Washington University in St. Louis
Washington University Open Scholarship

Volume 13

Washington University
Undergraduate Research Digest

Spring 2018

Biochemical and Sctructural Characterization of a Host Protein that Binds Ebola VP30

Gabe Small
Washington University in St. Louis

Follow this and additional works at: https://openscholarship.wustl.edu/wuurd_vol13

Recommended Citation

Small, Gabe, "Biochemical and Sctructural Characterization of a Host Protein that Binds Ebola VP30" (2018). *Volume 13*. 189.
https://openscholarship.wustl.edu/wuurd_vol13/189

This Abstracts S-Z is brought to you for free and open access by the Washington University Undergraduate Research Digest at Washington University Open Scholarship. It has been accepted for inclusion in Volume 13 by an authorized administrator of Washington University Open Scholarship. For more information, please contact digital@wumail.wustl.edu.

Biochemical and Structural Characterization of a Host Protein that Binds Ebola VP30

Gabe Small

Mentor: Gaya Amarasinghe

Ebola and Marburg viruses are negative sense RNA viruses that can cause high case fatality rates during outbreaks. Approximately 19 kb genome encodes for seven open reading frames. During virus replication, 7-10 multifunctional proteins are expressed, but viral replication and pathogenesis also require numerous cellular proteins. While the need for host factors in virus replication and pathogenesis has been long appreciated, our understanding of key host-virus interactions during filoviral infection and replication remain incomplete. In order to address this limitation, our collaborators recently performed a proteomic analysis, which identified RBBP6, an E3 ubiquitin ligase, as a cellular interactor of Ebola VP30 (eVP30). eVP30 is a viral protein critical for transcription initiation. In this study, we generated a series of recombinant RBBP6 and eVP30 truncation constructs. We performed in vitro pull-down assays to validate the initial proteomic identification of the eVP30/RBBP6 protein-protein interaction and defined key regions within RBBP6 that are critical for eVP30 binding. Furthermore, using purified eVP30 protein, we generated initial crystals with a RBBP6 binding peptide (RBBP6BP) and are currently refining X-ray diffraction data to develop a molecular model for RBBP6 interaction with eVP30. At the completion, we expect to define a key host-viral interface that modulates viral pathogenesis and define a novel target for potential development of antiviral therapeutics that target filoviruses.