

# Ashley Buckle

## List of Publications by Citations

**Source:** <https://exaly.com/author-pdf/8590770/ashley-buckle-publications-by-citations.pdf>

**Version:** 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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

143  
papers

5,869  
citations

40  
h-index

72  
g-index

169  
ext. papers

6,673  
ext. citations

6.4  
avg, IF

5.4  
L-index

#	Paper	IF	Citations
143	An overview of the serpin superfamily. <i>Genome Biology</i> , <b>2006</b> , 7, 216	18.3	437
142	Protein-protein recognition: crystal structural analysis of a barnase-barstar complex at 2.0-Å resolution. <i>Biochemistry</i> , <b>1994</b> , 33, 8878-89	3.2	303
141	T cell receptor recognition of a super-bulged major histocompatibility complex class I-bound peptide. <i>Nature Immunology</i> , <b>2005</b> , 6, 1114-22	19.1	234
140	A common fold mediates vertebrate defense and bacterial attack. <i>Science</i> , <b>2007</b> , 317, 1548-51	33.3	224
139	The MACPF/CDC family of pore-forming toxins. <i>Cellular Microbiology</i> , <b>2008</b> , 10, 1765-74	3.9	214
138	A structural model for GroEL-polypeptide recognition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>1997</b> , 94, 3571-5	11.5	188
137	The role of protein dynamics in the evolution of new enzyme function. <i>Nature Chemical Biology</i> , <b>2016</b> , 12, 944-950	11.7	166
136	Stability and function: two constraints in the evolution of barstar and other proteins. <i>Structure</i> , <b>1994</b> , 2, 945-51	5.2	152
135	Structural and energetic responses to cavity-creating mutations in hydrophobic cores: observation of a buried water molecule and the hydrophilic nature of such hydrophobic cavities. <i>Biochemistry</i> , <b>1996</b> , 35, 4298-305	3.2	145
134	GABA production by glutamic acid decarboxylase is regulated by a dynamic catalytic loop. <i>Nature Structural and Molecular Biology</i> , <b>2007</b> , 14, 280-6	17.6	144
133	Chaperone activity and structure of monomeric polypeptide binding domains of GroEL. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>1996</b> , 93, 15024-9	11.5	123
132	Refolding chromatography with immobilized mini-chaperones. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>1997</b> , 94, 3576-8	11.5	120
131	Structural basis for the inhibition of the essential <i>Plasmodium falciparum</i> M1 neutral aminopeptidase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2009</b> , 106, 2537-42	11.5	116
130	Crystal structural analysis of mutations in the hydrophobic cores of barnase. <i>Journal of Molecular Biology</i> , <b>1993</b> , 234, 847-60	6.5	112
129	Identification of the primary collagen-binding surface on human glycoprotein VI by site-directed mutagenesis and by a blocking phage antibody. <i>Blood</i> , <b>2004</b> , 103, 903-11	2.2	107
128	Control of the coagulation system by serpins. Getting by with a little help from glycosaminoglycans. <i>FEBS Journal</i> , <b>2005</b> , 272, 4842-51	5.7	100
127	Substrate-guided design of a potent and selective kallikrein-related peptidase inhibitor for kallikrein 4. <i>Chemistry and Biology</i> , <b>2009</b> , 16, 633-43		99

126	The crystal structure of AF1521 a protein from <i>Archaeoglobus fulgidus</i> with homology to the non-histone domain of macroH2A. <i>Journal of Molecular Biology</i> , <b>2003</b> , 330, 503-11	6.5	97
125	Consensus protein design. <i>Protein Engineering, Design and Selection</i> , <b>2016</b> , 29, 245-51	1.9	92
124	Subsite binding in an RNase: structure of a barnase-tetranucleotide complex at 1.76-A resolution. <i>Biochemistry</i> , <b>1994</b> , 33, 1644-53	3.2	80
123	The 1.6 A crystal structure of the catalytic domain of PlyB, a bacteriophage lysin active against <i>Bacillus anthracis</i> . <i>Journal of Molecular Biology</i> , <b>2007</b> , 366, 540-50	6.5	77
122	The 2.1A crystal structure of the far-red fluorescent protein HcRed: inherent conformational flexibility of the chromophore. <i>Journal of Molecular Biology</i> , <b>2005</b> , 349, 223-37	6.5	73
121	X-ray crystal structure of the streptococcal specific phage lysin PlyC. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, 12752-7	11.5	66
120	Structure of the <i>Plasmodium falciparum</i> M17 aminopeptidase and significance for the design of drugs targeting the neutral exopeptidases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2010</b> , 107, 2449-54	11.5	65
119	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 GroEL. <i>Biochemistry</i> , <b>2001</b> , 40, 4484-92	3.2	65
118	Structural response to mutation at a protein-protein interface. <i>Journal of Molecular Biology</i> , <b>1999</b> , 286, 1487-506	6.5	65
117	Loss of a metal-binding site in gelsolin leads to familial amyloidosis-Finnish type. <i>Nature Structural Biology</i> , <b>2002</b> , 9, 112-6		62
116	Design of highly stable functional GroEL minichaperones. <i>Protein Science</i> , <b>1999</b> , 8, 2186-93	6.3	62
115	Scabies mite inactivated serine protease paralogs inhibit the human complement system. <i>Journal of Immunology</i> , <b>2009</b> , 182, 7809-17	5.3	60
114	Laboratory evolution of protein conformational dynamics. <i>Current Opinion in Structural Biology</i> , <b>2018</b> , 50, 49-57	8.1	56
113	The high resolution crystal structure of the human tumor suppressor maspin reveals a novel conformational switch in the G-helix. <i>Journal of Biological Chemistry</i> , <b>2005</b> , 280, 22356-64	5.4	53
112	How pyridoxal 5Pphosphate differentially regulates human cytosolic and mitochondrial serine hydroxymethyltransferase oligomeric state. <i>FEBS Journal</i> , <b>2015</b> , 282, 1225-41	5.7	51
111	Mastering the canonical loop of serine protease inhibitors: enhancing potency by optimising the internal hydrogen bond network. <i>PLoS ONE</i> , <b>2011</b> , 6, e19302	3.7	49
110	<i>Yersinia enterocolitica</i> provides the link between thyroid-stimulating antibodies and their germline counterparts in Graves disease. <i>Journal of Immunology</i> , <b>2013</b> , 190, 5373-81	5.3	48
109	Epitope flexibility and dynamic footprint revealed by molecular dynamics of a pMHC-TCR complex. <i>PLoS Computational Biology</i> , <b>2012</b> , 8, e1002404	5	46

108	GroEL recognises sequential and non-sequential linear structural motifs compatible with extended beta-strands and alpha-helices. <i>Journal of Molecular Biology</i> , <b>1999</b> , 292, 163-72	6.5	44
107	The N terminus of the serpin, tengpin, functions to trap the metastable native state. <i>EMBO Reports</i> , <b>2007</b> , 8, 658-63	6.5	43
106	MUSTANG-MR structural sieving server: applications in protein structural analysis and crystallography. <i>PLoS ONE</i> , <b>2010</b> , 5, e10048	3.7	40
105	COOH-terminal clustering of autoantibody and T-cell determinants on the structure of GAD65 provide insights into the molecular basis of autoreactivity. <i>Diabetes</i> , <b>2008</b> , 57, 1293-301	0.9	40
104	The crystal structure of the transthyretin-like protein from <i>Salmonella dublin</i> , a prokaryote 5-hydroxyisourate hydrolase. <i>Journal of Molecular Biology</i> , <b>2006</b> , 359, 1389-99	6.5	40
103	The REFOLD database: a tool for the optimization of protein expression and refolding. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, D207-12	20.1	39
102	X-ray crystal structure of MENT: evidence for functional loop-sheet polymers in chromatin condensation. <i>EMBO Journal</i> , <b>2006</b> , 25, 3144-55	13	39
101	Stabilization of GroEL minichaperones by core and surface mutations. <i>Journal of Molecular Biology</i> , <b>2000</b> , 298, 917-26	6.5	36
100	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. <i>Folding &amp; Design</i> , <b>1996</b> , 1, 189-208		36
99	Federated repositories of X-ray diffraction images. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2008</b> , D64, 810-4		35
98	Protein engineering: the potential of remote mutations. <i>Biochemical Society Transactions</i> , <b>2019</b> , 47, 701-711	3.1	34
97	Understanding the structural dynamics of TCR-pMHC complex interactions. <i>Trends in Immunology</i> , <b>2014</b> , 35, 604-612	14.4	34
96	Structural biology of the GAD autoantigen. <i>Autoimmunity Reviews</i> , <b>2010</b> , 9, 148-52	13.6	34
95	Prodepth: predict residue depth by support vector regression approach from protein sequences only. <i>PLoS ONE</i> , <b>2009</b> , 4, e7072	3.7	33
94	Mechanism-based selection of a potent kallikrein-related peptidase 7 inhibitor from a versatile library based on the sunflower trypsin inhibitor SFTI-1. <i>Biopolymers</i> , <b>2013</b> , 100, 510-8	2.2	32
93	A structural double-mutant cycle: estimating the strength of a buried salt bridge in barnase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2002</b> , 58, 591-600		32
92	Energetic and structural analysis of the role of tryptophan 59 in FKBP12. <i>Biochemistry</i> , <b>2003</b> , 42, 2364-72	3.2	32
91	Catalytic diversity and cell wall binding repeats in the phage-encoded endolysins. <i>Molecular Microbiology</i> , <b>2018</b> , 110, 879-896	4.1	31

90	Oxidation of an exposed methionine instigates the aggregation of glyceraldehyde-3-phosphate dehydrogenase. <i>Journal of Biological Chemistry</i> , <b>2014</b> , 289, 26922-26936	5.4	30
89	Crystal, solution and in silico structural studies of dihydrodipicolinate synthase from the common grapevine. <i>PLoS ONE</i> , <b>2012</b> , 7, e38318	3.7	30
88	X-ray crystal structure of the fibrinolysis inhibitor alpha2-antiplasmin. <i>Blood</i> , <b>2008</b> , 111, 2049-52	2.2	29
87	Denisovan, modern human and mouse TNFAIP3 alleles tune A20 phosphorylation and immunity. <i>Nature Immunology</i> , <b>2019</b> , 20, 1299-1310	19.1	29
86	Structural and dynamic properties that govern the stability of an engineered fibronectin type III domain. <i>Protein Engineering, Design and Selection</i> , <b>2015</b> , 28, 67-78	1.9	28
85	REFOLD: an analytical database of protein refolding methods. <i>Protein Expression and Purification</i> , <b>2006</b> , 46, 166-71	2	28
84	Structure of the C-terminal sterile alpha-motif (SAM) domain of human p73 alpha. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2001</b> , 57, 545-51		27
83	The high resolution crystal structure of a native thermostable serpin reveals the complex mechanism underpinning the stressed to relaxed transition. <i>Journal of Biological Chemistry</i> , <b>2005</b> , 280, 8435-42	5.4	26
82	The X-ray crystal structure of Escherichia coli succinic semialdehyde dehydrogenase; structural insights into NADP+/enzyme interactions. <i>PLoS ONE</i> , <b>2010</b> , 5, e9280	3.7	26
81	Cofactor-dependent conformational heterogeneity of GAD65 and its role in autoimmunity and neurotransmitter homeostasis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, E2524-9	11.5	25
80	Structure of granzyme C reveals an unusual mechanism of protease autoinhibition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2009</b> , 106, 5587-92	11.5	24
79	Structural mechanisms of inactivation in scabies mite serine protease paralogues. <i>Journal of Molecular Biology</i> , <b>2009</b> , 390, 635-45	6.5	24
78	The matrix refolded. <i>Nature Methods</i> , <b>2005</b> , 2, 3	21.6	24
77	Recognition by host nuclear transport proteins drives disorder-to-order transition in Hendra virus V. <i>Scientific Reports</i> , <b>2018</b> , 8, 358	4.9	23
76	Previously Hidden Dynamics at the TCR-Peptide-MHC Interface Revealed. <i>Journal of Immunology</i> , <b>2018</b> , 200, 4134-4145	5.3	23
75	Direct and indirect mechanisms of KLK4 inhibition revealed by structure and dynamics. <i>Scientific Reports</i> , <b>2016</b> , 6, 35385	4.9	23
74	Crystallographic and molecular dynamics analysis of loop motions unmasking the peptidoglycan-binding site in stator protein MotB of flagellar motor. <i>PLoS ONE</i> , <b>2011</b> , 6, e18981	3.7	23
73	Modelling of Thyroid Peroxidase Reveals Insights into Its Enzyme Function and Autoantigenicity. <i>PLoS ONE</i> , <b>2015</b> , 10, e0142615	3.7	22

72	A redundant role of human thyroid peroxidase propeptide for cellular, enzymatic, and immunological activity. <i>Thyroid</i> , <b>2014</b> , 24, 371-82	6.2	22
71	Protein Folding Database (PFD 2.0): an online environment for the International Foldomics Consortium. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, D304-7	20.1	22
70	Development and Differentiation in Monobodies Based on the Fibronectin Type 3 Domain. <i>Cells</i> , <b>2020</b> , 9,	7.9	21
69	Conformational properties of the disease-causing Z variant of $\alpha$ -antitrypsin revealed by theory and experiment. <i>Biophysical Journal</i> , <b>2012</b> , 102, 2856-65	2.9	21
68	The $\beta$ importome of mammalian germ cell maturation provides novel insights for importin biology. <i>FASEB Journal</i> , <b>2014</b> , 28, 3480-93	0.9	20
67	A structural basis for loop C-sheet polymerization in serpins. <i>Journal of Molecular Biology</i> , <b>2008</b> , 376, 1348-59	6.5	20
66	PFD: a database for the investigation of protein folding kinetics and stability. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, D279-83	20.1	20
65	From minichaperone to GroEL 1: information on GroEL-polypeptide interactions from crystal packing of minichaperones. <i>Journal of Molecular Biology</i> , <b>2000</b> , 304, 873-81	6.5	19
64	Characterisation of peptide microarrays for studying antibody-antigen binding using surface plasmon resonance imagery. <i>PLoS ONE</i> , <b>2010</b> , 5, e12152	3.7	19
63	Reactive centre loop dynamics and serpin specificity. <i>Scientific Reports</i> , <b>2019</b> , 9, 3870	4.9	18
62	The rate of polyQ-mediated aggregation is dramatically affected by the number and location of surrounding domains. <i>Journal of Molecular Biology</i> , <b>2011</b> , 413, 879-87	6.5	18
61	Operation of the Australian Synchrotron for macromolecular crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2014</b> , 70, 2510-9		17
60	An analysis of the cross-reactivity of autoantibodies to GAD65 and GAD67 in diabetes. <i>PLoS ONE</i> , <b>2011</b> , 6, e18411	3.7	17
59	Integrating Experiment and Theory to Understand TCR-pMHC Dynamics. <i>Frontiers in Immunology</i> , <b>2018</b> , 9, 2898	8.4	17
58	Smoothing a rugged protein folding landscape by sequence-based redesign. <i>Scientific Reports</i> , <b>2016</b> , 6, 33958	4.9	16
57	PolyQ: a database describing the sequence and domain context of polyglutamine repeats in proteins. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, D272-6	20.1	16
56	Circumventing the stability-function trade-off in an engineered FN3 domain. <i>Protein Engineering, Design and Selection</i> , <b>2016</b> , 29, 541-550	1.9	15
55	Critical evaluation of in silico methods for prediction of coiled-coil domains in proteins. <i>Briefings in Bioinformatics</i> , <b>2016</b> , 17, 270-82	13.4	14

54	Structural determinants of GAD antigenicity. <i>Molecular Immunology</i> , <b>2009</b> , 47, 493-505	4.3	14
53	Molecular determinants of the substrate specificity of the complement-initiating protease, C1r. <i>Journal of Biological Chemistry</i> , <b>2013</b> , 288, 15571-80	5.4	13
52	Structural and dynamic requirements for optimal activity of the essential bacterial enzyme dihydrodipicolinate synthase. <i>PLoS Computational Biology</i> , <b>2012</b> , 8, e1002537	5	12
51	The Pu.1 target gene <i>Zbtb11</i> regulates neutrophil development through its integrase-like HHCC zinc finger. <i>Nature Communications</i> , <b>2017</b> , 8, 14911	17.4	11
50	Thyroid Peroxidase as an Autoantigen in Hashimoto's Disease: Structure, Function, and Antigenicity. <i>Hormone and Metabolic Research</i> , <b>2018</b> , 50, 908-921	3.1	11
49	Chimney: Reliable Computing and Data Management Platform in the Cloud <b>2015</b> ,		10
48	Structural characterization of the mechanism through which human glutamic acid decarboxylase auto-activates. <i>Bioscience Reports</i> , <b>2013</b> , 33, 137-44	4.1	10
47	Strategies for Increasing Protein Stability. <i>Methods in Molecular Biology</i> , <b>2020</b> , 2073, 163-181	1.4	10
46	Hybrid approaches to molecular simulation. <i>Current Opinion in Structural Biology</i> , <b>2012</b> , 22, 386-93	8.1	9
45	Prostate Cancer Risk-Associated Single-Nucleotide Polymorphism Affects Prostate-Specific Antigen Glycosylation and Its Function. <i>Clinical Chemistry</i> , <b>2019</b> , 65, e1-e9	5.5	9
44	A Comprehensive Phylogenetic Analysis of the Serpin Superfamily. <i>Molecular Biology and Evolution</i> , <b>2021</b> , 38, 2915-2929	8.3	8
43	Generation of AMBER force field parameters for zinc centres of M1 and M17 family aminopeptidases. <i>Journal of Biomolecular Structure and Dynamics</i> , <b>2018</b> , 36, 2595-2604	3.6	8
42	Wavelength-Dependent Fluorescent Immunosensors via Incorporation of Polarity Indicators near the Binding Interface of Antibody Fragments. <i>Analytical Chemistry</i> , <b>2019</b> , 91, 7631-7638	7.8	7
41	Recombinant protein quality evaluation: proposal for a minimal information standard. <i>Standards in Genomic Sciences</i> , <b>2011</b> , 5, 195-7		7
40	CLIMS: crystallography laboratory information management system. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2004</b> , 60, 1691-3		7
39	Genetic variation affecting DNA methylation and the human imprinting disorder, Beckwith-Wiedemann syndrome. <i>Clinical Epigenetics</i> , <b>2018</b> , 10, 114	7.7	7
38	REFOLDdb: a new and sustainable gateway to experimental protocols for protein refolding. <i>BMC Structural Biology</i> , <b>2017</b> , 17, 4	2.7	6
37	Refolding your protein with a little help from REFOLD. <i>Methods in Molecular Biology</i> , <b>2011</b> , 752, 45-57	1.4	6

36	Membrane proteins of <i>Pseudoalteromonas tunicata</i> during the transition from planktonic to extracellular matrix-adherent state. <i>Environmental Microbiology Reports</i> , <b>2011</b> , 3, 405-13	3.7	6
35	EGM: encapsulated gene-by-gene matching to identify gene orthologs and homologous segments in genomes. <i>Bioinformatics</i> , <b>2010</b> , 26, 2076-84	7.2	6
34	Thyroid Peroxidase Revisited - What's New?. <i>Hormone and Metabolic Research</i> , <b>2019</b> , 51, 765-769	3.1	6
33	Structural reconstruction of protein ancestry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, 3897-3902	11.5	5
32	Potent, multi-target serine protease inhibition achieved by a simplified $\beta$ -sheet motif. <i>PLoS ONE</i> , <b>2019</b> , 14, e0210842	3.7	5
31	KLK4 Inhibition by Cyclic and Acyclic Peptides: Structural and Dynamical Insights into Standard-Mechanism Protease Inhibitors. <i>Biochemistry</i> , <b>2019</b> , 58, 2524-2533	3.2	5
30	Computational methods for studying serpin conformational change and structural plasticity. <i>Methods in Enzymology</i> , <b>2011</b> , 501, 295-323	1.7	5
29	Mapping the Pathway and Dynamics of Bestatin Inhibition of the Plasmodium falciparum M1 Aminopeptidase PFA-M1. <i>ChemMedChem</i> , <b>2018</b> , 13, 2504-2513	3.7	5
28	The Role of Conformational Dynamics in Abacavir-Induced Hypersensitivity Syndrome. <i>Scientific Reports</i> , <b>2019</b> , 9, 10523	4.9	4
27	Regulation of Hemostasis by Heparin-Binding Serpins <b>2007</b> , 509-554		4
26	ARCHER $\beta$ -Research Tools for Research Data Management. <i>International Journal of Digital Curation</i> , <b>2009</b> , 4, 22-33	0.9	4
25	Conformational diversity facilitates antibody mutation trajectories and discrimination between foreign and self-antigens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2020</b> , 117, 22341-22350	11.5	4
24	Structural Studies of Thyroid Peroxidase Show the Monomer Interacting With Autoantibodies in Thyroid Autoimmune Disease. <i>Endocrinology</i> , <b>2020</b> , 161,	4.8	3
23	A colostrum trypsin inhibitor gene expressed in the Cape fur seal mammary gland during lactation. <i>Gene</i> , <b>2016</b> , 578, 7-16	3.8	3
22	Grid Interoperability: An Experiment in Bridging Grid Islands <b>2008</b> ,		3
21	Managing and mining protein crystallization data. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2006</b> , 62, 4-7	4.2	3
20	Dynamic Motion and Communication in the Streptococcal C1 Phage Lysin, PlyC. <i>PLoS ONE</i> , <b>2015</b> , 10, e0140219	3.7	3
19	Impact of HLA-DR Antigen Binding Cleft Rigidity on T Cell Recognition. <i>International Journal of Molecular Sciences</i> , <b>2020</b> , 21,	6.3	3



18	Solution structure of a soluble fragment derived from a membrane protein by shotgun proteolysis. <i>Protein Engineering, Design and Selection</i> , <b>2015</b> , 28, 445-50	1.9	2
17	Intrinsic limitations in mainstream methods of identifying network motifs in biology. <i>BMC Bioinformatics</i> , <b>2020</b> , 21, 165	3.6	2
16	Interactive visualization tools for the structural biologist. <i>Journal of Applied Crystallography</i> , <b>2013</b> , 46, 1518-1520	3.8	2
15	MrGrid: a portable grid based molecular replacement pipeline. <i>PLoS ONE</i> , <b>2010</b> , 5, e10049	3.7	2
14	Serpins in Prokaryotes <b>2007</b> , 131-162		2
13	High avidity drives the interaction between the streptococcal C1 phage endolysin, PlyC, with the cell surface carbohydrates of Group A Streptococcus. <i>Molecular Microbiology</i> , <b>2021</b> , 116, 397-415	4.1	2
12	Substrate Locking Promotes Dimer-Dimer Docking of an Enzyme Antibiotic Target. <i>Structure</i> , <b>2018</b> , 26, 948-959.e5	5.2	2
11	Structural Capacitance in Protein Evolution and Human Diseases. <i>Journal of Molecular Biology</i> , <b>2018</b> , 430, 3200-3217	6.5	1
10	Crystal structure of the inhibitor-free form of the serine protease kallikrein-4. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , <b>2019</b> , 75, 543-546	1.1	1
9	High-throughput protein structure determination using grid computing <b>2009</b> ,		1
8	Mutational and biophysical robustness in a prestabilized monobody. <i>Journal of Biological Chemistry</i> , <b>2021</b> , 296, 100447	5.4	1
7	Polymer End Group Control through a Decarboxylative Cobalt-Mediated Radical Polymerization: New Avenues for Synthesizing Peptide, Protein, and Nanomaterial Conjugates.. <i>Jacs Au</i> , <b>2022</b> , 2, 169-177		0
6	Enoxaparin augments alpha-1-antitrypsin inhibition of TMPRSS2, a promising drug combination against COVID-19.. <i>Scientific Reports</i> , <b>2022</b> , 12, 5207	4.9	0
5	Zbtb11, an Evolutionarily Conserved Pu.1-Regulated Transcriptional Repressor of TP53, Is Required for Neutrophil Development. <i>Blood</i> , <b>2015</b> , 126, 1180-1180	2.2	
4	Chapter 10. Structural Mechanisms of Inactivation in Proteolytically Inactive Serine Proteases from <i>Sarcoptes scabiei</i> . <i>RSC Drug Discovery Series</i> , <b>2011</b> , 229-241	0.6	
3	Ribosome Evolution and Structural Capacitance. <i>Frontiers in Molecular Biosciences</i> , <b>2019</b> , 6, 123	5.6	
2	Cyclic Peptide Serine Protease Inhibitors Based on the Natural Product SFTI-1 <b>2018</b> , 277-306		
1	Molecular basis of a redox switch: molecular dynamics simulations and surface plasmon resonance provide insight into reduced and oxidised angiotensinogen. <i>Biochemical Journal</i> , <b>2021</b> , 478, 3319-3330	3.8	

