

## Background/objective

Isozymes are enzymes that differ in sequence but catalyze the same chemical reaction. The evolutionary significance of the subset of isozymes that are co-localized in the same cellular compartment has remained a persistent question. Here, researchers used computational analysis of gene expression data from *Saccharomyces cerevisiae* to gain new understanding of the function of such isozymes.

## Approach

- ❖ Gene expression data for *S. cerevisiae* was computationally analyzed to identify environmental conditions under which isozyme expression diverged.
- ❖ Gene knockouts were compared under the identified environmental conditions.

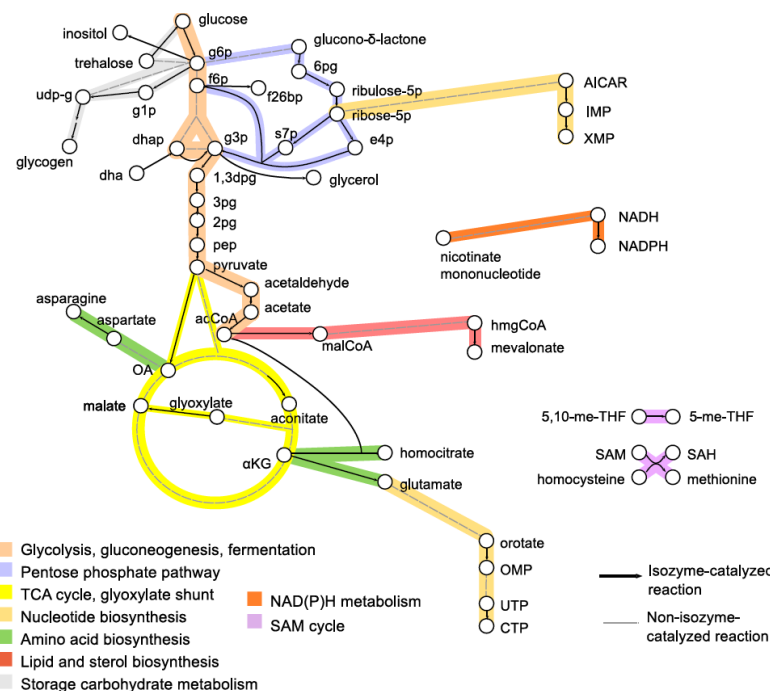
## Results

- ❖ The response of many isozymes diverged in response to carbon availability, indicating a role for such enzymes in optimizing control of carbon metabolism.
- ❖ Function was assigned to two minor central carbon metabolism enzymes: aconitase 2 (*ACO2*); and pyruvate kinase 2 (*PKY2*).

## Significance

- ❖ This study improves our understanding of how regulation of yeast central carbon metabolism resolves environment-dependent trade-offs.
- ❖ Understanding how isozymes fine-tune central carbon metabolism in response to different carbon sources will inform future efforts to engineer enzymes, including for bioproducts applications.

Bradley et al. 2019. "Minor Isozymes Tailor Yeast Metabolism to Carbon Availability." *mSystems*. 4:1-19. DOI:10.1128/mSystems.00170-18



**Co-localized isozyme-catalyzed reactions are enriched in the central carbon metabolism of *S. cerevisiae*. Heavy black lines indicate these reactions on the metabolic map above.**