

Dieter H Wolf

List of Publications by Year in descending order

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133
papers

12,447
citations

23567

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25787

108
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136
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136
docs citations

136
times ranked

10450
citing authors

#	ARTICLE	IF	CITATIONS
1	Oxygen Stress: A Regulator of Apoptosis in Yeast. <i>Journal of Cell Biology</i> , 1999, 145, 757-767.	5.2	963
2	Mutant analysis links the translocon and BiP to retrograde protein transport for ER degradation. <i>Nature</i> , 1997, 388, 891-895.	27.8	524
3	Protein dislocation from the ER requires polyubiquitination and the AAA-ATPase Cdc48. <i>Nature Cell Biology</i> , 2002, 4, 134-139.	10.3	489
4	The Active Sites of the Eukaryotic 20 S Proteasome and Their Involvement in Subunit Precursor Processing. <i>Journal of Biological Chemistry</i> , 1997, 272, 25200-25209.	3.4	446
5	NEW EMBO MEMBER'S REVIEW: For whom the bell tolls: protein quality control of the endoplasmic reticulum and the ubiquitin-proteasome connection. <i>EMBO Journal</i> , 2003, 22, 2309-2317.	7.8	376
6	Protein quality control and elimination of protein waste: The role of the ubiquitin-proteasome system. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2014, 1843, 182-196.	4.1	372
7	The medial-Golgi Ion Pump Pmr1 Supplies the Yeast Secretory Pathway with Ca ²⁺ and Mn ²⁺ Required for Glycosylation, Sorting, and Endoplasmic Reticulum-Associated Protein Degradation. <i>Molecular Biology of the Cell</i> , 1998, 9, 1149-1162.	2.1	369
8	Retrograde protein translocation: ERADication of secretory proteins in health and disease. <i>Trends in Biochemical Sciences</i> , 1999, 24, 266-270.	7.5	352
9	Proteasomes: destruction as a programme. <i>Trends in Biochemical Sciences</i> , 1996, 21, 96-102.	7.5	340
10	Der3p/Hrd1p Is Required for Endoplasmic Reticulum-associated Degradation of Misfolded Luminal and Integral Membrane Proteins. <i>Molecular Biology of the Cell</i> , 1998, 9, 209-222.	2.1	332
11	Endoplasmic reticulum degradation: reverse protein flow of no return. <i>FASEB Journal</i> , 1997, 11, 1227-1233.	0.5	249
12	Contribution of Proteasomal β^2 -Subunits to the Cleavage of Peptide Substrates Analyzed with Yeast Mutants. <i>Journal of Biological Chemistry</i> , 1998, 273, 25637-25646.	3.4	238
13	The proteasome: a proteolytic nanomachine of cell regulation and waste disposal. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2004, 1695, 19-31.	4.1	228
14	Cdc48: a power machine in protein degradation. <i>Trends in Biochemical Sciences</i> , 2011, 36, 515-523.	7.5	207
15	A genomic screen identifies Dsk2p and Rad23p as essential components of ER-associated degradation. <i>EMBO Reports</i> , 2004, 5, 692-697.	4.5	196
16	Analysis of two mutated vacuolar proteins reveals a degradation pathway in the endoplasmic reticulum or a related compartment of yeast. <i>FEBS Journal</i> , 1993, 218, 565-574.	0.2	184
17	Mammalian Bax triggers apoptotic changes in yeast. <i>FEBS Letters</i> , 1998, 438, 61-65.	2.8	180
18	The Cdc48 machine in endoplasmic reticulum associated protein degradation. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2012, 1823, 117-124.	4.1	170

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19	Use of Modular Substrates Demonstrates Mechanistic Diversity and Reveals Differences in Chaperone Requirement of ERAD. <i>Journal of Biological Chemistry</i> , 2003, 278, 35903-35913.	3.4	169
20	Endoplasmic Reticulum Degradation of a Mutated ATP-binding Cassette Transporter Pdr5 Proceeds in a Concerted Action of Sec61 and the Proteasome. <i>Journal of Biological Chemistry</i> , 1998, 273, 32848-32856.	3.4	166
21	Membrane Topology and Function of Der3/Hrd1p as a Ubiquitin-Protein Ligase (E3) Involved in Endoplasmic Reticulum Degradation. <i>Journal of Biological Chemistry</i> , 2001, 276, 10663-10669.	3.4	154
22	The Cytoplasmic Hsp70 Chaperone Machinery Subjects Misfolded and Endoplasmic Reticulum Import-incompetent Proteins to Degradation via the Ubiquitin-Proteasome System. <i>Molecular Biology of the Cell</i> , 2007, 18, 153-165.	2.1	148
23	Proteinases, proteolysis and biological control in the yeast <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 1985, 1, 139-157.	1.7	142
24	Catabolite Degradation of Fructose-1,6-bisphosphatase in the Yeast <i>Saccharomyces cerevisiae</i> : A Genome-wide Screen Identifies Eight Novel GID Genes and Indicates the Existence of Two Degradation Pathways. <i>Molecular Biology of the Cell</i> , 2003, 14, 1652-1663.	2.1	141
25	Degradation of misfolded protein in the cytoplasm is mediated by the ubiquitin ligase Ubr1. <i>FEBS Letters</i> , 2008, 582, 4143-4146.	2.8	139
26	Ricin A chain utilises the endoplasmic reticulum-associated protein degradation pathway to enter the cytosol of yeast. <i>FEBS Letters</i> , 1999, 459, 80-84.	2.8	138
27	Ubiquitin receptors and ERAD: A network of pathways to the proteasome. <i>Seminars in Cell and Developmental Biology</i> , 2007, 18, 780-791.	5.0	135
28	The Yeast GID Complex, a Novel Ubiquitin Ligase (E3) Involved in the Regulation of Carbohydrate Metabolism. <i>Molecular Biology of the Cell</i> , 2008, 19, 3323-3333.	2.1	132
29	N-glycosylation affects endoplasmic reticulum degradation of a mutated derivative of carboxypeptidase yscY in yeast. , 1996, 12, 1229-1238.		123
30	Proteasome β^2 -type subunits: unequal roles of propeptides in core particle maturation and a hierarchy of active site function. <i>Journal of Molecular Biology</i> , 1999, 291, 997-1013.	4.2	123
31	PRE5 and PRE6, the Last Missing Genes Encoding 20S Proteasome Subunits from Yeast? Indication for a Set of 14 Different Subunits in the Eukaryotic Proteasome Core. <i>Biochemistry</i> , 1994, 33, 12229-12237.	2.5	120
32	A genome-wide screen identifies Yos9p as essential for ER-associated degradation of glycoproteins. <i>FEBS Letters</i> , 2004, 577, 422-426.	2.8	117
33	Conformational constraints for protein self-cleavage in the proteasome. <i>Journal of Molecular Biology</i> , 1998, 279, 1187-1191.	4.2	113
34	Catabolite Inactivation of Fructose-1,6-bisphosphatase of <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 1995, 270, 26446-26450.	3.4	111
35	ER-Golgi Traffic Is a Prerequisite for Efficient ER Degradation. <i>Molecular Biology of the Cell</i> , 2002, 13, 1806-1818.	2.1	105
36	Protein Quality Control of the Endoplasmic Reticulum and Ubiquitin-Proteasome-Triggered Degradation of Aberrant Proteins: Yeast Pioneers the Path. <i>Annual Review of Biochemistry</i> , 2018, 87, 751-782.	11.1	104

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37	Endoplasmic reticulum associated protein degradation: A chaperone assisted journey to hell. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2010, 1803, 694-705.	4.1	103
38	Proteins of Newly Isolated Mutants and the Amino-terminal Proline Are Essential for Ubiquitin-Proteasome-catalyzed Catabolite Degradation of Fructose-1,6-bisphosphatase of <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 1998, 273, 25000-25005.	3.4	96
39	Stress-induced proteolysis in yeast. <i>Molecular Microbiology</i> , 1992, 6, 2437-2442.	2.5	92
40	Cystic Fibrosis Transmembrane Conductance Regulator Degradation Depends on the Lectins Htm1p/EDEM and the Cdc48 Protein Complex in Yeast. <i>Molecular Biology of the Cell</i> , 2004, 15, 4125-4135.	2.1	90
41	Vacuolar/lysosomal proteolysis: proteases, substrates mechanisms. <i>Current Opinion in Cell Biology</i> , 1993, 5, 990-996.	5.4	87
42	Exploring the Topology of the Gid Complex, the E3 Ubiquitin Ligase Involved in Catabolite-induced Degradation of Gluconeogenic Enzymes. <i>Journal of Biological Chemistry</i> , 2012, 287, 25602-25614.	3.4	84
43	Studies on a Carboxypeptidase Y Mutant of Yeast and Evidence for a Second Carboxypeptidase Activity. <i>FEBS Journal</i> , 1977, 73, 553-556.	0.2	81
44	PRE3, highly homologous to the human major histocompatibility complex-linked LMP2 (RING12) gene, codes for a yeast proteasome subunit necessary for the peptidylglutamyl-peptide hydrolyzing activity. <i>FEBS Letters</i> , 1994, 341, 193-196.	2.8	81
45	Ubc8p functions in catabolite degradation of fructose-1,6-bisphosphatase in yeast. <i>EMBO Journal</i> , 2000, 19, 2161-2167.	7.8	81
46	Importance of carbohydrate positioning in the recognition of mutated CPY for ER-associated degradation. <i>Journal of Cell Science</i> , 2005, 118, 1485-1492.	2.0	81
47	The proteasome/multicatalytic-multifunctional proteinase In vivo function in the ubiquitin-dependent N-end rule pathway of protein degradation in eukaryotes. <i>FEBS Letters</i> , 1992, 302, 192-196.	2.8	76
48	Der1p, a protein required for degradation of malformed soluble proteins of the endoplasmic reticulum: topology and Der1-like proteins. <i>FEMS Yeast Research</i> , 2004, 4, 721-729.	2.3	74
49	Studies on a Proteinase B Mutant of Yeast. <i>FEBS Journal</i> , 1979, 98, 375-384.	0.2	73
50	The Proteasomal Substrate Stm1 Participates in Apoptosis-like Cell Death in Yeast. <i>Molecular Biology of the Cell</i> , 2001, 12, 2422-2432.	2.1	73
51	Catabolite inactivation of fructose-1,6-bisphosphatase in yeast is mediated by the proteasome. <i>FEBS Letters</i> , 1994, 349, 270-274.	2.8	69
52	Sec61p is part of the endoplasmic reticulum-associated degradation machinery. <i>EMBO Journal</i> , 2009, 28, 2874-2884.	7.8	68
53	Proteinase yscE of yeast shows homology with the 20 S cylinder particles of <i>Xenopus laevis</i> . <i>FEBS Letters</i> , 1988, 239, 35-40.	2.8	67
54	Glucose-Induced Monoubiquitination of the <i>Saccharomyces cerevisiae</i> Galactose Transporter Is Sufficient To Signal Its Internalization. <i>Journal of Bacteriology</i> , 2001, 183, 3083-3088.	2.2	66

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55	Proteasomes of the yeast <i>S. cerevisiae</i> : genes, structure and functions. <i>Molecular Biology Reports</i> , 1995, 21, 3-10.	2.3	63
56	New proteolytic enzymes in yeast. <i>Archives of Biochemistry and Biophysics</i> , 1981, 207, 445-454.	3.0	62
57	Proteinase action in vitro versus proteinase function in vivo: mutants shed light on intracellular proteolysis in yeast. <i>Trends in Biochemical Sciences</i> , 1982, 7, 35-37.	7.5	62
58	Yeast Cycloheximide-resistant Mutants Are Proteasome Mutants Defective in Protein Degradation. <i>Molecular Biology of the Cell</i> , 1997, 8, 2487-2499.	2.1	62
59	Proteasomes: destruction as a programme. <i>Trends in Biochemical Sciences</i> , 1996, 21, 96-102.	7.5	62
60	Analysis of Proteinase A Function in Yeast. <i>FEBS Journal</i> , 1981, 121, 47-52.	0.2	61
61	Control of Metabolism in Yeast and other Lower Eukaryotes through Action of Proteinases. <i>Advances in Microbial Physiology</i> , 1981, 21, 267-338.	2.4	60
62	Site of catabolite inactivation. <i>Nature</i> , 1994, 369, 283-284.	27.8	57
63	Degradation of the yeast MAT1±2 transcriptional regulator is mediated by the proteasome. <i>FEBS Letters</i> , 1994, 354, 50-52.	2.8	56
64	Endoplasmic reticulum degradation. Reverse protein transport and its end in the proteasome. , 1999, 26, 125-130.		56
65	Previously unknown role for the ubiquitin ligase Ubr1 in endoplasmic reticulum-associated protein degradation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 15271-15276.	7.1	56
66	Carboxypeptidase S- and Carboxypeptidase Y-Deficient Mutants of <i>Saccharomyces cerevisiae</i> . <i>Journal of Bacteriology</i> , 1981, 147, 418-426.	2.2	55
67	A RING-H2 finger motif is essential for the function of Der3/Hrd1 in endoplasmic reticulum associated protein degradation in the yeast <i>Saccharomyces cerevisiae</i> . <i>FEBS Letters</i> , 1999, 448, 244-248.	2.8	53
68	Two Distinct Proteolytic Systems Responsible for Glucose-induced Degradation of Fructose-1,6-bisphosphatase and the Gal2p Transporter in the Yeast <i>Saccharomyces cerevisiae</i> Share the Same Protein Components of the Glucose Signaling Pathway. <i>Journal of Biological Chemistry</i> , 2002, 277, 8248-8254.	3.4	53
69	Proteinase yscD (oligopeptidase yscD). Structure, function and relationship of the yeast enzyme with mammalian thimet oligopeptidase (metalloendopeptidase, EP 24.15). <i>FEBS Journal</i> , 1994, 219, 627-639.	0.2	51
70	Endoplasmic reticulum-associated protein degradation – one model fits all?. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2004, 1695, 215-223.	4.1	51
71	Proteasome and cell cycle. <i>FEBS Letters</i> , 1993, 336, 34-36.	2.8	48
72	Aminopeptidase Co, a new yeast peptidase. <i>Biochemical and Biophysical Research Communications</i> , 1982, 109, 341-347.	2.1	46

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73	Re-entering the translocon from the luminal side of the endoplasmic reticulum. Studies on mutated carboxypeptidase yscY species. <i>FEBS Letters</i> , 1999, 443, 241-245.	2.8	46
74	Ubiquitin Ligase Hul5 Is Required for Fragment-specific Substrate Degradation in Endoplasmic Reticulum-associated Degradation. <i>Journal of Biological Chemistry</i> , 2008, 283, 16374-16383.	3.4	46
75	The ubiquitin-proteasome-system. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2014, 1843, 1.	4.1	45
76	In vivo biosynthesis of vacuolar proteinases in proteinase mutants of <i>Saccharomyces cerevisiae</i> . <i>Biochemical and Biophysical Research Communications</i> , 1982, 107, 770-778.	2.1	44
77	Biogenesis of the yeast vacuole (lysosome). Proteinase yscB contributes molecularly and kinetically to vacuolar hydrolase-precursor maturation. <i>FEBS Journal</i> , 1992, 207, 867-876.	0.2	41
78	Dfm1 Forms Distinct Complexes with Cdc48 and the ER Ubiquitin Ligases and Is Required for ERAD. <i>Traffic</i> , 2010, 11, 1363-1369.	2.7	41
79	DER7, encoding β -glucosidase I is essential for degradation of malformed glycoproteins of the endoplasmic reticulum. <i>FEMS Yeast Research</i> , 2004, 4, 815-820.	2.3	40
80	Yeast pheromone α -factor is synthesized as a high molecular weight precursor. <i>Biochemical and Biophysical Research Communications</i> , 1983, 116, 822-829.	2.1	39
81	Expression and Degradation of the Cystic Fibrosis Transmembrane Conductance Regulator in <i>Saccharomyces cerevisiae</i> . <i>Archives of Biochemistry and Biophysics</i> , 2001, 390, 195-205.	3.0	39
82	Gid9, a second RING finger protein contributes to the ubiquitin ligase activity of the Gid complex required for catabolite degradation. <i>FEBS Letters</i> , 2011, 585, 3856-3861.	2.8	39
83	Differential proteolytic sensitivity of yeast fatty acid synthetase subunits alpha and beta contributing to a balanced ratio of both fatty acid synthetase components. <i>FEBS Journal</i> , 1992, 203, 607-614.	0.2	38
84	Studies on the Yeast Proteasome Uncover Its Basic Structural Features and Multiple in vivo Functions. <i>Enzyme & Protein</i> , 1993, 47, 189-201.	1.4	38
85	The 26S proteasome of the yeast <i>Saccharomyces cerevisiae</i> . <i>FEBS Letters</i> , 1994, 355, 69-75.	2.8	38
86	Degradation of Ornithine Decarboxylase by the Mammalian and Yeast 26S Proteasome Complexes Requires all the Components of the Protease. <i>FEBS Journal</i> , 1995, 229, 276-283.	0.2	38
87	Proteolysis in eucaryotic cells: Aminopeptidases and dipeptidyl aminopeptidases of yeast revisited. <i>Archives of Biochemistry and Biophysics</i> , 1983, 226, 292-305.	3.0	37
88	Carboxypeptidase yscS: gene structure and function of the vacuolar enzyme. <i>FEBS Journal</i> , 1991, 197, 399-405.	0.2	37
89	Ubx4 Modulates Cdc48 Activity and Influences Degradation of Misfolded Proteins of the Endoplasmic Reticulum. <i>Journal of Biological Chemistry</i> , 2009, 284, 16082-16089.	3.4	36
90	Isolation of yeast mutants lacking proteinase B activity. <i>FEBS Letters</i> , 1978, 92, 121-124.	2.8	35

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91	Ubiquitin, a central component of selective cytoplasmic proteolysis, is linked to proteins residing at the locus of non-selective proteolysis, the vacuole. FEBS Letters, 1992, 301, 231-235.	2.8	34
92	RMND5 from <i>Xenopus laevis</i> Is an E3 Ubiquitin-Ligase and Functions in Early Embryonic Forebrain Development. PLoS ONE, 2015, 10, e0120342.	2.5	33
93	Vacuoles are not the sole compartments of proteolytic enzymes in yeast. FEBS Letters, 1984, 166, 321-325.	2.8	31
94	Biogenesis of the Yeast Vacuole (lysosome). The Use of Active-Site Mutants of Proteinase yscA to Determine the Necessity of the Enzyme for Vacuolar Proteinase Maturation and Proteinase yscB Stability. FEBS Journal, 1995, 231, 115-125.	0.2	30
95	Biogenesis of the yeast vacuole (lysosome). Mutation in the active site of the vacuolar serine proteinase yscB abolishes proteolytic maturation of its 73-kDa precursor to the 41.5-kDa pro-enzyme and a newly detected 41-kDa peptide. FEBS Journal, 1992, 203, 641-653.	0.2	29
96	Carboxypeptidase S from yeast: regulation of its activity during vegetative growth and differentiation. FEBS Letters, 1978, 91, 59-62.	2.8	28
97	Aminopeptidase yscII of yeast. Isolation of mutants and their biochemical and genetic analysis. FEBS Journal, 1988, 173, 589-598.	0.2	28
98	Regulation of the Gid ubiquitin ligase recognition subunit Gid4. FEBS Letters, 2018, 592, 3286-3294.	2.8	28
99	The proteinase yscB inhibitor (PBI2) gene of yeast and studies on the function of its protein product. FEBS Journal, 1991, 197, 1-7.	0.2	26
100	Hormone (pheromone) processing enzymes in yeast The carboxy-terminal processing enzyme of the mating pheromone α -factor, carboxypeptidase yscI \pm , is absent in α -factor maturation-defective <i>kex1</i> mutant cells. FEBS Letters, 1987, 221, 423-426.	2.8	23
101	Yos9, a control protein for misfolded glycosylated and non-glycosylated proteins in ERAD. FEBS Letters, 2011, 585, 3015-3019.	2.8	23
102	Mutations in the Yeast Proteasome β -Type Subunit Pre3 Uncover Position-dependent Effects on Proteasomal Peptidase Activity and in Vivo Function. Journal of Biological Chemistry, 1998, 273, 19443-19452.	3.4	22
103	Quality Control of a Cytoplasmic Protein Complex. Journal of Biological Chemistry, 2015, 290, 4677-4687.	3.4	22
104	Some characteristics of hormone (pheromone) processing enzymes in yeast. FEBS Letters, 1987, 218, 31-34.	2.8	20
105	Biogenesis of the yeast vacuole (lysosome) Active site mutation in the vacuolar aspartate proteinase yscA blocks maturation of vacuolar proteinases. FEBS Letters, 1991, 293, 62-66.	2.8	20
106	Proteinase yscD mutants of yeast. Isolation and characterization. FEBS Journal, 1987, 163, 339-346.	0.2	19
107	Lysosomal and non-lysosomal proteolysis in the eukaryotic cell: studies on yeast. Biochemical Society Transactions, 1991, 19, 724-725.	3.4	19
108	Molecular mass as a determinant for nuclear San1 α -dependent targeting of misfolded cytosolic proteins to proteasomal degradation. FEBS Letters, 2016, 590, 1765-1775.	2.8	18

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109	Tryptophan Synthase from Yeast. Purification by Affinity Chromatography, Physical Properties. FEBS Journal, 1974, 45, 269-276.	0.2	17
110	The proteinase yscA-inhibitor, IA3, gene Studies of cytoplasmic proteinase inhibitor deficiency on yeast physiology. FEBS Letters, 1991, 283, 78-84.	2.8	17
111	Absence of the Yeast Hsp31 Chaperones of the DJ-1 Superfamily Perturbs Cytoplasmic Protein Quality Control in Late Growth Phase. PLoS ONE, 2015, 10, e0140363.	2.5	17
112	The Cdc48â€“Ufd1â€“Npl4 complex is central in ubiquitinâ€“proteasome triggered catabolite degradation of fructose-1,6-bisphosphatase. Biochemical and Biophysical Research Communications, 2010, 394, 335-341.	2.1	16
113	Mutants of the deubiquitinating enzyme Ubp14 decipher pathway diversity of ubiquitinâ€“proteasome linked protein degradation. Biochemical and Biophysical Research Communications, 2006, 350, 329-333.	2.1	15
114	Mechanisms of cell regulation â€“ proteolysis, the big surprise. FEBS Letters, 2018, 592, 2515-2524.	2.8	15
115	Use of CPY* and Its Derivatives to Study Protein Quality Control in Various Cell Compartments. Methods in Molecular Biology, 2012, 832, 489-504.	0.9	14
116	Protein degradation in yeast. Biochemical Society Transactions, 1987, 15, 811-815.	3.4	12
117	The Hsp70 chaperone Ssa1 is essential for catabolite induced degradation of the gluconeogenic enzyme fructose-1,6-bisphosphatase. Biochemical and Biophysical Research Communications, 2010, 397, 447-452.	2.1	12
118	Yeast Genomics in the Elucidation of Endoplasmic Reticulum (ER) Quality Control and Associated Protein Degradation (ERQD). Methods in Enzymology, 2005, 399, 459-468.	1.0	9
119	Studies on the carboxypeptidase Y-inhibitor complex of yeast. Biochimica Et Biophysica Acta - Biomembranes, 1978, 527, 63-69.	2.6	8
120	Proteinases, proteolysis and regulation in yeast. Biochemical Society Transactions, 1985, 13, 279-283.	3.4	8
121	The ubiquitin clan: A protein family essential for life. FEBS Letters, 2011, 585, 2769-2771.	2.8	8
122	Ubiquitylation in the ERAD Pathway. Sub-Cellular Biochemistry, 2010, 54, 136-148.	2.4	7
123	Protein Quality Control in the Export Pathway. , 2002, , 180-213.		6
124	The Proteasome and Protein Degradation in Yeast. Advances in Experimental Medicine and Biology, 1996, 389, 197-202.	1.6	6
125	Biogenesis of the Yeast Vacuole (Lysosome). Signal Sequence Deletion of the Vacuolar Aspartic Proteinase yscA Does not Block Maturation of Vacuolar Proteinases. Biological Chemistry Hoppe-Seyler, 1993, 374, 1109-1116.	1.4	5
126	Mnl2, a novel component of the ER associated protein degradation pathway. Biochemical and Biophysical Research Communications, 2011, 414, 528-532.	2.1	5

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127	Purification and characterization of proteinase yscJ, a new yeast peptidase. FEBS Journal, 1992, 203, 571-575.	0.2	4
128	Purification and characterization of the cystinyl bond cleaving yeast aminopeptidase yscXVI. FEBS Letters, 1993, 322, 191-196.	2.8	4
129	From Proteasome to Lysosome: Studies on Yeast Demonstrate the Principles Of Protein Degradation in the Eukaryote Cell. Advances in Molecular and Cell Biology, 1998, , 43-70.	0.1	4
130	Waste disposal in plants: where and how?. Trends in Plant Science, 2003, 8, 461-462.	8.8	4
131	Endoplasmic Reticulum-Associated Protein Quality Control and Degradation: Genome-Wide Screen for ERAD Components. , 2005, 301, 289-292.		4
132	Characterization of protein quality control components via dual reporter-containing misfolded cytosolic model substrates. Analytical Biochemistry, 2016, 515, 14-21.	2.4	4
133	Biogenesis of the Yeast Vacuole (lysosome). The Use of Active-Site Mutants of Proteinase yscA to Determine the Necessity of the Enzyme for Vacuolar Proteinase Maturation and Proteinase yscB Stability. FEBS Journal, 1995, 231, 115-125.	0.2	0