

SFB 900 Seminar Series

ALL GUESTS ARE WELCOME

TITLE

Looking closely at the proper model: single-cell sequencing of coronavirus and herpesvirus infections

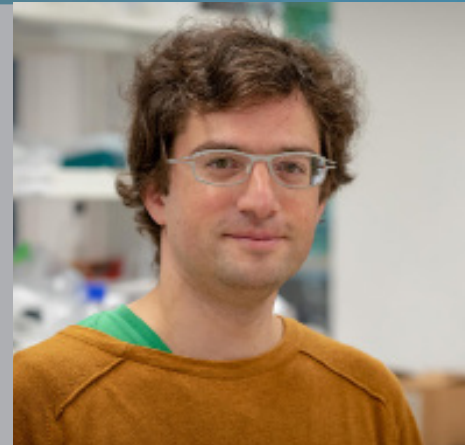
SPEAKER

Dr. Emanuel Wyler, Laboratory for RNA Biology and Posttranscriptional Regulation, Max Delbrück Center for Molecular Medicine (MDC) Berlin

LOCATION

Lecture Hall Q, building J06, MHH, Carl-Neuberg-Str.1
Hannover

only 20 people will be allowed in the audience, video conference will be provided



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01.09.
2020

5.00 PM (s.t.)

» Research of Emanuel Wyler, Landthaler Lab

Our main interest is the understanding of post-transcriptional regulatory networks that control gene expression. Post-transcriptional regulation is highly versatile and adaptable in exploiting cellular time and space. microRNAs and RNA-binding proteins play a key role in the regulation of spatial and temporal changes in protein synthesis through control of mRNA transport, storage and translation. Deregulation and failed coordination of these mechanisms contribute to the pathophysiological development and conditions. A prerequisite for a systems level understanding of post-transcriptional regulation is a transcriptome-wide high-resolution map of RNA-protein contacts that allows us to study how these interactions control the fate of mRNAs.

We are using a novel crosslinking-immunoprecipitation approach (PAR-CLIP) in combination with "deep-sequencing" to identify functional RNA-protein interactions at a nucleotide resolution (Hafner & Landthaler et al. [2010] Cell, 141). By using these RNA-protein interaction maps and combining them with cell-based and biochemical assays, we are aiming to understand the coordinated and combinatorial assembly of microRNAs, RNA-binding proteins and helicases on their target mRNAs as well as the structures and mechanisms guiding mRNA maturation, localization, turnover and protein synthesis in response to stress and environmental signals.