Report for MX-1615

The purpose of my research group is to better understand norovirus capsid flexibility with respect to receptor binding interactions and virus evolution with the ultimate aim of developing norovirus antivirals. We now have over 30 different X-ray structures. Below lists the results from the latest data collection.

HBGA binding to norovirus P domains

We successfully collected X-ray data for two new norovirus P domains. These were Hawaii virus (HV) and snow mountain virus (SMV), belonging to genogroup II genotype 1 (GII.1) and GII.2, respectively. This represents the first crystal structures of these two strains. We were unable to show any binding to histo-blood group antigens (HBGAs) with these two P domains. We will continue to test the binding with other techniques, however we believe these two viruses do not use the HBGAs, but some other receptor.

Crystal structure of norovirus RNA dependent RNA polymerase with ligands

We previously determined the first crystal structure of the RNA dependent RNA polymerase (RdRp) from the most dominant strain. We attempted to bind potential inhibitors to the RdRp, but were unsuccessful. We will continue to test other compounds in order to develop antivirals directed to the norovirus RdRp.