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Using Systems Approaches to Study Infectious Disease

There is a wide gap between the generation of large-scale biological data sets and more-detailed, structural and mechanistic studies. However, recent work that explicitly combine data from systems and structural biological approaches is having a profound effect on our ability to predict how mutations and small molecules affect atomic-level mechanisms, disrupt systems-level networks and ultimately lead to changes in organismal fitness. Our group aims to create a stronger bridge between these areas primarily using three types of data: genetic interactions, protein-protein interactions and post-translational modifications. Protein structural information helps to prioritize and functionally understand these large-scale datasets; conversely global, unbiasedly collected datasets helps inform the more mechanistic studies. Our efforts in this respect have been focused on a number of disease areas with a particular focus on pathogenesis, as we use these tools, and a number of viruses and bacteria, to systematically and quantitatively study the host-pathogen interface.

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