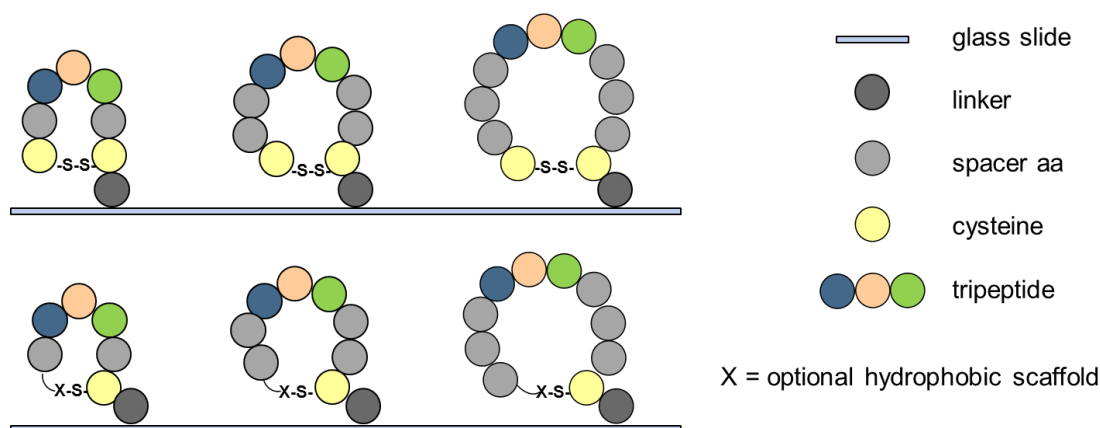




Full Combinatorial Constrained Tripeptide Libraries

PEPperPRINT's technology platform allows the synthesis of large combinatorial peptide libraries of thousands of peptides on microarrays, which are ideally suited for high throughput screening of peptide-protein interactions. In order to mimic conformational structures, we developed an on-chip peptide cyclization protocol. PEPperPRINT is currently looking for partners that are interested in full combinatorial constrained tripeptide libraries for e.g. peptide drug development or conformational epitope analysis. Please contact us for further information.



- Array Content:** Full combinatorial constrained tripeptide libraries with 6,859 peptides each microarray (cysteine is excluded)
- Ring Size:** Different ring sizes depending on the number of spacer amino acids; all motifs with one ring size on a single microarray
- Cyclization Method:** Disulfide or N-terminus to side-chain thioether bridging; the latter with or without inserted scaffolds for varying spatial orientations (X = aliphatic or aromatic cyclic scaffolds)
- Potential Applications:**
- (1) Primary screening library for e.g. conformational epitope analysis or peptide drug discovery
 - (2) Further optimization by full substitution scans of e.g. spacer amino acid positions or of tripeptide positions by non-physiological amino acids

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