# SpotMix™ Peptide Pools: a New Approach for Rapid Antigen Target Identification

M. Eckey, T. A. Teck, P. Holenya, J. Zerweck, N. Kolls, T. Knaute, U. Reimer, H. Wenschuh, F. Kern JPT Peptide Technologies GmbH, Berlin, Germany

\* Correspondence should be addressed to peptide@jpt.com

### Introduction

Enhancing specific immune responsiveness by vaccination is a promising therapeutic approach to infectious diseases and cancer. Its success, however, depends on the identification of suitable target antigens and epitopes. Stimulation with intact proteins or whole protein-spanning, overlapping peptide pools (PepMix<sup>TM</sup>) has been successfully used for that purpose. However, this approach comes with a significant effort in terms of time, labor and cost, in particular if many potential candidate proteins have to be analyzed.

Based on a method for the highly parallel synthesis of multiple peptides in low quantities, we developed a novel protocol which permits the production of equimolar pools of SPOT peptides the so called SpotMix<sup>TM</sup> peptide pools.

Here, we show examples comparing classic PepMix<sup>™</sup> peptide pools and SpotMix<sup>™</sup> peptide pools in T-cell stimulation assays like ELISpot and flow cytometry/intracellular cytokine staining (ICS).

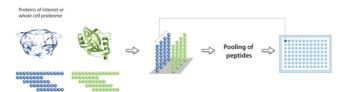


Figure 1: Peptide Pool concept. Overlapping 15-mer peptides covering the whole length of the protein of interest can be used for different functional T-cell assays like ELISpot and ICS.

### Methods

**PepMix™** peptide pools are manufactured using classical solid phase peptide synthesis on polystyrene resins. Peptides purification is performed by RP-HPLC. Purity is determined by HPLC-MS analysis.

SpotMix™ peptide pools: Synthesis is performed via fully automated SPOT-synthesis approach. Peptides are cleaved into Microtiter-plate wells, analyzed and quantified by LCMS and spin dried. Subsequently, the peptides are pooled and aliquoted.

 $\textbf{SpotMix}^{\textbf{TM}}$  **PLUS** are synthesized the same way with 100% quality controls (see also Table 1).

For this study the following proteins were produced as PepMix<sup>™</sup> peptide pools and SpotMix<sup>™</sup> PLUS peptide pools : UL83, UL55, EBNA1, EBNA3, BZLF1.

**Ex-vivo ELISpot:** Cryopreserved PBMCs were thawed and rested overnight Subsequently 2-3  $\times 10^5$  cells were either left untreated or stimulated with peptides for 16-20h. Each stimulant was tested in triplicates. The secretion of IFNy was detected using ALP coupled antibody and BCIP/NBT as substrate. Developed ELISpot plates were scanned using AID iSpot reader and analyzed with corresponding software.

FACS/ICS: Cryopreserved PBMCs were thawed and rested overnight . 2x10<sup>5</sup> cells were either left untreated or stimulated with peptides for 16h in the presence of Brefeldin A to inhibit cytokine secretion. After permeabilization and fixation, the cells were stained with fluorochrome-coupled antibodies against CD3, CD4, CD8 and IFNγ. Flow cytometry was performed on a BD accuri C6 and data analyzed with FlowJo X software.

Table 1 Comparative overview defining the different peptide pool approaches

	_		
	SpotMix <sup>™</sup>	SpotMix™ PLUS	PepMix™
Amount/Peptide	Varying (approx.5-20 μg)	10 μg /peptide (each peptide quantified)	From 1mg/peptide (each peptide quantified)
Peptide Purity	No purification	Purified by dialysis, if > 20 peptides/pool	Unpurified or purified by HPLC up to GxP grade
Peptide QC	5% peptides analyzed by LC-MS	100% peptides analyzed by LC-MS	100% peptide analyszed by LC-MS
Pool QC	None	none	Full QC for each peptide pool
Applications	Antigen discovery	Neo-epitope based immune monitoring, Antigen discovery	Clinical immune monitoring, preclinical & clinical research, immunotherapy

## Results

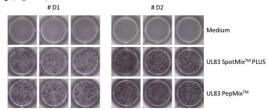


Figure 2: Ex-vivo ELISpot data. Exemplary wells of stimulation of donor #1 and #2 are shown

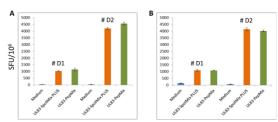


Figure 3: Comparison of two independent SpotMix<sup>™</sup> PLUS synthesis. A and B present quantified data obtained using two different Lots of UL83 SpotMix<sup>™</sup> PLUS in ELISpot experiments. Shown are mean values of triplicates (and standard deviation) presented as spot forming units (SFU) per Million cells.

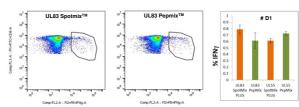


Figure 4: Comparative ICS. Left side: Exemplary ICS data with quantification of IFNγ positive cells (of cytotoxic T-lymphocytes) is depicted. The bar plots on the right side represent the mean values of duplicates and standard deviation minus background.

To obtain a broader view of the SpotMix<sup>™</sup> PLUS performance, we screened healthy donors for different Epstein-Barr Virus (EBV) antigens and compared the data to standard PepMixes<sup>™</sup> (Figure 5).

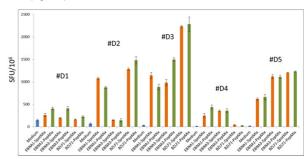


Figure 5: Screening of 5 donors for T-cell responses against 3 EBV antigens using ex-vivo ELISpot. Shown are the results comparing SpotMixes™ PLUS versus PepMixes™. Bars represent mean values of triplicates (and standard deviation) expressed as spot forming units (SFU) per Million cells.

# Summary

Comparisons between T-cell stimulation assays performed with the classic PepMix™ peptide pools and SpotMix™ PLUS pools demonstrate equivalence of these preparations. We envisage that these novel pools will significantly facilitate T-cell protein target discovery by permitting the synthesis of protein-spanning, overlapping peptide pools for many potential target antigens in parallel.