## Yale Systems Biology Institute

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## "Proteomics of Unperturbed Protein Degradation in *Escherichia coli*"

Protein degradation is a key regulatory mechanism to control protein levels. However, proteome-wide degradation measurements remain technically challenging and even in the well-studied E. coli model, reliable measurements remain scarce. Here, we quantify the degradation of ~2k E. coli proteins under 14 conditions by combining heavy isotope labeling with accurate multiplexed proteomics and find that E. coli recycles its cytoplasmic proteins when nitrogen is scarce. Furthermore, we show that protein degradation rates do not scale with division rates. With knockout experiments, we identify substrates of the known ATPdependent proteases but show that none is responsible for the cytoplasmic protein degradation in nitrogen starvation, suggesting that a major pathway in E. coli is still undiscovered. Thus, we introduce broadly-applicable technology for protein turnover measurements. We provide a rich resource for protein half-lives and protease substrates in E. coli that will allow researchers to complement genomics data to decipher the control of protein abundances.



Wednesday, July 20 at 1:00 pm Yale West Campus Conference Center 800 West Campus Drive, Event Room A West Haven, CT

~Lunch will be served~