Deubiquitinating enzymes and the proteasome regulate preferential sets of ubiquitin substrates.

Fredrik Trulsson^{1,#}, Vyacheslav Akimov^{2,#}, Mihaela Robu³, Nila van Overbeek¹, David Aureliano Pérez Berrocal¹, Rashmi G. Shah³, Jürgen Cox⁴, Girish M. Shah³, Blagoy Blagoev^{2,\$*}, Alfred C.O. Vertegaal^{1,\$*}.

- 1. Cell and Chemical Biology, Leiden University Medical Centre, Leiden, The Netherlands.
- 2. Department of Biochemistry and Molecular Biology, University of Southern Denmark, Odense, Denmark.
- Laboratory for Skin Cancer Research, CHU de Québec Laval University Hospital Research Centre, Québec (QC) Canada
- 4. Computational Systems Biochemistry Research Group, Max-Planck Institute of Biochemistry, Martinsried, Germany.
- # These authors contributed equally.
- \$ These authors jointly supervised this work.

*Correspondence: vertegaal@lumc.nl and bab@bmb.sdu.dk

Supplementary Information





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Supplementary Figure 1: Proteasome activity and Ub chains in response to E1, proteasome and DUB inhibition.

a Fluorescent scan of proteasome activity probe (Me₄BodipyFLAhx₃Leu₃VS) labelled proteasome subunits after 3h of indicated UPS inhibitor treatment or WIN 62,577 (WIN) (proteasome activator) in U2OS or HeLa cells, and immunoblot staining with anti Ub (P4D1), n=3 biologically independent samples. **b-d** Input and His10Ub purification of Ub substrates from cells treated for 3h with indicated UPS inhibitor, and combinations of UPS inhibitors, n=3 biologically independent samples. Membranes were stained for Ub K48 chains (Apu2) (**b**), Ub K63 chains (D7A11) (**c**) or SUMO2/3 (8A2) (**d**).





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PR619

Supplementary Figure 2: Dose and time course of DUB and proteasome inhibitors.

Immunoblots of U2OS cells treated for 10, 30, 60 or 180min with DMSO, MG132, PR619, Bortezomib or Carfilzomib at indicated concentrations. Membranes were stained for Ub (P4D1) and β -Actin (A5441). The Ub smear intensity was measured using ImageJ and normalized to the Actin loading control and plotted in Fig. 1k.

Supp	lementary	Figure	3
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b			DMSC	C				MG13	32				PR61	9	
		0.96	0.957	0.956	0.942	0.662	0.68	0.68	0.657	0.69	0.539	0.551	0.552	0.525	0.572
DMSO	0.96		0.953	0.955	0.941	0.684	0.686	0.701	0.661	0.689	0.556	0.568	0.563	0.54	0.584
	0.957	0.953		0.971	0.959	0.67	0.688	0.684	0.676	0.704	0.557	0.566	0.574	0.545	0.587
	0.956	0.955	0.971		0.964	0.664	0.678	0.686	0.663	0.693	0.539	0.547	0.551	0.522	0.568
	0.942	0.941	0.959	0.964		0.664	0.68	0.682	0.663	0.699	0.554	0.564	0.57	0.54	0.585
	0.662	0.684	0.67	0.664	0.664		0.885	0.816	0.863	0.848	0.611	0.599	0.582	0.555	0.598
	0.68	0.686	0.688	0.678	0.68	0.885		0.85	0.951	0.93	0.6	0.623	0.614	0.578	0.622
MG132	0.68	0.701	0.684	0.686	0.682	0.816	0.85		0.821	0.798	0.557	0.572	0.555	0.536	0.584
	0.657	0.661	0.676	0.663	0.663	0.863	0.951	0.821	,	0.932	0.585	0.609	0.605	0.565	0.605
	0.69	0.689	0.704	0.693	0.699	0.848	0.93	0.798	0.932	, . e	0.598	0.619	0.623	0.581	0.617
	0.539	0.556	0.557	0.539	0.554	0.611./	0.6	0.557	0.585	0.598		0.902	0.9	0.89	0.896
	0.551	0.568	0.566	0.547	0.564	0.599	0.622	0.572	0.609	0.619	0.902		0.945	0.941	0.943
PR619	0.552	0.563	0.574	0.551	0.57	0.582	0.614	0.555	0.605	0.623	0.9	0.945	, .	0.945	0.935
	0.525	0.54	0.545	0.522	0.54	0.555	0.578	0.536	0.565	0.581	0.89	0.941	0.945	, .	0.937
	0.572	0.584	0.587	0.568	0.585	0.598	0.622	0.584	0.605	0.617	0.896	0.943	0.935	0.937	

а												
		0.646	0.609	0.512	0.523	0.474	0.569	0.48	0.463	0.403	0.355	0.347
DMSO	0.646		0.712	0.518	0.512	0.592	0.457	0.538	0.476	0.363	0.384	0.381
	0.609	0.712		0.51	0.589	0.485	0.496	0.53	0.524	0.464	0.444	0.411
	0.512	0.518	0.51		0.628	0.683	0.526	0.533	0.522	0.409	0.395	0.379
TAK243	0.523	0.512	0.589	0.628		0.639	0.509	0.546	0.541	0.423	0.393	0.348
	0.474	0.592	0.485	0.683	0.639		0.488	0.571	0.599	0.414	0.4	0.378
	0.569	0.45/	0.495	0.526	0.509	0.488		0.591	0.566	0.375	0.354	0.335
MG132	0.48	0.538	0.53	0.533	0.546	0.571	0.591		0./1/	0.437	0.413	0.429
	0.463	0.476	0.524	0.522	0.541	0.599	0.566	0.717		0.527	0.413	0.405
	0.403	0.363	0.464	0.409	0.423	0.414	0.375	0.437	0.527		0.601	0.707
PROTS	0.335	0.384		0.395	0.353		0.351	0.413		0.601		0.659
	0.347	0.381	0.411	0.379	0.348	0.378	0.335	0.429	0.405	0.707	0.659	

DMSO TAK243 MG132 PR619

Supplementary Figure 3: Reproducibility and correlations of UbiSite DDA and DIA samples.

a Scatter plots of each UbiSite data-dependent acquisition sample (17 fractions) compared with each other, n=3. The Pearson correlation calculated in Perseus (1.6.15) of each comparison is annotated in blue above each scatter plot ³⁹. **b** Scatter plots of each UbiSite data-independent acquisition sample compared with each other, n=5. The Pearson correlation calculated in Perseus (1.6.15) of each comparison is annotated in blue above each scatter plot ³⁹.

Supplementary Figure 4



Supplementary Figure 4: Correlations of treatments in His10Ub data.

Scatter plots of each His10Ub replicate compared with each other after filtering out background binders as described in methods, n=3. The Pearson correlation calculated in Perseus (1.6.15) of each comparison is annotated in blue above each scatter plot ³⁹.





Supplementary Figure 5: Clustering of His10Ub data.

a Hierarchical clustering of His10Ub substrates identified in at least 3 replicates of one treatment and significant versus parental U2OS (student's T-test FDR=0.05 S0=0.1), with missing values imputed. LFQ intensity values were normalized by Z-score (subtraction of the mean). **b** Principal components analysis of the same data, were each treatment is colour coded using the components that explained the most variance, n=3.



Supplementary Figure 6: Ub site motifs and surface accessibility of Ub sites.

a-d Amino acid frequency adjacent to identified Ub sites (K, position 0), 15 amino acids downstream (-15) to 15 amino acids upstream (+15) for Ub sites that changed significantly in response to TAK243 (**a**), MG132 (**b**) and PR619 (**c**) treatments (student's T-test FDR=0.05 S0=0.1) or identified in DMSO but unchanged in all treatments (**d**) generated using Logomaker ⁴⁰. Frequencies are represented by character height where an Amino Acid ratio (AA ratio) of 1 represents 100% frequency. **e-g** Fold change difference of AA ratios compared to DMSO of Ub site motifs in TAK243 (**e**), MG132 (**f**) and PR619(**g**) treated cells, represented by character height. **h**, **i** The sequence window of 15 AAs upstream and downstream of the top 100 most enriched Ub sites in UbiSite data for PR619 or MG132 treated samples, with less than 1-fold difference in the other treatment, were analysed for surface accessibility with NetSurfP - 2.0 ⁴². Randomized sequences of 31 AAs were generated using The Sequence Manipulation Suite ⁴³. Accessible Surface Area (ASA) was plotted as a line graph in (**h**) and the Relative Solvent Accessibility (ASA/MaxASA) in (**i**).

Supplementary Figure 7

Supplementary Figure 7: diGly sites on enzymes and phosphorylation comodifications.

a Venn diagram of diGly sites identified using UbiSite DDA methodology on enzymes mapped to the BRENDA database, where proteins identified in at least one replicate in multiple treatments were considered as intersections, n=3 ⁶⁰. **b** Hierarchical clustering by Euclidean distance of diGly sites identified on enzymes mapped to the BRENDA database (pre-processed with k-means, 300 clusters, 1000 iterations). Values are represented as fold change versus DMSO (log2), n=3. **c** Venn diagram of diGly sites identified on enzymes mapped to the BRENDA database that contain "ubiquitin" in its protein name, where proteins identified in at least one replicate in multiple treatments were considered as intersections, n=3 ⁶⁰. **d** Hierarchical clustering by Euclidean distance of diGly sites identified on enzymes mapped to the BRENDA database that contain "ubiquitin" in its protein name, where proteins identified in at least one replicate in multiple treatments were considered as intersections, n=3 ⁶⁰. **d** Hierarchical clustering by Euclidean distance of diGly sites identified on enzymes mapped to the BRENDA database that contain "ubiquitin" in its protein name (pre-processed with k-means, 300 clusters, 1000 iterations). Values are represented as log2 fold change versus DMSO, n=3 ⁶⁰. **e** Venn diagram of Phospho sites on S, T and Y identified in UbiSite DDA data for each treatment, n=3. **f** Hierarchical clustering by Euclidean distance of phospho sites identified in UbiSite DDA samples (pre-processed with k-means, 300 clusters, 1000 iterations). Values are represented as log2, n=3.

Supplementary Figure 8

Supplementary Figure 8: UbiSite DIA diGly sites on enzymes.

a Hierarchical clustering by Euclidean distance of diGly sites identified using UbiSite DIA methodology on enzymes mapped to the BRENDA database (pre-processed with k-means, 300 clusters, 1000 iterations). Values are represented as fold change versus DMSO (log2), n=5 ⁶⁰. **b** Hierarchical clustering by Euclidean distance of diGly sites identified on enzymes mapped to the BRENDA database that contain "ubiquitin" in its protein name (pre-processed with k-means, 300 clusters, 1000 iterations). Values are represented as log2 fold change versus DMSO, n=5 ⁶⁰.

Supplementary Figure 9

Supplementary Figure 9: PR619 in combination with H₂O₂ induces PARylation without interfering with PARP1 or glycohydrolases.

a Immunoblot of PARylated proteins after 3h UPS inhibitor treatments as indicated, including the SUMO E1 inhibitor (ML792), the PARP1/2 inhibitor (Olaparib) on their own or in combination with increasing concentration of H₂O₂ (0.5mM, 1mM or 2mM), n=3 biologically independent samples. PARylation was probed with anti-PAR antibody (4335-MC-100) and actin was used as a loading control. b Input and elution of FLAG-IP from GMRSiP cells expressing FLAG tagged PARP1 using ten times more cells than Fig. 7h, treated with DMSO or 20µM PR619 for 3h. The membrane was probed with polyclonal PARP1-antibody (Alx-210-302), n=2 biologically independent samples. c PARylation in-vitro assay using PARP1, DNA and NAD with or without PR619 during incubation of PARylation mixture for 15min at 30°C. Membranes were probed for PARylated proteins (10H) and for PARP1 (Alx-210-302), n=3 biologically independent samples. d PARG assay: PARP1 auto-PARylated in-vitro using DNA and NAD was subjected to glycohydrolase treatment, in the presence or absence of PR619. PARylation was carried out by incubating the mixture for 15min at 30°C and the reaction was stopped by using either of the two PARP1 inhibitors PJ134 or Olaparib as indicated. Glycohydrolase was added to samples with or without PR619, and incubated for another 15 min at 30°C. The membrane was probed for PARylated proteins (10H) followed by probing for PARP1 (Alx-210-302), n=3 biologically independent samples.

Jurkat and Hep2 cells - 61,977 sites

Supplementary Figure 10: Ub sites identified compared to previous studies.

a All Ub sites identified in this study compared to Akimov *et al* ²⁵. **b** Comparison of Ub sites identified in this study to Ub sites previously known on PhosphoSitePlus ⁶².

Deubiquitinating enzymes and the proteasome regulate preferential sets of ubiquitin substrates.

Fredrik Trulsson^{1,5}, Vyacheslav Akimov^{2,5}, Mihaela Robu³, Nila van Overbeek¹, David Aureliano Pérez Berrocal¹, Rashmi G. Shah³, Jürgen Cox⁴, Girish M. Shah³, Blagoy Blagoev^{2,6*}, Alfred C.O. Vertegaal^{1,6*}.

- 1. Cell and Chemical Biology, Leiden University Medical Centre, Leiden, The Netherlands.
- 2. Department of Biochemistry and Molecular Biology, University of Southern Denmark, Odense, Denmark.
- Laboratory for Skin Cancer Research, CHU de Québec Laval University Hospital Research Centre, Québec (QC) Canada
- 4. Computational Systems Biochemistry Research Group, Max-Planck Institute of Biochemistry, Martinsried, Germany.
- 5. These authors contributed equally.
- 6. These authors jointly supervised this work.

*Correspondence: vertegaal@lumc.nl and bab@bmb.sdu.dk

Supplementary figures raw blots

1 2 3 4 5 6

1 2 3 4 5 6

1	No Probe	(Me4Bo	dipyFLAh	x3Leu3V٤
2	DMSO			
3	TAK243			
4	MG132			
5	PR619			
6	WIN62,57	7		

Replicate 2

Ubiquitin immunostaining

anti-Ub 1:1000 (Santa Cruz, Cat: sc-8017)

1 2 3 4 5 6 1 2 3 4 5 6

HeLa Cells

Replicate 3

HeLa Cells

U2OS cells

Replicate 1	anti-UbK48 1:1000 (Millipore, Cat:)	05-1307)	Replicate 2	
Input	1 2 3 4 5 6 7 8	Wells from left to right: 1 U2OS parental Input 2 U2OS UbHis10 DMSO 3 U2OS UbHis10 TAK243 4 U2OS UbHis10 MG132 5 U2OS UbHis10 PR619 6 U2OS UbHis10 TAK+MG 7 U2OS UbHis10 TAK+PR 8 U2OS UbHis10 MG+PR	12345678	Wells from left to right: 1 U2OS parental 2 U2OS UbHis10 DMSO 3 U2OS UbHis10 TAK243 4 U2OS UbHis10 MG132 5 U2OS UbHis10 PR619 6 U2OS UbHis10 TAK+MG 7 U2OS UbHis10 TAK+PR 8 U2OS UbHis10 MG+PR
His 10 Pulldown	1 2 3 4 5 6 7 8	His10 Pulldown	1 2 3 4 5 6 7 8	
Ponceau Input	1 2 3 4 5 6 7 8 191 97 64 51 39 28 19 14 7 19 14 7 19 19 19 19 19 19 19 19 19 19		1 2 3 4 5 6 7 8 191 97 64 51 39 28 19 14 7 Node-ing R	
	Input	1 2 3 4 5 6 7 8	Wells from left to right: 1 U2OS parental 2 U2OS UbHis10 DMSO 3 U2OS UbHis10 TAK243 4 U2OS UbHis10 MG132 5 U2OS UbHis10 PR619 6 U2OS UbHis10 TAK+MG 7 U2OS UbHis10 TAK+PR 8 U2OS UbHis10 MG+PR	
	His10 Pulldown	1 2 3 4 5 6 7 8		
		1 2 3 4 5 6 7 8 191 97 64 51 39 28 194 194 7		

Ubiquitin K48 Immunostaining

Supplementary Figure 1b

anti-Ub 1:1000 (Santa Cruz, Cat: s 8017) anti-actin 1:5000 (Sigma, Cat 45441	1 2 3 4 5 6 7 8 9 ¹⁰ 11 ¹²	1 DMSO 10min 2 DMSO 30min 3 DMSO 60min 4 DDMSO 180min 5 MG132 20UM 30min 6 MG132 20UM 30min 7 MG132 20UM 60min 8 MG132 20UM 180min 9 MG132 10UM 10min 10 MG132 10UM 30min 11 MG132 10UM 30min 12 MG132 10UM 30min	1 2 3 4 5 6 7 8 9 ¹⁰ 11 12 1 2 3 4 5 6 7 8 9 ¹⁰ 11 12 1 2 3 4 5 6 7 8 9 ¹⁰ 11 12	1 DMSO 10min 2 DMSO 30min 3 DMSO 60min 4 DMSO 180min 5 Bortezomib 200nM 10min 6 Bortezomib 200nM 30min 7 Bortezomib 200nM 60min 8 Bortezomib 100nM 10min 10 Bortezomib 100nM 30min 11 Bortezomib 100nM 60min 12 Bortezomib 100nM 180min
Replicate	2			
anti-Ub 1:1000 (Santa Cruz, Cat: s 8017) anti-actin 1:5000 (Sigma, Cat 45441	1 2 3 4 5 6 7 8 ^{9 10} 11 12 1 2 3 4 5 6 7 8 ^{9 10} 11 12	1 DMSO 10min 2 DMSO 30min 3 DMSO 60min 4 DMSO 180min 5 MG132 20uM 10min 6 MG132 20uM 30min 7 MG132 20uM 60min 8 MG132 20uM 80min 9 MG132 10uM 10min 10 MG132 10uM 30min 11 MG132 10uM 60min 12 MG132 10uM 180min	1 2 3 4 5 6 7 8 9 ¹⁰ 11 12 1 2 3 4 5 6 7 8 9 ¹⁰ 11 12	1 DMSO 10min 2 DMSO 30min 3 DMSO 60min 4 DMSO 180min 5 Bortezomib 200nM 10min 6 Bortezomib 200nM 30min 7 Bortezomib 200nM 60min 8 Bortezomib 100nM 10min 10 Bortezomib 100nM 30min 11 Bortezomib 100nM 60min 12 Bortezomib 100nM 180min
Replicate	3			
anti-Ub 1:1000 (Santa Cruz, Cat: s 8017)	1 2 3 4 ⁵ 6 7 8 9 10 11 12 1 2 3 4 ⁵ 6 7 8 9 10 11 12	1 DMSO 10min 2 DMSO 30min 3 DMSO 60min 4 DMSO 180min 5 MG132 20uM 10min 6 MG132 20uM 30min 7 MG132 20uM 80min 8 MG132 20uM 180min 9 MG132 10uM 10min 10 MG132 10uM 30min 11 MG132 10uM 60min 12 MG132 10uM 180min	1 2 3 4 5 6 7 8 9 ¹⁰ ₁₁ ¹²	1 DMSO 10min 2 DMSO 30min 3 DMSO 60min 4 DMSO 180min 5 Bortezomib 200nM 10min 6 Bortezomib 200nM 30min 7 Bortezomib 200nM 60min 8 Bortezomib 200nM 10min 9 Bortezomib 100nM 10min 10 Bortezomib 100nM 30min
anti-actin 1:5000			1 2 3 4 5 6 7 8 9 ¹⁰ 112	11 Bortezomib 100nM 60min 12 Bortezomib 100nM 180min

anti-actin 1:5000 (Sigma, Cat 45441

1 2 3 4 5 6 7 8 9 10₁₁12 anti-actin 1:5000

(Sigma, Cat 45441

5 Carfilzomib 2uM 10min 6 Carfilzomib 2uM 30min 7 Carfilzomib 2uM 60min 8 Carfilzomib 2uM 180min 9 Carfilzomib 1uM 10min 10 Carfilzomib 1uM 30min 11 Carfilzomib 1uM 60min 12 Carfilzomib 1uM 180min

1 2 3 4 5 6 7 8 9 10₁₁12

1 DMSO 10min
2 DMSO 30min
3 DMSO 60min
4 DMSO 180min
5 Bortezomib 50nM 10min
6 Bortezomib 50nM 30min
7 Bortezomib 50nM 60min
8 Bortezomib 50nM 180min
9 Carfilzomib 0.5uM 10min
10 Carfilzomib 0.5uM 30min
11 Carfilzomib 0.5uM 60min

12 Carfilzomib 0.5uM 180min

anti-actin 1:5000 (Sigma, Cat 45441

Replicate 1+2

Replicate 2+3

1 DMSO 10min 2 DMSO 30min 3 DMSO 60min 4 DMSO 180min 5 MG132 5uM 10min 6 MG132 5uM 30min 7 MG132 5uM 60min 8 MG132 5uM 180min B 9 MG132 5uM 10min 10 MG132 5uM 30min 11 MG132 5uM 60min 12 MG132 5uM 180min C Supplementary Figure 9a

Wells from left to right, starting at 1: 1 DMSO 2 TAK243 3 MG132 4 PR619 5 ML792 6 Olaparib 7 2 mM H2O2 + TAK243 8 1 mM H2O2 + TAK243 90.5 mM H2O2 + TAK243 102 mM H2O2 + ML792 11 1 mM H2O2 + ML792 12 0.5 mM H2O2 + ML792 Gel 2 Wells from left to right, starting at 1: 13 2 mM H2O2 14 1 mM H2O2 15 0.5 mM H2O2 16 2 mM H2O2 + PR619 17 1 mM H2O2 + PR619 18 0.5 mM H2O2 + PR619 192 mM H2O2 + MG1: 20 1 mM H2O2 + MG1; 21 0.5 mM H2O2 + MG132 22 2 mM H2O2 + Olaparib 23 1 mM H2O2 + Olaparib 24 0.5 mM H2O2 + Olaparib

Gel 1

Membrane

64 Membrane 28 14 191 64 51 39 28 14 14

Gel 1 Wells from left to right, starting at 1: 1 DMSO 2 TAK243 3 MG132 4 PR619 5 ML792 6 Olaparib 7 2 mM H2O2 + TAK243 8 1 mM H2O2 + TAK243 90.5 mM H2O2 + TAK243 10 2 mM H2O2 + ML792 11 1 mM H2O2 + ML792 12 0.5 mM H2O2 + ML792 Gel 2 Wells from left to right, starting at 1: 13 2 mM H2O2 14 1 mM H2O2 15 0.5 mM H2O2 16 2 mM H2O2 + MG1; 17 1 mM H2O2 + MG1; 18 0.5 mM H2O2 + MG132 192 mM H2O2 + PR619 20 1 mM H2O2 + PR619 21 0.5 mM H2O2 + PR619 22 2 mM H2O2 + Olaparib

23 1 mM H2O2 + Olaparib 24 0.5 mM H2O2 + Olaparib

Gel 1 Wells from left to right, starting at 1: 1 DMSO 2 TAK243 3 MG132 4 PR619 5 ML792 6 Olaparib . 7 2 mM H2O2 + TAK243 8 1 mM H2O2 + TAK243 90.5 mM H2O2 + TAK243 10 2 mM H2O2 + ML792 11 1 mM H2O2 + ML792 12 0.5 mM H2O2 + ML792 Gel 2 Wells from left to right, starting at 1: 13 2 mM H2O2 14 1 mM H2O2 15 0.5 mM H2O2 16 2 mM H2O2 + MG1: 17 1 mM H2O2 + MG1: 18 0.5 mM H2O2 + MG132 192 mM H2O2 + PR619 20 1 mM H2O2 + PR619 21 0.5 mM H2O2 + PR619 22 2 mM H2O2 + Olaparib 23 1 mM H2O2 + Olaparib 24 0.5 mM H2O2 + Olaparib

Membrane

Supplementary Fig. 9c (n=3)

Replicate 1

Replicate 2

Supplementary Fig. 9d (n=3)

Replicate 3

