

# Mark Hochstrasser

## List of Publications by Year in descending order

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178  
papers

22,538  
citations

10979

71  
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8618

146  
g-index

191  
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191  
docs citations

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times ranked

16272  
citing authors

#	ARTICLE	IF	CITATIONS
1	Selective microautophagy of proteasomes is initiated by ESCRT-0 and is promoted by proteasome ubiquitylation. <i>Journal of Cell Science</i> , 2022, 135, .	1.2	11
2	The CinB Nuclease from <i>Wolbachia</i> Is Sufficient for Induction of Cytoplasmic Incompatibility in <i>Drosophila</i> . <i>MBio</i> , 2022, 13, e0317721.	1.8	21
3	Cytoplasmic incompatibility: A <i>Wolbachia</i> toxin’s “antidote mechanism comes into view. <i>Current Biology</i> , 2022, 32, R287-R289.	1.8	3
4	Crystal Structures of <i>Wolbachia</i> CidA and CidB Reveal Determinants of Bacteria-induced Cytoplasmic Incompatibility and Rescue. <i>Nature Communications</i> , 2022, 13, 1608.	5.8	15
5	A versatile new tool derived from a bacterial deubiquitylase to detect and purify ubiquitylated substrates and their interacting proteins. <i>PLoS Biology</i> , 2022, 20, e3001501.	2.6	2
6	Conserved proline residues in the coiled coil OB domain linkers of Rpt proteins facilitate eukaryotic proteasome base assembly. <i>Journal of Biological Chemistry</i> , 2021, 296, 100660.	1.6	3
7	Histone sumoylation and chromatin dynamics. <i>Nucleic Acids Research</i> , 2021, 49, 6043-6052.	6.5	70
8	Yeast Nst1 is a novel component of P-bodies and is a specific suppressor of proteasome base assembly defects. <i>Molecular Biology of the Cell</i> , 2021, 32, ar6.	0.9	2
9	Protein quality control degron-containing substrates are differentially targeted in the cytoplasm and nucleus by ubiquitin ligases. <i>Genetics</i> , 2021, 217, 1-19.	1.2	14
10	Structural and mechanistic insights into the complexes formed by <i>Wolbachia</i> cytoplasmic incompatibility factors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	33
11	Ubiquitin Ligase Redundancy and Nuclear-Cytoplasmic Localization in Yeast Protein Quality Control. <i>Biomolecules</i> , 2021, 11, 1821.	1.8	22
12	Crystal structure of a guanine nucleotide exchange factor encoded by the scrub typhus pathogen <i>Orientia tsutsugamushi</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 30380-30390.	3.3	7
13	Histone sumoylation promotes Set3 histone-deacetylase complex-mediated transcriptional regulation. <i>Nucleic Acids Research</i> , 2020, 48, 12151-12168.	6.5	28
14	The Biochemistry of Cytoplasmic Incompatibility Caused by Endosymbiotic Bacteria. <i>Genes</i> , 2020, 11, 852.	1.0	33
15	Epigenetic Mechanisms Contribute to Evolutionary Adaptation of Gene Network Activity under Environmental Selection. <i>Cell Reports</i> , 2020, 33, 108306.	2.9	10
16	A deubiquitylase with an unusually high-affinity ubiquitin-binding domain from the scrub typhus pathogen <i>Orientia tsutsugamushi</i> . <i>Nature Communications</i> , 2020, 11, 2343.	5.8	22
17	The Sts1 nuclear import adaptor uses a noncanonical bipartite NLS and is directly degraded by the proteasome. <i>Journal of Cell Science</i> , 2020, 133, .	1.2	11
18	SUMO and cellular adaptive mechanisms. <i>Experimental and Molecular Medicine</i> , 2020, 52, 931-939.	3.2	22

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19	Microautophagy regulates proteasome homeostasis. <i>Current Genetics</i> , 2020, 66, 683-687.	0.8	24
20	A <i>Wolbachia</i> nuclease and its binding partner provide a distinct mechanism for cytoplasmic incompatibility. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 22314-22321.	3.3	82
21	The Ulp2 $\Sigma$ SUMO protease promotes transcription elongation through regulation of histone sumoylation. <i>EMBO Journal</i> , 2019, 38, e102003.	3.5	28
22	Endoplasmic reticulum stress differentially inhibits endoplasmic reticulum and inner nuclear membrane protein quality control degradation pathways. <i>Journal of Biological Chemistry</i> , 2019, 294, 19814-19830.	1.6	17
23	The Toxin "Antidote Model of Cytoplasmic Incompatibility: Genetics and Evolutionary Implications. <i>Trends in Genetics</i> , 2019, 35, 175-185.	2.9	111
24	Preface. <i>Methods in Enzymology</i> , 2019, 619, xv-xvii.	0.4	0
25	Preface. <i>Methods in Enzymology</i> , 2019, 618, xvii-xix.	0.4	0
26	Caution Does Not Preclude Predictive and Testable Models of Cytoplasmic Incompatibility: A Reply to Shropshire et al.. <i>Trends in Genetics</i> , 2019, 35, 399-400.	2.9	21
27	AMPK regulates ESCRT-dependent microautophagy of proteasomes concomitant with proteasome storage granule assembly during glucose starvation. <i>PLoS Genetics</i> , 2019, 15, e1008387.	1.5	21
28	Cholesterol increases protein levels of the E3 ligase MARCH6 and thereby stimulates protein degradation. <i>Journal of Biological Chemistry</i> , 2019, 294, 2436-2448.	1.6	33
29	Ubiquitin-dependent protein degradation at the endoplasmic reticulum and nuclear envelope. <i>Seminars in Cell and Developmental Biology</i> , 2019, 93, 111-124.	2.3	98
30	The <i>Wolbachia</i> cytoplasmic incompatibility enzyme CidB targets nuclear import and protamine-histone exchange factors. <i>ELife</i> , 2019, 8, .	2.8	61
31	Title is missing!. , 2019, 15, e1008387.		0
32	Title is missing!. , 2019, 15, e1008387.		0
33	Title is missing!. , 2019, 15, e1008387.		0
34	Title is missing!. , 2019, 15, e1008387.		0
35	DNA binding by the MAT $\pm$ 2 transcription factor controls its access to alternative ubiquitin-modification pathways. <i>Molecular Biology of the Cell</i> , 2018, 29, 542-556.	0.9	12
36	Distinct adaptive mechanisms drive recovery from aneuploidy caused by loss of the Ulp2 SUMO protease. <i>Nature Communications</i> , 2018, 9, 5417.	5.8	21

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37	Rapid degradation of progressive ankylosis protein (ANKH) in craniometaphyseal dysplasia. <i>Scientific Reports</i> , 2018, 8, 15710.	1.6	11
38	A <i>Wolbachia</i> deubiquitylating enzyme induces cytoplasmic incompatibility. <i>Nature Microbiology</i> , 2017, 2, 17007.	5.9	307
39	Adaptive aneuploidy counters a dysregulated SUMO system. <i>Cell Cycle</i> , 2017, 16, 383-385.	1.3	4
40	The DUB blade goes snicker-snack: Novel ubiquitin cleavage by a <i>Legionella</i> effector protein. <i>Cell Research</i> , 2017, 27, 845-846.	5.7	3
41	Proteasome Structure and Assembly. <i>Journal of Molecular Biology</i> , 2017, 429, 3500-3524.	2.0	275
42	A unified mechanism for proteolysis and autocatalytic activation in the 20S proteasome. <i>Nature Communications</i> , 2016, 7, 10900.	5.8	88
43	Recent progress in ubiquitin and ubiquitin-like protein (Ubl) signaling. <i>Cell Research</i> , 2016, 26, 389-390.	5.7	16
44	Substrate specificity of the ubiquitin and Ubl proteases. <i>Cell Research</i> , 2016, 26, 441-456.	5.7	92
45	A Conserved C-terminal Element in the Yeast Doa10 and Human MARCH6 Ubiquitin Ligases Required for Selective Substrate Degradation. <i>Journal of Biological Chemistry</i> , 2016, 291, 12105-12118.	1.6	36
46	The Regulation of Chromatin by Dynamic SUMO Modifications. <i>Methods in Molecular Biology</i> , 2016, 1475, 23-38.	0.4	7
47	Loss of the SUMO protease Ulp2 triggers a specific multichromosome aneuploidy. <i>Genes and Development</i> , 2016, 30, 1881-1894.	2.7	37
48	Protein Modification: Bacterial Effectors Rewrite the Rules of Ubiquitylation. <i>Current Biology</i> , 2016, 26, R539-R542.	1.8	2
49	Gyre and gimble in the proteasome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 12896-12898.	3.3	3
50	Assembly of an Evolutionarily Conserved Alternative Proteasome Isoform in Human Cells. <i>Cell Reports</i> , 2016, 14, 2962-2974.	2.9	39
51	Distinct Elements in the Proteasomal $\beta^5$ Subunit Propeptide Required for Autocatalytic Processing and Proteasome Assembly. <i>Journal of Biological Chemistry</i> , 2016, 291, 1991-2003.	1.6	15
52	SUMO Pathway Modulation of Regulatory Protein Binding at the Ribosomal DNA Locus in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2016, 202, 1377-1394.	1.2	22
53	Proteasomes: Isolation and Activity Assays. <i>Current Protocols in Cell Biology</i> , 2015, 67, 3.43.1-3.43.20.	2.3	29
54	STUBL-mediated degradation of the transcription factor MAT $\beta$ 2 requires degradation elements that coincide with corepressor binding sites. <i>Molecular Biology of the Cell</i> , 2015, 26, 3401-3412.	0.9	20

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55	A Single $\alpha$ Helix Drives Extensive Remodeling of the Proteasome Lid and Completion of Regulatory Particle Assembly. <i>Cell</i> , 2015, 163, 432-444.	13.5	73
56	Ubiquitin-dependent protein degradation at the yeast endoplasmic reticulum and nuclear envelope. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2015, 50, 1-17.	2.3	72
57	Site-specific cation release drives actin filament severing by vertebrate cofilin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 17821-17826.	3.3	45
58	The Intrinsically Disordered Sem1 Protein Functions as a Molecular Tether during Proteasome Lid Biogenesis. <i>Molecular Cell</i> , 2014, 53, 433-443.	4.5	64
59	Assembly of the 20S proteasome. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2014, 1843, 2-12.	1.9	80
60	Molecular Architecture and Assembly of the Eukaryotic Proteasome. <i>Annual Review of Biochemistry</i> , 2013, 82, 415-445.	5.0	330
61	N-terminal acetylation of the yeast Derlin Der1 is essential for Hrd1 ubiquitin-ligase activity toward luminal ER substrates. <i>Molecular Biology of the Cell</i> , 2013, 24, 890-900.	0.9	43
62	A Conserved Protein with AN1 Zinc Finger and Ubiquitin-like Domains Modulates Cdc48 (p97) Function in the Ubiquitin-Proteasome Pathway. <i>Journal of Biological Chemistry</i> , 2013, 288, 33682-33696.	1.6	23
63	Ulp2 SUMO Protease. , 2013, , 2362-2365.		0
64	The Doa4 Deubiquitylating Enzyme ( <i>Saccharomyces cerevisiae</i> ). , 2013, , 2049-2052.		0
65	Aberrant substrate engagement of the ER translocon triggers degradation by the Hrd1 ubiquitin ligase. <i>Journal of Cell Biology</i> , 2012, 197, 761-773.	2.3	59
66	Desumoylation of the Endoplasmic Reticulum Membrane VAP Family Protein Scs2 by Ulp1 and SUMO Regulation of the Inositol Synthesis Pathway. <i>Molecular and Cellular Biology</i> , 2012, 32, 64-75.	1.1	24
67	Function and regulation of SUMO proteases. <i>Nature Reviews Molecular Cell Biology</i> , 2012, 13, 755-766.	16.1	523
68	Split-Doa10: A Naturally Split Polytopic Eukaryotic Membrane Protein Generated by Fission of a Nuclear Gene. <i>PLoS ONE</i> , 2012, 7, e45194.	1.1	6
69	A new class of SUMO proteases. <i>EMBO Reports</i> , 2012, 13, 284-285.	2.0	10
70	Disulfide Engineering to Map Subunit Interactions in the Proteasome and Other Macromolecular Complexes. <i>Methods in Molecular Biology</i> , 2012, 832, 349-362.	0.4	5
71	Analysis of Protein Ubiquitination. <i>Current Protocols in Protein Science</i> , 2011, 66, Unit14.5.	2.8	29
72	Incorporation of the Rpn12 Subunit Couples Completion of Proteasome Regulatory Particle Lid Assembly to Lid-Base Joining. <i>Molecular Cell</i> , 2011, 44, 907-917.	4.5	63

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73	A conserved 20S proteasome assembly factor requires a C-terminal HbYX motif for proteasomal precursor binding. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 622-629.	3.6	70
74	Order of the Proteasomal ATPases and Eukaryotic Proteasome Assembly. <i>Cell Biochemistry and Biophysics</i> , 2011, 60, 13-20.	0.9	51
75	An Unusual Transmembrane Helix in the Endoplasmic Reticulum Ubiquitin Ligase Doa10 Modulates Degradation of Its Cognate E2 Enzyme. <i>Journal of Biological Chemistry</i> , 2011, 286, 20163-20174.	1.6	35
76	A WLM Protein with SUMO-Directed Protease Activity. <i>Molecular and Cellular Biology</i> , 2010, 30, 3734-3736.	1.1	6
77	SUMO-independent in vivo activity of a SUMO-targeted ubiquitin ligase toward a short-lived transcription factor. <i>Genes and Development</i> , 2010, 24, 893-903.	2.7	80
78	The Ubiquitinâ€“Proteasome System. , 2010, , 1293-1296.		0
79	Redundancy and variation in the ubiquitin-mediated proteolytic targeting of a transcription factor. <i>Cell Cycle</i> , 2010, 9, 4282-4285.	1.3	18
80	Designed Proteins To Modulate Cellular Networks. <i>ACS Chemical Biology</i> , 2010, 5, 545-552.	1.6	46
81	Heterohexameric Ring Arrangement of the Eukaryotic Proteasomal ATPases: Implications for Proteasome Structure and Assembly. <i>Molecular Cell</i> , 2010, 38, 393-403.	4.5	130
82	The SUMO-targeted ubiquitin ligase subunit Slx5 resides in nuclear foci and at sites of DNA breaks. <i>Cell Cycle</i> , 2009, 8, 1080-1089.	1.3	40
83	Essential Role of Nuclear Localization for Yeast Ulp2 SUMO Protease Function. <i>Molecular Biology of the Cell</i> , 2009, 20, 2196-2206.	0.9	31
84	A Tetrahedral Transition State at the Active Sites of the 20S Proteasome Is Coupled to Opening of the Î±-Ring Channel. <i>Structure</i> , 2009, 17, 1137-1147.	1.6	84
85	Small epitopeâ€“linker modules for PCRâ€“based Câ€“terminal tagging in <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 2009, 26, 185-192.	0.8	89
86	Origin and function of ubiquitin-like proteins. <i>Nature</i> , 2009, 458, 422-429.	13.7	670
87	Introduction to Intracellular Protein Degradation. <i>Chemical Reviews</i> , 2009, 109, 1479-1480.	23.0	9
88	Quantitative Proteomics Reveals the Function of Unconventional Ubiquitin Chains in Proteasomal Degradation. <i>Cell</i> , 2009, 137, 133-145.	13.5	948
89	Multiple Assembly Chaperones Govern Biogenesis of the Proteasome Regulatory Particle Base. <i>Cell</i> , 2009, 137, 887-899.	13.5	153
90	Identification of SUMO-Interacting Proteins by Yeast Two-Hybrid Analysis. <i>Methods in Molecular Biology</i> , 2009, 497, 107-120.	0.4	29

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91	Degradation of the bile salt export pump at endoplasmic reticulum in progressive familial intrahepatic cholestasis type II. <i>Hepatology</i> , 2008, 48, 1558-1569.	3.6	70
92	A multimeric assembly factor controls the formation of alternative 20S proteasomes. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 237-244.	3.6	144
93	Diversity of degradation signals in the ubiquitin-proteasome system. <i>Nature Reviews Molecular Cell Biology</i> , 2008, 9, 679-689.	16.1	701
94	Some assembly required: dedicated chaperones in eukaryotic proteasome biogenesis. <i>Biological Chemistry</i> , 2008, 389, 1143-1151.	1.2	38
95	Ulp2 and the DNA damage response: Desumoylation enables safe passage through mitosis. <i>Cell Cycle</i> , 2008, 7, 52-56.	1.3	13
96	An emerging role for thioester-linked polyubiquitin chains in protein degradation. <i>FASEB Journal</i> , 2008, 22, 605.7.	0.2	0
97	The Yeast Hex3-Slx8 Heterodimer Is a Ubiquitin Ligase Stimulated by Substrate Sumoylation. <i>Journal of Biological Chemistry</i> , 2007, 282, 34176-34184.	1.6	200
98	The Ulp2 SUMO Protease Is Required for Cell Division following Termination of the DNA Damage Checkpoint. <i>Molecular and Cellular Biology</i> , 2007, 27, 6948-6961.	1.1	40
99	A nuclear envelope protein linking nuclear pore basket assembly, SUMO protease regulation, and mRNA surveillance. <i>Journal of Cell Biology</i> , 2007, 178, 813-827.	2.3	99
100	Ubiquitin Ligation without a Ligase. <i>Developmental Cell</i> , 2007, 13, 4-6.	3.1	9
101	Autoregulation of an E2 enzyme by ubiquitin-chain assembly on its catalytic residue. <i>Nature Cell Biology</i> , 2007, 9, 422-427.	4.6	142
102	Î²-Subunit appendages promote 20S proteasome assembly by overcoming an Ump1-dependent checkpoint. <i>EMBO Journal</i> , 2007, 26, 2339-2349.	3.5	132
103	Modification of Proteins by Ubiquitin and Ubiquitin-Like Proteins. <i>Annual Review of Cell and Developmental Biology</i> , 2006, 22, 159-180.	4.0	1,352
104	Lingering Mysteries of Ubiquitin-Chain Assembly. <i>Cell</i> , 2006, 124, 27-34.	13.5	230
105	Cecile M. Pickart 1954-2006. <i>Nature Cell Biology</i> , 2006, 8, 542-543.	4.6	0
106	Spatially regulated ubiquitin ligation by an ER/nuclear membrane ligase. <i>Nature</i> , 2006, 443, 827-831.	13.7	155
107	Membrane and soluble substrates of the Doa10 ubiquitin ligase are degraded by distinct pathways. <i>EMBO Journal</i> , 2006, 25, 533-543.	3.5	249
108	The Short-Lived MatÎ±2 Transcriptional Repressor Is Protected from Degradation In Vivo by Interactions with Its Corepressors Tup1 and Ssn6. <i>Molecular and Cellular Biology</i> , 2006, 26, 371-380.	1.1	17

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109	A conserved late endosome targeting signal required for Doa4 deubiquitylating enzyme function. <i>Journal of Cell Biology</i> , 2006, 175, 825-835.	2.3	41
110	An amphipathic helix targets serum and glucocorticoid-induced kinase 1 to the endoplasmic reticulum-associated ubiquitin-conjugation machinery. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 11178-11183.	3.3	79
111	Membrane Topology of the Yeast Endoplasmic Reticulum-localized Ubiquitin Ligase Doa10 and Comparison with Its Human Ortholog TEB4 (MARCH-VI). <i>Journal of Biological Chemistry</i> , 2006, 281, 4646-4653.	1.6	126
112	Defining the SUMO-modified Proteome by Multiple Approaches in <i>Saccharomyces cerevisiae</i> *. <i>Journal of Biological Chemistry</i> , 2005, 280, 4102-4110.	1.6	354
113	Rtt106p is a histone chaperone involved in heterochromatin-mediated silencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 13410-13415.	3.3	110
114	Preparation and Characterization of Yeast and Human Desumoylating Enzymes. <i>Methods in Enzymology</i> , 2005, 398, 457-467.	0.4	3
115	Varshavsky's Contributions. <i>Science</i> , 2004, 306, 1290-1292.	6.0	11
116	Sem1, the yeast ortholog of a human BRCA2-binding protein, is a component of the proteasome regulatory particle that enhances proteasome stability. <i>Journal of Cell Science</i> , 2004, 117, 6447-6454.	1.2	94
117	Distinct Machinery Is Required in <i>Saccharomyces cerevisiae</i> for the Endoplasmic Reticulum-associated Degradation of a Multispanning Membrane Protein and a Soluble Luminal Protein. <i>Journal of Biological Chemistry</i> , 2004, 279, 38369-38378.	1.6	232
118	Ubiquitin signalling: what's in a chain?. <i>Nature Cell Biology</i> , 2004, 6, 571-572.	4.6	28
119	Plasticity in eucaryotic 20S proteasome ring assembly revealed by a subunit deletion in yeast. <i>EMBO Journal</i> , 2004, 23, 500-510.	3.5	85
120	NF- $\kappa$ B signaling: Flipping the Switch with Polyubiquitin Chains. <i>Current Biology</i> , 2004, 14, R898-R900.	1.8	25
121	Mechanism and function of deubiquitinating enzymes. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2004, 1695, 189-207.	1.9	799
122	Ubiquitin-dependent control of development in <i>Saccharomyces cerevisiae</i> . <i>Current Opinion in Microbiology</i> , 2004, 7, 647-654.	2.3	7
123	A superfamily of protein tags: ubiquitin, SUMO and related modifiers. <i>Trends in Biochemical Sciences</i> , 2003, 28, 321-328.	3.7	359
124	The Ubiquitin-Proteasome System. , 2003, , 347-350.		0
125	The Ulp1 SUMO isopeptidase. <i>Journal of Cell Biology</i> , 2003, 160, 1069-1082.	2.3	186
126	Ubiquitin-dependent degradation of the yeast Mat $\alpha$ 2 repressor enables a switch in developmental state. <i>Genes and Development</i> , 2003, 17, 2259-2270.	2.7	48



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127	MOLECULAR BIOLOGY: New Proteases in a Ubiquitin Stew. <i>Science</i> , 2002, 298, 549-552.	6.0	26
128	Assaying protein ubiquitination in <i>Saccharomyces cerevisiae</i> . <i>Methods in Enzymology</i> , 2002, 351, 248-257.	0.4	15
129	Analysis of Protein Ubiquitination. <i>Current Protocols in Protein Science</i> , 2002, 29, Unit 14.5.	2.8	8
130	New Structural Clues to Substrate Specificity in the "Ubiquitin System". <i>Molecular Cell</i> , 2002, 9, 453-454.	4.5	14
131	SP-RING for SUMO. <i>Cell</i> , 2001, 107, 5-8.	13.5	257
132	Unraveling the means to the end in ATP-dependent proteases. , 2001, 8, 294-296.		19
133	A conserved ubiquitin ligase of the nuclear envelope/endoplasmic reticulum that functions in both ER-associated and Matalpha 2 repressor degradation. <i>Genes and Development</i> , 2001, 15, 2660-2674.	2.7	421
134	Evolution and function of ubiquitin-like protein-conjugation systems. <i>Nature Cell Biology</i> , 2000, 2, E153-E157.	4.6	364
135	The Doa4 Deubiquitinating Enzyme Is Functionally Linked to the Vacuolar Protein-sorting and Endocytic Pathways. <i>Molecular Biology of the Cell</i> , 2000, 11, 3365-3380.	0.9	282
136	Analysis of the Deubiquitinating Enzymes of the Yeast <i>Saccharomyces cerevisiae</i> . <i>Biological Chemistry</i> , 2000, 381, 981-92.	1.2	162
137	The Yeast ULP2 ( SMT4 ) Gene Encodes a Novel Protease Specific for the Ubiquitin-Like Smt3 Protein. <i>Molecular and Cellular Biology</i> , 2000, 20, 2367-2377.	1.1	337
138	A viable ubiquitin-activating enzyme mutant for evaluating ubiquitin system function in <i>Saccharomyces cerevisiae</i> . <i>FEBS Letters</i> , 2000, 477, 193-198.	1.3	27
139	BIOCHEMISTRY: All in the Ubiquitin Family. <i>Science</i> , 2000, 289, 563-564.	6.0	106
140	The Doa4 Deubiquitinating Enzyme Is Required for Ubiquitin Homeostasis in Yeast. <i>Molecular Biology of the Cell</i> , 1999, 10, 2583-2594.	0.9	264
141	Interaction of the Doa4 Deubiquitinating Enzyme with the Yeast 26S Proteasome. <i>Molecular Biology of the Cell</i> , 1999, 10, 741-756.	0.9	118
142	A new protease required for cell-cycle progression in yeast. <i>Nature</i> , 1999, 398, 246-251.	13.7	672
143	Structure and functional analysis of the 26S proteasome subunits from plants. <i>Molecular Biology Reports</i> , 1999, 26, 137-146.	1.0	48
144	Eukaryotic 20S proteasome catalytic subunit propeptides prevent active site inactivation by N-terminal acetylation and promote particle assembly. <i>EMBO Journal</i> , 1999, 18, 3575-3585.	3.5	134

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145	Substrate Targeting in the Ubiquitin System. <i>Cell</i> , 1999, 97, 427-430.	13.5	417
146	Unified nomenclature for subunits of the <i>Saccharomyces cerevisiae</i> proteasome regulatory particle. <i>Trends in Biochemical Sciences</i> , 1998, 23, 244-245.	3.7	127
147	Degradation Signal Masking by Heterodimerization of MAT $\alpha$ 2 and MAT $\alpha$ 1 Blocks Their Mutual Destruction by the Ubiquitin-Proteasome Pathway. <i>Cell</i> , 1998, 94, 217-227.	13.5	189
148	An Evolutionarily Conserved Gene on Human Chromosome 5q33 encodes a Novel Deubiquitinating Enzyme. <i>Genomics</i> , 1998, 49, 411-418.	1.3	18
149	A Deubiquitinating Enzyme That Disassembles Free Polyubiquitin Chains Is Required for Development but Not Growth in <i>Dictyostelium</i> . <i>Journal of Biological Chemistry</i> , 1998, 273, 29178-29187.	1.6	44
150	The Deubiquitinating Enzymes. , 1998, , 99-125.		46
151	Ubiquitin-Dependent Degradation of Transcription Regulators. , 1998, , 279-302.		13
152	Molecular Organization of the 20S Proteasome Gene Family from <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 1998, 149, 677-692.	1.2	103
153	There's the Rub: a novel ubiquitin-like modification linked to cell cycle regulation. <i>Genes and Development</i> , 1998, 12, 901-907.	2.7	119
154	Identification of the yeast 20S proteasome catalytic centers and subunit interactions required for active-site formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997, 94, 7156-7161.	3.3	275
155	SUMO-1: Ubiquitin gains weight. <i>Trends in Cell Biology</i> , 1997, 7, 408-413.	3.6	79
156	In vivo disassembly of free polyubiquitin chains by yeast Ubp14 modulates rates of protein degradation by the proteasome. <i>EMBO Journal</i> , 1997, 16, 4826-4838.	3.5	211
157	UBIQUITIN-DEPENDENT PROTEIN DEGRADATION. <i>Annual Review of Genetics</i> , 1996, 30, 405-439.	3.2	1,566
158	Autocatalytic Subunit Processing Couples Active Site Formation in the 20S Proteasome to Completion of Assembly. <i>Cell</i> , 1996, 86, 961-972.	13.5	376
159	Protein Degradation or Regulation: Ub the Judge. <i>Cell</i> , 1996, 84, 813-815.	13.5	273
160	DUB-1, a deubiquitinating enzyme with growth-suppressing activity.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996, 93, 3275-3279.	3.3	166
161	The yeast SEN3 gene encodes a regulatory subunit of the 26S proteasome complex required for ubiquitin-dependent protein degradation in vivo. <i>Molecular and Cellular Biology</i> , 1995, 15, 6311-6321.	1.1	75
162	Ubiquitin, proteasomes, and the regulation of intracellular protein degradation. <i>Current Opinion in Cell Biology</i> , 1995, 7, 215-223.	2.6	859

#	ARTICLE	IF	CITATIONS
163	The DOA Pathway: Studies on the Functions and Mechanisms of Ubiquitin-dependent Protein Degradation in the Yeast <i>Saccharomyces cerevisiae</i> . Cold Spring Harbor Symposia on Quantitative Biology, 1995, 60, 503-513.	2.0	20
164	Degradation of the yeast MAT $\alpha$ 2 transcriptional regulator is mediated by the proteasome. FEBS Letters, 1994, 354, 50-52.	1.3	56
165	The yeast DOA4 gene encodes a deubiquitinating enzyme related to a product of the human tre-2 oncogene. Nature, 1993, 366, 313-319.	13.7	394
166	Multiple ubiquitin-conjugating enzymes participate in the in vivo degradation of the yeast MAT $\alpha$ 2 repressor. Cell, 1993, 74, 357-369.	13.5	415
167	Ubiquitin and intracellular protein degradation. Current Opinion in Cell Biology, 1992, 4, 1024-1031.	2.6	76
168	The short-lived MAT $\alpha$ 2 transcriptional regulator is ubiquitinated in vivo.. Proceedings of the National Academy of Sciences of the United States of America, 1991, 88, 4606-4610.	3.3	255
169	Functions of Intracellular Protein Degradation in Yeast. , 1991, 13, 307-329.		2
170	In vivo degradation of a transcriptional regulator: The yeast $\alpha$ 2 repressor. Cell, 1990, 61, 697-708.	13.5	251
171	Three-dimensional organization of <i>Drosophila melanogaster</i> interphase nuclei. II. Chromosome spatial organization and gene regulation.. Journal of Cell Biology, 1987, 104, 1471-1483.	2.3	108
172	Three-dimensional organization of <i>Drosophila melanogaster</i> interphase nuclei. I. Tissue-specific aspects of polytene nuclear architecture.. Journal of Cell Biology, 1987, 104, 1455-1470.	2.3	119
173	Chromosome structure in four wild-type polytene tissues of <i>Drosophila melanogaster</i> . Chromosoma, 1987, 95, 197-208.	1.0	28
174	Spatial organization of chromosomes in the salivary gland nuclei of <i>Drosophila melanogaster</i> .. Journal of Cell Biology, 1986, 102, 112-123.	2.3	256
175	Light microscope based analysis of three-dimensional structure: Applications to the study of <i>Drosophila</i> salivary gland nuclei. I. Data collection and analysis. Journal of Microscopy, 1985, 137, 241-252.	0.8	23
176	Characteristic folding pattern of polytene chromosomes in <i>Drosophila</i> salivary gland nuclei. Nature, 1984, 308, 414-421.	13.7	188
177	Properties of the T4 bacteriophage DNA replication apparatus: The T4 dda DNA helicase is required to pass a bound RNA polymerase molecule. Cell, 1983, 34, 115-123.	13.5	120
178	OtDUB from the Human Pathogen <i>Orientia tsutsugamushi</i> Modulates Host Membrane Trafficking by Multiple Mechanisms. Molecular and Cellular Biology, 0, , .	1.1	6