Insights into transcriptional and translational regulation by absolute protein expression profiling

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We developed a new simple and robust method, called Absolute Protein Expression profiling (APEX), which generates absolute protein abundances for measurements from large-scale mass spectrometry experiments. APEX relies upon correcting each protein's mass spectrometry sampling depth (observed peptide count) by learned probabilities for identifying the peptides. APEX abundances agree with measurements from controls, Western blotting, flow cytometry, and 2D gels, and known correlations with mRNA abundances and codon bias.

We use our method to characterize protein expression in *E.coli*, yeast and mouse, and quantify expression levels across ~3-4 orders of magnitude and for concentrations down to <500 hundred molecules/cell. We compare APEX-based protein abundances to other data of transcriptional and translational activity, and find that up to >70% of protein expression levels are based on mRNA expression. Both eukaryotic and prokaryotic proteins are set per mRNA molecules independently of overall protein concentration. In addition, APEX-based protein abundances can be applied to calculations of other protein characteristics such as degradation rates, and we discuss some examples.