

Alfred L Goldberg

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.

213
papers

45,167
citations

102
h-index

212
g-index

220
ext. papers

49,112
ext. citations

14.6
avg, IF

7.68
L-index

#	Paper	IF	Citations
213	Mammalian Ddi2 is a shuttling factor containing a retroviral protease domain that influences binding of ubiquitylated proteins and proteasomal degradation.. <i>Journal of Biological Chemistry</i> , 2022 , 101875	5.4	0
212	Mechanisms That Activate 26S Proteasomes and Enhance Protein Degradation. <i>Biomolecules</i> , 2021 , 11,	5.9	3
211	ClpX Is Essential and Activated by Single-Strand DNA Binding Protein in Mycobacteria. <i>Journal of Bacteriology</i> , 2021 , 203,	3.5	2
210	Protein Turnover Intracellular Protein Degradation 2021 , 212-224		
209	cGMP via PKG activates 26S proteasomes and enhances degradation of proteins, including ones that cause neurodegenerative diseases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 14220-14230	11.5	24
208	An allosteric switch regulates ClpP1P2 protease function as established by cryo-EM and methyl-TROSY NMR. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 5895-5906	11.5	25
207	Proteins containing ubiquitin-like (Ubl) domains not only bind to 26S proteasomes but also induce their activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 4664-4674	11.5	27
206	Multiple myeloma cells are exceptionally sensitive to heat shock, which overwhelms their proteostasis network and induces apoptosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 21588-21597	11.5	4
205	SIP/CacyBP promotes autophagy by regulating levels of BRUCE/Apollon, which stimulates LC3-I degradation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 13404-13413	11.5	24
204	PDE1 inhibition facilitates proteasomal degradation of misfolded proteins and protects against cardiac proteinopathy. <i>Science Advances</i> , 2019 , 5, eaaw5870	14.3	32
203	Inhibiting ubiquitination causes an accumulation of SUMOylated newly synthesized nuclear proteins at PML bodies. <i>Journal of Biological Chemistry</i> , 2019 , 294, 15218-15234	5.4	18
202	26S Proteasomes are rapidly activated by diverse hormones and physiological states that raise cAMP and cause Rpn6 phosphorylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 4228-4237	11.5	56
201	Development of high throughput screening methods for inhibitors of ClpC1P1P2 from Mycobacteria tuberculosis. <i>Analytical Biochemistry</i> , 2019 , 567, 30-37	3.1	7
200	The antibiotic cyclomarlin blocks arginine-phosphate-induced millisecond dynamics in the N-terminal domain of ClpC1 from. <i>Journal of Biological Chemistry</i> , 2018 , 293, 8379-8393	5.4	20
199	Rapid induction of p62 and GABARAPL1 upon proteasome inhibition promotes survival before autophagy activation. <i>Journal of Cell Biology</i> , 2018 , 217, 1757-1776	7.3	48
198	Impairment of protein degradation and proteasome function in hereditary neuropathies. <i>Glia</i> , 2018 , 66, 379-395	9	18
197	UBL domain of Usp14 and other proteins stimulates proteasome activities and protein degradation in cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E11642-E11650	11.5	230

196	Measuring the Overall Rate of Protein Breakdown in Cells and the Contributions of the Ubiquitin-Proteasome and Autophagy-Lysosomal Pathways. <i>Methods in Molecular Biology</i> , 2018 , 1844, 261-276	1.4	16
195	Methods to Rapidly Prepare Mammalian 26S Proteasomes for Biochemical Analysis. <i>Methods in Molecular Biology</i> , 2018 , 1844, 277-288	1.4	4
194	Measurement of the Multiple Activities of 26S Proteasomes. <i>Methods in Molecular Biology</i> , 2018 , 1844, 289-308	1.4	3
193	Exploring the Regulation of Proteasome Function by Subunit Phosphorylation. <i>Methods in Molecular Biology</i> , 2018 , 1844, 309-319	1.4	10
192	ZFAND5/ZNF216 is an activator of the 26S proteasome that stimulates overall protein degradation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E9550-E9559 ^{11.5}	11.5	21
191	Inhibition of the Proteasome β Site Sensitizes Triple-Negative Breast Cancer Cells to β Inhibitors and Suppresses Nrf1 Activation. <i>Cell Chemical Biology</i> , 2017 , 24, 218-230	8.2	55
190	The deubiquitinating enzyme Usp14 allosterically inhibits multiple proteasomal activities and ubiquitin-independent proteolysis. <i>Journal of Biological Chemistry</i> , 2017 , 292, 9830-9839	5.4	45
189	The Logic of the 26S Proteasome. <i>Cell</i> , 2017 , 169, 792-806	56.2	411
188	Regulating protein breakdown through proteasome phosphorylation. <i>Biochemical Journal</i> , 2017 , 474, 3355-3371	3.8	64
187	Acyldepsipeptide antibiotics kill mycobacteria by preventing the physiological functions of the ClpP1P2 protease. <i>Molecular Microbiology</i> , 2016 , 101, 194-209	4.1	51
186	Control of proteasomal proteolysis by mTOR. <i>Nature</i> , 2016 , 529, E1-2	50.4	53
185	Tau-driven 26S proteasome impairment and cognitive dysfunction can be prevented early in disease by activating cAMP-PKA signaling. <i>Nature Medicine</i> , 2016 , 22, 46-53	50.5	258
184	The requirements of yeast Hsp70 of SSA family for the ubiquitin-dependent degradation of short-lived and abnormal proteins. <i>Biochemical and Biophysical Research Communications</i> , 2016 , 475, 100-6	3.4	12
183	Structure and Functional Properties of the Active Form of the Proteolytic Complex, ClpP1P2, from <i>Mycobacterium tuberculosis</i> . <i>Journal of Biological Chemistry</i> , 2016 , 291, 7465-76	5.4	31
182	Reply to Vangala et al.: Complete inhibition of the proteasome reduces new proteasome production by causing Nrf1 aggregation. <i>Current Biology</i> , 2016 , 26, R836-R837	6.3	21
181	Coordinate regulation of autophagy and the ubiquitin proteasome system by MTOR. <i>Autophagy</i> , 2016 , 12, 1967-1970	10.2	41
180	Blocking Cancer Growth with Less POMP or Proteasomes. <i>Molecular Cell</i> , 2015 , 59, 143-5	17.6	5
179	Structural characterization of the interaction of Ubp6 with the 26S proteasome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 8626-31	11.5	86

178	Cleavage Specificity of Mycobacterium tuberculosis ClpP1P2 Protease and Identification of Novel Peptide Substrates and Boronate Inhibitors with Anti-bacterial Activity. <i>Journal of Biological Chemistry</i> , 2015 , 290, 11008-20	5.4	35
177	Regulation of autophagy and the ubiquitin-proteasome system by the FoxO transcriptional network during muscle atrophy. <i>Nature Communications</i> , 2015 , 6, 6670	17.4	357
176	The cyclic peptide ecumicin targeting ClpC1 is active against Mycobacterium tuberculosis in vivo. <i>Antimicrobial Agents and Chemotherapy</i> , 2015 , 59, 880-9	5.9	105
175	Muscle Wasting in Fasting Requires Activation of NF- κ B and Inhibition of AKT/Mechanistic Target of Rapamycin (mTOR) by the Protein Acetylase, GCN5. <i>Journal of Biological Chemistry</i> , 2015 , 290, 30269-79	5.4	31
174	Thiostrepton interacts covalently with Rpt subunits of the 19S proteasome and proteasome substrates. <i>Journal of Cellular and Molecular Medicine</i> , 2015 , 19, 2181-92	5.6	11
173	Muscle wasting in disease: molecular mechanisms and promising therapies. <i>Nature Reviews Drug Discovery</i> , 2015 , 14, 58-74	64.1	570
172	Compromising the 19S proteasome complex protects cells from reduced flux through the proteasome. <i>ELife</i> , 2015 , 4,	8.9	46
171	Autoubiquitination of the 26S proteasome on Rpn13 regulates breakdown of ubiquitin conjugates. <i>EMBO Journal</i> , 2014 , 33, 1159-76	13	116
170	Mechanisms of muscle growth and atrophy in mammals and Drosophila. <i>Developmental Dynamics</i> , 2014 , 243, 201-15	2.9	90
169	Proteasome-mediated processing of Nrf1 is essential for coordinate induction of all proteasome subunits and p97. <i>Current Biology</i> , 2014 , 24, 1573-1583	6.3	141
168	Re-examining class-I presentation and the DRiP hypothesis. <i>Trends in Immunology</i> , 2014 , 35, 144-52	14.4	68
167	Enhanced ubiquitin-dependent degradation by Nedd4 protects against β -synuclein accumulation and toxicity in animal models of Parkinson's disease. <i>Neurobiology of Disease</i> , 2014 , 64, 79-87	7.5	46
166	Trim32 reduces PI3K-Akt-FoxO signaling in muscle atrophy by promoting plakoglobin-PI3K dissociation. <i>Journal of Cell Biology</i> , 2014 , 204, 747-58	7.3	57
165	Lassomycin, a ribosomally synthesized cyclic peptide, kills mycobacterium tuberculosis by targeting the ATP-dependent protease ClpC1P1P2. <i>Chemistry and Biology</i> , 2014 , 21, 509-518		255
164	Myostatin/activin pathway antagonism: molecular basis and therapeutic potential. <i>International Journal of Biochemistry and Cell Biology</i> , 2013 , 45, 2333-47	5.6	185
163	The influence of skeletal muscle on systemic aging and lifespan. <i>Aging Cell</i> , 2013 , 12, 943-9	9.9	137
162	SIRT1 protein, by blocking the activities of transcription factors FoxO1 and FoxO3, inhibits muscle atrophy and promotes muscle growth. <i>Journal of Biological Chemistry</i> , 2013 , 288, 30515-30526	5.4	124
161	BMP signaling controls muscle mass. <i>Nature Genetics</i> , 2013 , 45, 1309-18	36.3	280

160	Mechanisms of skeletal muscle aging: insights from <i>Drosophila</i> and mammalian models. <i>DMM Disease Models and Mechanisms</i> , 2013 , 6, 1339-52	4.1	153
159	Why do cellular proteins linked to K63-polyubiquitin chains not associate with proteasomes?. <i>EMBO Journal</i> , 2013 , 32, 552-65	13	160
158	Immuno- and constitutive proteasomes do not differ in their abilities to degrade ubiquitinated proteins. <i>Cell</i> , 2013 , 152, 1184-94	56.2	80
157	Acetylation-mediated proteasomal degradation of core histones during DNA repair and spermatogenesis. <i>Cell</i> , 2013 , 153, 1012-24	56.2	203
156	The ATP costs and time required to degrade ubiquitinated proteins by the 26 S proteasome. <i>Journal of Biological Chemistry</i> , 2013 , 288, 29215-22	5.4	86
155	Ubiquitinated proteins activate the proteasomal ATPases by binding to Usp14 or Uch37 homologs. <i>Journal of Biological Chemistry</i> , 2013 , 288, 7781-7790	5.4	81
154	Lon-A Peptidase, Endopeptidase La 2013 , 3527-3533		1
153	S5a/Rpn10, a UIM-protein, as a universal substrate for ubiquitination. <i>Methods in Molecular Biology</i> , 2012 , 832, 653-60	1.4	3
152	Affinity purification of mammalian 26S proteasomes using an ubiquitin-like domain. <i>Methods in Molecular Biology</i> , 2012 , 832, 423-32	1.4	24
151	Cathepsins L and Z are critical in degrading polyglutamine-containing proteins within lysosomes. <i>Journal of Biological Chemistry</i> , 2012 , 287, 17471-17482	5.4	22
150	Ubiquitylation by Trim32 causes coupled loss of desmin, Z-bands, and thin filaments in muscle atrophy. <i>Journal of Cell Biology</i> , 2012 , 198, 575-89	7.3	134
149	Bacterial proteolytic complexes as therapeutic targets. <i>Nature Reviews Drug Discovery</i> , 2012 , 11, 777-89	64.1	82
148	The p97/VCP ATPase is critical in muscle atrophy and the accelerated degradation of muscle proteins. <i>EMBO Journal</i> , 2012 , 31, 3334-50	13	57
147	The direction of protein entry into the proteasome determines the variety of products and depends on the force needed to unfold its two termini. <i>Molecular Cell</i> , 2012 , 48, 601-11	17.6	47
146	Mycobacterium tuberculosis ClpP1 and ClpP2 function together in protein degradation and are required for viability in vitro and during infection. <i>PLoS Pathogens</i> , 2012 , 8, e1002511	7.6	130
145	The active ClpP protease from <i>M. tuberculosis</i> is a complex composed of a heptameric ClpP1 and a ClpP2 ring. <i>EMBO Journal</i> , 2012 , 31, 1529-41	13	83
144	Development of proteasome inhibitors as research tools and cancer drugs. <i>Journal of Cell Biology</i> , 2012 , 199, 583-8	7.3	184
143	Formation of nondegradable forked ubiquitin conjugates by ring-finger ligases and its prevention by S5a. <i>Methods in Molecular Biology</i> , 2012 , 832, 639-52	1.4	3

142	ATP binds to proteasomal ATPases in pairs with distinct functional effects, implying an ordered reaction cycle. <i>Cell</i> , 2011 , 144, 526-38	56.2	159
141	A conserved F box regulatory complex controls proteasome activity in <i>Drosophila</i> . <i>Cell</i> , 2011 , 145, 371-83	56.2	67
140	Structural basis for antigenic peptide precursor processing by the endoplasmic reticulum aminopeptidase ERAP1. <i>Nature Structural and Molecular Biology</i> , 2011 , 18, 604-13	17.6	151
139	Blm10 protein promotes proteasomal substrate turnover by an active gating mechanism. <i>Journal of Biological Chemistry</i> , 2011 , 286, 42830-9	5.4	61
138	Ubiquitin ligase Nedd4 promotes alpha-synuclein degradation by the endosomal-lysosomal pathway. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 17004-9	11.5	163
137	Misfolded PrP impairs the UPS by interaction with the 20S proteasome and inhibition of substrate entry. <i>EMBO Journal</i> , 2011 , 30, 3065-77	13	86
136	Keeping proteasomes under control--a role for phosphorylation in the nucleus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 18573-4	11.5	19
135	Bortezomib--Scientific Origins and Its Tortuous Path to the Clinic 2011 , 1-27		4
134	Interactions of PAN's C-termini with archaeal 20S proteasome and implications for the eukaryotic proteasome-ATPase interactions. <i>EMBO Journal</i> , 2010 , 29, 692-702	13	90
133	Puromycin-sensitive aminopeptidase protects against aggregation-prone proteins via autophagy. <i>Human Molecular Genetics</i> , 2010 , 19, 4573-86	5.6	51
132	Muscle wasting in aged, sarcopenic rats is associated with enhanced activity of the ubiquitin proteasome pathway. <i>Journal of Biological Chemistry</i> , 2010 , 285, 39597-608	5.4	156
131	Peroxisome proliferator-activated receptor gamma coactivator 1alpha or 1beta overexpression inhibits muscle protein degradation, induction of ubiquitin ligases, and disuse atrophy. <i>Journal of Biological Chemistry</i> , 2010 , 285, 19460-71	5.4	165
130	Characterization of the Brain 26S Proteasome and its Interacting Proteins. <i>Frontiers in Molecular Neuroscience</i> , 2010 , 3,	6.1	82
129	ATP-dependent steps in the binding of ubiquitin conjugates to the 26S proteasome that commit to degradation. <i>Molecular Cell</i> , 2010 , 40, 671-81	17.6	135
128	Hsp104 is essential for the selective degradation in yeast of polyglutamine expanded ataxin-1 but not most misfolded proteins generally. <i>Biochemical and Biophysical Research Communications</i> , 2010 , 391, 1056-61	3.4	10
127	Reversal of cancer cachexia and muscle wasting by ActRIIB antagonism leads to prolonged survival. <i>Cell</i> , 2010 , 142, 531-43	56.2	661
126	Functional Consequences of Nucleotide Binding to the Proteasomal ATPases. <i>FASEB Journal</i> , 2010 , 24, 1b84	0.9	
125	The ubiquitin-interacting motif protein, S5a, is ubiquitinated by all types of ubiquitin ligases by a mechanism different from typical substrate recognition. <i>Journal of Biological Chemistry</i> , 2009 , 284, 12622-32	5.4	39

124	During muscle atrophy, thick, but not thin, filament components are degraded by MuRF1-dependent ubiquitylation. <i>Journal of Cell Biology</i> , 2009 , 185, 1083-95	7.3	437
123	S5a promotes protein degradation by blocking synthesis of nondegradable forked ubiquitin chains. <i>EMBO Journal</i> , 2009 , 28, 1867-77	13	70
122	Isolation of mammalian 26S proteasomes and p97/VCP complexes using the ubiquitin-like domain from HHR23B reveals novel proteasome-associated proteins. <i>Biochemistry</i> , 2009 , 48, 2538-49	3.2	137
121	Getting to first base in proteasome assembly. <i>Cell</i> , 2009 , 138, 25-8	56.2	64
120	Ubiquitinated proteins activate the proteasome by binding to Usp14/Ubp6, which causes 20S gate opening. <i>Molecular Cell</i> , 2009 , 36, 794-804	17.6	174
119	Mechanism of gate opening in the 20S proteasome by the proteasomal ATPases. <i>Molecular Cell</i> , 2008 , 30, 360-8	17.6	296
118	Coordinate activation of autophagy and the proteasome pathway by FoxO transcription factor. <i>Autophagy</i> , 2008 , 4, 378-80	10.2	128
117	Heat shock and oxygen radicals stimulate ubiquitin-dependent degradation mainly of newly synthesized proteins. <i>Journal of Cell Biology</i> , 2008 , 182, 663-73	7.3	145
116	What the Archaeal PAN Proteasome Complex and Bacterial ATP-Dependent Proteases Can Teach Us About the 26S Proteasome 2008 , 215-247		
115	The internal sequence of the peptide-substrate determines its N-terminus trimming by ERAP1. <i>PLoS ONE</i> , 2008 , 3, e3658	3.7	67
114	On prions, proteasomes, and mad cows. <i>New England Journal of Medicine</i> , 2007 , 357, 1150-2	59.2	19
113	Certain pairs of ubiquitin-conjugating enzymes (E2s) and ubiquitin-protein ligases (E3s) synthesize nondegradable forked ubiquitin chains containing all possible isopeptide linkages. <i>Journal of Biological Chemistry</i> , 2007 , 282, 17375-86	5.4	326
112	ATP-induced structural transitions in PAN, the proteasome-regulatory ATPase complex in Archaea. <i>Journal of Biological Chemistry</i> , 2007 , 282, 22921-9	5.4	39
111	Rapid disuse and denervation atrophy involve transcriptional changes similar to those of muscle wasting during systemic diseases. <i>FASEB Journal</i> , 2007 , 21, 140-55	0.9	429
110	Functions of the proteasome: from protein degradation and immune surveillance to cancer therapy. <i>Biochemical Society Transactions</i> , 2007 , 35, 12-7	5.1	290
109	FoxO3 controls autophagy in skeletal muscle in vivo. <i>Cell Metabolism</i> , 2007 , 6, 458-71	24.6	1393
108	FoxO3 coordinately activates protein degradation by the autophagic/lysosomal and proteasomal pathways in atrophying muscle cells. <i>Cell Metabolism</i> , 2007 , 6, 472-83	24.6	1141
107	Docking of the proteasomal ATPases' carboxyl termini in the 20S proteasome's alpha ring opens the gate for substrate entry. <i>Molecular Cell</i> , 2007 , 27, 731-44	17.6	405

106	c-IAP1 cooperates with Myc by acting as a ubiquitin ligase for Mad1. <i>Molecular Cell</i> , 2007 , 28, 914-22	17.6	66
105	PGC-1alpha protects skeletal muscle from atrophy by suppressing FoxO3 action and atrophy-specific gene transcription. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 16260-5	11.5	708
104	Importance of the different proteolytic sites of the proteasome and the efficacy of inhibitors varies with the protein substrate. <i>Journal of Biological Chemistry</i> , 2006 , 281, 8582-90	5.4	315
103	Tripeptidyl peptidase II is the major peptidase needed to trim long antigenic precursors, but is not required for most MHC class I antigen presentation. <i>Journal of Immunology</i> , 2006 , 177, 1434-43	5.3	80
102	Protein degradation by the ubiquitin-proteasome pathway in normal and disease states. <i>Journal of the American Society of Nephrology: JASN</i> , 2006 , 17, 1807-19	12.7	816
101	Protein Degradation and Turnover 2006 ,		1
100	Proteasomes and their associated ATPases: a destructive combination. <i>Journal of Structural Biology</i> , 2006 , 156, 72-83	3.4	95
99	hRpn13/ADRM1/GP110 is a novel proteasome subunit that binds the deubiquitinating enzyme, UCH37. <i>EMBO Journal</i> , 2006 , 25, 5742-53	13	189
98	Preparation of hybrid (19S-20S-PA28) proteasome complexes and analysis of peptides generated during protein degradation. <i>Methods in Enzymology</i> , 2005 , 398, 336-52	1.7	23
97	ATP binding to PAN or the 26S ATPases causes association with the 20S proteasome, gate opening, and translocation of unfolded proteins. <i>Molecular Cell</i> , 2005 , 20, 687-98	17.6	206
96	Nobel committee tags ubiquitin for distinction. <i>Neuron</i> , 2005 , 45, 339-44	13.9	35
95	Monitoring activity and inhibition of 26S proteasomes with fluorogenic peptide substrates. <i>Methods in Enzymology</i> , 2005 , 398, 364-78	1.7	253
94	Protein misfolding and cellular defense mechanisms in neurodegenerative diseases 2005 , 108-130		
93	The membrane-associated inhibitor of apoptosis protein, BRUCE/Apollon, antagonizes both the precursor and mature forms of Smac and caspase-9. <i>Journal of Biological Chemistry</i> , 2005 , 280, 174-82	5.4	68
92	The FOXO3a transcription factor regulates cardiac myocyte size downstream of AKT signaling. <i>Journal of Biological Chemistry</i> , 2005 , 280, 20814-23	5.4	260
91	The ER aminopeptidase, ERAP1, trims precursors to lengths of MHC class I peptides by a "molecular ruler" mechanism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 17107-12	11.5	238
90	Pathway for degradation of peptides generated by proteasomes: a key role for thimet oligopeptidase and other metallopeptidases. <i>Journal of Biological Chemistry</i> , 2004 , 279, 46723-32	5.4	146
89	Post-proteasomal antigen processing for major histocompatibility complex class I presentation. <i>Nature Immunology</i> , 2004 , 5, 670-7	19.1	204

88	Multiple types of skeletal muscle atrophy involve a common program of changes in gene expression. <i>FASEB Journal</i> , 2004 , 18, 39-51	0.9	1163
87	Eukaryotic proteasomes cannot digest polyglutamine sequences and release them during degradation of polyglutamine-containing proteins. <i>Molecular Cell</i> , 2004 , 14, 95-104	17.6	319
86	Foxo transcription factors induce the atrophy-related ubiquitin ligase atrogin-1 and cause skeletal muscle atrophy. <i>Cell</i> , 2004 , 117, 399-412	56.2	2133
85	IGF-I stimulates muscle growth by suppressing protein breakdown and expression of atrophy-related ubiquitin ligases, atrogin-1 and MuRF1. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2004 , 287, E591-601	6	436
84	Protein Degradation 2004 , 484-492		
83	TNF-alpha increases ubiquitin-conjugating activity in skeletal muscle by up-regulating UbcH2/E220k. <i>FASEB Journal</i> , 2003 , 17, 1048-57	0.9	200
82	Protein degradation and protection against misfolded or damaged proteins. <i>Nature</i> , 2003 , 426, 895-9	50.4	1644
81	The cytosolic endopeptidase, thimet oligopeptidase, destroys antigenic peptides and limits the extent of MHC class I antigen presentation. <i>Immunity</i> , 2003 , 18, 429-40	32.3	125
80	ATP hydrolysis by the proteasome regulatory complex PAN serves multiple functions in protein degradation. <i>Molecular Cell</i> , 2003 , 11, 69-78	17.6	210
79	The caspase-like sites of proteasomes, their substrate specificity, new inhibitors and substrates, and allosteric interactions with the trypsin-like sites. <i>Journal of Biological Chemistry</i> , 2003 , 278, 35869-77	5.4	146
78	An IFN-gamma-induced aminopeptidase in the ER, ERAP1, trims precursors to MHC class I-presented peptides. <i>Nature Immunology</i> , 2002 , 3, 1169-76	19.1	414
77	Properties of the hybrid form of the 26S proteasome containing both 19S and PA28 complexes. <i>EMBO Journal</i> , 2002 , 21, 2636-45	13	161
76	Patterns of gene expression in atrophying skeletal muscles: response to food deprivation. <i>FASEB Journal</i> , 2002 , 16, 1697-712	0.9	264
75	The importance of the proteasome and subsequent proteolytic steps in the generation of antigenic peptides. <i>Molecular Immunology</i> , 2002 , 39, 147-64	4.3	273
74	What do we really know about the ubiquitin-proteasome pathway in muscle atrophy?. <i>Current Opinion in Clinical Nutrition and Metabolic Care</i> , 2001 , 4, 183-90	3.8	308
73	Proteasome inhibitors: from research tools to drug candidates. <i>Chemistry and Biology</i> , 2001 , 8, 739-58		916
72	The molecular chaperone DnaJ is required for the degradation of a soluble abnormal protein in Escherichia coli. <i>Journal of Biological Chemistry</i> , 2001 , 276, 3920-8	5.4	44
71	Major histocompatibility complex class I-presented antigenic peptides are degraded in cytosolic extracts primarily by thimet oligopeptidase. <i>Journal of Biological Chemistry</i> , 2001 , 276, 36474-81	5.4	119

70	The unfolding of substrates and ubiquitin-independent protein degradation by proteasomes. <i>Biochimie</i> , 2001 , 83, 311-8	4.6	80
69	Cellular defenses against unfolded proteins: a cell biologist thinks about neurodegenerative diseases. <i>Neuron</i> , 2001 , 29, 15-32	13.9	870
68	The axial channel of the proteasome core particle is gated by the Rpt2 ATPase and controls both substrate entry and product release. <i>Molecular Cell</i> , 2001 , 7, 1143-52	17.6	347
67	Proteins are unfolded on the surface of the ATPase ring before transport into the proteasome. <i>Molecular Cell</i> , 2001 , 8, 1339-49	17.6	215
66	PAN, the proteasome-activating nucleotidase from archaeobacteria, is a protein-unfolding molecular chaperone. <i>Nature Cell Biology</i> , 2000 , 2, 833-9	23.4	303
65	Why does threonine, and not serine, function as the active site nucleophile in proteasomes?. <i>Journal of Biological Chemistry</i> , 2000 , 275, 14831-7	5.4	102
64	Ca ²⁺ -free calmodulin and calmodulin damaged by in vitro aging are selectively degraded by 26 S proteasomes without ubiquitination. <i>Journal of Biological Chemistry</i> , 2000 , 275, 20295-301	5.4	89
63	A new model of cancer cachexia: contribution of the ubiquitin-proteasome pathway. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 1999 , 277, E332-41	6	25
62	Rapid degradation of an abnormal protein in <i>Escherichia coli</i> proceeds through repeated cycles of association with GroEL. <i>Journal of Biological Chemistry</i> , 1999 , 274, 37743-9	5.4	35
61	An archaeobacterial ATPase, homologous to ATPases in the eukaryotic 26 S proteasome, activates protein breakdown by 20 S proteasomes. <i>Journal of Biological Chemistry</i> , 1999 , 274, 26008-14	5.4	135
60	The sizes of peptides generated from protein by mammalian 26 and 20 S proteasomes. Implications for understanding the degradative mechanism and antigen presentation. <i>Journal of Biological Chemistry</i> , 1999 , 274, 3363-71	5.4	429
59	Proteolysis and class I major histocompatibility complex antigen presentation. <i>Immunological Reviews</i> , 1999 , 172, 49-66	11.3	192
58	Degradation of cell proteins and the generation of MHC class I-presented peptides. <i>Annual Review of Immunology</i> , 1999 , 17, 739-79	34.7	789
57	Muscle protein breakdown and the critical role of the ubiquitin-proteasome pathway in normal and disease states. <i>Journal of Nutrition</i> , 1999 , 129, 227S-237S	4.1	518
56	Ubiquitin conjugation by the N-end rule pathway and mRNAs for its components increase in muscles of diabetic rats. <i>Journal of Clinical Investigation</i> , 1999 , 104, 1411-20	15.9	140
55	Proteasome inhibitors: valuable new tools for cell biologists. <i>Trends in Cell Biology</i> , 1998 , 8, 397-403	18.3	1188
54	The N-end rule pathway catalyzes a major fraction of the protein degradation in skeletal muscle. <i>Journal of Biological Chemistry</i> , 1998 , 273, 25216-22	5.4	106
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1	Duo-activation of PKA and PKG by PDE1 inhibition facilitates proteasomal degradation of misfolded proteins and protects against proteinopathy		2