

# Resource Summary Report

Generated by [dkNET](#) on Sep 12, 2026

## Yeast Resource Center

RRID:SCR\_007942

Type: Tool

### Proper Citation

Yeast Resource Center (RRID:SCR\_007942)

### Resource Information

**URL:** <http://depts.washington.edu/yeastrc/>

**Proper Citation:** Yeast Resource Center (RRID:SCR\_007942)

**Description:** Biomedical technology research center that (1) exploits the budding yeast *Saccharomyces cerevisiae* to develop novel technologies for investigating and characterizing protein function and protein structure (2) facilitates research and extension of new technologies through collaboration, and (3) actively disseminates data and technology to the research community. Through collaboration, the YRC freely provides resources and expertise in six core technology areas: Protein Tandem Mass Spectrometry, Protein Sequence-Function Relationships, Quantitative Phenotyping, Protein Structure Prediction and Design, Fluorescence Microscopy, Computational Biology.

**Abbreviations:** YRC

**Synonyms:** YRC

**Resource Type:** biomedical technology research center, training resource

**Keywords:** systems biology technology center, protein function, protein structure, mass spectrometry, protein, structure prediction, fluorescence microscopy, computational biology, sequence, function, phenotyping

**Funding:** NCRR ;  
NIGMS P41 GM103533

**Resource Name:** Yeast Resource Center

**Resource ID:** SCR\_007942

**Alternate IDs:** nif-0000-03650

**Record Creation Time:** 20220129T080244+0000

## Ratings and Alerts

No rating or validation information has been found for Yeast Resource Center.

No alerts have been found for Yeast Resource Center.

---

## Data and Source Information

**Source:** [SciCrunch Registry](#)

---

## Usage and Citation Metrics

We found 6 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [dkNET](#) .

Wu S, et al. (2017) Independent regulation of gene expression level and noise by histone modifications. PLoS computational biology, 13(6), e1005585.

Topalidou I, et al. (2016) The EARP Complex and Its Interactor EIPR-1 Are Required for Cargo Sorting to Dense-Core Vesicles. PLoS genetics, 12(5), e1006074.

Kollman JM, et al. (2015) Ring closure activates yeast ??TuRC for species-specific microtubule nucleation. Nature structural & molecular biology, 22(2), 132.

Breker M, et al. (2014) LoQAtE--Localization and Quantitation ATlas of the yeast proteome. A new tool for multiparametric dissection of single-protein behavior in response to biological perturbations in yeast. Nucleic acids research, 42(Database issue), D726.

Ma CH, et al. (2013) Temporal sequence and cell cycle cues in the assembly of host factors at the yeast 2 micron plasmid partitioning locus. Nucleic acids research, 41(4), 2340.

Shimogawa MM, et al. (2006) Mps1 phosphorylation of Dam1 couples kinetochores to microtubule plus ends at metaphase. Current biology : CB, 16(15), 1489.