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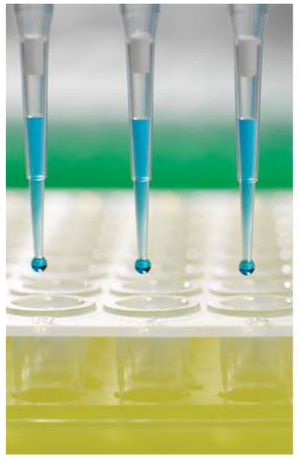
Peptide Libraries



GenScript
The Biology CRO

Your Innovation Partner in Drug Discovery!

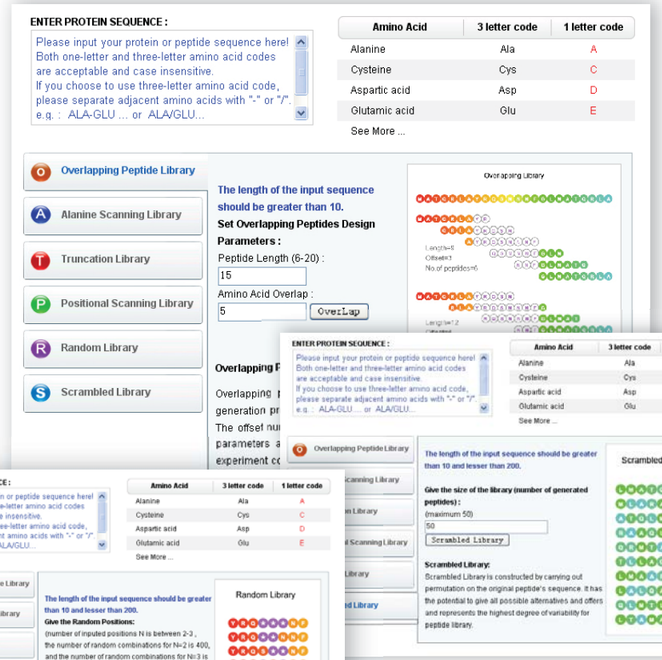
GenScript Peptide Libraries

More choices than an army knife!!

Peptide Libraries

Peptide libraries are commanding assets in the fast-growing field of proteomics and its related subfields including GPCR ligand screening, protein-protein interaction, functional proteome, nucleic acid binding, enzyme substrate and inhibitor screening, antigen and epitope screening, discovery of signal molecules, peptide/protein cross talking, etc. They all have significant contributions to modern drug discovery.

GenScript has developed a rapid high-throughput parallel peptide synthesis platform equipped with six powerful peptide library generation protocols. They can be effectively used in epitope mapping and sequence optimization.

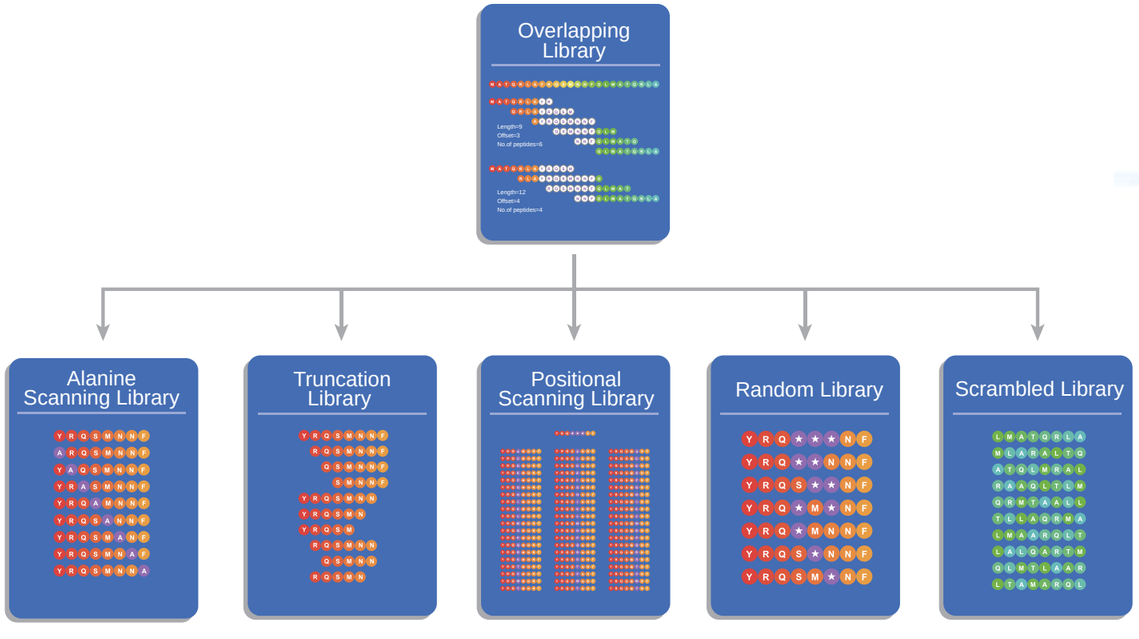


Peptide Screening Tools

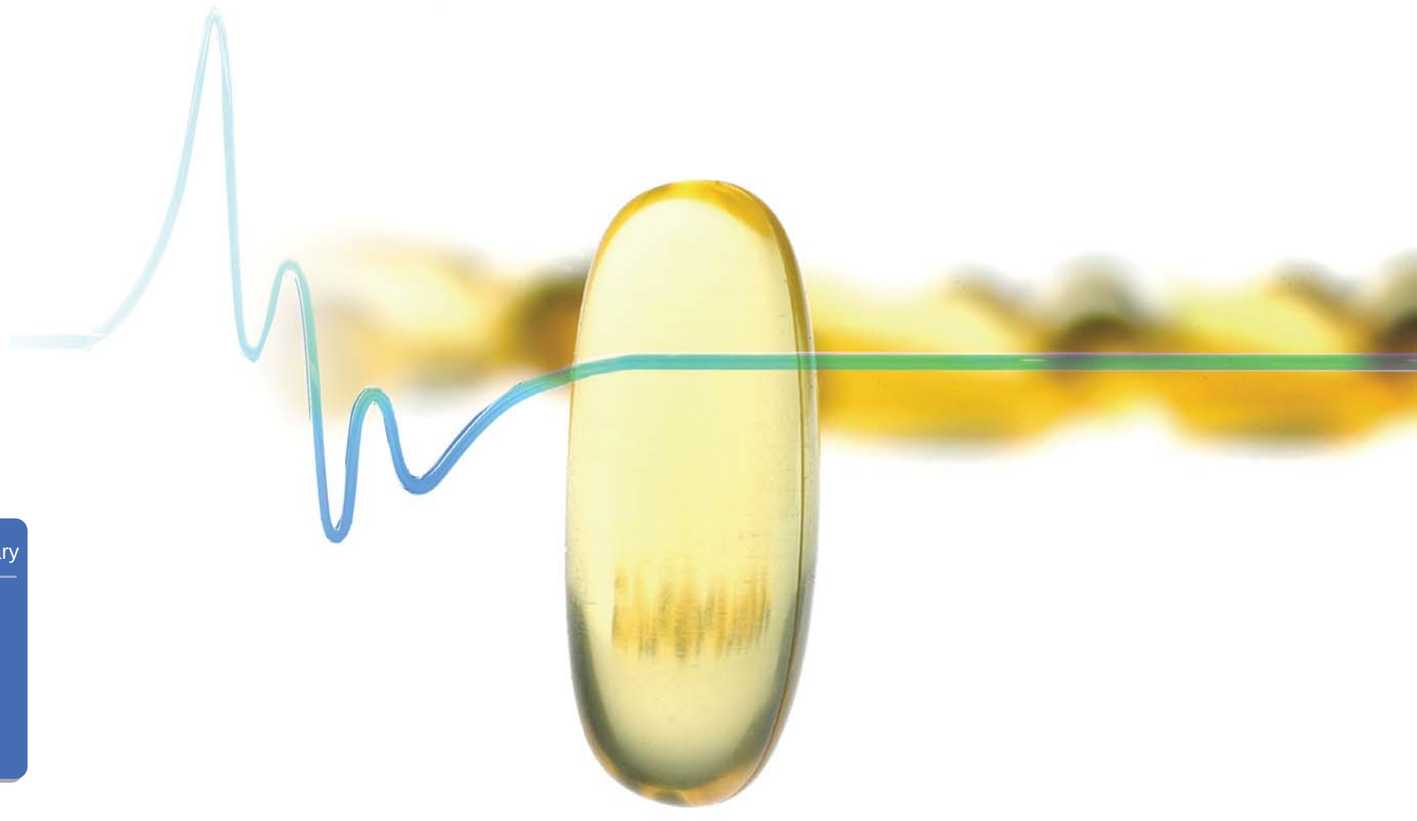
Combinatorial peptide libraries and HTS compound arrays are key players in drug discovery. These libraries can be used to screen highly active compounds such as antigenic peptides, receptor ligands, antimicrobial compounds, and enzyme inhibitors. Some of the applications of peptide screening tools are as follows:

1. Epitope mapping studies.
2. Vaccine research.
3. High-throughput protein-protein interaction analysis.
4. Customized peptide microarray production.
5. Kinase assays.

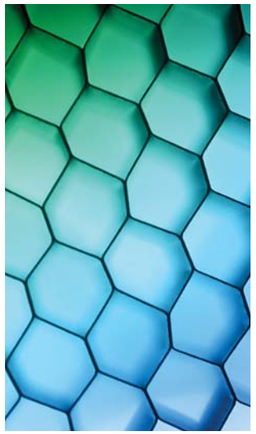
GenScript has developed six powerful screening tools for generating peptide libraries. They are overlapping peptide library, alanine scanning library, truncation library, positional scanning library, random library, and scrambled library which are necessary tools in epitope identification and sequence optimization for structure-activity studies.



Flexible strategies for your peptide-based drug research!



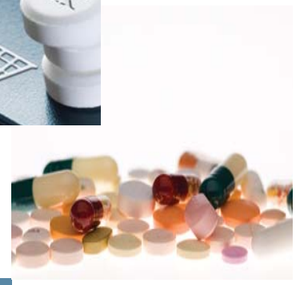
Overlapping Peptide Library

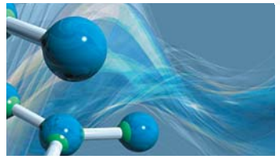


Overlapping peptide library can be used for linear and continuous epitope mapping, which can in turn be used to figure out which part of a given protein or peptide contains the essential amino acids that contribute to its functionality. Characterized by two parameters, fragment length and offset number, each library is generated by breaking the original protein or peptide into many equal-length overlapping fragments, each has 8 to 20 residues in size. As a general guideline, a peptide fragment must be at least six residues in length for it to cover an epitope. The offset number is the number of amino acid residues shifted between adjacent fragments and it reflects the degree of overlap.

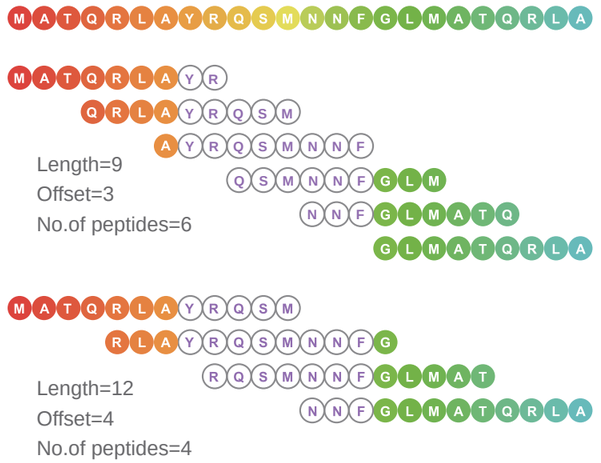
Careful selections of the offset number and the fragment length can minimize the experiment costs while maximizing data value. The offset number is usually chosen to be 1/3 of the fragment length. Usually, longer fragments are difficult to synthesize but the library generates fewer fragments. Also, it is more likely for the fragments to cover an epitope. The combination of low offset number and short fragment length generates the most number of fragments while the combination of high offset number and long fragment length produces the least number of fragments.

The overlapping peptide library has many applications. For example, the library can be used for the T-cell epitope determination in the areas of infectious diseases, oncology, and vaccine development.





Overlapping Library



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Alanine Scanning Library

Alanine scanning library is able to identify specific amino acid residues responsible for the peptide's function, stability, and conformation. Alanine, the smallest chiral amino acid, is used to substitute each non-alanine residue one at a time. Subsequently, corresponding change in epitope activity can be measured. Substitution of key amino acid residue(s) with alanine causes diminished epitope activity. This library enables us to quickly determine each individual amino acid's contribution to the peptide's functionality.

Alanine Scanning Library

References

- Weiss GA, Watanabe CK, Zhong A, Goddard A, and Sidhu SS. Rapid mapping of protein functional epitopes by combinatorial alanine scanning. Proc. Natl. Acad. Sci. U S A. Aug 2000 1; 97(16): 8950-4
- Richardson PL. The determination and use of optimized protease substrates in drug discovery and development. Curr. Pharm. Des. 2002; 8(28): 2559-81.
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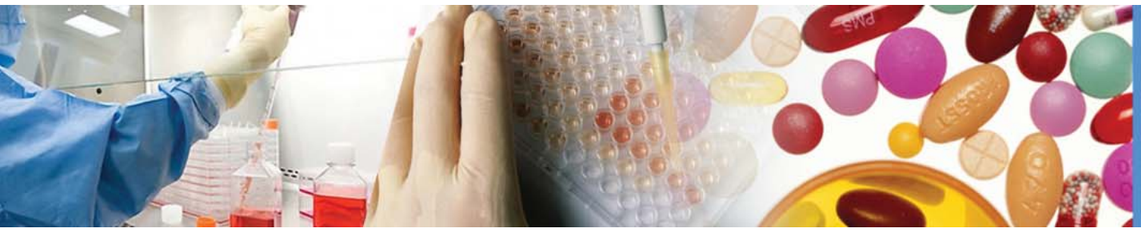
- Levine KB, Hamill S, Cloherty EK, and Carruthers A. Alanine scanning mutagenesis of the human erythrocyte glucose transporter putative ATP binding domain. Blood Cells Mol. Dis. Jan-Feb 2001; 27(1): 139-42.
- Sidhu SS, and Kossiakoff AA. Exploring and designing protein function with restricted diversity. Curr. Opin. Chem. Biol. Jun 2007; 11(3): 347-54.



Truncation Library

Truncation library allows researchers to determine the minimum length required for epitope activity. The library is generated through a systematic truncation of the peptide's sequence from each terminus. Knowing the positions of key residues via Alanine Scanning Library studies, the truncation fragments can be centered around them.

In many cases, truncation library screening gives knowledge about the peptides with enhanced proteolytic stability. It can act as a tool to investigate peptide drugs undergo metabolic degradation, which is a major inhibiting factor bringing these drugs to the market.

Truncation Library

References

- Svenson J, Stensen W, Brandsdal BO, Haug BE, Monrad J, and Svendsen JS. Antimicrobial peptides with stability toward tryptic degradation. Biochemistry. Mar 2008 25; 47(12): 3777-88.
- Bolger GB, Baillie GS, Li X, Lynch MJ, Herzyk P, MohamedA, Mitchell LH, McCahill A, Hundsrucker C, Klussmann E, Adams DR, and Houslay MD. Scanning peptide array analyses identify overlapping binding sites for the signalling scaffold proteins, beta-arrestin and RACK1, in cAMP-specific phosphodiesterase PDE4D5. Biochem. J. Aug 2006; 15; 398(1): 23-36.
- Ostermeier M, Nixon AE, Shim JH, and Benkovic SJ. Combinatorial protein engineering by incremental truncation. Proc. Natl. Acad. Sci. U S A. Mar 1999 30; 96(7): 3562-7.
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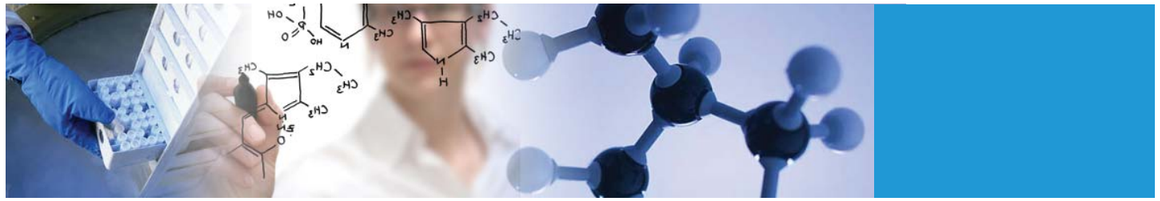
- Horswill AR, Naumann TA, and Benkovic SJ. Using incremental truncation to create libraries of hybrid enzymes. Methods Enzymol. 2004; 388: 50-60.

Positional Scanning Library



Positional scanning library is an important tool for peptide sequence optimization. It identifies amino acids of interest at a given position or positions and substitutes the amino acid(s) at that position with all other natural amino acids one at a time. It generates high value data by locating potential more favorable residue(s) at specified position(s) for enhanced peptide activity.

In particular, positional scanning library has been used to identify T-cell epitopes from complex mixtures of proteins. In addition, this type of library can also be used to locate substrates with interdependent subsite with only minimum synthesis and screening.

References

- Weiss GA, Watanabe CK, Zhong A, Goddard A, and Sidhu SS. Rapid mapping of protein functional epitopes by combinatorial alanine scanning. Proc. Natl. Acad. Sci. U S A. Aug 2000 1; 97(16): 8950-4
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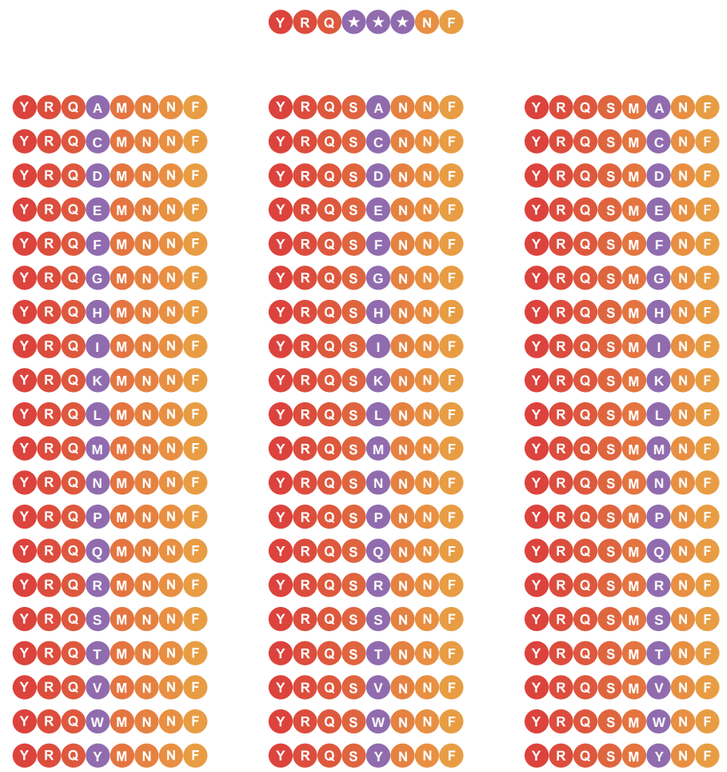

Random Library

Random library is an indispensable tool for sequence optimization. It has the ability to generate alternative peptides that could have the potential for enhanced activity. We substitute selected residues randomly and simultaneously with all other 20 natural amino acids via a shotgun approach. Our random library fabricates as many variations as possible within the selected amino acid residues.

Random Library

References

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- Horswill AR, Naumann TA, and Benkovic SJ. Using incremental truncation to create libraries of hybrid enzymes. Methods Enzymol. 2004; 388: 50-60.

Scrambled Library

Scrambled library brings the highest degree of variability for peptide library. The library is constructed through sequence permutation of the original peptide. Representing all possible alternative peptides, the scrambled library creates an ideal scenario for sequence optimization. It can be used to probe target molecules of interest including proteins, antibodies, DNAs, etc.

Scrambled Library

References

- Jiang QS, and Wang SQ. Design and screening of antisense oligodeoxynucleotides against PAI-1 mRNA in endothelial cells in vitro. Acta. Pharmacol. Sin. Aug 2006; 27(8): 1018-23.
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- Keizer DW, Miles LA, Li F, Nair M, Anders RF, Coley AM, Foley M, and Norton RS. Structures of phage-display peptides that bind to the malarial surface protein, apical membrane antigen 1, and block erythrocyte invasion. Biochemistry. Aug 2003; 26; 42(33): 9915-23.

Peptide Library Services

Key Features

- Flexible Purity Choices: Crude, >70%, >80%, >90% and >95% purity are available to meet your multiple demands.
- No Cross-Contamination: Peptides are supplied in individual fully labeled vials.
- Comprehensive Modifications: Our modification service includes labeling, the incorporation of unnatural amino acids, and peptide cyclization with disulfide bridges.
- Stringent Quality Control: GenScript provides COA, MS and HPLC validation data for each peptide.

Service Specifications

Crude Peptide Library (Catalog No.: SC1177)

1. 1-4 mg (5-9 mg, 10-20 mg are also available) for each crude peptide
2. Peptide length of 5-20 AA
3. Certificate of Analysis, RP-HPLC(optional) and mass spectrum for each peptide
4. Modifications including biotin, fluorescence, and unnatural amino acid etc.
5. 1-2 weeks typical turnaround time
6. Minimum order size is 24 peptides

Purified Peptide Library (Catalog No.: SC1487)

1. 1-4 mg for each peptide
2. Purity: Choice of >70%, >80%, >90% or >95% by RP-HPLC
3. Peptide length of 5-18 AA
4. Certificate of Analysis, RP-HPLC and mass spectrum for each peptide
5. Modifications including biotin, fluorescence, and unnatural amino acid etc.
6. 2-3 weeks typical turnaround time
7. Minimum order size is 24 peptides

Delivery Specifications

The typical delivery consists of:

- Lyophilized unbound peptides in individual fully labeled vials
- COA, MS and HPLC data

Quotations and Ordering:

Order online: www.genscript.com

Order by email: peptide@genscript.com

Order by phone: 1-877-436-7274 (Toll-Free) 1-732-885-9188

Order by fax: 1-732-210-0262 1-732-885-5878