# Modeling the contribution of allosteric regulation for flux control in the central carbon metabolism of *E. coli*

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## Abstract

Redesign of microbial metabolism is a critical step in biotechnology for the production of industrially relevant compounds. Central carbon metabolism provides the energy and building blocks required for cellular growth and synthesis of the desired byproducts and, consequently, it is the main target for intervention in most rational strain design approaches. However, the complexity of central carbon metabolism is still not completely understood. Recent studies in different organisms show that flux control in central carbon metabolism is predominantly regulated by non-transcriptional mechanisms, leaving post-translational modifications, allosteric regulation, and thermodynamics as main candidates. In this work, we extend a model of central carbon metabolism of *E.coli* with allosteric interactions in order to reveal a hidden topology in metabolic networks. We use this model to integrate a multi-*omic* dataset containing transcript, protein, flux and metabolite levels to further dissect and analyze the contribution of allosteric regulation for metabolic flux control.