Prospector™ Custom Peptide Libraries

Prospector™ custom peptide libraries allow the rapid screening of many peptides for bioreactivity. Overlapping peptide libraries can be used to investigate immune responses in detail and provide an opportunity to screen the immunological responsiveness of every optimal-length epitope in a given protein. They can be applied in a number of immunological assays including ELISPOT and ELISA. Additionally, by generating a peptide library to test variations of the most common version of a particular epitope, it is possible to determine how specific amino acid mutations affect T and B cell or substrate recognition.

To meet the huge demand generated by the large number of applications for peptide libraries, we have significantly increased our peptide library product range:

Prospector™ Peptide Library Product Range

Code	Description	Purity	Quantity	QC	Estimated Dispatch
PP97	Prospector™ Pure97	>97%	>1 mg	100% LC-MS	Enquire
PP95	Prospector™ Pure95	>95%	>1 mg	100% LC-MS	3-4 weeks <200
PP90	Prospector™ Pure90	>90%	>1 mg	100% LC-MS	3-4 weeks <200
PP80	Prospector™ Pure80	>80%	>1 mg	100% LC-MS	3-4 weeks <500
PP70	Prospector™ Pure70	>70%	1-5 mg	100% LC-MS	3-4 weeks <500
PPLC	Prospector™ LCMS	Crude	1-5 mg	100% LC-MS	2-3 weeks <500
P0L	Prospector PEPscreen®	Crude	0.5-2 mg	100% MS or 100% LC-MS	2-3 weeks <500
PPLX	Prospector™ Lightning-X Peptides with C-terminal amino acid of choice	Crude	50-100 nmol	5% LC-MS	2-3 weeks <10,000
PPLG	Prospector™ Lightning-G Peptides with C-term. Gly	Crude	50-100 nmol	5% LC-MS	2-3 weeks <10,000

Prospector™ Pure

Our Prospector™ Pure purified peptide libraries deliver on the most exacting requirements and at prices that help you break new ground on research driven by synthetic peptides. Unlike the synthesis of individual purified peptides, these libraries are made using a parallel synthesis platform that guarantees minimal product variance, and delivery is in an easy to handle tube-array format. Our high throughput purification combined with 100% LC-MS analysis ensures that you do not have to lose critical path time on your projects just because you need to work with purified and fully analyzed peptides. Our technology also has the flexibility to meet multiple design parameters, such as N- and C-terminal modifications and non-standard amino acids.

Prospector™

Prospector™ libraries deliver highly attractive prices and exacting 100% LC-MS quality control (QC). Though these libraries are not purified, they are synthesized using the same reliable platform as our purified products and the resulting peptides have high average purity. For example, for Prospector PEPscreen®, the average purity of 10mers is ~86% and the average purity of 15mers is ~73%. The features of Prospector™ make it an ideal product for epitope discovery applications, giving you the comfort of comprehensive QC so you know absolutely what you are working with.

Unlike some commercial peptide libraries available, Prospector™ has no hidden set-up charges. A single price is charged per peptide, and the order size starts at only 24 or 48 peptides. Prospector PEPscreen®: Custom Peptide Libraries accommodate peptides from 6-20 amino acids; information in the table below about all other Prospector™ libraries is based on peptides from 7 to 15 amino acids; peptides up to 40 amino acids in length can be made using the technology platform, but quantities and dispatch times will vary, depending on the specification.

Dr. Vesna Blazevic, FIT Biotech, Finland "ProImmune's PEPscreen®: Custom Peptide Library has played a central role in my research into DNA based and HIV vaccines in both IFNγ and IL-2 ELISPOT assays. Working in preclinical and clinical settings, I have found the library to be an easy and reliable way of screening for T cell epitopes. The peptides were easy to dissolve, of a very good quality and showed no non-specific background in the ELISPOT assay. My decision to purchase products from ProImmune was based on the fact that they are a good price, of a superior quality and have fast delivery."	Karen Fitzmaurice, Trinity College Dublin, Ireland "Our study aimed to characterize the $CD8^+$ T cell responses associated with certain class I alleles linked to favourable outcomes in HCV infection. We chose a PEPscreen®: Custom Peptide Library of overlapping peptides spanning the HCV genome to use in ELISPOT assays. As well as the fact that the peptide library was of good quality and easy to reconstitute for use in the assays, I also found the price to be competitive and the service I received was excellent.

Technical support from ProImmune's experts

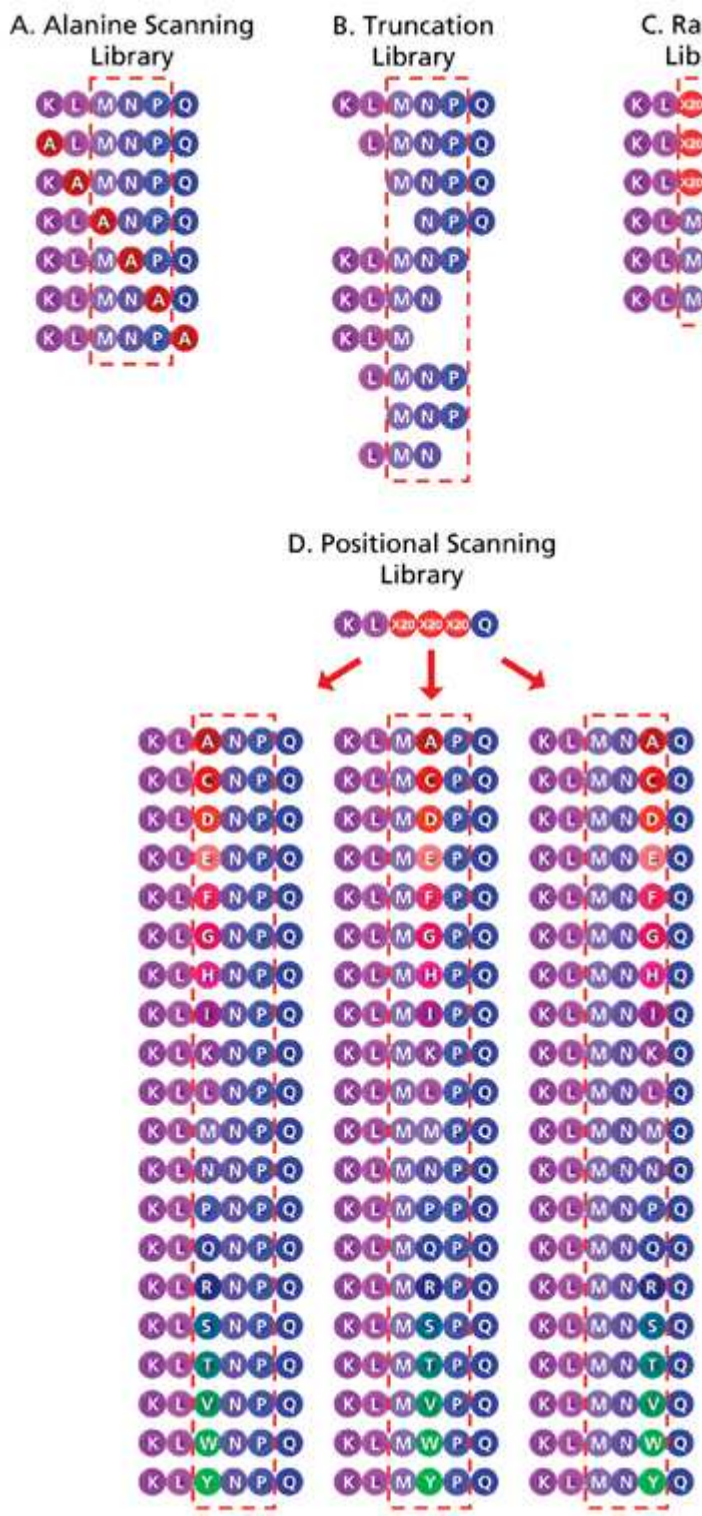
Our technical and applications support team can offer advice on library design, peptide solubilization, experimental set-up, and analysis. Relating to design, we can advise on the best overlap or offset of peptides to be used in your target application, and then using your full-length protein sequence, we can generate the list of peptides for your library. Assistance with experimental set-up and analysis is available for applications such as ELISPOT, ELISA, cell culture, immunization protocols and flow cytometry. Additionally, ProImmune offers outsourcing of cellular analysis services, such as ELISPOT and intracellular cytokine staining. The Prospector™ peptide library technology can be used for a number of different types of library, including overlapping peptide library, alanine scanning library, truncation library, random library and positional scanning library

Overlapping Peptide Library

The overlapping peptide library is most commonly used for linear, continuous epitope mapping, where the aim is to generate a library of overlapping peptide sequences of specific length and specific offset, to cover the entire native protein sequence. Choice of the appropriate peptide length and offset number depends on the application of the peptides and also affects both the cost of the peptide set and the usefulness of the data obtained from the experiment. Examples of design parameters for selected applications are shown in the following table:

Application	Length	Offset
ELISPOT		
$CD4^+$ and $CD8^+$ T cell epitope mapping	15-20	1-5
$CD8^+$ T cell epitope mapping	8-15	1-5
MHC-Peptide Binding Assays		
$CD4^+$ T cell epitope mapping	15	1-3
$CD8^+$ T cell epitope mapping	9-10	1
B cell epitope mapping	15-20	5-10

Epitope identification is followed by studies to demonstrate structure and function relationships of peptide sequences, usually by peptide sequence optimization and structure stabilization. Synthesis of alternative types of peptide library can greatly assist the sequence optimization process. The figure shows a schematic representation of the different strategies in constructing peptide libraries for sequence optimization.



A. Alanine Scanning Library
Alanine is systematically substituted into each amino acid position in the identified epitope. This strategy identifies the amino acids in the native sequence that are essential for activity. Substitution of an essential amino acid results in a reduction in peptide activity, and the degree of reduction in activity is usually taken as a relative measure of the importance of the amino acid being substituted.

B. Truncation Library
This strategy determines the minimum length required for optimum peptide activity by generating a set of peptides with systematic truncation of the flanking residues. If the essential amino acids are known, the direction of truncation can be selected around them, as opposed to systematic truncation from both ends of the peptide sequence.

C. Random Library
Selected residues in the peptide sequence (wobbles) are simultaneously substituted with a mixture of all 20 amino acids, or a mixture of specific amino acids. In practise, this strategy is usually used for preliminary identification of a group of active sequences that can then be re-synthesized to validate the initial results.

D. Positional Scanning Library
A selected position or positions in a peptide sequence are each systematically replaced with different amino acids in order to determine the preferred amino acid residues at these positions, measured by corresponding increases in activity.

Figure 1: Schematic representation of the different strategies in constructing peptide libraries for sequence optimization. The presumed essential positions are enclosed in the dotted box.

Peptide Library Solubilization

Complete solubilization of peptides is important for successful screening of peptide activities. Peptides can be fully active only if they are completely solubilized and are able to assume the correct conformation for binding to their receptors. As the number of peptides in a set increases, so does the potential solubility variation of the peptides within the set. Therefore, in order to obtain accurate and reliable peptide activity data, careful attention should be devoted to the process of dissolving peptide sets.

The strategy for dissolving the PEPscreen® peptide set, and any of the other Prospector™ Libraries, is different from dissolving individual peptides. For individual peptides, conditions are chosen for optimum solubility based on the given peptide sequence. However, for peptide sets, conditions are chosen in an effort to dissolve as many of the peptides in the set as possible in the first solubilization attempt. Suggested common strategies are schematically represented in figure 2.

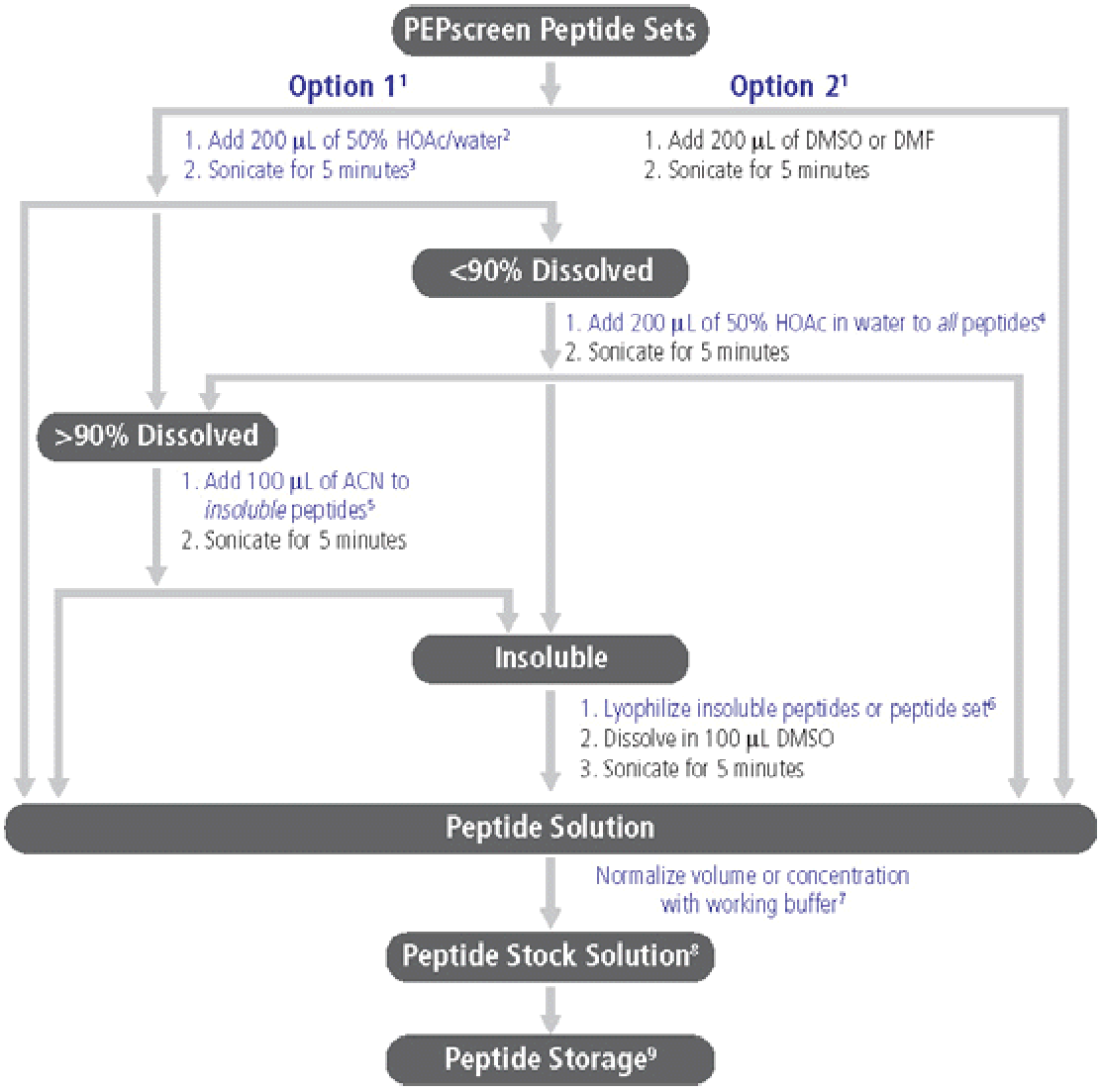


Figure 2: Suggested strategies for peptide library solubilization.

Quality Control

The power of high throughput LC-MS analysis

LC-MS means analysis by combined sequential liquid chromatography and mass spectrometry. Liquid chromatography is used to determine different species in each peptide and what proportion each species has overall. Mass spectrometry determines the molecular mass of a species and indicates by implication the molecular composition of a species. LC-MS quality control determines the mass spec of the major peak found by liquid chromatography. Combining the two methods means that it is possible to determine with certainty that the purified peptide is the species of interest. Prospector™ library peptides that fail quality control will be remade once. If a peptide still does not reach its specification the customer will be contacted to discuss options for re-synthesis.

For the Prospector PEPscreen® product, MALDI-TOF Mass Spectrometry (MS) is performed on 100% of samples. Each peptide must meet both the MS analysis and the final gross weight criteria to pass quality control. For a peptide to pass the MS criterion the desired molecular mass must be one of the three major ions. Peptides that fail quality control by MS will be remade once. Subsequent failed peptides are supplied as part of the order, and are labeled accordingly in the accompanying paperwork, allowing the user to decide whether or not to include the peptide in their studies.

Product Format

Prospector™ Pure, Prospector™ LCMS and Prospector PEPscreen®

Peptides are dried as a thin film at the bottom of individual tubes. This is to prevent the peptide from smearing throughout the inside of the tube during transit, which can make resuspension in small volumes difficult. Tubes are individually capped and arranged in a standard 8 x 12 tube array for compatibility with high throughput assays. This format also allows the flexibility to select only the tubes of interest and rearrange them into a convenient assay format. Each tube is clearly labeled in case the tubes are accidentally mixed.

Prospector™ Lightning

The peptides are dried as a thin film in a 96-well plate, with clear labeling for peptide set identification.

Contact us to request a quotation tailored to your needs:

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ST27 Version 1.2 January 2011