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**An *in vitro* recapitulation of proteolytic antigen degradation and peptide capture by class II MHC**

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Much insight in antigen processing and epitope selection has been gained from studies that analyze the repertoire of peptides that are presented on the surface of antigen presenting cells in the form of complexes with major histocompatibility complex (MHC) molecules. A cell-free equivalent composed of purified protein components that recapitulates the proteolytic degradation of antigen and the loading of the resulting fragments onto class II MHC molecules may be a powerful experimental platform for conducting further investigation into antigen presentation by class II MHC molecules. Such a system could be useful for the *de novo* candidate identification of immunodominant pathogen-derived class II MHC epitopes with potentially none of the background that one might get from using a cell-based system. Here we describe our efforts toward establishing a system in which proteolytic fragments of an influenza hemagglutinin (HA) protein are selected for their ability to associate with the human class II MHC molecule HLA-DR1, and are subsequently identified by mass spectrometry.