Post-Translational Modification Data in the *Saccharomyces* Genome Database

Sage T. Hellerstedt, Stacia R. Engel, Shuai Weng, J. Michael Cherry, and The SGD Project
Stanford University, School of Medicine, Stanford CA

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).

Where are PTM data at SGD?

Summary | Sequence | Protein | Gene Ontology | Phenotype | Interactions | Regulation | Expression | Literature

HHT1 / YBR010W
- Protein Overview
- Experimental Data
- Domains and Classification
- Sequence
- External Identifiers
- Resources

HHT1 / YBR010W Protein

Protein Help

Aliases: BUR5 [1], SIN2 [2]
Protein Product: histone H3
Feature Type: ORF, Verified
Description: Histone H3; core histone protein required for chromatin assembly, part of heterochromatin-mediated telomeric and HM silencing; one of two identical histone H3 proteins (see HHT2); regulated by acetylation, methylation, and phosphorylation; H3K14 acetylation plays an important role in the unfolding of strongly positioned nucleosomes during repair of UV damage [3 4 5 6 7 8 9 10 11]

1) From the Locus page go to the Protein tab
2) Scroll down, or use left navigation menu, to find Sequence

Data is available:

1) As highlighted residues in amino acid sequence or

2) In tabular form

Strain

S288C - Reference Genome

Choose your strain

```
  1 MARTKQTARK STGGKAPRKQ LASKAARKSA PSTGGVKKPH RYKPGTVALR EIRRFQKSTE
 61 LLIRKLPFQR LVREIAQDFK TDLRFQSSAI GALQESVEAY LVSLFEDTNL AAIHAKRVTI
121 QKKDIKLARR LRGERS*
```

* Blue amino acids indicate modification sites. More information below.

Download Sequence (.fsa)

Highlighted residue represents modification site

Post-translational Modifications - S288C — 95 entries for 19 sites

Filter table

Site	Modification	Modifier	Reference
K5	demethylation	JHD2	De Vos D, et al. (2011) PMID: 21760613
K5	acetylation	GCN5	Guillemette B, et al. (2011) PMID: 21483810
K5	methylation	SET1	Soares LM and Buratowski S (2012) PMID: 22431730
K5	monomethylation		Yang L, et al. (2010) PMID: 19699711
K5	dimethylation		Yang L, et al. (2010) PMID: 19699711
K5	trimethylation		Yang L, et al. (2010) PMID: 19699711
K5	methylation	SET1	Nakanishi S, et al. (2009) PMID: 19667127
K5	trimethylation	SET1	Laribee RN, et al. (2007) PMID: 17389396
K5	trimethylation	SET1	Lee JS, et al. (2012) PMID: 22549955
K10	acetylation		Lavoie H, et al. (2010) PMID: 20231876

Showing 11 to 20 of 95 entries | 10 records per page | « 1 2 3 ... 9 10 »

Download (.txt)

Table includes modification site (amino acid and position in protein sequence), type of modification, modifier (if determined), and reference information

Filter by site, modification, modifier, or reference

Data curated from small scale and high-throughput studies

Data available for download

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sgd-helpdesk@lists.stanford.edu