Tania A Baker

List of Publications by Year
in descending order

159	12,781	26626 56	28296 105
papers	citations	h-index	g-index

171	171	171	7037
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	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
2	ClpP1P2 peptidase activity promotes biofilm formation in Pseudomonas aeruginosa. Molecular Microbiology, 2021, 115, 1094-1109.	2.5	15
3	Heat activates the AAA+ HslUV protease by melting an axial autoinhibitory plug. Cell Reports, 2021, 34, 108639.	6.4	7
4	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
5	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
6	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
7	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
8	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
9	Regulation of Antimycin Biosynthesis Is Controlled by the ClpXP Protease. MSphere, 2020, 5, .	2.9	5
10	Structures of the ATP-fueled ClpXP proteolytic machine bound to protein substrate. ELife, 2020, 9, .	6.0	105
11	Mitochondrial ClpX activates an essential biosynthetic enzyme through partial unfolding. ELife, 2020, 9, .	6.0	21
12	ClpAP proteolysis does not require rotation of the ClpA unfoldase relative to ClpP. ELife, 2020, 9, .	6.0	9
13	Structural basis of ClpXP recognition and unfolding of ssrA-tagged substrates. ELife, 2020, 9, .	6.0	48
14	Roles of the ClpX IGF loops in ClpP association, dissociation, and protein degradation. Protein Science, 2019, 28, 756-765.	7.6	25
15	N domain of the Lon AAA+ protease controls assembly and substrate choice. Protein Science, 2019, 28, 1239-1251.	7.6	10
16	Interactions between a subset of substrate side chains and AAA+ motor pore loops determine grip during protein unfolding. ELife, 2019, 8, .	6.0	20
17	Direct proteolytic control of an extracytoplasmic function RNA polymerase sigma factor. Access Microbiology, 2019, 1, .	0.5	0
18	Mechanical Protein Unfolding and Degradation. Annual Review of Physiology, 2018, 80, 413-429.	13.1	70

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19	Structure of the Mitochondrial Aminolevulinic Acid Synthase, a Key Heme Biosynthetic Enzyme. Structure, 2018, 26, 580-589.e4.	3.3	38
20	Hingeâ€“Linker Elements in the AAA+ Protein Unfoldase ClpX Mediate Intersubunit Communication, Assembly, and Mechanical Activity. Biochemistry, 2018, 57, 6787-6796.	2.5	18
21	Deciphering the Role of ATPase Domains of CLPA using Single-Molecule Optical Tweezers. Biophysical Journal, 2018, 114, 170a.	0.5	0
22	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
23	Mutation in human CLPX elevates levels of Î´- aminolevulinate synthase and protoporphyrin IX to promote erythropoietic protoporphyria. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E8045-E8052.	7.1	69
24	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
25	Two Isoforms of Clp Peptidase in Pseudomonas aeruginosa Control Distinct Aspects of Cellular Physiology. Journal of Bacteriology, 2017, 199, .	2.2	37
26	A Structurally Dynamic Region of the HslU Intermediate Domain Controls Protein Degradation and ATP Hydrolysis. Structure, 2016, 24, 1766-1777.	3.3	9
27	Mechanistic insights into bacterial AAA+ proteases and protein-remodelling machines. Nature Reviews Microbiology, 2016, 14, 33-44.	28.6	243
28	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
29	Structural Basis of an N-Degron Adaptor with More Stringent Specificity. Structure, 2016, 24, 232-242.	3.3	27
30	Oxidization without substrate unfolding triggers proteolysis of the peroxide-sensor, PerR. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E23-31.	7.1	32
31	A Dominant Mutation in Mitochondrial Unfoldase CLPX Results in Erythropoietic Protoporphyria. Blood, 2016, 128, 77-77.	1.4	0
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	Mitochondrial ClpX Activates a Key Enzyme for Heme Biosynthesis and Erythropoiesis. Cell, 2015, 161, 858-867.	28.9	95
36	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

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37	Deciphering the Roles of Multicomponent Recognition Signals by the AAA + Unfoldase ClpX. Journal of Molecular Biology, 2015, 427, 2966-2982.	4.2	11
38	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
39	Dissection of Axial-Pore Loop Function during Unfolding and Translocation by a AAA+ Proteolytic Machine. Cell Reports, 2015, 12, 1032-1041.	6.4	48
40	NOA1, a Novel ClpXP Substrate, Takes an Unexpected Nuclear Detour Prior to Mitochondrial Import. PLoS ONE, 2014, 9, e103141.	2.5	24
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	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
45	Stochastic but Highly Coordinated Protein Unfolding and Translocation by the ClpXP Proteolytic Machine. Cell, 2014, 158, 647-658.	28.9	120
46	Mechanochemical basis of protein degradation by a double-ring AAA+ machine. Nature Structural and Molecular Biology, 2014, 21, 871-875.	8.2	77
47	Mechanical Protein Unfolding and Translocation by AAA+ Proteases. Biophysical Journal, 2014, 106, 246a.	0.5	0
48	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
49	Engineering fluorescent protein substrates for the AAA+ Lon protease. Protein Engineering, Design and Selection, 2013, 26, 299-305.	2.1	22
50	Distinct Quaternary Structures of Lon Protease Control Substrate Degradation. Biophysical Journal, 2013, 104, 554a.	0.5	0
51	Nucleotide Binding and Conformational Switching in the Hexameric Ring of a AAA+ Machine. Cell, 2013, 153, 628-639.	28.9	97
52	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
53	RpoS proteolysis is controlled directly by ATP levels in Escherichia coli. Genes and Development, 2012, 26, 548-553.	5.9	52
54	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

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55	Segregation of molecules at cell division reveals native protein localization. Nature Methods, 2012, 9, 480-482.	19.0	287
56	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
57	ClpXP, an ATP-powered unfolding and protein-degradation machine. Biochimica Et Biophysica Acta - Molecular Cell Research, 2012, 1823, 15-28.	4.1	384
58	Small-Molecule Control of Protein Degradation Using Split Adaptors. ACS Chemical Biology, 2011, 6, 1205-1213.	3.4	35
59	AAA+ Proteases: ATP-Fueled Machines of Protein Destruction. Annual Review of Biochemistry, 2011, 80, 587-612.	11.1	638
60	Single-Molecule Protein Unfolding and Translocation by an ATP-Fueled Proteolytic Machine. Cell, 2011, 145, 257-267.	28.9	251
61	Proteolysis in the Escherichia coli heat shock response: a player at many levels. Current Opinion in Microbiology, 2011, 14, 194-199.	5.1	46
62	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
63	Regulatory Cohesion of Cell Cycle and Cell Differentiation through Interlinked Phosphorylation and Second Messenger Networks. Molecular Cell, 2011, 43, 550-560.	9.7	169
64	Stepwise Unfolding of a Î² Barrel Protein by the AAA+ ClpXP Protease. Journal of Molecular Biology, 2011, 413, 4-16.	4.2	66
65	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
66	The IbpA and IbpB small heatâ€shock proteins are substrates of the AAA+ Lon protease. Molecular Microbiology, 2010, 75, 1539-1549.	2.5	74
67	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
68	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
69	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
70	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
71	Engineering Synthetic Adaptors and Substrates for Controlled ClpXP Degradation. Journal of Biological Chemistry, 2009, 284, 21848-21855.	3.4	22
72	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

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73	Controlled degradation by ClpXP protease tunes the levels of the excision repair protein UvrA to the extent of DNA damage. Molecular Microbiology, 2009, 71, 912-924.	2.5	30
74	Polypeptide Translocation by the AAA+ ClpXP Protease Machine. Chemistry and Biology, 2009, 16, 605-612.	6.0	61
75	Structures of Asymmetric ClpX Hexamers Reveal Nucleotide-Dependent Motions in a AAA+ Protein-Unfolding Machine. Cell, 2009, 139, 744-756.	28.9	231
76	Proteolysis in the SOS response and metal homeostasis in Escherichia coli. Research in Microbiology, 2009, 160, 677-683.	2.1	27
77	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
78	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
79	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
80	Asymmetric Nucleotide Transactions of the HslUV Protease. Journal of Molecular Biology, 2008, 380, 946-957.	4.2	47
81	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
82	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
83	The Molecular Basis of N-End Rule Recognition. Molecular Cell, 2008, 32, 406-414.	9.7	85
84	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
85	Tuning the Strength of a Bacterial N-end Rule Degradation Signal. Journal of Biological Chemistry, 2008, 283, 24600-24607.	3.4	50
86	Dissecting the roles of MuB in Mu transposition: ATP regulation of DNA binding is not essential for target delivery. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 12101-12107.	7.1	6
87	Ligand-Controlled Proteolysis of the Escherichia coli Transcriptional Regulator ZntR. Journal of Bacteriology, 2007, 189, 3017-3025.	2.2	47
88	Design principles of the proteolytic cascade governing the ÂE-mediated envelope stress response in Escherichia coli: keys to graded, buffered, and rapid signal transduction. Genes and Development, 2007, 21, 124-136.	5.9	101
89	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
90	ClpS modulates but is not essential for bacterial N-end rule degradation. Genes and Development, 2007, 21, 403-408.	5.9	64

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91	The Dynamic Mu Transpososome: MuB Activation Prevents Disintegration. Journal of Molecular Biology, 2007, 374, 1158-1171.	4.2	6
92	Altered Specificity of a AAA+ Protease. Molecular Cell, 2007, 25, 161-166.	9.7	44
93	Distinct Static and Dynamic Interactions Control ATPase-Peptidase Communication in a AAA+ Protease. Molecular Cell, 2007, 27, 41-52.	9.7	113
94	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
95	Arthur Kornberg (1918â€“2007). Nature, 2007, 450, 809-809.	27.8	1
96	Structure and Substrate Specificity of an SspB Ortholog: Design Implications for AAA+ Adaptors. Structure, 2007, 15, 1296-1305.	3.3	18
97	Proteomic Profiling of ClpXP Substrates after DNA Damage Reveals Extensive Instability within SOS Regulon. Molecular Cell, 2006, 22, 193-204.	9.7	172
98	Engineering Controllable Protein Degradation. Molecular Cell, 2006, 22, 701-707.	9.7	202
99	ATP-dependent proteases of bacteria: recognition logic and operating principles. Trends in Biochemical Sciences, 2006, 31, 647-653.	7.5	258
100	The tmRNA system for ribosome rescue and targeted protein degradation.. FASEB Journal, 2006, 20, A1474.	0.5	4
101	Remodeling protein complexes: Insights from the AAA+ unfoldase ClpX and Mu transposase. Protein Science, 2005, 14, 1945-1954.	7.6	46
102	Nucleotide-dependent substrate recognition by the AAA+ HslUV protease. Nature Structural and Molecular Biology, 2005, 12, 245-251.	8.2	63
103	Versatile modes of peptide recognition by the AAA+ adaptor protein SspB. Nature Structural and Molecular Biology, 2005, 12, 520-525.	8.2	39
104	Rebuilt AAA + motors reveal operating principles for ATP-fuelled machines. Nature, 2005, 437, 1115-1120.	27.8	344
105	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
106	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
107	Asymmetric Interactions of ATP with the AAA+ ClpX6 Unfoldase: Allosteric Control of a Protein Machine. Cell, 2005, 121, 1017-1027.	28.9	158
108	Reorganization of the Mu Transpososome Active Sites during a Cooperative Transition between DNA Cleavage and Joining. Journal of Biological Chemistry, 2004, 279, 5135-5145.	3.4	8

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109	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
110	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
111	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
112	Communication between ClpX and ClpP during substrate processing and degradation. Nature Structural and Molecular Biology, 2004, 11, 404-411.	8.2	128
113	Sculpting the Proteome with AAA+ Proteases and Disassembly Machines. Cell, 2004, 119, 9-18.	28.9	398
114	Nucleotide-Dependent Substrate Handoff from the SspB Adaptor to the AAA+ ClpXP Protease. Molecular Cell, 2004, 16, 343-350.	9.7	68
115	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
116	Bivalent Tethering of SspB to ClpXP Is Required for Efficient Substrate Delivery. Molecular Cell, 2004, 13, 443-449.	9.7	57
117	Mu Transpososome Architecture Ensures that Unfolding by ClpX or Proteolysis by ClpXP Remodels but Does Not Destroy the Complex. Chemistry and Biology, 2003, 10, 463-472.	6.0	24
118	DNA gyrase requirements distinguish the alternate pathways of Mu transposition. Molecular Microbiology, 2003, 47, 397-409.	2.5	18
119	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
120	Energy-dependent degradation: Linkage between ClpX-catalyzed nucleotide hydrolysis and protein-substrate processing. Protein Science, 2003, 12, 893-902.	7.6	55
121	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
122	Expression of N-formylated proteins in Escherichia coli. Protein Expression and Purification, 2003, 32, 317-322.	1.3	17
123	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
124	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
125	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
126	Effect of Mutations in the C-terminal Domain of Mu B on DNA Binding and Interactions with Mu A Transposase. Journal of Biological Chemistry, 2003, 278, 31210-31217.	3.4	7

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127	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
128	The terminal nucleotide of the Mu genome controls catalysis of DNA strand transfer. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 7509-7514.	7.1	7
129	Latent ClpX-recognition signals ensure LexA destruction after DNA damage. Genes and Development, 2003, 17, 1084-1089.	5.9	99
130	DNA Recognition Sites Activate MuA Transposase to Perform Transposition of Non-Mu DNA. Journal of Biological Chemistry, 2002, 277, 7694-7702.	3.4	20
131	Sequence and Positional Requirements for DNA Sites in a Mu Transpososome. Journal of Biological Chemistry, 2002, 277, 7703-7712.	3.4	15
132	Characterization of a Specificity Factor for an AAA+ ATPase. Chemistry and Biology, 2002, 9, 1237-1245.	6.0	89
133	ClpX-Mediated Remodeling of Mu Transpososomes. Molecular Cell, 2001, 8, 449-454.	9.7	48
134	Differential role of the Mu B protein in phage Mu integration vs. replication: mechanistic insights into two transposition pathways. Molecular Microbiology, 2001, 40, 141-155.	2.5	9
135	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
136	Molecular determinants of complex formation between Clp/Hsp100 ATPases and the ClpP peptidase. Nature Structural Biology, 2001, 8, 230-233.	9.7	234
137	Comparative architecture of transposase and integrase complexes. , 2001, 8, 302-307.		168
138	A Specificity-Enhancing Factor for the ClpXP Degradation Machine. Science, 2000, 289, 2354-2356.	12.6	297
139	Dynamics of Substrate Denaturation and Translocation by the ClpXP Degradation Machine. Molecular Cell, 2000, 5, 639-648.	9.7	307
140	MOLECULAR BIOLOGY: Transposase Team Puts a Headlock on DNA. Science, 2000, 289, 73-74.	12.6	9
141	Trapped in the act. Nature, 1999, 401, 29-30.	27.8	8
142	Polymerases and the Replisome: Machines within Machines. Cell, 1998, 92, 295-305.	28.9	322
143	An ATPâ€“ADP switch in MuB controls progression of the Mu transposition pathway. EMBO Journal, 1998, 17, 5509-5518.	7.8	49
144	Mutational Analysis of the Mu Transposase. Journal of Biological Chemistry, 1998, 273, 31358-31365.	3.4	21

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145	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
146	The Interwoven Architecture of the Mu Transposase Couples DNA Synapsis to Catalysis. Cell, 1996, 85, 257-269.	28.9	90
147	Assembly of phage Mu transpososomes: Cooperative transitions assisted by protein and DNA scaffolds. Cell, 1995, 83, 375-385.	28.9	43
148	Replication arrest. Cell, 1995, 80, 521-524.	28.9	40
149	Bacteriophage Mu: a transposing phage that integrates like retroviruses. Seminars in Virology, 1995, 6, 53-63.	3.9	5
150	Replication Initiation: A new controller in Escherichia coli. Current Biology, 1994, 4, 945-946.	3.9	6
151	Untangling the steps in chromosome segregation. Current Biology, 1993, 3, 94-96.	3.9	0
152	Proteinâ€"DNA assemblies controlling lytic develÃ²pment of bacteriophage Mu. Current Opinion in Genetics and Development, 1993, 3, 708-712.	3.3	7
153	Division of labor among monomers within the Mu transposase tetramer. Cell, 1993, 74, 723-733.	28.9	115
154	Assembly of the active form of the transposase-Mu DNA complex: A critical control point in Mu transposition. Cell, 1992, 70, 303-311.	28.9	167
155	Genetics and Enzymology of DNA Replication in Escherichia Coli. Annual Review of Genetics, 1992, 26, 447-477.	7.6	65
156	MuB protein allosterically activates strand transfer by the transposase of phage Mu. Cell, 1991, 65, 1003-1013.	28.9	106
157	. . . and then there were two. Nature, 1991, 353, 794-795.	27.8	7
158	Transcriptional activation of initiation of replication from the E. coli chromosomal origin: An RNA-DNA hybrid near oriC. Cell, 1988, 55, 113-123.	28.9	256
159	Extensive unwinding of the plasmid template during staged enzymatic initiation of DNA replication from the origin of the Escherichia coli chromosome. Cell, 1986, 45, 53-64.	28.9	273