

# Plasticity of the Malleobactin Pathway and its Impact on Siderophore Action in Human Pathogenic Bacteria.

Franke J, Ishida K, Hertweck C (2015) Plasticity of the Malleobactin Pathway and its Impact on Siderophore Action in Human Pathogenic Bacteria. *Chemistry* 21(22), 8010-8014.

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## Abstract

The human pathogenic bacteria *Burkholderia mallei*, *Burkholderia pseudomallei*, and *Burkholderia thailandensis* harbor a highly conserved gene cluster coding for the biosynthesis of the long sought-after malleobactins. Four new, unexpected congeners of the malleobactin family that were isolated and fully characterized in this study feature unusual deviations from the parent, ornibactin-like architecture. Thus, the malleobactin non-ribosomal peptide synthetase (NRPS) has a rare flexibility that yields diverse peptide backbones, of which one candidate confers pronounced siderophore activity ( $EC_{50}$  : 8.4  $\mu$ M, CAS assay). These findings not only unveil a highly diverse assembly line but also are an important addition to the knowledgebase of the pathogens' metabolomes.

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**doi:** 10.1002/chem.201500757

**PMID:** 25873483