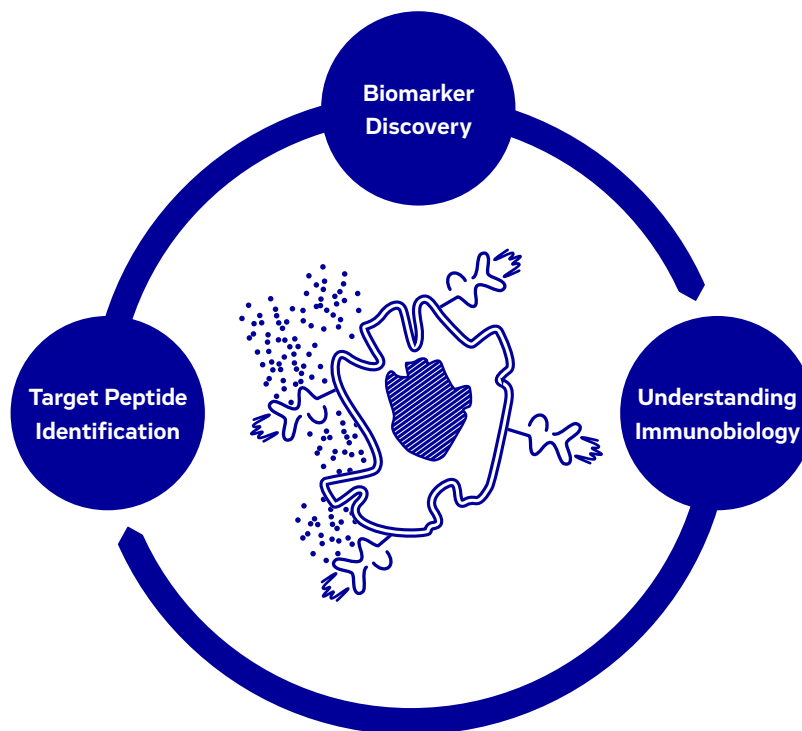

Deciphering the immunopeptidome for neoantigen identification

- ▶ Identification of naturally presented HLA class I- and II-bound peptides from cancerous cells and tissues is crucial to leverage the development of immunology-based therapies
- ▶ Underlying therapeutic principles can be harnessed to fight infectious diseases
- ▶ Evotec's immunopeptidomics platform enables the unbiased identification of novel immunotherapeutic targets
- ▶ Identification of diagnostic and monitoring biomarker signatures in normal and altered cells from cohort studies
- ▶ Supports biological insight into the connection between T cells and MHC-presenting cells





- ▶ Evotec's highly optimised experimental strategy in combination with its industry-leading capabilities in high-end quantitative mass spectrometry reaches highest sensitivity required to distinguish disease-specific (neo)antigens from normally presented peptides
- ▶ Integrating whole exome sequencing and/or transcriptomics data will power neoepitope discovery
- ▶ Advanced statistics and bioinformatics for systems-wide data analysis and in-depth data interpretation facilitates peptide prioritisation
- ▶ Identification of up to a thousand peptides per sample
- ▶ Direct detection of presented peptides in contrast to approaches solely based on computation-intensive *in silico* predictions
- ▶ Validation and highly accurate quantification of individual peptides through targeted mass spectrometry (PRM-MS)

