Contribution ID: **15** Type: **Poster**

Exploiting protein structure predictions and structural homology to identify viral immune evasion strategies.

Viruses are infamously efficient at employing homology as a mechanism of immune evasion by imitating host proteins to escape immune response. This might be exploited to identify new virus-host interactions. We have implemented a computational workflow, tested on the Human Cytomegalovirus (HCMV), which conducts structural homology search to list viral proteins and their homologs in humans. Matched human proteins are filtered for immune-related functions and their interacting partners are collated from databases. Finally, it predicts structures of complexes between the immune-mimicking viral proteins and their respective human counterparts. Complexes predicted at high quality are validated in vitro. By characterizing the interaction of these proteins, we hope to shed light on new immune evasion mechanisms employed by HCMV and other viruses.

I want to give a Lightning Talk

no

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Session Classification: Poster Session