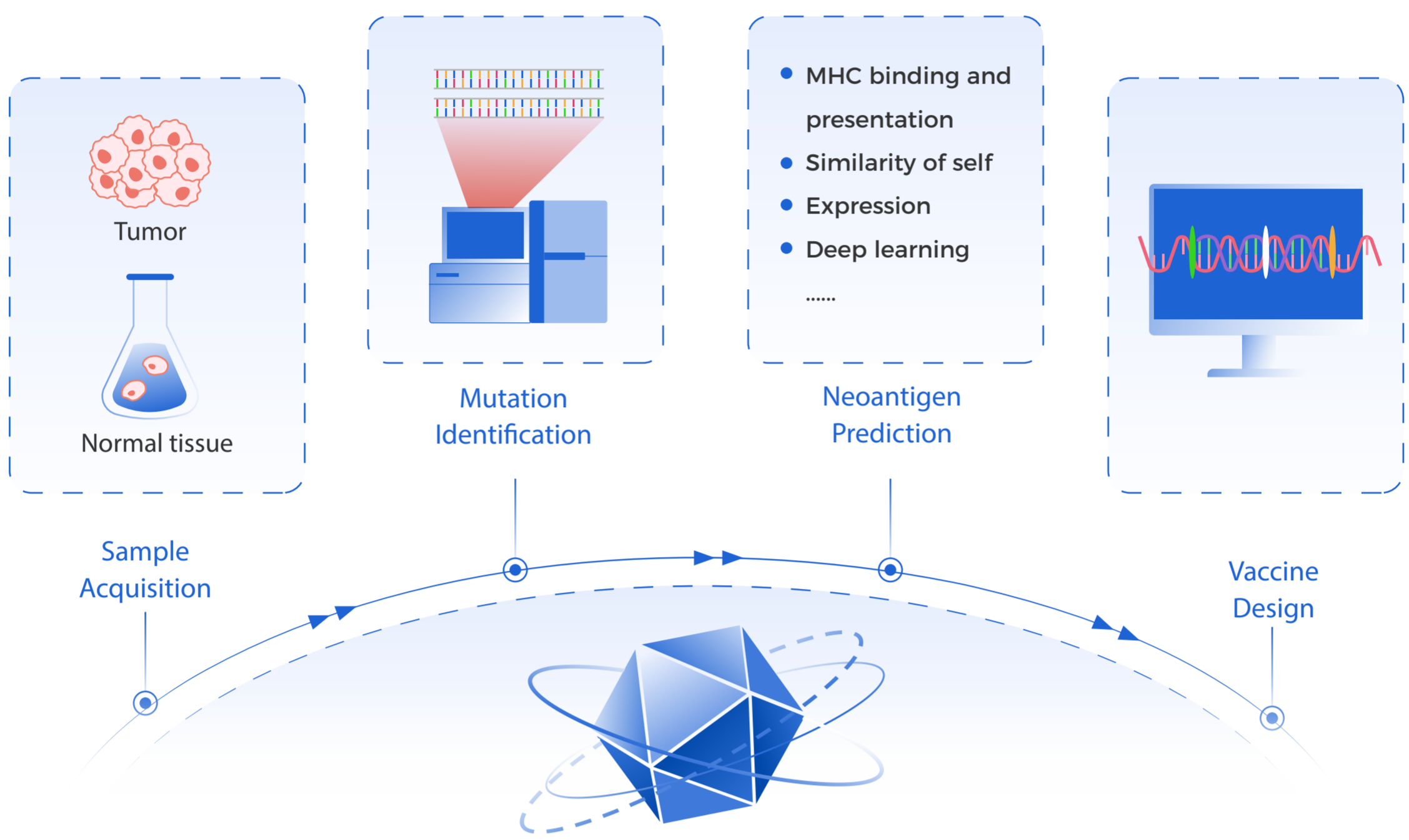


Personalized Cancer Vaccines Neoantigen Discovery

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Design Individualized Neoantigen Vaccine

- Next-generation sequencing of healthy tissue and tumor biopsy samples are conducted.
- The tumor and normal DNA sequencing data are compared to identify tumor-specific mutations.
- Mutations are prioritized as vaccine candidates on the basis on their potential to elicit T-cell responses by computational approaches including major histocompatibility complex (MHC) binding prediction, quantification of mutant transcript expression, and other features.
- Design individualized and multi-specific neoantigen vaccines using the selected vaccine platform.



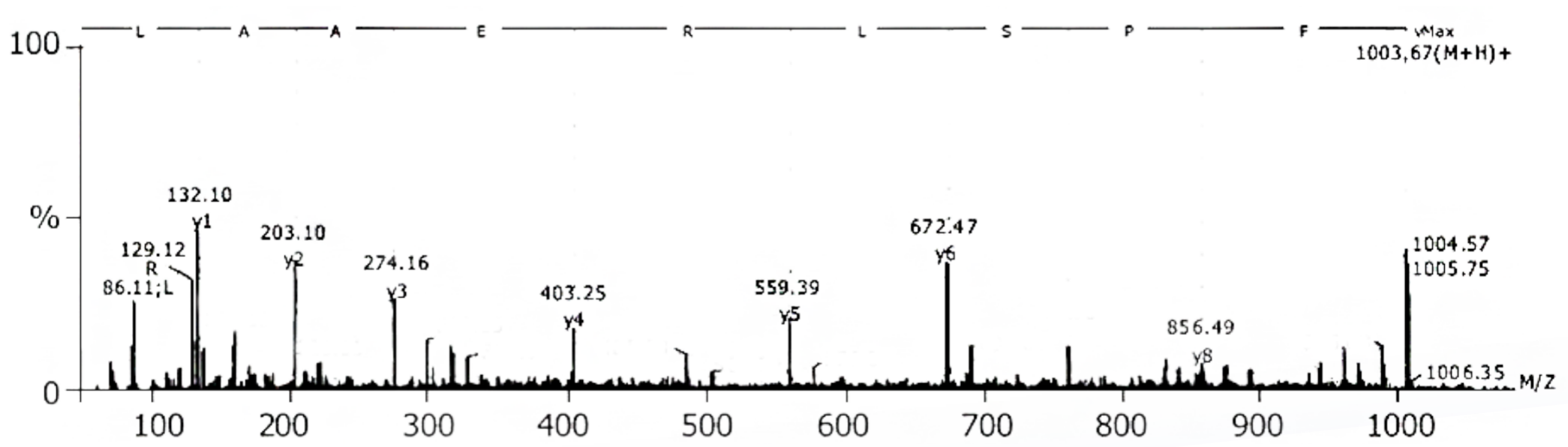
Neoantigen Prediction

MHC binding prediction data

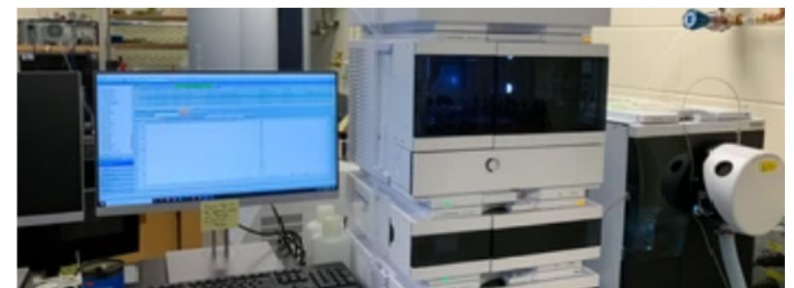
| Allele | Peptide Length | Sequence | IC ₅₀ (nM) |
|------------|----------------|-----------|-----------------------|
| HLA A*0201 | 9 | MGQIVTMFE | 24531.2 |
| HLA A*0201 | 9 | GQIVTMFEA | 398.0 |
| HLA A*0201 | 9 | QIVTMFEAL | 7456.9 |
| HLA A*0201 | 9 | IVTMFEALP | 24129.3 |
| HLA A*0201 | 9 | VTMFEALPH | 23998.4 |
| HLA A*0201 | 9 | TMFEALPHI | 9.6 |
| HLA A*0201 | 9 | MFEALPHII | 19645.1 |

*A lower number (IC₅₀) indicates higher affinity

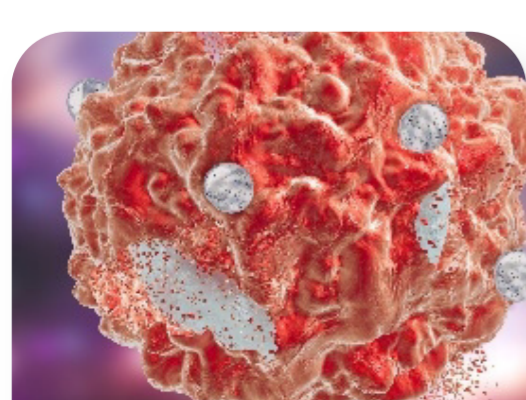
Mass Spectrometry (MS) Analysis for Neoantigen Discovery



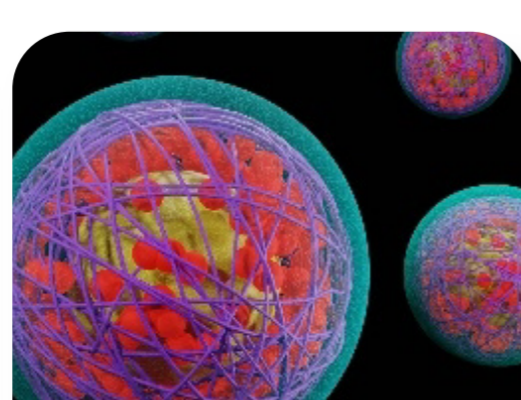
Mass spectrometry analysis of tumor immune peptides can be used to identify mutant MHC-binding neoantigen ligands



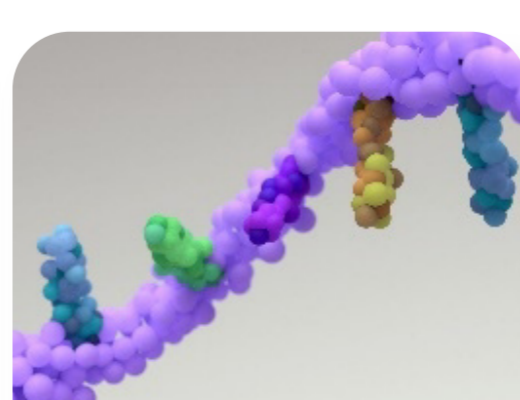
Personalized Cancer Vaccines-related Services



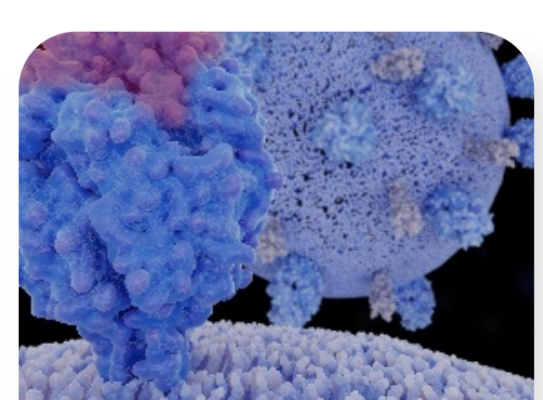
Tumor Antigens
in Silico Prediction



Cancer Vaccine
Delivery Systems



Nucleic Acid-based
Cancer Vaccine



Antigen Peptide
Cancer Vaccine