
Peptide-MHC Structure Prediction With Mixed Residue and Atom Graph Neural Network

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Abstract

Neoantigen-targeting vaccines have achieved breakthrough success in cancer immunotherapy by eliciting immune responses against neoantigens, which are proteins uniquely produced by cancer cells. During the immune response, the interactions between peptides and major histocompatibility complexes (MHC) play an important role as peptides must be bound and presented by MHC to be recognised by the immune system. However, only limited experimentally determined peptide-MHC (pMHC) structures are available, and *in-silico* structure modelling is therefore used for studying their interactions. Current approaches mainly use Monte Carlo sampling and energy minimisation, and are often computationally expensive. On the other hand, the advent of large high-quality proteomic data sets has led to an unprecedented opportunity for deep learning-based methods with pMHC structure prediction becoming feasible with these trained protein folding models. In this work, we present a graph neural network-based model for pMHC structure prediction, which takes an amino acid-level pMHC graph and an atomic-level peptide graph as inputs and predicts the peptide backbone conformation. With a novel weighted reconstruction loss, the trained model achieved a similar accuracy to AlphaFold 2, requiring only 1.7M learnable parameters compared to 93M, representing a more than 98% reduction in the number of required parameters.

1 Introduction

Cancer immunotherapeutics have revolutionised the field of oncology by using the patient’s immune system to trigger tumour regression [Finck et al., 2020, Waldman et al., 2020]. Among them, cancer vaccines aim to induce and enhance tumour-specific T-cell responses in patients by delivering targeted immunogenic neoepitopes [Blass and Ott, 2021]. The cellular immune response activation towards an antigen relies on a series of tightly regulated biological processes whose keystones are the major histocompatibility complexes (MHC). These essential cell surface proteins bind peptides and display them to the intercellular space where they can interact with immune cells. The features underlying the binding and presentation of antigenic peptides are therefore key to understanding the immune response and have valuable health implications.

However, the MHC is a highly polymorphic protein and there are 20^9 possible 9-mer peptide sequences, with limited structural information available in public databases [Berman et al., 2000]. In-silico structure modelling methods are thereby applied for predicting peptide-MHC (pMHC)

structures. State-of-the-art methods mostly rely on energy minimisation strategies via random sampling but require a long computation time, making scalability a challenge [Abella et al., 2019, Parizi et al., 2022]. The advent of large high-quality proteomic data has led to an unprecedented opportunity for deep learning-based protein folding methods such as AlphaFold 2 [Jumper et al., 2021], OmegaFold [Wu et al., 2022], and ESMFold [Lin et al., 2022], which have been proven to predict reliable and accurate protein structures. Furthermore, these trained models can be fine-tuned on pMHC structures for other downstream tasks such as binding prediction [Motmaen et al., 2022].

In this paper, we propose a graph neural network (GNN) that takes an amino acid residue graph for the pMHC interface and an atom graph for the peptide as inputs to predict the peptide backbone conformation. A post-processing step recovers the full-atom coordinates and constructs the entire pMHC structure. By training on a novel weighted reconstruction loss, the proposed GNN predicted accurate structures with similar performance compared to AlphaFold 2 [Jumper et al., 2021] and pMHC fine-tuned AlphaFold 2 [Motmaen et al., 2022] with only 1.7M learnable parameters, which represents a more than 98% reduction in the number of parameters. We demonstrate that the predicted structures are closer to native structures, both in terms of geometry and biological consistency. Furthermore, we show that our method considerably improves upon others in terms of fulfilling biological constraints on peptide positioning within certain areas of the MHC called binding pockets [Nguyen et al., 2021].

2 Methods

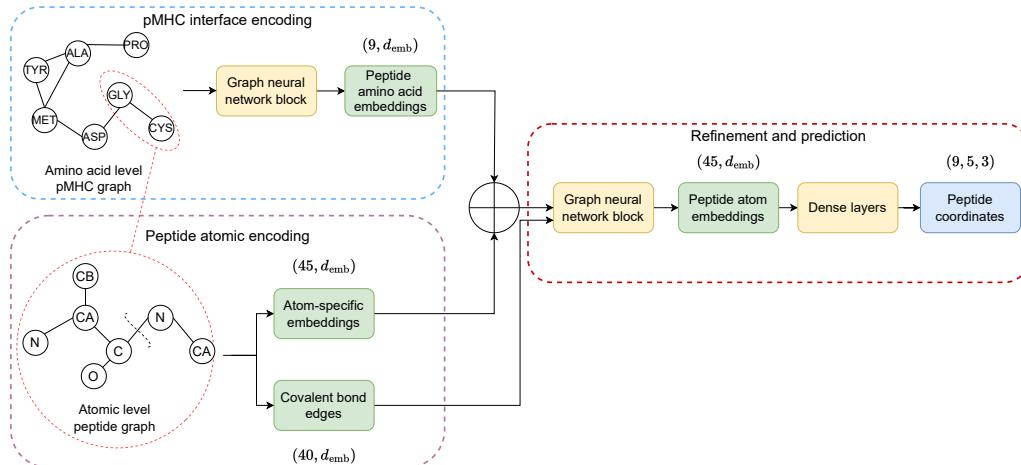


Figure 1: Neural Network Architecture. Each model stage (pMHC interface encoding, peptide atomic encoding, refinement and prediction) are represented by a rectangular dashed box in light blue, mauve, and red, respectively. Model layers and layers’ inputs/outputs are represented by rectangular colour-filled boxes, in yellow and green, respectively. The blue-filled rectangular box represents the final model output (peptide atom coordinates).

2.1 pMHC Graph Representation

Unlike protein folding models that predict structures from amino acid sequences and pairwise features of template structures, in this work, we propose to input an initial conformation by replacing the residues in the template structure with target ones. Specifically, given a target pMHC, we identify a template pMHC structure from a set of experimentally determined pMHC structures via peptide sequence similarity and replace the amino acid residues with target ones for both peptide and MHC. In other words, we input the target pMHC sequence with the conformation from the selected template.

The resulting pMHC structure is represented by two graphs, one representing the pMHC interface at the amino acid-level to capture the interaction between the peptide and MHC, and another one representing the peptide on the atom-level to refine the information for conformation prediction.

The pMHC graph consists of the amino acid residues of the peptide together with the α_1 and α_2 domains of the MHC [Wilson and Fremont, 1993]. Nodes represent residues, with edges connecting nodes if the distance between the C_α of the corresponding residues is smaller than 8 Å, following Xia and Ku [2021]. For each node, the features include the type of amino acid, Kidera factors [Kidera et al., 1985], Atchley factors [Atchley et al., 2005], and the coordinates of the C_α , O , C_{carbo} , N and C_β atoms of the residue. For glycine, a virtual C_β position is computed following Cock et al. [2009]. For each edge, the features include the edge classes depending on the bond type (covalent or non-covalent) and the chains (peptide or MHC) of the nodes it connects to.

The peptide graph consists of the backbone atoms (C_α , O , C_{carbo} , and N) and C_β atoms. Nodes represent atoms, with edges connecting nodes if a covalent bond exists between the corresponding atoms. The node features encode the atom classes and the edge features encode the edge classes depending on whether it is a single or double covalent bond and whether the atoms it connects come from the same residue.

2.2 Neural Network Architecture

The neural network consists of three stages (Figure 1). First, the amino acid-level pMHC graph is fed into a GNN block and each amino acid residue is represented by a node embedding. Meanwhile the atom-level peptide graph is constructed where atom features are encoded and summed with their corresponding residue embeddings. The resulting embeddings together with the atom-level peptide graph are fed into another GNN block to refine the atom embeddings. Finally, each atom's coordinates are predicted from their embeddings via two shared dense layers.

The key component is the GNN block which consists of four message passing layers with an multi-head attention mechanism [Shi et al., 2021]. The message passing layer is wrapped into a Transformer-like architecture involving a ReLU-activated feed-forward network. To reduce the impact of distant neighbours, the distance between each pair of nodes is considered in the denominator inside the message passing layer:

$$\mathbf{x}_i = \mathbf{W}_1 \mathbf{x}_i + \sum_{j \in \text{Nbr}(i)} \alpha_{ij} \mathbf{m}_{ij}, \quad (1)$$

$$\mathbf{m}_{ij} = \mathbf{W}_2 \mathbf{x}_j^t + \mathbf{W}_3 \mathbf{x}_{ij}^t, \quad (2)$$

$$\alpha_{ij} = \text{softmax} \left(\frac{(\mathbf{W}_4 \mathbf{x}_i)^\top (\mathbf{W}_5 \mathbf{x}_j + \mathbf{W}_6 \mathbf{x}_{ij})}{d_{ij} \sqrt{d_{\text{emb}}}} \right) \quad (3)$$

where $\mathbf{W}_1, \mathbf{W}_2, \mathbf{W}_3, \mathbf{W}_4, \mathbf{W}_5$ and \mathbf{W}_6 are learnable parameters of shape $d_{\text{emb}} \times d_{\text{emb}}$; \mathbf{x}_i is the embedding for node i ; \mathbf{x}_{ij} is the embedding for edge between node i and j , and j iterates through all neighbour nodes of i ; \mathbf{m}_{ij} , α_{ij} , and d_{ij} are the message, attention, distance from node j to i , respectively; and d_{emb} is the dimension of the embedding.

2.3 Loss

We propose a novel loss L_{Struct} to ensure chemical and geometric constraints on the peptide structure. It includes 1) L_{MSE} (Appendix A.1), a mean squared error (MSE) of atom coordinates between ground truth and prediction, 2) L_{Intra} (Appendix A.2), a MSE of pairwise distances between atoms inside each residue, 3) L_{Inter} (Appendix A.3), a MSE of pairwise distances between atoms across different residues, 4) L_{Dihedral} (Appendix A.4), a MSE of the trigonometric functions (cos and sin) of dihedral angles:

$$L_{\text{Struct}} = L_{\text{MSE}} + \lambda_1 L_{\text{Intra}} + \lambda_2 L_{\text{Inter}} + \lambda_3 L_{\text{Dihedral}}, \quad (4)$$

where λ_1, λ_2 and λ_3 are hyper-parameters.

2.4 Post-processing

For each peptide residue, as the network outputs only the backbone and C_β atom coordinates, calculation of side chain atoms is necessary to obtain a full-atomic structure. We use the Rosetta Packer algorithm [Leaver-Fay et al., 2011] which selects the side chain conformations from the 2010 BBDep Rotamer library [Shapovalov and Dunbrack, 2011], such that the overall energy (Rosetta

REF15 energy [Alford et al., 2017]) of the structure is minimised, similar to the post-processing applied by Jumper et al. [2021] in AlphaFold 2. During the post-processing, only side chain atoms are updated, the predicted backbone atoms remain unchanged.

3 Experiment Setting

3.1 Data

We focus on MHC class I with a data set of 749 pMHC crystal structures retrieved from the Research Collaboratory for Structural Bioinformatics (RCSB) Protein Data Bank (PDB) [Berman et al., 2000]. Structures with any missing backbone or C_β atom and with non-9-mer peptides were removed. The β -2 microglobulin chain was not used in this work. After this process, 458 structures were kept. The structures were further split into train, validation, and test sets such that the test set matched the same as the one used by Motmaen et al. [2022] with no peptide shared between the splits. The resulting data set contains 293, 36, and 38 structures for train, validation, and test split, respectively. PDB IDs and amino acid frequencies of each subset are provided in Appendix B. All structures were aligned into the same coordinate system based only on the MHC C_α atoms with respect to a randomly chosen structure (PDB code: 1AKJ).

3.2 Metrics

We calculated the root mean square deviation (RMSD) on backbone and full-atom peptide structures for evaluation. Structures predicted by AlphaFold 2 and OmegaFold were aligned with respect to the 1AKJ MHC chain prior to evaluation. Additionally, we considered a mean average error (MAE) of the dihedral angles ϕ and ψ , averaged across the peptide. As the peptide positioning has to fulfil biological constraints and be inserted into MHC surrounding areas called binding pockets [Nguyen et al., 2021], we evaluated whether the predicted structures exhibit accurate binding positions by calculating the MAE on distances from the peptide to the MHC binding pockets (Appendix C). The total reweighted and attractive energy scores with Rosetta [Raveh et al., 2011] were reported to quantitatively assess the biological consistency of the structures.

3.3 Implementation

The GNN model was implemented with PyTorch Geometric [Fey and Lenssen, 2019] and trained on a Nvidia A100 40GB GPU. The optimiser was Adam with an initial learning rate of 3×10^{-4} . Hyperparameters were empirically set without extensive tuning (Appendix D). The official implementation of AlphaFold 2 monomer [Jumper et al., 2021], pMHC fine-tuned AlphaFold 2 [Motmaen et al., 2022], and OmegaFold [Wu et al., 2022] were used for benchmarking.

4 Results

Table 1: Metrics on test set per model. The reported values are average with standard deviation.

Metric (Unit)	GNN	AlphaFold 2 [Jumper et al., 2021]	Fine-tuned AlphaFold 2 [Motmaen et al., 2022]	OmegaFold [Wu et al., 2022]
Backbone RMSD (\AA)	1.26 ± 0.64	1.18 ± 0.61	1.19 ± 0.62	22.62 ± 11.21
Full-atom RMSD (\AA)	2.51 ± 1.01	2.11 ± 1.12	2.07 ± 1.11	23.43 ± 11.10
Dihedral MAE ($^\circ$)	25.80 ± 12.55	20.76 ± 12.13	21.41 ± 12.53	63.85 ± 16.75
Binding Pocket A MAE (\AA)	0.11 ± 0.15	0.24 ± 0.52	0.28 ± 0.54	16.48 ± 9.24
Binding Pocket B MAE (\AA)	0.25 ± 0.16	0.29 ± 0.54	0.35 ± 0.56	13.41 ± 7.88
Binding Pocket C MAE (\AA)	0.42 ± 0.30	0.49 ± 0.60	0.58 ± 0.72	9.14 ± 8.16
Binding Pocket D MAE (\AA)	0.36 ± 0.36	0.43 ± 0.48	0.49 ± 0.50	12.44 ± 8.64
Binding Pocket E MAE (\AA)	0.49 ± 0.37	0.56 ± 0.67	0.58 ± 0.75	11.40 ± 9.38
Binding Pocket F MAE (\AA)	0.10 ± 0.09	0.25 ± 0.54	0.31 ± 0.60	14.72 ± 9.37
Attractive score MAE (kcal/mol)	185.44 ± 83.15	340.72 ± 86.01	342.82 ± 85.04	189.91 ± 84.88
Total energy score MAE (kcal/mol)	147.19 ± 53.04	306.96 ± 86.21	305.14 ± 88.19	199.63 ± 64.54

The metrics of the proposed model together with the baselines AlphaFold 2 [Jumper et al., 2021], pMHC fine-tuned AlphaFold 2 [Motmaen et al., 2022], and OmegaFold [Wu et al., 2022] are reported

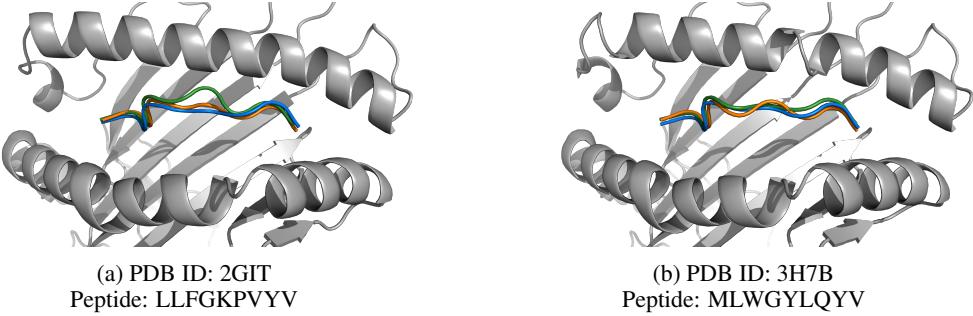


Figure 2: Examples of predicted structures. Experimental, GNN, and AlphaFold 2 fine-tuned predicted peptide are represented in green, blue, and orange, respectively. The MHC chain is represented in grey. AlphaFold 2 structures are not represented to simplify visualisation. GNN matches AlphaFold 2 fine-tuned structures and captures most of the peptide backbone shape and curvatures.

in Table 1 and their distributions in Figure 6 (Appendix E). For the GNN, results for the first seed are given in Table 1 and for four other seeds in Table 9 (Appendix E). The proposed method achieved on average 1.26 Å and 2.51 Å backbone and full-atom RMSD, respectively. This is comparable with the AlphaFold 2-based counterparts, despite having only 1.7M learnable parameters compared to 93M in AlphaFold 2. High backbone accuracy is necessary since full-atom structures are produced based on the backbone coordinates, therefore small errors in the backbone might propagate and have large effects on the side-chains. OmegaFold, on the other hand, generated inaccurate results with an RMSD of >10 Å (Figure 7 in Appendix E). The average dihedral MAE of the GNN is 26°, which is acceptable since the Packer algorithm uses a dihedral angle resolution of 10°. When comparing the distance to binding pockets, the proposed method achieved lower MAE, meaning that our method predicted structures better satisfying the constraints on the anchor residues. In terms of energies, all models predicted structures with higher energy scores than native, but the proposed method achieved the smallest difference, suggesting that structures predicted by the GNN are energetically more consistent with native structures than other methods. Examples of the predicted pMHC structures are visualised in Figure 2. Ablation studies were performed to analyse the impact of the proposed novel loss functions. The results are summarised in Table 10 in Appendix F, showing that additional loss terms led to improved structure geometry (dihedral angles) and more energetically consistent structures. Binding pockets were less impacted by the new loss terms, with the overall peptide position in the binding groove predominantly determined via the MSE loss term.

5 Conclusion and Discussion

In this work, we proposed a novel graph neural network architecture taking both residue-level and atom-level graphs to predict full-atomic pMHC structures. By minimising the composed losses on atom coordinates, pairwise distances, and dihedral angles, we demonstrated that a lightweight model with only 1.7M parameters is capable of producing accurate and biologically consistent structures, which is comparable to large protein folding models such as AlphaFold 2 (93M parameters). While the proposed method achieved plausible results, it solely predicts the backbone and C_β atoms for the peptide and relies on the Rosetta Packer algorithm to obtain full-atomic structures. Extending the network to predict full-atom pMHC structures may enable us to achieve higher accuracy, and to further reduce inference time. Moreover, the experiments were focused only on the interactions between 9-mer peptides and MHC class I. Future work could include extending the model to peptides of variable length and MHC class II to build a universal structure prediction model for pMHC complexes.

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A Loss

A.1 Mean Squared Error Loss

The role of the mean squared error loss is to give the correct overall shape and position in the space of the peptide atoms. There are 9 amino acids and 5 atoms per amino acid. Let $y_a^{(j)}$ and $\hat{y}_a^{(j)}$ denote the true and predicted coordinates of the j^{th} atom in the a^{th} amino acid of the peptide, respectively. As some peptide residues are more variable than others, residue-wise weights (denoted by w_a) are added to strengthen the attention given to the middle amino acids. Raw residue-wise weights are calculated by running the model with uniform weighting (i.e. $w_a = 1/9$) and then extracting the residue-wise MSE loss on the validation subset. Weights w_a are normalised to sum to 1 and the values are provided in Table 2. The formula of this loss is given by:

$$L_{\text{MSE}} = \frac{1}{45} \sum_{a=1}^9 \sum_{j=1}^5 w_a \|y_a^{(j)} - \hat{y}_a^{(j)}\|^2. \quad (5)$$

Table 2: MSE weights values per amino acid.

Residue	1	2	3	4	5	6	7	8	9
Weight	0.0356	0.0308	0.0621	0.1201	0.2900	0.1927	0.1117	0.0684	0.0887

A.2 Intra-residue Loss

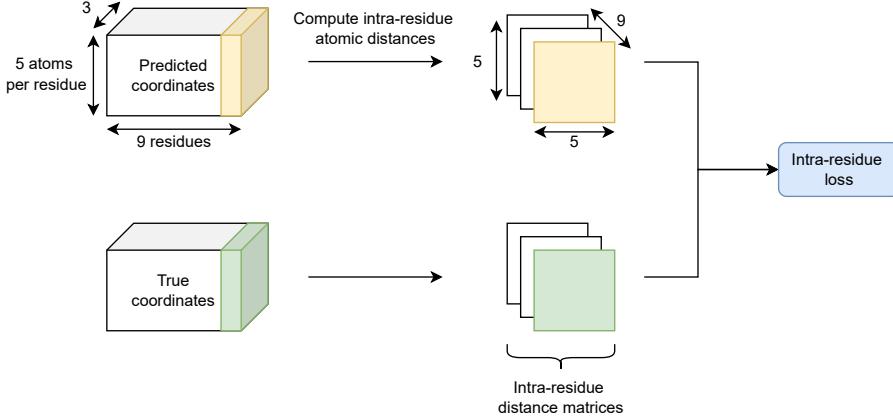


Figure 3: Intra-residue loss computation process

Let $d_a^{(j,k)}$ and $\hat{d}_a^{(j,k)}$ denote the distances between the j^{th} and k^{th} atoms in the a^{th} amino acid of the peptide for the ground truth and predicted structures, respectively:

$$d_a^{(j,k)} = \|y_a^{(k)} - y_a^{(j)}\|, \quad (6)$$

$$\hat{d}_a^{(j,k)} = \|\hat{y}_a^{(k)} - \hat{y}_a^{(j)}\|. \quad (7)$$

The intra-residue loss is defined as (Figure 3):

$$L_{\text{Intra}} = \frac{1}{225} \sum_{a=1}^9 \sum_{j=1}^5 \sum_{k=1}^5 \|d_a^{(j,k)} - \hat{d}_a^{(j,k)}\|^2. \quad (8)$$

The intra-residue loss adds constraints on the local geometry inside each peptide amino acid residue.

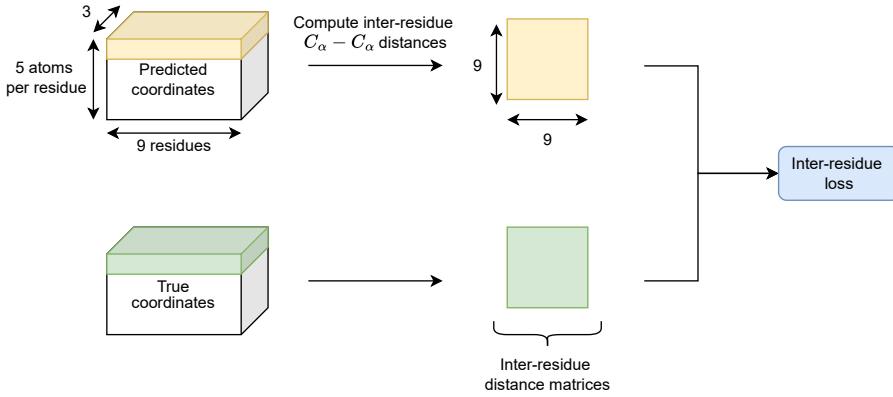


Figure 4: Inter-residue loss computation process

A.3 Inter-residue Loss

Let $d_{a,b}$ and $\hat{d}_{a,b}$ denote the distances between the C_α atoms of the a^{th} and b^{th} amino acids of the peptide for the ground truth and predicted structures, respectively:

$$d_{a,b} = \|y_a^{(0)} - y_b^{(0)}\|, \quad (9)$$

$$\hat{d}_{a,b} = \|\hat{y}_a^{(0)} - \hat{y}_b^{(0)}\|, \quad (10)$$

where $y_a^{(0)}$ and $\hat{y}_a^{(0)}$ represent the coordinates of the C_α atom for a^{th} amino acid of peptide for the ground truth and predicted structures, respectively.

The inter-residue loss is defined as (Figure 4):

$$L_{\text{Inter}} = \frac{1}{81} \sum_{a=1}^9 \sum_{b=1}^9 \|d_{a,b} - \hat{d}_{a,b}\|^2 \quad (11)$$

The inter-residue loss adds constraints on the geometry between peptide amino acid residues.

A.4 Dihedral Loss

Let ϕ^j and ψ^j denote the j^{th} dihedral angles of rotation over the $N-C_\alpha$ and $C_\alpha-C$ covalent bonds of the peptide [Ramachandran et al., 1963]. Following Xia and Ku [2021], the dihedral loss is defined as:

$$\begin{aligned} L_{\text{Dihedral}} &= \frac{1}{8} \sum_{j=1}^8 (\sin(\psi^j) - \sin(\hat{\psi}^j))^2 + (\cos(\psi^j) - \cos(\hat{\psi}^j))^2 \\ &\quad (\sin(\phi^j) - \sin(\hat{\phi}^j))^2 + (\cos(\phi^j) - \cos(\hat{\phi}^j))^2 \end{aligned} \quad (12)$$

B Data

The PDB IDs for the training, validation, and test sets are listed in Table 3, Table 4, and Table 5, respectively. The amino acid frequencies at each peptide position are illustrated in Figure 5 for each data subset.

Table 3: Train set PDB IDs.

PDB ID									
1A1O	1T1X	2PYE	3L3J	3RL1	5EO1	5VWH	6P23	6VMC	7LFZ
1A9B	1T1Y	2X4S	3L3K	3SKM	5EU4	5W69	6P27	6VMX	7LG0
1A9E	1T1Z	2X4U	3LKN	3TO2	5EU5	5W6A	6P2C	6VQO	7LG3
1AKJ	1T21	2XPG	3LKO	3UPR	5EU6	5WLG	6P2F	6VR1	7LGD
1CG9	1T22	3AM8	3LKP	3V5D	5F9J	5WMN	6P2S	6VR5	7M8U
1EEY	1TVB	3BH9	3LKK	3V5H	5GSR	5WMO	6P64	6VRM	7MJ6
1EEZ	1TVH	3BHB	3LKR	3V5K	5HHO	5WMR	6PA1	6VRN	7MJ9
1EFX	1W0V	3BZF	3LKS	4EUP	5HHP	5WSH	6PTB	6W51	7MJA
1G7P	1W0W	3C9N	3LV3	4HWZ	5HHQ	5XOS	6PTE	6XQA	7MKB
1HHJ	1WBZ	3CCH	3MR9	4I4W	5IEK	5XOT	6R2L	6Y26	7MLE
1HSA	1XR8	3D18	3MRB	4K7F	5IM7	6BJ2	6SS7	6Y27	7N1A
1I1F	1XR9	3FQR	3MRC	4L8D	5INC	6BJ3	6SS8	6Y28	7N1B
1I1Y	1YDP	3FQT	3MRD	4LCY	5MEN	6BJ8	6SS9	6Y29	7N1E
1I7T	1ZT7	3FQW	3MRF	4MNQ	5MEO	6D2T	6SSA	6Y2A	7N1F
1I7U	2A83	3FT4	3MRG	4N8V	5MEP	6EWA	6UJO	6Y2B	7N6D
1JHT	2BCK	3GSQ	3MRH	4NNY	5MEQ	6EWC	6UK4	6Z9V	7N6E
1JUF	2BNR	3GSR	3MRI	4N05	5MER	6EWO	6ULI	6Z9W	7P3D
1M6O	2BSR	3GSU	3MRJ	4O2C	5N6B	6GL1	6ULN	7CIR	7P3E
1N2R	2BST	3GSV	3MRK	4O2E	5NME	6ID4	6ULR	7DUU	7RM4
1P7Q	2C7U	3GSW	3MRL	4QRP	5NMG	6J1V	6UZM	7EJL	7RRG
1Q94	2CIK	3GSX	3MYJ	4QRQ	5NMK	6J1W	6UZO	7EJM	7RTD
1QEW	2DYP	3I6G	3PWJ	4QRS	5T7G	6J29	6UZP	7EJN	7RTR
1QR1	2F53	3I6L	3PWL	4QRT	5TS1	6JTP	6UZS	7F4W	7S8R
1S8D	2F54	3KPM	3PWN	4QRU	5TXS	6MT5	6VB0	7JYW	
1S9W	2GTW	3KPO	3PWP	4U1S	5VGD	6NCA	6VB1	7KGP	
1S9X	2GTZ	3KPQ	3QDJ	5BRZ	5VGE	6O4Y	6VB2	7KGQ	
1S9Y	2GUO	3KPR	3QEQQ	5BS0	5VUD	6O4Z	6VM7	7KGR	
1SYS	2H6P	3L3D	3QFD	5E00	5VUF	6O9B	6VM8	7KGS	
1SYV	2P5E	3L3G	3QFJ	5ENW	5VVP	6O9C	6VM9	7L1B	
1T1W	2P5W	3L3I	3REW	5EO0	5VWF	6OPD	6VMA	7L1C	

Table 4: Validation set PDB IDs.

PDB ID									
1AIM	1W72	3BH8	4I48	5D2L	5NMF	6MT6	6UK2	7KGO	
1HHG	2J8U	3CC5	4L29	5D2N	5SWQ	6PYJ	6VB4	7LG2	
1LP9	2VLR	3KYN	4NQX	5EU3	6JOZ	6PYV	7BBG	7LGT	
1QRN	2X4O	4E5X	5B39	5HHN	6MT4	6PZ5	7EU2	7M8T	

Table 5: Test set PDB IDs.

PDB ID									
1E27	1QQD	2FWO	3D25	3KYO	4QRR	5DEG	5TRZ	6G9Q	6VB7
1I7R	1VGK	2GIT	3H7B	3MRE	4U1H	5FA3	5U98	6GH1	7JYV
1JGE	1X7Q	3BVN	3KLA	3SKO	4U1N	5IB2	5VWJ	6J2A	
1JPG	2BVP	3BXN	3KPP	4HX1	4Z77	5IND	5WMQ	6Q3S	

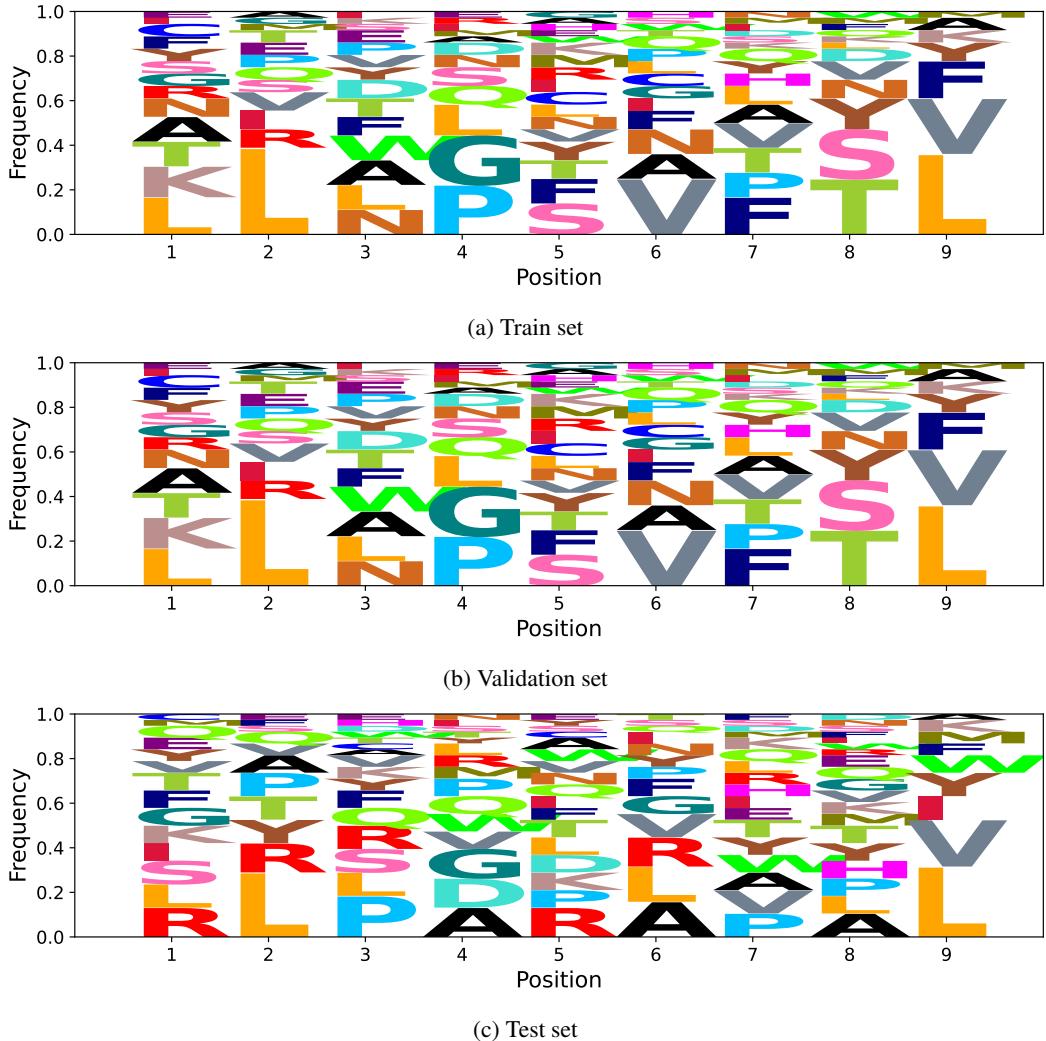


Figure 5: Sequence logo plots representing the amino acid frequencies at each peptide position and for each data subset.

C Distance to Binding Pockets

Binding pockets are areas on the MHC chain that play a key role in how the peptide binds to the MHC [Nguyen et al., 2021]. Each binding pocket corresponds to a group of residues, named anchor residues that can bind to one or two peptide residues. Nguyen et al. [2021] have identified six distinct binding pockets (A to F), along with their corresponding anchor residues (on the MHC chain) and peptide residues. Specifically, for each binding pocket, there are two fixed sets of residues on peptide and MHC chain. Let \mathcal{P}_k and \mathcal{M}_k denote the residue index sets for binding pocket k for peptide and MHC, respectively. The C_α position on these residues are therefore denoted by $y_i^{(0)}, y_j^{(0)}$ for ground truth structure and $\hat{y}_i^{(0)}, \hat{y}_j^{(0)}$ for predicted structure. In this work, we assess how well the structures reflect the position of the peptide relatively to these binding pockets by measuring the average $C_\alpha - C_\alpha$ distance between the corresponding peptide and anchor residues as follows:

$$d_{\text{BP}} = \frac{1}{|\mathcal{P}_k| |\mathcal{M}_k|} \sum_{i \in \mathcal{P}_k} \sum_{j \in \mathcal{M}_k} \|y_i^{(0)} - y_j^{(0)}\|, \quad (13)$$

$$\hat{d}_{\text{BP}} = \frac{1}{|\mathcal{P}_k| |\mathcal{M}_k|} \sum_{i \in \mathcal{P}_k} \sum_{j \in \mathcal{M}_k} \|\hat{y}_i^{(0)} - \hat{y}_j^{(0)}\|. \quad (14)$$

Table 6: Binding pocket peptide and MHC anchor residues from Nguyen et al. [2021].

Binding pocket	Peptide residue(s)	MHC anchor residues
A	1	5, 7, 59, 63, 66, 159, 163, 167, 171
B	2	7, 9, 24, 34, 45, 63, 66, 67, 70, 99
C	3, 5, 6	9, 70, 73, 74, 97
D	3, 5, 6	99, 114, 155, 156, 159, 160
E	3, 5	97, 114, 147, 152, 156
F	9	77, 80, 81, 84, 95, 123, 143, 146, 147

D Experiments Parameters

GNN and training hyper-parameters are defined in Table 7 and Table 8, respectively.

Table 7: Neural network hyper-parameters

Block	Number of layers	Input size	Output size
Node embedding	1	15	128
Edge embedding	1	6	128
GNN block	4 with 4 heads each	128	128
Prediction head	2	128/128	128/3

Table 8: Training hyper-parameters

Parameter	Value	Parameter	Value
Max epochs	70	Output shape	(9, 5, 3)
Batch size	10	Intra-residue loss weight λ_1	3.0
Input dimension	15	Inter-residue loss weight λ_2	0.5
Embedding dimension d_{emb}	128	Dihedral loss weight λ_3	0.25

AlphaFold 2 original and fine-tuned models were trained using Motmaen et al. [2022] implementation¹ with original and fine-tuned weights respectively. Motmaen et al. [2022] use a 200 residue gap trick to add the peptide sequence. For OmegaFold, we use Wu et al. [2022] implementation² with a 30 glycine residue gap trick as shown more successful by Tsaban et al. [2022].

¹https://github.com/phbradley/alphafold_finetune

²<https://github.com/HeliXonProtein/OmegaFold>

E Results

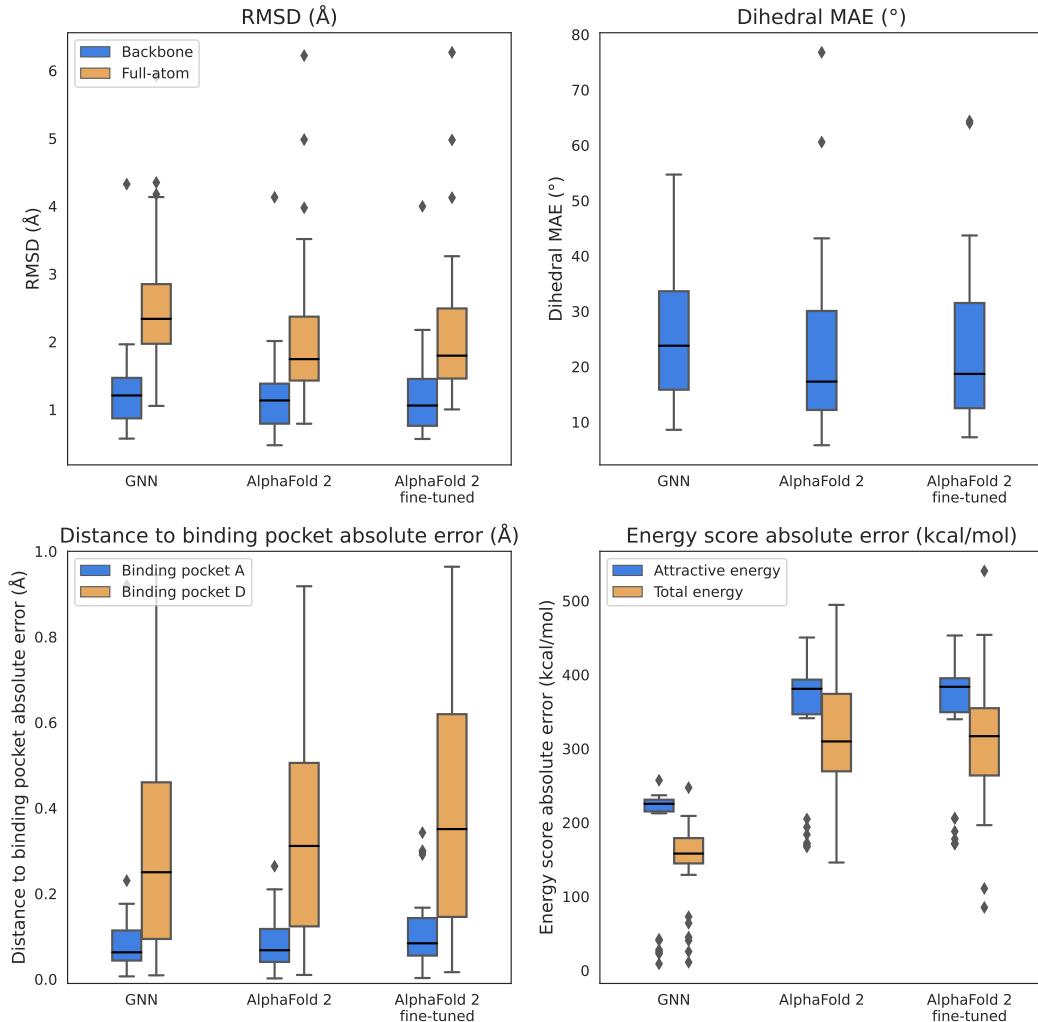


Figure 6: Boxplots of distributions of RMSD (top-left), dihedral MAE (top-right), distance to binding pocket absolute error (bottom-left) and energy score absolute error (bottom-right). To simplify the visualisation, OmegaFold results are not displayed and only binding pockets A and D are represented.

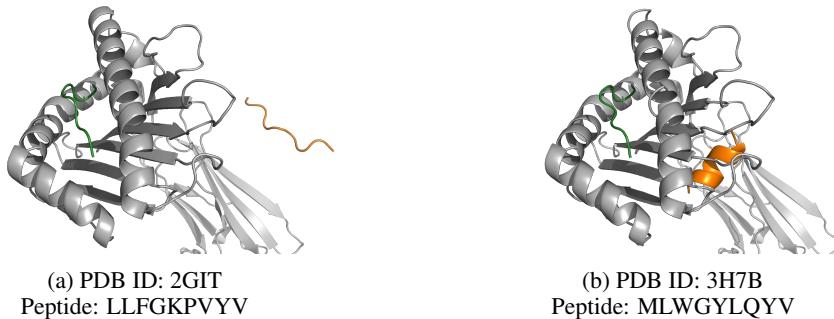


Figure 7: Examples of incorrectly predicted structures by OmegaFold. Experimental and OmegaFold peptide are represented in green and orange respectively. The MHC chain is represented in grey.

Table 9: Metrics on test set per seed. The reported values are average with standard deviation across the test set.

Metric (Unit)	Seed 1	Seed 2	Seed 3	Seed 4	Seed 5
Backbone RMSD (Å)	1.26 ± 0.64	1.21 ± 0.71	1.23 ± 0.65	1.23 ± 0.65	1.23 ± 0.62
Full-atom RMSD (Å)	2.51 ± 1.01	2.42 ± 1.12	2.43 ± 1.06	2.43 ± 1.06	2.60 ± 1.00
Dihedral MAE (°)	25.80 ± 12.55	30.04 ± 16.01	28.10 ± 13.86	28.10 ± 13.86	34.37 ± 18.10
Binding Pocket A MAE (Å)	0.11 ± 0.15	0.07 ± 0.14	0.06 ± 0.14	0.07 ± 0.15	0.06 ± 0.14
Binding Pocket B MAE (Å)	0.25 ± 0.16	0.20 ± 0.16	0.17 ± 0.15	0.22 ± 0.16	0.21 ± 0.16
Binding Pocket C MAE (Å)	0.42 ± 0.30	0.43 ± 0.31	0.39 ± 0.28	0.35 ± 0.29	0.41 ± 0.27
Binding Pocket D MAE (Å)	0.36 ± 0.36	0.37 ± 0.39	0.34 ± 0.31	0.37 ± 0.38	0.37 ± 0.34
Binding Pocket E MAE (Å)	0.49 ± 0.37	0.46 ± 0.32	0.50 ± 0.43	0.50 ± 0.35	0.54 ± 0.42
Binding Pocket F MAE (Å)	0.10 ± 0.09	0.09 ± 0.09	0.10 ± 0.09	0.12 ± 0.08	0.10 ± 0.08
Attractive score MAE (kcal/mol)	185.44 ± 83.15	186.44 ± 82.41	185.75 ± 82.92	185.35 ± 83.05	186.15 ± 83.60
Total energy score MAE (kcal/mol)	147.19 ± 53.04	142.43 ± 56.73	143.39 ± 47.87	143.90 ± 52.13	160.13 ± 82.38

F Loss Ablation

We trained the same GNN model with different combinations of loss terms. We compared different cases where additional loss terms were removed individually, and when only the MSE loss was kept. The results are reported in Table 10 and examples of predicted structures for both cases are visualised in Figure 8.

Table 10: Metrics on test set per model. The reported values are average with standard deviation across the test set.

Metric (Unit)	Full loss	MSE only	$\lambda_1 = 0$	$\lambda_2 = 0$	$\lambda_3 = 0$
Backbone RMSD (Å)	1.26 ± 0.64	1.29 ± 0.68	1.32 ± 0.66	1.24 ± 0.66	1.31 ± 0.71
Full-atom RMSD (Å)	2.51 ± 1.01	2.63 ± 1.13	2.67 ± 1.16	2.55 ± 1.14	2.64 ± 1.11
Dihedral MAE (°)	25.80 ± 12.55	31.01 ± 14.62	29.09 ± 16.83	29.01 ± 16.45	35.51 ± 17.57
Binding Pocket A MAE (Å)	0.11 ± 0.15	0.08 ± 0.15	0.06 ± 0.15	0.06 ± 0.14	0.07 ± 0.15
Binding Pocket B MAE (Å)	0.25 ± 0.16	0.29 ± 0.19	0.19 ± 0.15	0.19 ± 0.17	0.25 ± 0.16
Binding Pocket C MAE (Å)	0.42 ± 0.30	0.42 ± 0.32	0.41 ± 0.29	0.45 ± 0.34	0.34 ± 0.29
Binding Pocket D MAE (Å)	0.36 ± 0.36	0.37 ± 0.39	0.40 ± 0.37	0.35 ± 0.33	0.36 ± 0.35
Binding Pocket E MAE (Å)	0.49 ± 0.37	0.46 ± 0.38	0.55 ± 0.39	0.49 ± 0.40	0.47 ± 0.37
Binding Pocket F MAE (Å)	0.10 ± 0.09	0.11 ± 0.10	0.11 ± 0.09	0.11 ± 0.08	0.10 ± 0.09
Attractive score MAE (kcal/mol)	185.44 ± 83.15	190.20 ± 79.68	192.23 ± 80.19	190.60 ± 80.05	190.89 ± 80.64
Total energy score MAE (kcal/mol)	147.19 ± 53.04	165.00 ± 73.17	149.20 ± 63.33	168.73 ± 76.98	157.32 ± 57.40

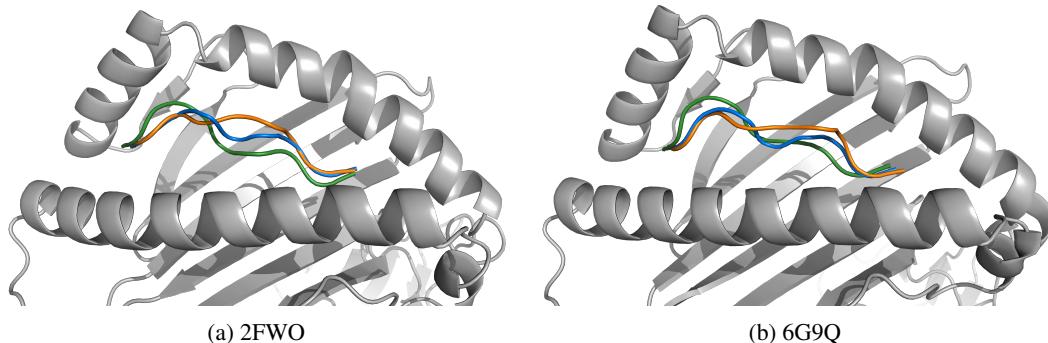


Figure 8: Examples of predicted structures. Experimental, GNN with full loss, and GNN with MSE loss only predicted peptide are represented in green, blue, and orange, respectively. The MHC chain is represented in grey.

G Running time

We provide in Table 11 the inference time for each model per structure. We assess the running time on one A100 40GB GPU and 8 e2-standard 64 GB CPUs. Note that the Packer only runs on CPU and is not assessed on GPU. We hypothesise that the GNN inference running faster on CPU compared to GPU is due to the low compute requirements of the forward pass with the memory transfer from main to GPU memory dominating the cost.

Table 11: Inference running time in seconds per structure per model on CPU and GPU.

Model	CPU	GPU
GNN	0.064	0.35
Packer	6.73	NA
AlphaFold 2	303.16	4.61
OmegaFold	1917.00	26.48