In silico TCR drug design

Neoantigen/immunopeptide identification (HLA02-specific) → **Neoantigen – HLA binding ability validation** → **Prediction of novel peptides that bind neoantigens** → **Peptide Prioritization (binding affinity, stability, interaction)** → **Cross-target prediction** → **Structure prediction of a new peptide linked with anti-CD3 scFv domain** → **Developability Prediction**

ML training on existing datasets (e.g. TSNAdb, IEDB, TESLA, NCI, in-house WGS/WES/RNA-Seq)

DDA/DIA MS spectra of HLA-1 eluted peptides (T vs N)

- NetMHCpan
- MHCflurry
- IEDB Analysis Resource

- AutoDock Vina
- DeepAffinity (GPU)
- FlexPepDock*
- AMBER
- CHARMM

- IEDB
- VDJdb
- McPAS-TCR
- Tbadb
- ImmuneCode

- **SwissADME**: solubility and drug-likeness.
- **ADMETlab 3.0**
- **PRIME:** immunogenicity.
- **ToxiM**: toxicity.
- FoldX: folding stability

- FragPipe
- DIA-NN
- MSFragger
- **Proteome Discoverer**
- **MaxQuant**

De Novo Peptide Design (ML training):
- ProteinMPNN: Generate peptide sequences that are likely to interact with a target protein.
- AlphaDesign
- EvoBind
- DeepProtein
- **AlphaProteo (2024)**

- **AlphaFold**
- **RosettaFold**
- **RosettaAntibody**

Lab validation

```
>T=0.1, sample=0, score=1.2431, seq_recovery=0.1000
GGNAVGVGDS
```

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Science (2022); Immunity (2023)