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Structural characterization of SARS-Cov-2 spike derived peptides presented by the Human Leukocyte Antigen A*29:02.

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The rapid emergence of SARS-Cov-2 out of Wuhan, China, in late 2019 has resulted in the current outbreak that has crippled social and economic development worldwide. With over four million deaths, significant efforts are being made to generate a viable treatment option. It has been well established that T lymphocytes destroy infected cells. These T cells also produce long lasting immunity through the proliferation of memory cells which recognize future viral invasion.

Activation of T lymphocytes is achieved through the recognition of Human Leukocyte Antigens (HLA) surface receptors on infected cells. These HLA molecules present viral peptides to T cells which are able to recognize and activate against these antigens.

However, due to the highly polymorphic nature of HLA molecules, it remains unclear how different peptides bind to the vast number of HLA molecules affect the stimulation of the adaptive immune response.

The focus of this project is on a singular HLA, HLA-A*29:02, found in approximately 3% of the world's population. We wish to structurally analyse various peptides presented by HLA-A*29:02 derived from the SARS-Cov-2 spike protein and determine how COVID-19 variants and their mutations might different in their presentation to T cells.

Through the use of X-ray crystallography, we will gain deeper insights into how theses peptides are presented. This will further our understanding of how our own immune system responds to these antigens and may also help to in designing long lasting therapies such as peptide vaccines.

Level of Expertise

Student

Presenter Gender

Man

Pronouns

He/Him

Which facility did you use for your research

Australian Synchrotron

Students Only - Are you interested in AINSE student funding

Yes

Do you wish to take part in the Student Poster Slam

Yes

Condition of submission

Yes

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