

FASSBERG

SEMINAR SERIES



Uwe Ohler
**Max Delbrück Center for
Molecular Medicine, Berlin**

special
date & time

Computational and genomics approaches to dissect post-transcriptional gene regulation

Deep sequencing protocols now enable the large-scale identification of the targets of regulatory non-coding RNAs as well as RNA-binding proteins, and they also enable the profiling of different steps of gene regulation, from nascent transcription to translation. I will present ongoing work on quantifying translation at the isoform level from ribosome profiling data, as well as deep learning approaches to identify functional binding sites and their features from cross-linking and immunoprecipitation compendia. Our contributions help moving the field forward towards an interpretation of the effects of non-coding sequence variation.

Host: Patrick Cramer



Thursday / 11.04.2019 / 13:00
Max Planck Institute for Biophysical Chemistry
Ludwig Prandtl Hall / Administration Building

