



AB045. P016. Profile of neoepitopes on human pancreas tumor tissue by proteomics

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Abstract: Mutated peptide ligands could be attractive targets for cancer immunotherapy. For direct identification of clinically relevant neoepitopes, we have surveyed the pancreatic cancer-associated immunopeptidome by using advanced mass spectrometry (MS) analysis. Peptides are biochemically purified from human leucocyte antigens (HLA) class I and II binding peptides from pancreas

tumors followed by sample clean using C18 columns. The purified peptides were analyzed by Q Exactive plus hybrid quadrupole-Orbitrap mass spectrometer, followed by bioinformatics analysis. Totally, we identified novel 34,247 peptide sequences from HLA class I binding peptides. The distribution of peptide length showed that 9-amino acid (AA) are the most abundant, followed by 10-AA and 8-AA, with a frequency of 3,580, 2,463, and 2,368 respectively. We will do genomic sequencing to verify the proteomic profile of these neoepitopes.

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