



# Catherine H. Schein, PhD

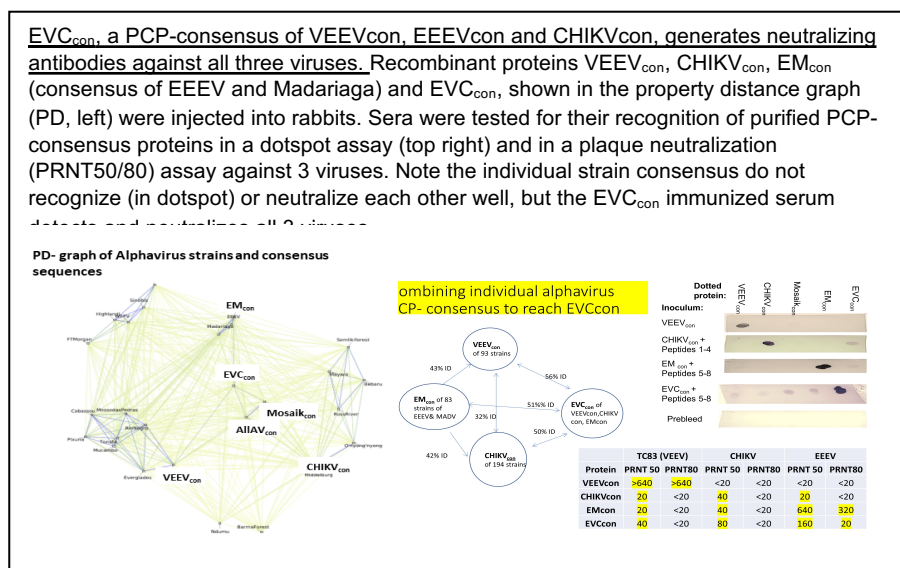
## Adjunct Professor

### Biochemistry and Molecular Biology

*Tackling Variability in RNA viruses*

Dr. Schein is a medicinal biochemist with experience in soluble protein production in bacteria, interferon and cytokine mechanisms, catabolic reactions of ribonucleases and autophagy, databases of allergens and viruses (SDAP, Flavitrack), bacterial toxin inhibitors, protein structure and computational drug design. All of this experience contributes to the current research in her lab group on broad spectrum antigens for vaccines designed with physicochemical property (PCP)- consensus and motif recognition, and synthetic conformational epitope mimetics (constrained and click chemistry peptides and proteins).

**Abstract:** The recent SARS-CoV-2 (COVID-19) epidemic has highlighted how the high variability of RNA viruses can present major obstacles to designing effective vaccines, therapies and diagnostics. However, long before coronaviruses became an existential threat, it was recognized that circulating RNA viruses, including poliovirus, influenza, dengue, West Nile, chikungunya etc. are not stable, but mixtures of evolving sequences differing from one another at a few positions. We have developed and validated, in 4 different virus groups, a suite of programs to identify regions of PCP-motifs and PCP-consensus sequences, as well as alignment-free methods to cluster sequences based on property distance (PD-Graph).



A PCP-consensus, which is closest in its properties to all the sequences used to calculate it, provides a rational reference for a given virus type. More importantly, it can be combined with experimental data to design single antigens that generate protective antibodies against virus groups with up to 68% diversity.

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