

From Antigen Recognition to Radionuclide Delivery: Structural Studies of HLA-A and Siderocalin-HOPO-Eu Complexes

Alex Gao^{1,2}, Michael Stark^{1,3}, Dr. Peter Rupert¹, Sabriyah Morshed¹, Dr. Roland Strong^{1,4}

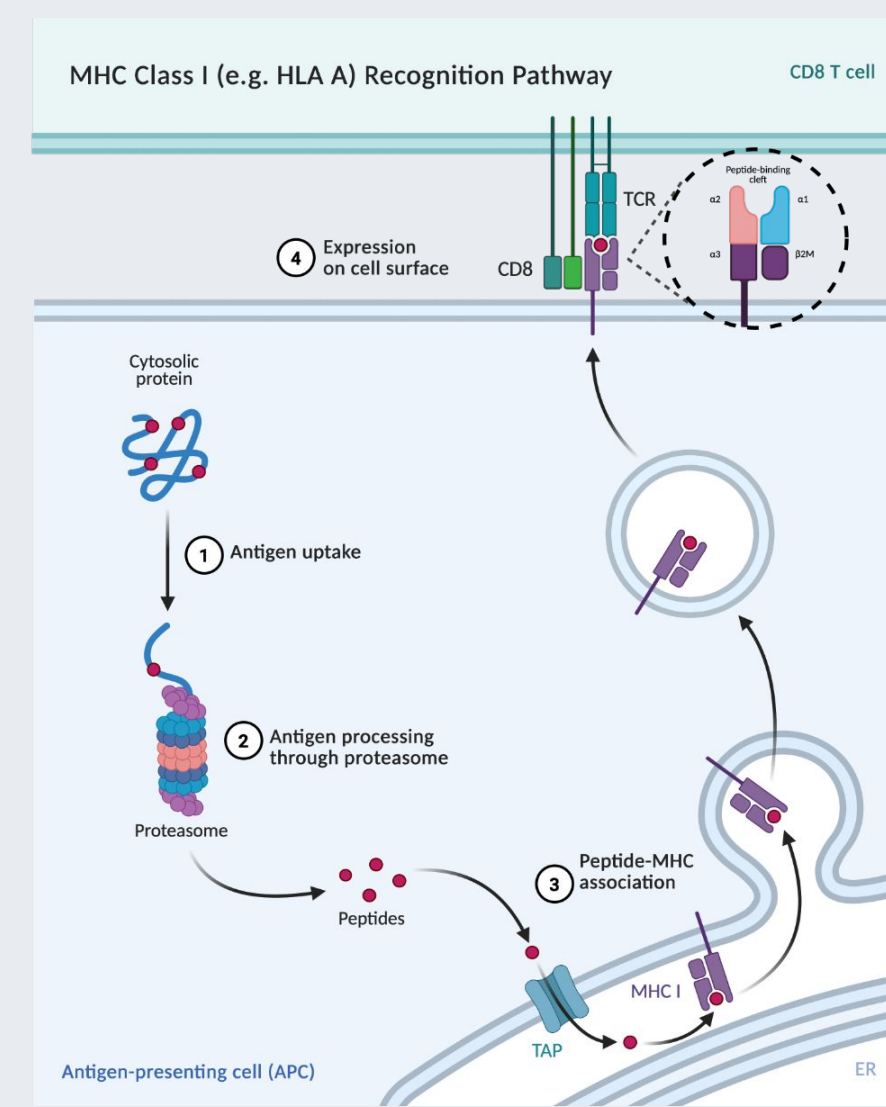
¹Fred Hutchinson Cancer Center, Seattle, WA, ²University of Chicago, Chicago, IL, ³Thomas Jefferson High School, Denver CO, ⁴University of Washington, Seattle, WA

Background and Motivation: Structural Biology for Targeted Cancer Therapy

Targeted Cancer Therapy Requires Two Complementary Capabilities

1. We Must Define a Tumor Specific Target

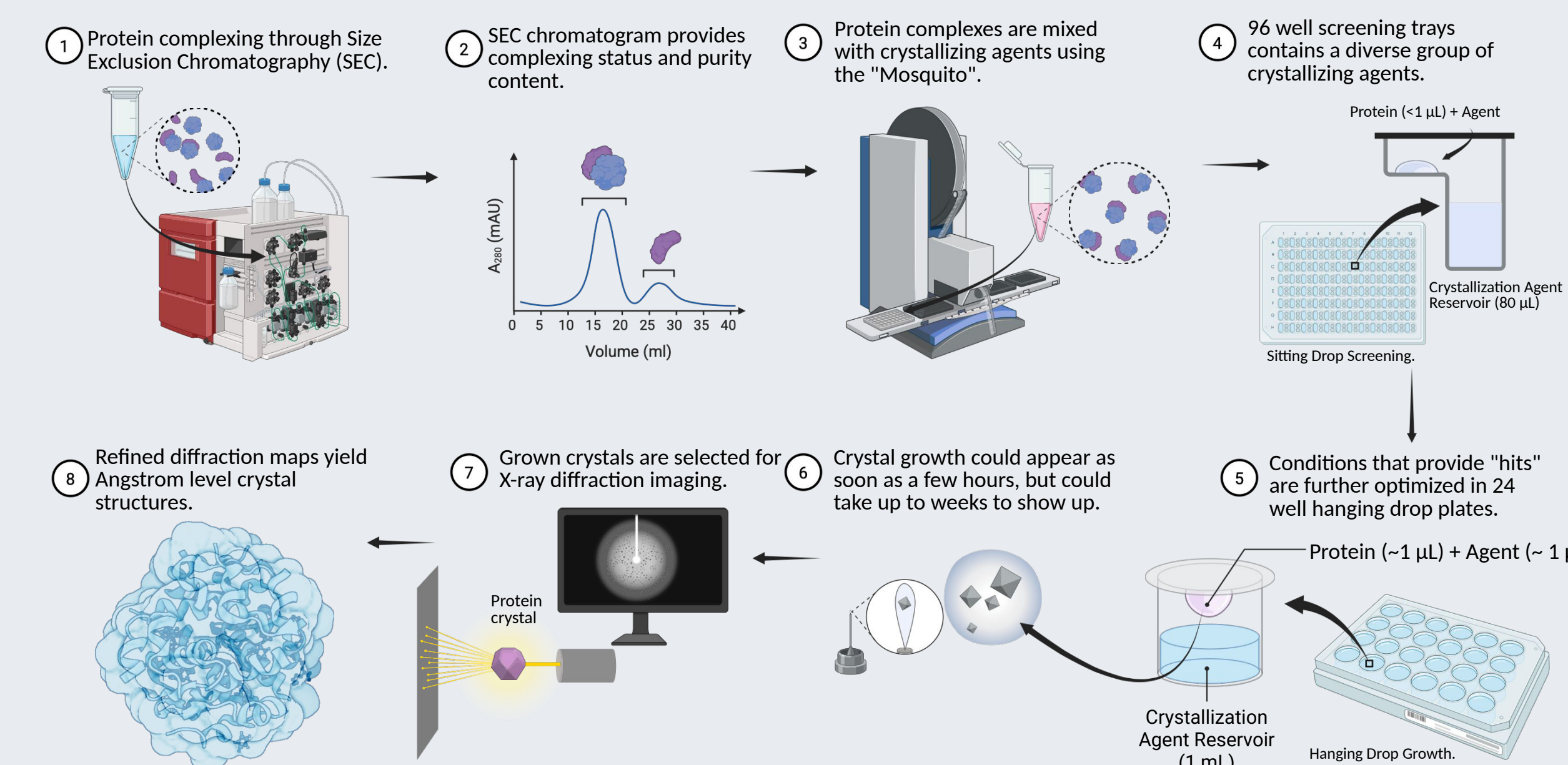
- Human papillomavirus (HPV) drives the production of oncogenic proteins, including the E6 protein that functions as a **molecular glue** to the **ubiquitin ligase** for the tumor suppressor p53.
- Cell surface MHC Class I proteins (**HLA-A, -B, -C**) display peptides derived primarily from intracellular proteins on the cell surface for immune recognition. (**Figure 1: HLA-A Antigen Presentation**)



2. We Must Accurately Deliver the Therapeutic Payload

- Current radiotherapies run into **severe off target toxicity**, as the radioactive dose is **not** localized only to the tumor.
- Siderocalin (Scn)** forms high-affinity noncovalent complexes with lanthanide loaded HOPO chelators.
- Structural based **engineering** could improve chelator retention and provide a potential modular platform for radioactive metal delivery when coupled to a **tumor targeting module**.

Crystallography Workflow



1. Engineered SCTs Stabilize Peptide-HLA Complexes

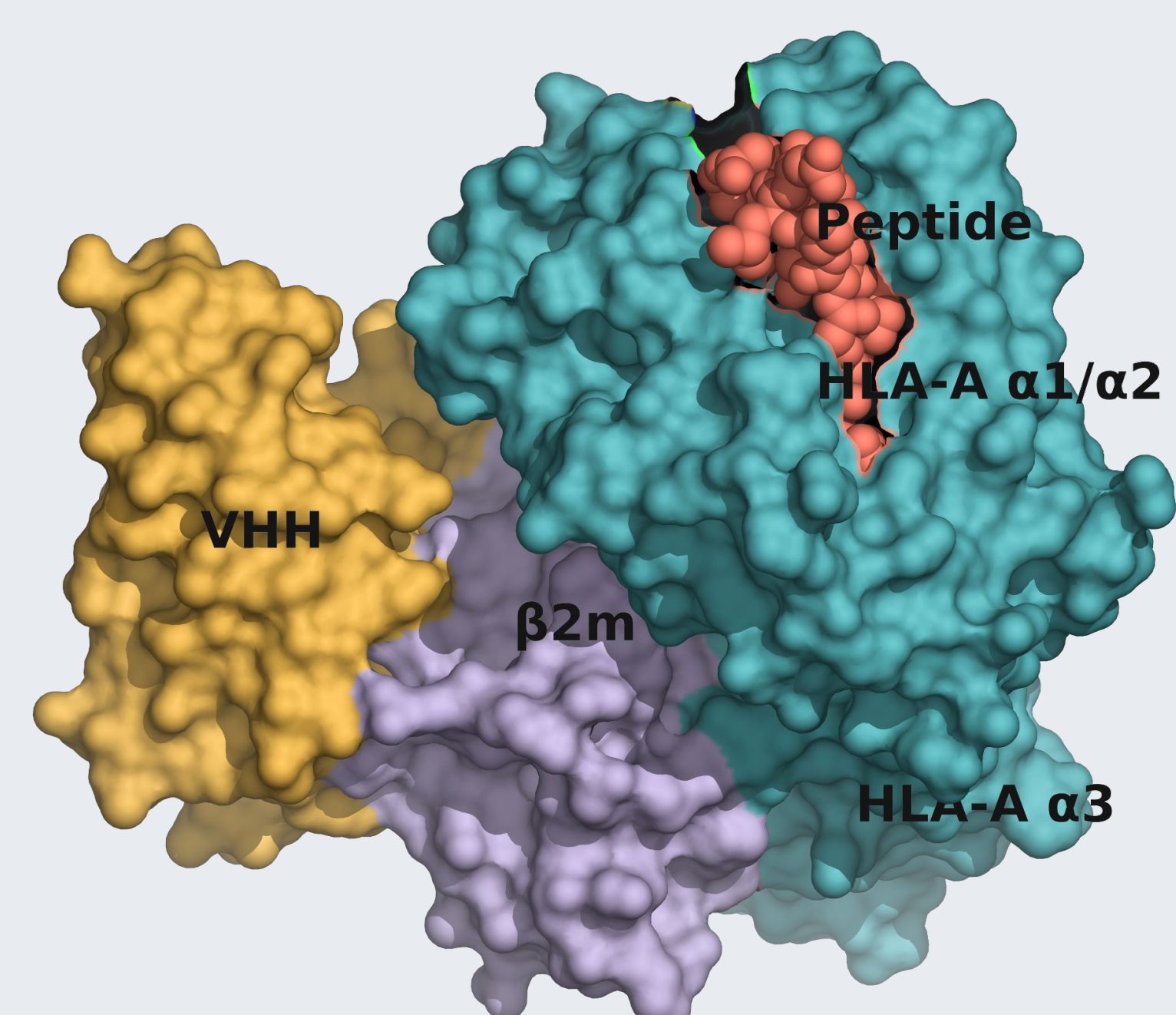


Figure 2: Single Chain Trimer Design. A Single Chain Trimer (SCT) is an **engineered mimic** of our pHLA A presentation system. The SCT links a peptide from HPV, β 2-microglobulin (B2M), and the HLA-A heavy chain. An engineered disulfide between a linker and the heavy chain stabilizes peptide loading, while the AD01 VHH binds B2M as a peptide-independent **crystallization chaperone**.

2. HLA Allele Alters Presentation of the Same Peptide

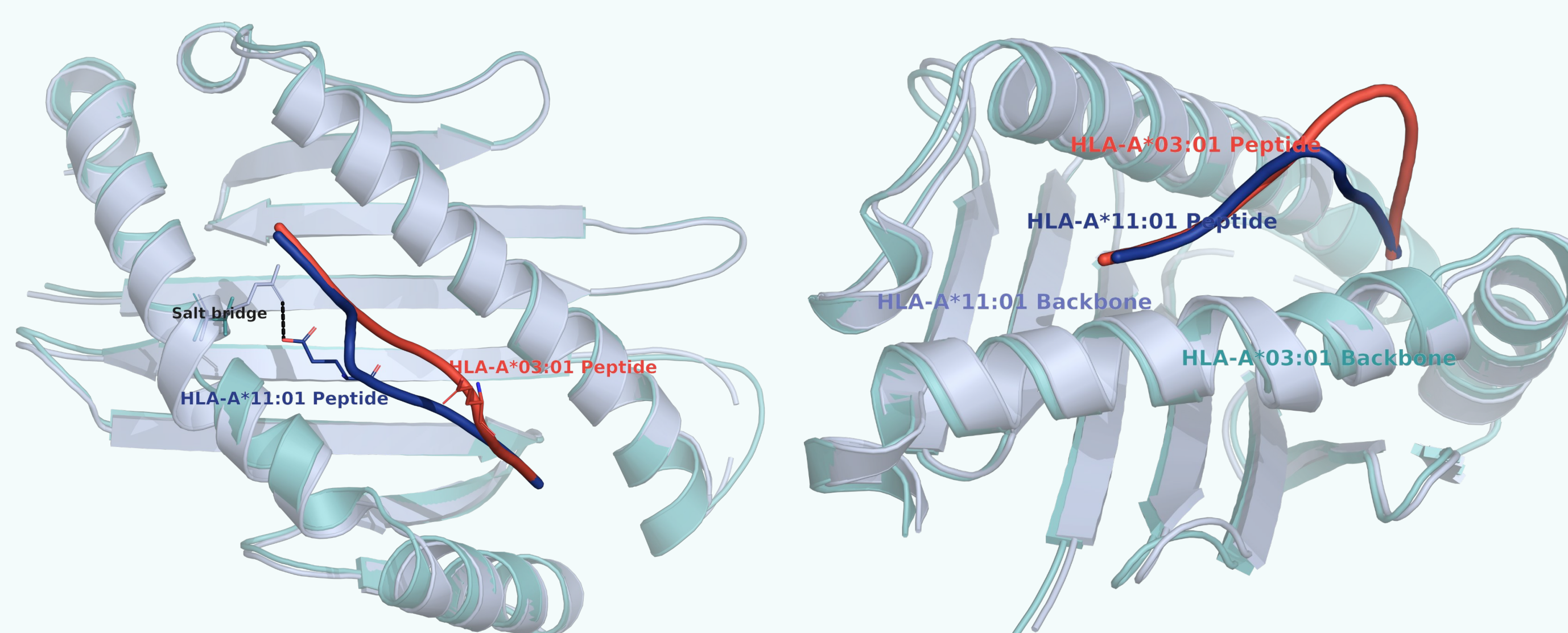
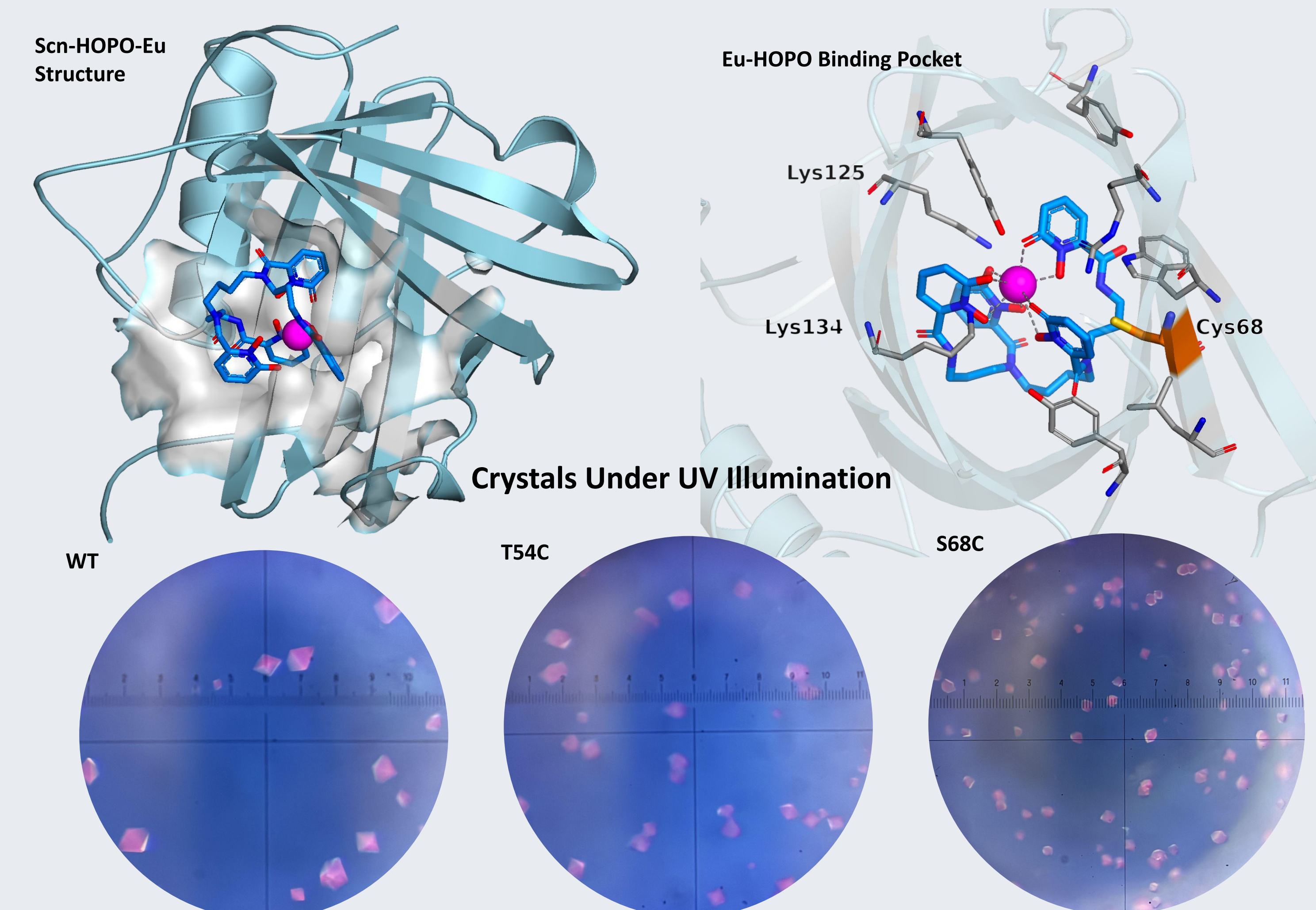


Figure 3: Allele dependent presentation of the HPV16 E6 13-mer. HLA-A*03:01 and HLA-A*11:01 are two different yet **structurally homologous** HLA alleles. However, when the same 13-mer peptide SVYGTTLTLEQQYNK is aligned to the two binding grooves, these peptides adopt different presentation conformations. Our structures (**Left: Side View, Right: Top View**) indicate that a distinct salt bridge in the HLA-A*11:01 α -helix may contribute to a tighter binding conformer.

Same peptide sequence $\neq$ Same antigenic surface.

5. Siderocalin Retains Eu-HOPO Binding Across Cysteine Variants



3. Partial Peptide Disorder Observed in HLA-A*03:01-AD01 Crystal

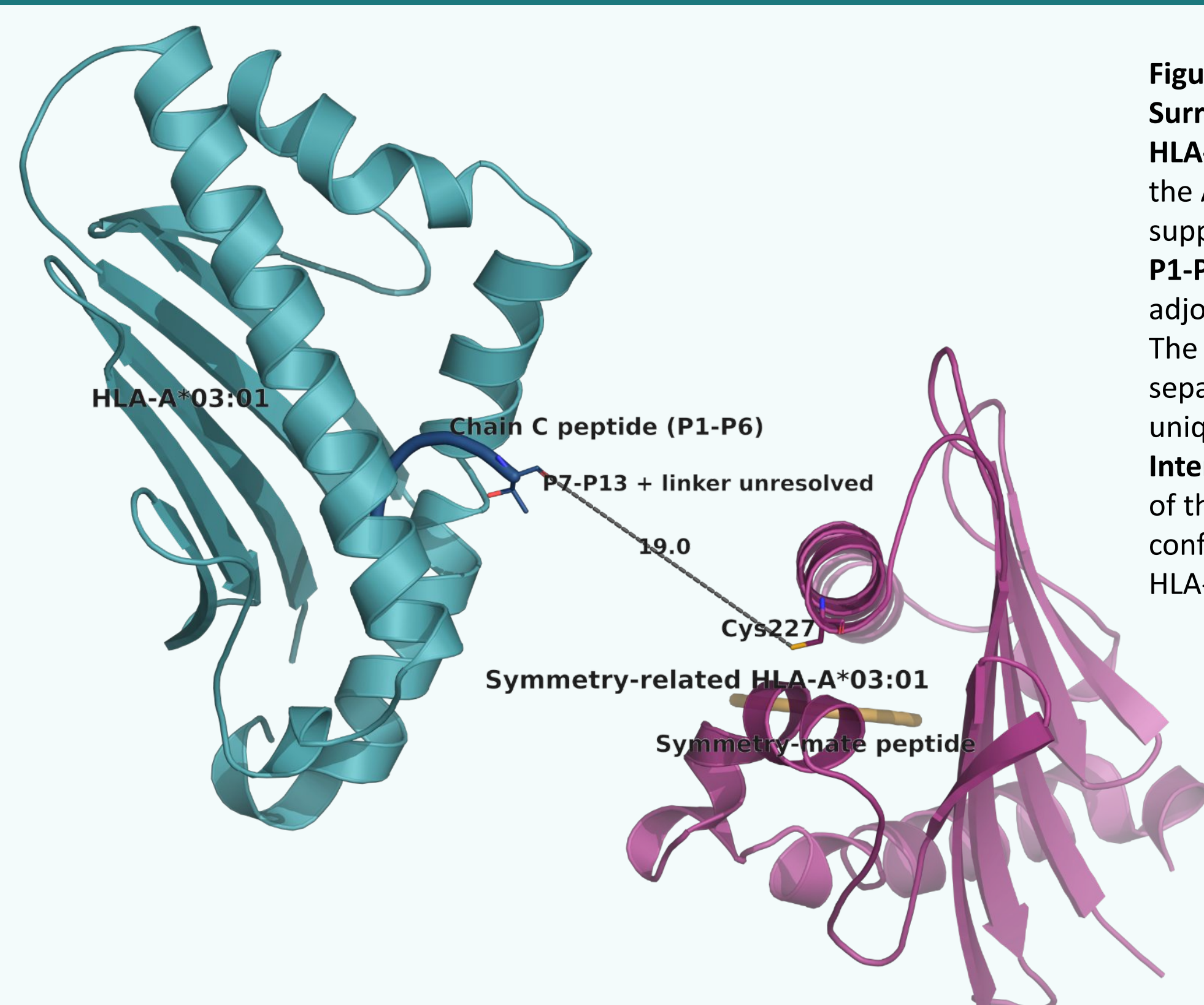


Figure 4: The Crystal Environment Surrounding a Partially Solved HLA-A*03:01 Peptide. In chain C of the Asymmetric Unit, our density supports the **positioning of residues P1-P6**, whereas P7-P13 and the adjoining linker remain unresolved. The nearby symmetry mate is separated by only $\sim 19\text{\AA}$, suggesting a unique crystal packing contact. **Interpretation:** The C-terminal region of the 13-mer may retain substantial conformational flexibility within the HLA-A*03:01 construct.

4. Peptide Length Reshapes HLA-A*11:01 Antigenic Surface

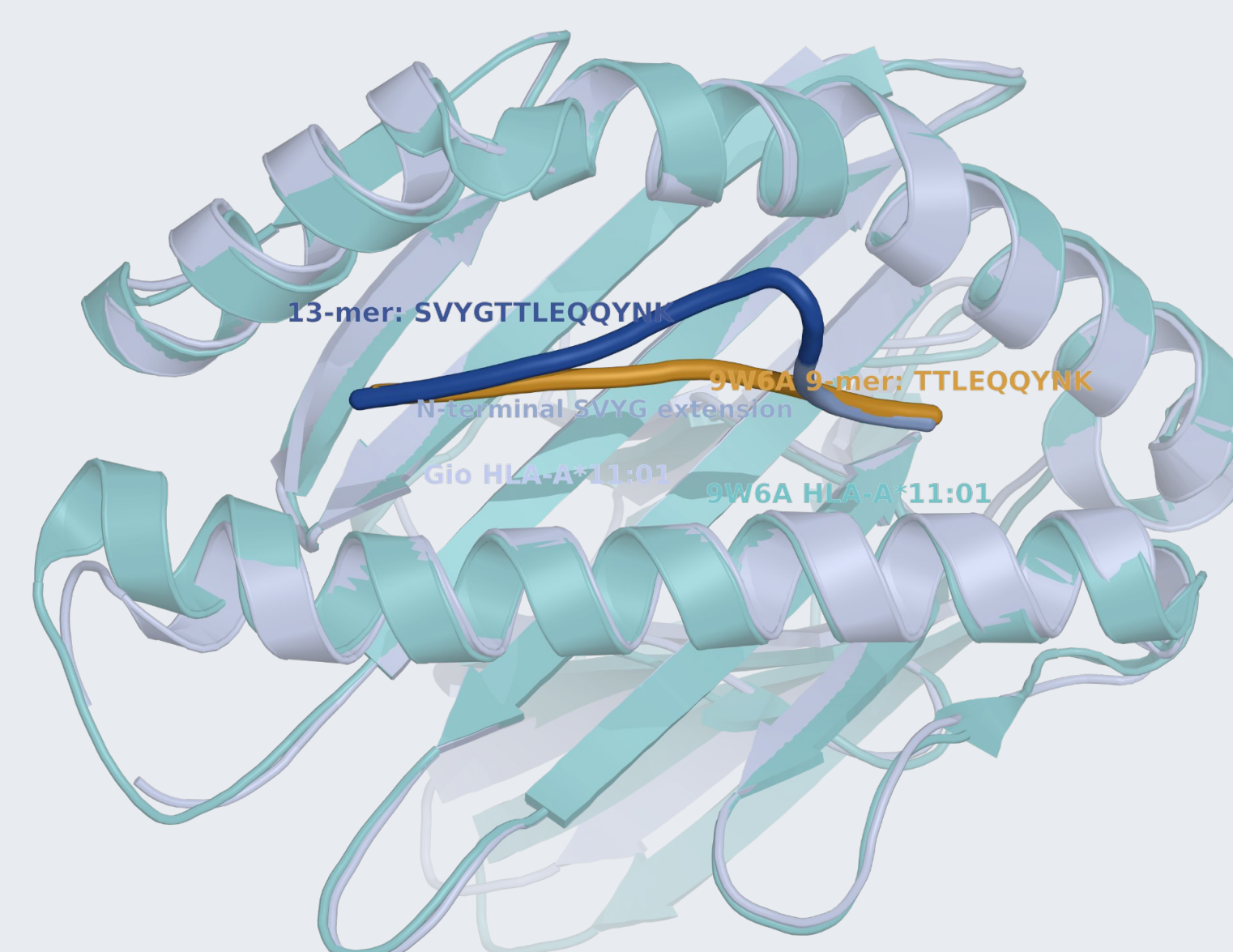


Figure 5: Structural comparison between nested HPV16 E6 peptides presented by HLA-A*11:01. HLA-A*11:01 recognizes and displays both the 13-mer SVYGTTLTLEQQYNK and the N-terminally reduced 9-mer TLEQQYNK (PDB: 9W6A)². The difference in **four** residues alter the peptide presentation conformation, where the 13-mer is more revealing and less enclosed than the respective 9-mer.

6. Engineering a Covalent Lanthanide Chelator Platform

- Why engineer siderocalin?** Siderocalin binds lanthanide 3,4,3 HOPO complexes with high affinity, providing a protein scaffold for transporting radioactive metals. However, despite being a nanomolar-affinity binder, the wild type interactions are **non-covalent**, which may result in the premature deposition of radioactive metals.
- Why introduce cysteine?** Two coordinated cysteines form a **covalent** disulfide linkage. T54C and S68C are tested as engineered thiol handles. For disulfide bond formation with the HOPO chelator, a cysteine needs to be installed properly on 3,4,3 HOPO as **well**. Our first round test demonstrates that both mutations preserve the original **non-covalent** scaffold compatibility.
- Why does it matter?** Subsequent testing with both mutant Scn and **engineered HOPO** could potentially result in a **covalent radiometal cargo delivery system** that might reduce unintentional payload dissociation.

References & Acknowledgements

References: ¹ Finton KAK et al. *Front Immunol.* 2023;14:1170462. ² Wang J et al. RCSB Protein Data Bank, **9W6A**. We thank Giovanni M. Loia and Kathryn A. Finton for permission to use and compare unpublished HLA-A*11:01 SCT structural data, and Roland Strong, Peter Rupert, Michael Stark, and Sabriyah Morshed for experimental mentorship and collaboration. Molecular structures were visualized in PyMOL (Schrödinger, LLC); schematics were created with BioRender.com. This work is supported by the NIAID. The Fred Hutch Summer Undergraduate Research Program is supported in part by the University of Chicago, Fred Hutch Internship Program, and participating laboratories/research groups.