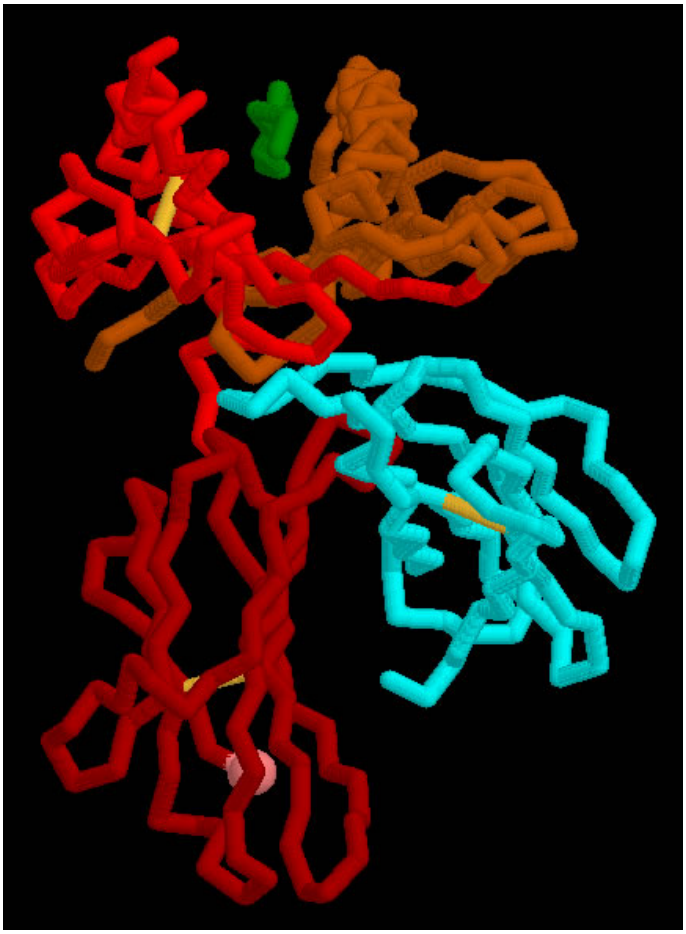
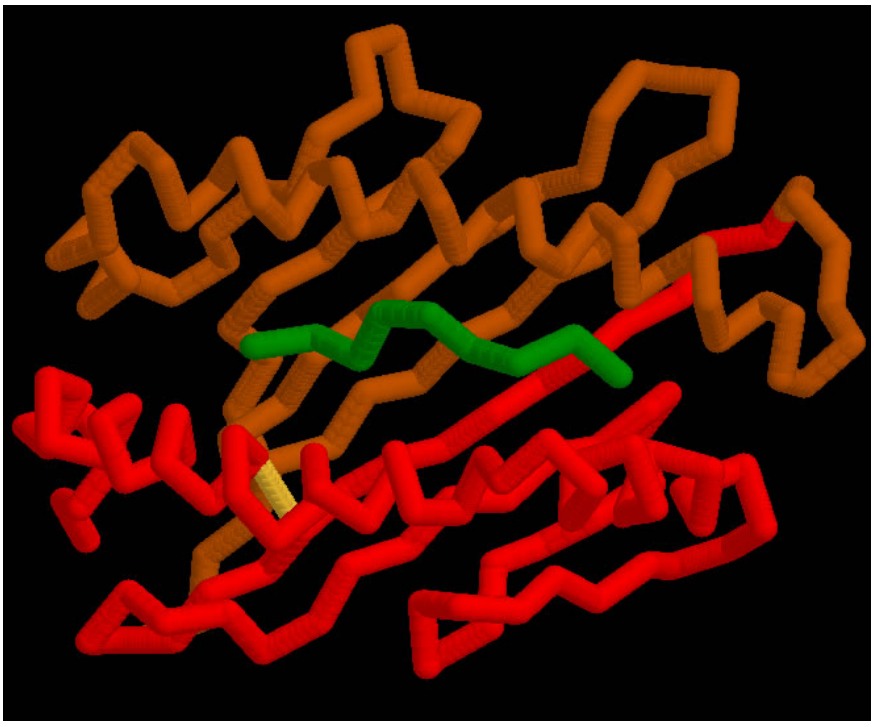
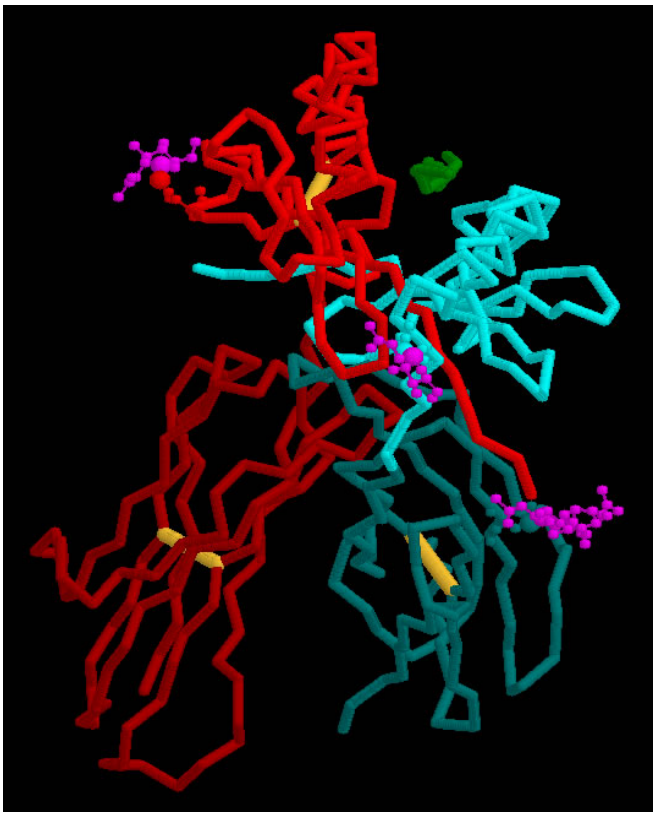
VISUAL MHC.



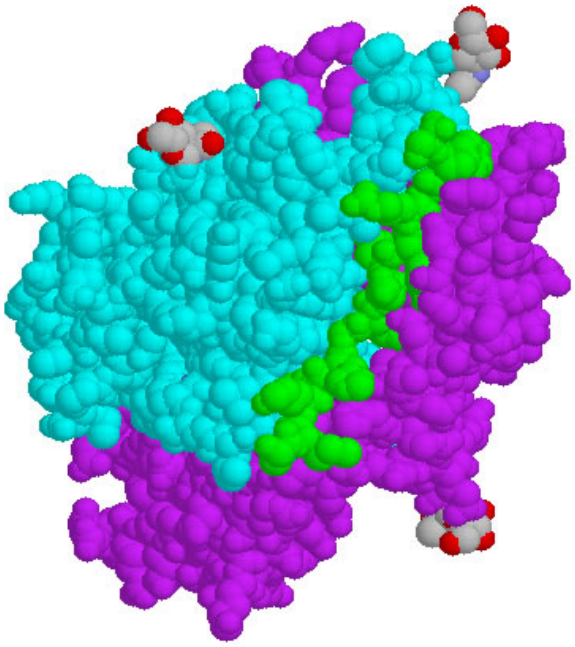
From MolVis, RasMol, and Chime come some pretty useful structures. This is the extracellular domain of an **MHC Class I** molecule, seen from the side. In brown at upper right is the alpha-1 domain and in red at the upper left, the alpha-2 domain, of Class I. The dull red domain below is membrane proximal alpha-3. In blue is β_2-microglobulin, which is invariant, stabilizes the folding of the alpha chain, is not inserted into the plasma membrane, and is not coded for within the MHC. The floating green blob is the antigenic peptide; it's not floating at all except in this stick view, it's making many contacts with the MHC (see the van der Waals view on the next page).



Here's the T cell's view. The peptide is making hydrophobic or electrostatic contacts with both the alpha helices as well as with residues on the beta sheet below.

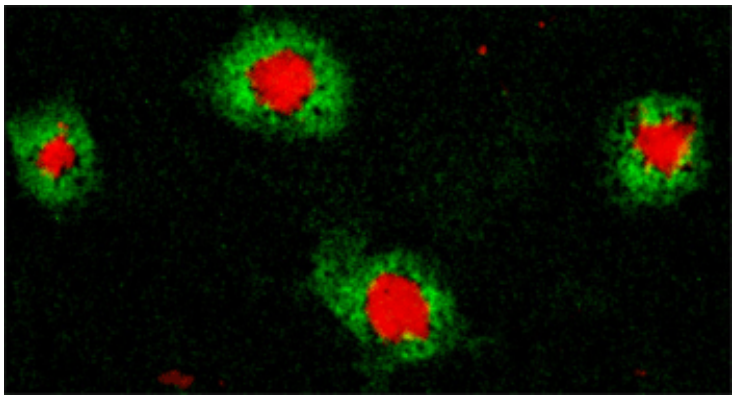


This is **MHC Class II**. It has two chains, alpha and beta. The alpha-1 and beta-1 domains jointly form the cleft in which the green antigenic peptide sits. Alpha-2 and beta-2 domains below are membrane-proximal, attached to the transmembrane stretches which are not shown here. You can also see the stabilizing disulphide bonds that are essential parts of the structure of immunoglobulin fold domains. And some nice purple carbohydrate.



Another T cell's view of a loaded MHC Class II. This picture shows nicely how well embedded the peptide is. In Class II the peptides are tucked in and peep out; those associating with Class I tend to be a bit longer, and drape over the cleft like a foot-long hotdog in a bun.

Pucker Up: An antigen-presenting cell's view of the "**immunological synapses**" of 4 T cells. The T cell receptors (stained red) are clustered in the centers of the synapse, and accessory adhesion molecules (in green) surround them.[1]



[1] Kaizuka, Y. et al. 2007. Mechanisms for segregating T cell receptor and adhesion molecules during immunological synapse formation in Jurkat T cells. PNAS 104:**20296-20301**