Title: Defining the mechanisms of gene expression control in the Hepatitis A virus (NCN/SONATA BIS).

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www: https://shorturl.at/JGpmn

Project description:

Upon infection, viruses hijack the cell's translational machinery and use it to synthesize copious quantities of viral proteins. However, viral gene expression must be tightly controlled to ensure that individual viral proteins are produced at the right time and in sufficient quantities to support viral replication. Most viruses use some form of transcriptional regulation, in which individual viral genes are transcribed only in the amounts needed. Other viruses, including those in the *Picornaviridae* family, rely entirely on posttranscriptional regulation of gene expression. However, the mechanisms involved are still poorly understood.

Aim:

Our goal is to define the gene regulatory strategies used by the Hepatitis A virus, a model picornavirus and important human pathogen. This work will involve the use of Ribo-seq profiling to investigate the role of translational regulation (e.g. ribosome frameshifting, cryptic translation initiation, etc.) for Hepatitis A gene expression. The resulting datasets may also provide insights into the translational regulation of host cell mRNAs during the course of infection. In this project, you will learn: mammalian cell culture and viral infection, CRISPR/Cas9 gene editing, high-throughput sequencing approaches such as Ribo-seq, and data analysis.

Requirements:

- MSc degree in biology, biochemistry, or related field
- Solid knowledge in at least one of the following disciplines: molecular biology, biochemistry, or microbiology
- Basic hands-on experience in molecular biology
- Written and spoken fluency in English
- Willingness to learn and take on new challenges, ability to work independently, analytical thinking
- Good interpersonal skills and a collaborative attitude

Number of positions available: 1

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