

Introduction

PepSlide® software provides peptide array users with easy-to-use tools to save their time and manual work, as well as to make their discovery more easily. It supports the whole process from design to printing and to analysis of peptide arrays.

The software is natively supported on Windows and Mac OS X. It is available with flexible and attractive pricing models. The 14-day trial version with full functionality and support is free. You can easily request a free trial by means of the product website [1].

Peptide Array Design

The design tool - PepSlide® Designer - facilitates generation and layout of peptide libraries on microarray formats. It provides interactive tools for generating three types of peptide libraries:

- **Substitution:** Alternatives of a peptide generated by substituting residues at specified positions with desired amino acids.
- **Overlapping:** Overlapping peptides translated from a protein.
- **Random:** Peptides generated stochastically.

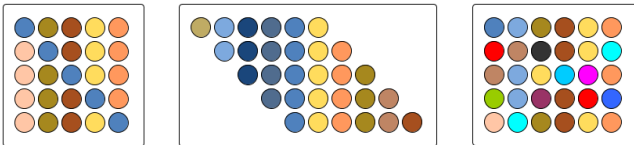


Fig. 1: Peptide Library Generation Tools.

The graphical array editor enables flexible layout of peptide libraries and controls on microarray formats. You can then use array design files, saved in PSF format, to print and to analyze the peptide arrays.

Peptide Array Data Analysis

The analysis tool - PepSlide® Analyzer - supports microarray image analysis and quantification of microarray data. This includes automatic batch processing of multiple microarray images.

In addition, you can benefit from analyses that directly support peptide array applications such as epitope mapping, biomarker discovery, and characterization or optimization of peptides.

Microarray Image Analysis

PepSlide® Analyzer supports TIFF images and array files of PSF or GAL format. It provides a comprehensive set of image processing and array rotation tools. Background correction is handled automatically with local methods or more finely with background controls.

Two spot finding methods are available for data quantification (Fig. 2): *Fixed-Spot* quantifies the spots according to their layout in the array file, while *Flex-Spot* can flexibly and precisely detect the spots' signal.

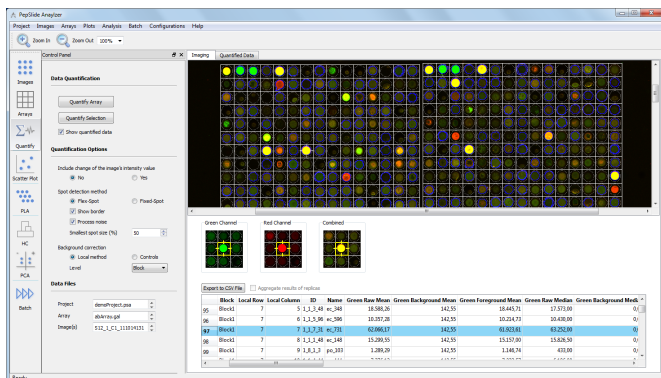


Fig. 2: Microarray Image Analysis & Data Quantification.

Automatic alignment of the array, or grids, with the image is supported. You can setup a batch for quantifying a large number of microarray images. The batch results can be used directly with data mining tools.

Peptide Library Analysis

PepSlide® Analyzer facilitates analysis of peptide libraries. If e.g. a target protein or antigen is translated into overlapping peptides for epitope mapping, the software can suggest a grouped list of peptides which represent an epitope of a serum sample (Fig. 3).

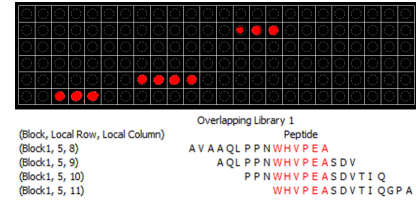


Fig. 3: Epitope Mapping Support.

Fig. 4 shows variants of the peptide NYGKY and their "response". Here, the (P)-axis lists residues of the peptide and the (S)-axis contains 20 amino acids for substituting, thus a "point" in the (PS)-plane features a variant whose response is represented in terms of the bar height. This tool enables convenient examination of variants and peptide optimization.

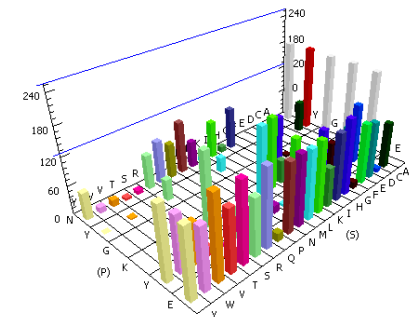


Fig. 4: Peptide Characterization & Optimization Support.

Biomarker Discovery Support

The following data mining tools, in combination with peptide library analysis tools, assist you to identify biomarkers.

- **Principal Component Analysis:** to discover peptides and samples that influence the microarray study, and
- **Hierarchical Clustering Analysis** (Fig. 5): to find their relationship.

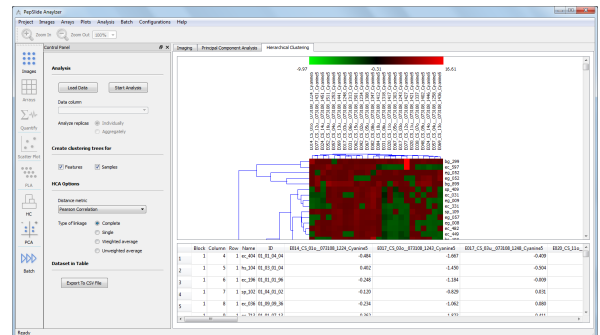


Fig. 5: Hierarchical Clustering Analysis.

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[1] PepSlide®. Peptide Array Design and Analysis Software. www.sicasy.de/pepslide/