

Invited: “Going Viral” with Biological Sequence Analysis

Daniel Schwartz

Department of Physiology and Neurobiology

University of Connecticut

Storrs, CT, USA

daniel.schwartz@uconn.edu

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Viruses have been implicated as the causative agents for a variety of cancers as well as diseases of the major physiological systems (e.g., nervous, respiratory, immune, reproductive, etc.), and viral infections have consistently ranked among the leading causes of death worldwide. Although viruses exhibit extreme biological diversity, plainly evidenced by the Baltimore classification of their genomes, they are united by their dependence on host-cell machinery to accomplish the task of self-replication. Thus, the ability to identify host-cell interaction partners to viral proteins is of central importance to understanding viral pathogenesis. This presentation will describe

progress toward building a map of potential viral interactors on the basis of protein post-translational modification (PTM) motifs embedded within viral primary structure. The use of the motif-x and scan-x tools for the extraction and prediction of short linear protein motifs on a number of enzymatic data sets will be discussed. Additionally, the presentation will outline the development and cross-validation of the virPTM database, an online repository for viral post-translational modifications, and will also illustrate how viral sequence analysis can be used to generate testable biological hypotheses as well as design rational therapeutic strategies for the treatment of viral diseases.