Ashley Buckle

List of Publications by Year
in descending order

150 papers	7,281 citations	66336 42 h-index	64791 79 g-index
169 all docs	169 docs citations	169 times ranked	9528 citing authors

#	Article	IF	Citations
1	Polymer End Group Control through a Decarboxylative Cobalt-Mediated Radical Polymerization: New Avenues for Synthesizing Peptide, Protein, and Nanomaterial Conjugates. Jacs Au, 2022, 2, 169-177.	7.9	4
2	Enoxaparin augments alpha-1-antitrypsin inhibition of TMPRSS2, a promising drug combination against COVID-19. Scientific Reports, 2022, 12, 5207.	3.3	8
3	A metal ionâ€"dependent conformational switch modulates activity of the Plasmodium M17 aminopeptidase. Journal of Biological Chemistry, 2022, 298, 102119.	3.4	1
4	A Comprehensive Phylogenetic Analysis of the Serpin Superfamily. Molecular Biology and Evolution, 2021, 38, 2915-2929.	8.9	39
5	High avidity drives the interaction between the streptococcal C1 phage endolysin, PlyC, with the cell surface carbohydrates of Group A Streptococcus. Molecular Microbiology, 2021, 116, 397-415.	2.5	9
6	Assessing Respiratory Immune Responses to Haemophilus Influenzae. Journal of Visualized Experiments, 2021, , .	0.3	1
7	Molecular basis of a redox switch: molecular dynamics simulations and surface plasmon resonance provide insight into reduced and oxidised angiotensinogen. Biochemical Journal, 2021, 478, 3319-3330.	3.7	1
8	Mutational and biophysical robustness in a prestabilized monobody. Journal of Biological Chemistry, 2021, 296, 100447.	3.4	6
9	Conformational diversity facilitates antibody mutation trajectories and discrimination between foreign and self-antigens. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 22341-22350.	7.1	15
10	Development and Differentiation in Monobodies Based on the Fibronectin Type 3 Domain. Cells, 2020, 9, 610.	4.1	35
11	Structural Studies of Thyroid Peroxidase Show the Monomer Interacting With Autoantibodies in Thyroid Autoimmune Disease. Endocrinology, 2020, 161, .	2.8	10
12	Intrinsic limitations in mainstream methods of identifying network motifs in biology. BMC Bioinformatics, 2020, 21, 165.	2.6	2
13	Strategies for Increasing Protein Stability. Methods in Molecular Biology, 2020, 2073, 163-181.	0.9	21
14	Impact of HLA-DR Antigen Binding Cleft Rigidity on T Cell Recognition. International Journal of Molecular Sciences, 2020, 21, 7081.	4.1	7
15	The Role of Conformational Dynamics in Abacavir-Induced Hypersensitivity Syndrome. Scientific Reports, 2019, 9, 10523.	3.3	6
16	Crystal structure of the inhibitor-free form of the serine protease kallikrein-4. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 543-546.	0.8	1
17	Potent, multi-target serine protease inhibition achieved by a simplified Î²-sheet motif. PLoS ONE, 2019, 14, e0210842.	2.5	7
18	Wavelength-Dependent Fluorescent Immunosensors via Incorporation of Polarity Indicators near the Binding Interface of Antibody Fragments. Analytical Chemistry, 2019, 91, 7631-7638.	6.5	9

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19	KLK4 Inhibition by Cyclic and Acyclic Peptides: Structural and Dynamical Insights into Standard-Mechanism Protease Inhibitors. Biochemistry, 2019, 58, 2524-2533.	2.5	13
20	Protein engineering: the potential of remote mutations. Biochemical Society Transactions, 2019, 47, 701-711.	3.4	62
21	Reactive centre loop dynamics and serpin specificity. Scientific Reports, 2019, 9, 3870.	3.3	33
22	Ribosome Evolution and Structural Capacitance. Frontiers in Molecular Biosciences, 2019, 6, 123.	3.5	0
23	Thyroid Peroxidase Revisited â€“ WhatÊ¼s New?. Hormone and Metabolic Research, 2019, 51, 765-769.	1.5	15
24	Denisovan, modern human and mouse TNFAIP3 alleles tune A20 phosphorylation and immunity. Nature Immunology, 2019, 20, 1299-1310.	14.5	53
25	Prostate Cancer Risk-Associated Single-Nucleotide Polymorphism Affects Prostate-Specific Antigen Glycosylation and Its Function. Clinical Chemistry, 2019, 65, e1-e9.	3.2	17
26	Recognition by host nuclear transport proteins drives disorder-to-order transition in Hendra virus V. Scientific Reports, 2018, 8, 358.	3.3	32
27	Previously Hidden Dynamics at the TCRâ€“Peptideâ€“MHC Interface Revealed. Journal of Immunology, 2018, 200, 4134-4145.	0.8	34
28	REFOLDdb: a new and sustainable gateway to experimental protocols for protein refolding. BMC Structural Biology, 2018, 17, 4.	2.3	11
29	Laboratory evolution of protein conformational dynamics. Current Opinion in Structural Biology, 2018, 50, 49-57.	5.7	87
30	Generation of AMBER force field parameters for zinc centres of M1 and M17 family aminopeptidases. Journal of Biomolecular Structure and Dynamics, 2018, 36, 2595-2604.	3.5	13
31	Catalytic diversity and cell wall binding repeats in the phageâ€encoded endolysins. Molecular Microbiology, 2018, 110, 879-896.	2.5	58
32	Integrating Experiment and Theory to Understand TCR-pMHC Dynamics. Frontiers in Immunology, 2018, 9, 2898.	4.8	23
33	Thyroid Peroxidase as an Autoantigen in Hashimotoâ€™s Disease: Structure, Function, and Antigenicity. Hormone and Metabolic Research, 2018, 50, 908-921.	1.5	29
34	Mapping the Pathway and Dynamics of Bestatin Inhibition of the Plasmodium falciparum M1 Aminopeptidase PfAâ€M1. ChemMedChem, 2018, 13, 2504-2513.	3.2	9
35	Genetic variation affecting DNA methylation and the human imprinting disorder, Beckwith-Wiedemann syndrome. Clinical Epigenetics, 2018, 10, 114.	4.1	10
36	Substrate Locking Promotes Dimer-Dimer Docking of an Enzyme Antibiotic Target. Structure, 2018, 26, 948-959.e5.	3.3	5

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37	Structural Capacitance in Protein Evolution and Human Diseases. Journal of Molecular Biology, 2018, 430, 3200-3217.	4.2	3
38	The Pu.1 target gene Zbtb11 regulates neutrophil development through its integrase-like HHCC zinc finger. Nature Communications, 2017, 8, 14911.	12.8	27
39	Structural reconstruction of protein ancestry. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 3897-3902.	7.1	12
40	PolyQ 2.0: an improved version of PolyQ, a database of human polyglutamine proteins. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw021.	3.0	3
41	The PU.1 target gene Zbtb11 regulates neutrophil but not macrophage development via a novel zinc finger. Experimental Hematology, 2016, 44, S83.	0.4	0
42	Circumventing the stability-function trade-off in an engineered FN3 domain. Protein Engineering, Design and Selection, 2016, 29, 541-550.	2.1	17
43	The role of protein dynamics in the evolution of new enzyme function. Nature Chemical Biology, 2016, 12, 944-950.	8.0	252
44	Smoothing a rugged protein folding landscape by sequence-based redesign. Scientific Reports, 2016, 6, 33958.	3.3	22
45	Direct and indirect mechanisms of KLK4 inhibition revealed by structure and dynamics. Scientific Reports, 2016, 6, 35385.	3.3	28
46	KinetochoreDB: a comprehensive online resource for the kinetochore and its related proteins. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw019.	3.0	0
47	Consensus protein design. Protein Engineering, Design and Selection, 2016, 29, 245-251.	2.1	160
48	A colostrum trypsin inhibitor gene expressed in the Cape fur seal mammary gland during lactation. Gene, 2016, 578, 7-16.	2.2	5
49	Critical evaluation ofin silicomethods for prediction of coiled-coil domains in proteins. Briefings in Bioinformatics, 2016, 17, 270-282.	6.5	22
50	Modelling of Thyroid Peroxidase Reveals Insights into Its Enzyme Function and Autoantigenicity. PLoS ONE, 2015, 10, e0142615.	2.5	36
51	Chiminey: Reliable Computing and Data Management Platform in the Cloud. , 2015, , .		14
52	How pyridoxal 5â€²â€phosphate differentially regulates human cytosolic and mitochondrial serine hydroxymethyltransferase oligomeric state. FEBS Journal, 2015, 282, 1225-1241.	4.7	78
53	Structural and dynamic properties that govern the stability of an engineered fibronectin type III domain. Protein Engineering, Design and Selection, 2015, 28, 67-78.	2.1	31
54	Solution structure of a soluble fragment derived from a membrane protein by shotgun proteolysis. Protein Engineering, Design and Selection, 2015, 28, 445-450.	2.1	4

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55	Dynamic Motion and Communication in the Streptococcal C1 Phage Lysin, PlyC. PLoS ONE, 2015, 10, e0140219.	2.5	3
56	Zbtb11, an Evolutionarily Conserved Pu.1-Regulated Transcriptional Repressor of TP53, Is Required for Neutrophil Development. Blood, 2015, 126, 1180-1180.	1.4	0
57	PLP-Dependent Enzymes. BioMed Research International, 2014, 2014, 1-2.	1.9	8
58	A Redundant Role of Human Thyroid Peroxidase Propeptide for Cellular, Enzymatic, and Immunological Activity. Thyroid, 2014, 24, 371-382.	4.5	25
59	Cofactor-dependent conformational heterogeneity of GAD65 and its role in autoimmunity and neurotransmitter homeostasis. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E2524-E2529.	7.1	34
60	Operation of the Australian Store.Synchrotron for macromolecular crystallography. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2510-2519.	2.5	21
61	Understanding the structural dynamics of TCR-pMHC interactions. Trends in Immunology, 2014, 35, 604-612.	6.8	54
62	Oxidation of an Exposed Methionine Instigates the Aggregation of Glyceraldehyde-3-phosphate Dehydrogenase. Journal of Biological Chemistry, 2014, 289, 26922-26936.	3.4	41
63	The Î±â€importome of mammalian germ cell maturation provides novel insights for importin biology. FASEB Journal, 2014, 28, 3480-3493.	0.5	24
64	Yersinia enterocolitica Provides the Link between Thyroid-Stimulating Antibodies and Their Germline Counterparts in Gravesâ€™ Disease. Journal of Immunology, 2013, 190, 5373-5381.	0.8	62
65	Structural characterization of the mechanism through which human glutamic acid decarboxylase auto-activates. Bioscience Reports, 2013, 33, 137-44.	2.4	16
66	Molecular Determinants of the Substrate Specificity of the Complement-initiating Protease, C1r. Journal of Biological Chemistry, 2013, 288, 15571-15580.	3.4	16
67	Interactive visualization tools for the structural biologist. Journal of Applied Crystallography, 2013, 46, 1518-1520.	4.5	4
68	Mechanismâ€based selection of a potent kallikreinâ€related peptidase 7 inhibitor from a versatile library based on the sunflower trypsin inhibitor SFTIâ€1. Biopolymers, 2013, 100, 510-518.	2.4	38
69	Epitope Flexibility and Dynamic Footprint Revealed by Molecular Dynamics of a pMHC-TCR Complex. PLoS Computational Biology, 2012, 8, e1002404.	3.2	54
70	Structural and Dynamic Requirements for Optimal Activity of the Essential Bacterial Enzyme Dihydrodipicolinate Synthase. PLoS Computational Biology, 2012, 8, e1002537.	3.2	16
71	X-ray crystal structure of the streptococcal specific phage lysin PlyC. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 12752-12757.	7.1	80
72	Conformational Properties of the Disease-Causing Z Variant of Î±1-Antitrypsin Revealed by Theory and Experiment. Biophysical Journal, 2012, 102, 2856-2865.	0.5	24

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73	Hybrid approaches to molecular simulation. Current Opinion in Structural Biology, 2012, 22, 386-393.	5.7	11
74	Crystal, Solution and In silico Structural Studies of Dihydrodipicolinate Synthase from the Common Grapevine. PLoS ONE, 2012, 7, e38318.	2.5	32
75	The Rate of PolyQ-Mediated Aggregation Is Dramatically Affected by the Number and Location of Surrounding Domains. Journal of Molecular Biology, 2011, 413, 879-887.	4.2	20
76	Refolding Your Protein with a Little Help from REFOLD. Methods in Molecular Biology, 2011, 752, 45-57.	0.9	8
77	Membrane proteins of Pseudoalteromonas tunicata during the transition from planktonic to extracellular matrixâ€adherent state. Environmental Microbiology Reports, 2011, 3, 405-413.	2.4	6
78	Recombinant protein quality evaluation: proposal for a minimal information standard. Standards in Genomic Sciences, 2011, 5, 195-197.	1.5	8
79	PolyQ: a database describing the sequence and domain context of polyglutamine repeats in proteins. Nucleic Acids Research, 2011, 39, D272-D276.	14.5	18
80	Computational Methods for Studying Serpin Conformational Change and Structural Plasticity. Methods in Enzymology, 2011, 501, 295-323.	1.0	5
81	An Analysis of the Cross-Reactivity of Autoantibodies to GAD65 and GAD67 in Diabetes. PLoS ONE, 2011, 6, e18411.	2.5	24
82	Crystallographic and Molecular Dynamics Analysis of Loop Motions Unmasking the Peptidoglycan-Binding Site in Stator Protein MotB of Flagellar Motor. PLoS ONE, 2011, 6, e18981.	2.5	28
83	Mastering the Canonical Loop of Serine Protease Inhibitors: Enhancing Potency by Optimising the Internal Hydrogen Bond Network. PLoS ONE, 2011, 6, e19302.	2.5	61
84	Chapter 10. Structural Mechanisms of Inactivation in Proteolytically Inactive Serine Proteases from Sarcoptes scabiei. RSC Drug Discovery Series, 2011, , 229-241.	0.3	0
85	Structural biology of the GAD autoantigen. Autoimmunity Reviews, 2010, 9, 148-152.	5.8	42
86	MUSTANG-MR Structural Sieving Server: Applications in Protein Structural Analysis and Crystallography. PLoS ONE, 2010, 5, e10048.	2.5	47
87	MrGrid: A Portable Grid Based Molecular Replacement Pipeline. PLoS ONE, 2010, 5, e10049.	2.5	2
88	EGM: encapsulated gene-by-gene matching to identify gene orthologs and homologous segments in genomes. Bioinformatics, 2010, 26, 2076-2084.	4.1	7
89	Structure of the Plasmodium falciparum M17 aminopeptidase and significance for the design of drugs targeting the neutral exopeptidases. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 2449-2454.	7.1	80
90	The X-Ray Crystal Structure of Escherichia coli Succinic Semialdehyde Dehydrogenase; Structural Insights into NADP+/Enzyme Interactions. PLoS ONE, 2010, 5, e9280.	2.5	31

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91	Characterisation of Peptide Microarrays for Studying Antibody-Antigen Binding Using Surface Plasmon Resonance Imagery. PLoS ONE, 2010, 5, e12152.	2.5	20
92	High-throughput protein structure determination using grid computing. , 2009, , .		1
93	Structural basis for the inhibition of the essential Plasmodium falciparum M1 neutral aminopeptidase. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 2537-2542.	7.1	133
94	Structure of granzyme C reveals an unusual mechanism of protease autoinhibition. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 5587-5592.	7.1	25
95	Scabies Mite Inactivated Serine Protease Paralogs Inhibit the Human Complement System. Journal of Immunology, 2009, 182, 7809-7817.	0.8	89
96	Substrate-Guided Design of a Potent and Selective Kallikrein-Related Peptidase Inhibitor for Kallikrein 4. Chemistry and Biology, 2009, 16, 633-643.	6.0	109
97	Structural Mechanisms of Inactivation in Scabies Mite Serine Protease Paralogues. Journal of Molecular Biology, 2009, 390, 635-645.	4.2	33
98	Structural determinants of GAD antigenicity. Molecular Immunology, 2009, 47, 493-505.	2.2	16
99	Prodepth: Predict Residue Depth by Support Vector Regression Approach from Protein Sequences Only. PLoS ONE, 2009, 4, e7072.	2.5	40
100	ARCHER â€“ e-Research Tools for Research Data Management. International Journal of Digital Curation, 2009, 4, 22-33.	0.2	7
101	Federated repositories of X-ray diffraction images. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 810-814.	2.5	42
102	The MACPF/CDC family of pore-forming toxins. Cellular Microbiology, 2008, 10, 1765-1774.	2.1	250
103	A Structural Basis for Loop C-Sheet Polymerization in Serpins. Journal of Molecular Biology, 2008, 376, 1348-1359.	4.2	20
104	Grid Interoperability: An Experiment in Bridging Grid Islands. , 2008, , .		3
105	ARCHER – An Enabler of Research Data Management. , 2008, , .		1
106	COOH-Terminal Clustering of Autoantibody and T-Cell Determinants on the Structure of GAD65 Provide Insights Into the Molecular Basis of Autoreactivity. Diabetes, 2008, 57, 1293-1301.	0.6	43
107	X-ray crystal structure of the fibrinolysis inhibitor Î±2-antiplasmin. Blood, 2008, 111, 2049-2052.	1.4	35
108	Protein Folding Database (PFD 2.0): an online environment for the International Foldeomics Consortium. Nucleic Acids Research, 2007, 35, D304-D307.	14.5	24

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109	The 1.6ÂÃ... Crystal Structure of the Catalytic Domain of PlyB, a Bacteriophage Lysin Active Against Bacillus anthracis. Journal of Molecular Biology, 2007, 366, 540-550.	4.2	81
110	eResearch Solutions for High Throughput Structural Biology. , 2007, , .		2
111	A Common Fold Mediates Vertebrate Defense and Bacterial Attack. Science, 2007, 317, 1548-1551.	12.6	261
112	The N terminus of the serpin, tengpin, functions to trap the metastable native state. EMBO Reports, 2007, 8, 658-663.	4.5	48
113	GABA production by glutamic acid decarboxylase is regulated by a dynamic catalytic loop. Nature Structural and Molecular Biology, 2007, 14, 280-286.	8.2	189
114	Serpins in Prokaryotes. , 2007, , 131-162.		6
115	Regulation of Hemostasis by Heparin-Binding Serpins. , 2007, , 509-554.		4
116	An overview of the serpin superfamily. Genome Biology, 2006, 7, 216.	9.6	550
117	The REFOLD database: a tool for the optimization of protein expression and refolding. Nucleic Acids Research, 2006, 34, D207-D212.	14.5	42
118	The Crystal Structure of the Transthyretin-like Protein from Salmonella dublin, a Prokaryote 5-Hydroxyisourate Hydrolase. Journal of Molecular Biology, 2006, 359, 1389-1399.	4.2	42
119	REFOLD: An analytical database of protein refolding methods. Protein Expression and Purification, 2006, 46, 166-171.	1.3	31
120	X-ray crystal structure of MENT: evidence for functional loopâ€“sheet polymers in chromatin condensation. EMBO Journal, 2006, 25, 3144-3155.	7.8	41
121	T cell receptor recognition of a 'super-bulged' major histocompatibility complex class Iâ€“bound peptide. Nature Immunology, 2005, 6, 1114-1122.	14.5	280
122	The matrix refolded. Nature Methods, 2005, 2, 3-3.	19.0	29
123	Control of the coagulation system by serpins. FEBS Journal, 2005, 272, 4842-4851.	4.7	117
124	Managing and mining protein crystallization data. Proteins: Structure, Function and Bioinformatics, 2005, 62, 4-7.	2.6	3
125	The High Resolution Crystal Structure of the Human Tumor Suppressor Maspin Reveals a Novel Conformational Switch in the G-helix. Journal of Biological Chemistry, 2005, 280, 22356-22364.	3.4	69
126	The High Resolution Crystal Structure of a Native Thermostable Serpin Reveals the Complex Mechanism Underpinning the Stressed to Relaxed Transition. Journal of Biological Chemistry, 2005, 280, 8435-8442.	3.4	29

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127	The 2.1Ã… Crystal Structure of the Far-red Fluorescent Protein HcRed: Inherent Conformational Flexibility of the Chromophore. Journal of Molecular Biology, 2005, 349, 223-237.	4.2	79
128	PFD: a database for the investigation of protein folding kinetics and stability. Nucleic Acids Research, 2004, 33, D279-D283.	14.5	21
129	CLIMS: Crystallography Laboratory Information Management System. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 1691-1693.	2.5	9
130	Identification of the primary collagen-binding surface on human glycoprotein VI by site-directed mutagenesis and by a blocking phage antibody. Blood, 2004, 103, 903-911.	1.4	116
131	Energetic and Structural Analysis of the Role of Tryptophan 59 in FKBP12. Biochemistry, 2003, 42, 2364-2372.	2.5	34
132	The Crystal Structure of AF1521 a Protein from Archaeoglobus fulgidus with Homology to the Non-histone Domain of MacroH2A. Journal of Molecular Biology, 2003, 330, 503-511.	4.2	113
133	A structural double-mutant cycle: estimating the strength of a buried salt bridge in barnase. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 591-600.	2.5	36
134	Loss of a metal-binding site in gelsolin leads to familial amyloidosisâ€"Finnish type. Nature Structural Biology, 2002, 9, 112-116.	9.7	67
135	The Binding of Bis-ANS to the Isolated GroEL Apical Domain Fragment Induces the Formation of a Folding Intermediate with Increased Hydrophobic Surface Not Observed in Tetradecameric GroELâ€. Biochemistry, 2001, 40, 4484-4492.	2.5	68
136	Structure of the C-terminal sterile Î±-motif (SAM) domain of human p73Î±. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 545-551.	2.5	28
137	Stabilization of GroEL minichaperones by core and surface mutations. Journal of Molecular Biology, 2000, 298, 917-926.	4.2	37
138	From Minichaperone to GroEL 1: Information on GroEL-Polypeptide Interactions from Crystal Packing of Minichaperonesâ€. Journal of Molecular Biology, 2000, 304, 873-881.	4.2	19
139	Design of highly stable functional GroEL minichaperones. Protein Science, 1999, 8, 2186-2193.	7.6	73
140	Structural response to mutation at a protein-protein interface 1 1Edited by R. Huber. Journal of Molecular Biology, 1999, 286, 1487-1506.	4.2	72
141	GroEL recognises sequential and non-sequential linear structural motifs compatible with extended Î²-strands and Î±-helices 1 1Edited by J. Karn. Journal of Molecular Biology, 1999, 292, 163-172.	4.2	46
142	A structural model for GroEL-polypeptide recognition. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 3571-3575.	7.1	201
143	Refolding chromatography with immobilized mini-chaperones. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 3576-3578.	7.1	126
144	Structural and Energetic Responses to Cavity-Creating Mutations in Hydrophobic Cores:Â Observation of a Buried Water Molecule and the Hydrophilic Nature of Such Hydrophobic Cavitiesâ€¡. Biochemistry, 1996, 35, 4298-4305.	2.5	154

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145	Chaperone activity and structure of monomeric polypeptide binding domains of GroEL. Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 15024-15029.	7.1	137
146	Towards the complete structural characterization of a protein folding pathway: the structures of the denatured, transition and native states for the association/folding of two complementary fragments of cleaved chymotrypsin inhibitor 2. Direct evidence for a nucleation-condensation mechanism. Folding & Design, 1996, 1, 189-208.	4.5	37
147	Stability and function: two constraints in the evolution of barstar and other proteins. Structure, 1994, 2, 945-951.	3.3	165
148	Protein-protein recognition: Crystal structural analysis of a barnase-barstar complex at 2.0-.ANG. resolution. Biochemistry, 1994, 33, 8878-8889.	2.5	366
149	Subsite Binding in an RNase: Structure of a Barnase-Tetranucleotide Complex at 1.76-.ANG. Resolution. Biochemistry, 1994, 33, 1644-1653.	2.5	90
150	Crystal Structural Analysis of Mutations in the Hydrophobic Cores of Barnase. Journal of Molecular Biology, 1993, 234, 847-860.	4.2	118