After translation by a ribosome, a protein can undergo modifications known as post-translational modifications (PTMs). Through the covalent addition or removal of various functional groups, PTMs increase the functional diversity of the proteome. At the Saccharomyces Genome Database (SGD; www.yeastgenome.org), we have been actively expanding our protein data to include manually curated post-translational modification information for the model organism Saccharomyces cerevisiae. Examples of PTM types we are currently curating from the literature include, but are not limited to: phosphorylation, acetylation, methylation, ubiquitination, and sumoylation. These data are displayed in the amino acid sequence section of SGD Protein pages as highlighted residues, including the protein modifier when available. Post-translational modification information is often critical to understanding mature protein function and regulation, thus we include the PTM data in SGD as part of our continuing mission to educate students, enable bench research, and facilitate scientific discovery. This work is supported by a grant from the NHGRI (U41 HG001315).