July 30, 2025 – August 13, 2025

Peptide Preparation for Docking and Early Trial-and-Error Optimization

After designing several candidate peptides, I transitioned to preparing them for molecular docking simulations.

- Protonation states
- Bond angles
- Rotatable bonds
- File formats
- Structural optimization settings

Through iteration, I successfully prepared a set of structurally stable peptides ready for docking trials.

August 18, 2025 – August 20, 2025

Initial Docking Trials and Data Recording

With peptides prepared, I began testing their predicted binding strength to my selected target structures. For each docking simulation, I recorded:

- Binding affinity scores
- Predicted interaction energies
- Hydrogen bond formation
- Interaction residues
- Orientation of binding

Rather than selecting a single “winner,” I chose to carry forward the top three candidates for further optimization. This avoided premature narrowing of variables.

August 21, 2025 – September 2, 2025

Temporary Pause and Continued Literature Review

During this period, I took a short break from active computational work. However, I continued reading immunology and structural biology literature to better contextualize my results.

This reflection period was valuable. It allowed me to:

- Re-evaluate whether my docking model aligned with biological reality
- Consider limitations of in silico binding predictions
- Think critically about potential off-target interactions

September 2025

Professional Outreach and Mentor Feedback

I met with my teacher, Ms. Sleiman, to review the structure and clarity of my project. She provided feedback on the clarity of hypothesis articulation, variable control explanation, and how to present computational methodology clearly.

Following this, I reached out to several professionals for mentorship and feedback:

- Dr. Markus Geuking
- Dr. Maura Ruyechan
- Dr. Hailey Gorman

My goal was not only validation but critical evaluation. I wanted experts to identify weaknesses in:

- Experimental design
- Biological plausibility
- Overstated conclusions
- Computational limitations

Meetings were scheduled, and I prepared summaries of my work to present in a professional format.

October 2025

Professional Consultations and Implementation of Recommendations

During meetings with the professionals, I received detailed feedback. Key recommendations included:

- Avoid overstating therapeutic claims
- Emphasize the computational and theoretical nature of the study
- Strengthen the explanation of controls and off-target risk
- Improve clarity regarding stereochemistry considerations
- Consider further optimization strategies beyond manual sequence changes

I incorporated discussions of limitations, including:

- Docking algorithm assumptions
- Lack of dynamic simulation
- Absence of in vitro validation
- Simplification of immune microenvironment complexity

November 2025

Advanced Optimization Using AI-Based Peptide Evolution

In November, Dr. Markus Geuking suggested exploring AI-assisted peptide evolution tools if accessible.

The AI-generated modifications introduced changes in:

- Amino acid charge distribution
- Side-chain polarity
- Steric bulk
- Predicted hydrogen bonding capacity

I evaluated:

- Whether the changes were chemically reasonable
- Whether increased binding affinity came at the cost of specificity
- Whether stereochemical integrity was maintained

The newly generated peptides were then:

1. Modelled into 3D structures
2. Energy minimized
3. Prepared for docking
4. Docked against the same target structures
5. Compared directly against the original base peptides

December 2025

Reduced Activity and Light Research

- Overall narrative coherence
- Strength of the hypothesis
- Logical flow from design to optimization
- Areas requiring clearer explanation

January 2026

Finalization, Presentation Preparation, and Analytical Refinement

- Designed my trifold board
- Organized figures logically
- Refined graphs and docking result visuals
- Strengthened the conclusion section
- Clarified limitations
- Improved wording to avoid overstated medical claims
- The peptides show promising computational binding trends.
- AI-assisted optimization can enhance predicted affinity.
- Further in vitro and in vivo validation would be required before any therapeutic consideration.