

# Robert T Sauer

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

281  
papers

21,727  
citations

82  
h-index

135  
g-index

294  
ext. papers

23,642  
ext. citations

12.9  
avg, IF

7.02  
L-index

#	Paper	IF	Citations
281	Division of labor between the pore-1 loops of the D1 and D2 AAA+ rings coordinates substrate selectivity of the ClpAP protease. <i>Journal of Biological Chemistry</i> , <b>2021</b> , 101407	5.4	0
280	ClpP1P2 peptidase activity promotes biofilm formation in <i>Pseudomonas aeruginosa</i> . <i>Molecular Microbiology</i> , <b>2021</b> , 115, 1094-1109	4.1	3
279	Heat activates the AAA+ HslUV protease by melting an axial autoinhibitory plug. <i>Cell Reports</i> , <b>2021</b> , 34, 108639	10.6	1
278	Structure and function of ClpXP, a AAA+ proteolytic machine powered by probabilistic ATP hydrolysis.. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , <b>2021</b> , 1-17	8.7	2
277	The Non-dominant AAA+ Ring in the ClpAP Protease Functions as an Anti-stalling Motor to Accelerate Protein Unfolding and Translocation. <i>Cell Reports</i> , <b>2020</b> , 30, 2644-2654.e3	10.6	9
276	Acydepsipeptide Antibiotics and a Bioactive Fragment Thereof Differentially Perturb <i>Mycobacterium tuberculosis</i> ClpXP1P2 Activity in vitro. <i>ACS Chemical Biology</i> , <b>2020</b> ,	4.9	6
275	Structures of the ATP-fueled ClpXP proteolytic machine bound to protein substrate. <i>ELife</i> , <b>2020</b> , 9,	8.9	50
274	ClpAP proteolysis does not require rotation of the ClpA unfoldase relative to ClpP. <i>ELife</i> , <b>2020</b> , 9,	8.9	8
273	Structural basis of ClpXP recognition and unfolding of ssrA-tagged substrates. <i>ELife</i> , <b>2020</b> , 9,	8.9	8
272	Modular and coordinated activity of AAA+ active sites in the double-ring ClpA unfoldase of the ClpAP protease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2020</b> , 117, 25455-25463	11.5	7
271	The Intrinsically Disordered N-terminal Extension of the ClpS Adaptor Reprograms Its Partner AAA+ ClpAP Protease. <i>Journal of Molecular Biology</i> , <b>2020</b> , 432, 4908-4921	6.5	4
270	Multistep substrate binding and engagement by the AAA+ ClpXP protease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2020</b> , 117, 28005-28013	11.5	10
269	A mutagenesis screen for essential plastid biogenesis genes in human malaria parasites. <i>PLoS Biology</i> , <b>2019</b> , 17, e3000136	9.7	19
268	Roles of the ClpX IGF loops in ClpP association, dissociation, and protein degradation. <i>Protein Science</i> , <b>2019</b> , 28, 756-765	6.3	17
267	Interactions between a subset of substrate side chains and AAA+ motor pore loops determine grip during protein unfolding. <i>ELife</i> , <b>2019</b> , 8,	8.9	11
266	Mechanical Protein Unfolding and Degradation. <i>Annual Review of Physiology</i> , <b>2018</b> , 80, 413-429	23.1	43
265	Structure of the Mitochondrial Aminolevulinic Acid Synthase, a Key Heme Biosynthetic Enzyme. <i>Structure</i> , <b>2018</b> , 26, 580-589.e4	5.2	28

264	Structural and Functional Analysis of E. coli Cyclopropane Fatty Acid Synthase. <i>Structure</i> , <b>2018</b> , 26, 1251-1258.e3		
263	Hinge-Linker Elements in the AAA+ Protein Unfoldase ClpX Mediate Intersubunit Communication, Assembly, and Mechanical Activity. <i>Biochemistry</i> , <b>2018</b> , 57, 6787-6796	3.2	9
262	Covalently linked HslU hexamers support a probabilistic mechanism that links ATP hydrolysis to protein unfolding and translocation. <i>Journal of Biological Chemistry</i> , <b>2017</b> , 292, 5695-5704	5.4	9
261	Rational Design of Selective and Bioactive Inhibitors of the Mycobacterium tuberculosis Proteasome. <i>ACS Infectious Diseases</i> , <b>2017</b> , 3, 176-181	5.5	16
260	Effect of directional pulling on mechanical protein degradation by ATP-dependent proteolytic machines. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, E6306-E6313	11.5	28
259	Small molecule inhibition of apicomplexan FtsH1 disrupts plastid biogenesis in human pathogens. <i>ELife</i> , <b>2017</b> , 6,	8.9	35
258	Mechanistic insights into bacterial AAA+ proteases and protein-remodelling machines. <i>Nature Reviews Microbiology</i> , <b>2016</b> , 14, 33-44	22.2	179
257	Highly Dynamic Interactions Maintain Kinetic Stability of the ClpXP Protease During the ATP-Fueled Mechanical Cycle. <i>ACS Chemical Biology</i> , <b>2016</b> , 11, 1552-1560	4.9	19
256	Structural Basis of an N-Degron Adaptor with More Stringent Specificity. <i>Structure</i> , <b>2016</b> , 24, 232-42	5.2	23
255	Origin and Functional Evolution of the Cdc48/p97/VCP AAA+ Protein Unfolding and Remodeling Machine. <i>Journal of Molecular Biology</i> , <b>2016</b> , 428, 1861-9	6.5	45
254	A Structurally Dynamic Region of the HslU Intermediate Domain Controls Protein Degradation and ATP Hydrolysis. <i>Structure</i> , <b>2016</b> , 24, 1766-1777	5.2	5
253	The AAA+ FtsH Protease Degrades an ssrA-Tagged Model Protein in the Inner Membrane of Escherichia coli. <i>Biochemistry</i> , <b>2016</b> , 55, 5649-5652	3.2	10
252	A conserved activation cluster is required for allosteric communication in HtrA-family proteases. <i>Structure</i> , <b>2015</b> , 23, 517-526	5.2	22
251	Assaying the kinetics of protein denaturation catalyzed by AAA+ unfolding machines and proteases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2015</b> , 112, 5377-82	11.5	21
250	Subunit asymmetry and roles of conformational switching in the hexameric AAA+ ring of ClpX. <i>Nature Structural and Molecular Biology</i> , <b>2015</b> , 22, 411-6	17.6	32
249	Deciphering the Roles of Multicomponent Recognition Signals by the AAA+ Unfoldase ClpX. <i>Journal of Molecular Biology</i> , <b>2015</b> , 427, 2966-82	6.5	8
248	Steric clashes with bound OMP peptides activate the DegS stress-response protease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2015</b> , 112, 3326-31	11.5	10
247	Dissection of Axial-Pore Loop Function during Unfolding and Translocation by a AAA+ Proteolytic Machine. <i>Cell Reports</i> , <b>2015</b> , 12, 1032-41	10.6	39

246	Substrate-guided optimization of the syringolins yields potent proteasome inhibitors with activity against leukemia cell lines. <i>Bioorganic and Medicinal Chemistry</i> , <b>2015</b> , 23, 6218-22	3.4	8
245	An ALS disease mutation in Cdc48/p97 impairs 20S proteasome binding and proteolytic communication. <i>Protein Science</i> , <b>2015</b> , 24, 1521-7	6.3	17
244	Examination of a Structural Model of Peptidomimicry by Cyclic Acyldepsipeptide Antibiotics in Their Interaction with the ClpP Peptidase. <i>ChemBioChem</i> , <b>2015</b> , 16, 1875-1879	3.8	7
243	Coordinated gripping of substrate by subunits of a AAA+ proteolytic machine. <i>Nature Chemical Biology</i> , <b>2015</b> , 11, 201-6	11.7	49
242	Roles of the N domain of the AAA+ Lon protease in substrate recognition, allosteric regulation and chaperone activity. <i>Molecular Microbiology</i> , <b>2014</b> , 91, 66-78	4.1	30
241	Distinct regulatory mechanisms balance DegP proteolysis to maintain cellular fitness during heat stress. <i>Genes and Development</i> , <b>2014</b> , 28, 902-11	12.6	18
240	Restriction of the conformational dynamics of the cyclic acyldepsipeptide antibiotics improves their antibacterial activity. <i>Journal of the American Chemical Society</i> , <b>2014</b> , 136, 1922-9	16.4	65
239	A simple fragment of cyclic acyldepsipeptides is necessary and sufficient for ClpP activation and antibacterial activity. <i>ChemBioChem</i> , <b>2014</b> , 15, 2216-20	3.8	26
238	Remodeling of a delivery complex allows ClpS-mediated degradation of N-degron substrates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, E3853-9	11.5	35
237	Stochastic but highly coordinated protein unfolding and translocation by the ClpXP proteolytic machine. <i>Cell</i> , <b>2014</b> , 158, 647-58	56.2	95
236	Mechanochemical basis of protein degradation by a double-ring AAA+ machine. <i>Nature Structural and Molecular Biology</i> , <b>2014</b> , 21, 871-5	17.6	63
235	Crystal structure of Mycobacterium tuberculosis ClpP1P2 suggests a model for peptidase activation by AAA+ partner binding and substrate delivery. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, E4587-95	11.5	66
234	Substrate delivery by the AAA+ ClpX and ClpC1 unfoldases activates the mycobacterial ClpP1P2 peptidase. <i>Molecular Microbiology</i> , <b>2014</b> , 93, 617-28	4.1	43
233	Overexpression of CupB5 activates alginate overproduction in Pseudomonas aeruginosa by a novel AlgW-dependent mechanism. <i>Molecular Microbiology</i> , <b>2014</b> , 93, 415-25	4.1	6
232	Architecture and assembly of the archaeal Cdc48*20S proteasome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, E1687-94	11.5	49
231	Dual molecular signals mediate the bacterial response to outer-membrane stress. <i>Science</i> , <b>2013</b> , 340, 837-41	33.3	130
230	Antibacterial activity of and resistance to small molecule inhibitors of the ClpP peptidase. <i>ACS Chemical Biology</i> , <b>2013</b> , 8, 2669-77	4.9	44
229	A mutation in the N domain of Escherichia coli lon stabilizes dodecamers and selectively alters degradation of model substrates. <i>Journal of Bacteriology</i> , <b>2013</b> , 195, 5622-8	3.5	9

228	Mutagenic dissection of the sequence determinants of protein folding, recognition, and machine function. <i>Protein Science</i> , <b>2013</b> , 22, 1675-87	6.3	4
227	Engineering fluorescent protein substrates for the AAA+ Lon protease. <i>Protein Engineering, Design and Selection</i> , <b>2013</b> , 26, 299-305	1.9	18
226	Allosteric regulation of DegS protease subunits through a shared energy landscape. <i>Nature Chemical Biology</i> , <b>2013</b> , 9, 90-6	11.7	26
225	Nucleotide binding and conformational switching in the hexameric ring of a AAA+ machine. <i>Cell</i> , <b>2013</b> , 153, 628-39	56.2	91
224	Bipartite determinants mediate an evolutionarily conserved interaction between Cdc48 and the 20S peptidase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, 3327-32	11.5	52
223	Distinct quaternary structures of the AAA+ Lon protease control substrate degradation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, E2002-8	11.5	47
222	ClpXP, an ATP-powered unfolding and protein-degradation machine. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , <b>2012</b> , 1823, 15-28	4.9	287
221	The I domain of the AAA+ HslUV protease coordinates substrate binding, ATP hydrolysis, and protein degradation. <i>Protein Science</i> , <b>2012</b> , 21, 188-98	6.3	12
220	Protein unfolding and degradation by the AAA+ Lon protease. <i>Protein Science</i> , <b>2012</b> , 21, 268-78	6.3	36
219	Dynamic and static components power unfolding in topologically closed rings of a AAA+ proteolytic machine. <i>Nature Structural and Molecular Biology</i> , <b>2012</b> , 19, 616-22	17.6	51
218	Cage assembly of DegP protease is not required for substrate-dependent regulation of proteolytic activity or high-temperature cell survival. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, 7263-8	11.5	48
217	Identification of the Cdc48 $\alpha$ 20S proteasome as an ancient AAA+ proteolytic machine. <i>Science</i> , <b>2012</b> , 337, 843-6	33.3	100
216	AAA+ proteases: ATP-fueled machines of protein destruction. <i>Annual Review of Biochemistry</i> , <b>2011</b> , 80, 587-612	29.1	525
215	Signal integration by DegS and RseB governs the $\sigma$ <sup>E</sup> -mediated envelope stress response in <i>Escherichia coli</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2011</b> , 108, 2106-11	11.5	53
214	Covalent linkage of distinct substrate degrons controls assembly and disassembly of DegP proteolytic cages. <i>Cell</i> , <b>2011</b> , 145, 67-78	56.2	63
213	Single-molecule protein unfolding and translocation by an ATP-fueled proteolytic machine. <i>Cell</i> , <b>2011</b> , 145, 257-67	56.2	205
212	The ClpS adaptor mediates staged delivery of N-end rule substrates to the AAA+ ClpAP protease. <i>Molecular Cell</i> , <b>2011</b> , 43, 217-28	17.6	50
211	Stepwise unfolding of a $\beta$ barrel protein by the AAA+ ClpXP protease. <i>Journal of Molecular Biology</i> , <b>2011</b> , 413, 4-16	6.5	56

210	Small-molecule control of protein degradation using split adaptors. <i>ACS Chemical Biology</i> , <b>2011</b> , 6, 1205-13	21
209	Design, construction and characterization of a set of insulated bacterial promoters. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, 1131-41	20.1 237
208	The IbpA and IbpB small heat-shock proteins are substrates of the AAA+ Lon protease. <i>Molecular Microbiology</i> , <b>2010</b> , 75, 1539-49	4.1 49
207	The AAA+ ClpX machine unfolds a keystone subunit to remodel the Mu transpososome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2010</b> , 107, 2437-42	11.5 19
206	Allostery is an intrinsic property of the protease domain of DegS: implications for enzyme function and evolution. <i>Journal of Biological Chemistry</i> , <b>2010</b> , 285, 34039-47	5.4 29
205	Control of substrate gating and translocation into ClpP by channel residues and ClpX binding. <i>Journal of Molecular Biology</i> , <b>2010</b> , 399, 707-18	6.5 66
204	Multiple sequence signals direct recognition and degradation of protein substrates by the AAA+ protease HslUV. <i>Journal of Molecular Biology</i> , <b>2010</b> , 403, 420-9	6.5 7
203	Versatile modes of peptide recognition by the ClpX N domain mediate alternative adaptor-binding specificities in different bacterial species. <i>Protein Science</i> , <b>2010</b> , 19, 242-54	6.3 15
202	Molecular basis of substrate selection by the N-end rule adaptor protein ClpS. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2009</b> , 106, 8888-93	11.5 47
201	Analyzing the interaction of RseA and RseB, the two negative regulators of the sigmaE envelope stress response, using a combined bioinformatic and experimental strategy. <i>Journal of Biological Chemistry</i> , <b>2009</b> , 284, 5403-13	5.4 9
200	Engineering synthetic adaptors and substrates for controlled ClpXP degradation. <i>Journal of Biological Chemistry</i> , <b>2009</b> , 284, 21848-21855	5.4 18
199	Degrans in protein substrates program the speed and operating efficiency of the AAA+ Lon proteolytic machine. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2009</b> , 106, 18503-8	11.5 65
198	Single-molecule denaturation and degradation of proteins by the AAA+ ClpXP protease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2009</b> , 106, 19340-5	11.5 33
197	OMP peptides activate the DegS stress-sensor protease by a relief of inhibition mechanism. <i>Structure</i> , <b>2009</b> , 17, 1411-21	5.2 39
196	Control of <i>Pseudomonas aeruginosa</i> AlgW protease cleavage of MucA by peptide signals and MucB. <i>Molecular Microbiology</i> , <b>2009</b> , 72, 368-79	4.1 67
195	Polypeptide translocation by the AAA+ ClpXP protease machine. <i>Chemistry and Biology</i> , <b>2009</b> , 16, 605-12	50
194	Structures of asymmetric ClpX hexamers reveal nucleotide-dependent motions in a AAA+ protein-unfolding machine. <i>Cell</i> , <b>2009</b> , 139, 744-56	56.2 218
193	OMP peptides modulate the activity of DegS protease by differential binding to active and inactive conformations. <i>Molecular Cell</i> , <b>2009</b> , 33, 64-74	17.6 41

192	Protein unfolding by a AAA+ protease is dependent on ATP-hydrolysis rates and substrate energy landscapes. <i>Nature Structural and Molecular Biology</i> , <b>2008</b> , 15, 139-45	17.6	98
191	Distinct structural elements of the adaptor ClpS are required for regulating degradation by ClpAP. <i>Nature Structural and Molecular Biology</i> , <b>2008</b> , 15, 288-94	17.6	41
190	Pore loops of the AAA+ ClpX machine grip substrates to drive translocation and unfolding. <i>Nature Structural and Molecular Biology</i> , <b>2008</b> , 15, 1147-51	17.6	215
189	Asymmetric nucleotide transactions of the HslUV protease. <i>Journal of Molecular Biology</i> , <b>2008</b> , 380, 946-53	17.6	46
188	Diverse pore loops of the AAA+ ClpX machine mediate unassisted and adaptor-dependent recognition of ssrA-tagged substrates. <i>Molecular Cell</i> , <b>2008</b> , 29, 441-50	17.6	121
187	Unique contacts direct high-priority recognition of the tetrameric Mu transposase-DNA complex by the AAA+ unfoldase ClpX. <i>Molecular Cell</i> , <b>2008</b> , 30, 39-50	17.6	30
186	The molecular basis of N-end rule recognition. <i>Molecular Cell</i> , <b>2008</b> , 32, 406-14	17.6	73
185	Forced extraction of targeted components from complex macromolecular assemblies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2008</b> , 105, 11685-90	11.5	20
184	Tuning the strength of a bacterial N-end rule degradation signal. <i>Journal of Biological Chemistry</i> , <b>2008</b> , 283, 24600-7	5.4	46
183	Recognition of misfolded proteins by Lon, a AAA(+) protease. <i>Genes and Development</i> , <b>2008</b> , 22, 2267-77	12.6	169
182	Revisiting the mechanism of macrolide-antibiotic resistance mediated by ribosomal protein L22. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2008</b> , 105, 18261-6	11.5	36
181	Evolution of the ssrA degradation tag in <i>Mycoplasma</i> : specificity switch to a different protease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2008</b> , 105, 16113-8	11.5	48
180	The tmRNA system for translational surveillance and ribosome rescue. <i>Annual Review of Biochemistry</i> , <b>2007</b> , 76, 101-24	29.1	253
179	Altered tethering of the SspB adaptor to the ClpXP protease causes changes in substrate delivery. <i>Journal of Biological Chemistry</i> , <b>2007</b> , 282, 11465-73	5.4	23
178	Structure and substrate specificity of an SspB ortholog: design implications for AAA+ adaptors. <i>Structure</i> , <b>2007</b> , 15, 1296-305	5.2	16
177	Inhibition of regulated proteolysis by RseB. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2007</b> , 104, 3771-6	11.5	68
176	Direct and adaptor-mediated substrate recognition by an essential AAA+ protease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2007</b> , 104, 6590-5	11.5	77
175	ClpS modulates but is not essential for bacterial N-end rule degradation. <i>Genes and Development</i> , <b>2007</b> , 21, 403-8	12.6	57

174	Allosteric activation of DegS, a stress sensor PDZ protease. <i>Cell</i> , <b>2007</b> , 131, 572-83	56.2	101
173	Altered specificity of a AAA+ protease. <i>Molecular Cell</i> , <b>2007</b> , 25, 161-6	17.6	35
172	Distinct static and dynamic interactions control ATPase-peptidase communication in a AAA+ protease. <i>Molecular Cell</i> , <b>2007</b> , 27, 41-52	17.6	96
171	ATP-dependent proteases of bacteria: recognition logic and operating principles. <i>Trends in Biochemical Sciences</i> , <b>2006</b> , 31, 647-53	10.3	217
170	Proteomic profiling of ClpXP substrates after DNA damage reveals extensive instability within SOS regulon. <i>Molecular Cell</i> , <b>2006</b> , 22, 193-204	17.6	131
169	Engineering controllable protein degradation. <i>Molecular Cell</i> , <b>2006</b> , 22, 701-7	17.6	156
168	Asymmetric interactions of ATP with the AAA+ ClpX6 unfoldase: allosteric control of a protein machine. <i>Cell</i> , <b>2005</b> , 121, 1017-27	56.2	145
167	Cytoplasmic degradation of ssrA-tagged proteins. <i>Molecular Microbiology</i> , <b>2005</b> , 57, 1750-61	4.1	113
166	Ribosome rescue: tmRNA tagging activity and capacity in Escherichia coli. <i>Molecular Microbiology</i> , <b>2005</b> , 58, 456-66	4.1	91
165	Nucleotide-dependent substrate recognition by the AAA+ HslUV protease. <i>Nature Structural and Molecular Biology</i> , <b>2005</b> , 12, 245-51	17.6	55
164	Versatile modes of peptide recognition by the AAA+ adaptor protein SspB. <i>Nature Structural and Molecular Biology</i> , <b>2005</b> , 12, 520-5	17.6	36
163	Rebuilt AAA + motors reveal operating principles for ATP-fuelled machines. <i>Nature</i> , <b>2005</b> , 437, 1115-20	50.4	299
162	Partitioning between unfolding and release of native domains during ClpXP degradation determines substrate selectivity and partial processing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2005</b> , 102, 1390-5	11.5	86
161	Sequence determinants of a conformational switch in a protein structure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2005</b> , 102, 18344-9	11.5	27
160	Consolidating critical binding determinants by noncyclic rearrangement of protein secondary structure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2005</b> , 102, 2305-9	11.5	5
159	Specificity versus stability in computational protein design. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2005</b> , 102, 12724-9	11.5	118
158	Role of the processing pore of the ClpX AAA+ ATPase in the recognition and engagement of specific protein substrates. <i>Genes and Development</i> , <b>2004</b> , 18, 369-74	12.6	129
157	Modulating substrate choice: the SspB adaptor delivers a regulator of the extracytoplasmic-stress response to the AAA+ protease ClpXP for degradation. <i>Genes and Development</i> , <b>2004</b> , 18, 2292-301	12.6	160



156	Ribosomal protein S1 binds mRNA and tmRNA similarly but plays distinct roles in translation of these molecules. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2004</b> , 101, 13454-9	11.5	48
155	SspB delivery of substrates for ClpXP proteolysis probed by the design of improved degradation tags. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2004</b> , 101, 12136-41	11.5	41
154	Communication between ClpX and ClpP during substrate processing and degradation. <i>Nature Structural and Molecular Biology</i> , <b>2004</b> , 11, 404-11	17.6	109
153	Computational and Experimental Probes of Symmetry Mismatches in the Arc Repressor-DNA Complex. <i>Journal of Molecular Biology</i> , <b>2004</b> , 340, 253-253	6.5	
152	Sculpting the proteome with AAA(+) proteases and disassembly machines. <i>Cell</i> , <b>2004</b> , 119, 9-18	56.2	361
151	Nucleotide-dependent substrate handoff from the SspB adaptor to the AAA+ ClpXP protease. <i>Molecular Cell</i> , <b>2004</b> , 16, 343-50	17.6	63
150	Effects of local protein stability and the geometric position of the substrate degradation tag on the efficiency of ClpXP denaturation and degradation. <i>Journal of Structural Biology</i> , <b>2004</b> , 146, 130-40	3.4	52
149	Computational and experimental probes of symmetry mismatches in the Arc repressor-DNA complex. <i>Journal of Molecular Biology</i> , <b>2004</b> , 340, 253-61	6.5	4
148	Bivalent tethering of SspB to ClpXP is required for efficient substrate delivery: a protein-design study. <i>Molecular Cell</i> , <b>2004</b> , 13, 443-9	17.6	52
147	Distinct peptide signals in the UmuD and UmuD <sub>Q</sub> subunits of UmuD/D <sub>Q</sub> mediate tethering and substrate processing by the ClpXP protease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2003</b> , 100, 13219-24	11.5	86
146	Latent ClpX-recognition signals ensure LexA destruction after DNA damage. <i>Genes and Development</i> , <b>2003</b> , 17, 1084-9	12.6	77
145	Role of an N(cap) residue in determining the stability and operator-binding affinity of Arc repressor. <i>Biophysical Chemistry</i> , <b>2003</b> , 100, 341-50	3.5	9
144	C-terminal domain mutations in ClpX uncouple substrate binding from an engagement step required for unfolding. <i>Molecular Microbiology</i> , <b>2003</b> , 48, 67-76	4.1	12
143	Nickel coordination is regulated by the DNA-bound state of NikR. <i>Nature Structural Biology</i> , <b>2003</b> , 10, 126-30		60
142	Crystal structure of the nickel-responsive transcription factor NikR. <i>Nature Structural and Molecular Biology</i> , <b>2003</b> , 10, 794-9	17.6	151
141	Energy-dependent degradation: Linkage between ClpX-catalyzed nucleotide hydrolysis and protein-substrate processing. <i>Protein Science</i> , <b>2003</b> , 12, 893-902	6.3	49
140	Structure of a delivery protein for an AAA+ protease in complex with a peptide degradation tag. <i>Molecular Cell</i> , <b>2003</b> , 12, 365-72	17.6	79
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2	Structural basis of ClpXP recognition and unfolding of ssrA-tagged substrates		2
1	Structures of the ATP-fueled ClpXP proteolytic machine bound to protein substrate		4