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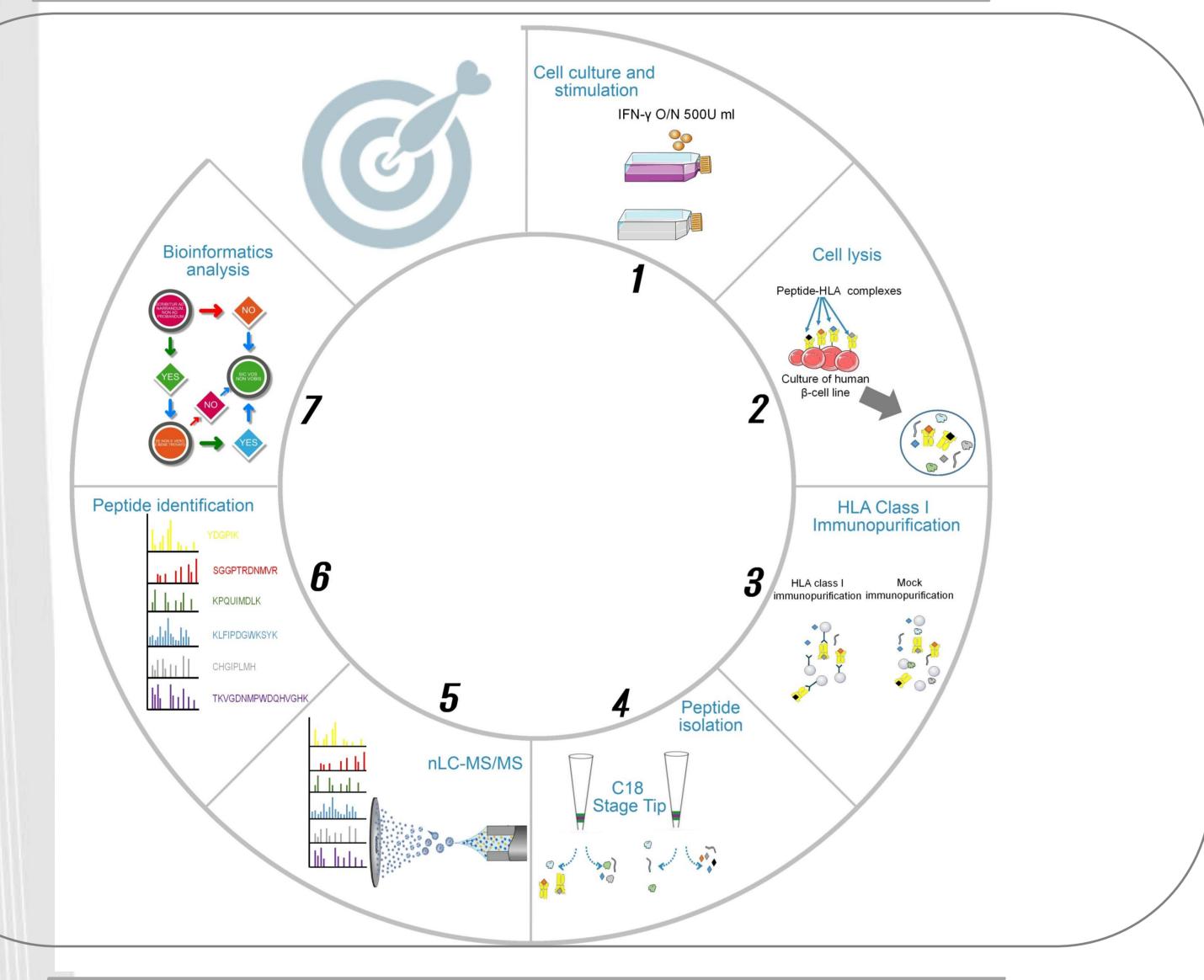
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1. Introduction

Type 1 diabetes (T1D) is an autoimmune disease in which autoreactive CD8+ T cells destroy pancreatic β cells. This destruction is triggered by the recognition of peptide fragments (epitopes), which are derived from protein antigens and presented at the β -cell surface in the pocket of HLA class I molecules.

We aimed at identifying these peptides by HLA peptidomics. This strategy consists in purifying the peptide-HLA complexes from β cells and to analyze the eluted peptides by mass spectrometry.

2. Material and methods



4. Conclusions

HLA peptidomics identified preproinsulin sequences already described as major CD8+ T-cell epitopes, thus directly validating our approach.

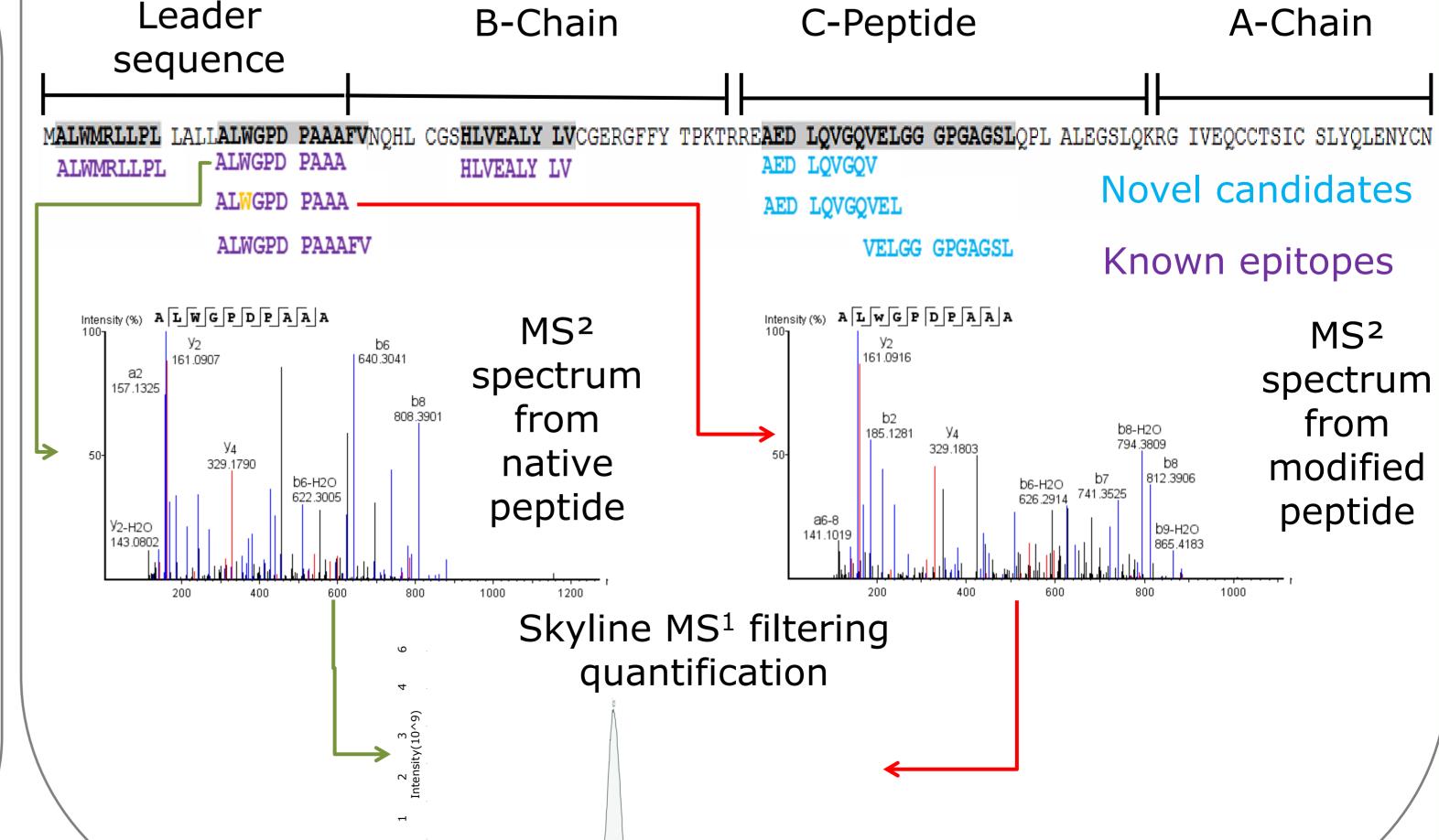
Some of these peptides are post-translationally modified and could thus behave as neo-antigens.

Major T1D associated CD8+ T cell epitope PPI_{15-24} (ALWGPDPAAA) has been identified, both under unmodified and modified (trp->Kynurenin) forms.

95 additional candidate epitopes derived from 52 unique proteins are under study.

3. Bioinformatic pipeline and results Number of peptides N=4,908PEAKS MAXQUANT MASCOT SEQUEST Technical N=1,302 ← reproducibility YES N = 3,606Biological reproducibility YES N=3,606 Biological replicate 1 Algorithm N=1,266 ← concordance YES N=2,340Peptide Length 9 > = N < = 12YES N=2,093Peptide length (aminoacids) Sample Mock HLA-specific YES | N=1,751 |Log2 of normalized AUC Protein-tissue network visualization Non-ubiquitous N=1,546 NO YES N = 205Pancreas PTM expression variants N = 38N = 64

102 peptides identified, 16 are derived from preproinsulin including 9 post-translationally modified variants



Acknowledgments