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# Bacterial Genomes Mining

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[dx.doi.org/10.17504/protocols.io.4r3l2obw4v1y/v1](https://dx.doi.org/10.17504/protocols.io.4r3l2obw4v1y/v1)

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The fast development of genome sequencing technologies and the power of advanced computational analyses of the DNA sequences dramatically increased the potential for natural product discovery. Our knowledge on the biosynthesis of secondary metabolites by bacteria is constantly expanding, thereby adding new information that connects biosynthetic genes with metabolites of particular chemical classes. With the cost-effective and rapid increase in the number of bacterial genomes sequenced, one challenge encountered in current drug discovery efforts is how to effectively prioritize those strains with the greatest ability to produce new compounds and understand the extent of biosynthetic potential that exists in nature.

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