Robert T Sauer

List of Publications by Year
in descending order

281	25,063	4960 84	9589 142
papers	citations	h-index	g-index

294	294	294	13091
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Transcription Factors: Structural Families and Principles of DNA Recognition. Annual Review of Biochemistry, 1992, 61, 1053-1095.	11.1	1,425
2	AAA+ Proteases: ATP-Fueled Machines of Protein Destruction. Annual Review of Biochemistry, 2011, 80, 587-612.	11.1	638
3	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
4	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
5	Alternative packing arrangements in the hydrophobic core of Î»represser. Nature, 1989, 339, 31-36.	27.8	418
6	Î» Repressor and croâ€"components of an efficient molecular switch. Nature, 1981, 294, 217-223.	27.8	410
7	Sculpting the Proteome with AAA+ Proteases and Disassembly Machines. Cell, 2004, 119, 9-18.	28.9	398
8	ClpXP, an ATP-powered unfolding and protein-degradation machine. Biochimica Et Biophysica Acta - Molecular Cell Research, 2012, 1823, 15-28.	4.1	384
9	The SsrA-SmpB system for protein tagging, directed degradation and ribosome rescue. Nature Structural Biology, 2000, 7, 449-455.	9.7	363
10	Rebuilt AAA + motors reveal operating principles for ATP-fuelled machines. Nature, 2005, 437, 1115-1120.	27.8	344
11	Are buried salt bridges important for protein stability and conformational specificity?. Nature Structural and Molecular Biology, 1995, 2, 122-128.	8.2	327
12	Dynamics of Substrate Denaturation and Translocation by the ClpXP Degradation Machine. Molecular Cell, 2000, 5, 639-648.	9.7	307
13	Design, construction and characterization of a set of insulated bacterial promoters. Nucleic Acids Research, 2011, 39, 1131-1141.	14.5	302
14	A Specificity-Enhancing Factor for the ClpXP Degradation Machine. Science, 2000, 289, 2354-2356.	12.6	297
15	The tmRNA System for Translational Surveillance and Ribosome Rescue. Annual Review of Biochemistry, 2007, 76, 101-124.	11.1	296
16	DNA recognition by Î²-sheets in the Arc repressorâ€"operator crystal structure. Nature, 1994, 367, 754-757.	27.8	287
17	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
18	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

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19	ATP-dependent proteases of bacteria: recognition logic and operating principles. Trends in Biochemical Sciences, 2006, 31, 647-653.	7.5	258
20	Single-Molecule Protein Unfolding and Translocation by an ATP-Fueled Proteolytic Machine. Cell, 2011, 145, 257-267.	28.9	251
21	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
22	Mechanistic insights into bacterial AAA+ proteases and protein-remodelling machines. Nature Reviews Microbiology, 2016, 14, 33-44.	28.6	243
23	Molecular determinants of complex formation between Clp/Hsp100 ATPases and the ClpP peptidase. Nature Structural Biology, 2001, 8, 230-233.	9.7	234
24	Equilibrium dissociation and unfolding of the arc repressor dimer. Biochemistry, 1989, 28, 7139-7143.	2.5	233
25	Structures of Asymmetric ClpX Hexamers Reveal Nucleotide-Dependent Motions in a AAA+ Protein-Unfolding Machine. Cell, 2009, 139, 744-756.	28.9	231
26	The role of internal packing interactions in determining the structure and stability of a protein. Journal of Molecular Biology, 1991, 219, 359-376.	4.2	219
27	Recognition of misfolded proteins by Lon, a AAA⁺ protease. Genes and Development, 2008, 22, 2267-2277.	5.9	216
28	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
29	Engineering Controllable Protein Degradation. Molecular Cell, 2006, 22, 701-707.	9.7	202
30	Structural and energetic consequences of disruptive mutations in a protein core. Biochemistry, 1992, 31, 4324-4333.	2.5	183
31	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
32	Reverse hydrophobic effects relieved by amino-acid substitutions at a protein surface. Nature, 1990, 344, 363-364.	27.8	172
33	Proteomic Profiling of ClpXP Substrates after DNA Damage Reveals Extensive Instability within SOS Regulon. Molecular Cell, 2006, 22, 193-204.	9.7	172
34	Crystal structure of the nickel-responsive transcription factor NikR. Nature Structural and Molecular Biology, 2003, 10, 794-799.	8.2	165
35	p22 Arc Repressor: Folding Kinetics of a Single-Domain, Dimeric Protein. Biochemistry, 1994, 33, 1125-1133.	2.5	164
36	Dual Molecular Signals Mediate the Bacterial Response to Outer-Membrane Stress. Science, 2013, 340, 837-841.	12.6	159

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37	[76] Bacteriophage Î» repressor and cro protein: Interactions with operator DNA. Methods in Enzymology, 1980, 65, 839-856.	1.0	158
38	Asymmetric Interactions of ATP with the AAA+ ClpX6 Unfoldase: Allosteric Control of a Protein Machine. Cell, 2005, 121, 1017-1027.	28.9	158
39	Lambda repressor mutations that increase the affinity and specificity of operator binding. Cell, 1985, 42, 549-558.	28.9	157
40	Regulatory functions of the Î» repressor reside in the amino-terminal domain. Nature, 1979, 279, 396-400.	27.8	155
41	Sequence space, folding and protein design. Current Opinion in Structural Biology, 1996, 6, 3-10.	5.7	154
42	Cooperatively folded proteins in random sequence libraries. Nature Structural Biology, 1995, 2, 856-864.	9.7	149
43	Regulation of High Affinity Nickel Uptake in Bacteria. Journal of Biological Chemistry, 2000, 275, 19735-19741.	3.4	148
44	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
45	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
46	Changing the DNA-binding specificity of a repressor. Cell, 1983, 35, 777-783.	28.9	140
47	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
48	The N-terminal arms of Î» repressor wrap around the operator DNA. Nature, 1982, 298, 441-443.	27.8	136
49	Contributions of a hydrogen bond/salt bridge network to the stability of secondary and tertiary structure in Î» repressor. Protein Science, 1994, 3, 2217-2225.	7.6	135
50	Diverse effects of mutations in the signal sequence on the secretion of Î²-lactamase in Salmonella typhimurium. Cell, 1982, 30, 903-914.	28.9	134
51	Cytoplasmic degradation of ssrA-tagged proteins. Molecular Microbiology, 2005, 57, 1750-1761.	2.5	134
52	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
53	DNA sequence of the bacteriophage Î» cI gene. Nature, 1978, 276, 301-302.	27.8	131
54	Primary structure of the Î» repressor. Biochemistry, 1978, 17, 1092-1100.	2.5	129

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55	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
56	Communication between ClpX and ClpP during substrate processing and degradation. Nature Structural and Molecular Biology, 2004, 11, 404-411.	8.2	128
57	P22 Arc Repressor: Transition State Properties Inferred from Mutational Effects on the Rates of Protein Unfolding and Refolding. Biochemistry, 1995, 34, 13914-13919.	2.5	127
58	Differential DNA-binding specificity of the engrailed homeodomain: The role of residue 50. Biochemistry, 1994, 33, 9187-9194.	2.5	120
59	Stochastic but Highly Coordinated Protein Unfolding and Translocation by the ClpXP Proteolytic Machine. Cell, 2014, 158, 647-658.	28.9	120
60	Stabilization of Î» repressor against thermal denaturation by site-directed Glyâ†'Ala changes in Î±-helix 3. Proteins: Structure, Function and Bioinformatics, 1986, 1, 43-46.	2.6	116
61	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
62	PDZ-like Domains Mediate Binding Specificity in the Clp/Hsp100 Family of Chaperones and Protease Regulatory Subunits. Cell, 1997, 91, 939-947.	28.9	115
63	Allosteric Activation of DegS, a Stress Sensor PDZ Protease. Cell, 2007, 131, 572-583.	28.9	114
64	Distinct Static and Dynamic Interactions Control ATPase-Peptidase Communication in a AAA+ Protease. Molecular Cell, 2007, 27, 41-52.	9.7	113
65	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
66	Identification of the Cdc48â€¢20 S Proteasome as an Ancient AAA+ Proteolytic Machine. Science, 2012, 337, 843-846.	12.6	111
67	Ribosome rescue: tmRNA tagging activity and capacity inEscherichia coli. Molecular Microbiology, 2005, 58, 456-466.	2.5	109
68	NikR is a ribbonâ€helixâ€helix DNAâ€binding protein. Protein Science, 1999, 8, 2494-2500.	7.6	109
69	Protein stability effects of a complete set of alanine substitutions in Arc repressor. Nature Structural Biology, 1994, 1, 518-523.	9.7	107
70	Evolution of a Protein Fold in Vitro. Science, 1999, 284, 325-327.	12.6	105
71	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
72	Structures of the ATP-fueled ClpXP proteolytic machine bound to protein substrate. ELife, 2020, 9, .	6.0	105

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73	NikR Repressor. Chemistry and Biology, 2002, 9, 1141-1148.	6.0	102
74	Identification of protein folds: Matching hydrophobicity patterns of sequence sets with solvent accessibility patterns of known structures. Proteins: Structure, Function and Bioinformatics, 1990, 7, 257-264.	2.6	101
75	Latent ClpX-recognition signals ensure LexA destruction after DNA damage. Genes and Development, 2003, 17, 1084-1089.	5.9	99
76	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
77	Probing the roles of residues at the e and g positions of the GCN4 leucine zipper by combinatorial mutagenesis. Protein Science, 1993, 2, 1072-1084.	7.6	97
78	Dexamethasoneâˆ’Methotrexate:â€‰ An Efficient Chemical Inducer of Protein Dimerization In Vivo. Journal of the American Chemical Society, 2000, 122, 4247-4248.	13.7	97
79	Nucleotide Binding and Conformational Switching in the Hexameric Ring of a AAA+ Machine. Cell, 2013, 153, 628-639.	28.9	97
80	Amino acid substitutions that increase the thermal stability of the Î» Cro protein. Proteins: Structure, Function and Bioinformatics, 1989, 5, 202-210.	2.6	96
81	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
82	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
83	Sequence Determinants of C-terminal Substrate Recognition by the Tsp Protease. Journal of Biological Chemistry, 1996, 271, 2589-2593.	3.4	92
84	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
85	Protein Stabilization by Removal of Unsatisfied Polar Groups:â€‰ Computational Approaches and Experimental Tests. Biochemistry, 1996, 35, 7621-7625.	2.5	89
86	Characterization of a Specificity Factor for an AAA+ ATPase. Chemistry and Biology, 2002, 9, 1237-1245.	6.0	89
87	Phage P22 tail protein: gene and amino acid sequence. Biochemistry, 1982, 21, 5811-5815.	2.5	88
88	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
89	Specificity of Minor-Groove and Major-Groove Interactions in a Homeodomain-DNA Complex. Biochemistry, 1995, 34, 14601-14608.	2.5	86
90	The Molecular Basis of N-End Rule Recognition. Molecular Cell, 2008, 32, 406-414.	9.7	85

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91	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
92	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
93	Covalent Linkage of Distinct Substrate Degrons Controls Assembly and Disassembly of DegP Proteolytic Cages. Cell, 2011, 145, 67-78.	28.9	81
94	Primary structure of the imml immunity region of bacteriophage P22. Journal of Molecular Biology, 1983, 168, 699-713.	4.2	79
95	Nonlinear Free Energy Relationships in Arc Repressor Unfolding Imply the Existence of Unstable, Native-like Folding Intermediatesâ€. Biochemistry, 1996, 35, 4795-4802.	2.5	79
96	Major groove DNA recognition by Î²-sheets: the ribbon-helix-helix family of gene regulatory proteins. Current Opinion in Structural Biology, 1994, 4, 36-43.	5.7	78
97	An evolutionary bridge to a new protein fold. Nature Structural Biology, 2000, 7, 1129-1132.	9.7	78
98	Bacteriophage P22 Mnt repressor. Journal of Molecular Biology, 1987, 195, 311-322.	4.2	77
99	[27] Random mutagenesis of protein sequences using oligonucleotide cassettes. Methods in Enzymology, 1991, 208, 564-586.	1.0	77
100	P22 Arc repressor: Enhanced expression of unstable mutants by addition of polar Câ€terminal sequences. Protein Science, 1993, 2, 2198-2205.	7.6	77
101	Control of Pseudomonas aeruginosa AlgW protease cleavage of MucA by peptide signals and MucB. Molecular Microbiology, 2009, 72, 368-379.	2.5	77
102	Mechanochemical basis of protein degradation by a double-ring AAA+ machine. Nature Structural and Molecular Biology, 2014, 21, 871-875.	8.2	77
103	Primary structure of the phage P22 repressor and its gene c2. Biochemistry, 1981, 20, 3591-3598.	2.5	74
104	Isolation and analysis of arc repressor mutants: Evidence for an unusual mechanism of DNA binding. Proteins: Structure, Function and Bioinformatics, 1986, 1, 302-311.	2.6	74
105	Functionally acceptable substitutions in two Î±-helical regions of Î» repressor. Proteins: Structure, Function and Bioinformatics, 1990, 7, 306-316.	2.6	74
106	The IbpA and IbpB small heatâ€shock proteins are substrates of the AAA+ Lon protease. Molecular Microbiology, 2010, 75, 1539-1549.	2.5	74
107	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
108	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

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109	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
110	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
111	Câ€terminal specific protein degradation: Activity and substrate specificity of the Tsp protease. Protein Science, 1995, 4, 1507-1515.	7.6	70
112	Signal Detection by the PhoQ Sensor-Transmitter. Journal of Biological Chemistry, 1996, 271, 26630-26636.	3.4	70
113	Mechanical Protein Unfolding and Degradation. Annual Review of Physiology, 2018, 80, 413-429.	13.1	70
114	Identification of Active Site Residues of the Tsp Protease. Journal of Biological Chemistry, 1995, 270, 28864-28868.	3.4	69
115	Î» Repressor: A Model System for Understanding Proteinâ€“DNA Interactions and Protein Stability. Advances in Protein Chemistry, 1990, 40, 1-61.	4.4	68
116	Nucleotide-Dependent Substrate Handoff from the SspB Adaptor to the AAA+ ClpXP Protease. Molecular Cell, 2004, 16, 343-350.	9.7	68
117	Solution Structure of Dimeric Mnt Repressor (1-76). Biochemistry, 1994, 33, 15036-15045.	2.5	67
118	Phage lambda repressor revertants. Journal of Molecular Biology, 1985, 186, 53-63.	4.2	66
119	Understanding protein hydrogen bond formation with kinetic H/D amide isotope effects. Nature Structural Biology, 2002, 9, 458-463.	9.7	66
120	Stepwise Unfolding of a Î² Barrel Protein by the AAA+ ClpXP Protease. Journal of Molecular Biology, 2011, 413, 4-16.	4.2	66
121	Arc repressor is tetrameric when bound to operator DNA. Biochemistry, 1990, 29, 11189-11195.	2.5	65
122	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
123	Nickel coordination is regulated by the DNA-bound state of NikR. Nature Structural Biology, 2003, 10, 126-130.	9.7	64
124	ClpS modulates but is not essential for bacterial N-end rule degradation. Genes and Development, 2007, 21, 403-408.	5.9	64
125	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
126	Nucleotide-dependent substrate recognition by the AAA+ HslUV protease. Nature Structural and Molecular Biology, 2005, 12, 245-251.	8.2	63

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127	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
128	Dimerization of the operator binding domain of phage .lambda. repressor. Biochemistry, 1987, 26, 897-904.	2.5	62
129	Equilibrium Stability and Sub-Millisecond Refolding of a Designed Single-Chain Arc Repressorâ€. Biochemistry, 1996, 35, 13878-13884.	2.5	62
130	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
131	Polypeptide Translocation by the AAA+ ClpXP Protease Machine. Chemistry and Biology, 2009, 16, 605-612.	6.0	61
132	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
133	Stability and DNA Binding of the Phd Protein of the Phage P1 Plasmid Addiction System. Journal of Biological Chemistry, 1999, 274, 2652-2657.	3.4	59
134	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
135	Antibacterial Activity of and Resistance to Small Molecule Inhibitors of the ClpP Peptidase. ACS Chemical Biology, 2013, 8, 2669-2677.	3.4	58
136	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
137	Bivalent Tethering of SspB to ClpXP Is Required for Efficient Substrate Delivery. Molecular Cell, 2004, 13, 443-449.	9.7	57
138	Covalent Attachment of Arc Repressor Subunits by a Peptide Linker Enhances Affinity for Operator DNAâ€. Biochemistry, 1996, 35, 109-116.	2.5	56
139	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
140	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
141	Coordinated gripping of substrate by subunits of a AAA+ proteolytic machine. Nature Chemical Biology, 2015, 11, 201-206.	8.0	56
142	Assembly of the arc repressor-operator complex: cooperative interactions between DNA-bound dimers. Biochemistry, 1993, 32, 1354-1363.	2.5	55
143	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
144	Energy-dependent degradation: Linkage between ClpX-catalyzed nucleotide hydrolysis and protein-substrate processing. Protein Science, 2003, 12, 893-902.	7.6	55

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145	Isolation of .lambda. repressor mutants with defects in cooperative operator binding. Biochemistry, 1993, 32, 9073-9079.	2.5	54
146	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
147	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
148	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
149	TraY proteins of F and related episomes are members of the Arc and Mnt repressor family. Journal of Molecular Biology, 1990, 211, 5-6.	4.2	53
150	Acceleration of the refolding of Arc repressor by nucleic acids and other polyanions. Nature Structural Biology, 1999, 6, 569-573.	9.7	53
151	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
152	Interaction of the bacteriophage P22 arc repressor with operator DNA. Journal of Molecular Biology, 1987, 195, 323-331.	4.2	52
153	Î» Repressor mutants that are better substrates for RecA-mediated cleavage. Journal of Molecular Biology, 1989, 206, 29-39.	4.2	52
154	[12] Analysis of DNA-protein interactions by affinity coelectrophoresis. Methods in Enzymology, 1991, 208, 196-210.	1.0	52
155	The Doc Toxin and Phd Antidote Proteins of the Bacteriophage P1 Plasmid Addiction System Form a Heterotrimeric Complex. Journal of Biological Chemistry, 1999, 274, 16813-16818.	3.4	51
156	Toxin-Antitoxin Pairs in Bacteria. Cell, 2003, 112, 2-4.	28.9	51
157	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
158	Î» Repressor inactivation: Properties of purified indâ€™ proteins in the autodigestion and RecA-mediated cleavage reactions. Journal of Molecular Biology, 1986, 192, 39-47.	4.2	50
159	Tuning the Strength of a Bacterial N-end Rule Degradation Signal. Journal of Biological Chemistry, 2008, 283, 24600-24607.	3.4	50
160	The tetramerization domain of the Mnt repressor consists of two right-handed coiled coils. Nature Structural Biology, 1999, 6, 755-759.	9.7	49
161	Dissection of Axial-Pore Loop Function during Unfolding and Translocation by a AAA+ Proteolytic Machine. Cell Reports, 2015, 12, 1032-1041.	6.4	48
162	Structural basis of ClpXP recognition and unfolding of ssrA-tagged substrates. ELife, 2020, 9, .	6.0	48

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163	Asymmetric Nucleotide Transactions of the HslUV Protease. Journal of Molecular Biology, 2008, 380, 946-957.	4.2	47
164	Small molecule inhibition of apicomplexan FtsH1 disrupts plastid biogenesis in human pathogens. ELife, 2017, 6, .	6.0	47
165	Increasing and decreasing protein stability: Effects of revertant substitutions on the thermal denaturation of phage ? repressor. Journal of Cellular Biochemistry, 1985, 29, 217-224.	2.6	46
166	Critical side-chain interactions at a subunit interface in the Arc repressor dimer. Biochemistry, 1995, 34, 3344-3351.	2.5	46
167	Tolerance of a protein helix to multiple alanine and valine substitutions. Folding & Design, 1998, 3, 119-126.	4.5	46
168	Interaction of mutant Î» repressors with operator and non-operator DNA. Journal of Molecular Biology, 1986, 192, 27-38.	4.2	45
169	Tolerance of a protein to multiple polarâ€toâ€hydrophobic surface substitutions. Protein Science, 1999, 8, 318-325.	7.6	45
170	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
171	Altered Specificity of a AAA+ Protease. Molecular Cell, 2007, 25, 161-166.	9.7	44
172	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
173	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
174	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
175	Scanning mutagenesis of the Arc represser as a functional probe of operator recognition. Nature Structural Biology, 1994, 1, 164-168.	9.7	42
176	Domain structure and quaternary organization of the bacteriophage P22 Erf protein. Journal of Molecular Biology, 1983, 171, 401-418.	4.2	41
177	Control of phage P22 tail protein expression by transcription termination. Journal of Molecular Biology, 1983, 164, 561-572.	4.2	41
178	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
179	OMP Peptides Activate the DegS Stress-Sensor Protease by a Relief of Inhibition Mechanism. Structure, 2009, 17, 1411-1421.	3.3	40
180	Protein unfolding and degradation by the AAA+ Lon protease. Protein Science, 2012, 21, 268-278.	7.6	40

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