Repurposing the peroxisome in *Sacchromyces cerevisiae* for Compartmentalizing Multi-Enzyme Metabolic Pathways

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Engineered metabolic pathways often suffer from undesired interactions with the production host's native cellular processes. Evolution has solved the problem of metabolic crosstalk by segregating distinct cellular functions into membrane-bound organelles. We aim to follow this blueprint by repurposing one of these organelles – specifically the peroxisome of *Saccharomyces cerevisiae* – for compartmentalizing heterologous metabolic pathways. Towards this goal, we are working to 1) improve the targeting efficiency of non-native enzyme cargo to the peroxisome, 2) determine the natural chemical composition of the peroxisomal lumen, and 3) demonstrate successful compartmentalization of a model pathway. Ultimately, this work will contribute to the development of a synthetic organelle that can limit metabolic crosstalk and improve production efficiency for a variety of engineered pathways.