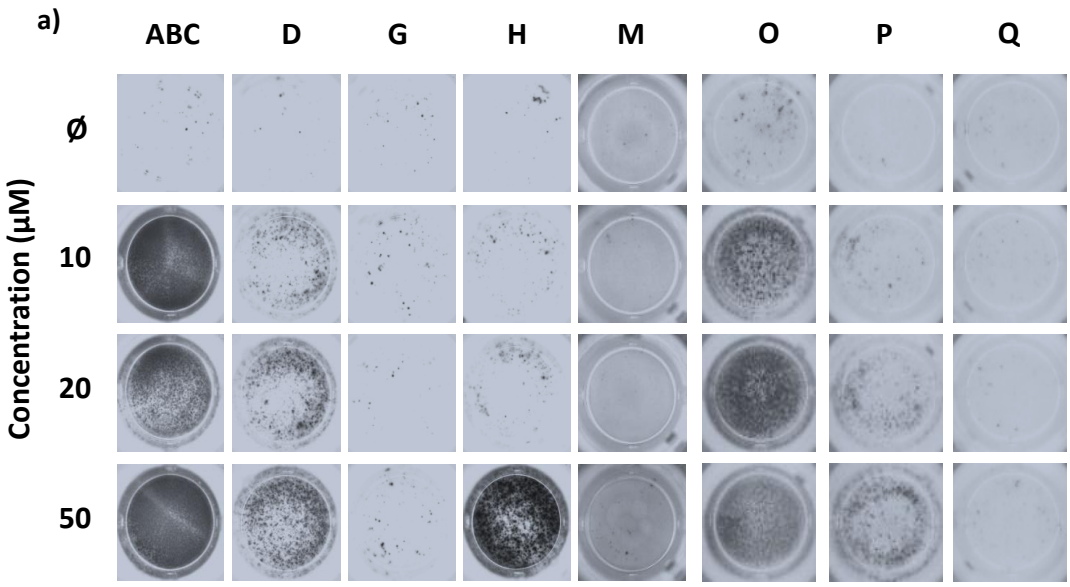
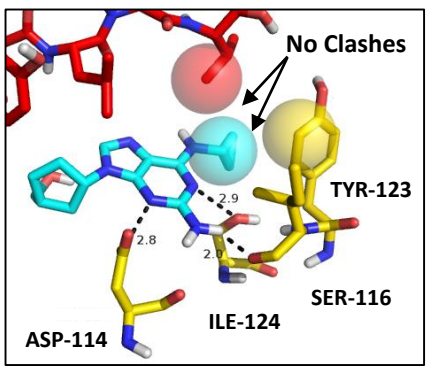
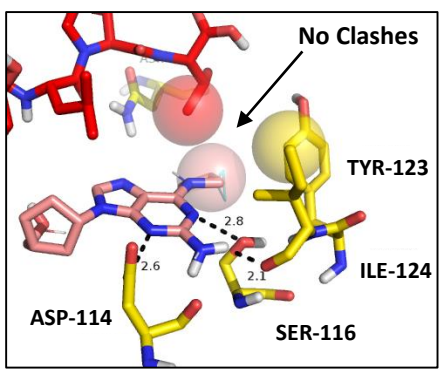
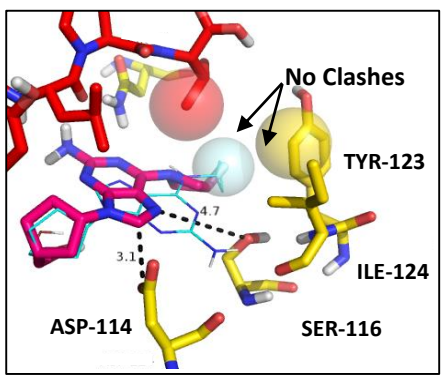
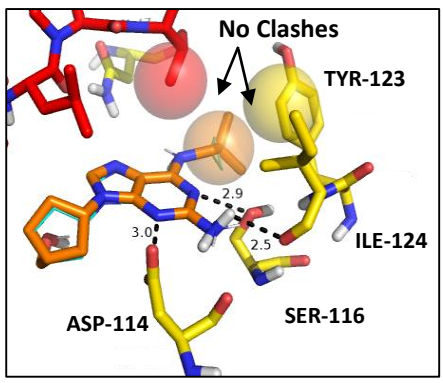


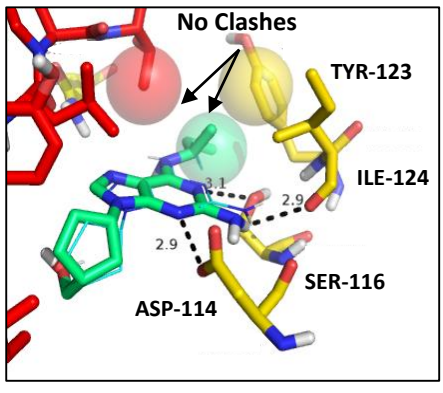


T-cell activity

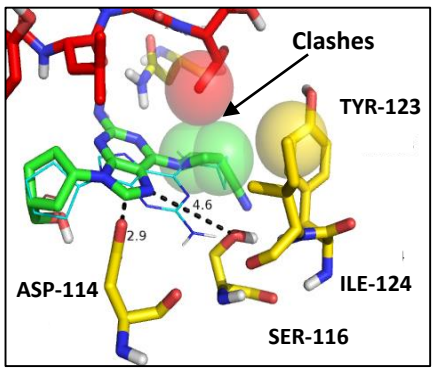


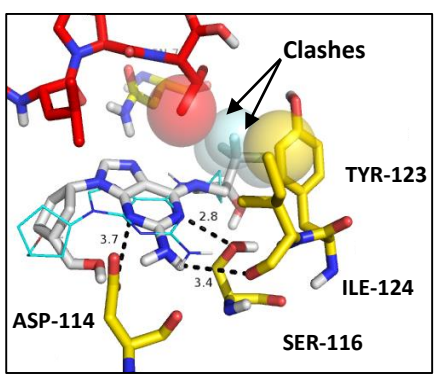






No T-cell activity





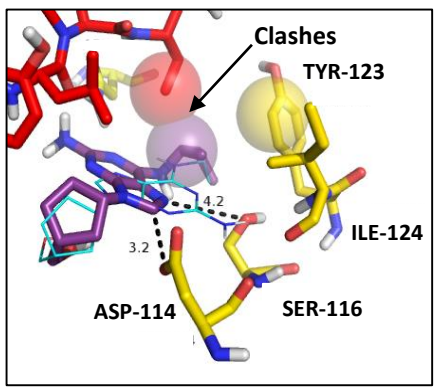


Figure 2. Direct comparison of the CD8⁺ T-cell activity of abacavir substituted analogues and the binding orientations within the F-pocket of HLA-B*57:01. a) Representative ELIspot images from wells containing abacavir and analogues D, G, H, M, O, P and Q at concentrations of 0, 10, 20 and 50μM. b) Crystal structure binding orientation of abacavir c) Crystal structure binding orientation of analogues capable of activating abacavir-responsive T-cell clones i) D (azetidine), ii) H (azetidine-fluoro), iii) O (isobutylamino) and iv) P (S-$_{sec}$-butyl amino) within the F-pocket of HLA-B*57:01. d) Crystal structure binding orientation of abacavir analogues with no cross-reactivity with abacavir responsive T-cell clones i) G (azetidine-3-carbonitrile), ii) M (azetidine-trifluoromethyl), iv) Q (R-$_{sec}$-butyl amino) within the F-pocket of HLA-B*57:01. Crystal structure of HLA-B*57:01 (PDB:3UPR). Stick representation of the peptide, (HSITYLLPV) shown in red. Key amino acid residues are shown as yellow sticks. All non-polar hydrogen atoms removed. Key hydrogen bond interactions shown as black dashes. Spheres used to illustrate the atomic radii of the atoms in the functional groups of abacavir and substituted analogues, peptide (HSITYLLPV) and HLA-B*57:01 amino acids. Abacavir structure superimposed over analogues shown as blue lines.