

CEIPEX MU TOPIC 4

Položka / Field	Obsah / Content
NAME	Dominik Hrebík, Ph.D.
CEIPEX RESEARCH TOPIC LEVEL2	Structural Biology: structural virology
NAME OF THE RESEARCH GROUP	Dominik Hrebík Research Group
TOPIC	One Protein to Rule Them All: Decoding the Multifunctionality of Paramyxovirus Matrix Proteins
ABSTRACT	How can a single viral structural protein perform radically different functions across an infected cell? Paramyxovirus matrix protein M is best known for driving virus assembly by linking the viral membrane to the nucleocapsid and ultimately forming a static lattice in the mature virus. Yet M also enters the nucleus and nucleolus, interacts with mitochondria, redirects host translation, binds the AP-3 adaptor complex, and cooperates with actin during viral budding. The molecular basis connecting these diverse activities remains unknown. Using representative viruses from the family Paramyxoviridae, the successful candidate will combine whole-cell cryo-FIB-SEM, correlative microscopy, cryo-electron tomography, and subtomogram averaging to visualise M-associated changes in the nucleolus, mitochondria, ribosome organisation, viral factories, and budding sites. Structural observations will be validated using high-resolution fluorescence microscopy, functional mutants, rescue experiments, and proteomics. In parallel, purified M will be reconstituted on defined membranes and with host factors to uncover the interactions that drive its structural transitions. At the interface of structural virology, cell biology, and advanced cryo-imaging, this project offers an opportunity to uncover how viral proteins reorganise infected cells across scales – from molecular assemblies to whole-cell architecture – and to redefine M as a dynamic regulator of infection rather than a passive structural component.
WEBPAGE OF THE RESEARCH GROUP/CONTACT	https://www.muni.cz/lide/376324-dominik-hrebik