 10, 2019
1:00 p.m.**

Location:

**Mount Sinai Hospital
Level 3 Conferences Rooms L3-201-202-203
60 Murray Street, 3rd floor**

Hosts: Dr. Anne-Claude Gingras & Dr. Daniel Schramek

Dr. de Boer received his PhD in Molecular Genetics in 2014 for his work in the laboratory of Prof. Timothy Hughes at the University of Toronto. There, he used machine learning, genomics and synthetic sequence design to understand how genes were designed by the cell, i.e. how DNA sequence guides where transcription occurs (see, e.g. PMID:24170600). He also created the YeTFaSCo database which continues to be a useful resource for the yeast community (PMID: 22102575). Moving to the laboratory of Prof. Aviv Regev (Broad Institute) for his postdoctoral work, he used diverse computational approaches to understand how RNA and chromatin change in disease and across cell states, and pioneered new approaches for the analysis of emerging data types such as single cell ATAC-seq. Importantly, he also generated ideal “Big Data” to solve the cis-regulatory logic of yeast (<https://www.biorxiv.org/content/early/2018/09/19/224907>). In his own group, he will focus on the regulation of mammalian transcription, by using a combination of genomics, synthetic biology, machine learning and experimentation. This will address fundamental questions such as: What turns a DNA sequence into a regulatory output? How do non-coding genetic variants cause disease? How do regulatory sequences evolve?