



BiophysTO Lunchtime Seminar Series

Date

Thursday, November 16, 2017
12:00 pm (noon)

Location

McLennan Physical Laboratories,
Room MP606, 60 St. George Street

Streaming

Seminar live streamed to
DV3129 @ UTM

**Pizza & refreshments
provided**

Dr. James M. Rini

University of Toronto
Department of Biochemistry &
Department of Molecular Genetics

Human Coronavirus Adaptation and Evolution

The coronavirus S-protein is responsible for host cell receptor binding and fusion of the viral and host cell membranes. Among coronaviruses it has evolved to recognize various host cell receptors that include both proteins and carbohydrates. The S-protein is also a major target of the host immune system and antibodies against it provide a route to viral neutralization. Using structural and biochemical approaches, we are characterizing the S-protein-receptor interaction of two human coronaviruses, HCoV-229E and HCoV-OC43. We have shown that the receptor binding domain (RBD) of the HCoV-229E S-protein has segregated into 6 phylogenetic classes whose viruses have successively replaced each other in the human population over the past 50 years. Biochemical characterization shows that the 6 RBDs differ in their receptor (aminopeptidase N) binding affinity and their ability to be bound by a neutralizing antibody, determinants of fitness on which selection can act. Our characterization of the OC43 S-protein interaction with its receptor (9-O-acetylsialic acid) also suggests an ongoing adaptation in the human population. Taken together, our results provide insight into immune evasion, the optimization of receptor binding affinity, and the acquisition of new receptor interactions, interrelated process that drive the emergence of new viral threats.

Host: Dr. Walid A. Houry



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