# Deep learning of antibody epitopes using positional permutation vectors

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## BACKGROUND

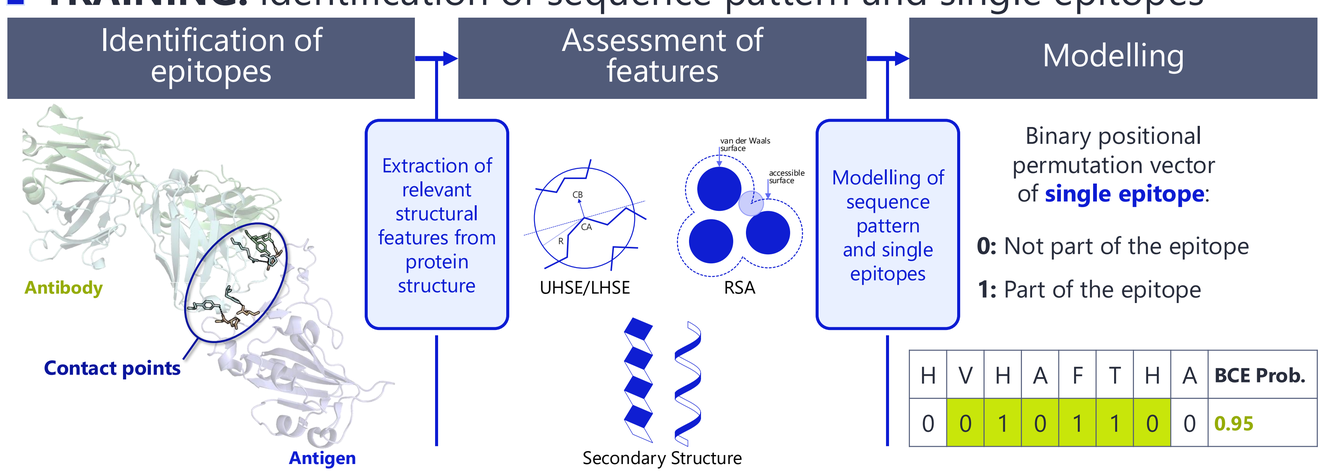
- Knowledge of the precise coordinates of antibody epitopes are crucial in vaccine design, therapeutic antibody engineering, and optimizing diagnostic and therapeutic applications in molecular medicine [2-4].
- Experimental approaches to capture antibody epitope are time consuming, laborious, and expensive. Therefore, not amenable to be applied on a large-scale for comprehensive BCE mapping and screening [5].
- Herein, we use ML based epitope profiling of SARS-Cov-2 Spike variants to identify conserved and variant specific epitopes.
- We then applied a mutation policy to generate an artificial spike protein bearing a set of epitope with broad coverage of variants
- Finally, we generated mRNA-LNP vaccines encoding for the AI designed antigen and compared its neutralization effect on different SARS variant after immunization in the mouse.

## OBJECTIVE

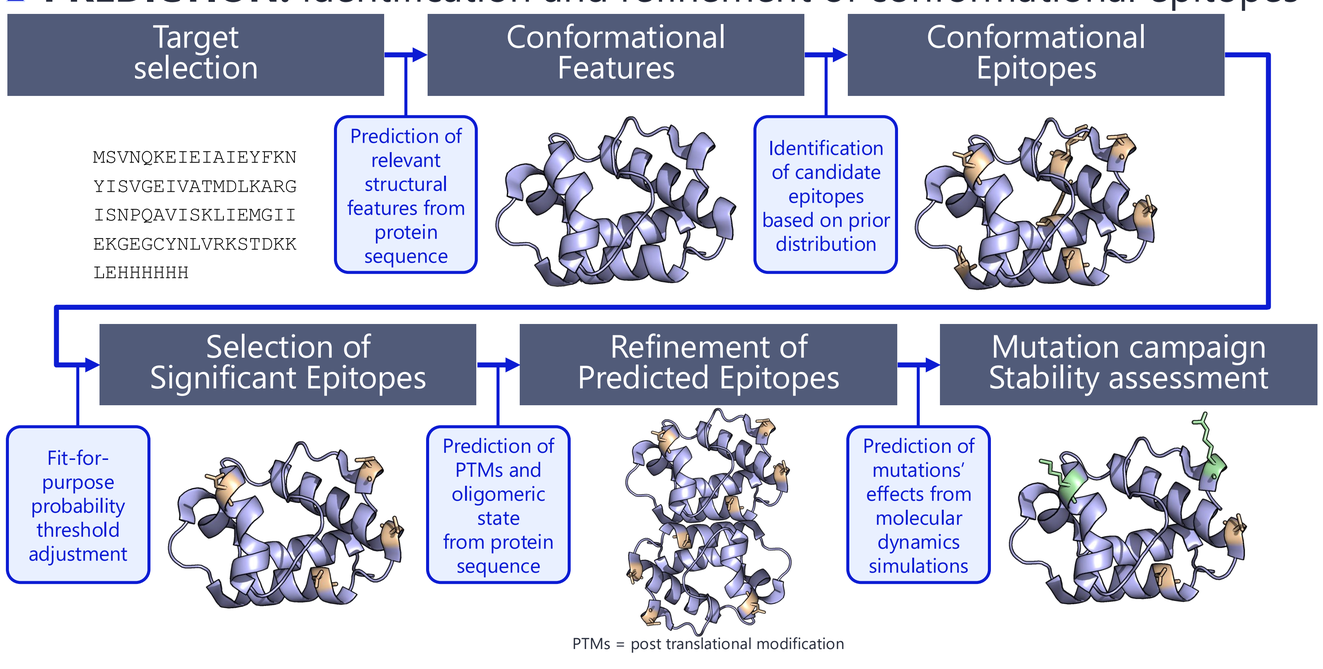
To accurately **predict B cell epitopes** of relevance using state-of-the-art technologies, therefore accelerating the **drug development** for challenging diseases areas and indications, and enabling various treatment modalities e.g. monoclonal antibodies, antibody-drug conjugates and more [6].

## OUR PLATFORM

**TRAINING:** identification of sequence pattern and single epitopes



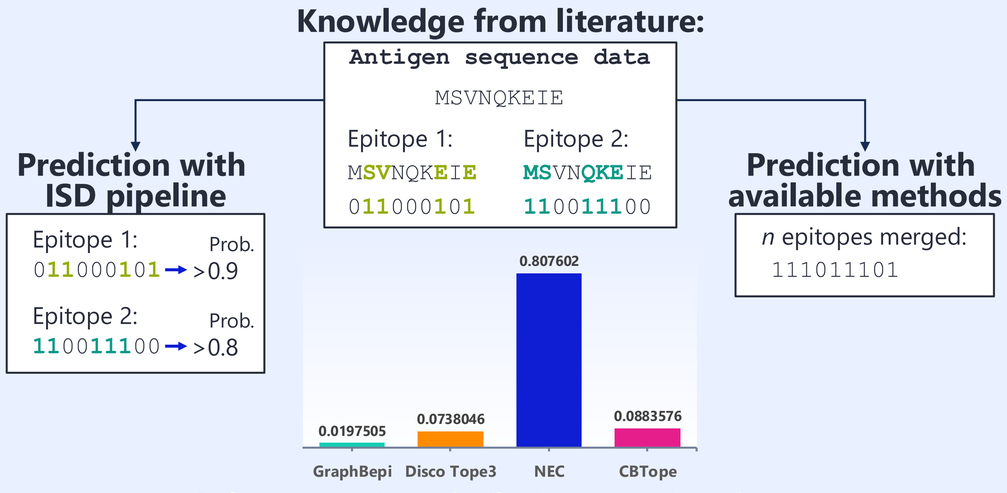

**PREDICTION:** identification and refinement of conformational epitopes




## ADVANTAGES

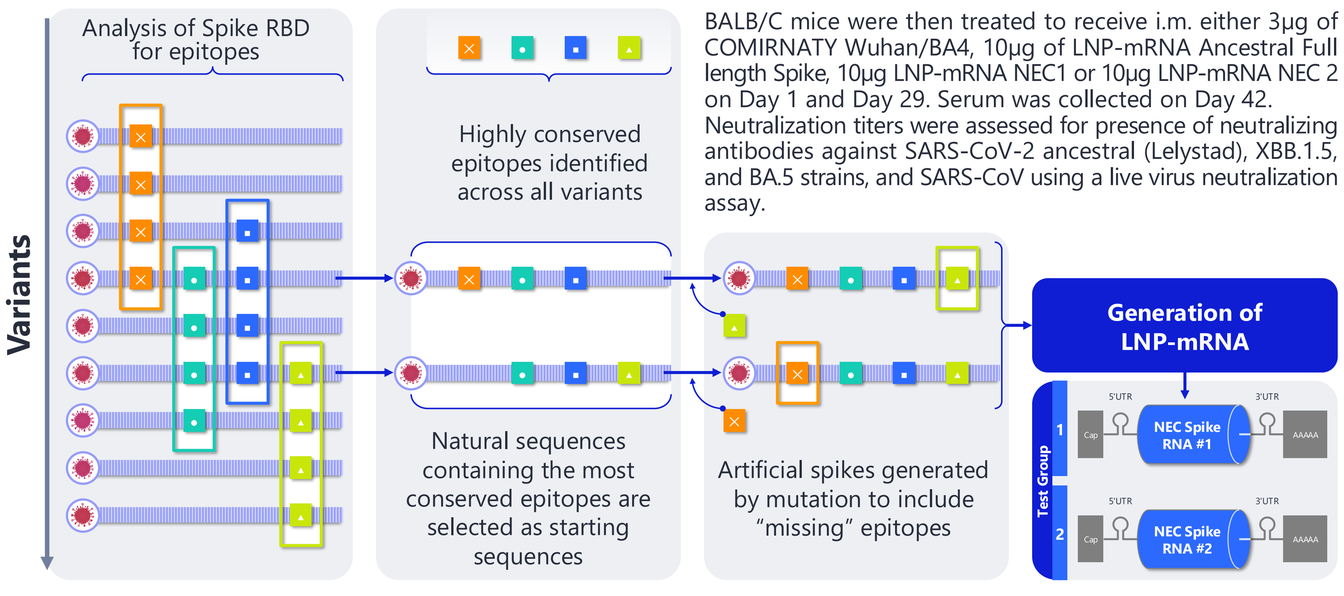
1. Use of state-of-art neural network .
2. Identification of separated epitopes.
3. No need for 3D structures of proteins.
4. Accurate conformational epitope predictions.
5. Broad application across therapeutic areas.
   - **Epitope-specific vaccines.** E.g. peptide-based, subunit-based, virus-like particles, mRNA or DNA-based, conjugate vaccines.
   - **Engineering epitope-specific antibodies.** E.g. neutralizing, tumor-specific, anti-toxin, autoimmune diseases antibodies.
   - **Mutation campaign on specific epitopes.** E.g. to gain broader protection.

## BENCHMARK COMPARISON




*Performance on epitopes identification on a proprietary dataset.*

## APPLICATION: novel SARS-CoV-2 vaccines




BALB/C mice were then treated to receive i.m. either 3µg of COMIRNATY Wuhan/BA4, 10µg of LNP-mRNA Ancestral Full length Spike, 10µg LNP-mRNA NEC1 or 10µg LNP-mRNA NEC 2 on Day 1 and Day 29. Serum was collected on Day 42. Neutralization titers were assessed for presence of neutralizing antibodies against SARS-CoV-2 ancestral (Lelystad), XBB.1.5, and BA.5 strains, and SARS-CoV using a live virus neutralization assay.

- ✓ Top level neutralization
- ≤ Neutralization lower than Top Performer
- ✗ Comparable to negative control (GFP-mRNA)

| Vaccine treatment | Neutralization assay: Ancestral | BA.5 Omicron | XBB.1.5 Omicron | SARS-Cov-1 |
|---|---|---|---|---|
| Commercial Gen 2 vaccine | ✓ | ✓ | ≤ | ✗ |
| Ancestral Spike RNA | ✓ | ✗ | ✗ | ✗ |
| NEC Spike RNA #1 | ✓ | ✓ | ✓ | ✓ |
| NEC Spike RNA #2 | ✓ | ✓ | ✓ | ✓ |

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**References**
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[5] G. Cia et al. Brief Bioinform. (2023). [6] I. Vardaxis et al. Comput Struct Biotechnol J. (2024)

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