Robert T Sauer

List of Publications by Year
in descending order

281 papers	25,063 citations	4960 84 h-index	9589 142 g-index
294 all docs	294 docs citations	294 times ranked	13091 citing authors

#	Article	IF	Citations
1	Acyldepsipeptide Antibiotics and a Bioactive Fragment Thereof Differentially Perturb Mycobacterium tuberculosis ClpXP1P2 Activity in Vitro. ACS Chemical Biology, 2023, 18, 724-733.	3.4	12
2	Structure and function of ClpXP, a AAA+â€‰proteolytic machine powered by probabilistic ATP hydrolysis. Critical Reviews in Biochemistry and Molecular Biology, 2022, 57, 188-204.	5.2	17
3	ClpP1P2 peptidase activity promotes biofilm formation in Pseudomonas aeruginosa. Molecular Microbiology, 2021, 115, 1094-1109.	2.5	15
4	Heat activates the AAA+ HslUV protease by melting an axial autoinhibitory plug. Cell Reports, 2021, 34, 108639.	6.4	7
5	Division of labor between the pore-1 loops of the D1 and D2 AAA+ rings coordinates substrate selectivity of the ClpAP protease. Journal of Biological Chemistry, 2021, , 101407.	3.4	2
6	Modular and coordinated activity of AAA+ active sites in the double-ring ClpA unfoldase of the ClpAP protease. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 25455-25463.	7.1	11
7	The Intrinsically Disordered N-terminal Extension of the ClpS Adaptor Reprograms Its Partner AAA + ClpAP Protease. Journal of Molecular Biology, 2020, 432, 4908-4921.	4.2	7
8	Multistep substrate binding and engagement by the AAA+ ClpXP protease. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 28005-28013.	7.1	16
9	The Non-dominant AAA+ Ring in the ClpAP Protease Functions as an Anti-stalling Motor to Accelerate Protein Unfolding and Translocation. Cell Reports, 2020, 30, 2644-2654.e3.	6.4	21
10	Structures of the ATP-fueled ClpXP proteolytic machine bound to protein substrate. ELife, 2020, 9, .	6.0	105
11	ClpAP proteolysis does not require rotation of the ClpA unfoldase relative to ClpP. ELife, 2020, 9, .	6.0	9
12	Structural basis of ClpXP recognition and unfolding of ssrA-tagged substrates. ELife, 2020, 9, .	6.0	48
13	A mutagenesis screen for essential plastid biogenesis genes in human malaria parasites. PLoS Biology, 2019, 17, e3000136.	5.6	37
14	Roles of the ClpX IGF loops in ClpP association, dissociation, and protein degradation. Protein Science, 2019, 28, 756-765.	7.6	25
15	Interactions between a subset of substrate side chains and AAA+ motor pore loops determine grip during protein unfolding. ELife, 2019, 8, .	6.0	20
16	Mechanical Protein Unfolding and Degradation. Annual Review of Physiology, 2018, 80, 413-429.	13.1	70
17	Structure of the Mitochondrial Aminolevulinic Acid Synthase, a Key Heme Biosynthetic Enzyme. Structure, 2018, 26, 580-589.e4.	3.3	38
18	Hingeâ€"Linker Elements in the AAA+ Protein Unfoldase ClpX Mediate Intersubunit Communication, Assembly, and Mechanical Activity. Biochemistry, 2018, 57, 6787-6796.	2.5	18

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19	Structural and Functional Analysis of E.Âcoli Cyclopropane Fatty Acid Synthase. Structure, 2018, 26, 1251-1258.e3.	3.3	27
20	Covalently linked HslU hexamers support a probabilistic mechanism that links ATP hydrolysis to protein unfolding and translocation. Journal of Biological Chemistry, 2017, 292, 5695-5704.	3.4	13
21	Rational Design of Selective and Bioactive Inhibitors of the Mycobacterium tuberculosis Proteasome. ACS Infectious Diseases, 2017, 3, 176-181.	3.8	19
22	Effect of directional pulling on mechanical protein degradation by ATP-dependent proteolytic machines. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E6306-E6313.	7.1	44
23	Small molecule inhibition of apicomplexan FtsH1 disrupts plastid biogenesis in human pathogens. ELife, 2017, 6, .	6.0	47
24	A Structurally Dynamic Region of the HslU Intermediate Domain Controls Protein Degradation and ATP Hydrolysis. Structure, 2016, 24, 1766-1777.	3.3	9
25	The AAA+ FtsH Protease Degrades an ssrA-Tagged Model Protein in the Inner Membrane of Escherichia coli. Biochemistry, 2016, 55, 5649-5652.	2.5	18
26	Mechanistic insights into bacterial AAA+ proteases and protein-remodelling machines. Nature Reviews Microbiology, 2016, 14, 33-44.	28.6	243
27	Highly Dynamic Interactions Maintain Kinetic Stability of the ClpXP Protease During the ATP-Fueled Mechanical Cycle. ACS Chemical Biology, 2016, 11, 1552-1560.	3.4	29
28	Structural Basis of an N-Degron Adaptor with More Stringent Specificity. Structure, 2016, 24, 232-242.	3.3	27
29	Origin and Functional Evolution of the Cdc48/p97/VCP AAA+ Protein Unfolding and Remodeling Machine. Journal of Molecular Biology, 2016, 428, 1861-1869.	4.2	60
30	<scp>A</scp>n <scp>ALS</scp> disease mutation in <scp>C</scp>dc48/p97 impairs 20<scp>S</scp> proteasome binding and proteolytic communication. Protein Science, 2015, 24, 1521-1527.	7.6	19
31	Examination of a Structural Model of Peptidomimicry by Cyclic Acyldepsipeptide Antibiotics in Their Interaction with the ClpP Peptidase. ChemBioChem, 2015, 16, 1875-1879.	2.6	7
32	Coordinated gripping of substrate by subunits of a AAA+ proteolytic machine. Nature Chemical Biology, 2015, 11, 201-206.	8.0	56
33	A Conserved Activation Cluster Is Required for Allosteric Communication in HtrA-Family Proteases. Structure, 2015, 23, 517-526.	3.3	32
34	Assaying the kinetics of protein denaturation catalyzed by AAA+ unfolding machines and proteases. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 5377-5382.	7.1	29
35	Subunit asymmetry and roles of conformational switching in the hexameric AAA+ ring of ClpX. Nature Structural and Molecular Biology, 2015, 22, 411-416.	8.2	36
36	Deciphering the Roles of Multicomponent Recognition Signals by the AAA + Unfoldase ClpX. Journal of Molecular Biology, 2015, 427, 2966-2982.	4.2	11

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37	Steric clashes with bound OMP peptides activate the DegS stress-response protease. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 3326-3331.	7.1	19
38	Dissection of Axial-Pore Loop Function during Unfolding and Translocation by a AAA+ Proteolytic Machine. Cell Reports, 2015, 12, 1032-1041.	6.4	48
39	Substrate-guided optimization of the syringolins yields potent proteasome inhibitors with activity against leukemia cell lines. Bioorganic and Medicinal Chemistry, 2015, 23, 6218-6222.	3.0	8
40	Substrate delivery by the <scp>AAA</scp>+ <scp>ClpX</scp> and <scp>ClpC1</scp> unfoldases activates the mycobacterial <scp>ClpP1P2</scp> peptidase. Molecular Microbiology, 2014, 93, 617-628.	2.5	62
41	Overexpression of <scp>CupB</scp>5 activates alginate overproduction in <scp>P</scp>seudomonas aeruginosa by a novel <scp>AlgW</scp>â€dependent mechanism. Molecular Microbiology, 2014, 93, 415-425.	2.5	15
42	Architecture and assembly of the archaeal Cdc48â‹…20S proteasome. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E1687-94.	7.1	53
43	Roles of the <scp>N</scp> domain of the <scp>AAA</scp>+ <scp>Lon</scp> protease in substrate recognition, allosteric regulation and chaperone activity. Molecular Microbiology, 2014, 91, 66-78.	2.5	36
44	Distinct regulatory mechanisms balance DegP proteolysis to maintain cellular fitness during heat stress. Genes and Development, 2014, 28, 902-911.	5.9	29
45	Restriction of the Conformational Dynamics of the Cyclic Acyldepsipeptide Antibiotics Improves Their Antibacterial Activity. Journal of the American Chemical Society, 2014, 136, 1922-1929.	13.7	73
46	A Simple Fragment of Cyclic Acyldepsipeptides Is Necessary and Sufficient for ClpP Activation and Antibacterial Activity. ChemBioChem, 2014, 15, 2216-2220.	2.6	29
47	Remodeling of a delivery complex allows ClpS-mediated degradation of N-degron substrates. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E3853-9.	7.1	38
48	Stochastic but Highly Coordinated Protein Unfolding and Translocation by the ClpXP Proteolytic Machine. Cell, 2014, 158, 647-658.	28.9	120
49	Mechanochemical basis of protein degradation by a double-ring AAA+ machine. Nature Structural and Molecular Biology, 2014, 21, 871-875.	8.2	77
50	Crystal structure of Mycobacterium tuberculosis ClpP1P2 suggests a model for peptidase activation by AAA+ partner binding and substrate delivery. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E4587-95.	7.1	82
51	Dual Molecular Signals Mediate the Bacterial Response to Outer-Membrane Stress. Science, 2013, 340, 837-841.	12.6	159
52	Antibacterial Activity of and Resistance to Small Molecule Inhibitors of the ClpP Peptidase. ACS Chemical Biology, 2013, 8, 2669-2677.	3.4	58
53	A Mutation in the N Domain of Escherichia coli Lon Stabilizes Dodecamers and Selectively Alters Degradation of Model Substrates. Journal of Bacteriology, 2013, 195, 5622-5628.	2.2	10
54	Mutagenic dissection of the sequence determinants of protein folding, recognition, and machine function. Protein Science, 2013, 22, 1675-1687.	7.6	4

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55	Engineering fluorescent protein substrates for the AAA+ Lon protease. Protein Engineering, Design and Selection, 2013, 26, 299-305.	2.1	22
56	Allosteric regulation of DegS protease subunits through a shared energy landscape. Nature Chemical Biology, 2013, 9, 90-96.	8.0	40
57	Nucleotide Binding and Conformational Switching in the Hexameric Ring of a AAA+ Machine. Cell, 2013, 153, 628-639.	28.9	97
58	Bipartite determinants mediate an evolutionarily conserved interaction between Cdc48 and the 20 S peptidase. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 3327-3332.	7.1	56
59	Distinct quaternary structures of the AAA+ Lon protease control substrate degradation. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E2002-8.	7.1	64
60	Cage assembly of DegP protease is not required for substrate-dependent regulation of proteolytic activity or high-temperature cell survival. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 7263-7268.	7.1	51
61	Identification of the Cdc48â€¢20 S Proteasome as an Ancient AAA+ Proteolytic Machine. Science, 2012, 337, 843-846.	12.6	111
62	The I domain of the AAA+ HslUV protease coordinates substrate binding, ATP hydrolysis, and protein degradation. Protein Science, 2012, 21, 188-198.	7.6	13
63	Protein unfolding and degradation by the AAA+ Lon protease. Protein Science, 2012, 21, 268-278.	7.6	40
64	Dynamic and static components power unfolding in topologically closed rings of a AAA+ proteolytic machine. Nature Structural and Molecular Biology, 2012, 19, 616-622.	8.2	56
65	ClpXP, an ATP-powered unfolding and protein-degradation machine. Biochimica Et Biophysica Acta - Molecular Cell Research, 2012, 1823, 15-28.	4.1	384
66	Small-Molecule Control of Protein Degradation Using Split Adaptors. ACS Chemical Biology, 2011, 6, 1205-1213.	3.4	35
67	AAA+ Proteases: ATP-Fueled Machines of Protein Destruction. Annual Review of Biochemistry, 2011, 80, 587-612.	11.1	638
68	Signal integration by DegS and RseB governs the Ïƒ ^E -mediated envelope stress response in Escherichia coli. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 2106-2111.	7.1	63
69	Covalent Linkage of Distinct Substrate Degrons Controls Assembly and Disassembly of DegP Proteolytic Cages. Cell, 2011, 145, 67-78.	28.9	81
70	Single-Molecule Protein Unfolding and Translocation by an ATP-Fueled Proteolytic Machine. Cell, 2011, 145, 257-267.	28.9	251
71	The ClpS Adaptor Mediates Staged Delivery of N-End Rule Substrates to the AAA+ ClpAP Protease. Molecular Cell, 2011, 43, 217-228.	9.7	59
72	Stepwise Unfolding of a Î² Barrel Protein by the AAA+ ClpXP Protease. Journal of Molecular Biology, 2011, 413, 4-16.	4.2	66

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73	Design, construction and characterization of a set of insulated bacterial promoters. Nucleic Acids Research, 2011, 39, 1131-1141.	14.5	302
74	Versatile modes of peptide recognition by the ClpX N domain mediate alternative adaptorâ€binding specificities in different bacterial species. Protein Science, 2010, 19, 242-254.	7.6	20
75	The IbpA and IbpB small heatâ€shock proteins are substrates of the AAA+ Lon protease. Molecular Microbiology, 2010, 75, 1539-1549.	2.5	74
76	The AAA+ ClpX machine unfolds a keystone subunit to remodel the Mu transpososome. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 2437-2442.	7.1	20
77	Allostery Is an Intrinsic Property of the Protease Domain of DegS. Journal of Biological Chemistry, 2010, 285, 34039-34047.	3.4	37
78	Control of Substrate Gating and Translocation into ClpP by Channel Residues and ClpX Binding. Journal of Molecular Biology, 2010, 399, 707-718.	4.2	74
79	Multiple Sequence Signals Direct Recognition and Degradation of Protein Substrates by the AAA+ Protease HslUV. Journal of Molecular Biology, 2010, 403, 420-429.	4.2	10
80	Molecular basis of substrate selection by the N-end rule adaptor protein ClpS. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 8888-8893.	7.1	54
81	Analyzing the Interaction of RseA and RseB, the Two Negative Regulators of the ÏƒE Envelope Stress Response, Using a Combined Bioinformatic and Experimental Strategy. Journal of Biological Chemistry, 2009, 284, 5403-5413.	3.4	11
82	Engineering Synthetic Adaptors and Substrates for Controlled ClpXP Degradation. Journal of Biological Chemistry, 2009, 284, 21848-21855.	3.4	22
83	Degrons in protein substrates program the speed and operating efficiency of the AAA+ Lon proteolytic machine. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 18503-18508.	7.1	72
84	Single-molecule denaturation and degradation of proteins by the AAA+ ClpXP protease. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 19340-19345.	7.1	41
85	OMP Peptides Activate the DegS Stress-Sensor Protease by a Relief of Inhibition Mechanism. Structure, 2009, 17, 1411-1421.	3.3	40
86	Control of Pseudomonas aeruginosa AlgW protease cleavage of MucA by peptide signals and MucB. Molecular Microbiology, 2009, 72, 368-379.	2.5	77
87	Polypeptide Translocation by the AAA+ ClpXP Protease Machine. Chemistry and Biology, 2009, 16, 605-612.	6.0	61
88	Structures of Asymmetric ClpX Hexamers Reveal Nucleotide-Dependent Motions in a AAA+ Protein-Unfolding Machine. Cell, 2009, 139, 744-756.	28.9	231
89	OMP Peptides Modulate the Activity of DegS Protease by Differential Binding to Active and Inactive Conformations. Molecular Cell, 2009, 33, 64-74.	9.7	44
90	Protein unfolding by a AAA+ protease is dependent on ATP-hydrolysis rates and substrate energy landscapes. Nature Structural and Molecular Biology, 2008, 15, 139-145.	8.2	116

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91	Distinct structural elements of the adaptor ClpS are required for regulating degradation by ClpAP. Nature Structural and Molecular Biology, 2008, 15, 288-294.	8.2	45
92	Pore loops of the AAA+ ClpX machine grip substrates to drive translocation and unfolding. Nature Structural and Molecular Biology, 2008, 15, 1147-1151.	8.2	244
93	Asymmetric Nucleotide Transactions of the HslUV Protease. Journal of Molecular Biology, 2008, 380, 946-957.	4.2	47
94	Diverse Pore Loops of the AAA+ ClpX Machine Mediate Unassisted and Adaptor-Dependent Recognition of ssrA-Tagged Substrates. Molecular Cell, 2008, 29, 441-450.	9.7	146
95	Unique Contacts Direct High-Priority Recognition of the Tetrameric Mu Transposase-DNA Complex by the AAA+ Unfoldase ClpX. Molecular Cell, 2008, 30, 39-50.	9.7	32
96	The Molecular Basis of N-End Rule Recognition. Molecular Cell, 2008, 32, 406-414.	9.7	85
97	Forced extraction of targeted components from complex macromolecular assemblies. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 11685-11690.	7.1	21
98	Tuning the Strength of a Bacterial N-end Rule Degradation Signal. Journal of Biological Chemistry, 2008, 283, 24600-24607.	3.4	50
99	Recognition of misfolded proteins by Lon, a AAA⁺ protease. Genes and Development, 2008, 22, 2267-2277.	5.9	216
100	Revisiting the mechanism of macrolide-antibiotic resistance mediated by ribosomal protein L22. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 18261-18266.	7.1	44
101	Evolution of the ssrA degradation tag in Mycoplasma : Specificity switch to a different protease. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 16113-16118.	7.1	65
102	Inhibition of regulated proteolysis by RseB. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 3771-3776.	7.1	73
103	Direct and adaptor-mediated substrate recognition by an essential AAA+ protease. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 6590-6595.	7.1	84
104	ClpS modulates but is not essential for bacterial N-end rule degradation. Genes and Development, 2007, 21, 403-408.	5.9	64
105	Allosteric Activation of DegS, a Stress Sensor PDZ Protease. Cell, 2007, 131, 572-583.	28.9	114
106	Altered Specificity of a AAA+ Protease. Molecular Cell, 2007, 25, 161-166.	9.7	44
107	Distinct Static and Dynamic Interactions Control ATPase-Peptidase Communication in a AAA+ Protease. Molecular Cell, 2007, 27, 41-52.	9.7	113
108	The tmRNA System for Translational Surveillance and Ribosome Rescue. Annual Review of Biochemistry, 2007, 76, 101-124.	11.1	296

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109	Altered Tethering of the SspB Adaptor to the ClpXP Protease Causes Changes in Substrate Delivery. Journal of Biological Chemistry, 2007, 282, 11465-11473.	3.4	28
110	Structure and Substrate Specificity of an SspB Ortholog: Design Implications for AAA+ Adaptors. Structure, 2007, 15, 1296-1305.	3.3	18
111	Proteomic Profiling of ClpXP Substrates after DNA Damage Reveals Extensive Instability within SOS Regulon. Molecular Cell, 2006, 22, 193-204.	9.7	172
112	Engineering Controllable Protein Degradation. Molecular Cell, 2006, 22, 701-707.	9.7	202
113	ATP-dependent proteases of bacteria: recognition logic and operating principles. Trends in Biochemical Sciences, 2006, 31, 647-653.	7.5	258
114	Cytoplasmic degradation of ssrA-tagged proteins. Molecular Microbiology, 2005, 57, 1750-1761.	2.5	134
115	Ribosome rescue: tmRNA tagging activity and capacity inEscherichia coli. Molecular Microbiology, 2005, 58, 456-466.	2.5	109
116	Nucleotide-dependent substrate recognition by the AAA+ HslUV protease. Nature Structural and Molecular Biology, 2005, 12, 245-251.	8.2	63
117	Versatile modes of peptide recognition by the AAA+ adaptor protein SspB. Nature Structural and Molecular Biology, 2005, 12, 520-525.	8.2	39
118	Rebuilt AAA + motors reveal operating principles for ATP-fuelled machines. Nature, 2005, 437, 1115-1120.	27.8	344
119	Partitioning between unfolding and release of native domains during ClpXP degradation determines substrate selectivity and partial processing. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 1390-1395.	7.1	94
120	Sequence determinants of a conformational switch in a protein structure. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 18344-18349.	7.1	30
121	Consolidating critical binding determinants by noncyclic rearrangement of protein secondary structure. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 2305-2309.	7.1	6
122	Specificity versus stability in computational protein design. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 12724-12729.	7.1	129
123	Asymmetric Interactions of ATP with the AAA+ ClpX6 Unfoldase: Allosteric Control of a Protein Machine. Cell, 2005, 121, 1017-1027.	28.9	158
124	Role of the processing pore of the ClpX AAA+ ATPase in the recognition and engagement of specific protein substrates. Genes and Development, 2004, 18, 369-374.	5.9	146
125	Modulating substrate choice: the SspB adaptor delivers a regulator of the extracytoplasmic-stress response to the AAA+ protease ClpXP for degradation. Genes and Development, 2004, 18, 2292-2301.	5.9	175
126	Ribosomal protein S1 binds mRNA and tmRNA similarly but plays distinct roles in translation of these molecules. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 13454-13459.	7.1	54

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127	SspB delivery of substrates for ClpXP proteolysis probed by the design of improved degradation tags. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 12136-12141.	7.1	57
128	Signaling degradation. Nature Structural and Molecular Biology, 2004, 11, 800-802.	8.2	5
129	Communication between ClpX and ClpP during substrate processing and degradation. Nature Structural and Molecular Biology, 2004, 11, 404-411.	8.2	128
130	Computational and Experimental Probes of Symmetry Mismatches in the Arc Repressor?DNA Complex. Journal of Molecular Biology, 2004, 340, 253-253.	4.2	0
131	Sculpting the Proteome with AAA+ Proteases and Disassembly Machines. Cell, 2004, 119, 9-18.	28.9	398
132	Nucleotide-Dependent Substrate Handoff from the SspB Adaptor to the AAA+ ClpXP Protease. Molecular Cell, 2004, 16, 343-350.	9.7	68
133	Effects of local protein stability and the geometric position of the substrate degradation tag on the efficiency of ClpXP denaturation and degradation. Journal of Structural Biology, 2004, 146, 130-140.	2.8	54
134	Computational and Experimental Probes of Symmetry Mismatches in the Arc Repressorâ€"DNA Complex. Journal of Molecular Biology, 2004, 340, 253-261.	4.2	4
135	Bivalent Tethering of SspB to ClpXP Is Required for Efficient Substrate Delivery. Molecular Cell, 2004, 13, 443-449.	9.7	57
136	C-terminal domain mutations in ClpX uncouple substrate binding from an engagement step required for unfolding. Molecular Microbiology, 2003, 48, 67-76.	2.5	13
137	Nickel coordination is regulated by the DNA-bound state of NikR. Nature Structural Biology, 2003, 10, 126-130.	9.7	64
138	Crystal structure of the nickel-responsive transcription factor NikR. Nature Structural and Molecular Biology, 2003, 10, 794-799.	8.2	165
139	Energy-dependent degradation: Linkage between ClpX-catalyzed nucleotide hydrolysis and protein-substrate processing. Protein Science, 2003, 12, 893-902.	7.6	55
140	Structure of a Delivery Protein for an AAA+ Protease in Complex with a Peptide Degradation Tag. Molecular Cell, 2003, 12, 365-372.	9.7	87
141	Expression of N-formylated proteins in Escherichia coli. Protein Expression and Purification, 2003, 32, 317-322.	1.3	17
142	Cleavage of the A Site mRNA Codon during Ribosome Pausing Provides a Mechanism for Translational Quality Control. Molecular Cell, 2003, 12, 903-911.	9.7	203
143	Solution Structure of Switch Arc, a Mutant with 310 Helices Replacing a Wild-type Î²-Ribbon. Journal of Molecular Biology, 2003, 326, 899-909.	4.2	13
144	Toxin-Antitoxin Pairs in Bacteria. Cell, 2003, 112, 2-4.	28.9	51

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145	OMP Peptide Signals Initiate the Envelope-Stress Response by Activating DegS Protease via Relief of Inhibition Mediated by Its PDZ Domain. Cell, 2003, 113, 61-71.	28.9	456
146	Linkage between ATP Consumption and Mechanical Unfolding during the Protein Processing Reactions of an AAA+ Degradation Machine. Cell, 2003, 114, 511-520.	28.9	277
147	Proteomic Discovery of Cellular Substrates of the ClpXP Protease Reveals Five Classes of ClpX-Recognition Signals. Molecular Cell, 2003, 11, 671-683.	9.7	563
148	Flexible Linkers Leash the Substrate Binding Domain of SspB to a Peptide Module that Stabilizes Delivery Complexes with the AAA+ ClpXP Protease. Molecular Cell, 2003, 12, 355-363.	9.7	91
149	STRUCTURAL BIOLOGY: A Glimpse into tmRNA-Mediated Ribosome Rescue. Science, 2003, 300, 72-73.	12.6	2
150	Distinct peptide signals in the UmuD and UmuD' subunits of UmuD/D' mediate tethering and substrate processing by the ClpXP protease. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 13219-13224.	7.1	98
151	Latent ClpX-recognition signals ensure LexA destruction after DNA damage. Genes and Development, 2003, 17, 1084-1089.	5.9	99
152	Stop codons preceded by rare arginine codons are efficient determinants of SsrA tagging inEscherichia coli. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 3440-3445.	7.1	105
153	Proline Residues at the C Terminus of Nascent Chains Induce SsrA Tagging during Translation Termination. Journal of Biological Chemistry, 2002, 277, 33825-33832.	3.4	139
154	Tsp and Related Tail-Specific Proteases. The Enzymes, 2002, 22, 373-386.	1.7	1
155	Characterization of a Specificity Factor for an AAA+ ATPase. Chemistry and Biology, 2002, 9, 1237-1245.	6.0	89
156	Mutational studies of protein stability and folding of the hyperstable MYL Arc repressor variant. Biophysical Chemistry, 2002, 101-102, 35-42.	2.8	6
157	Role of an Ncap residue in determining the stability and operator-binding affinity of Arc repressor. Biophysical Chemistry, 2002, 100, 341-350.	2.8	13
158	Understanding protein hydrogen bond formation with kinetic H/D amide isotope effects. Nature Structural Biology, 2002, 9, 458-463.	9.7	66
159	NikR Repressor. Chemistry and Biology, 2002, 9, 1141-1148.	6.0	102
160	Simultaneous and functional binding of SmpB and EF-TuÂ·GTP to the alanyl acceptor arm of tmRNA. Journal of Molecular Biology, 2001, 314, 9-21.	4.2	96
161	Preferential Heterodimer Formation via Undercompensated Electrostatic Interactions. Journal of the American Chemical Society, 2001, 123, 1264-1265.	13.7	17
162	Assignments of the 1H,13C, and 15N resonances of the substrate-binding SSD domain from Lon protease. Journal of Biomolecular NMR, 2001, 21, 387-388.	2.8	3

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163	Characterization of the N-terminal repeat domain of Escherichia coli ClpA--A class I Clp/HSP100 ATPase. Protein Science, 2001, 10, 551-559.	7.6	55
164	Effects of protein stability and structure on substrate processing by the ClpXP unfolding and degradation machine. EMBO Journal, 2001, 20, 3092-3100.	7.8	132
165	Molecular determinants of complex formation between Clp/Hsp100 ATPases and the ClpP peptidase. Nature Structural Biology, 2001, 8, 230-233.	9.7	234
166	Identification of Endogenous SsrA-tagged Proteins Reveals Tagging at Positions Corresponding to Stop Codons. Journal of Biological Chemistry, 2001, 276, 28509-28515.	3.4	112
167	Overlapping recognition determinants within the ssrA degradation tag allow modulation of proteolysis. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 10584-10589.	7.1	262
168	An evolutionary bridge to a new protein fold. Nature Structural Biology, 2000, 7, 1129-1132.	9.7	78
169	The SsrA-SmpB system for protein tagging, directed degradation and ribosome rescue. Nature Structural Biology, 2000, 7, 449-455.	9.7	363
170	Regulation of High Affinity Nickel Uptake in Bacteria. Journal of Biological Chemistry, 2000, 275, 19735-19741.	3.4	148
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