MX1457

The purpose of this experiment was the following:

1. Saga P domain

A new norovirus viral spike (Saga P domain) was produced and crystallized. Complexes of viral spike and receptor (histo-blood group antigens – HBGAs) were crystallized. We successfully collected data on these complexes (including HBGAs: A trisaccharide, B trisaccharide, H2 trisaccharide, LeA trisaccharide, LeY tetrasaccharide, L fucose). The resolution was between 1.2 and 1.8A for most data sets. We are now refining these structures and preparing the paper. However, we would like to collect some more data sets with additional HBGAs.

2. 026 P Particle

The viral spike protein was developed to form a tetramer. This tetramer was found to have better ability to bind receptor, although the details of the inter-connections between the dimers were not previously known. We have now solved this structure and found that the lower section of the P domains were connected, making available the outermost section of the P domain available to the surface. We are preparing some further experiments with this structure, including complexes with HBGAs to better understand the binding interactions with the recpetors.

3. SMV P domain

A new norovirus P domain was crystallized. The structure was solved. We also solved the complex structure of the P domain with various HBGAs. However, we will need to collect a number of additional data sets to be sure of our results.