Numerous proteins with unique characteristics are degraded by the 26S proteasome following monoubiquitination

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The “canonical” proteasomal degradation signal is a substrate-anchored polyubiquitin chain. However, a handful of proteins were shown to be targeted following monoubiquitination. In this study, we established—in both human and yeast cells—a systematic approach for the identification of monoubiquitination-dependent proteasomal substrates. The cellular wild-type polymerizable ubiquitin was replaced with ubiquitin that cannot form chains. Using proteomic ways, and, in humans, are structurally less disordered. We suggest that monoubiquitination-depending degradation is more widespread than assumed previously, and plays key roles in various cellular processes.

monoubiquitination | 26S proteasome | protein degradation | ubiquitin replacement

Polymers of ubiquitin (Ub) are formed on proteasomal substrates in eukaryotic cells by the concerted action of three enzymes: the Ub-activating enzyme (E1), a Ub-carrier protein (E2; known also as Ub-conjugating enzyme (UBC)), and a Ub ligase (E3), which is the specific substrate-recognition element of the system. The Ub chains typically consist of multiple moieties linked to one another via an isopeptide bond between the C-terminal Gly residue of the distinct moiety and the ε-NH₂ group of Lys,6 of the proximal one (1). In addition, the system can also catalyze modification by a single Ub moiety (monoubiquitination) or multiple single Ub moieties (multiple monoubiquitinations), each modifying a distinct lysine residue (2). Generally, monoubiquitination has been conceived as a nondestructive signal. Furthermore, it has been suggested that efficient proteasomal targeting requires a chain with a minimal length of four Ub moieties (3). Monoubiquitination is known to be involved in multiple biological processes. For example, monoubiquitination of proteins containing a ubiquitin-binding domain (UBD) often mediates autoinhibition by a UBD–Ub interaction (4, 5). Signal transduction by membrane receptors, such as the EGFR, is attenuated by monoubiquitination-mediated receptor internalization (6). The subcellular localization of small GTPases is controlled, among other posttranslational modifications, by monoubiquitination (7, 8), and histone monoubiquitination regulates nucleosomal structure, thus affecting gene expression (9). Emerging reports indicate, however, that several substrates can be degraded following monoubiquitination (10–13). Partial degradation/processing of the p105 precursor of NF-kB, which results in release of the p50 active subunit of the transcription factor, is dependent on multiple monoubiquitinations (14). Importantly, these findings demonstrate that the proteasome can recognize a single Ub moiety (moieties) and imply the existence of monoubiquitination vs. polyubiquitination “decision” mechanisms. In this context, a previous study has suggested that the chain length required for proteasomal degradation is determined by the size of the substrate, and possibly other characteristics that affect the affinity of the modified substrate to the proteasome. Specifically, it was suggested that substrates smaller than 150 aa are degraded following monoubiquitination, whereas longer substrates require longer chains. Thus, a dynamic model was proposed, according to which the chain elongates to a point where the affinity to the proteasome is high enough to secure a stable binding

Significance

A substrate-conjugated polyubiquitin chain is accepted as the “canonical” proteasomal degradation signal. Using a cellular (human and yeast) proteomic screen in the exclusive presence of nonpolymerizable ubiquitin, we show that a large group of proteins is degraded by the proteasome following monoubiquitination. The screen also unraveled polyubiquitin-dependent substrates, as they are stabilized in the presence of this ubiquitin mutant. Notably, monoubiquitination- and polyubiquitination-dependent substrates display distinct important characteristics. Monoubiquitinated proteins are of lower molecular mass and of lesser structural disorder. The two groups can be assigned to defined cellular pathways. Furthermore, some of the characteristics are confined to either human or yeast cells, suggesting that the mechanism of action/recognition of the ubiquitin system in the two organisms are different somehow.


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The authors declare no conflict of interest.

See Commentary on page 8894.

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of the conjugated substrate, its concomitant detachment from the E3, and its subsequent degradation (15). Another study demonstrated that restricting the number of ubiquitinatable Lys residues can switch the mode of modification necessary for degradation from multiple monoubiquitinations to polyubiquitination, suggesting that, in the cell, the masking of Lys residues by protein–protein interactions or post-translational modifications can affect the mode of ubiquitination (11).

However, all of these studies have been carried out using specific substrates. Therefore, general conclusions regarding monoubiquitination-dependent degradation mechanisms, the population of substrates that are degraded following this modification, and importantly, whether they have common distinct characteristics, have remained limited.

In this study, we used a systematic proteomic approach for the identification and characterization of monoubiquitination-dependent proteasomal substrates. By silencing the endogenous WT Ub followed by expression of nonpolymerizable lysineless Ub, we identified numerous substrates in both mammalian and yeast cells that are targeted by the proteasome following monoubiquitination or multiple monoubiquitinations. Interestingly, we confirmed a previous hypothesis (15) that there is a correlation between the length of the substrate and its requirement for either monoubiquitination or polyubiquitination. Also, the monoubiquitinated substrates are enriched in specific pathways [e.g., oxidative stress, carbohydrate transport, and components of the ubiquitin–proteasome system (UPS) itself] and, in humans, are structurally less disordered.

Results

Establishing a System for Induction of Monoubiquitination in Cells. In general, to model monoubiquitination (or multiple monoubiquitinations), we silenced endogenous Ub expression and replaced it with a lysineless Ub (UbK0). This nonpolymerizable Ub species, in which all seven Lys residues were replaced with Arg, can modify each Lys in the target substrate only once and cannot be further ubiquitinated (16–19).

To study monoubiquitination in yeast, we used a modification of a previously described Ub replacement method (20). Briefly, all of the Ub-coding genes were deleted and replaced by galactose-inducible Ub (ΔUb strain), and either copper-inducible UbWT or UbK0 (ΔUbWT or ΔUbK0, respectively). Thus, Ub expression can be silenced by adding glucose, and Ub reexpression can be induced by adding copper to the growth medium (Fig. 1A). To validate Ub silencing and reexpression, ΔUbΔUbWT and ΔUbΔUbK0 yeast strains were treated with glucose and copper. As shown in Fig. 1B, Ub expression was efficiently suppressed, and both UbWT and UbK0 were markedly expressed.

To assess monoubiquitination in human cells, we used a modification of a previously described Ub replacement model in human cultured cells (21). Briefly, endogenous Ub is silenced in U2OS cells by a Ub-specific tetracycline-induced shRNA (shUb), and either HA-UbWT or HA-UbK0 is expressed following infection with an adenoviral vector (Fig. 1B). To evaluate Ub silencing efficiency, we monitored Ub and Ub conjugates level in U2OSΔK0 cells following tetracycline treatment. As demonstrated in Fig. 1C, the level of both Ub and Ub–protein conjugates were significantly decreased. In the endogenous Ub-silenced cells, both HA-UbWT and HA-UbK0 were efficiently expressed and assembled into high-molecular-mass conjugates following adenoviral expression (Fig. 1C). It should be noted that the pattern of conjugation appears similar for both UbWT and UbK0 expression. This is probably due to the numerous substrates with a broad range of molecular mass that are conjugated, and from the possibility that many of them are modified by multiple monoubiquitinations.

To demonstrate Ub replacement using an additional method, we quantified Ub using mass spectrometry (MS). As shown in Fig. S1A, tryptic digestion of UbWT and UbK0 yields both common and differential MS-detectable peptides. To assess Ub replacement in yeast, we treated ΔUbΔUbWT cells with glucose and copper and quantified Ub-derived peptides by MS. As illustrated in Fig. S1B, UbK0 was markedly more abundant than endogenous Ub. To evaluate UbK0 expression in human cells, we overexpressed HA-UbK0 via adenoviral infection using increasing multiplicities of infection (MOIs). As displayed in Fig. S1C, UbK0 expression level was MOI dependent and significantly exceeded the level of endogenous Ub.

Taken together, these data demonstrate the effectiveness of our Ub replacement strategies and suggest that our experimental systems are suitable for studying protein monoubiquitination.

Systematic Identification of Monoubiquitination-Dependent Proteasome Substrates. To identify substrates that are degraded following monoubiquitination, we replaced Ub with either UbWT or UbK0 (as a control). We then used anti-K-ε-GG immunoprecipitation (Fig. S2) to enrich and quantify by MS GlyGly-modified peptides derived from tryptic digestion of ubiquitinated proteins (Fig. S2). This method enabled us to identify ubiquitination sites (Ubsites). To verify that the ubiquitinated proteins serve indeed as proteolytic substrates, we monitored the level of nonmodified peptides derived from them (Fig. 2A). To ascertain reproducibility, we performed several independent biological replicates for each model organism, using both stable isotope labeling by amino acids in cell culture (SILAC) and label-free quantification (Table S1). As shown in Fig. 2B, identification of the proteins was quite reproducible. Similar to previous data (22), identification of Ubsites within proteins was less reproducible.

This established experimental setup enabled us to discriminate between proteins degraded following modification by monoubiquitination (or multiple monoubiquitination), and those that are degraded

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Fig. 1. Replacement of endogenous Ub by UbK0 in yeast and mammalian cells. (A) Workflow describing Ub silencing and reexpression (see a detailed description under Experimental Procedures). (B) Ub replacement in yeast cells. ΔUb, ΔUbWT, and ΔUbK0 yeast cells were treated for Ub silencing and Ub reexpression as indicated. Yeast cells were analyzed by trichloroacetic acid (TCA) lysis followed by SDS PAGE and Western blotting (WB) using the indicated antibodies. (C) Ub replacement in human cells. (i) Ub silencing. To silence Ub, U2OsΔK0 cells were treated with tetracycline (1 μg/mL) for the indicated times. (ii) Ub reexpression. Following Ub silencing, cells were infected with viral vectors expressing UbWT or UbK0. In both panels, lysates were analyzed via SDS PAGE followed by WB using the indicated antibodies.
Figure 2. Identification of monoubiquitination- and polyubiquitination-dependent proteasomal substrates. (A) Experimental workflow. See a detailed description in Results. (B) Ubiquitination sites and ubiquitinated proteins identified in independent experiments. See Table S1 for experiment names. (C) The algorithm used for classification to monoubiquitination- and polyubiquitination-dependent substrates.
points to important differences in the mode of recognition of the UPS in the two species. Yeast apparently operates much more by the traditional signal, polyubiquitin, whereas in humans monoubiquitination is used almost as frequently as polyubiquitination to mark proteins for degradation. The difference may arise from a combination of factors such as using different sets of conjugating enzymes (E2s and E3s), different preferences for local sequence and structural features of substrates, and the recognition elements of the proteasome. Some of these issues are addressed below.

In previous studies, it has been shown that protein ubiquitination and degradation are intimately linked with structural disorder. Intrinsically disordered protein regions lack a well-defined tertiary structure, yet they fulfill important functional roles linked with their highly flexible and adaptable structure (25–27). Structural disorder correlates with all three elements of degradation signals: location of the ubiquitin ligase recognition motif on substrates, the Lys residue(s) to which ubiquitin is attached, and a nearby long disordered region (LDR) (a region of at least 30 consecutive disordered residues) that initiates the unfolding of the substrate engaged with the proteasome (15, 28–30). Structural disorder may also be required for ubiquitin conjugation itself, in two different ways. It is repeatedly reported that the mutation of the Lys residue that is the site of modification does not usually abrogate sensitivity to UPS degradation (11, 31), because flexibility of the substrate enables multiple modifications on neighboring Lys resides. By a similar logic, the buildup of a polyubiquitin chain can also benefit from local structural disorder, because it enables the processive addition of subsequent ubiquitin moieties to the end of the growing polyubiquitin chain.

To test whether these disorder features may be related to the use of monoubiquitination vs. polyubiquitination, we tested whether predicted structural disorder of proteins differs in the different datasets (Fig. 4A). We found significant differences between yeast and human proteins: in yeast, the occurrence of structural disorder does not differ between monoubiquitinated and polyubiquitinated substrates, whereas in human cells, structural disorder prevails in polyubiquitinated substrates. Given that polyubiquitin is a stronger signal, we presume that

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Table 1. Putative ubiquitination-mediated proteasomal substrates
structural disorder is primarily used for the buildup of the polyubiquitin chain. Because yeast relies more heavily on polyubiquitination, yet its polyubiquitinated substrates do not have more disorder, it is possible that their E3 ligases differ from humans in some critical features. These can be their number/redundancy, structural disorder, or binding heterogeneity, the structural disorder of which ensures processive addition of ubiquitin moieties in the ubiquitin chain.

These differences also have to manifest themselves in the local disorder of the protein chain around the ubiquitinated Lys residues. In general, the sites of posttranslational modifications (PTMs) in proteins tend to exhibit local disorder, as studied in detail for phosphorylation (32) and also ubiquitination (28). In our entire dataset, the lysines that are the sites of ubiquitination tend to be locally disordered, but even more importantly, they show a highly characteristic difference between the two species. In yeast, monoubiquitination sites, whereas in human cells polyubiquitination sites, are significantly more disordered (Fig. 4B). Our interpretation, again, is that these differences point to likely differences in the UPS in the two species. In yeast, monoubiquitination sites, whereas in human cells polyubiquitination sites, are significantly more disordered (Fig. 4B). The distinction between the signaling strength and functionality of monoubiquitin and polyubiquitin chains in yeast and human cells is also reflected in characteristic differences in the proximity of LDRs to Ub sites, which might be the sites of initiation of proteasomal degradation (28–30). The need of such assistance for monoubiquitination sites in yeast is apparent from the larger proportion of such sites that are close to an LDR (Fig. 4C), and probably also by a larger proportion of such sites that are close to the termini of the proteins, which are generally flexible (Fig. S3B).

Conservation in evolution can be an important indicator of the functionality of PTM sites. For example, functional phosphorylation sites (i.e., shown to have a functional role by direct or indirect evidence, e.g., mutagenesis and/or functional assays) evolve significantly slower than those without evidence for a functional role (34). Interestingly, Ub sites are significantly more conserved in human cells than in yeast (Fig. S3C) (these differences are significant because the phylogenetic coverage of the respective multiple alignments is comparable). These results infer that yeast sites are under a significantly lower evolutionary pressure, which may point to the fact that they are functionally more promiscuous.

Physical Characteristics of the Proteins Play a Role in Their Mode of Ubiquitination: (ii) Size of the Protein. In a previous study, we demonstrated that substrates degraded following conjugation of a single Ub moiety are usually shorter than 150 aa (15), which suggests that monoubiquitination is a weaker signal. Consistently, we found in this study a significant enrichment of shorter proteins among monoubiquitinated substrates in both yeast and human (Fig. S3D). This difference is not reflected in a preference of multiple modifications in longer proteins: there are no significant differences in the length of substrates that are degraded after the attachment of a single vs. multiple monoubiquitin or polyubiquitin chains (Fig. S3E).

Monoubiquitination- and Polyubiquitination-Dependent Substrates Are Differentially Enriched in Specific Biological Processes. To characterize the two different modes of ubiquitination in a cellular function perspective, we searched for enriched gene ontology (GO) terms, using the GOrilla tool (35, 36). As illustrated in Fig. 5A, it appears that monoubiquitination-dependent proteasomal substrates are enriched in oxidative stress response and carbohydrate transport pathways. As presented in Fig. 5B, molecular-function–specific GO terms were also identified. For example, monoubiquitination-dependent substrates were found enriched among ribosomal and proteasomal subunits. Similarities between the monoubiquitinated and polyubiquitinated substrates were also observed, as Ub system components were enriched in both groups. Interestingly, however, monoubiquitinated substrates consisted of mostly Ub ligases, E3s (e.g., HERC3, ITCH, XIAP), whereas polyubiquitinated substrates were enriched with Ub-conjugating enzymes, E2s (e.g., UBE2J1, UBE2T, and UBE2L6).

Ubiquitination Site Sequence Analysis Reveals Unique Patterns. Previous studies have demonstrated motifs and sequence patterns specific for protein posttranslational modifications such as phosphorylation, acetylation, and SUMOylation (29, 30, 37, 38). To identify Ub site motifs, we analyzed our data using the Motif-X algorithm (39), sites that have to be supported by local disorder, probably more for initiation of degradation than modification (29). In human cells, the sites of polyubiquitination are significantly more disordered, probably as much for the processive buildup of the polyubiquitin chain as for initiation of degradation (as suggested above). These are genuine differences and do not result from the natural tendency of lysines to be locally disordered, which, as disorder-promoting amino acids, tend to be located in disordered regions of proteins (33) (Fig. S3A).

**Fig. 3.** Validation of representative candidate substrates degraded by the proteasome following monoubiquitination and polyubiquitination. (A, Upper) MCF7 cells were cotransfected with plasmids coding for GOT1-HA or CDC20-HA along with plasmids coding for UbWT or UbK6 as indicated. (Lower) ΔUbWT and ΔUbK6 yeast cells were transformed with plasmids coding for Gre1p-HA or Ard1p-HA, and Ub replacement was carried out as described in Fig. 1. In all experiments, substrate stability was monitored as described in Experimental Procedures. (B, Upper) MCF7 cells were transfected with either GOT1-HA or CDC20-HA, followed by the treatment with epoxomicin (2 μM, 24 h) as indicated. (Lower) ΔPDR5 yeast cells (strain Y12409 from the EUROSCARF collection) were transformed with plasmids coding for either Arp1p-HA or Gre1p-HA. Strains were treated with cycloheximide (CHX) and bortezomib (100 μM each) as indicated. Samples were collected at the indicated time points. Cell lysates were analyzed via SDS/PAGE followed by WB using the indicated antibodies.
Consistent with previous findings (24), no specific motif was found when analyzing all identified Ubsites in either yeast or human cells. To analyze Ubsite amino acid composition, all identified Ubsites were examined. We constructed an alignment of peptides that are surrounding each modified Lys residue. Residue- and position-specific amino acid occurrences were calculated and were compared with the corresponding proteomic occurrence in a lysine-centered peptide. As depicted in Fig. S4A, ubiquitination sites demonstrated residues-specific enrichment (e.g., Ala, Gly, Gln) and underrepresentation (e.g., Cys, His, Lys, Met, Trp) for both yeast and human cells. Enrichment of Glu, and to a lesser extent Asp, was specific to yeast sites. Importantly, for several amino acids, the enrichment factor depended on the proximity to the modified Lys, suggesting that these residues can affect conjugation mechanisms.

To compare the ubiquitination site composition of monoubiquitination- vs. polyubiquitination-dependent substrates, we performed the above analysis for each group separately. As shown in Fig. S4 B and C, each group displays a unique pattern of enrichment factors, and several differences can be observed between the patterns of monoubiquitination- and polyubiquitination-dependent substrates.

Discussion
In this study, we identified 82 yeast and 220 mammalian proteins that are degraded by the proteasome following monoubiquitination. These significant numbers point to a much broader phenomenon to what was considered until recently as an exception. Therefore, it allows for analysis that sheds light on the mechanisms that underlie the different modes of ubiquitination. Because we did not use proteasome inhibitors, it is likely that some low level, rapidly degrading proteins were below the detection threshold, and therefore the numbers are probably larger.

Experimentally, we replaced UbWT with UbK0 in cells to enforce monoubiquitination. This strategy has been used successfully to inhibit polyubiquitination-dependent proteasomal degradation (14, 17–19). Other methods to study monoubiquitination have been reported, such as inhibition of polyubiquitin chain formation by methylated Ub (40), or detection by Western blotting of specific substrates that appear to be monoubiquitinated (10). However, using methylated Ub is limited to cell-free systems, and using endogenous Ub can identify only individual substrates. Therefore, these methods limit the ability to identify and characterize the broad population of target substrates degraded by the proteasome following monoubiquitination and polyubiquitination. Thus, UbWT-to-UbK0 replacement in cells seemed to be the most suitable strategy for our objective of carrying out a proteome-wide screen to identify these two distinct populations.

Notably, although efficient UbK0 expression inhibits polyubiquitination, it may still support the conjugation of several UbK0 molecules to a protein substrate, resulting in multiple monoubiquitinations. In our study, we included monoubiquitinated...
and multiple-monoubiquitinated substrates in the same group, as discriminating between the two is complicated experimentally.

Importantly, in our screen, we decided not to use proteasome inhibitors as a tool to identify substrates that are nevertheless degraded following Ub replacement; the reason being that, in human cells infected with adenoviral HA-Ub+WT, we could not observe up-regulation of Ub conjugates following treatment with a proteasome inhibitor (Fig. S5A). It should be noted that the proteasome in the control cells was active (Fig. S5A), and its inhibition was efficient (Fig. SSC). This finding is consistent with partial proteasome inhibition by free Ub chains that are accumulated due to the high level of HA-Ub+WT (41). Also, the use of proteasome inhibitors is challenging in yeast cells, as low permeability results in low cellular concentration of the drugs (42). Notably, in human cells, it was reported that proteasome inhibitors impair protein synthesis in a selective manner, thus affecting the proteome in more than one mode. Therefore, interpretation of proteomic data of experiments carried out in their presence is not straightforward (43). Accordingly, we have adapted alternative classification criteria to identify monoubiquitinated vs. ubiquitinated proteasomal substrates based on MS analyses of the proteome and ubiquitome under normal conditions and where only monoUb is available (Results and Fig. 2B). To confirm our results and to nevertheless relate them to proteasomal degradation, we integrated data from previous studies (23, 24, 44) and constructed a reference list of known ubiquitin–proteasome substrates (Dataset S3). Compared with this list, our polyubiquitination-dependent substrates were highly enriched with known proteasomal substrates (P valueYeast = 6.90 × 10⁻²² and P valuehuman = 5.06 × 10⁻³, by hypergeometric test). Furthermore, our monoubiquitination-dependent candidates were also highly enriched with proteasomal substrates (P valuehuman = 1.10 × 10⁻³⁶). These findings strongly suggest that our experimental model is faithful and offers a reliable method for the identification of UPS substrates. Furthermore, we validated biochemically that several randomly sampled monoubiquitination and polyubiquitination-dependent candidates that emerged from the screen do indeed belong to their respective predicted categories (Fig. 3).

Reportedly, membrane proteins such as receptor tyrosine kinases (RTKs) (45) are subjected to monoubiquitination-dependent lysosomal degradation. To specifically identify proteasomal substrates in the absence of proteasome inhibitors, plasma membrane proteins were excluded from our screen.

It is interesting to refer to specific proteins that were identified in previous studies as targeted by monoubiquitination. For example, Syndecan-4 (12) did exhibit site K0/WT ratio < 1 (for Lys105) but was detected in one replicate only. Cks-2 (15) displayed protein K0/WT ratio < 1 at the protein level but had conflicting ratios at site level. Other substrates including Pax-3 (13) and α-synuclein (10) could not be detected, probably due to low abundance in the bone-derived U2OS cells (46). Taken together, it seems that our results are in agreement with random previous data but should be further substantiated by experiments in cells from different tissues.

From the bioinformatics analyses of the substrates, several important and intriguing conclusions can be drawn. First, in agreement with previous studies in which it was shown that substrates of up to 150 residues can be degraded following monoubiquitination (15), we found that the distribution of monoubiquitination-dependent substrates is shifted toward shorter proteins (Fig. S3D).
Furthermore, a difference between yeast and human is also apparent when comparing the ratio of monoubiquitination- and polyubiquitination-dependent substrates. Yeast relies more heavily on polyubiquitination, whereas human cells use both monoubiquitination and polyubiquitination with a similar frequency. This difference can be interpreted if structural disorder is considered as shown by our own data (Fig. 4 and Fig. S3), and if we assume that a single ubiquitin moiety is a weaker signal for degradation than polyubiquitin. As suggested, local structural disorder is involved in various steps of the UPS cascade, from recognition motifs of E3 ligases through local disorder of ubiquitination sites to an LDR initiation site of substrate unfolding (28–30).

We have screened our monoubiquitination-dependent substrates for enriched biological-process-related GO terms and found a highly significant overrepresentation of genes associated with carbohydrate transport and oxidative stress response pathways (Fig. S4). Because carbohydrate transporters are plasma membrane proteins, this finding is consistent with previous studies that demonstrated membrane receptors down-regulation via monoubiquitination-mediated endocytosis (47). Notably, as this pathway results in lysosomal/vacuolar rather than proteasomal degradation, this finding highlights the challenge in distinguishing between these two degradation modes using our experimental system. Oxidative stress was shown to activate cellular signal transduction cascades, and to result in gene expression modulation (48). The enrichment of oxidative stress response proteins in our monoubiquitination-dependent substrates may suggest that they are regulated by a common monoubiquitinating E3 ligase(s). Thus, oxidative stress-mediated down-regulation of this putative E3 may result in up-regulation of oxidative stress pathway components and activate the respective cellular response. Consistently, microarray experiments have shown that the expression of the E3s UBR1 and HUL4, and the E2s CDC43, RAD6, and UBC11, is decreased following exposure to oxidative stress (49).

UPS components were enriched in both groups (Fig. S5). This finding most likely represents the previously reported autoubiquitination sites (43). Analysis of relative amino acid abundance to characterize ubiquitination sites (55) reflect site-level promiscuity, which is supported by low identification of a ubiquitination-site motif in this study and in others (24, 25).

The UPS is a multi-substrate system that degrades a broad spectrum of proteins by ubiquitination, with a large number of proteins being ubiquitinated by more than one E3 ligase (26). This study demonstrates that oxidative stress-mediated degradation for the sake of construction. Physiol Rev 82(2):373–428.


