PEPSCAN
Part of the Biosynth Group

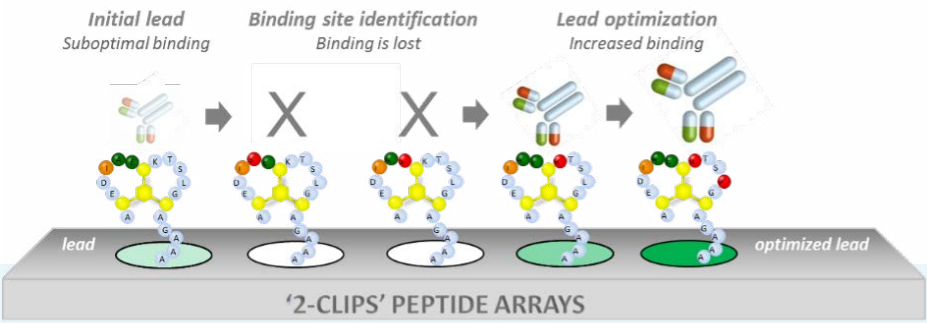
BROCHURE

Peptide Lead Optimization

Need to improve the affinity of your lead peptide? Does your lead peptide not yet display the high activity for the target needed for an active drug that also works in vivo? Pepscan's Lead Optimization helps you bring your candidate peptide to the next level. Our highly skilled project team is well-equipped with many years of experience in peptide lead optimization.

What is Peptide Lead Optimization?

Lead optimization is a critical step in the design of novel peptide-based drugs. Most peptide leads display interesting properties for therapeutic drugs, but the binding is suboptimal. Typical affinities to the target protein are usually in the (sub)micromolar range, or the stability to proteolytic degradation is insufficient. This is where Pepscan's Lead Optimization team comes in.



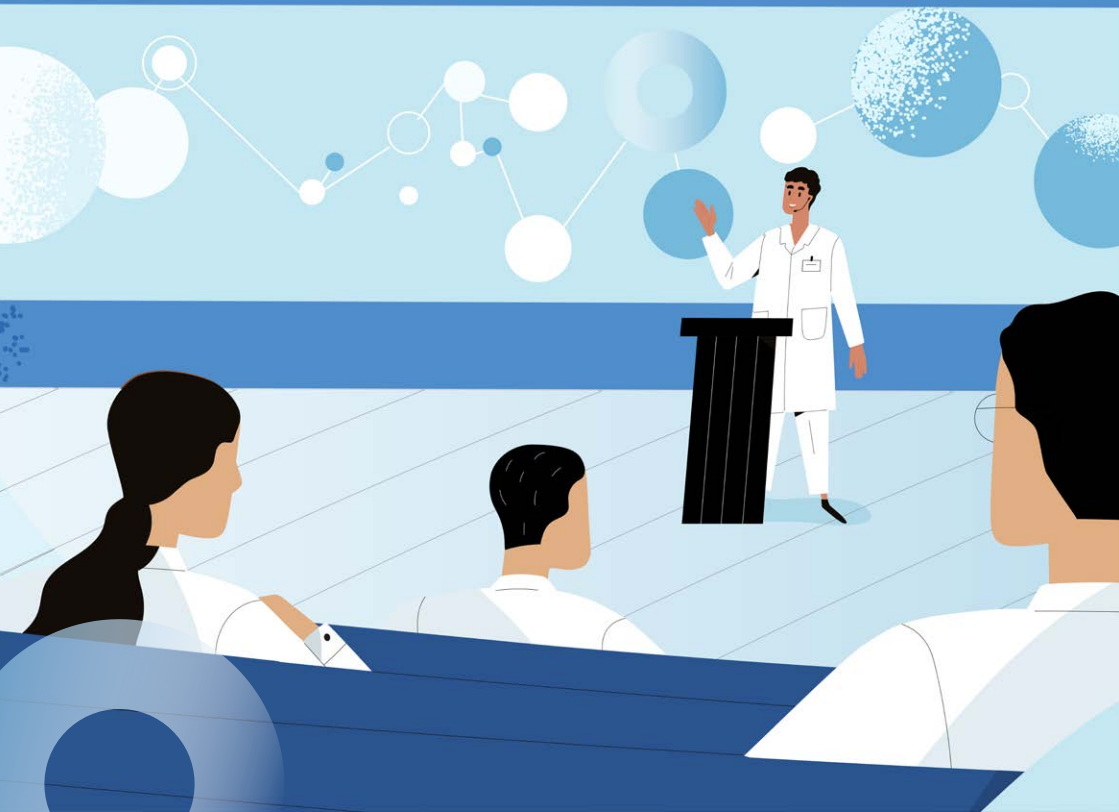
Three Ways to Optimize Peptide Leads

1. Through amino acid replacement analysis
2. By constraining peptides using CLIPS™ technology
3. By adjusting the peptide length or size

Pepscan combines these methods in iterative screening rounds. The affinity of peptide-based lead drug candidates can be improved up to **1,000 times**.

What Pepscan Offers

1. Support in designing the most efficient and economical library to help you compute lists of peptide library sequences
2. Unique libraries of 3D-constrained (CLIPS™) peptides if the 3D conformation of your peptide is crucial
3. Wide range of library design options, each tailored to your specific research questions
4. Peptide libraries produced with different types of non-natural amino acid variants, such as 1- or 2-naphthylalanine, tert-butylalanine, nor-isoleucine, nor-leucine, nor-valine, etc., or backbone N-methylations, or typical post-translational modifications, such as serine/threonine/tyrosine phosphorylation or arginine/lysine methylations



Why Choose Lead Optimization at Pepscan?

- Detailed insights into the critical amino acids of a lead peptide
- Improved binding affinity by introducing a large variety of non-natural amino acids
- Additional insights through mutational analysis and alanine scanning (AlaScan)
- Development of an enhanced molecule by constraining it (e.g. using CLIPS™) for better pharmacokinetic properties
- Inclusion of various in-house functional assays to determine proteolytic and/or enzymatic stability profiles of a lead peptide candidate

Case Studies

Pepscan designs the most efficient and economical libraries for you, with a full list of peptide sequences. If the 3D conformation of your peptide is important for activity, we also provide libraries of 3D-constrained (CLIPS™) peptides. A wide range of peptide libraries is made available, each tailored to your specific research needs.

Read about our achievements.

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About Pepscan

Pepscan is an all-in-one partner in peptides, building on 25 years of experience in advancing and applying peptide expertise to facilitate customers in the development and manufacturing of peptides. At our end-to-end facility in Lelystad, the Netherlands, we offer a range of proprietary technologies, phage display capabilities, a lead-optimization microarray platform, and production facilities for R&D- to GMP-grade peptides to a worldwide customer base.

Find out more about Pepscan.