



ICLR 2026

Quantifying Cross-Attention Interaction in Transformers for Interpreting TCR-pMHC Binding

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Project Page: <https://qcai.jiarui.li/>



ICLR
International Conference On
Learning Representations



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BACKGROUNDS

TCR-pMHC Binding Prediction



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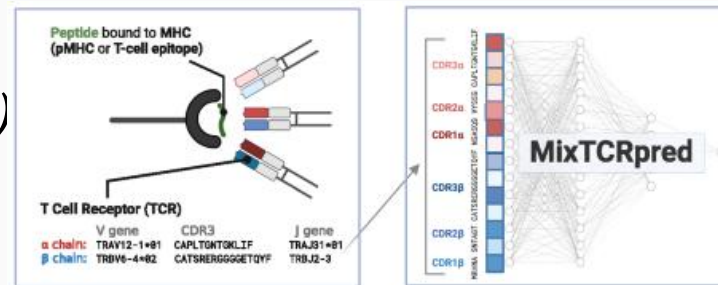
INPUTS:

1. CDR3 α Chain (e.g., $[ALGDHSGSWQLI]$)
2. CDR3 β Chain (e.g., $[ASSLRTGANSDYT]$)
3. Peptide (e.g., $[GVYATSSAVRLR]$)

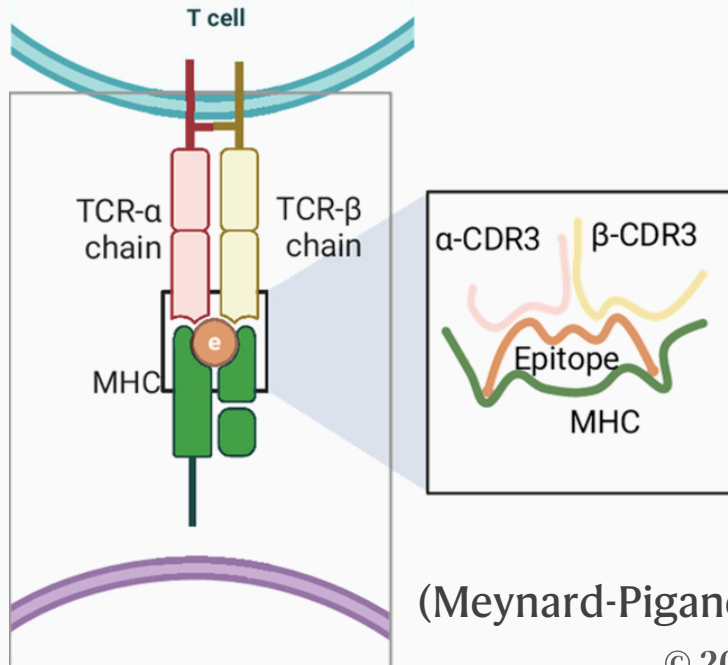
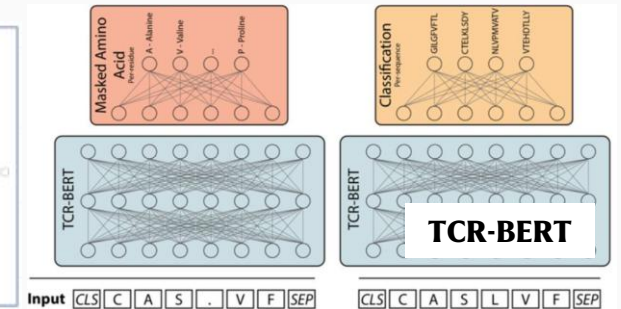
OUTPUTS:

1. Binder/non-binder (*True/False*)

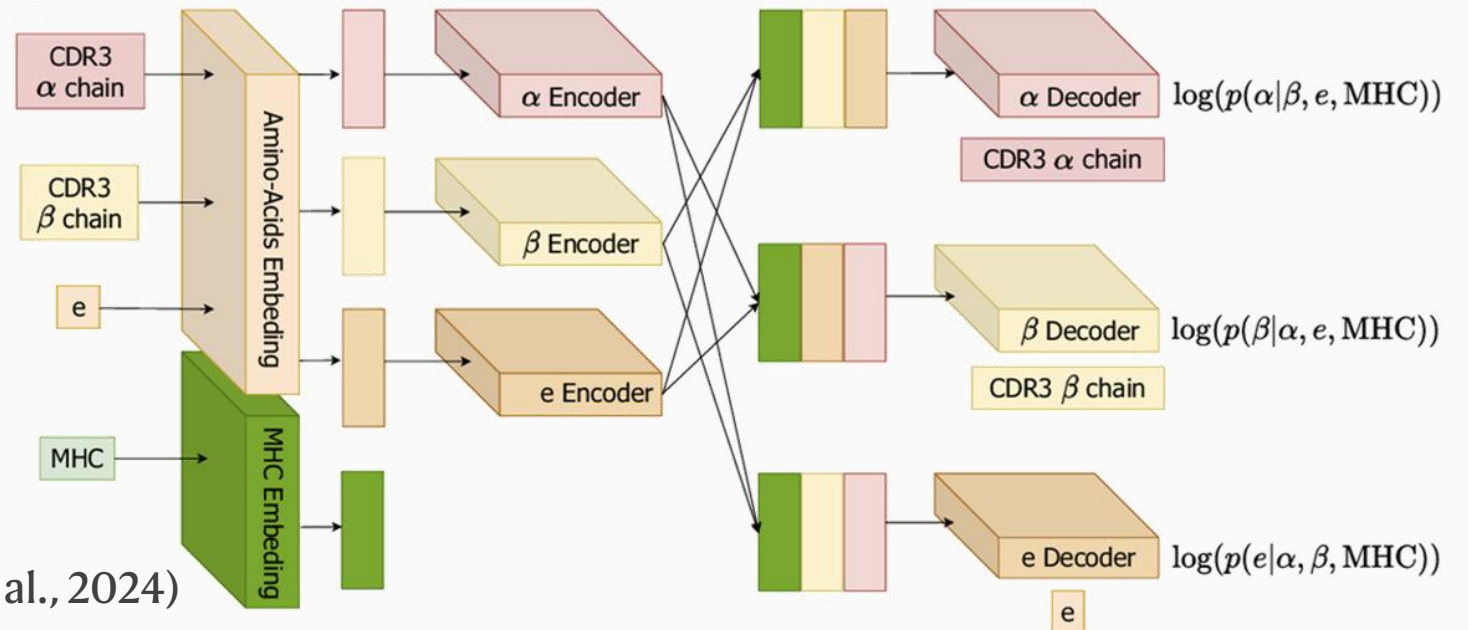
(Groce et al, 2024)



(Wu et al, 2024)



(Meynard-Piganeau et al., 2024)



BACKGROUNDS

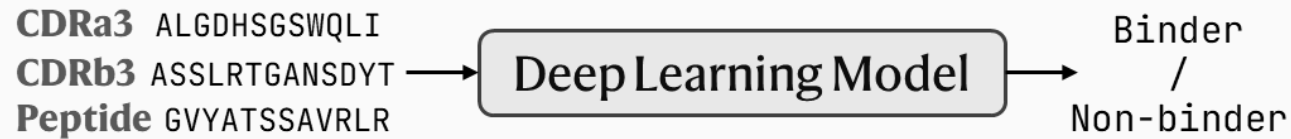
Interpretable Machine Learning



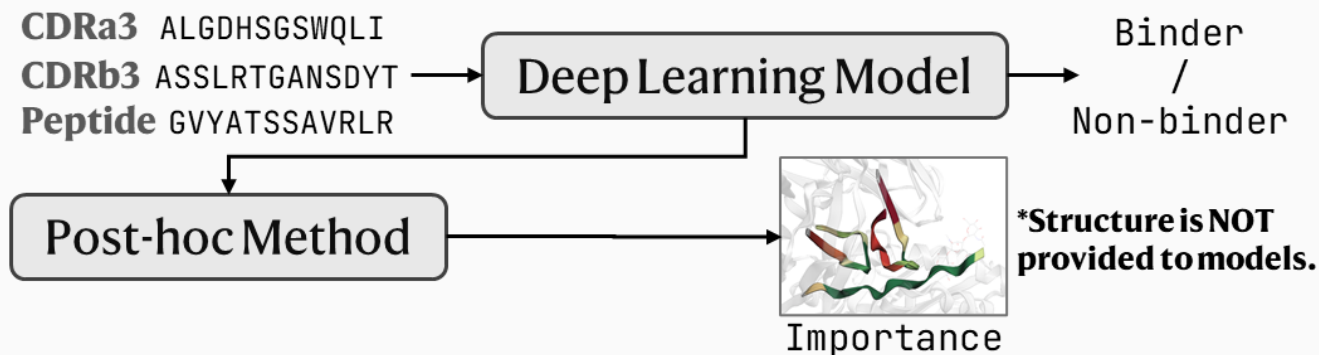
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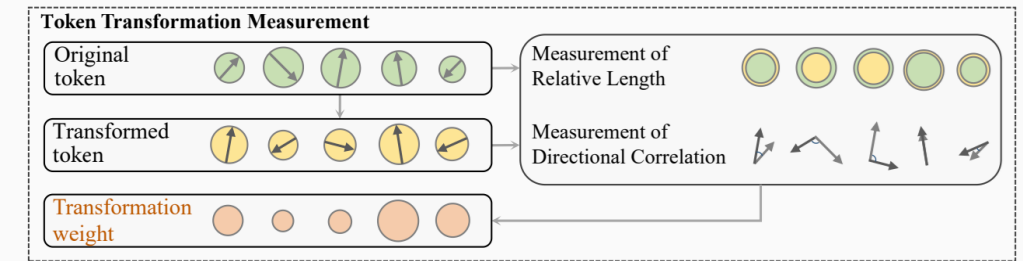
Black Box



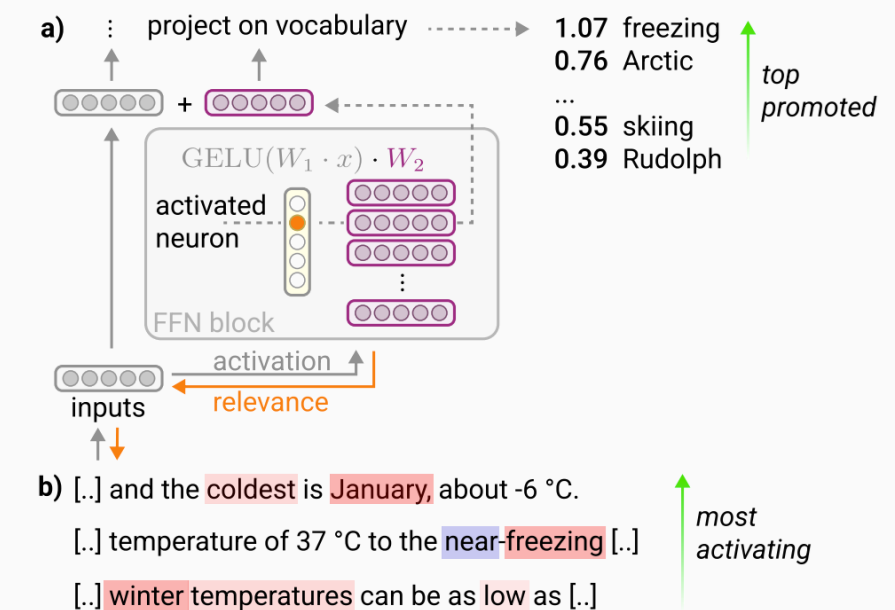
Post-hoc Interpretation



TokenTM (Wu et al., 2024)



AttnLRP (Achtibat et al., 2024)

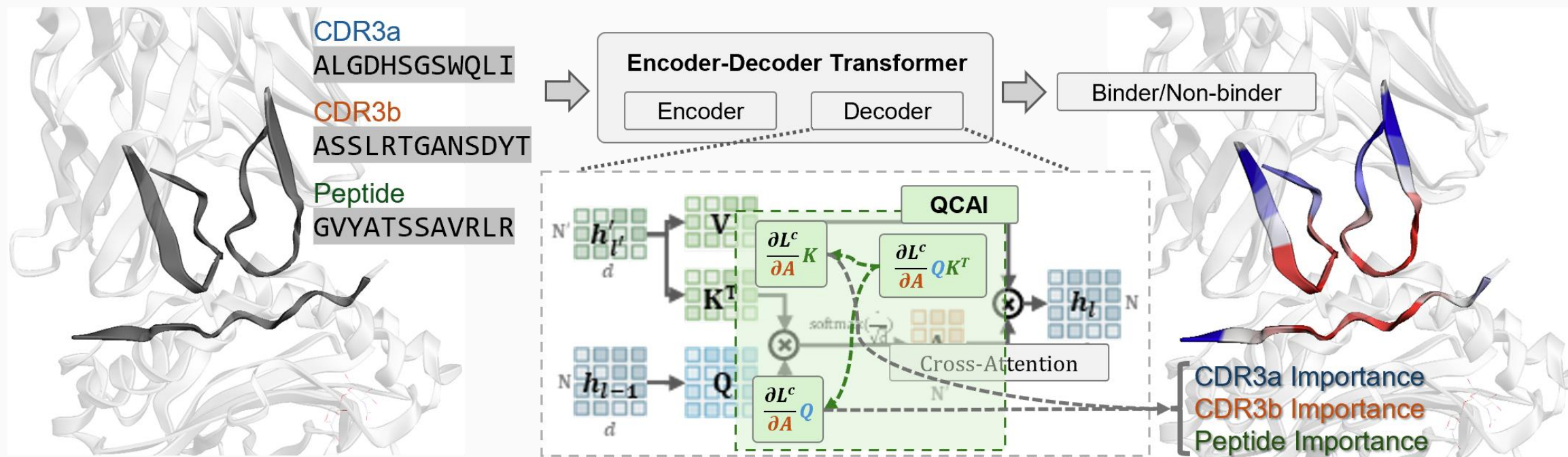


OUR APPROACH

Quantifying Cross-Attention Interaction



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OUR APPROACH

TCR-XAI Benchmark & BRHR



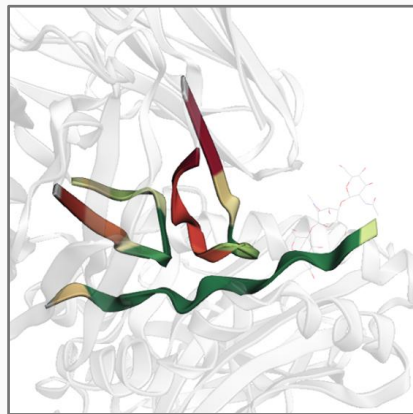
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TCR-XAI

Explanation Quantitative Benchmark

274 High Resolution TCR-pMHC Complex Structural Data from **STCRDab** (Leem et al., 2018) and **TCR3d 2.0** (Lin et al., 2025)



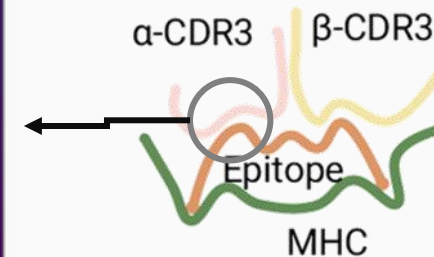
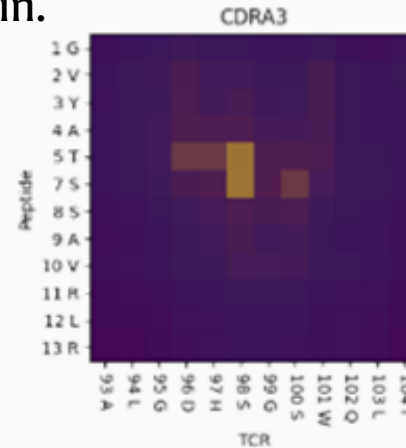
How much agreement?

BRHR

Binding Region Hit Rate

Importance vs. Binding Structure

- Residue importance correlates with binding structure: more interactions \rightarrow higher importance in the model.
- **BRHR.k**: Measures whether the top-k important residues in one chain align with the top-k residues closest to the other chain.



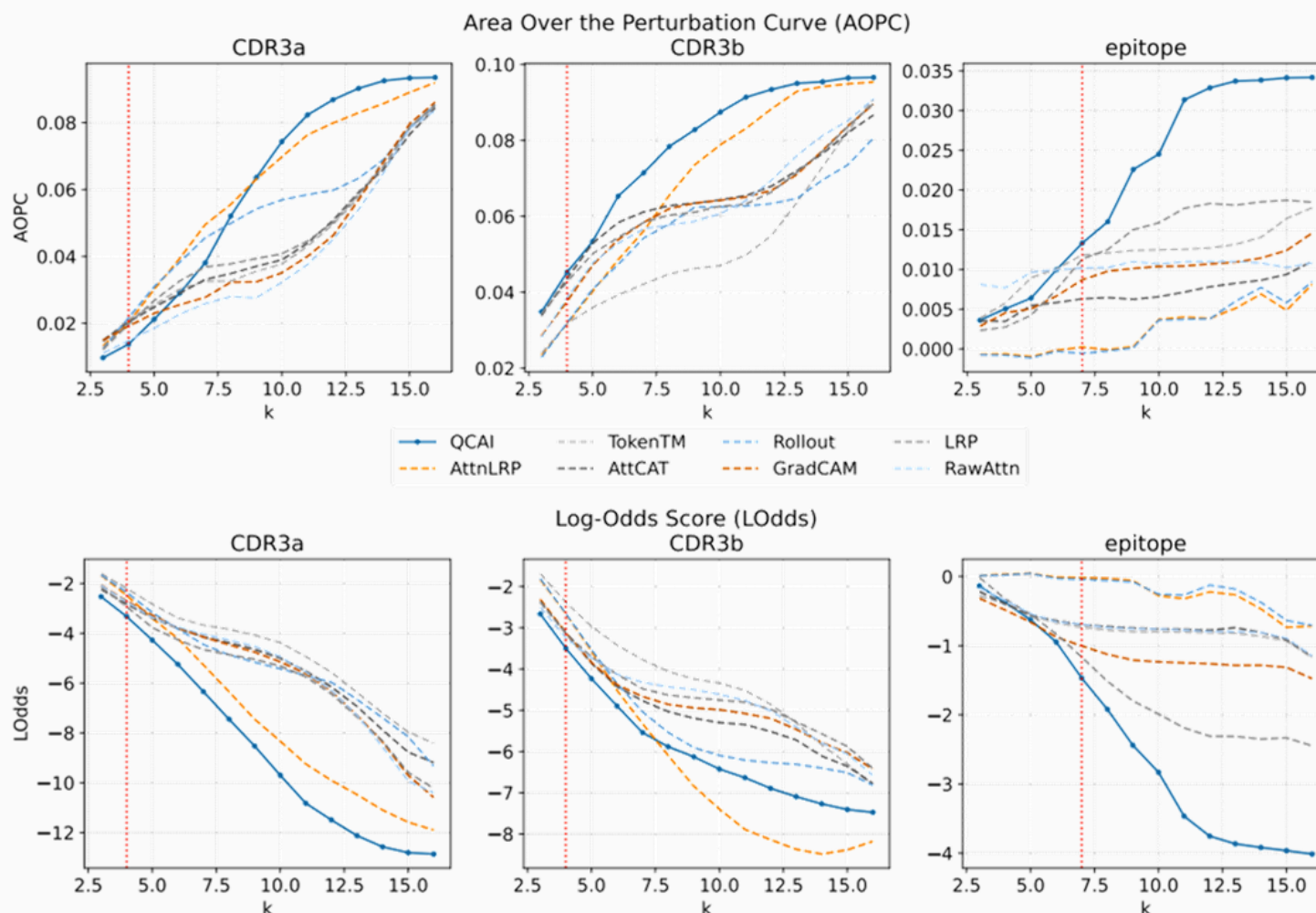
Use **distance** between two given chains to quantitatively evaluate **explanation quality**.

RESULTS

Perturbation Experiments



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LOdds

Log-Odds Score

$$\text{LOdds}(k) = \frac{1}{N} \sum_{i=1}^N \log \frac{p(\hat{y}|\tilde{\mathbf{x}}_i^k)}{p(\hat{y}|\mathbf{x}_i)}$$

AOPC

Area Over the Perturbation Curve

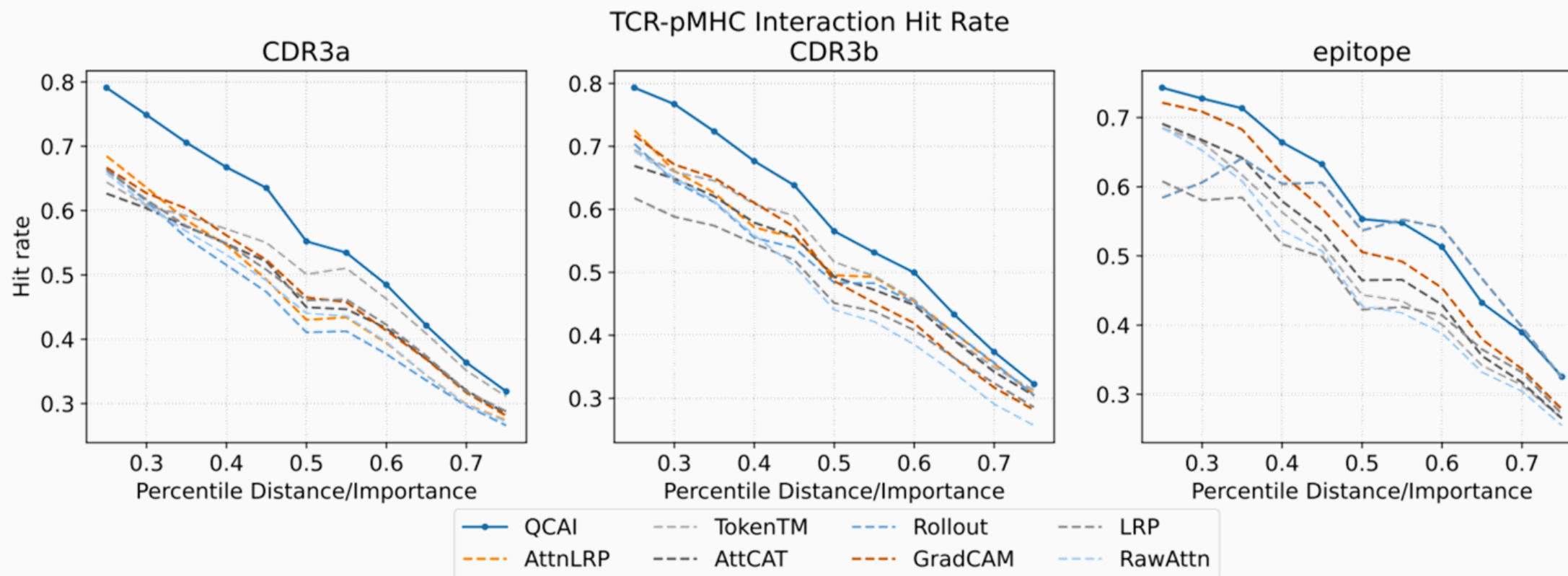
$$\text{AOPC}(k) = \frac{1}{N} \sum_{i=1}^N p(\hat{y}|\mathbf{x}_i) - p(\hat{y}|\tilde{\mathbf{x}}_i^k),$$

RESULTS

Binding Region Hit Rate



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Binding Site Hit Rate (BRHR)

compares top-ranked residues by explanation score against top interacting residues by distance.

RESULTS

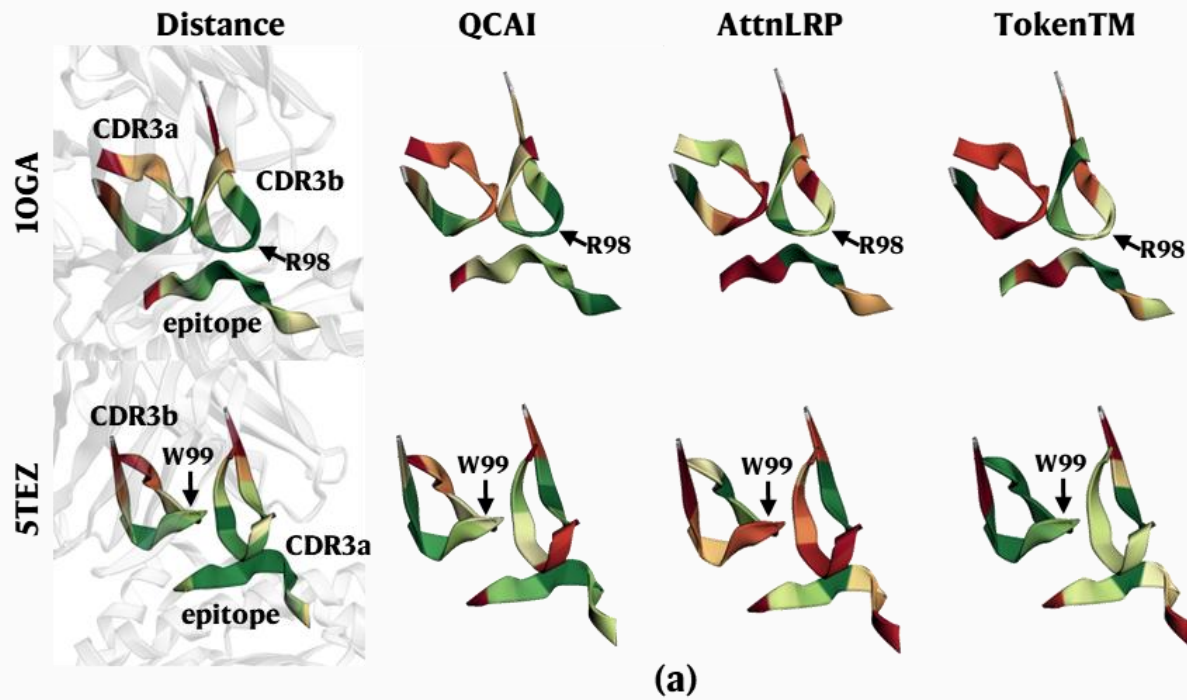
Case Studies



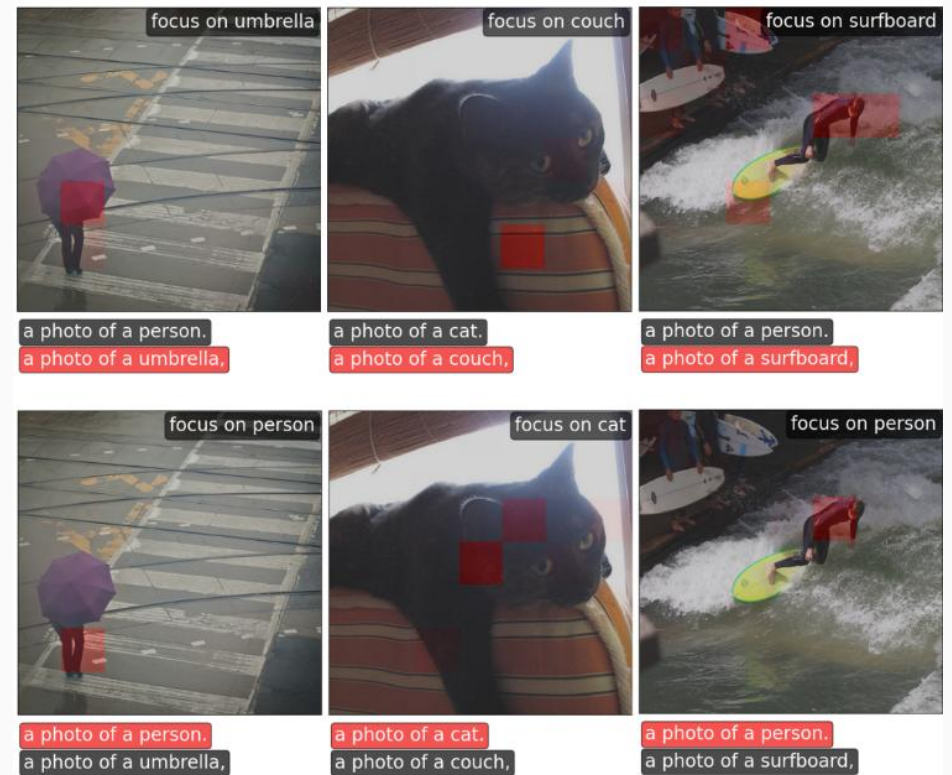
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TULIP for Influenza Matrix Protein



Vision Language Model on ImageNet



CONCLUSION

Summary & Future Study



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- **QCAI:** Quantifying Cross-Attention Interaction
- **TCR-XAI:** Quantitative Benchmark for TCR-pMHC Explanation Evaluation
- Cross-Attention Role in TCR-pMHC Binding Prediction
- **QCAI Application:**
 - Explanation-Guided Model Design (*Li et al., 2025, ACM-BCB*)
 - Inherent Explainable Model for TCR-pMHC Binding

**Project Page for Code,
Data, and Models**
(<https://qcai.jiarui.li/>)

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