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Characterization of SARS-CoV-2 peptides presented by Human Leukocyte Antigen molecules

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To date, the COVID-19 pandemic has claimed 970,000 lives and afflicted more than 31 million individuals. Although a global effort has been enacted for vaccines and drug discovery, our rudimentary understanding of SARS-CoV-2 infection and our own immune defense against this infection remains unclear. Our immune system can naturally overcome viral infection through the presentation of viral protein fragments or peptides (p) via human leukocyte antigen (HLA) molecules. These peptide-HLA complexes (pHLAs) are recognized by cytotoxic T cells that can activate, proliferate, and kill infected cells. T cells also retain memory of their encounter with the virus, and will respond faster during re-infection. How peptides are presented on the cell surface by HLA molecules impact T cell recognition and influence the outcome of viral clearance, and therefore, outcome of the disease. Although SARS and SARS-CoV2 cause severe acute respiratory syndrome, other coronavirus strains (229E, OCE43, HKU1, and NL63) only cause the common cold. These coronaviruses share similar peptide sequences that can be presented by HLAs, meaning that prior exposure to a less severe strain of coronavirus may infer immunity via memory T cells if similar peptides are presented in the same structural fashion. Using protein crystallography and X-ray diffraction at the Australian Synchrotron, we have characterized the presentation of SARS-CoV-2 peptides, which could influence vaccine strategies and provide a basis for research in T cell therapy.

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