

Andreas Matouschek

List of Publications by Year in descending order

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86
papers

9,579
citations

53794

45
h-index

58581

82
g-index

92
all docs

92
docs citations

92
times ranked

6614
citing authors

#	ARTICLE	IF	CITATIONS
1	The folding of an enzyme. <i>Journal of Molecular Biology</i> , 1992, 224, 771-782.	4.2	855
2	Mapping the transition state and pathway of protein folding by protein engineering. <i>Nature</i> , 1989, 340, 122-126.	27.8	715
3	Transient folding intermediates characterized by protein engineering. <i>Nature</i> , 1990, 346, 440-445.	27.8	501
4	The folding of an enzyme. <i>Journal of Molecular Biology</i> , 1992, 224, 783-804.	4.2	421
5	An unstructured initiation site is required for efficient proteasome-mediated degradation. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 830-837.	8.2	404
6	ATP-Dependent Proteases Degrade Their Substrates by Processively Unraveling Them from the Degradation Signal. <i>Molecular Cell</i> , 2001, 7, 627-637.	9.7	380
7	Aggregated and Monomeric α -Synuclein Bind to the S6 ² Proteasomal Protein and Inhibit Proteasomal Function. <i>Journal of Biological Chemistry</i> , 2003, 278, 11753-11759.	3.4	364
8	The folding of an enzyme. <i>Journal of Molecular Biology</i> , 1992, 224, 805-818.	4.2	269
9	Targeting proteins for degradation. <i>Nature Chemical Biology</i> , 2009, 5, 815-822.	8.0	260
10	Inefficient degradation of truncated polyglutamine proteins by the proteasome. <i>EMBO Journal</i> , 2004, 23, 4307-4318.	7.8	258
11	Detection and characterization of a folding intermediate in barnase by NMR. <i>Nature</i> , 1990, 346, 488-490.	27.8	241
12	The folding of an enzyme. <i>Journal of Molecular Biology</i> , 1992, 224, 819-835.	4.2	222
13	Regulated protein turnover: snapshots of the proteasome in action. <i>Nature Reviews Molecular Cell Biology</i> , 2014, 15, 122-133.	37.0	212
14	Cyclophilin catalyzes protein folding in yeast mitochondria.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995, 92, 6319-6323.	7.1	206
15	Application of physical organic chemistry to engineered mutants of proteins: Hammond postulate behavior in the transition state of protein folding.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1993, 90, 7814-7818.	7.1	199
16	Intrinsically Disordered Segments Affect Protein Half-Life in the Cell and during Evolution. <i>Cell Reports</i> , 2014, 8, 1832-1844.	6.4	192
17	The folding of an enzyme. <i>Journal of Molecular Biology</i> , 1992, 224, 847-859.	4.2	169
18	Lack of a Robust Unfoldase Activity Confers a Unique Level of Substrate Specificity to the Universal AAA Protease FtsH. <i>Molecular Cell</i> , 2003, 11, 659-669.	9.7	163

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19	Protein unfolding by mitochondria. <i>EMBO Reports</i> , 2000, 1, 404-410.	4.5	160
20	Protein unfolding – an important process in vivo?. <i>Current Opinion in Structural Biology</i> , 2003, 13, 98-109.	5.7	153
21	Defining the geometry of the two-component proteasome degron. <i>Nature Chemical Biology</i> , 2011, 7, 161-167.	8.0	149
22	Active unfolding of precursor proteins during mitochondrial protein import. <i>EMBO Journal</i> , 1997, 16, 6727-6736.	7.8	140
23	Movement of the position of the transition state in protein folding. <i>Biochemistry</i> , 1995, 34, 13656-13662.	2.5	133
24	Protein unfolding in the cell. <i>Trends in Biochemical Sciences</i> , 2004, 29, 593-600.	7.5	125
25	Protein unfolding by the mitochondrial membrane potential. <i>Nature Structural Biology</i> , 2002, 9, 301-307.	9.7	119
26	Mitochondria unfold precursor proteins by unraveling them from their N-termini. <i>Nature Structural Biology</i> , 1999, 6, 1132-1138.	9.7	110
27	The dimensions of the protein import channels in the outer and inner mitochondrial membranes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999, 96, 13086-13090.	7.1	109
28	Controlling a Single Protein in a Nanopore through Electrostatic Traps. <i>Journal of the American Chemical Society</i> , 2008, 130, 4081-4088.	13.7	109
29	Disordered Proteinaceous Machines. <i>Chemical Reviews</i> , 2014, 114, 6806-6843.	47.7	109
30	Sequence composition of disordered regions fine-tunes protein half-life. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 214-221.	8.2	109
31	Substrate selection by the proteasome during degradation of protein complexes. <i>Nature Chemical Biology</i> , 2009, 5, 29-36.	8.0	108
32	A conserved processing mechanism regulates the activity of transcription factors Cubitus interruptus and NF- κ B. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 1045-1053.	8.2	106
33	Paradigms of protein degradation by the proteasome. <i>Current Opinion in Structural Biology</i> , 2014, 24, 156-164.	5.7	102
34	The proteasome 19S cap and its ubiquitin receptors provide a versatile recognition platform for substrates. <i>Nature Communications</i> , 2020, 11, 477.	12.8	101
35	The folding of an enzyme. <i>Journal of Molecular Biology</i> , 1992, 224, 837-845.	4.2	100
36	Recognition of Client Proteins by the Proteasome. <i>Annual Review of Biophysics</i> , 2017, 46, 149-173.	10.0	99

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37	Effect of protein structure on mitochondrial import. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 15435-15440.	7.1	94
38	Rad23 escapes degradation because it lacks a proteasome initiation region. Nature Communications, 2011, 2, 192.	12.8	87
39	[6] Protein engineering in analysis of protein folding pathways and stability. Methods in Enzymology, 1991, 202, 82-112.	1.0	81
40	Hsp60-independent protein folding in the matrix of yeast mitochondria.. EMBO Journal, 1996, 15, 764-774.	7.8	81
41	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.	2.1	71
42	ATP-dependent Proteases Differ Substantially in Their Ability to Unfold Globular Proteins. Journal of Biological Chemistry, 2009, 284, 18674-18684.	3.4	69
43	Concurrent Translocation of Multiple Polypeptide Chains through the Proteasomal Degradation Channel. Journal of Biological Chemistry, 2002, 277, 34760-34765.	3.4	57
44	Conserved Sequence Preferences Contribute to Substrate Recognition by the Proteasome. Journal of Biological Chemistry, 2016, 291, 14526-14539.	3.4	56
45	Ubiquitin-like domains can target to the proteasome but proteolysis requires a disordered region. EMBO Journal, 2016, 35, 1522-1536.	7.8	52
46	Sequence- and Species-Dependence of Proteasomal Processivity. ACS Chemical Biology, 2012, 7, 1444-1453.	3.4	50
47	\hat{I}^2 -Synuclein Reduces Proteasomal Inhibition by \hat{I}^{\pm} -Synuclein but Not \hat{I}^3 -Synuclein. Journal of Biological Chemistry, 2005, 280, 7562-7569.	3.4	49
48	The Structure of Precursor Proteins during Import into Mitochondria. Journal of Biological Chemistry, 1999, 274, 12759-12764.	3.4	47
49	Top-Down 193-nm Ultraviolet Photodissociation Mass Spectrometry for Simultaneous Determination of Polyubiquitin Chain Length and Topology. Analytical Chemistry, 2015, 87, 1812-1820.	6.5	41
50	The Force Exerted by the Membrane Potential during Protein Import into the Mitochondrial Matrix. Biophysical Journal, 2004, 86, 3647-3652.	0.5	38
51	Protein targeting to ATP-dependent proteases. Current Opinion in Structural Biology, 2008, 18, 43-51.	5.7	36
52	A Rapid and Versatile Method for Generating Proteins with Defined Ubiquitin Chains. Biochemistry, 2016, 55, 1898-1908.	2.5	36
53	Mechanisms of substrate recognition by the 26S proteasome. Current Opinion in Structural Biology, 2021, 67, 161-169.	5.7	34
54	A Three-part Signal Governs Differential Processing of Gli1 and Gli3 Proteins by the Proteasome. Journal of Biological Chemistry, 2011, 286, 39051-39058.	3.4	33

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55	A masked initiation region in retinoblastoma protein regulates its proteasomal degradation. <i>Nature Communications</i> , 2020, 11, 2019.	12.8	33
56	To degrade or release: ubiquitin-chain remodeling. <i>Trends in Cell Biology</i> , 2007, 17, 419-421.	7.9	29
57	Finding a protein's Achilles heel. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 674-676.	8.2	27
58	Proteasomal Degradation from Internal Sites Favors Partial Proteolysis <i>via</i> Remote Domain Stabilization. <i>ACS Chemical Biology</i> , 2011, 6, 1087-1095.	3.4	27
59	Substrate selection by the proteasome through initiation regions. <i>Protein Science</i> , 2019, 28, 1222-1232.	7.6	26
60	An Inducible System for Rapid Degradation of Specific Cellular Proteins Using Proteasome Adaptors. <i>PLoS ONE</i> , 2016, 11, e0152679.	2.5	25
61	Hsp60-independent protein folding in the matrix of yeast mitochondria. <i>EMBO Journal</i> , 1996, 15, 764-74.	7.8	25
62	Barreling through the outer membrane. , 2001, 8, 284-286.		24
63	Pathway and stability of protein folding. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 1991, 332, 171-176.	4.0	22
64	An assay for 26S proteasome activity based on fluorescence anisotropy measurements of dye-labeled protein substrates. <i>Analytical Biochemistry</i> , 2016, 509, 50-59.	2.4	22
65	Effect of the protein import machinery at the mitochondrial surface on precursor stability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 12991-12996.	7.1	21
66	Pathway of protein folding. <i>Faraday Discussions</i> , 1992, 93, 183.	3.2	13
67	Regulation of Proteasomal Degradation by Modulating Proteasomal Initiation Regions. <i>ACS Chemical Biology</i> , 2015, 10, 2537-2543.	3.4	13
68	Mouse Mammary Tumor Virus Signal Peptide Uses a Novel p97-Dependent and Derlin-Independent Retrotranslocation Mechanism To Escape Proteasomal Degradation. <i>MBio</i> , 2017, 8, .	4.1	12
69	Where to start and when to stop. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 668-670.	8.2	10
70	Mechanical unfolding of spectrin reveals a super-exponential dependence of unfolding rate on force. <i>Scientific Reports</i> , 2019, 9, 11101.	3.3	9
71	Physical-organic molecular biology: pathway and stability of protein folding. <i>Pure and Applied Chemistry</i> , 1991, 63, 187-194.	1.9	7
72	How to pick a protein and pull at it. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 1135-1136.	8.2	7

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73	Scalable In Vitro Proteasome Activity Assay. <i>Methods in Molecular Biology</i> , 2018, 1844, 321-341.	0.9	7
74	Import and Folding of Proteins by Mitochondria. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 1995, 60, 609-617.	1.1	6
75	Recognizing misfolded proteins in the endoplasmic reticulum. , 2000, 7, 265-266.		5
76	An Ancient Portal to Proteolysis. <i>Science</i> , 2012, 337, 813-814.	12.6	5
77	Making It Easier to Regulate Protein Stability. <i>Chemistry and Biology</i> , 2010, 17, 917-918.	6.0	3
78	Pup grows up: in vitro characterization of the degradation of pupylated proteins. <i>EMBO Journal</i> , 2010, 29, 1163-1164.	7.8	3
79	Ramping up degradation for proliferation. <i>Nature Cell Biology</i> , 2016, 18, 141-142.	10.3	3
80	Use of Multiple Ion Fragmentation Methods to Identify Protein Cross-Links and Facilitate Comparison of Data Interpretation Algorithms. <i>Journal of Proteome Research</i> , 2020, 19, 2758-2771.	3.7	3
81	Chance, Destiny, and the Inner Workings of ClpXP. <i>Cell</i> , 2014, 158, 479-480.	28.9	2
82	Decoding without the cipher. <i>Nature Chemical Biology</i> , 2019, 15, 210-212.	8.0	2
83	Design principles that protect the proteasome from self-destruction. <i>Protein Science</i> , 2022, 31, 556-567.	7.6	2
84	ATP-Dependent Proteases: The Cell's Degradation Machines. , 0, , 239-260.		1
85	1P041 SELECTING PROTEINS FOR DEGRADATION: THE INITIATION STEP(Proteins-functions, methodology,) Tj ETQq _{0,1} 1 0.784314 rgBT ₀		
86	How ClpX Unfolds GFP in Stages by Pulling. <i>Journal of Molecular Biology</i> , 2011, 413, 1-3.	4.2	0