Proteins do not always function in isolation, but often interact with other proteins, nucleic acids, or small molecules to form stable macromolecular complexes that play roles in important cellular processes and pathways. One of the goals of Saccharomyces Genome Database (SGD; www.yeastgenome.org) is to provide a complete picture of budding yeast biological processes. To this end, we collaborated with the Molecular Interactions team that produces the IntAct database at EMBL-EBI to manually curate the complete yeast complexome. These data, from a total of 585 complexes, were initially available in YeastMine (https://yeastmine.yeastgenome.org/yeastmine/begin.do), our data warehouse, as well as the Complex Portal (https://www.ebi.ac.uk/complexportal/home).

We have now incorporated macromolecular complex data into our main SGD database and designed pages to make these data easily available to researchers. The pages will contain referenced summaries focused on the composition and function of individual complexes. In addition, detailed information about subunits' stoichiometry and association within the complex, and the physical structure of the complex will be displayed when available. Finally, we will have network diagrams displaying shared members and GO annotations between complexes. Macromolecular complexes will continue to be updated and curated as more data become available. SGD is funded by the NIH-NHGRI [U41HG001315].