

Robert T Sauer

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#	Paper	IF	Citations
281	Transcription factors: structural families and principles of DNA recognition. <i>Annual Review of Biochemistry</i> , 1992 , 61, 1053-95	29.1	1284
280	AAA+ proteases: ATP-fueled machines of protein destruction. <i>Annual Review of Biochemistry</i> , 2011 , 80, 587-612	29.1	525
279	Proteomic discovery of cellular substrates of the ClpXP protease reveals five classes of ClpX-recognition signals. <i>Molecular Cell</i> , 2003 , 11, 671-83	17.6	465
278	OMP peptide signals initiate the envelope-stress response by activating DegS protease via relief of inhibition mediated by its PDZ domain. <i>Cell</i> , 2003 , 113, 61-71	56.2	412
277	Alternative packing arrangements in the hydrophobic core of lambda repressor. <i>Nature</i> , 1989 , 339, 31-6	50.4	376
276	Sculpting the proteome with AAA(+) proteases and disassembly machines. <i>Cell</i> , 2004 , 119, 9-18	56.2	361
275	lambda Repressor and cro--components of an efficient molecular switch. <i>Nature</i> , 1981 , 294, 217-23	50.4	359
274	The SsrA-SmpB system for protein tagging, directed degradation and ribosome rescue. <i>Nature Structural Biology</i> , 2000 , 7, 449-55		327
273	Are buried salt bridges important for protein stability and conformational specificity?. <i>Nature Structural and Molecular Biology</i> , 1995 , 2, 122-8	17.6	305
272	Rebuilt AAA + motors reveal operating principles for ATP-fuelled machines. <i>Nature</i> , 2005 , 437, 1115-20	50.4	299
271	ClpXP, an ATP-powered unfolding and protein-degradation machine. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2012 , 1823, 15-28	4.9	287
270	Dynamics of substrate denaturation and translocation by the ClpXP degradation machine. <i>Molecular Cell</i> , 2000 , 5, 639-48	17.6	271
269	A specificity-enhancing factor for the ClpXP degradation machine. <i>Science</i> , 2000 , 289, 2354-6	33.3	260
268	DNA recognition by beta-sheets in the Arc repressor-operator crystal structure. <i>Nature</i> , 1994 , 367, 754-75	50.4	260
267	The tmRNA system for translational surveillance and ribosome rescue. <i>Annual Review of Biochemistry</i> , 2007 , 76, 101-24	29.1	253
266	Linkage between ATP consumption and mechanical unfolding during the protein processing reactions of an AAA+ degradation machine. <i>Cell</i> , 2003 , 114, 511-20	56.2	244
265	Design, construction and characterization of a set of insulated bacterial promoters. <i>Nucleic Acids Research</i> , 2011 , 39, 1131-41	20.1	237

264	Overlapping recognition determinants within the <i>ssrA</i> degradation tag allow modulation of proteolysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001 , 98, 10584-9	11.5	224
263	Equilibrium dissociation and unfolding of the Arc repressor dimer. <i>Biochemistry</i> , 1989 , 28, 7139-43	3.2	223
262	Structures of asymmetric ClpX hexamers reveal nucleotide-dependent motions in a AAA+ protein-unfolding machine. <i>Cell</i> , 2009 , 139, 744-56	56.2	218
261	ATP-dependent proteases of bacteria: recognition logic and operating principles. <i>Trends in Biochemical Sciences</i> , 2006 , 31, 647-53	10.3	217
260	Pore loops of the AAA+ ClpX machine grip substrates to drive translocation and unfolding. <i>Nature Structural and Molecular Biology</i> , 2008 , 15, 1147-51	17.6	215
259	Single-molecule protein unfolding and translocation by an ATP-fueled proteolytic machine. <i>Cell</i> , 2011 , 145, 257-67	56.2	205
258	Molecular determinants of complex formation between Clp/Hsp100 ATPases and the ClpP peptidase. <i>Nature Structural Biology</i> , 2001 , 8, 230-3		205
257	The role of internal packing interactions in determining the structure and stability of a protein. <i>Journal of Molecular Biology</i> , 1991 , 219, 359-76	6.5	198
256	Cleavage of the A site mRNA codon during ribosome pausing provides a mechanism for translational quality control. <i>Molecular Cell</i> , 2003 , 12, 903-11	17.6	190
255	Mechanistic insights into bacterial AAA+ proteases and protein-remodelling machines. <i>Nature Reviews Microbiology</i> , 2016 , 14, 33-44	22.2	179
254	Recognition of misfolded proteins by Lon, a AAA(+) protease. <i>Genes and Development</i> , 2008 , 22, 2267-77	12.6	169
253	Structural and energetic consequences of disruptive mutations in a protein core. <i>Biochemistry</i> , 1992 , 31, 4324-33	3.2	164
252	Reverse hydrophobic effects relieved by amino-acid substitutions at a protein surface. <i>Nature</i> , 1990 , 344, 363-4	50.4	161
251	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> , 2004 , 18, 2292-301	12.6	160
250	P22 Arc repressor: folding kinetics of a single-domain, dimeric protein. <i>Biochemistry</i> , 1994 , 33, 1125-33	3.2	160
249	Engineering controllable protein degradation. <i>Molecular Cell</i> , 2006 , 22, 701-7	17.6	156
248	Crystal structure of the nickel-responsive transcription factor NikR. <i>Nature Structural and Molecular Biology</i> , 2003 , 10, 794-9	17.6	151
247	Asymmetric interactions of ATP with the AAA+ ClpX6 unfoldase: allosteric control of a protein machine. <i>Cell</i> , 2005 , 121, 1017-27	56.2	145

246	Regulatory functions of the lambda repressor reside in the amino-terminal domain. <i>Nature</i> , 1979 , 279, 396-400	50.4	142
245	Sequence space, folding and protein design. <i>Current Opinion in Structural Biology</i> , 1996 , 6, 3-10	8.1	141
244	Regulation of high affinity nickel uptake in bacteria. Ni ²⁺ -Dependent interaction of NikR with wild-type and mutant operator sites. <i>Journal of Biological Chemistry</i> , 2000 , 275, 19735-41	5.4	139
243	Lambda repressor mutations that increase the affinity and specificity of operator binding. <i>Cell</i> , 1985 , 42, 549-58	56.2	139
242	Bacteriophage lambda repressor and cro protein: interactions with operator DNA. <i>Methods in Enzymology</i> , 1980 , 65, 839-56	1.7	139
241	Proteomic profiling of ClpXP substrates after DNA damage reveals extensive instability within SOS regulon. <i>Molecular Cell</i> , 2006 , 22, 193-204	17.6	131
240	Dual molecular signals mediate the bacterial response to outer-membrane stress. <i>Science</i> , 2013 , 340, 837-41	33.3	130
239	Proline residues at the C terminus of nascent chains induce SsrA tagging during translation termination. <i>Journal of Biological Chemistry</i> , 2002 , 277, 33825-32	5.4	130
238	Role of the processing pore of the ClpX AAA+ ATPase in the recognition and engagement of specific protein substrates. <i>Genes and Development</i> , 2004 , 18, 369-74	12.6	129
237	Contributions of a hydrogen bond/salt bridge network to the stability of secondary and tertiary structure in lambda repressor. <i>Protein Science</i> , 1994 , 3, 2217-25	6.3	127
236	Changing the DNA-binding specificity of a repressor. <i>Cell</i> , 1983 , 35, 777-83	56.2	126
235	Diverse effects of mutations in the signal sequence on the secretion of beta-lactamase in <i>Salmonella typhimurium</i> . <i>Cell</i> , 1982 , 30, 903-14	56.2	123
234	Cooperatively folded proteins in random sequence libraries. <i>Nature Structural Biology</i> , 1995 , 2, 856-64		122
233	The N-terminal arms of lambda repressor wrap around the operator DNA. <i>Nature</i> , 1982 , 298, 441-3	50.4	122
232	DNA sequence of the bacteriophage gamma cl gene. <i>Nature</i> , 1978 , 276, 301-2	50.4	122
231	Diverse pore loops of the AAA+ ClpX machine mediate unassisted and adaptor-dependent recognition of ssrA-tagged substrates. <i>Molecular Cell</i> , 2008 , 29, 441-50	17.6	121
230	P22 Arc repressor: transition state properties inferred from mutational effects on the rates of protein unfolding and refolding. <i>Biochemistry</i> , 1995 , 34, 13914-9	3.2	121
229	Effects of protein stability and structure on substrate processing by the ClpXP unfolding and degradation machine. <i>EMBO Journal</i> , 2001 , 20, 3092-100	13	120

228	Specificity versus stability in computational protein design. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 12724-9	11.5	118
227	Primary structure of the lambda repressor. <i>Biochemistry</i> , 1978 , 17, 1092-100	3.2	114
226	Cytoplasmic degradation of ssrA-tagged proteins. <i>Molecular Microbiology</i> , 2005 , 57, 1750-61	4.1	113
225	Communication between ClpX and ClpP during substrate processing and degradation. <i>Nature Structural and Molecular Biology</i> , 2004 , 11, 404-11	17.6	109
224	Differential DNA-binding specificity of the engrailed homeodomain: the role of residue 50. <i>Biochemistry</i> , 1994 , 33, 9187-94	3.2	109
223	PDZ-like domains mediate binding specificity in the Clp/Hsp100 family of chaperones and protease regulatory subunits. <i>Cell</i> , 1997 , 91, 939-47	56.2	106
222	Stabilization of lambda repressor against thermal denaturation by site-directed Gly----Ala changes in alpha-helix 3. <i>Proteins: Structure, Function and Bioinformatics</i> , 1986 , 1, 43-6	4.2	103
221	Identification of endogenous SsrA-tagged proteins reveals tagging at positions corresponding to stop codons. <i>Journal of Biological Chemistry</i> , 2001 , 276, 28509-15	5.4	102
220	Protein stability effects of a complete set of alanine substitutions in Arc repressor. <i>Nature Structural Biology</i> , 1994 , 1, 518-23		102
219	NikR is a ribbon-helix-helix DNA-binding protein. <i>Protein Science</i> , 1999 , 8, 2494-500	6.3	101
218	Allosteric activation of DegS, a stress sensor PDZ protease. <i>Cell</i> , 2007 , 131, 572-83	56.2	101
217	Identification of the Cdc48 Δ 0S proteasome as an ancient AAA+ proteolytic machine. <i>Science</i> , 2012 , 337, 843-6	33.3	100
216	NikR repressor: high-affinity nickel binding to the C-terminal domain regulates binding to operator DNA. <i>Chemistry and Biology</i> , 2002 , 9, 1141-8		99
215	Protein unfolding by a AAA+ protease is dependent on ATP-hydrolysis rates and substrate energy landscapes. <i>Nature Structural and Molecular Biology</i> , 2008 , 15, 139-45	17.6	98
214	Evolution of a protein fold in vitro. <i>Science</i> , 1999 , 284, 325-8	33.3	97
213	Distinct static and dynamic interactions control ATPase-peptidase communication in a AAA+ protease. <i>Molecular Cell</i> , 2007 , 27, 41-52	17.6	96
212	Stop codons preceded by rare arginine codons are efficient determinants of SsrA tagging in Escherichia coli. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 3440-5	11.5	96
211	Stochastic but highly coordinated protein unfolding and translocation by the ClpXP proteolytic machine. <i>Cell</i> , 2014 , 158, 647-58	56.2	95

210	Identification of protein folds: matching hydrophobicity patterns of sequence sets with solvent accessibility patterns of known structures. <i>Proteins: Structure, Function and Bioinformatics</i> , 1990 , 7, 257-64	4.2	92
209	Nucleotide binding and conformational switching in the hexameric ring of a AAA+ machine. <i>Cell</i> , 2013 , 153, 628-39	56.2	91
208	Ribosome rescue: tmRNA tagging activity and capacity in Escherichia coli. <i>Molecular Microbiology</i> , 2005 , 58, 456-66	4.1	91
207	Simultaneous and functional binding of SmpB and EF-Tu-TP to the alanyl acceptor arm of tmRNA. <i>Journal of Molecular Biology</i> , 2001 , 314, 9-21	6.5	91
206	Dexamethasone/Methotrexate: An Efficient Chemical Inducer of Protein Dimerization In Vivo. <i>Journal of the American Chemical Society</i> , 2000 , 122, 4247-4248	16.4	90
205	Amino acid substitutions that increase the thermal stability of the lambda Cro protein. <i>Proteins: Structure, Function and Bioinformatics</i> , 1989 , 5, 202-10	4.2	87
204	Distinct peptide signals in the UmuD and UmuD _C subunits of UmuD/D _C mediate tethering and substrate processing by the ClpXP protease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 13219-24	11.5	86
203	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> , 2005 , 102, 1390-5	11.5	86
202	Probing the roles of residues at the e and g positions of the GCN4 leucine zipper by combinatorial mutagenesis. <i>Protein Science</i> , 1993 , 2, 1072-84	6.3	86
201	Sequence determinants of C-terminal substrate recognition by the Tsp protease. <i>Journal of Biological Chemistry</i> , 1996 , 271, 2589-93	5.4	85
200	Protein stabilization by removal of unsatisfied polar groups: computational approaches and experimental tests. <i>Biochemistry</i> , 1996 , 35, 7621-5	3.2	84
199	Structure of a delivery protein for an AAA+ protease in complex with a peptide degradation tag. <i>Molecular Cell</i> , 2003 , 12, 365-72	17.6	79
198	Flexible linkers leash the substrate binding domain of SspB to a peptide module that stabilizes delivery complexes with the AAA+ ClpXP protease. <i>Molecular Cell</i> , 2003 , 12, 355-63	17.6	79
197	Characterization of a specificity factor for an AAA+ ATPase: assembly of SspB dimers with ssrA-tagged proteins and the ClpX hexamer. <i>Chemistry and Biology</i> , 2002 , 9, 1237-45		78
196	Nonlinear free energy relationships in Arc repressor unfolding imply the existence of unstable, native-like folding intermediates. <i>Biochemistry</i> , 1996 , 35, 4795-802	3.2	78
195	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> , 2007 , 104, 6590-5	11.5	77
194	Latent ClpX-recognition signals ensure LexA destruction after DNA damage. <i>Genes and Development</i> , 2003 , 17, 1084-9	12.6	77
193	Phage P22 tail protein: gene and amino acid sequence. <i>Biochemistry</i> , 1982 , 21, 5811-5	3.2	75

192	The molecular basis of N-end rule recognition. <i>Molecular Cell</i> , 2008 , 32, 406-14	17.6	73
191	P22 Arc repressor: enhanced expression of unstable mutants by addition of polar C-terminal sequences. <i>Protein Science</i> , 1993 , 2, 2198-205	6.3	73
190	Specificity of minor-groove and major-groove interactions in a homeodomain-DNA complex. <i>Biochemistry</i> , 1995 , 34, 14601-8	3.2	72
189	An evolutionary bridge to a new protein fold. <i>Nature Structural Biology</i> , 2000 , 7, 1129-32		71
188	Major groove DNA recognition by β sheets: the ribbon-helix-helix family of gene regulatory proteins. <i>Current Opinion in Structural Biology</i> , 1994 , 4, 36-43	8.1	70
187	Bacteriophage P22 Mnt repressor. DNA binding and effects on transcription in vitro. <i>Journal of Molecular Biology</i> , 1987 , 195, 311-22	6.5	70
186	Primary structure of the imm1 immunity region of bacteriophage P22. <i>Journal of Molecular Biology</i> , 1983 , 168, 699-713	6.5	70
185	Functionally acceptable substitutions in two alpha-helical regions of lambda repressor. <i>Proteins: Structure, Function and Bioinformatics</i> , 1990 , 7, 306-16	4.2	69
184	Inhibition of regulated proteolysis by RseB. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 3771-6	11.5	68
183	Control of <i>Pseudomonas aeruginosa</i> AlgW protease cleavage of MucA by peptide signals and MucB. <i>Molecular Microbiology</i> , 2009 , 72, 368-79	4.1	67
182	Crystal structure of <i>Mycobacterium tuberculosis</i> 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> , 2014 , 111, E4587-95	11.5	66
181	Control of substrate gating and translocation into ClpP by channel residues and ClpX binding. <i>Journal of Molecular Biology</i> , 2010 , 399, 707-18	6.5	66
180	Random mutagenesis of protein sequences using oligonucleotide cassettes. <i>Methods in Enzymology</i> , 1991 , 208, 564-86	1.7	66
179	Primary structure of the phage P22 repressor and its gene c2. <i>Biochemistry</i> , 1981 , 20, 3591-8	3.2	66
178	Restriction of the conformational dynamics of the cyclic acyldepsipeptide antibiotics improves their antibacterial activity. <i>Journal of the American Chemical Society</i> , 2014 , 136, 1922-9	16.4	65
177	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> , 2009 , 106, 18503-8	11.5	65
176	Understanding protein hydrogen bond formation with kinetic H/D amide isotope effects. <i>Nature Structural Biology</i> , 2002 , 9, 458-63		64
175	Mechanochemical basis of protein degradation by a double-ring AAA+ machine. <i>Nature Structural and Molecular Biology</i> , 2014 , 21, 871-5	17.6	63

174	Covalent linkage of distinct substrate degrons controls assembly and disassembly of DegP proteolytic cages. <i>Cell</i> , 2011 , 145, 67-78	56.2	63
173	Nucleotide-dependent substrate handoff from the SspB adaptor to the AAA+ ClpXP protease. <i>Molecular Cell</i> , 2004 , 16, 343-50	17.6	63
172	Arc repressor is tetrameric when bound to operator DNA. <i>Biochemistry</i> , 1990 , 29, 11189-95	3.2	61
171	Nickel coordination is regulated by the DNA-bound state of NikR. <i>Nature Structural Biology</i> , 2003 , 10, 126-30		60
170	Isolation and analysis of arc repressor mutants: evidence for an unusual mechanism of DNA binding. <i>Proteins: Structure, Function and Bioinformatics</i> , 1986 , 1, 302-11	4.2	60
169	Equilibrium stability and sub-millisecond refolding of a designed single-chain Arc repressor. <i>Biochemistry</i> , 1996 , 35, 13878-84	3.2	59
168	Solution structure of dimeric Mnt repressor (1-76). <i>Biochemistry</i> , 1994 , 33, 15036-45	3.2	59
167	C-terminal specific protein degradation: activity and substrate specificity of the Tsp protease. <i>Protein Science</i> , 1995 , 4, 1507-15	6.3	58
166	ClpS modulates but is not essential for bacterial N-end rule degradation. <i>Genes and Development</i> , 2007 , 21, 403-8	12.6	57
165	Stability and DNA binding of the phd protein of the phage P1 plasmid addiction system. <i>Journal of Biological Chemistry</i> , 1999 , 274, 2652-7	5.4	57
164	Signal detection by the PhoQ sensor-transmitter. Characterization of the sensor domain and a response-impaired mutant that identifies ligand-binding determinants. <i>Journal of Biological Chemistry</i> , 1996 , 271, 26630-6	5.4	57
163	Stepwise unfolding of a β barrel protein by the AAA+ ClpXP protease. <i>Journal of Molecular Biology</i> , 2011 , 413, 4-16	6.5	56
162	Nucleotide-dependent substrate recognition by the AAA+ HslUV protease. <i>Nature Structural and Molecular Biology</i> , 2005 , 12, 245-51	17.6	55
161	Identification of active site residues of the Tsp protease. <i>Journal of Biological Chemistry</i> , 1995 , 270, 28864-8	5.4	55
160	Lambda repressor: a model system for understanding protein-DNA interactions and protein stability. <i>Advances in Protein Chemistry</i> , 1990 , 40, 1-61		55
159	Covalent attachment of Arc repressor subunits by a peptide linker enhances affinity for operator DNA. <i>Biochemistry</i> , 1996 , 35, 109-16	3.2	54
158	Signal integration by DegS and RseB governs the σ ^E -mediated envelope stress response in Escherichia coli. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 2106-11	11.5	53
157	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> , 2013 , 110, 3327-32	11.5	52

156	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> , 2004 , 146, 130-40	3.4	52
155	Bivalent tethering of SspB to ClpXP is required for efficient substrate delivery: a protein-design study. <i>Molecular Cell</i> , 2004 , 13, 443-9	17.6	52
154	Dimerization of the operator binding domain of phage lambda repressor. <i>Biochemistry</i> , 1987 , 26, 897-904.	3.2	52
153	Dynamic and static components power unfolding in topologically closed rings of a AAA+ proteolytic machine. <i>Nature Structural and Molecular Biology</i> , 2012 , 19, 616-22	17.6	51
152	Characterization of the N-terminal repeat domain of Escherichia coli ClpA-A class I Clp/HSP100 ATPase. <i>Protein Science</i> , 2001 , 10, 551-9	6.3	51
151	Assembly of the Arc repressor-operator complex: cooperative interactions between DNA-bound dimers. <i>Biochemistry</i> , 1993 , 32, 1354-63	3.2	51
150	The ClpS adaptor mediates staged delivery of N-end rule substrates to the AAA+ ClpAP protease. <i>Molecular Cell</i> , 2011 , 43, 217-28	17.6	50
149	Polypeptide translocation by the AAA+ ClpXP protease machine. <i>Chemistry and Biology</i> , 2009 , 16, 605-12		50
148	TraY proteins of F and related episomes are members of the Arc and Mnt repressor family. <i>Journal of Molecular Biology</i> , 1990 , 211, 5-6	6.5	50
147	Phage lambda repressor revertants. Amino acid substitutions that restore activity to mutant proteins. <i>Journal of Molecular Biology</i> , 1985 , 186, 53-63	6.5	50
146	Structures of the ATP-fueled ClpXP proteolytic machine bound to protein substrate. <i>ELife</i> , 2020 , 9,	8.9	50
145	Coordinated gripping of substrate by subunits of a AAA+ proteolytic machine. <i>Nature Chemical Biology</i> , 2015 , 11, 201-6	11.7	49
144	Architecture and assembly of the archaeal Cdc48*20S proteasome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, E1687-94	11.5	49
143	The IbpA and IbpB small heat-shock proteins are substrates of the AAA+ Lon protease. <i>Molecular Microbiology</i> , 2010 , 75, 1539-49	4.1	49
142	Energy-dependent degradation: Linkage between ClpX-catalyzed nucleotide hydrolysis and protein-substrate processing. <i>Protein Science</i> , 2003 , 12, 893-902	6.3	49
141	The Doc toxin and Phd antidote proteins of the bacteriophage P1 plasmid addiction system form a heterotrimeric complex. <i>Journal of Biological Chemistry</i> , 1999 , 274, 16813-8	5.4	49
140	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> , 2012 , 109, 7263-8	11.5	48
139	Evolution of the ssrA degradation tag in Mycoplasma: specificity switch to a different protease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 16113-8	11.5	48

138	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> , 2004 , 101, 13454-9	11.5	48
137	Acceleration of the refolding of Arc repressor by nucleic acids and other polyanions. <i>Nature Structural Biology</i> , 1999 , 6, 569-73		48
136	Analysis of DNA-protein interactions by affinity coelectrophoresis. <i>Methods in Enzymology</i> , 1991 , 208, 196-210	1.7	48
135	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> , 2013 , 110, E2002-8	11.5	47
134	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> , 2009 , 106, 8888-93	11.5	47
133	Isolation of lambda repressor mutants with defects in cooperative operator binding. <i>Biochemistry</i> , 1993 , 32, 9073-9	3.2	47
132	Lambda repressor mutants that are better substrates for RecA-mediated cleavage. <i>Journal of Molecular Biology</i> , 1989 , 206, 29-39	6.5	47
131	Interaction of the bacteriophage P22 Arc repressor with operator DNA. <i>Journal of Molecular Biology</i> , 1987 , 195, 323-31	6.5	47
130	Lambda repressor inactivation: properties of purified ind- proteins in the autodigestion and RecA-mediated cleavage reactions. <i>Journal of Molecular Biology</i> , 1986 , 192, 39-47	6.5	47
129	Asymmetric nucleotide transactions of the HslUV protease. <i>Journal of Molecular Biology</i> , 2008 , 380, 946-53	6.5	46
128	Tuning the strength of a bacterial N-end rule degradation signal. <i>Journal of Biological Chemistry</i> , 2008 , 283, 24600-7	5.4	46
127	The tetramerization domain of the Mnt repressor consists of two right-handed coiled coils. <i>Nature Structural Biology</i> , 1999 , 6, 755-9		46
126	Origin and Functional Evolution of the Cdc48/p97/VCP AAA+ Protein Unfolding and Remodeling Machine. <i>Journal of Molecular Biology</i> , 2016 , 428, 1861-9	6.5	45
125	Antibacterial activity of and resistance to small molecule inhibitors of the ClpP peptidase. <i>ACS Chemical Biology</i> , 2013 , 8, 2669-77	4.9	44
124	Mechanical Protein Unfolding and Degradation. <i>Annual Review of Physiology</i> , 2018 , 80, 413-429	23.1	43
123	Substrate delivery by the AAA+ ClpX and ClpC1 unfoldases activates the mycobacterial ClpP1P2 peptidase. <i>Molecular Microbiology</i> , 2014 , 93, 617-28	4.1	43
122	Critical side-chain interactions at a subunit interface in the Arc repressor dimer. <i>Biochemistry</i> , 1995 , 34, 3344-51	3.2	43
121	OMP peptides modulate the activity of DegS protease by differential binding to active and inactive conformations. <i>Molecular Cell</i> , 2009 , 33, 64-74	17.6	41

120	Distinct structural elements of the adaptor ClpS are required for regulating degradation by ClpAP. <i>Nature Structural and Molecular Biology</i> , 2008 , 15, 288-94	17.6	41
119	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> , 2004 , 101, 12136-41	11.5	41
118	Tolerance of a protein to multiple polar-to-hydrophobic surface substitutions. <i>Protein Science</i> , 1999 , 8, 318-25	6.3	40
117	Toxin-antitoxin pairs in bacteria: killers or stress regulators?. <i>Cell</i> , 2003 , 112, 2-4	56.2	40
116	Domain structure and quaternary organization of the bacteriophage P22 Erf protein. <i>Journal of Molecular Biology</i> , 1983 , 171, 401-18	6.5	40
115	Increasing and decreasing protein stability: effects of revertant substitutions on the thermal denaturation of phage lambda repressor. <i>Journal of Cellular Biochemistry</i> , 1985 , 29, 217-24	4.7	40
114	Dissection of Axial-Pore Loop Function during Unfolding and Translocation by a AAA+ Proteolytic Machine. <i>Cell Reports</i> , 2015 , 12, 1032-41	10.6	39
113	OMP peptides activate the DegS stress-sensor protease by a relief of inhibition mechanism. <i>Structure</i> , 2009 , 17, 1411-21	5.2	39
112	Interaction of mutant lambda repressors with operator and non-operator DNA. <i>Journal of Molecular Biology</i> , 1986 , 192, 27-38	6.5	39
111	Scanning mutagenesis of the Arc repressor as a functional probe of operator recognition. <i>Nature Structural Biology</i> , 1994 , 1, 164-8		37
110	Protein unfolding and degradation by the AAA+ Lon protease. <i>Protein Science</i> , 2012 , 21, 268-78	6.3	36
109	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> , 2008 , 105, 18261-6	11.5	36
108	Versatile modes of peptide recognition by the AAA+ adaptor protein SspB. <i>Nature Structural and Molecular Biology</i> , 2005 , 12, 520-5	17.6	36
107	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> , 2014 , 111, E3853-9	11.5	35
106	Small molecule inhibition of apicomplexan FtsH1 disrupts plastid biogenesis in human pathogens. <i>ELife</i> , 2017 , 6,	8.9	35
105	Altered specificity of a AAA+ protease. <i>Molecular Cell</i> , 2007 , 25, 161-6	17.6	35
104	Tolerance of a protein helix to multiple alanine and valine substitutions. <i>Folding & Design</i> , 1998 , 3, 119-26		34
103	Crystal structure, folding, and operator binding of the hyperstable Arc repressor mutant PL8. <i>Biochemistry</i> , 1995 , 34, 1405-12	3.2	34

102	Deletion of the <i>prc</i> (<i>tsp</i>) gene provides evidence for additional tail-specific proteolytic activity in <i>Escherichia coli</i> K-12. <i>Molecular Genetics and Genomics</i> , 1994 , 242, 237-40		34
101	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> , 2009 , 106, 19340-5	11.5	33
100	Protein folding from a combinatorial perspective. <i>Folding & Design</i> , 1996 , 1, R27-30		33
99	Control of phage P22 tail protein expression by transcription termination. <i>Journal of Molecular Biology</i> , 1983 , 164, 561-72	6.5	33
98	Subunit asymmetry and roles of conformational switching in the hexameric AAA+ ring of ClpX. <i>Nature Structural and Molecular Biology</i> , 2015 , 22, 411-6	17.6	32
97	Formation of a denatured dimer limits the thermal stability of Arc repressor. <i>Journal of Molecular Biology</i> , 1997 , 273, 692-700	6.5	32
96	¹ H-NMR study of the lambda operator site OL1: assignment of the imino and adenine H2 resonances. <i>Nucleic Acids Research</i> , 1984 , 12, 4035-47	20.1	32
95	Roles of the N domain of the AAA+ Lon protease in substrate recognition, allosteric regulation and chaperone activity. <i>Molecular Microbiology</i> , 2014 , 91, 66-78	4.1	30
94	Unique contacts direct high-priority recognition of the tetrameric Mu transposase-DNA complex by the AAA+ unfoldase ClpX. <i>Molecular Cell</i> , 2008 , 30, 39-50	17.6	30
93	An essential proline in lambda repressor is required for resistance to intracellular proteolysis. <i>Biochemistry</i> , 1990 , 29, 7563-71	3.2	30
92	Bacteriophage P22 Cro protein: sequence, purification, and properties. <i>Biochemistry</i> , 1986 , 25, 251-6	3.2	30
91	Allostery is an intrinsic property of the protease domain of DegS: implications for enzyme function and evolution. <i>Journal of Biological Chemistry</i> , 2010 , 285, 34039-47	5.4	29
90	Evidence for partial secondary structure formation in the transition state for arc repressor refolding and dimerization. <i>Biochemistry</i> , 2000 , 39, 8308-14	3.2	29
89	Domains of Mnt repressor: roles in tetramer formation, protein stability, and operator DNA binding. <i>Biochemistry</i> , 1995 , 34, 13109-16	3.2	29
88	Structure of the Mitochondrial Aminolevulinic Acid Synthase, a Key Heme Biosynthetic Enzyme. <i>Structure</i> , 2018 , 26, 580-589.e4	5.2	28
87	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> , 2017 , 114, E6306-E6313	11.5	28
86	Striking stabilization of Arc repressor by an engineered disulfide bond. <i>Biochemistry</i> , 2000 , 39, 12494-503.2		28
85	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> , 2005 , 102, 18344-9	11.5	27

84	A simple fragment of cyclic acyldepsipeptides is necessary and sufficient for ClpP activation and antibacterial activity. <i>ChemBioChem</i> , 2014 , 15, 2216-20	3.8	26
83	Allosteric regulation of DegS protease subunits through a shared energy landscape. <i>Nature Chemical Biology</i> , 2013 , 9, 90-6	11.7	26
82	Mutational analysis of protein stability. <i>Current Opinion in Structural Biology</i> , 1992 , 2, 46-51	8.1	25
81	NMR studies of Arc repressor mutants: proton assignments, secondary structure, and long-range contacts for the thermostable proline-8----leucine variant of Arc. <i>Biochemistry</i> , 1989 , 28, 9813-25	3.2	24
80	Structural Basis of an N-Degron Adaptor with More Stringent Specificity. <i>Structure</i> , 2016 , 24, 232-42	5.2	23
79	Altered tethering of the SspB adaptor to the ClpXP protease causes changes in substrate delivery. <i>Journal of Biological Chemistry</i> , 2007 , 282, 11465-73	5.4	23
78	A conserved activation cluster is required for allosteric communication in HtrA-family proteases. <i>Structure</i> , 2015 , 23, 517-526	5.2	22
77	P22 Arc repressor: role of cooperativity in repression and binding to operators with altered half-site spacing. <i>Journal of Molecular Biology</i> , 1995 , 249, 729-42	6.5	22
76	¹ H NMR aromatic spectrum of the operator binding domain of the lambda repressor: resonance assignment with application to structure and dynamics. <i>Biochemistry</i> , 1987 , 26, 890-7	3.2	22
75	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> , 2015 , 112, 5377-82	11.5	21
74	Small-molecule control of protein degradation using split adaptors. <i>ACS Chemical Biology</i> , 2011 , 6, 1205-13	4.3	21
73	Forced extraction of targeted components from complex macromolecular assemblies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 11685-90	11.5	20
72	Dramatic changes in DNA-binding specificity caused by single residue substitutions in an Arc/Mnt hybrid repressor. <i>Nature Structural and Molecular Biology</i> , 1995 , 2, 1115-22	17.6	20
71	The Mnt repressor of bacteriophage P22: role of C-terminal residues in operator binding and tetramer formation. <i>Biochemistry</i> , 1988 , 27, 2088-94	3.2	20
70	A mutagenesis screen for essential plastid biogenesis genes in human malaria parasites. <i>PLoS Biology</i> , 2019 , 17, e3000136	9.7	19
69	Highly Dynamic Interactions Maintain Kinetic Stability of the ClpXP Protease During the ATP-Fueled Mechanical Cycle. <i>ACS Chemical Biology</i> , 2016 , 11, 1552-1560	4.9	19
68	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> , 2010 , 107, 2437-42	11.5	19
67	The solution structure and dynamics of an Arc repressor mutant reveal premelting conformational changes related to DNA binding. <i>Biochemistry</i> , 1999 , 38, 6035-42	3.2	19

66	Distinct regulatory mechanisms balance DegP proteolysis to maintain cellular fitness during heat stress. <i>Genes and Development</i> , 2014 , 28, 902-11	12.6	18
65	Engineering fluorescent protein substrates for the AAA+ Lon protease. <i>Protein Engineering, Design and Selection</i> , 2013 , 26, 299-305	1.9	18
64	Engineering synthetic adaptors and substrates for controlled ClpXP degradation. <i>Journal of Biological Chemistry</i> , 2009 , 284, 21848-21855	5.4	18
63	Solution NMR studies of intact lambda repressor. <i>Journal of Biomolecular Structure and Dynamics</i> , 1983 , 1, 151-7	3.6	18
62	Roles of the ClpX IGF loops in ClpP association, dissociation, and protein degradation. <i>Protein Science</i> , 2019 , 28, 756-765	6.3	17
61	An ALS disease mutation in Cdc48/p97 impairs 20S proteasome binding and proteolytic communication. <i>Protein Science</i> , 2015 , 24, 1521-7	6.3	17
60	Rational Design of Selective and Bioactive Inhibitors of the Mycobacterium tuberculosis Proteasome. <i>ACS Infectious Diseases</i> , 2017 , 3, 176-181	5.5	16
59	Structure and substrate specificity of an SspB ortholog: design implications for AAA+ adaptors. <i>Structure</i> , 2007 , 15, 1296-305	5.2	16
58	Biophysical characterization of the TraY protein of Escherichia coli F factor. <i>Journal of Biological Chemistry</i> , 1998 , 273, 1329-33	5.4	16
57	Versatile modes of peptide recognition by the ClpX N domain mediate alternative adaptor-binding specificities in different bacterial species. <i>Protein Science</i> , 2010 , 19, 242-54	6.3	15
56	Expression of N-formylated proteins in Escherichia coli. <i>Protein Expression and Purification</i> , 2003 , 32, 317-22	2	15
55	Preferential heterodimer formation via undercompensated electrostatic interactions. <i>Journal of the American Chemical Society</i> , 2001 , 123, 1264-5	16.4	15
54	Solution structure of switch Arc, a mutant with 3(10) helices replacing a wild-type beta-ribbon. <i>Journal of Molecular Biology</i> , 2003 , 326, 899-909	6.5	13
53	Lac repressor at last. <i>Structure</i> , 1996 , 4, 219-22	5.2	13
52	Structural and Functional Analysis of E. coli Cyclopropane Fatty Acid Synthase. <i>Structure</i> , 2018 , 26, 1251-1258.e8	4.258	12
51	The I domain of the AAA+ HslUV protease coordinates substrate binding, ATP hydrolysis, and protein degradation. <i>Protein Science</i> , 2012 , 21, 188-98	6.3	12
50	C-terminal domain mutations in ClpX uncouple substrate binding from an engagement step required for unfolding. <i>Molecular Microbiology</i> , 2003 , 48, 67-76	4.1	12
49	The lambda and P22 phage repressors. <i>Journal of Biomolecular Structure and Dynamics</i> , 1983 , 1, 1011-22	3.6	12

48	Interactions between a subset of substrate side chains and AAA+ motor pore loops determine grip during protein unfolding. <i>ELife</i> , 2019 , 8,	8.9	11
47	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> , 2015 , 112, 3326-31	11.5	10
46	A streptomycin selection for DNA-binding activity. <i>Methods in Enzymology</i> , 1991 , 208, 604-19	1.7	10
45	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> , 2020 , 117, 28005-28013	11.5	10
44	The AAA+ FtsH Protease Degrades an ssrA-Tagged Model Protein in the Inner Membrane of Escherichia coli. <i>Biochemistry</i> , 2016 , 55, 5649-5652	3.2	10
43	Covalently linked HslU hexamers support a probabilistic mechanism that links ATP hydrolysis to protein unfolding and translocation. <i>Journal of Biological Chemistry</i> , 2017 , 292, 5695-5704	5.4	9
42	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> , 2020 , 30, 2644-2654.e3	10.6	9
41	A mutation in the N domain of Escherichia coli lon stabilizes dodecamers and selectively alters degradation of model substrates. <i>Journal of Bacteriology</i> , 2013 , 195, 5622-8	3.5	9
40	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> , 2009 , 284, 5403-13	5.4	9
39	Role of an N(cap) residue in determining the stability and operator-binding affinity of Arc repressor. <i>Biophysical Chemistry</i> , 2003 , 100, 341-50	3.5	9
38	Hinge-Linker Elements in the AAA+ Protein Unfoldase ClpX Mediate Intersubunit Communication, Assembly, and Mechanical Activity. <i>Biochemistry</i> , 2018 , 57, 6787-6796	3.2	9
37	Deciphering the Roles of Multicomponent Recognition Signals by the AAA+ Unfoldase ClpX. <i>Journal of Molecular Biology</i> , 2015 , 427, 2966-82	6.5	8
36	Substrate-guided optimization of the syringolins yields potent proteasome inhibitors with activity against leukemia cell lines. <i>Bioorganic and Medicinal Chemistry</i> , 2015 , 23, 6218-22	3.4	8
35	Crystallization of the Arc repressor. <i>Journal of Molecular Biology</i> , 1985 , 185, 445-6	6.5	8
34	ClpAP proteolysis does not require rotation of the ClpA unfoldase relative to ClpP. <i>ELife</i> , 2020 , 9,	8.9	8
33	Structural basis of ClpXP recognition and unfolding of ssrA-tagged substrates. <i>ELife</i> , 2020 , 9,	8.9	8
32	Examination of a Structural Model of Peptidomimicry by Cyclic Acyldepsipeptide Antibiotics in Their Interaction with the ClpP Peptidase. <i>ChemBioChem</i> , 2015 , 16, 1875-1879	3.8	7
31	Multiple sequence signals direct recognition and degradation of protein substrates by the AAA+ protease HslUV. <i>Journal of Molecular Biology</i> , 2010 , 403, 420-9	6.5	7

30	Interactions of Arg2 in the Mnt N-terminal arm with the central and flanking regions of the Mnt operator. <i>Journal of Molecular Biology</i> , 2000 , 301, 959-73	6.5	7
29	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> , 2020 , 117, 25455-25463	11.5	7
28	Acyldepsipeptide Antibiotics and a Bioactive Fragment Thereof Differentially Perturb Mycobacterium tuberculosis ClpXP1P2 Activity in vitro. <i>ACS Chemical Biology</i> , 2020 ,	4.9	6
27	Overexpression of CupB5 activates alginate overproduction in Pseudomonas aeruginosa by a novel AlgW-dependent mechanism. <i>Molecular Microbiology</i> , 2014 , 93, 415-25	4.1	6
26	Mutational studies of protein stability and folding of the hyperstable MYL Arc repressor variant. <i>Biophysical Chemistry</i> , 2002 , 101-102, 35-42	3.5	6
25	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> , 2005 , 102, 2305-9	11.5	5
24	Role of operator subsites in Arc repression. <i>Journal of Molecular Biology</i> , 1996 , 264, 233-42	6.5	5
23	Quaternary structure and function in phage lambda repressor: 1H-NMR studies of genetically altered proteins. <i>Journal of Biomolecular Structure and Dynamics</i> , 1987 , 5, 539-56	3.6	5
22	A Structurally Dynamic Region of the HslU Intermediate Domain Controls Protein Degradation and ATP Hydrolysis. <i>Structure</i> , 2016 , 24, 1766-1777	5.2	5
21	Mutagenic dissection of the sequence determinants of protein folding, recognition, and machine function. <i>Protein Science</i> , 2013 , 22, 1675-87	6.3	4
20	Computational and experimental probes of symmetry mismatches in the Arc repressor-DNA complex. <i>Journal of Molecular Biology</i> , 2004 , 340, 253-61	6.5	4
19	NMR structure determination of the tetramerization domain of the Mnt repressor: An asymmetric alpha-helical assembly in slow exchange. <i>Journal of Biomolecular NMR</i> , 1999 , 15, 39-53	3	4
18	Protein-Protein Interactions in DNA Recognition: H-NMR Studies of Lambda cl Repressors Genetically Altered by Site-Directed Mutagenesis. <i>Biophysical Journal</i> , 1986 , 49, 29-33	2.9	4
17	Structures of the ATP-fueled ClpXP proteolytic machine bound to protein substrate		4
16	The Intrinsically Disordered N-terminal Extension of the ClpS Adaptor Reprograms Its Partner AAA+ ClpAP Protease. <i>Journal of Molecular Biology</i> , 2020 , 432, 4908-4921	6.5	4
15	Assignments of the 1H,13C, and 15N resonances of the substrate-binding SSD domain from Lon protease. <i>Journal of Biomolecular NMR</i> , 2001 , 21, 387-8	3	3
14	ClpP1P2 peptidase activity promotes biofilm formation in Pseudomonas aeruginosa. <i>Molecular Microbiology</i> , 2021 , 115, 1094-1109	4.1	3
13	Structural biology. A glimpse into tmRNA-mediated ribosome rescue. <i>Science</i> , 2003 , 300, 72-3	33.3	2

12	Structure and dynamics of the tetrameric mnt repressor and a model for its DNA complex. <i>Journal of Biomolecular Structure and Dynamics</i> , 2000 , 17 Suppl 1, 113-22	3.6	2
11	Mutagenesis of the Arc Repressor Using Synthetic Primers with Random Nucleotide Substitutions 1973 , 243-256		2
10	Structural basis of ClpXP recognition and unfolding of ssrA-tagged substrates		2
9	Genetic Methods in High-Resolution NMR Studies of Proteins 1986 , 37-48		2
8	Structure and function of ClpXP, a AAA+ proteolytic machine powered by probabilistic ATP hydrolysis.. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2021 , 1-17	8.7	2
7	Tsp and Related Tail-Specific Proteases. <i>The Enzymes</i> , 2002 , 22, 373-386	2.3	1
6	Multistep substrate binding and engagement by the AAA+ ClpXP protease		1
5	Heat activates the AAA+ HslUV protease by melting an axial autoinhibitory plug. <i>Cell Reports</i> , 2021 , 34, 108639	10.6	1
4	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> , 2021 , 101407	5.4	0
3	Computational and Experimental Probes of Symmetry Mismatches in the Arc Repressor?DNA Complex. <i>Journal of Molecular Biology</i> , 2004 , 340, 253-253	6.5	
2	Surface areas of unfolded proteins. <i>Nature</i> , 1990 , 348, 397	50.4	
1	Identifying the Determinants of Protein Function and Stability 1987 , 177-198		