Absolute Quantification of Protein and mRNA Abundances Demonstrate Variability in Gene-Specific Translation Efficiency in Yeast

Protein synthesis is the most energy-consuming process in a proliferating cell, and understanding what controls protein abundances represents a key question in biology and biotechnology. We quantified absolute abundances of 5,354 mRNAs and 2,198 proteins in Saccharomyces cerevisiae under ten environmental conditions and protein turnover for 1,384 proteins under a reference condition. The overall correlation between mRNA and protein abundances across all conditions was low (0.46), but for differentially expressed proteins (n = 202), the median mRNA-protein correlation was 0.88. We used these data to model translation efficiencies and found that they vary more than 400-fold between genes. Non-linear regression analysis detected that mRNA abundance and translation elongation were the dominant factors controlling protein synthesis, explaining 61% and 15% of its variance. Metabolic flux balance analysis further showed that only mitochondrial fluxes were positively associated with changes at the transcript level. The present dataset represents a crucial expansion to the current resources for future studies on yeast physiology.