

Dieter H Wolf

List of Publications by Year in descending order

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133
papers

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23567

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times ranked

10450
citing authors

#	ARTICLE	IF	CITATIONS
1	Protein Quality Control of the Endoplasmic Reticulum and Ubiquitinâ€“Proteasome-Triggered Degradation of Aberrant Proteins: Yeast Pioneers the Path. <i>Annual Review of Biochemistry</i> , 2018, 87, 751-782.	11.1	104
2	Mechanisms of cell regulation â€“ proteolysis, the big surprise. <i>FEBS Letters</i> , 2018, 592, 2515-2524.	2.8	15
3	Regulation of the Gid ubiquitin ligase recognition subunit Gid4. <i>FEBS Letters</i> , 2018, 592, 3286-3294.	2.8	28
4	Characterization of protein quality control components via dual reporter-containing misfolded cytosolic model substrates. <i>Analytical Biochemistry</i> , 2016, 515, 14-21.	2.4	4
5	Molecular mass as a determinant for nuclear San1â€“dependent targeting of misfolded cytosolic proteins to proteasomal degradation. <i>FEBS Letters</i> , 2016, 590, 1765-1775.	2.8	18
6	RMND5 from <i>Xenopus laevis</i> Is an E3 Ubiquitin-Ligase and Functions in Early Embryonic Forebrain Development. <i>PLoS ONE</i> , 2015, 10, e0120342.	2.5	33
7	Quality Control of a Cytoplasmic Protein Complex. <i>Journal of Biological Chemistry</i> , 2015, 290, 4677-4687.	3.4	22
8	Absence of the Yeast Hsp31 Chaperones of the DJ-1 Superfamily Perturbs Cytoplasmic Protein Quality Control in Late Growth Phase. <i>PLoS ONE</i> , 2015, 10, e0140363.	2.5	17
9	Protein quality control and elimination of protein waste: The role of the ubiquitinâ€“proteasome system. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2014, 1843, 182-196.	4.1	372
10	The ubiquitinâ€“proteasome-system. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2014, 1843, 1.	4.1	45
11	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
12	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
13	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
14	Use of CPY* and Its Derivatives to Study Protein Quality Control in Various Cell Compartments. <i>Methods in Molecular Biology</i> , 2012, 832, 489-504.	0.9	14
15	Mnl2, a novel component of the ER associated protein degradation pathway. <i>Biochemical and Biophysical Research Communications</i> , 2011, 414, 528-532.	2.1	5
16	Cdc48: a power machine in protein degradation. <i>Trends in Biochemical Sciences</i> , 2011, 36, 515-523.	7.5	207
17	The ubiquitin clan: A protein family essential for life. <i>FEBS Letters</i> , 2011, 585, 2769-2771.	2.8	8
18	Yos9, a control protein for misfolded glycosylated and non-glycosylated proteins in ERAD. <i>FEBS Letters</i> , 2011, 585, 3015-3019.	2.8	23

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19	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
20	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
21	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
22	The Cdc48â€“Ufd1â€“Npl4 complex is central in ubiquitinâ€“proteasome triggered catabolite degradation of fructose-1,6-bisphosphatase. <i>Biochemical and Biophysical Research Communications</i> , 2010, 394, 335-341.	2.1	16
23	The Hsp70 chaperone Ssa1 is essential for catabolite induced degradation of the gluconeogenic enzyme fructose-1,6-bisphosphatase. <i>Biochemical and Biophysical Research Communications</i> , 2010, 397, 447-452.	2.1	12
24	Ubiquitylation in the ERAD Pathway. <i>Sub-Cellular Biochemistry</i> , 2010, 54, 136-148.	2.4	7
25	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
26	Sec61p is part of the endoplasmic reticulum-associated degradation machinery. <i>EMBO Journal</i> , 2009, 28, 2874-2884.	7.8	68
27	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
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	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
30	The Cytoplasmic Hsp70 Chaperone Machinery Subjects Misfolded and Endoplasmic Reticulum Import-incompetent Proteins to Degradation via the Ubiquitinâ€“Proteasome System. <i>Molecular Biology of the Cell</i> , 2007, 18, 153-165.	2.1	148
31	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
32	Mutants of the deubiquitinating enzyme Ubp14 decipher pathway diversity of ubiquitinâ€“proteasome linked protein degradation. <i>Biochemical and Biophysical Research Communications</i> , 2006, 350, 329-333.	2.1	15
33	Endoplasmic Reticulum-Associated Protein Quality Control and Degradation: Genome-Wide Screen for ERAD Components. , 2005, 301, 289-292.		4
34	Yeast Genomics in the Elucidation of Endoplasmic Reticulum (ER) Quality Control and Associated Protein Degradation (ERQD). <i>Methods in Enzymology</i> , 2005, 399, 459-468.	1.0	9
35	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
36	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

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37	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
38	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
39	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
40	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
41	DER7, encoding α -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
42	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
43	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
44	Waste disposal in plants: where and how?. <i>Trends in Plant Science</i> , 2003, 8, 461-462.	8.8	4
45	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
46	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
47	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
48	ER-Golgi Traffic Is a Prerequisite for Efficient ER Degradation. <i>Molecular Biology of the Cell</i> , 2002, 13, 1806-1818.	2.1	105
49	Protein Quality Control in the Export Pathway. , 2002, , 180-213.		6
50	Protein dislocation from the ER requires polyubiquitination and the AAA-ATPase Cdc48. <i>Nature Cell Biology</i> , 2002, 4, 134-139.	10.3	489
51	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
52	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
53	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
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	Ubc8p functions in catabolite degradation of fructose-1,6-bisphosphatase in yeast. EMBO Journal, 2000, 19, 2161-2167.	7.8	81
56	Oxygen Stress: A Regulator of Apoptosis in Yeast. Journal of Cell Biology, 1999, 145, 757-767.	5.2	963
57	Endoplasmic reticulum degradation. Reverse protein transport and its end in the proteasome. , 1999, 26, 125-130.		56
58	Retrograde protein translocation: ERADication of secretory proteins in health and disease. Trends in Biochemical Sciences, 1999, 24, 266-270.	7.5	352
59	Re-entering the translocon from the luminal side of the endoplasmic reticulum. Studies on mutated carboxypeptidase yscY species. FEBS Letters, 1999, 443, 241-245.	2.8	46
60	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> . FEBS Letters, 1999, 448, 244-248.	2.8	53
61	Ricin A chain utilises the endoplasmic reticulum-associated protein degradation pathway to enter the cytosol of yeast. FEBS Letters, 1999, 459, 80-84.	2.8	138
62	Proteasome $\hat{2}$ -type subunits: unequal roles of propeptides in core particle maturation and a hierarchy of active site function. Journal of Molecular Biology, 1999, 291, 997-1013.	4.2	123
63	Mammalian Bax triggers apoptotic changes in yeast. FEBS Letters, 1998, 438, 61-65.	2.8	180
64	Conformational constraints for protein self-cleavage in the proteasome. Journal of Molecular Biology, 1998, 279, 1187-1191.	4.2	113
65	Der3p/Hrd1p Is Required for Endoplasmic Reticulum-associated Degradation of Misfolded Luminal and Integral Membrane Proteins. Molecular Biology of the Cell, 1998, 9, 209-222.	2.1	332
66	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> . Journal of Biological Chemistry, 1998, 273, 25000-25005.	3.4	96
67	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
68	Endoplasmic Reticulum Degradation of a Mutated ATP-binding Cassette Transporter Pdr5 Proceeds in a Concerted Action of Sec61 and the Proteasome. Journal of Biological Chemistry, 1998, 273, 32848-32856.	3.4	166
69	The <i>medial</i> -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. Molecular Biology of the Cell, 1998, 9, 1149-1162.	2.1	369
70	Mutations in the Yeast Proteasome $\hat{2}$ -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
71	Contribution of Proteasomal $\hat{2}$ -Subunits to the Cleavage of Peptide Substrates Analyzed with Yeast Mutants. Journal of Biological Chemistry, 1998, 273, 25637-25646.	3.4	238
72	Yeast Cycloheximide-resistant <i>cr1</i> Mutants Are Proteasome Mutants Defective in Protein Degradation. Molecular Biology of the Cell, 1997, 8, 2487-2499.	2.1	62

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73	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
74	Endoplasmic reticulum degradation: reverse protein flow of no return. <i>FASEB Journal</i> , 1997, 11, 1227-1233.	0.5	249
75	Mutant analysis links the translocon and BiP to retrograde protein transport for ER degradation. <i>Nature</i> , 1997, 388, 891-895.	27.8	524
76	Proteasomes: destruction as a programme. <i>Trends in Biochemical Sciences</i> , 1996, 21, 96-102.	7.5	340
77	N-glycosylation affects endoplasmic reticulum degradation of a mutated derivative of carboxypeptidase yscY in yeast. , 1996, 12, 1229-1238.		123
78	The Proteasome and Protein Degradation in Yeast. <i>Advances in Experimental Medicine and Biology</i> , 1996, 389, 197-202.	1.6	6
79	Proteasomes: destruction as a programme. <i>Trends in Biochemical Sciences</i> , 1996, 21, 96-102.	7.5	62
80	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. <i>FEBS Journal</i> , 1995, 231, 115-125.	0.2	0
81	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
82	Proteasomes of the yeast <i>S. cerevisiae</i> : genes, structure and functions. <i>Molecular Biology Reports</i> , 1995, 21, 3-10.	2.3	63
83	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
84	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. <i>FEBS Journal</i> , 1995, 231, 115-125.	0.2	30
85	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
86	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
87	Degradation of the yeast MAT1±2 transcriptional regulator is mediated by the proteasome. <i>FEBS Letters</i> , 1994, 354, 50-52.	2.8	56
88	The 26S proteasome of the yeast <i>Saccharomyces cerevisiae</i> . <i>FEBS Letters</i> , 1994, 355, 69-75.	2.8	38
89	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
90	Site of catabolite inactivation. <i>Nature</i> , 1994, 369, 283-284.	27.8	57

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91	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
92	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
93	Purification and characterization of the cystinyl bond cleaving yeast aminopeptidase yscXVI. <i>FEBS Letters</i> , 1993, 322, 191-196.	2.8	4
94	Proteasome and cell cycle. <i>FEBS Letters</i> , 1993, 336, 34-36.	2.8	48
95	Vacuolar/lysosomal proteolysis: proteases, substrates mechanisms. <i>Current Opinion in Cell Biology</i> , 1993, 5, 990-996.	5.4	87
96	Biogenesis of the Yeast Vacuole (Lysosome). Signal Sequence Deletion of the Vacuolar Aspartic Proteinase yscA Does not Block Maturation of Vacuolar Proteinases. <i>Biological Chemistry Hoppe-Seyler</i> , 1993, 374, 1109-1116.	1.4	5
97	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
98	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
99	Ubiquitin, a central component of selective cytoplasmic proteolysis, is linked to proteins residing at the locus of non-selective proteolysis, the vacuole. <i>FEBS Letters</i> , 1992, 301, 231-235.	2.8	34
100	Purification and characterization of proteinase yscJ, a new yeast peptidase. <i>FEBS Journal</i> , 1992, 203, 571-575.	0.2	4
101	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
102	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. <i>FEBS Journal</i> , 1992, 203, 641-653.	0.2	29
103	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
104	Stress-induced proteolysis in yeast. <i>Molecular Microbiology</i> , 1992, 6, 2437-2442.	2.5	92
105	The proteinase yscA-inhibitor, IA3, gene Studies of cytoplasmic proteinase inhibitor deficiency on yeast physiology. <i>FEBS Letters</i> , 1991, 283, 78-84.	2.8	17
106	Biogenesis of the yeast vacuole (lysosome) Active site mutation in the vacuolar aspartate proteinase yscA blocks maturation of vacuolar proteinases. <i>FEBS Letters</i> , 1991, 293, 62-66.	2.8	20
107	Lysosomal and non-lysosomal proteolysis in the eukaryotic cell: studies on yeast. <i>Biochemical Society Transactions</i> , 1991, 19, 724-725.	3.4	19
108	The proteinase yscB inhibitor (PBI2) gene of yeast and studies on the function of its protein product. <i>FEBS Journal</i> , 1991, 197, 1-7.	0.2	26

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109	Carboxypeptidase yscS: gene structure and function of the vacuolar enzyme. FEBS Journal, 1991, 197, 399-405.	0.2	37
110	Aminopeptidase yscII of yeast. Isolation of mutants and their biochemical and genetic analysis. FEBS Journal, 1988, 173, 589-598.	0.2	28
111	Proteinase yscE of yeast shows homology with the 20 S cylinder particles of <i>Xenopus laevis</i> . FEBS Letters, 1988, 239, 35-40.	2.8	67
112	Protein degradation in yeast. Biochemical Society Transactions, 1987, 15, 811-815.	3.4	12
113	Hormone (pheromone) processing enzymes in yeast The carboxy-terminal processing enzyme of the mating pheromone $\hat{1}\pm$ -factor, carboxypeptidase yscI \pm , is absent in $\hat{1}\pm$ -factor maturation-defective <i>kek1</i> mutant cells. FEBS Letters, 1987, 221, 423-426.	2.8	23
114	Some characteristics of hormone (pheromone) processing enzymes in yeast. FEBS Letters, 1987, 218, 31-34.	2.8	20
115	Proteinase yscD mutants of yeast. Isolation and characterization. FEBS Journal, 1987, 163, 339-346.	0.2	19
116	Proteinases, proteolysis and regulation in yeast. Biochemical Society Transactions, 1985, 13, 279-283.	3.4	8
117	Proteinases, proteolysis and biological control in the yeast <i>Saccharomyces cerevisiae</i> . Yeast, 1985, 1, 139-157.	1.7	142
118	Vacuoles are not the sole compartments of proteolytic enzymes in yeast. FEBS Letters, 1984, 166, 321-325.	2.8	31
119	Proteolysis in eucaryotic cells: Aminopeptidases and dipeptidyl aminopeptidases of yeast revisited. Archives of Biochemistry and Biophysics, 1983, 226, 292-305.	3.0	37
120	Yeast pheromone $\hat{1}\pm$ -factor is synthesized as a high molecular weight precursor. Biochemical and Biophysical Research Communications, 1983, 116, 822-829.	2.1	39
121	Proteinase action in vitro versus proteinase function in vivo: mutants shed light on intracellular proteolysis in yeast. Trends in Biochemical Sciences, 1982, 7, 35-37.	7.5	62
122	In vivo biosynthesis of vacuolar proteinases in proteinase mutants of <i>Saccharomyces cerevisiae</i> . Biochemical and Biophysical Research Communications, 1982, 107, 770-778.	2.1	44
123	Aminopeptidase Co, a new yeast peptidase. Biochemical and Biophysical Research Communications, 1982, 109, 341-347.	2.1	46
124	New proteolytic enzymes in yeast. Archives of Biochemistry and Biophysics, 1981, 207, 445-454.	3.0	62
125	Control of Metabolism in Yeast and other Lower Eukaryotes through Action of Proteinases. Advances in Microbial Physiology, 1981, 21, 267-338.	2.4	60
126	Analysis of Proteinase A Function in Yeast. FEBS Journal, 1981, 121, 47-52.	0.2	61

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127	Carboxypeptidase S- and Carboxypeptidase Y-Deficient Mutants of <i>Saccharomyces cerevisiae</i> . <i>Journal of Bacteriology</i> , 1981, 147, 418-426.	2.2	55
128	Studies on a Proteinase B Mutant of Yeast. <i>FEBS Journal</i> , 1979, 98, 375-384.	0.2	73
129	Carboxypeptidase S from yeast: regulation of its activity during vegetative growth and differentiation. <i>FEBS Letters</i> , 1978, 91, 59-62.	2.8	28
130	Isolation of yeast mutants lacking proteinase B activity. <i>FEBS Letters</i> , 1978, 92, 121-124.	2.8	35
131	Studies on the carboxypeptidase Y-inhibitor complex of yeast. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 1978, 527, 63-69.	2.6	8
132	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
133	Tryptophan Synthase from Yeast. Purification by Affinity Chromatography, Physical Properties. <i>FEBS Journal</i> , 1974, 45, 269-276.	0.2	17