

Jill Trehwella

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.

137 papers	5,388 citations	43 h-index	67 g-index
161 ext. papers	5,892 ext. citations	5.4 avg, IF	5.47 L-index

#	Paper	IF	Citations
137	Recent advances in small-angle scattering and its expanding impact in structural biology.. <i>Structure</i> , 2022 , 30, 15-23	5.2	6
136	Contrasting DNA-binding behaviour by ISL1 and LHX3 underpins differential gene targeting in neuronal cell specification. <i>Journal of Structural Biology: X</i> , 2021 , 5, 100043	2.9	
135	Growing a thriving international community for small-angle scattering through collaboration. <i>Journal of Applied Crystallography</i> , 2021 , 54, 1029-1033	3.8	2
134	E3 ubiquitin-protein ligase TRIM21-mediated lysine capture by UBE2E1 reveals substrate-targeting mode of a ubiquitin-conjugating E2. <i>Journal of Biological Chemistry</i> , 2019 , 294, 11404-11419	5.4	5
133	Mutation in a flexible linker modulates binding affinity for modular complexes. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019 , 87, 425-429	4.2	1
132	An optimized SEC-SAXS system enabling high X-ray dose for rapid SAXS assessment with correlated UV measurements for biomolecular structure analysis. <i>Journal of Applied Crystallography</i> , 2018 , 51, 97-111	3.8	41
131	The C-Terminal Zinc Fingers of ZBTB38 are Novel Selective Readers of DNA Methylation. <i>Journal of Molecular Biology</i> , 2018 , 430, 258-271	6.5	18
130	Small Angle Scattering and Structural Biology: Data Quality and Model Validation. <i>Advances in Experimental Medicine and Biology</i> , 2018 , 1105, 77-100	3.6	2
129	Bayesian inference of protein conformational ensembles from limited structural data. <i>PLoS Computational Biology</i> , 2018 , 14, e1006641	5	20
128	Archiving of Integrative Structural Models. <i>Advances in Experimental Medicine and Biology</i> , 2018 , 1105, 261-272	3.6	4
127	Structural properties of a haemophore facilitate targeted elimination of the pathogen <i>Porphyromonas gingivalis</i> . <i>Nature Communications</i> , 2018 , 9, 4097	17.4	15
126	2017 publication guidelines for structural modelling of small-angle scattering data from biomolecules in solution: an update. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017 , 73, 710-728	5.5	145
125	PDB-Dev: a Prototype System for Depositing Integrative/Hybrid Structural Models. <i>Structure</i> , 2017 , 25, 1317-1318	5.2	58
124	Small-angle scattering and 3D structure interpretation. <i>Current Opinion in Structural Biology</i> , 2016 , 40, 1-7	8.1	29
123	Structural Characterization of the Extracellular Domain of CASPR2 and Insights into Its Association with the Novel Ligand Contactin1. <i>Journal of Biological Chemistry</i> , 2016 , 291, 5788-5802	5.4	21
122	Clinically Linked Mutations in the Central Domains of Cardiac Myosin-Binding Protein C with Distinct Phenotypes Show Differential Structural Effects. <i>Structure</i> , 2016 , 24, 105-115	5.2	10
121	The outer-membrane export signal of <i>Porphyromonas gingivalis</i> type IX secretion system (T9SS) is a conserved C-terminal β -sandwich domain. <i>Scientific Reports</i> , 2016 , 6, 23123	4.9	37

120	Mutation-Induced Population Shift in the MexR Conformational Ensemble Disengages DNA Binding: A Novel Mechanism for MarR Family Derepression. <i>Structure</i> , 2016 , 24, 1311-1321	5.2	10
119	A Highly Conserved Yet Flexible Linker Is Part of a Polymorphic Protein-Binding Domain in Myosin-Binding Protein C. <i>Structure</i> , 2016 , 24, 2000-2007	5.2	12
118	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. <i>Structure</i> , 2015 , 23, 1156-67	5.2	131
117	The structure of human SFPQ reveals a coiled-coil mediated polymer essential for functional aggregation in gene regulation. <i>Nucleic Acids Research</i> , 2015 , 43, 3826-40	20.1	81
116	Structural basis of interprotein electron transfer in bacterial sulfite oxidation. <i>ELife</i> , 2015 , 4, e09066	8.9	14
115	Report of the wwPDB Small-Angle Scattering Task Force: data requirements for biomolecular modeling and the PDB. <i>Structure</i> , 2013 , 21, 875-81	5.2	65
114	K7del is a common TPM2 gene mutation associated with nemaline myopathy and raised myofibre calcium sensitivity. <i>Brain</i> , 2013 , 136, 494-507	11.2	29
113	Publication guidelines for structural modelling of small-angle scattering data from biomolecules in solution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012 , 68, 620-6		107
112	Effects of gadolinium chelate on the evolution of the nanoscale structure in peptide hydrogels. <i>Biopolymers</i> , 2012 , 98, 50-8	2.2	4
111	Reliable structural interpretation of small-angle scattering data from bio-molecules in solution--the importance of quality control and a standard reporting framework. <i>BMC Structural Biology</i> , 2012 , 12, 9	2.7	14
110	Calmodulin binds a highly extended HIV-1 MA protein that refolds upon its release. <i>Biophysical Journal</i> , 2012 , 103, 541-549	2.9	12
109	Solution structure studies of monomeric human TIP47/perilipin-3 reveal a highly extended conformation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012 , 80, 2046-55	4.2	11
108	The role of heme binding by DNA-protective protein from starved cells (Dps) in the Tolerance of Porphyromonas gingivalis to heme toxicity. <i>Journal of Biological Chemistry</i> , 2012 , 287, 42243-58	5.4	16
107	The motif of human cardiac myosin-binding protein C is required for its Ca ²⁺ -dependent interaction with calmodulin. <i>Journal of Biological Chemistry</i> , 2012 , 287, 31596-607	5.4	14
106	Solution structure of the LIM-homeodomain transcription factor complex Lhx3/Ldb1 and the effects of a pituitary mutation on key Lhx3 interactions. <i>PLoS ONE</i> , 2012 , 7, e40719	3.7	7
105	Effects of macromolecular crowding on an intrinsically disordered protein characterized by small-angle neutron scattering with contrast matching. <i>Biophysical Journal</i> , 2011 , 100, 1120-8	2.9	62
104	A novel structure of an antikinase and its inhibitor. <i>Journal of Molecular Biology</i> , 2011 , 405, 214-26	6.5	17
103	The N-terminal domains of myosin binding protein C can bind polymorphically to F-actin. <i>Journal of Molecular Biology</i> , 2011 , 412, 379-86	6.5	45

102	The C0C1 fragment of human cardiac myosin binding protein C has common binding determinants for both actin and myosin. <i>Journal of Molecular Biology</i> , 2011 , 413, 908-13	6.5	29
101	Human cardiac myosin binding protein C: structural flexibility within an extended modular architecture. <i>Journal of Molecular Biology</i> , 2011 , 414, 735-48	6.5	34
100	Reflections of a Woman Scientist in the Year 2011. <i>Australian Journal of Chemistry</i> , 2011 , 64, 666	1.2	
99	The structure of TTHA0988 from <i>Thermus thermophilus</i> , a KipI-KipA homologue incorrectly annotated as an allophanate hydrolase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011 , 67, 105-11		7
98	Fractal dimension of an intrinsically disordered protein: small-angle X-ray scattering and computational study of the bacteriophage Φ N protein. <i>Protein Science</i> , 2011 , 20, 1955-70	6.3	33
97	Sol and gel states in peptide hydrogels visualized by Gd(III)-enhanced magnetic resonance imaging. <i>Biopolymers</i> , 2011 , 96, 734-43	2.2	10
96	Invited review: probing the structures of muscle regulatory proteins using small-angle solution scattering. <i>Biopolymers</i> , 2011 , 95, 505-16	2.2	4
95	Effects of chain length on oligopeptide hydrogelation. <i>Soft Matter</i> , 2011 , 7, 2624-2631	3.6	7
94	Activation of the retroviral budding factor ALIX. <i>Journal of Virology</i> , 2011 , 85, 9222-6	6.6	38
93	Structural basis for partial redundancy in a class of transcription factors, the LIM homeodomain proteins, in neural cell type specification. <i>Journal of Biological Chemistry</i> , 2011 , 286, 42971-80	5.4	31
92	A chemically modified alpha-amylase with a molten-globule state has entropically driven enhanced thermal stability. <i>Protein Engineering, Design and Selection</i> , 2010 , 23, 769-80	1.9	29
91	Binding of N-Terminus Fragments of Cardiac Myosin-Binding C-protein to Actin. <i>Biophysical Journal</i> , 2010 , 98, 157a	2.9	3
90	Changes in small-angle X-ray scattering parameters observed upon binding of ligand to rabbit muscle pyruvate kinase are not correlated with allosteric transitions. <i>Biochemistry</i> , 2010 , 49, 7202-9	3.2	14
89	LIM domain binding proteins 1 and 2 have different oligomeric states. <i>Journal of Molecular Biology</i> , 2010 , 399, 133-44	6.5	33
88	Calmodulin disrupts the structure of the HIV-1 MA protein. <i>Journal of Molecular Biology</i> , 2010 , 400, 702-15	6.5	17
87	Effect of temperature during assembly on the structure and mechanical properties of peptide-based materials. <i>Biomacromolecules</i> , 2010 , 11, 1502-6	6.9	24
86	¹ H, ¹³ C and ¹⁵ N backbone and side chain resonance assignments of the N-terminal domain of the histidine kinase inhibitor KipI from <i>Bacillus subtilis</i> . <i>Biomolecular NMR Assignments</i> , 2010 , 4, 167-9	0.7	1
85	The macromolecular architecture of extracellular domain of alphaNRXN1: domain organization, flexibility, and insights into trans-synaptic disposition. <i>Structure</i> , 2010 , 18, 1044-53	5.2	28

84	Small-angle scattering for structural biology--expanding the frontier while avoiding the pitfalls. <i>Protein Science</i> , 2010 , 19, 642-57	6.3	298
83	A novel approach for enhancing the catalytic efficiency of a protease at low temperature: reduction in substrate inhibition by chemical modification. <i>Biotechnology and Bioengineering</i> , 2009 , 103, 676-86	4.9	40
82	Structure of the sporulation histidine kinase inhibitor Sda from <i>Bacillus subtilis</i> and insights into its solution state. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009 , 65, 574-81		9
81	A picornaviral loop-to-loop replication complex. <i>Journal of Structural Biology</i> , 2009 , 166, 251-62	3.4	16
80	Domain organization of the monomeric form of the Tom70 mitochondrial import receptor. <i>Journal of Molecular Biology</i> , 2009 , 388, 1043-58	6.5	33
79	Solution structure of ectodomains of the insulin receptor family: the ectodomain of the type 1 insulin-like growth factor receptor displays asymmetry of ligand binding accompanied by limited conformational change. <i>Journal of Molecular Biology</i> , 2009 , 394, 878-92	6.5	28
78	Small-angle scattering and neutron contrast variation for studying bio-molecular complexes. <i>Methods in Molecular Biology</i> , 2009 , 544, 307-23	1.4	40
77	Characterization of the solution structure of a neuroligin/beta-neurexin complex. <i>Chemico-Biological Interactions</i> , 2008 , 175, 150-5	5	7
76	Ligand-induced conformational changes and conformational dynamics in the solution structure of the lactose repressor protein. <i>Journal of Molecular Biology</i> , 2008 , 376, 466-81	6.5	49
75	Small-angle X-ray scattering reveals the N-terminal domain organization of cardiac myosin binding protein C. <i>Journal of Molecular Biology</i> , 2008 , 377, 1186-99	6.5	55
74	Small-angle X-ray scattering of reduced ribonuclease A: effects of solution conditions and comparisons with a computational model of unfolded proteins. <i>Journal of Molecular Biology</i> , 2008 , 377, 1576-92	6.5	36
73	Evolution of quaternary structure in a homotetrameric enzyme. <i>Journal of Molecular Biology</i> , 2008 , 380, 691-703	6.5	70
72	Histidine kinase regulation by a cyclophilin-like inhibitor. <i>Journal of Molecular Biology</i> , 2008 , 384, 422-356.5		26
71	Subdividing repressor function: DNA binding affinity, selectivity, and allostery can be altered by amino acid substitution of nonconserved residues in a LacI/GalR homologue. <i>Biochemistry</i> , 2008 , 47, 8058-69	3.2	23
70	The different views from small angles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 4967-8	11.5	15
69	Cardiac myosin-binding protein C decorates F-actin: implications for cardiac function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 18360-5	11.5	99
68	Refined solution structure of the 82-kDa enzyme malate synthase G from joint NMR and synchrotron SAXS restraints. <i>Journal of Biomolecular NMR</i> , 2008 , 40, 95-106	3	93
67	MULCh: modules for the analysis of small-angle neutron contrast variation data from biomolecular assemblies. <i>Journal of Applied Crystallography</i> , 2008 , 41, 222-226	3.8	128

66	Synaptic arrangement of the neuroligin/beta-neurexin complex revealed by X-ray and neutron scattering. <i>Structure</i> , 2007 , 15, 693-705	5.2	60
65	The structure of the KinA-Sda complex suggests an allosteric mechanism of histidine kinase inhibition. <i>Journal of Molecular Biology</i> , 2007 , 368, 407-20	6.5	59
64	Phosphorylation-dependent conformational transition of the cardiac specific N-extension of troponin I in cardiac troponin. <i>Journal of Molecular Biology</i> , 2007 , 373, 706-22	6.5	73
63	Ligand-induced conformational changes via flexible linkers in the amino-terminal region of the inositol 1,4,5-trisphosphate receptor. <i>Journal of Molecular Biology</i> , 2007 , 373, 1269-80	6.5	43
62	Structural themes and variations in protein kinase A as seen by small-angle scattering and neutron contrast variation. <i>European Biophysics Journal</i> , 2006 , 35, 585-9	1.9	2
61	Neutrons reveal how nature uses structural themes and variation in biological regulation. <i>Physica B: Condensed Matter</i> , 2006 , 385-386, 825-830	2.8	6
60	Protein kinase A targeting and activation as seen by small-angle solution scattering. <i>European Journal of Cell Biology</i> , 2006 , 85, 655-62	6.1	5
59	Coassembling Peptide-Based Biomaterials: Effects of Pairing Equal and Unequal Chain Length Oligopeptides. <i>Chemistry of Materials</i> , 2006 , 18, 6157-6162	9.6	41
58	Solution scattering reveals large differences in the global structures of type II protein kinase A isoforms. <i>Journal of Molecular Biology</i> , 2006 , 357, 880-9	6.5	32
57	Refinement of multidomain protein structures by combination of solution small-angle X-ray scattering and NMR data. <i>Journal of the American Chemical Society</i> , 2005 , 127, 16621-8	16.4	185
56	Ca ²⁺ -induced structural changes in phosphorylase kinase detected by small-angle X-ray scattering. <i>Protein Science</i> , 2005 , 14, 1039-48	6.3	22
55	The conformationally dynamic C helix of the RIalpha subunit of protein kinase A mediates isoform-specific domain reorganization upon C subunit binding. <i>Journal of Biological Chemistry</i> , 2005 , 280, 35521-7	5.4	18
54	C subunits binding to the protein kinase A RI alpha dimer induce a large conformational change. <i>Journal of Biological Chemistry</i> , 2004 , 279, 19084-90	5.4	36
53	Differential effects of substrate on type I and type II PKA holoenzyme dissociation. <i>Biochemistry</i> , 2004 , 43, 5629-36	3.2	49
52	Conformational differences among solution structures of the type Ialpha, IIalpha and IIbeta protein kinase A regulatory subunit homodimers: role of the linker regions. <i>Journal of Molecular Biology</i> , 2004 , 337, 1183-94	6.5	50
51	Solution structure of heavy meromyosin by small-angle scattering. <i>Journal of Biological Chemistry</i> , 2003 , 278, 6034-40	5.4	8
50	Further insights into calmodulin-myosin light chain kinase interaction from solution scattering and shape restoration. <i>Biochemistry</i> , 2003 , 42, 10579-88	3.2	43
49	Small-angle neutron scattering with contrast variation reveals spatial relationships between the three subunits in the ternary cardiac troponin complex and the effects of troponin I phosphorylation. <i>Biochemistry</i> , 2003 , 42, 7790-800	3.2	44

48	Mechanisms associated with cGMP binding and activation of cGMP-dependent protein kinase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 2380-5	11.5	59
47	A structural model of the catalytic subunit-regulatory subunit dimeric complex of the cAMP-dependent protein kinase. <i>Journal of Biological Chemistry</i> , 2002 , 277, 12423-31	5.4	26
46	Small-angle solution scattering reveals information on conformational dynamics in calcium-binding proteins and in their interactions with regulatory targets. <i>Methods in Molecular Biology</i> , 2002 , 173, 137-54	1.4	5
45	The solution structure of a cardiac troponin C-troponin I-troponin T complex shows a somewhat compact troponin C interacting with an extended troponin I-troponin T component. <i>Biochemistry</i> , 2002 , 41, 15654-63	3.2	53
44	Activation of myosin light chain kinase requires translocation of bound calmodulin. <i>Journal of Biological Chemistry</i> , 2001 , 276, 4535-8	5.4	26
43	Functional dynamics of the hydrophobic cleft in the N-domain of calmodulin. <i>Biophysical Journal</i> , 2001 , 80, 2082-92	2.9	71
42	There is communication between all four Ca(2+)-bindings sites of calcineurin B. <i>Biochemistry</i> , 2001 , 40, 12094-102	3.2	29
41	Nanoscale Science and Technology at Los Alamos National Laboratory. <i>Journal of Nanoparticle Research</i> , 2000 , 2, 249-266	2.3	1
40	Large-scale shape changes in proteins and macromolecular complexes. <i>Annual Review of Physical Chemistry</i> , 2000 , 51, 355-80	15.7	64
39	Calmodulin remains extended upon binding to smooth muscle caldesmon: a combined small-angle scattering and fourier transform infrared spectroscopy study. <i>Biochemistry</i> , 2000 , 39, 3979-87	3.2	25
38	A model of troponin-I in complex with troponin-C using hybrid experimental data: the inhibitory region is a beta-hairpin. <i>Protein Science</i> , 2000 , 9, 1312-26	6.3	45
37	A Day in the World Science Alliance. <i>Science</i> , 1999 , 286, 2104-2106	33.3	
36	Troponin I inhibitory peptide (96-115) has an extended conformation when bound to skeletal muscle troponin C. <i>Biochemistry</i> , 1999 , 38, 6911-7	3.2	22
35	The solution structure of the DNA double-stranded break repair protein Ku and its complex with DNA: a neutron contrast variation study. <i>Biochemistry</i> , 1999 , 38, 2152-9	3.2	15
34	The solution structure of the Sac7d/DNA complex: a small-angle X-ray scattering study. <i>Biochemistry</i> , 1999 , 38, 10247-55	3.2	29
33	Global conformational changes control the reactivity of methane monooxygenase. <i>Biochemistry</i> , 1999 , 38, 6752-60	3.2	39
32	Calmodulin binding to myosin light chain kinase begins at substoichiometric Ca ²⁺ concentrations: a small-angle scattering study of binding and conformational transitions. <i>Biochemistry</i> , 1998 , 37, 17810-7	3.2	35
31	Neutron-scattering studies reveal further details of the Ca ²⁺ /calmodulin-dependent activation mechanism of myosin light chain kinase. <i>Biochemistry</i> , 1998 , 37, 13997-4004	3.2	50

30	The assembly of immunoglobulin-like modules in titin: implications for muscle elasticity. <i>Journal of Molecular Biology</i> , 1998 , 284, 761-77	6.5	75
29	Quaternary structures of a catalytic subunit-regulatory subunit dimeric complex and the holoenzyme of the cAMP-dependent protein kinase by neutron contrast variation. <i>Journal of Biological Chemistry</i> , 1998 , 273, 30448-59	5.4	45
28	Myosin light chain kinase: functional domains and structural motifs. <i>Acta Physiologica Scandinavica</i> , 1998 , 164, 471-82		61
27	Progressive cyclic nucleotide-induced conformational changes in the cGMP-dependent protein kinase studied by small angle X-ray scattering in solution. <i>Journal of Biological Chemistry</i> , 1997 , 272, 31929-36	5.4	44
26	Neutron Resonance Scattering Shows Specific Binding of Plutonium to the Calcium-Binding Sites of the Protein Calmodulin and Yields Precise Distance Information. <i>Journal of the American Chemical Society</i> , 1997 , 119, 5118-5125	16.4	18
25	Structures of calmodulin and a functional myosin light chain kinase in the activated complex: a neutron scattering study. <i>Biochemistry</i> , 1997 , 36, 6017-23	3.2	66
24	Insights into biomolecular function from small-angle scattering. <i>Current Opinion in Structural Biology</i> , 1997 , 7, 702-8	8.1	44
23	The relative orientation of Gla and EGF domains in coagulation factor X is altered by Ca ²⁺ binding to the first EGF domain. A combined NMR-small angle X-ray scattering study. <i>Biochemistry</i> , 1996 , 35, 11547-59	3.2	76
22	The Structure of the Muscle Protein Complex 4Ca ²⁺ -Troponin C-Troponin I 1996 , 137-147		
21	Conformationally constrained analogs of protein kinase inhibitor (6-22)amide: effect of turn structures in the center of the peptide on inhibition of cAMP-dependent protein kinase. <i>Protein Science</i> , 1995 , 4, 405-15	6.3	5
20	Structures of fd gene 5 protein-nucleic acid complexes: a combined solution scattering and electron microscopy study. <i>Journal of Molecular Biology</i> , 1995 , 249, 576-94	6.5	36
19	Troponin I encompasses an extended troponin C in the Ca(2+)-bound complex: a small-angle X-ray and neutron scattering study. <i>Biochemistry</i> , 1994 , 33, 8233-9	3.2	89
18	A model structure of the muscle protein complex 4Ca ²⁺ -troponin C-troponin I derived from small-angle scattering data: implications for regulation. <i>Biochemistry</i> , 1994 , 33, 12800-6	3.2	111
17	The solution structures of calmodulin and its complexes with synthetic peptides based on target enzyme binding domains. <i>Cell Calcium</i> , 1992 , 13, 377-90	4	36
16	Orienting rigid and flexible biological assemblies in ferrofluids for small-angle neutron scattering studies. <i>Biophysical Journal</i> , 1991 , 60, 1178-89	2.9	14
15	Potential biophysical application of the Los Alamos infrared free electron laser: DNA spectroscopy. <i>Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment</i> , 1990 , 296, 809-813	1.2	2
14	Small-angle scattering studies show distinct conformations of calmodulin in its complexes with two peptides based on the regulatory domain of the catalytic subunit of phosphorylase kinase. <i>Biochemistry</i> , 1990 , 29, 9316-24	3.2	71
13	Ordered macromolecular structures in ferrofluid mixtures. <i>Physical Review Letters</i> , 1989 , 62, 1667-1670	7.4	29

12	Calmodulin and troponin C structures studied by Fourier transform infrared spectroscopy: effects of Ca ²⁺ and Mg ²⁺ binding. <i>Biochemistry</i> , 1989 , 28, 1294-301	3.2	94
11	Changes in the structure of calmodulin induced by a peptide based on the calmodulin-binding domain of myosin light chain kinase. <i>Biochemistry</i> , 1989 , 28, 6757-64	3.2	118
10	Comparison of the crystal and solution structures of calmodulin and troponin C. <i>Biochemistry</i> , 1988 , 27, 909-15	3.2	317
9	Neutron diffraction studies of bacteriorhodopsin. <i>Physica B: Physics of Condensed Matter & C: Atomic, Molecular and Plasma Physics, Optics</i> , 1986 , 136, 249-251		
8	¹ H N.M.R Studies of High-Spin Complexes of Soybean Leghemoglobin. Interactions Between the Distal Histidine and Acetate, Formate and Fluoride Ligands. <i>Australian Journal of Chemistry</i> , 1986 , 39, 317	1.2	5
7	Stability of transmembrane regions in bacteriorhodopsin studied by progressive proteolysis. <i>Journal of Membrane Biology</i> , 1985 , 88, 233-47	2.3	37
6	Assignment of segments of the bacteriorhodopsin sequence to positions in the structural map. <i>Biophysical Journal</i> , 1983 , 42, 233-41	2.9	64
5	Differences in the heme environment of soybean leghemoglobin components shown by ¹ H-NMR spectroscopy. <i>BBA - Proteins and Proteomics</i> , 1982 , 700, 171-177		7
4	¹ H-NMR studies of ferric soybean leghemoglobin: assignment of hyperfine shifted resonances of complexes with cyanide, nicotinate, pyridine and azide. <i>Biochimica Et Biophysica Acta (BBA) - Protein Structure</i> , 1980 , 625, 202-20		26
3	Molecular basis for proton-dependent anion binding by soybean leghaemoglobin a. <i>Nature</i> , 1979 , 280, 87-88	50.4	22
2	Spin state equilibria in soybean ferric leghemoglobin and its complexes with formate and acetate. <i>Biochemical and Biophysical Research Communications</i> , 1979 , 88, 713-21	3.4	8
1	Small-Angle Scattering of Neutrons and X-Rays1-11		