

CASSIS and SMIPS: promoter-based prediction of secondary metabolite gene clusters in eukaryotic genomes.

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Abstract

Secondary metabolites (SM) are structurally diverse natural products of high pharmaceutical importance. Genes involved in their biosynthesis are often organized in clusters, i.e., are co-localized and co-expressed. In silico cluster prediction in eukaryotic genomes remains problematic mainly due to the high variability of the clusters' content and lack of other distinguishing sequence features.

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