

Mark Hochstrasser

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

170
papers

19,292
citations

67
h-index

138
g-index

191
ext. papers

21,063
ext. citations

14.3
avg, IF

7.3
L-index

#	Paper	IF	Citations
170	The CinB Nuclease from <i>Neisseria meningitidis</i> Is Sufficient for Induction of Cytoplasmic Incompatibility in <i>Escherichia coli</i> . <i>MBio</i> , 2022 , e0317721	7.8	3
169	Cytoplasmic incompatibility: A Wolbachia toxin-antidote mechanism comes into view.. <i>Current Biology</i> , 2022 , 32, R287-R289	6.3	0
168	Crystal Structures of Wolbachia CidA and CidB Reveal Determinants of Bacteria-induced Cytoplasmic Incompatibility and Rescue.. <i>Nature Communications</i> , 2022 , 13, 1608	17.4	2
167	Ubiquitin Ligase Redundancy and Nuclear-Cytoplasmic Localization in Yeast Protein Quality Control.. <i>Biomolecules</i> , 2021 , 11,	5.9	2
166	Structural and mechanistic insights into the complexes formed by cytoplasmic incompatibility factors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	8
165	Protein quality control degron-containing substrates are differentially targeted in the cytoplasm and nucleus by ubiquitin ligases. <i>Genetics</i> , 2021 , 217, 1-19	4	3
164	Histone sumoylation and chromatin dynamics. <i>Nucleic Acids Research</i> , 2021 , 49, 6043-6052	20.1	23
163	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	5.4	1
162	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	3.5	0
161	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	17.4	6
160	The Sts1 nuclear import adapter uses a non-canonical bipartite nuclear localization signal and is directly degraded by the proteasome. <i>Journal of Cell Science</i> , 2020 , 133,	5.3	4
159	SUMO and cellular adaptive mechanisms. <i>Experimental and Molecular Medicine</i> , 2020 , 52, 931-939	12.8	6
158	Microautophagy regulates proteasome homeostasis. <i>Current Genetics</i> , 2020 , 66, 683-687	2.9	10
157	Crystal structure of a guanine nucleotide exchange factor encoded by the scrub typhus pathogen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 30380-30390	11.5	1
156	Histone sumoylation promotes Set3 histone-deacetylase complex-mediated transcriptional regulation. <i>Nucleic Acids Research</i> , 2020 , 48, 12151-12168	20.1	14
155	The Biochemistry of Cytoplasmic Incompatibility Caused by Endosymbiotic Bacteria. <i>Genes</i> , 2020 , 11,	4.2	17
154	Epigenetic Mechanisms Contribute to Evolutionary Adaptation of Gene Network Activity under Environmental Selection. <i>Cell Reports</i> , 2020 , 33, 108306	10.6	3

153	The Toxin-Antidote Model of Cytoplasmic Incompatibility: Genetics and Evolutionary Implications. <i>Trends in Genetics</i> , 2019 , 35, 175-185	8.5	65
152	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	8.5	15
151	A 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	11.5	46
150	The Ulp2 SUMO protease promotes transcription elongation through regulation of histone sumoylation. <i>EMBO Journal</i> , 2019 , 38, e102003	13	14
149	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	5.4	4
148	The cytoplasmic incompatibility enzyme CidB targets nuclear import and protamine-histone exchange factors. <i>ELife</i> , 2019 , 8,	8.9	35
147	AMPK regulates ESCRT-dependent microautophagy of proteasomes concomitant with proteasome storage granule assembly during glucose starvation. <i>PLoS Genetics</i> , 2019 , 15, e1008387	6	13
146	Cholesterol increases protein levels of the E3 ligase MARCH6 and thereby stimulates protein degradation. <i>Journal of Biological Chemistry</i> , 2019 , 294, 2436-2448	5.4	17
145	Ubiquitin-dependent protein degradation at the endoplasmic reticulum and nuclear envelope. <i>Seminars in Cell and Developmental Biology</i> , 2019 , 93, 111-124	7.5	55
144	AMPK regulates ESCRT-dependent microautophagy of proteasomes concomitant with proteasome storage granule assembly during glucose starvation 2019 , 15, e1008387		
143	AMPK regulates ESCRT-dependent microautophagy of proteasomes concomitant with proteasome storage granule assembly during glucose starvation 2019 , 15, e1008387		
142	AMPK regulates ESCRT-dependent microautophagy of proteasomes concomitant with proteasome storage granule assembly during glucose starvation 2019 , 15, e1008387		
141	AMPK regulates ESCRT-dependent microautophagy of proteasomes concomitant with proteasome storage granule assembly during glucose starvation 2019 , 15, e1008387		
140	DNA binding by the MAT α transcription factor controls its access to alternative ubiquitin-modification pathways. <i>Molecular Biology of the Cell</i> , 2018 , 29, 542-556	3.5	9
139	Distinct adaptive mechanisms drive recovery from aneuploidy caused by loss of the Ulp2 SUMO protease. <i>Nature Communications</i> , 2018 , 9, 5417	17.4	12
138	Rapid degradation of progressive ankylosis protein (ANKH) in craniometaphyseal dysplasia. <i>Scientific Reports</i> , 2018 , 8, 15710	4.9	6
137	A Wolbachia deubiquitylating enzyme induces cytoplasmic incompatibility. <i>Nature Microbiology</i> , 2017 , 2, 17007	26.6	198
136	The DUB blade goes snicker-snack: Novel ubiquitin cleavage by a Legionella effector protein. <i>Cell Research</i> , 2017 , 27, 845-846	24.7	2

135	Proteasome Structure and Assembly. <i>Journal of Molecular Biology</i> , 2017 , 429, 3500-3524	6.5	169
134	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	11.5	3
133	Assembly of an Evolutionarily Conserved Alternative Proteasome Isoform in Human Cells. <i>Cell Reports</i> , 2016 , 14, 2962-74	10.6	27
132	Distinct Elements in the Proteasomal β Subunit Propeptide Required for Autocatalytic Processing and Proteasome Assembly. <i>Journal of Biological Chemistry</i> , 2016 , 291, 1991-2003	5.4	11
131	SUMO Pathway Modulation of Regulatory Protein Binding at the Ribosomal DNA Locus in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2016 , 202, 1377-94	4	19
130	A unified mechanism for proteolysis and autocatalytic activation in the 20S proteasome. <i>Nature Communications</i> , 2016 , 7, 10900	17.4	66
129	Substrate specificity of the ubiquitin and Ubl proteases. <i>Cell Research</i> , 2016 , 26, 441-56	24.7	70
128	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, 12105-18	5.4	18
127	The Regulation of Chromatin by Dynamic SUMO Modifications. <i>Methods in Molecular Biology</i> , 2016 , 1475, 23-38	1.4	7
126	Loss of the SUMO protease Ulp2 triggers a specific multichromosome aneuploidy. <i>Genes and Development</i> , 2016 , 30, 1881-94	12.6	26
125	Protein Modification: Bacterial Effectors Rewrite the Rules of Ubiquitylation. <i>Current Biology</i> , 2016 , 26, R539-R542	6.3	2
124	STUBL-mediated degradation of the transcription factor MAT α requires degradation elements that coincide with corepressor binding sites. <i>Molecular Biology of the Cell</i> , 2015 , 26, 3401-12	3.5	12
123	A Single Helix Drives Extensive Remodeling of the Proteasome Lid and Completion of Regulatory Particle Assembly. <i>Cell</i> , 2015 , 163, 432-44	56.2	60
122	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	8.7	60
121	Proteasomes: Isolation and Activity Assays. <i>Current Protocols in Cell Biology</i> , 2015 , 67, 3.43.1-3.43.20	2.3	17
120	The intrinsically disordered Sem1 protein functions as a molecular tether during proteasome lid biogenesis. <i>Molecular Cell</i> , 2014 , 53, 433-43	17.6	49
119	Assembly of the 20S proteasome. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2014 , 1843, 2-12	4.9	62
118	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, 17821-6	11.5	32

117	Molecular architecture and assembly of the eukaryotic proteasome. <i>Annual Review of Biochemistry</i> , 2013 , 82, 415-45	29.1	266
116	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	3.5	32
115	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	5.4	16
114	Ulp2 SUMO Protease 2013 , 2362-2365		
113	The Doa4 Deubiquitylating Enzyme (<i>Saccharomyces cerevisiae</i>) 2013 , 2049-2052		
112	Function and regulation of SUMO proteases. <i>Nature Reviews Molecular Cell Biology</i> , 2012 , 13, 755-66	48.7	402
111	Split-Doa10: a naturally split polytopic eukaryotic membrane protein generated by fission of a nuclear gene. <i>PLoS ONE</i> , 2012 , 7, e45194	3.7	4
110	A new class of SUMO proteases. <i>EMBO Reports</i> , 2012 , 13, 284-5	6.5	9
109	Aberrant substrate engagement of the ER translocon triggers degradation by the Hrd1 ubiquitin ligase. <i>Journal of Cell Biology</i> , 2012 , 197, 761-73	7.3	49
108	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	4.8	17
107	Disulfide engineering to map subunit interactions in the proteasome and other macromolecular complexes. <i>Methods in Molecular Biology</i> , 2012 , 832, 349-62	1.4	5
106	Analysis of protein ubiquitination. <i>Current Protocols in Protein Science</i> , 2011 , Chapter 14, Unit14.5	3.1	19
105	Incorporation of the Rpn12 subunit couples completion of proteasome regulatory particle lid assembly to lid-base joining. <i>Molecular Cell</i> , 2011 , 44, 907-17	17.6	52
104	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, 622-9	17.6	56
103	Order of the proteasomal ATPases and eukaryotic proteasome assembly. <i>Cell Biochemistry and Biophysics</i> , 2011 , 60, 13-20	3.2	36
102	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, 20163-74	5.4	23
101	A WLM protein with SUMO-directed protease activity. <i>Molecular and Cellular Biology</i> , 2010 , 30, 3734-6	4.8	6
100	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	12.6	69

99 The Ubiquitin-Proteasome System **2010**, 1293-1296

98	Redundancy and variation in the ubiquitin-mediated proteolytic targeting of a transcription factor. <i>Cell Cycle</i> , 2010 , 9, 4282-5	4.7	17
97	Designed proteins to modulate cellular networks. <i>ACS Chemical Biology</i> , 2010 , 5, 545-52	4.9	41
96	Heterohexameric ring arrangement of the eukaryotic proteasomal ATPases: implications for proteasome structure and assembly. <i>Molecular Cell</i> , 2010 , 38, 393-403	17.6	116
95	The SUMO-targeted ubiquitin ligase subunit Slx5 resides in nuclear foci and at sites of DNA breaks. <i>Cell Cycle</i> , 2009 , 8, 1080-9	4.7	34
94	Essential role of nuclear localization for yeast Ulp2 SUMO protease function. <i>Molecular Biology of the Cell</i> , 2009 , 20, 2196-206	3.5	29
93	A tetrahedral transition state at the active sites of the 20S proteasome is coupled to opening of the alpha-ring channel. <i>Structure</i> , 2009 , 17, 1137-47	5.2	72
92	Small epitope-linker modules for PCR-based C-terminal tagging in <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 2009 , 26, 185-92	3.4	69
91	Origin and function of ubiquitin-like proteins. <i>Nature</i> , 2009 , 458, 422-9	50.4	591
90	Quantitative proteomics reveals the function of unconventional ubiquitin chains in proteasomal degradation. <i>Cell</i> , 2009 , 137, 133-45	56.2	832
89	Multiple assembly chaperones govern biogenesis of the proteasome regulatory particle base. <i>Cell</i> , 2009 , 137, 887-99	56.2	132
88	Identification of SUMO-interacting proteins by yeast two-hybrid analysis. <i>Methods in Molecular Biology</i> , 2009 , 497, 107-20	1.4	26
87	A multimeric assembly factor controls the formation of alternative 20S proteasomes. <i>Nature Structural and Molecular Biology</i> , 2008 , 15, 237-44	17.6	120
86	Diversity of degradation signals in the ubiquitin-proteasome system. <i>Nature Reviews Molecular Cell Biology</i> , 2008 , 9, 679-90	48.7	593
85	Some assembly required: dedicated chaperones in eukaryotic proteasome biogenesis. <i>Biological Chemistry</i> , 2008 , 389, 1143-51	4.5	36
84	Ulp2 and the DNA damage response: desumoylation enables safe passage through mitosis. <i>Cell Cycle</i> , 2008 , 7, 52-6	4.7	11
83	Biochemical Functions of Ubiquitin and Ubiquitin-like Protein Conjugation 2008 , 249-278		2
82	Degradation of the bile salt export pump at endoplasmic reticulum in progressive familial intrahepatic cholestasis type II. <i>Hepatology</i> , 2008 , 48, 1558-69	11.2	61

81	An emerging role for thioester-linked polyubiquitin chains in protein degradation. <i>FASEB Journal</i> , 2008 , 22, 605-7	0.9	
80	Autoregulation of an E2 enzyme by ubiquitin-chain assembly on its catalytic residue. <i>Nature Cell Biology</i> , 2007 , 9, 422-7	23.4	129
79	beta-Subunit appendages promote 20S proteasome assembly by overcoming an Ump1-dependent checkpoint. <i>EMBO Journal</i> , 2007 , 26, 2339-49	13	118
78	The yeast Hex3.Slx8 heterodimer is a ubiquitin ligase stimulated by substrate sumoylation. <i>Journal of Biological Chemistry</i> , 2007 , 282, 34176-84	5.4	178
77	The Ulp2 SUMO protease is required for cell division following termination of the DNA damage checkpoint. <i>Molecular and Cellular Biology</i> , 2007 , 27, 6948-61	4.8	38
76	A nuclear envelope protein linking nuclear pore basket assembly, SUMO protease regulation, and mRNA surveillance. <i>Journal of Cell Biology</i> , 2007 , 178, 813-27	7.3	84
75	Ubiquitin ligation without a ligase. <i>Developmental Cell</i> , 2007 , 13, 4-6	10.2	8
74	The short-lived Matalpha2 transcriptional repressor is protected from degradation in vivo by interactions with its corepressors Tup1 and Ssn6. <i>Molecular and Cellular Biology</i> , 2006 , 26, 371-80	4.8	15
73	A conserved late endosome-targeting signal required for Doa4 deubiquitylating enzyme function. <i>Journal of Cell Biology</i> , 2006 , 175, 825-35	7.3	37
72	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, 11178-83	11.5	71
71	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, 4646-53	5.4	112
70	Modification of proteins by ubiquitin and ubiquitin-like proteins. <i>Annual Review of Cell and Developmental Biology</i> , 2006 , 22, 159-80	12.6	1184
69	Lingering mysteries of ubiquitin-chain assembly. <i>Cell</i> , 2006 , 124, 27-34	56.2	216
68	Cecile M. Pickart 1954-2006. <i>Nature Cell Biology</i> , 2006 , 8, 542-3	23.4	
67	Spatially regulated ubiquitin ligation by an ER/nuclear membrane ligase. <i>Nature</i> , 2006 , 443, 827-31	50.4	129
66	Membrane and soluble substrates of the Doa10 ubiquitin ligase are degraded by distinct pathways. <i>EMBO Journal</i> , 2006 , 25, 533-43	13	212
65	Defining the SUMO-modified proteome by multiple approaches in <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2005 , 280, 4102-10	5.4	318
64	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, 13410-5	11.5	95

63	Preparation and characterization of yeast and human desumoylating enzymes. <i>Methods in Enzymology</i> , 2005 , 398, 457-67	1.7	3
62	Varshavsky's contributions. <i>Science</i> , 2004 , 306, 1290-2	33.3	9
61	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, 6447-54	5.3	78
60	Distinct machinery is required in <i>Saccharomyces cerevisiae</i> for the endoplasmic reticulum-associated degradation of a multispinning membrane protein and a soluble luminal protein. <i>Journal of Biological Chemistry</i> , 2004 , 279, 38369-78	5.4	207
59	Plasticity in eucaryotic 20S proteasome ring assembly revealed by a subunit deletion in yeast. <i>EMBO Journal</i> , 2004 , 23, 500-10	13	69
58	NF-kappaB signaling: flipping the switch with polyubiquitin chains. <i>Current Biology</i> , 2004 , 14, R898-900	6.3	23
57	Mechanism and function of deubiquitinating enzymes. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2004 , 1695, 189-207	4.9	678
56	Ubiquitin-dependent control of development in <i>Saccharomyces cerevisiae</i> . <i>Current Opinion in Microbiology</i> , 2004 , 7, 647-54	7.9	6
55	Ubiquitin-dependent degradation of the yeast Mat(alpha)2 repressor enables a switch in developmental state. <i>Genes and Development</i> , 2003 , 17, 2259-70	12.6	39
54	A superfamily of protein tags: ubiquitin, SUMO and related modifiers. <i>Trends in Biochemical Sciences</i> , 2003 , 28, 321-8	10.3	321
53	The Ubiquitin-Proteasome System 2003 , 347-350		
52	The Ulp1 SUMO isopeptidase: distinct domains required for viability, nuclear envelope localization, and substrate specificity. <i>Journal of Cell Biology</i> , 2003 , 160, 1069-81	7.3	163
51	Molecular biology. New proteases in a ubiquitin stew. <i>Science</i> , 2002 , 298, 549-52	33.3	20
50	Assaying protein ubiquitination in <i>Saccharomyces cerevisiae</i> . <i>Methods in Enzymology</i> , 2002 , 351, 248-57	1.7	14
49	Analysis of protein ubiquitination. <i>Current Protocols in Protein Science</i> , 2002 , Chapter 14, Unit 14.5	3.1	7
48	New structural clues to substrate specificity in the "ubiquitin system". <i>Molecular Cell</i> , 2002 , 9, 453-4	17.6	13
47	A conserved ubiquitin ligase of the nuclear envelope/endoplasmic reticulum that functions in both ER-associated and Matalpha2 repressor degradation. <i>Genes and Development</i> , 2001 , 15, 2660-74	12.6	360
46	SP-RING for SUMO: new functions bloom for a ubiquitin-like protein. <i>Cell</i> , 2001 , 107, 5-8	56.2	233

45	Evolution and function of ubiquitin-like protein-conjugation systems. <i>Nature Cell Biology</i> , 2000 , 2, E153-73.4	323
44	The Doa4 deubiquitinating enzyme is functionally linked to the vacuolar protein-sorting and endocytic pathways. <i>Molecular Biology of the Cell</i> , 2000 , 11, 3365-80	3.5 264
43	Analysis of the deubiquitinating enzymes of the yeast <i>Saccharomyces cerevisiae</i> . <i>Biological Chemistry</i> , 2000 , 381, 981-92	4.5 146
42	The yeast ULP2 (SMT4) gene encodes a novel protease specific for the ubiquitin-like Smt3 protein. <i>Molecular and Cellular Biology</i> , 2000 , 20, 2367-77	4.8 314
41	A viable ubiquitin-activating enzyme mutant for evaluating ubiquitin system function in <i>Saccharomyces cerevisiae</i> . <i>FEBS Letters</i> , 2000 , 477, 193-8	3.8 25
40	Biochemistry. All in the ubiquitin family. <i>Science</i> , 2000 , 289, 563-4	33.3 94
39	The Doa4 deubiquitinating enzyme is required for ubiquitin homeostasis in yeast. <i>Molecular Biology of the Cell</i> , 1999 , 10, 2583-94	3.5 246
38	Interaction of the Doa4 deubiquitinating enzyme with the yeast 26S proteasome. <i>Molecular Biology of the Cell</i> , 1999 , 10, 741-56	3.5 111
37	A new protease required for cell-cycle progression in yeast. <i>Nature</i> , 1999 , 398, 246-51	50.4 611
36	Structure and functional analysis of the 26S proteasome subunits from plants. <i>Molecular Biology Reports</i> , 1999 , 26, 137-46	2.8 36
35	Eukaryotic 20S proteasome catalytic subunit propeptides prevent active site inactivation by N-terminal acetylation and promote particle assembly. <i>EMBO Journal</i> , 1999 , 18, 3575-85	13 116
34	Substrate targeting in the ubiquitin system. <i>Cell</i> , 1999 , 97, 427-30	56.2 395
33	Unified nomenclature for subunits of the <i>Saccharomyces cerevisiae</i> proteasome regulatory particle. <i>Trends in Biochemical Sciences</i> , 1998 , 23, 244-5	10.3 111
32	Degradation signal masking by heterodimerization of MAT α 2 and MAT α 1 blocks their mutual destruction by the ubiquitin-proteasome pathway. <i>Cell</i> , 1998 , 94, 217-27	56.2 172
31	An evolutionarily conserved gene on human chromosome 5q33-q34, UBH1, encodes a novel deubiquitinating enzyme. <i>Genomics</i> , 1998 , 49, 411-8	4.3 17
30	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, 29178-87	5.4 39
29	The Deubiquitinating Enzymes 1998 , 99-125	33
28	Ubiquitin-Dependent Degradation of Transcription Regulators 1998 , 279-302	10

27	Molecular organization of the 20S proteasome gene family from <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 1998 , 149, 677-92	4	95
26	There's the rub: a novel ubiquitin-like modification linked to cell cycle regulation. <i>Genes and Development</i> , 1998 , 12, 901-7	12.6	109
25	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, 7156-61	11.5	248
24	SUMO-1: Ubiquitin gains weight. <i>Trends in Cell Biology</i> , 1997 , 7, 408-13	18.3	68
23	In vivo disassembly of free polyubiquitin chains by yeast Ubp14 modulates rates of protein degradation by the proteasome. <i>EMBO Journal</i> , 1997 , 16, 4826-38	13	184
22	Ubiquitin-dependent protein degradation. <i>Annual Review of Genetics</i> , 1996 , 30, 405-39	14.5	1445
21	Autocatalytic subunit processing couples active site formation in the 20S proteasome to completion of assembly. <i>Cell</i> , 1996 , 86, 961-72	56.2	338
20	Protein degradation or regulation: Ub the judge. <i>Cell</i> , 1996 , 84, 813-5	56.2	255
19	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, 3275-9	11.5	157
18	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, 6311-21	4.8	69
17	Ubiquitin, proteasomes, and the regulation of intracellular protein degradation. <i>Current Opinion in Cell Biology</i> , 1995 , 7, 215-23	9	763
16	The DOA pathway: studies on the functions and mechanisms of ubiquitin-dependent protein degradation in the yeast <i>Saccharomyces cerevisiae</i> . <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 1995 , 60, 503-13	3.9	18
15	Degradation of the yeast MAT alpha 2 transcriptional regulator is mediated by the proteasome. <i>FEBS Letters</i> , 1994 , 354, 50-2	3.8	50
14	Multiple ubiquitin-conjugating enzymes participate in the in vivo degradation of the yeast MAT alpha 2 repressor. <i>Cell</i> , 1993 , 74, 357-69	56.2	383
13	The yeast DOA4 gene encodes a deubiquitinating enzyme related to a product of the human <i>trc-2</i> oncogene. <i>Nature</i> , 1993 , 366, 313-9	50.4	360
12	Ubiquitin and intracellular protein degradation. <i>Current Opinion in Cell Biology</i> , 1992 , 4, 1024-31	9	73
11	The short-lived MAT alpha 2 transcriptional regulator is ubiquitinated in vivo. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1991 , 88, 4606-10	11.5	236
10	Functions of intracellular protein degradation in yeast. <i>Genetic Engineering</i> , 1991 , 13, 307-29		1

9	In vivo degradation of a transcriptional regulator: the yeast alpha 2 repressor. <i>Cell</i> , 1990 , 61, 697-708	56.2	235
8	Three-dimensional organization of <i>Drosophila melanogaster</i> interphase nuclei. II. Chromosome spatial organization and gene regulation. <i>Journal of Cell Biology</i> , 1987 , 104, 1471-83	7.3	94
7	Three-dimensional organization of <i>Drosophila melanogaster</i> interphase nuclei. I. Tissue-specific aspects of polytene nuclear architecture. <i>Journal of Cell Biology</i> , 1987 , 104, 1455-70	7.3	106
6	Chromosome structure in four wild-type polytene tissues of <i>Drosophila melanogaster</i> . The 87A and 87C heat shock loci are induced unequally in the midgut in a manner dependent on growth temperature. <i>Chromosoma</i> , 1987 , 95, 197-208	2.8	25
5	Spatial organization of chromosomes in the salivary gland nuclei of <i>Drosophila melanogaster</i> . <i>Journal of Cell Biology</i> , 1986 , 102, 112-23	7.3	224
4	Light microscope based analysis of three-dimensional structure: applications to the study of <i>Drosophila</i> salivary gland nuclei. I. Data collection and analysis. <i>Journal of Microscopy</i> , 1985 , 137, 241-52	1.9	18
3	Characteristic folding pattern of polytene chromosomes in <i>Drosophila</i> salivary gland nuclei. <i>Nature</i> , 1984 , 308, 414-21	50.4	162
2	Properties of the T4 bacteriophage DNA replication apparatus: the T4 dda DNA helicase is required to pass a bound RNA polymerase molecule. <i>Cell</i> , 1983 , 34, 115-23	56.2	112
1	Ubiquitin and Ubiquitin-like Protein Conjugation249		