Jennifer L Martin

List of Publications by Year
in descending order

135 papers	7,484 citations	53794 45 h-index	58581 82 g-index
142 all docs	142 docs citations	142 times ranked	7487 citing authors

#	Article	IF	Citations
1	Thioredoxin â€"a fold for all reasons. Structure, 1995, 3, 245-250.	3.3	746
2	Human Sulfotransferases and Their Role in Chemical Metabolism. Toxicological Sciences, 2006, 90, 5-22.	3.1	582
3	Crystal structure of the DsbA protein required for disulphide bond formation in vivo. Nature, 1993, 365, 464-468.	27.8	396
4	Protein disulfide isomerase: the structure of oxidative folding. Trends in Biochemical Sciences, 2006, 31, 455-464.	7.5	293
5	DSB proteins and bacterial pathogenicity. Nature Reviews Microbiology, 2009, 7, 215-225.	28.6	260
6	Post-crystallization treatments for improving diffraction quality of protein crystals. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 1173-1180.	2.5	180
7	Structure of a Human Carcinogen-converting Enzyme, SULT1A1. Journal of Biological Chemistry, 2003, 278, 7655-7662.	3.4	151
8	Crystal structures of reduced and oxidized DsbA: investigation of domain motion and thiolate stabilization. Structure, 1998, 6, 757-767.	3.3	147
9	Targeting virulence not viability in the search for future antibacterials. British Journal of Clinical Pharmacology, 2015, 79, 208-215.	2.4	144
10	Structure of the Munc18c/Syntaxin4 N-peptide complex defines universal features of the N-peptide binding mode of Sec1/Munc18 proteins. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 8773-8778.	7.1	131
11	Structure of West Nile Virus NS3 Protease: Ligand Stabilization of the Catalytic Conformation. Journal of Molecular Biology, 2009, 385, 1568-1577.	4.2	131
12	Ten Simple Rules to Achieve Conference Speaker Gender Balance. PLoS Computational Biology, 2014, 10, e1003903.	3.2	125
13	Solving the Î±-Conotoxin Folding Problem: Efficient Selenium-Directed On-Resin Generation of More Potent and Stable Nicotinic Acetylcholine Receptor Antagonists. Journal of the American Chemical Society, 2010, 132, 3514-3522.	13.7	124
14	Crystal structure of Toll-like receptor adaptor MAL/TIRAP reveals the molecular basis for signal transduction and disease protection. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 14879-14884.	7.1	123
15	Crystal structure of human catecholamine sulfotransferase 1 1Edited by R. Huber. Journal of Molecular Biology, 1999, 293, 521-530.	4.2	119
16	Molecular Dissection of the Munc18c/Syntaxin4 Interaction: Implications for Regulation of Membrane Trafficking. Traffic, 2006, 7, 1408-1419.	2.7	106
17	The Structure of Human SULT1A1 Crystallized with Estradiol. Journal of Biological Chemistry, 2005, 280, 41482-41486.	3.4	103
18	Possible roles for Munc18-1 domain 3a and Syntaxin1 N-peptide and C-terminal anchor in SNARE complex formation. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 1040-1045.	7.1	101

#	Article	IF	Citations
19	The 1.1 Ã¥ crystal structure of the neuronal acetylcholine receptor antagonist, Î±-conotoxin PnIA from Conus pennaceus. Structure, 1996, 4, 417-423.	3.3	99
20	Combined X-ray and NMR Analysis of the Stability of the Cyclotide Cystine Knot Fold That Underpins Its Insecticidal Activity and Potential Use as a Drug Scaffold. Journal of Biological Chemistry, 2009, 284, 10672-10683.	3.4	96
21	Structure and Function of DsbA, a Key Bacterial Oxidative Folding Catalyst. Antioxidants and Redox Signaling, 2011, 14, 1729-1760.	5.4	96
22	Crystal structures of the DsbG disulfide isomerase reveal an unstable disulfide. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 8876-8881.	7.1	95
23	Properties of the Thioredoxin Fold Superfamily Are Modulated by a Single Amino Acid Residue. Journal of Biological Chemistry, 2009, 284, 10150-10159.	3.4	93
24	Structural analysis of three His32 mutants of DsbA: Support for an electrostatic role of His32 in DsbA stability. Protein Science, 1997, 6, 1893-1900.	7.6	82
25	Crystal Structure of Escherichia coli Xanthine Phosphoribosyltransferase. Biochemistry, 1997, 36, 4125-4134.	2.5	79
26	The uncharged surface features surrounding the active site ofEscherichia coliDsbA are conserved and are implicated in peptide binding. Protein Science, 1997, 6, 1148-1156.	7.6	78
27	Substrate-Based Cyclic Peptidomimetics of Phe-Ile-Val That Inhibit HIV-1 Protease Using a Novel Enzyme-Binding Mode. Journal of the American Chemical Society, 1996, 118, 3375-3379.	13.7	77
28	Dehydration Converts DsbG Crystal Diffraction from Low to High Resolution. Structure, 2003, 11, 139-145.	3.3	77
29	An Inflammatory Role for the Mammalian Carboxypeptidase Inhibitor Latexin: Relationship to Cystatins and the Tumor Suppressor TIG1. Structure, 2005, 13, 309-317.	3.3	71
30	Structural basis for recruitment of tandem hotdog domains in acyl-CoA thioesterase 7 and its role in inflammation. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 10382-10387.	7.1	71
31	Structure of CcmG/DsbE at 1.14 Ã... Resolution. Structure, 2002, 10, 973-979.	3.3	69
32	Comparative studies of Munc18c and Munc18-1 reveal conserved and divergent mechanisms of Sec1/Munc18 proteins. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E3271-80.	7.1	69
33	Synthesis, Stability, Antiviral Activity, and Protease-Bound Structures of Substrate-Mimicking Constrained Macrocyclic Inhibitors of HIV-1 Protease. Journal of Medicinal Chemistry, 2000, 43, 3495-3504.	6.4	68
34	Structure of TcpG, the DsbA protein folding catalyst from Vibrio cholerae. Journal of Molecular Biology, 1997, 268, 137-146.	4.2	66
35	Structures of free and complexed forms of Escherichia coli xanthine-guanine phosphoribosyltransferase 1 1Edited by R. Huber. Journal of Molecular Biology, 1998, 282, 875-889.	4.2	63
36	Crystallography and proteinâ€“protein interactions: biological interfaces and crystal contacts. Biochemical Society Transactions, 2008, 36, 1438-1441.	3.4	61

#	Article	IF	Citations
37	Getting the Adrenaline Going. Structure, 2001, 9, 977-985.	3.3	60
38	Low-resolution solution structures of Munc18:Syntaxin protein complexes indicate an open binding mode driven by the Syntaxin N-peptide. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 9816-9821.	7.1	59
39	Molecular Recognition of Macrocyclic Peptidomimetic Inhibitors by HIV-1 Proteaseâ€,â€¡. Biochemistry, 1999, 38, 7978-7988.	2.5	56
40	Active Site Mutations and Substrate Inhibition in Human Sulfotransferase 1A1 and 1A3. Journal of Biological Chemistry, 2004, 279, 18799-18805.	3.4	56
41	Staphylococcus aureus DsbA Does Not Have a Destabilizing Disulfide. Journal of Biological Chemistry, 2008, 283, 4261-4271.	3.4	56
42	The name's bondâ€¦â€¦disulfide bond. Current Opinion in Structural Biology, 2007, 17, 691-698.	5.7	53
43	Human cytosolic sulfotransferase SULT1A1. International Journal of Biochemistry and Cell Biology, 2007, 39, 685-689.	2.8	52
44	Improved Success of Sparse Matrix Protein Crystallization Screening with Heterogeneous Nucleating Agents. PLoS ONE, 2007, 2, e1091.	2.5	49
45	Countering Cooperative Effects in Protease Inhibitors Using Constrained Î²-Strand-Mimicking Templates in Focused Combinatorial Libraries. Journal of Medicinal Chemistry, 2004, 47, 1641-1651.	6.4	47
46	The Munc18-1 domain 3a loop is essential for neuroexocytosis but not for syntaxin-1A transport to the plasma membrane. Journal of Cell Science, 2013, 126, 2353-2360.	2.0	47
47	DisarmingBurkholderia pseudomallei: Structural and Functional Characterization of a Disulfide Oxidoreductase (DsbA) Required for VirulenceIn Vivo. Antioxidants and Redox Signaling, 2014, 20, 606-617.	5.4	47
48	Application of Fragmentâ€Based Screening to the Design of Inhibitors of Escherichia coli DsbA. Angewandte Chemie - International Edition, 2015, 54, 2179-2184.	13.8	46
49	Crystal structures of free, IMP-, and GMP-bound Escherichia coli hypoxanthine phosphoribosyltransferase. Protein Science, 2009, 11, 1626-1638.	7.6	44
50	Federated repositories of X-ray diffraction images. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 810-814.	2.5	42
51	Peptide Inhibitors of the Escherichia coli DsbA Oxidative Machinery Essential for Bacterial Virulence. Journal of Medicinal Chemistry, 2015, 58, 577-587.	6.4	42
52	Fragment-based screening by X-ray crystallography, MS and isothermal titration calorimetry to identify PNMT (phenylethanolamine N-methyltransferase) inhibitors. Biochemical Journal, 2010, 431, 51-61.	3.7	41
53	Crystallization of DsbA, an Escherichia coli Protein Required for Disulphide Bond Formation in Vivo. Journal of Molecular Biology, 1993, 230, 1097-1100.	4.2	40
54	Comparison of the Binding of 3-Fluoromethyl-7-sulfonyl-1,2,3,4-tetrahydroisoquinolines with Their Isosteric Sulfonamides to the Active Site of PhenylethanolamineN-Methyltransferase1. Journal of Medicinal Chemistry, 2006, 49, 5424-5433.	6.4	40

#	Article	IF	Citations
55	United we stand: combining structural methods. Current Opinion in Structural Biology, 2008, 18, 617-622.	5.7	39
56	Structural and Functional Characterization of the Oxidoreductase Î±-DsbA1 fromWolbachia pipientis. Antioxidants and Redox Signaling, 2009, 11, 1485-1500.	5.4	39
57	Four structural subclasses of the antivirulence drug target disulfide oxidoreductase DsbA provide a platform for design of subclass-specific inhibitors. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 1391-1401.	2.3	39
58	In vivooxidative protein folding can be facilitated by oxidationÃ¢Â€Â“reduction cycling. Molecular Microbiology, 2010, 75, 13-28.	2.5	38
59	Structural Insights into the Role of the Cyclic Backbone in a Squash Trypsin Inhibitor. Journal of Biological Chemistry, 2013, 288, 36141-36148.	3.4	38
60	SNARE-ing the structures of Sec1/Munc18 proteins. Current Opinion in Structural Biology, 2014, 29, 44-51.	5.7	35
61	Inhibition of Diverse DsbA Enzymes in Multi-DsbA Encoding Pathogens. Antioxidants and Redox Signaling, 2018, 29, 653-666.	5.4	35
62	The Arabidopsis B3 Domain Protein VERNALIZATION1 (VRN1) Is Involved in Processes Essential for Development, with Structural and Mutational Studies Revealing Its DNA-binding Surface. Journal of Biological Chemistry, 2013, 288, 3198-3207.	3.4	32
63	Laboratory evolution of one disulfide isomerase to resemble another. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 11670-11675.	7.1	31
64	Molecular recognition of physiological substrate noradrenaline by the adrenaline-synthesizing enzyme PNMT and factors influencing its methyltransferase activity. Biochemical Journal, 2009, 422, 463-471.	3.7	30
65	Cortactin Adopts a Globular Conformation and Bundles Actin into Sheets. Journal of Biological Chemistry, 2008, 283, 16187-16193.	3.4	29
66	Rv2969c, essential for optimal growth inMycobacterium tuberculosis, is a DsbA-like enzyme that interacts with VKOR-derived peptides and has atypical features of DsbA-like disulfide oxidases. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1981-1994.	2.5	29
67	Evaluating protein:protein complex formation using synchrotron radiation circular dichroism spectroscopy. Proteins: Structure, Function and Bioinformatics, 2008, 70, 1142-1146.	2.6	28
68	Characterization of the DsbA Oxidative Folding Catalyst fromPseudomonas aeruginosaReveals a Highly Oxidizing Protein that Binds Small Molecules. Antioxidants and Redox Signaling, 2010, 12, 921-931.	5.4	28
69	Small Molecule Inhibitors of Disulfide Bond Formation by the Bacterial DsbAâ€“DsbB Dual Enzyme System. ACS Chemical Biology, 2015, 10, 957-964.	3.4	27
70	Structural, Mutagenic, and Kinetic Analysis of the Binding of Substrates and Inhibitors of Human Phenylethanolamine N-Methyltransferase. Journal of Medicinal Chemistry, 2005, 48, 7243-7252.	6.4	26
71	Enzyme Adaptation to Inhibitor Binding:â€‰ A Cryptic Binding Site in Phenylethanolamine N-Methyltransferase. Journal of Medicinal Chemistry, 2007, 50, 4845-4853.	6.4	26
72	Molecular Recognition of Sub-micromolar Inhibitors by the Epinephrine-Synthesizing Enzyme Phenylethanolamine N-Methyltransferase. Journal of Medicinal Chemistry, 2004, 47, 37-44.	6.4	25

#	Article	IF	Citations
73	Mode of Binding of Methyl Acceptor Substrates to the Adrenaline-Synthesizing Enzyme Phenylethanolamine N-Methyltransferase:â€‰ Implications for Catalysis. Biochemistry, 2005, 44, 16875-16885.	2.5	24
74	Comparative Sequence, Structure and Redox Analyses of Klebsiella pneumoniae DsbA Show That Anti-Virulence Target DsbA Enzymes Fall into Distinct Classes. PLoS ONE, 2013, 8, e80210.	2.5	24
75	Comparison of three commercial sparse-matrix crystallization screens. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 769-772.	2.5	23
76	An automatable screen for the rapid identification of proteins amenable to refolding. Proteomics, 2006, 6, 1750-1757.	2.2	22
77	The mammalian DUF59 protein Fam96a forms two distinct types of domain-swapped dimer. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 637-648.	2.5	22
78	Crystal Structures of Highly Constrained Substrate and Hydrolysis Products Bound to HIV-1 Protease. Implications for the Catalytic Mechanism. Biochemistry, 2008, 47, 3736-3744.	2.5	21
79	A shape-shifting redox foldase contributes to Proteus mirabilis copper resistance. Nature Communications, 2017, 8, 16065.	12.8	21
80	The 1.2â€…Ã… resolution crystal structure of TcpG, theVibrio choleraeDsbA disulfide-forming protein required for pilus and cholera-toxin production. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1290-1302.	2.5	20
81	Crystal Structure of the Dithiol Oxidase DsbA Enzyme from Proteus Mirabilis Bound Non-covalently to an Active Site Peptide Ligand. Journal of Biological Chemistry, 2014, 289, 19810-19822.	3.4	20
82	The Acidic Nature of the CcmG Redox-Active Center Is Important for Cytochrome c Maturation in Escherichia coli. Journal of Bacteriology, 2004, 186, 4030-4033.	2.2	19
83	Modelling the structure of latexinâ€“carboxypeptidase A complex based on chemical cross-linking and molecular docking. Protein Engineering, Design and Selection, 2006, 19, 9-16.	2.1	19
84	Disulfide isomerase activity of the dynamic, trimeric ScsC protein is primed by the tandem immunoglobulin-fold domain of ScsB. Journal of Biological Chemistry, 2018, 293, 5793-5805.	3.4	19
85	Protein Structure Determination Using a Combination of Cross-linking, Mass Spectrometry, and Molecular Modeling. Methods in Molecular Biology, 2008, 426, 459-474.	0.9	18
86	Membrane Curvature Protein Exhibits Interdomain Flexibility and Binds a Small GTPase. Journal of Biological Chemistry, 2012, 287, 40996-41006.	3.4	17
87	Fragment library screening identifies hits that bind to the non-catalytic surface of Pseudomonas aeruginosa DsbA1. PLoS ONE, 2017, 12, e0173436.	2.5	17
88	The Weak Complex between RhoGAP Protein ARHGAP22 and Signal Regulatory Protein 14-3-3 Has 1â^¶2 Stoichiometry and a Single Peptide Binding Mode. PLoS ONE, 2012, 7, e41731.	2.5	17
89	Incorporating a TEV cleavage site reduces the solubility of nine recombinant mouse proteins. Protein Expression and Purification, 2006, 50, 68-73.	1.3	16
90	Structure of the Acinetobacter baumannii Dithiol Oxidase DsbA Bound to Elongation Factor EF-Tu Reveals a Novel Protein Interaction Site. Journal of Biological Chemistry, 2014, 289, 19869-19880.	3.4	16

#	Article	IF	Citations
91	Virtual Screening of Peptide and Peptidomimetic Fragments Targeted to Inhibit Bacterial Dithiol Oxidase DsbA. PLoS ONE, 2015, 10, e0133805.	2.5	16
92	Rapid Elaboration of Fragments into Leads by X-ray Crystallographic Screening of Parallel Chemical Libraries (REFiL_X). Journal of Medicinal Chemistry, 2020, 63, 6863-6875.	6.4	16
93	Focusing in on structural genomics: The University of Queensland structural biology pipeline. New Biotechnology, 2006, 23, 281-289.	2.7	14
94	Reconciling the regulatory role of Munc18 proteins in SNARE-complex assembly. IUCrJ, 2014, 1, 505-513.	2.2	14
95	The structure of the caspase recruitment domain of BinCARD reveals that all three cysteines can be oxidized. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 774-784.	2.5	13
96	Towards selective lysophospholipid GPCR modulators. Trends in Pharmacological Sciences, 2014, 35, 219-226.	8.7	13
97	Virulence of the Melioidosis Pathogen Burkholderia pseudomallei Requires the Oxidoreductase Membrane Protein DsbB. Infection and Immunity, 2018, 86, .	2.2	13
98	The Î±-Proteobacteria Wolbachia pipientis Protein Disulfide Machinery Has a Regulatory Mechanism Absent in Î³-Proteobacteria. PLoS ONE, 2013, 8, e81440.	2.5	12
99	Life inside and out: making and breaking protein disulfide bonds inChlamydia. Critical Reviews in Microbiology, 2019, 45, 33-50.	6.1	11
100	Crystallization and preliminary diffraction studies of native and selenomethionine CcmG (CycY, DsbE). Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 1293-1295.	2.5	10
101	Interrogating Fragments Using a Protein Thermal Shift Assay. Australian Journal of Chemistry, 2013, 66, 1502.	0.9	10
102	Structural and Biochemical Characterization of Chlamydia trachomatis DsbA Reveals a Cysteine-Rich and Weakly Oxidising Oxidoreductase. PLoS ONE, 2016, 11, e0168485.	2.5	10
103	Crystal structure and site-directed mutagenesis of circular bacteriocin plantacyclin B21AG reveals cationic and aromatic residues important for antimicrobial activity. Scientific Reports, 2020, 10, 17398.	3.3	10
104	Cloning, expression, purification and characterization of a DsbA-like protein from Wolbachia pipientis. Protein Expression and Purification, 2008, 59, 266-273.	1.3	9
105	Modification of recombinatorial cloning for small affinity tag fusion protein construct generation. Analytical Biochemistry, 2005, 346, 327-329.	2.4	8
106	Backbone resonance assignments of the monomeric DUF59 domain of human Fam96a. Biomolecular NMR Assignments, 2013, 7, 117-120.	0.8	8
107	Recombinant expression of Munc18c in a baculovirus system and interaction with syntaxin4. Protein Expression and Purification, 2003, 31, 305-310.	1.3	7
108	Pilot studies on the parallel production of soluble mouse proteins in a bacterial expression system. Journal of Structural and Functional Genomics, 2005, 6, 13-20.	1.2	7

#	Article	IF	Citations
109	The Multidrug Resistance IncA/C Transferable Plasmid Encodes a Novel Domain-swapped Dimeric Protein-disulfide Isomerase. Journal of Biological Chemistry, 2014, 289, 2563-2576.	3.4	7
110	NMR fragment screening reveals a novel small molecule binding site near the catalytic surface of the disulfideâ€“dithiol oxidoreductase enzyme DsbA from Burkholderia pseudomallei. Journal of Biomolecular NMR, 2020, 74, 595-611.	2.8	7
111	Salmonella enterica BcfH Is a Trimeric Thioredoxin-Like Bifunctional Enzyme with Both Thiol Oxidase and Disulfide Isomerase Activities. Antioxidants and Redox Signaling, 2021, 35, 21-39.	5.4	7
112	Crystallization of PNMT, the adrenaline-synthesizing enzyme, is critically dependent on a high protein concentration. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 314-315.	2.5	6
113	A method for screening the temperature dependence of three-dimensional crystal formation. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 559-562.	2.5	6
114	Crystallization of the C-terminal domain of the mouse brain cytosolic long-chain acyl-CoA thioesterase. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 133-135.	0.7	6
115	Crystallization and preliminary X-ray diffraction of the Munc18câ€“syntaxin41â€“29complex. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 524-528.	0.7	5
116	A Medium or High Throughput Protein Refolding Assay. Methods in Molecular Biology, 2008, 426, 269-275.	0.9	5
117	Sent packing: protein engineering generates a new crystal form ofPseudomonas aeruginosaDsbA1 with increased catalytic surface accessibility. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 2386-2395.	2.5	5
118	Engineered variants provide new insight into the structural properties important for activity of the highly dynamic, trimeric protein disulfide isomerase ScsC from Proteus mirabilis. Acta Crystallographica Section D: Structural Biology, 2019, 75, 296-307.	2.3	5
119	Prediction of Burkholderia pseudomallei DsbA substrates identifies potential virulence factors and vaccine targets. PLoS ONE, 2020, 15, e0241306.	2.5	5
120	Disulfide-linked dimers of human adrenaline synthesizing enzyme PNMT are catalytically active. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2005, 1750, 82-92.	2.3	4
121	The atypical thiolâ€“disulfide exchange protein Î±-DsbA2 fromWolbachia pipientisis a homotrimeric disulfide isomerase. Acta Crystallographica Section D: Structural Biology, 2019, 75, 283-295.	2.3	4
122	The nature of the Syntaxin4 C-terminus affects Munc18c-supported SNARE assembly. PLoS ONE, 2017, 12, e0183366.	2.5	4
123	Backbone and side chain 1H, 15N and 13C assignments for the oxidised and reduced forms of the oxidoreductase protein DsbA from Staphylococcus aureus. Biomolecular NMR Assignments, 2010, 4, 25-28.	0.8	3
124	Oxidoreductase disulfide bond proteins DsbA and DsbB form an active redox pair in Chlamydia trachomatis, a bacterium with disulfide dependent infection and development. PLoS ONE, 2019, 14, e0222595.	2.5	3
125	Antivirulence DsbA inhibitors attenuate Salmonella enterica serovar Typhimurium fitness without detectable resistance. FASEB BioAdvances, 2021, 3, 231-242.	2.4	3
126	Milligram Quantities of Homogeneous Recombinant Full-Length Mouse Munc18c from Escherichia coli Cultures. PLoS ONE, 2013, 8, e83499.	2.5	3

#	Article	IF	Citations
127	The suppressor of copper sensitivity protein C from Caulobacter crescentus is a trimeric disulfide isomerase that binds copper(I) with subpicomolar affinity. Acta Crystallographica Section D: Structural Biology, 2022, 78, 337-352.	2.3	3
128	Expression, purification and preliminary X-ray diffraction studies of VERNALIZATION1208â€“341fromArabidopsis thaliana. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 291-294.	0.7	2
129	Revisiting interaction specificity reveals neuronal and adipocyte Munc18 membrane fusion regulatory proteins differ in their binding interactions with partner SNARE Syntaxins. PLoS ONE, 2017, 12, e0187302.	2.5	2
130	Interaction between Plate Make and Protein in Protein Crystallisation Screening. PLoS ONE, 2009, 4, e7851.	2.5	2
131	Identification and characterization of two drug-like fragments that bind to the same cryptic binding pocket of Burkholderia pseudomallei DsbA. Acta Crystallographica Section D: Structural Biology, 2022, 78, 75-90.	2.3	2
132	SEC-uring membrane fusion: a sneak peek at SNARE-complex assembly driven by Sec1â€“Munc18 proteins. Nature Structural and Molecular Biology, 2015, 22, 756-758.	8.2	1
133	Overview of the Pipeline for Structural and Functional Characterization of Macrophage Proteins at the University of Queensland. Methods in Molecular Biology, 2008, 426, 577-587.	0.9	1
134	Studying Munc18:Syntaxin Interactions Using Small-Angle Scattering. Methods in Molecular Biology, 2019, 1860, 115-144.	0.9	0
135	Expression, purification and characterization of the suppressor of copper sensitivity (Scs) B membrane protein from Proteus mirabilis. Protein Expression and Purification, 2022, 193, 106047.	1.3	0