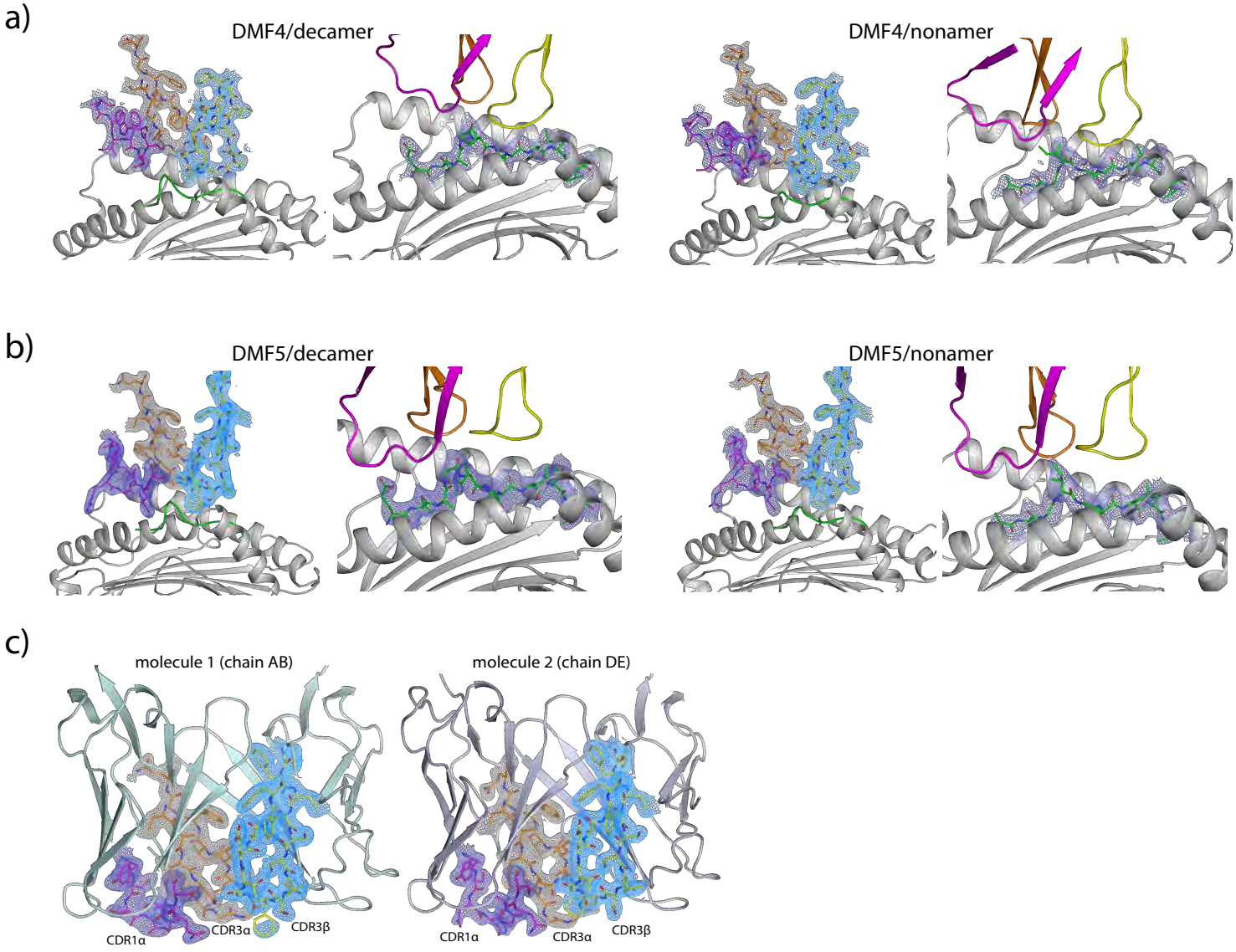
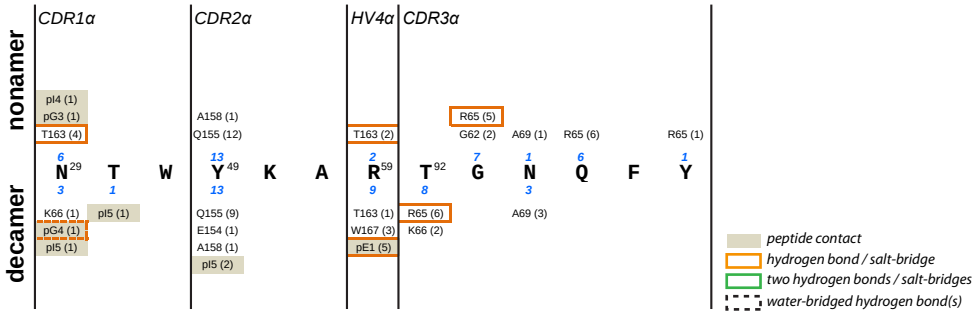


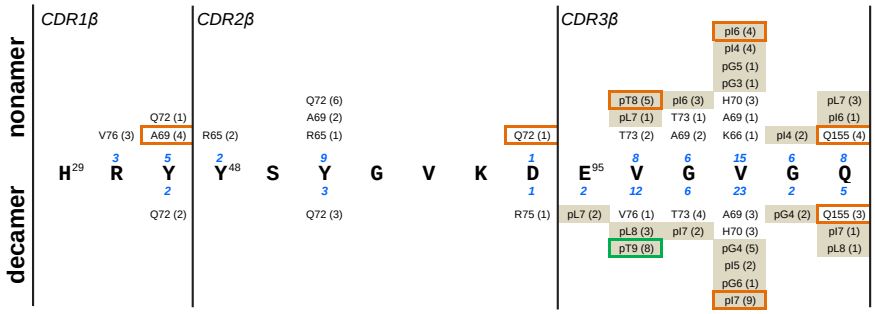
Supplemental Fig. 1. $2F_o$-F_c electron density contoured at 1σ for the DMF4 (A) and DMF5 (B) TCR-peptide/HLA-A2 ternary complexes and the free DMF5 TCR (C). For the ternary complexes, density for the CDR1α , CDR3α, and CDR3β loops and the peptides are shown. CDR1α loops are magenta with dark blue mesh, CDR3α loops are orange with grey mesh, and CDR3β loops are yellow with light blue mesh.

a) contacts in DMF4 structures

α chain

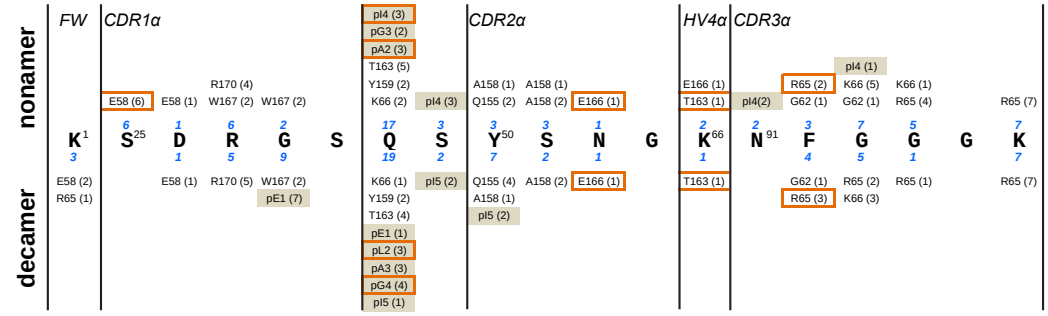


β chain

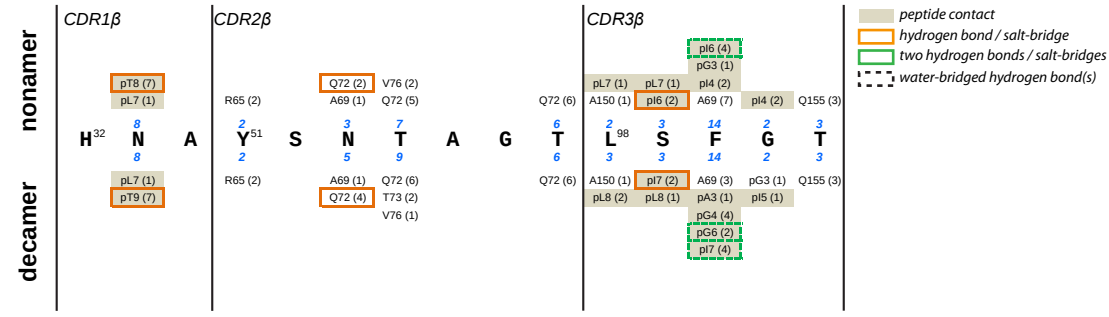


b) contacts in DMF5 structures

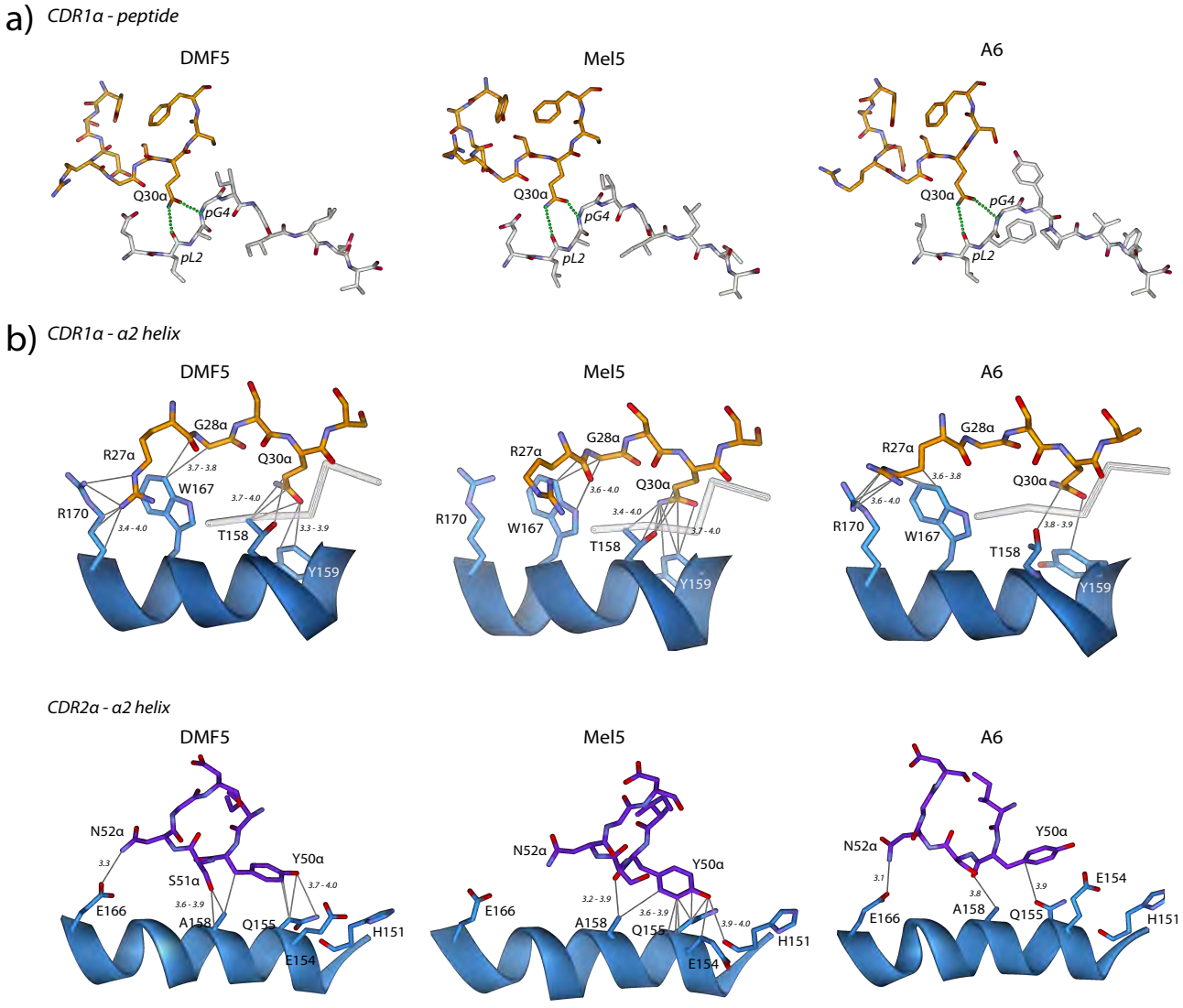
α chain



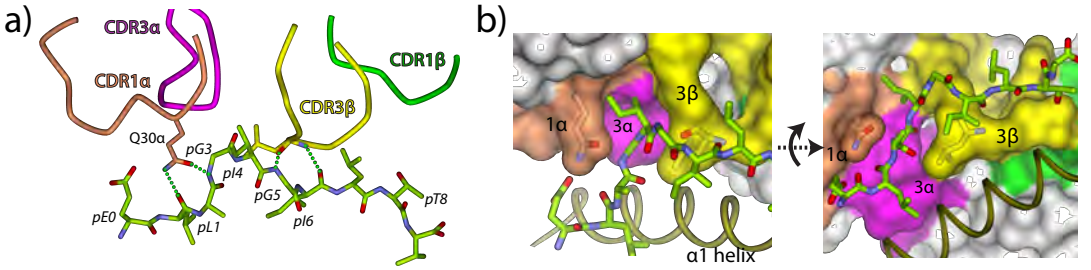
β chain



Supplemental Fig. 2. Intermolecular contacts in the two DMF4-peptide/HLA-A2 interfaces (A) and the two DMF5-peptide/HLA-A2 interfaces (B). For both panels, TCR CDR loop sequences are shown across the center rows, with the α chain in the top panel and the β chain in the bottom. The number of contacts to each TCR amino acid is in blue, with nonamer contacts above the sequence and decamer contacts below. HLA-A2 or peptide amino acids forming contacts are also shown, with the number of contacts given in parentheses. Superscripts on the first number of each loop sequence give the amino acid numbers. Peptide residues are shaded grey. Orange outlines indicate a residue is involved in a single hydrogen bond or salt-bridge, green outlines indicate two or more hydrogen bonds or salt-bridges. Dashed outlines indicate one or more water-mediated hydrogen bond. Contacts were tabulted with a distance cutoff of ≤ 4 Å.



Supplemental Fig. 3. Interactions made by the Vα 12-2 CDR1α/CDR2β loops in the ternary complexes DMF5, Mel5, and A6 form with peptide/HLA-A2. A) The backbone conformation of CDR1α in the DMF5, Mel5, and A6 ternary structures is the same, and in all three structures Gln30α engages the N-terminal portions of the peptides identically. Dotted green lines illustrate hydrogen bonds made by Gln30 of CDR1α to the peptide backbone. B) Patterns of van der Waals contacts between residues of CDR1α of DMF5 and HLA-A2 (top panel) and CDR2α of DMF5 and HLA-A2 (bottom panel) in the DMF5, Mel5, and A6 ternary complexes.



Supplemental Fig. 4. The Mel5 TCR accomodates the bulge in the MART-1 decamer via a slot formed by CDR1α, CDR3α, and CDR3β, analogous to the mechanism used by DMF5.