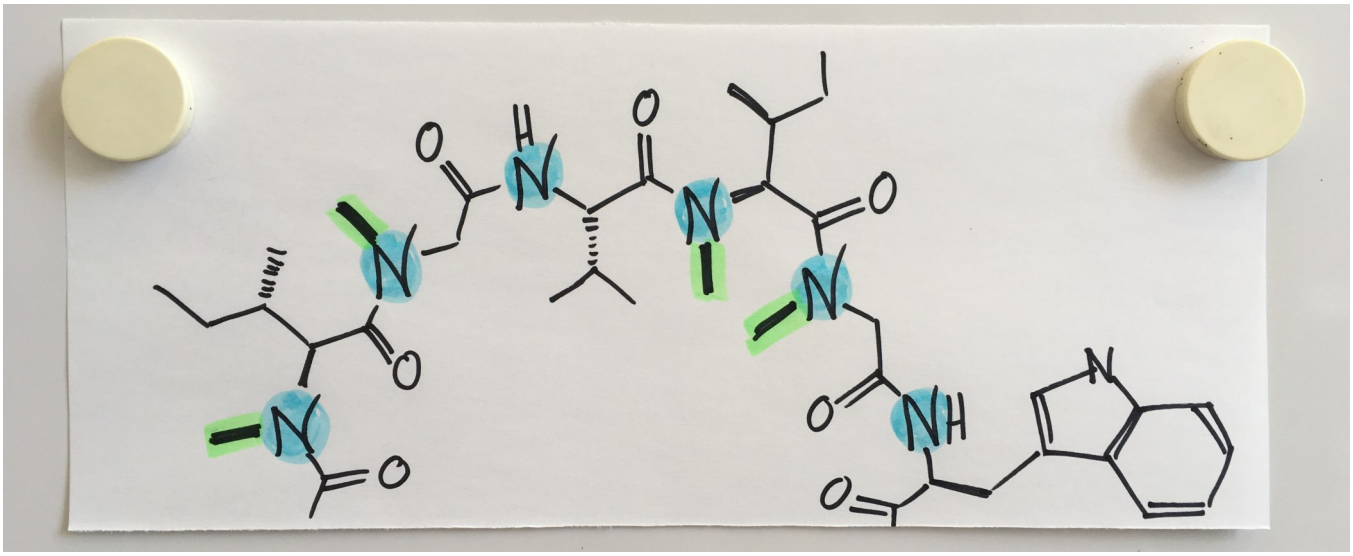
ETH zürich

Licensing Opportunity

De novo generation of libraries of backbone N-methylated peptides for drug development



Summary

A newly discovered biosynthetic pathway allows the de novo generation of large libraries of backbone N-methylated peptides in bacteria and yeast. These libraries can be screened in vitro or in vivo for backbone N-methylated peptides that bind to target proteins. These peptides are promising leads for the development of therapeutic peptides due to their modification.

Background

Backbone N-methylation can improve the oral availability, metabolic stability, membrane permeability and target selectivity of peptides. Currently, this modification is often added (chemically) retroactively to leads for therapeutic peptides to improve their pharmacological properties. This procedure is technically challenging and often negatively affects the biological activity of the lead peptides.

Invention

The OphA enzyme from the jack-o-lantern mushroom is capable of posttranslational backbone N-methylation of a wide range of different peptides and is functional in the cytoplasm of bacteria and yeast.

Features & Benefits

- Proactive rather than retroactive backbone N-methylation of peptide libraries
- High library complexities due to genetic coding of the peptides and promiscuity of modifying enzyme
- Combination with established in vivo and in vitro screening procedures due to library generation in bacteria and yeast

Fields of Application

- Production of peptide drug libraries for screening

Patent Status

- PCT/EP2017/058327

Publication

- van der Velden NS, Kälin N, Helf MJ, Piel J, Freeman MF, Künzler M. “Autocatalytic backbone N-methylation in a family of ribosomal peptide natural products.” Nature Chemical Biology 13, 833-835 (2017)

Technology Readiness Level

1 2 **3** 4 5 6 7 8 9

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