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 immunoncology-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
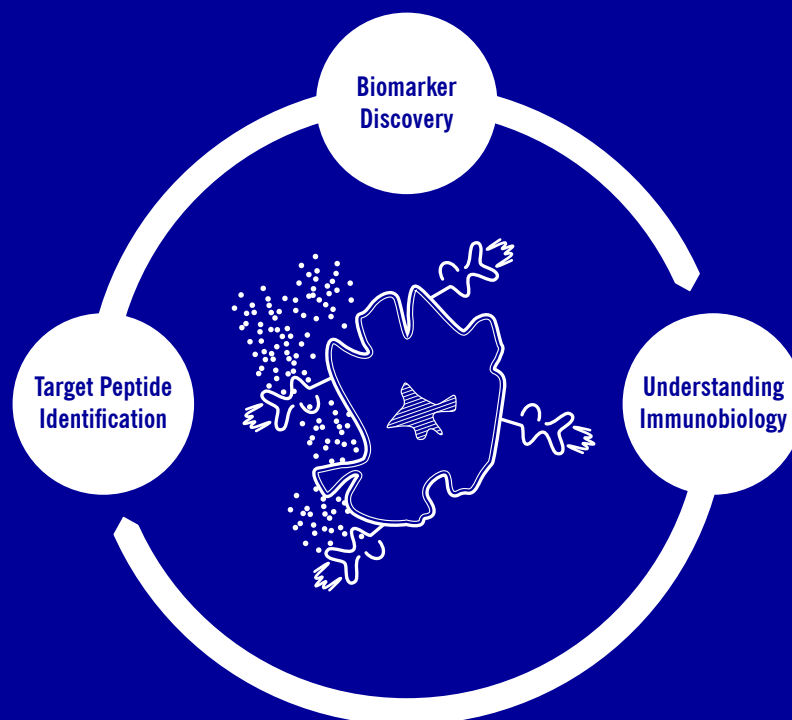
▸ Evotec's highly optimised experimental strategy in combination with its industry-leading capabilities in high-end quantitative mass spectrometry reaches highest sensitivity required to distinguish disease-specific (neo)antigens from normally presented peptides

▸ Integrating whole exome sequencing and/or transciptomics 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)

Cancer tissue

Matched healthy tissue

Purification and enrichment of HLA class I- and class II-bound peptides

LC-MS/MS analysis

Identification tumor specific mutations and sequence variants (WES/transcriptomics) and their transcription (transcriptomics)

Sample tailored sequence database to process MS raw files with MaxQuant including cancer mutational events

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  1 MERRRLWGSI QSRYISMSVW TSPRRLVELA GQSLLKDEAL AIAALELLPR ELFPPLFMAA
 61 FDGRHSQTLK AMVQAWPFTC LPLGVLMKGQ HLHLETFKAV LDGLDVLLAQ EVRPRRWKLQ
121 VLDLRKNSHQ DFWTVWSGNR ASLYSFPEPE AAQPMTKKRK VDGLSTEAEQ PFIPVEVLVD
181 LFLKEGACDE LFSYLIEKVK RKKNVLRLCC KKLKIFAMPM QDIKMILKMV QLDSIEDLEV
241 TCTWKLPTLA KFSPYLGQMI NLRRLLLSHI HASSYISPEK EEQYIAQFTS QFLSLQCLQA
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▸ QC (Length distribution, affinity predictions)
▸ Identification of presented tumor-specific and tumor-associated antigens
▸ Differential presentation analysis in comparison with healthy or adjacent tissue
▸ Antigen priorization