OncoPept*VAC*™

Identify prioritized neo-antigens and neo-epitopes quickly

OncoPept*VAC*™ is an end-to-end genomics platform delivering prioritized T-cell neo-epitopes that can be used as DNA or peptide vaccines for cancer immunotherapy

Highlights

- Time saving – generates a short and comprehensive list of tumor-specific mutant peptides for your vaccine program
- State-of-the-art prediction of HLA-types, antigen processing and MHC-peptide binding
- Proprietary strategy to select the most-relevant candidate neo-antigens for validation

Key Benefits

DNA/Peptide Vaccine composition

Benefits	Features
Identify cancer variants with high specificity and sensitivity	• Robust NGS platform with optimized variant calling pipeline
Identify cancer mutations that are potentially HLA-binding	• Sensitive HLA typing and HLA expression analysis • Accurate mapping of expressed variants • Proprietary neo-epitope selection with multiple prioritization steps • Greater than 2-log reduction in the number of prioritized peptides
Identify cancer mutations that are potentially T-cell binding	• Automatic identification of TCR-binding mutations based on the position of the amino acid within the peptide • Utilizes the chemical structure of the amino acids to predict rules of TCR binding

DNA/Peptide Vaccine structure
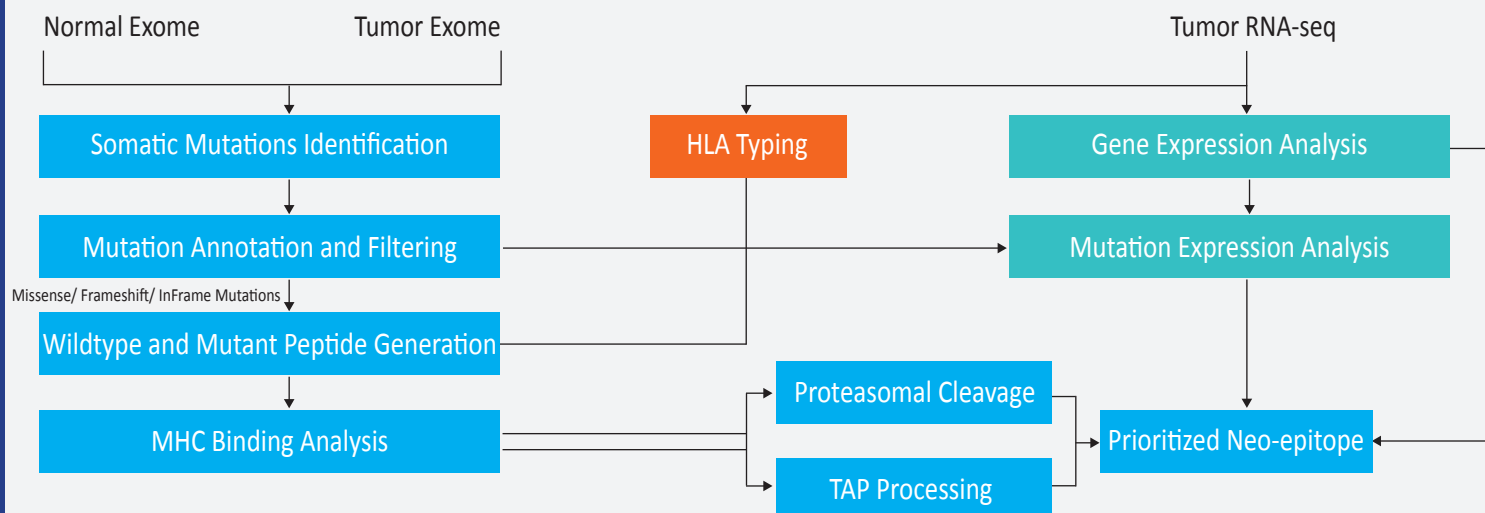
Create optimum length of the peptide or DNA vaccine	• Generates peptide of optimum length to preserve the position of the mutant amino acid at the HLA-binding or TCR-binding sites
Ensure the peptide/DNA vaccines are processed correctly to produce HLA-binding neo-epitope	• Creates the sequence of the peptide/DNA with optimum proteasomal/ immunoproteasomal processing sites to ensure generation of core HLA binding peptide

DNA/Peptide Vaccine validation

Assay to determine efficient presentation of peptides by antigen presenting cells, such as dendritic cells*	• Generates peptide of optimum length to preserve the position of the mutant amino acid at the HLA-binding or TCR-binding sites
Ensures that the predicted peptide can activate T-cells*	• T-cell activation assay using patient-derived T-cells, dendritic cells and exogenously added peptides

Workflow

Normal Exome   Tumor Exome   Tumor RNA-seq

| Somatic Mutations Identification | HLA Typing | Gene Expression Analysis |

| Mutation Annotation and Filtering | | Mutation Expression Analysis |

Missense/ Frameshift/ InFrame Mutations

| Wildtype and Mutant Peptide Generation |

| Proteasomal Cleavage |

| MHC Binding Analysis | | Prioritized Neo-epitope |

| TAP Processing |

Key Deliverables

- ✓ Exome Sequence – somatic variant identification
- ✓ RNA sequence – variant expression
- ✓ HLA typing
- ✓ Vaccine candidates
- ✓ All data files

Key Metrics

Sequencing Method	• Illumina Hi-Seq Platform
Bioinformatics	• Both Proprietary and Public tools
Depth	• DNA (150X); RNA (60-80 million reads)
Turn Around Time	• 4 weeks (Rapid TAT available at additional cost)
Sample Requirements	• Tumor only or tumor with matched normal
Sample Types	• Frozen tumor, FFPE, Blood
DNA Input Required	• 1µg-4µg
RNA Input Required	• 300ng-1µg
Blood Required	• 2-5 million blood cells
FFPE Required	• 3 X10 micron slides
Frozen tumor Required	• 300µg – 1mg

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