MS02-2-7 Structural characterisation of influenza epitopes presented by a prevalent Indigenous Australian Human Leukocyte Antigen
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Abstract
Influenza is a highly infectious respiratory disease caused by the influenza virus. Previous research has shown that Indigenous Australians are at higher risk of developing severe symptoms associated with influenza infection than non-Indigenous Australians. In the event of a pandemic outbreak, Indigenous Australians are more likely to be hospitalised due to influenza infection (16%) than non-Indigenous Australians, despite only making up a small portion (2.5%) of the total population. The underlying immunological reason for this susceptibility is still unclear, but may be due to their distinct immunogenetics. In particular, Indigenous Australians have distinctive Human Leukocyte Antigen (HLA) expression profiles that impact on the selection and presentation of peptide antigens to anti-viral T cells, which plays a critical role in the clearance of the virus.
Our work is focused on HLA-B*13:01, a prevalent HLA allele in the Indigenous Australian population. There is no data regarding how the HLA-B*13:01 molecule might select and bind to peptide antigens for subsequent presentation to T cells. Here, we have characterised HLA-B*13:01 presenting influenza epitopes and their recognition by T cell receptors at the atomic level using X-ray crystallography at the Australian Synchrotron. This provides the first insight into HLA-B*13:01 peptide presentation and the T cell recognition mechanism in great detail. Our structures of HLA-B*13:01 revealed characteristics unique to this HLA molecule which are important for T cell recognition and could help further understand the T cell-mediated response restricted to this HLA.