Andreas Matouschek

List of Publications by Year
in descending order

86	9,579	53660 45	58464 82
papers	citations	h-index	g-index

92	92	92	6614
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Design principles that protect the proteasome from selfâ€destruction. Protein Science, 2022, 31, 556-567.	3.1	2
2	Mechanisms of substrate recognition by the 26S proteasome. Current Opinion in Structural Biology, 2021, 67, 161-169.	2.6	34
3	Use of Multiple Ion Fragmentation Methods to Identify Protein Cross-Links and Facilitate Comparison of Data Interpretation Algorithms. Journal of Proteome Research, 2020, 19, 2758-2771.	1.8	3
4	The proteasome 19S cap and its ubiquitin receptors provide a versatile recognition platform for substrates. Nature Communications, 2020, 11, 477.	5.8	101
5	A masked initiation region in retinoblastoma protein regulates its proteasomal degradation. Nature Communications, 2020, 11, 2019.	5.8	33
6	Mechanical unfolding of spectrin reveals a super-exponential dependence of unfolding rate on force. Scientific Reports, 2019, 9, 11101.	1.6	9
7	Substrate selection by the proteasome through initiation regions. Protein Science, 2019, 28, 1222-1232.	3.1	26
8	Decoding without the cipher. Nature Chemical Biology, 2019, 15, 210-212.	3.9	2
9	Scalable In Vitro Proteasome Activity Assay. Methods in Molecular Biology, 2018, 1844, 321-341.	0.4	7
10	Recognition of Client Proteins by the Proteasome. Annual Review of Biophysics, 2017, 46, 149-173.	4.5	99
11	Mouse Mammary Tumor Virus Signal Peptide Uses a Novel p97-Dependent and Derlin-Independent Retrotranslocation Mechanism To Escape Proteasomal Degradation. MBio, 2017, 8, .	1.8	12
12	An Inducible System for Rapid Degradation of Specific Cellular Proteins Using Proteasome Adaptors. PLoS ONE, 2016, 11, e0152679.	1.1	25
13	Conserved Sequence Preferences Contribute to Substrate Recognition by the Proteasome. Journal of Biological Chemistry, 2016, 291, 14526-14539.	1.6	56
14	Ubiquitinâ€like domains can target to the proteasome but proteolysis requires a disordered region. EMBO Journal, 2016, 35, 1522-1536.	3.5	52
15	An assay for 26S proteasome activity based on fluorescence anisotropy measurements of dye-labeled protein substrates. Analytical Biochemistry, 2016, 509, 50-59.	1.1	22
16	Ramping up degradation for proliferation. Nature Cell Biology, 2016, 18, 141-142.	4.6	3
17	A Rapid and Versatile Method for Generating Proteins with Defined Ubiquitin Chains. Biochemistry, 2016, 55, 1898-1908.	1.2	36
18	Sequence composition of disordered regions fine-tunes protein half-life. Nature Structural and Molecular Biology, 2015, 22, 214-221.	3.6	109

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19	Top-Down 193-nm Ultraviolet Photodissociation Mass Spectrometry for Simultaneous Determination of Polyubiquitin Chain Length and Topology. Analytical Chemistry, 2015, 87, 1812-1820.	3.2	41
20	Regulation of Proteasomal Degradation by Modulating Proteasomal Initiation Regions. ACS Chemical Biology, 2015, 10, 2537-2543.	1.6	13
21	Intrinsically Disordered Segments Affect Protein Half-Life in the Cell and during Evolution. Cell Reports, 2014, 8, 1832-1844.	2.9	192
22	Paradigms of protein degradation by the proteasome. Current Opinion in Structural Biology, 2014, 24, 156-164.	2.6	102
23	Disordered Proteinaceous Machines. Chemical Reviews, 2014, 114, 6806-6843.	23.0	109
24	Regulated protein turnover: snapshots of the proteasome in action. Nature Reviews Molecular Cell Biology, 2014, 15, 122-133.	16.1	212
25	Chance, Destiny, and the Inner Workings of ClpXP. Cell, 2014, 158, 479-480.	13.5	2
26	An Ancient Portal to Proteolysis. Science, 2012, 337, 813-814.	6.0	5
27	Sequence- and Species-Dependence of Proteasomal Processivity. ACS Chemical Biology, 2012, 7, 1444-1453.	1.6	50
28	Proteasomal Degradation from Internal Sites Favors Partial Proteolysis via Remote Domain Stabilization. ACS Chemical Biology, 2011, 6, 1087-1095.	1.6	27
29	How ClpX Unfolds GFP in Stages by Pulling. Journal of Molecular Biology, 2011, 413, 1-3.	2.0	0
30	Defining the geometry of the two-component proteasome degron. Nature Chemical Biology, 2011, 7, 161-167.	3.9	149
31	Rad23 escapes degradation because it lacks a proteasome initiation region. Nature Communications, 2011, 2, 192.	5.8	87
32	A Three-part Signal Governs Differential Processing of Gli1 and Gli3 Proteins by the Proteasome. Journal of Biological Chemistry, 2011, 286, 39051-39058.	1.6	33
33	Making It Easier to Regulate Protein Stability. Chemistry and Biology, 2010, 17, 917-918.	6.2	3
34	Pup grows up: in vitro characterization of the degradation of pupylated proteins. EMBO Journal, 2010, 29, 1163-1164.	3.5	3
35	Substrate selection by the proteasome during degradation of protein complexes. Nature Chemical Biology, 2009, 5, 29-36.	3.9	108
36	Targeting proteins for degradation. Nature Chemical Biology, 2009, 5, 815-822.	3.9	260

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37	ATP-dependent Proteases Differ Substantially in Their Ability to Unfold Globular Proteins. Journal of Biological Chemistry, 2009, 284, 18674-18684.	1.6	69
38	How to pick a protein and pull at it. Nature Structural and Molecular Biology, 2008, 15, 1135-1136.	3.6	7
39	Protein targeting to ATP-dependent proteases. Current Opinion in Structural Biology, 2008, 18, 43-51.	2.6	36
40	Controlling a Single Protein in a Nanopore through Electrostatic Traps. Journal of the American Chemical Society, 2008, 130, 4081-4088.	6.6	109
41	1P041 SELECTING PROTEINS FOR DEGRADATION: THE INITIATION STEP(Proteins-functions, methodology,) Tj ETQq1 1 0.784314 rgBT	0.0	0
42	To degrade or release: ubiquitin-chain remodeling. Trends in Cell Biology, 2007, 17, 419-421.	3.6	29
43	Where to start and when to stop. Nature Structural and Molecular Biology, 2006, 13, 668-670.	3.6	10
44	A conserved processing mechanism regulates the activity of transcription factors Cubitus interruptus and NF-Î¹B. Nature Structural and Molecular Biology, 2005, 12, 1045-1053.	3.6	106
45	Effect of protein structure on mitochondrial import. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 15435-15440.	3.3	94
46	Î²-Synuclein Reduces Proteasomal Inhibition by Î±-Synuclein but Not Î³-Synuclein. Journal of Biological Chemistry, 2005, 280, 7562-7569.	1.6	49
47	Inefficient degradation of truncated polyglutamine proteins by the proteasome. EMBO Journal, 2004, 23, 4307-4318.	3.5	258
48	An unstructured initiation site is required for efficient proteasome-mediated degradation. Nature Structural and Molecular Biology, 2004, 11, 830-837.	3.6	404
49	Protein unfolding in the cell. Trends in Biochemical Sciences, 2004, 29, 593-600.	3.7	125
50	The Force Exerted by the Membrane Potential during Protein Import into the Mitochondrial Matrix. Biophysical Journal, 2004, 86, 3647-3652.	0.2	38
51	Protein unfolding â€" an important process in vivo?. Current Opinion in Structural Biology, 2003, 13, 98-109.	2.6	153
52	Finding a protein's Achilles heel. Nature Structural and Molecular Biology, 2003, 10, 674-676.	3.6	27
53	Lack of a Robust Unfoldase Activity Confers a Unique Level of Substrate Specificity to the Universal AAA Protease FtsH. Molecular Cell, 2003, 11, 659-669.	4.5	163
54	Aggregated and Monomeric Î±-Synuclein Bind to the S6â€² Proteasomal Protein and Inhibit Proteasomal Function. Journal of Biological Chemistry, 2003, 278, 11753-11759.	1.6	364

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55	Concurrent Translocation of Multiple Polypeptide Chains through the Proteasomal Degradation Channel. Journal of Biological Chemistry, 2002, 277, 34760-34765.	1.6	57
56	Protein unfolding by the mitochondrial membrane potential. Nature Structural Biology, 2002, 9, 301-307.	9.7	119
57	ATP-Dependent Proteases Degrade Their Substrates by Processively Unraveling Them from the Degradation Signal. Molecular Cell, 2001, 7, 627-637.	4.5	380
58	Barreling through the outer membrane. , 2001, 8, 284-286.		24
59	Recognizing misfolded proteins in the endoplasmic reticulum. , 2000, 7, 265-266.		5
60	Protein unfolding by mitochondria. EMBO Reports, 2000, 1, 404-410.	2.0	160
61	Effect of the protein import machinery at the mitochondrial surface on precursor stability. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 12991-12996.	3.3	21
62	The Structure of Precursor Proteins during Import into Mitochondria. Journal of Biological Chemistry, 1999, 274, 12759-12764.	1.6	47
63	The dimensions of the protein import channels in the outer and inner mitochondrial membranes. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 13086-13090.	3.3	109
64	Mitochondria unfold precursor proteins by unraveling them from their N-termini. Nature Structural Biology, 1999, 6, 1132-1138.	9.7	110
65	Active unfolding of precursor proteins during mitochondrial protein import. EMBO Journal, 1997, 16, 6727-6736.	3.5	140
66	Hsp60-independent protein folding in the matrix of yeast mitochondria.. EMBO Journal, 1996, 15, 764-774.	3.5	81
67	Hsp60-independent protein folding in the matrix of yeast mitochondria. EMBO Journal, 1996, 15, 764-74.	3.5	25
68	Cyclophilin catalyzes protein folding in yeast mitochondria.. Proceedings of the National Academy of Sciences of the United States of America, 1995, 92, 6319-6323.	3.3	206
69	Movement of the position of the transition state in protein folding. Biochemistry, 1995, 34, 13656-13662.	1.2	133
70	Import and Folding of Proteins by Mitochondria. Cold Spring Harbor Symposia on Quantitative Biology, 1995, 60, 609-617.	2.0	6
71	Extrapolation to water of kinetic and equilibrium data for the unfolding of barnase in urea solutions. Protein Engineering, Design and Selection, 1994, 7, 1089-1095.	1.0	71
72	Application of physical organic chemistry to engineered mutants of proteins: Hammond postulate behavior in the transition state of protein folding.. Proceedings of the National Academy of Sciences of the United States of America, 1993, 90, 7814-7818.	3.3	199

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73	Pathway of protein folding. Faraday Discussions, 1992, 93, 183.	1.6	13
74	The folding of an enzyme. Journal of Molecular Biology, 1992, 224, 783-804.	2.0	421
75	The folding of an enzyme. Journal of Molecular Biology, 1992, 224, 805-818.	2.0	269
76	The folding of an enzyme. Journal of Molecular Biology, 1992, 224, 819-835.	2.0	222
77	The folding of an enzyme. Journal of Molecular Biology, 1992, 224, 771-782.	2.0	855
78	The folding of an enzyme. Journal of Molecular Biology, 1992, 224, 837-845.	2.0	100
79	The folding of an enzyme. Journal of Molecular Biology, 1992, 224, 847-859.	2.0	169
80	Pathway and stability of protein folding. Philosophical Transactions of the Royal Society B: Biological Sciences, 1991, 332, 171-176.	1.8	22
81	Physical-organic molecular biology: pathway and stability of protein folding. Pure and Applied Chemistry, 1991, 63, 187-194.	0.9	7
82	[6] Protein engineering in analysis of protein folding pathways and stability. Methods in Enzymology, 1991, 202, 82-112.	0.4	81
83	Transient folding intermediates characterized by protein engineering. Nature, 1990, 346, 440-445.	13.7	501
84	Detection and characterization of a folding intermediate in barnase by NMR. Nature, 1990, 346, 488-490.	13.7	241
85	Mapping the transition state and pathway of protein folding by protein engineering. Nature, 1989, 340, 122-126.	13.7	715
86	ATP-Dependent Proteases: The Cell's Degradation Machines. , 0, , 239-260.		1