

Genome mining for ribosomally synthesized and post-translationally modified peptides (RiPPs) in anaerobic bacteria.

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Abstract

Ribosomally synthesized and post-translationally modified peptides (RiPPs) are a diverse group of biologically active bacterial molecules. Due to the conserved genomic arrangement of many of the genes involved in their synthesis, these secondary metabolite biosynthetic pathways can be predicted from genome sequence data. To date, however, despite the myriad of sequenced genomes covering many branches of the bacterial phylogenetic tree, such an analysis for a broader group of bacteria like anaerobes has not been attempted.

Beteiligte Forschungseinheiten

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