MARSI: metabolite analogues for rational strain improvement

Metabolite analogues (MAs) mimic the structure of native metabolites, can competitively inhibit their utilization in enzymatic reactions, and are commonly used as selection tools for isolating desirable mutants of industrial microorganisms. Genome-scale metabolic models representing all biochemical reactions in an organism can be used to predict effects of MAs on cellular phenotypes. Here, we present the Metabolite Analogues for Rational Strain Improvement (MARSI) framework. MARSI provides a rational approach to strain improvement by searching for metabolites as targets instead of genes or reactions. The designs found by MARSI can be implemented by supplying MAs in the culture media, enabling metabolic rewiring without the use of recombinant DNA technologies that cannot always be used due to regulations. To facilitate experimental implementation, MARSI provides tools to identify candidate MAs to a target metabolite from a database of known drugs and analogues.

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