

Each row in the table corresponds to one protein group.

A. Protein IDs: SGD ORFs, including all proteins that could be identified from the peptides identified. Protein ids are ordered by number of peptides identified (most to least).

B. First Id: A representative protein in the group that had a maximal number of peptide identified.

C. SGD Id: Mapping from first id to SGD identifier

D. Gene Name: Mapped from SGD

E. ControlCDC48 Ratio: Ratio of *cdc48-3+His8Ub*/wt

F. OneToOne Ratio: Ratio of *wt+His8Ub*/*wt+His8Ub*

G. CDC48 Ratio: Ratio of *cdc48-3+His8Ub*/ *wt+His8Ub*

H. Ubx2 Ratio: Ratio of *ubx2Δ+His8Ub*/ *wt+His8Ub*

I. Ubx3 Ratio: Ratio of *ubx3Δ+His8Ub*/ *wt+His8Ub*

J. Ubx4 Ratio: Ratio of *ubx4Δ+His8Ub*/ *wt+His8Ub*

K. Ubx5 Ratio: Ratio of *ubx5Δ+His8Ub*/ *wt+His8Ub*

L. Ubx6 Ratio: Ratio of *ubx6Δ+His8Ub*/ *wt+His8Ub*

M. Ubx7 Ratio: Ratio of *ubx7Δ+His8Ub*/ *wt+His8Ub*

N. InScud: Whether protein id is listed in SCUD database as a Ub-conjugated protein

O. Ub Enzyme: Type of UPS enzyme (if any)

P. Valid Substrate: Passed filtering thresholds (i.e., not changed in OneToOne and significantly up in ControlCDC48)

Q. Quantified in All Experiments: Quantified in CDC48, Ubx2, Ubx3, Ubx4, Ubx5, Ubx6 and Ubx7

R. Proteins: Number for proteins in the protein group

S. Peptides: Total number of peptides assigned to protein group

T. Razor + unique peptides: Number of peptides assigned to the protein group for quantitative purposes

U. Unique peptides: Number of peptides uniquely assigned to the protein group

V. Sequence coverage [%]: Percent sequence coverage of the first id protein

W. PEP: Posterior error probability of protein identification as calculated by MaxQuant

X. Reverse: “+” if the protein identified was a decoy

Y. Contaminant: “+” if the protein identified was a contaminant such as keratin or trypsin

Z. ControlCDC48 Ratio Log2: Log₂ ratio of *cdc48-3+His8Ub/wt*

AA. ControlCDC48 Std Error: Standard error of the log₂ ratio of *cdc48-3+His8Ub/wt* as calculated by the bootstrap statistical models

AB. ControlCDC48 Evidence Counts: Number of different peptide ratios used to calculate the log₂ ratio of *cdc48-3+His8Ub/wt*

AC. ControlCDC48 p-val 1:1: Two sided, one-sample location test p-value of log₂ ratio and standard error of *cdc48-3+His8Ub/wt* relative to a log₂ ratio of 0.0 (i.e., a ratio of 1.0)

AD. ControlCDC48 p-val 1:1 One Sided < 0: One sided, one-sample location test p-value of log₂ ratio and standard error of *cdc48-3+His8Ub/wt* relative to a log₂ ratio of 0.0 (i.e., a ratio of 1.0)

AE. OneToOne Ratio Log2: Log₂ ratio of *wt+His8Ub/wt+His8Ub*

AF. OneToOne Std Error: Standard error of the log₂ ratio of *wt+His8Ub/wt+His8Ub* as calculated by the bootstrap statistical models

AG. OneToOne Evidence Counts: Number of different peptide ratios used to calculate the log₂ ratio of *wt+His8Ub/wt+His8Ub*

AH. OneToOne p-val 1:1: Two sided, one-sample location test p-value of log₂ ratio and standard error of *wt+His8Ub/wt+His8Ub* relative to a log₂ ratio of 0.0 (i.e., a ratio of 1.0)

AI. OneToOne p-val <10% Change: Two sided, one-sample location test p-value of log₂ ratio and standard error of *wt+His8Ub/wt+His8Ub* relative to a protein fold change < 10%

AJ. CDC48 Ratio Log2: Log₂ ratio of *cdc48-3+His8Ub/ wt+His8Ub*

AK. CDC48 Std Error: Standard error of the log₂ ratio of *cdc48-3+His8Ub/ wt+His8Ub* as calculated by the bootstrap statistical models

AL. CDC48 Evidence Counts: Number of different peptide ratios used to calculate the log₂ ratio of *cdc48-3+His8Ub/ wt+His8Ub*

AM. CDC48 p-val 1:1: Two sided, one-sample location test p-value of log₂ ratio and standard error of *cdc48-3+His8Ub/ wt+His8Ub* relative to a log₂ ratio of 0.0 (i.e., a ratio of 1.0)

AN. CDC48 1:1 IsSig @ 0.05 p-val BH Corrected: True if log₂ ratio of *cdc48-3+His8Ub/ wt+His8Ub* is significantly different from 0.0 (p-value < 0.05) after correcting for multiple hypothesis testing using the Benjamini and Hochberg method

AO. CDC48 p-val <10% Change: Two sided, one-sample location test p-value of \log_2 ratio and standard error of *cdc48-3+His8Ub/ wt+His8Ub* relative to a protein fold change < 10%

AP. Ubx2 Ratio Log2: \log_2 ratio of *ubx2Δ+His8Ub/ wt+His8Ub*

AQ. Ubx2 Std Error: Standard error of the \log_2 ratio of *ubx2Δ+His8Ub/ wt+His8Ub* as calculated by the bootstrap statistical models

AR. Ubx2 Evidence Counts: Number of different peptide ratios used to calculate the \log_2 ratio of *ubx2Δ+His8Ub/ wt+His8Ub*

AS. Ubx2 p-val 1:1: Two sided, one-sample location test p-value of \log_2 ratio and standard error of *ubx2Δ+His8Ub/ wt+His8Ub* relative to a \log_2 ratio of 0.0 (i.e., a ratio of 1.0)

AT. Ubx2 1:1 IsSig @ 0.05 p-val BH Corrected: True if \log_2 ratio of *ubx2Δ+His8Ub/ wt+His8Ub* is significantly different from 0.0 (p-value < 0.05) after correcting for multiple hypothesis testing using the Benjamini and Hochberg method

AU. Ubx2 p-val <10% Change: Two sided, one-sample location test p-value of \log_2 ratio and standard error of *ubx2Δ+His8Ub/ wt+His8Ub* relative to a protein fold change < 10%

AV. Ubx3 Ratio Log2: \log_2 ratio of *ubx3Δ+His8Ub/ wt+His8Ub*

AW. Ubx3 Std Error: Standard error of the \log_2 ratio of *ubx3Δ+His8Ub/ wt+His8Ub* as calculated by the bootstrap statistical models

AX. Ubx3 Evidence Counts: Number of different peptide ratios used to calculate the \log_2 ratio of *ubx3Δ+His8Ub/ wt+His8Ub*

AY. Ubx3 p-val 1:1: Two sided, one-sample location test p-value of \log_2 ratio and standard error of *ubx3Δ+His8Ub/ wt+His8Ub* relative to a \log_2 ratio of 0.0 (i.e., a ratio of 1.0)

AZ. Ubx3 1:1 IsSig @ 0.05 p-val BH Corrected: True if \log_2 ratio of *ubx3Δ+His8Ub/ wt+His8Ub* is significantly different from 0.0 (p-value < 0.05) after correcting for multiple hypothesis testing using the Benjamini and Hochberg method

BA. Ubx3 p-val <10% Change: Two sided, one-sample location test p-value of \log_2 ratio and standard error of *ubx3Δ+His8Ub/ wt+His8Ub* relative to a protein fold change < 10%

BB. Ubx4 Ratio Log2: \log_2 ratio of *ubx4Δ+His8Ub/ wt+His8Ub*

BC. Ubx4 Std Error: Standard error of the \log_2 ratio of *ubx4Δ+His8Ub/ wt+His8Ub* as calculated by the bootstrap statistical models

BD. Ubx4 Evidence Counts: Number of different peptide ratios used to calculate the \log_2 ratio of *ubx4Δ+His8Ub/ wt+His8Ub*

BE. Ubx4 p-val 1:1: Two sided, one-sample location test p-value of \log_2 ratio and standard error of *ubx4 Δ +His8Ub/ wt+His8Ub* relative to a \log_2 ratio of 0.0 (i.e., a ratio of 1.0)

BF. Ubx4 1:1 IsSig @ 0.05 p-val BH Corrected: True if \log_2 ratio of *ubx4 Δ +His8Ub/ wt+His8Ub* is significantly different from 0.0 (p-value < 0.05) after correcting for multiple hypothesis testing using the Benjamini and Hochberg method

BG. Ubx4 p-val <10% Change: Two sided, one-sample location test p-value of \log_2 ratio and standard error of *ubx4 Δ +His8Ub/ wt+His8Ub* relative to a protein fold change < 10%

BH. Ubx5 Ratio Log2: \log_2 ratio of *ubx5 Δ +His8Ub/ wt+His8Ub*

BI. Ubx5 Std Error: Standard error of the \log_2 ratio of *ubx5 Δ +His8Ub/ wt+His8Ub* as calculated by the bootstrap statistical models

BJ. Ubx5 Evidence Counts: Number of different peptide ratios used to calculate the \log_2 ratio of *ubx5 Δ +His8Ub/ wt+His8Ub*

BK. Ubx5 p-val 1:1: Two sided, one-sample location test p-value of \log_2 ratio and standard error of *ubx5 Δ +His8Ub/ wt+His8Ub* relative to a \log_2 ratio of 0.0 (i.e., a ratio of 1.0)

BL. Ubx5 1:1 IsSig @ 0.05 p-val BH Corrected: True if \log_2 ratio of *ubx5 Δ +His8Ub/ wt+His8Ub* is significantly different from 0.0 (p-value < 0.05) after correcting for multiple hypothesis testing using the Benjamini and Hochberg method

BM. Ubx5 p-val <10% Change: Two sided, one-sample location test p-value of \log_2 ratio and standard error of *ubx5 Δ +His8Ub/ wt+His8Ub* relative to a protein fold change < 10%

BN. Ubx6 Ratio Log2: \log_2 ratio of *ubx6 Δ +His8Ub/ wt+His8Ub*

BO. Ubx6 Std Error: Standard error of the \log_2 ratio of *ubx6 Δ +His8Ub/ wt+His8Ub* as calculated by the bootstrap statistical models

BP. Ubx6 Evidence Counts: Number of different peptide ratios used to calculate the \log_2 ratio of *ubx6 Δ +His8Ub/ wt+His8Ub*

BQ. Ubx6 p-val 1:1: Two sided, one-sample location test p-value of \log_2 ratio and standard error of *ubx6 Δ +His8Ub/ wt+His8Ub* relative to a \log_2 ratio of 0.0 (i.e., a ratio of 1.0)

BR. Ubx6 1:1 IsSig @ 0.05 p-val BH Corrected: True if \log_2 ratio of *ubx6 Δ +His8Ub/ wt+His8Ub* is significantly different from 0.0 (p-value < 0.05) after correcting for multiple hypothesis testing using the Benjamini and Hochberg method

BS. Ubx6 p-val <10% Change: Two sided, one-sample location test p-value of \log_2 ratio and standard error of *ubx6 Δ +His8Ub/ wt+His8Ub* relative to a protein fold change < 10%

BT. Ubx7 Ratio Log2: \log_2 ratio of *ubx7 Δ +His8Ub/ wt+His8Ub*

BU. Ubx7 Std Error: Standard error of the \log_2 ratio of *ubx7 Δ +His8Ub*/ *wt+His8Ub* as calculated by the bootstrap statistical models

BV. Ubx7 Evidence Counts: Number of different peptide ratios used to calculate the \log_2 ratio of *ubx7 Δ +His8Ub*/ *wt+His8Ub*

BW. Ubx7 p-val 1:1: Two sided, one-sample location test p-value of \log_2 ratio and standard error of *ubx7 Δ +His8Ub*/ *wt+His8Ub* relative to a \log_2 ratio of 0.0 (i.e., a ratio of 1.0)

BX. Ubx7 1:1 IsSig @ 0.05 p-val BH Corrected: True if \log_2 ratio of *ubx7 Δ +His8Ub*/ *wt+His8Ub* is significantly different from 0.0 (p-value < 0.05) after correcting for multiple hypothesis testing using the Benjamini and Hochberg method

BY. Ubx7 p-val <10% Change: Two sided, one-sample location test p-value of \log_2 ratio and standard error of *ubx7 Δ +His8Ub*/ *wt+His8Ub* relative to a protein fold change < 10%

BZ. id: Protein group identifier