Glycation, the nonenzymatic modification of proteins by sugars and sugar metabolites, is thought to cause protein dysfunction associated with diabetes and other diseases. However, due to reliance on crude glycated protein mixtures, the effects of precise modifications are poorly understood. Using peptides containing chemically synthesized glycation products, we found that some reported effects of glycated proteins may be due to contaminating methylglyoxal (MGO), a metabolic byproduct and glycating agent. To better understand the effects of MGO in biological systems, we created a fluorogenic sensor for its detection. Our sensor exhibited excellent selectivity for MGO over structurally related species, and allowed MGO visualization in live cells for the first time. Part 2: Protein folding is a prerequisite for protein engineering, but the majority of heterologous proteins fold poorly and fail to express in E. coli, precluding investigation of many interesting targets. We created a system for evolving proteins with improved folding using phage-assisted continuous evolution (PACE). Using a PACE-compatible “AND” gate, we simultaneously selected for protein activity as well as folding to evolve better-expressing antibody fragments that retained antigen binding activity. We also evolved cytidine deaminases with improved expression that increased the apparent activity of Cas9-derived base editors. This system allows rapid evolution of better-folded protein variants and may be used to increase the number of proteins accessible to engineering efforts in E. coli.