

Cy Mj Jeffries

List of Publications by Year in descending order

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77
papers

4,266
citations

147566

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123241

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83
all docs

83
docs citations

83
times ranked

5785
citing authors

#	ARTICLE	IF	CITATIONS
1	<i>ATSAS 3.0</i>: expanded functionality and new tools for small-angle scattering data analysis. Journal of Applied Crystallography, 2021, 54, 343-355.	1.9	512
2	Versatile sample environments and automation for biological solution X-ray scattering experiments at the P12 beamline (PETRA III, DESY). Journal of Applied Crystallography, 2015, 48, 431-443.	1.9	508
3	SASBDB, a repository for biological small-angle scattering data. Nucleic Acids Research, 2015, 43, D357-D363.	6.5	279
4	Of barn owls and bankers: a lush variety of $\hat{1}\pm\hat{1}^2$ hydrolases. Structure, 1999, 7, R141-R146.	1.6	220
5	Correlation Map, a goodness-of-fit test for one-dimensional X-ray scattering spectra. Nature Methods, 2015, 12, 419-422.	9.0	195
6	SASBDB: Towards an automatically curated and validated repository for biological scattering data. Protein Science, 2020, 29, 66-75.	3.1	158
7	Consensus Bayesian assessment of protein molecular mass from solution X-ray scattering data. Scientific Reports, 2018, 8, 7204.	1.6	154
8	Preparing monodisperse macromolecular samples for successful biological small-angle X-ray and neutron-scattering experiments. Nature Protocols, 2016, 11, 2122-2153.	5.5	142
9	Selection, biophysical and structural analysis of synthetic nanobodies that effectively neutralize SARS-CoV-2. Nature Communications, 2020, 11, 5588.	5.8	132
10	Limiting radiation damage for high-brilliance biological solution scattering: practical experience at the EMBL P12 beamline PETRAIII. Journal of Synchrotron Radiation, 2015, 22, 273-279.	1.0	112
11	Cardiac myosin-binding protein C decorates F-actin: Implications for cardiac function. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 18360-18365.	3.3	107
12	Automated Pipeline for Purification, Biophysical and X-Ray Analysis of Biomacromolecular Solutions. Scientific Reports, 2015, 5, 10734.	1.6	99
13	MICREDOXÂ® development of a ferricyanide-mediated rapid biochemical oxygen demand method using an immobilised Proteus vulgaris biocomponent. Biosensors and Bioelectronics, 2004, 20, 524-532.	5.3	79
14	Small-angle X-ray and neutron scattering. Nature Reviews Methods Primers, 2021, 1, .	11.8	77
15	Effects of Macromolecular Crowding on an Intrinsically Disordered Protein Characterized by Small-Angle Neutron Scattering with Contrast Matching. Biophysical Journal, 2011, 100, 1120-1128.	0.2	71
16	Machine Learning Methods for X-Ray Scattering Data Analysis from Biomacromolecular Solutions. Biophysical Journal, 2018, 114, 2485-2492.	0.2	71
17	Structural Analysis of Influenza A Virus Matrix Protein M1 and Its Self-Assemblies at Low pH. PLoS ONE, 2013, 8, e82431.	1.1	60
18	Small-Angle X-ray Scattering Reveals the N-Terminal Domain Organization of Cardiac Myosin Binding Protein C. Journal of Molecular Biology, 2008, 377, 1186-1199.	2.0	56

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19	Cooperative folding of intrinsically disordered domains drives assembly of a strong elongated protein. <i>Nature Communications</i> , 2015, 6, 7271.	5.8	52
20	The N-Terminal Domains of Myosin Binding Protein C Can Bind Polymorphically to F-Actin. <i>Journal of Molecular Biology</i> , 2011, 412, 379-386.	2.0	50
21	Domain-swap polymerization drives the self-assembly of the bacterial flagellar motor. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 197-203.	3.6	48
22	Adding Size Exclusion Chromatography (SEC) and Light Scattering (LS) Devices to Obtain High-Quality Small Angle X-Ray Scattering (SAXS) Data. <i>Crystals</i> , 2020, 10, 975.	1.0	48
23	Activation of the Retroviral Budding Factor ALIX. <i>Journal of Virology</i> , 2011, 85, 9222-9226.	1.5	47
24	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, 1269-1280.	2.0	46
25	Characterisation of a thermophilic L-glutamate dehydrogenase biosensor for amperometric determination of L-glutamate by flow injection analysis. <i>Biosensors and Bioelectronics</i> , 1999, 14, 171-178.	5.3	43
26	K7del is a common TPM2 gene mutation associated with nemaline myopathy and raised myofibre calcium sensitivity. <i>Brain</i> , 2013, 136, 494-507.	3.7	42
27	Evaluation of a thermophile enzyme for a carbon paste amperometric biosensor: L-glutamate dehydrogenase. <i>Biosensors and Bioelectronics</i> , 1997, 12, 225-232.	5.3	38
28	LIM Domain Binding Proteins 1 and 2 Have Different Oligomeric States. <i>Journal of Molecular Biology</i> , 2010, 399, 133-144.	2.0	38
29	Human Cardiac Myosin Binding Protein C: Structural Flexibility within an Extended Modular Architecture. <i>Journal of Molecular Biology</i> , 2011, 414, 735-748.	2.0	37
30	The CD27L and CTP1L Endolysins Targeting Clostridia Contain a Built-in Trigger and Release Factor. <i>PLoS Pathogens</i> , 2014, 10, e1004228.	2.1	37
31	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, 42971-42980.	1.6	35
32	The COC1 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, 908-913.	2.0	34
33	Competition between LIM-binding domains. <i>Biochemical Society Transactions</i> , 2008, 36, 1393-1397.	1.6	33
34	The Macromolecular Architecture of Extracellular Domain of $\hat{\pm}$ NRXN1: Domain Organization, Flexibility, and Insights into Trans-Synaptic Disposition. <i>Structure</i> , 2010, 18, 1044-1053.	1.6	30
35	Stabilization of a binary protein complex by intein-mediated cyclization. <i>Protein Science</i> , 2006, 15, 2612-2618.	3.1	29
36	Histidine Kinase Regulation by a Cyclophilin-like Inhibitor. <i>Journal of Molecular Biology</i> , 2008, 384, 422-435.	2.0	29

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37	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.	1.6	29
38	Smaller capillaries improve the small-angle X-ray scattering signal and sample consumption for biomacromolecular solutions. <i>Journal of Synchrotron Radiation</i> , 2018, 25, 1113-1122.	1.0	27
39	Insights into herpesvirus assembly from the structure of the pUL7:pUL51 complex. <i>ELife</i> , 2020, 9, .	2.8	27
40	Influenza virus Matrix Protein M1 preserves its conformation with pH, changing multimerization state at the priming stage due to electrostatics. <i>Scientific Reports</i> , 2017, 7, 16793.	1.6	25
41	Structure-Based Identification and Functional Characterization of a Lipocalin in the Malaria Parasite <i>Plasmodium falciparum</i> . <i>Cell Reports</i> , 2020, 31, 107817.	2.9	23
42	A picornaviral loop-to-loop replication complex. <i>Journal of Structural Biology</i> , 2009, 166, 251-262.	1.3	21
43	The modular structure of haemagglutinin/adhesin regions in gingipains of <i>Porphyromonas gingivalis</i> . <i>Molecular Microbiology</i> , 2011, 81, 1358-1373.	1.2	20
44	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, 31596-31607.	1.6	19
45	pUL21 is a viral phosphatase adaptor that promotes herpes simplex virus replication and spread. <i>PLoS Pathogens</i> , 2021, 17, e1009824.	2.1	19
46	Calmodulin Disrupts the Structure of the HIV-1 MA Protein. <i>Journal of Molecular Biology</i> , 2010, 400, 702-714.	2.0	18
47	Structural basis for DNA recognition and allosteric control of the retinoic acid receptors RAR α /RXR. <i>Nucleic Acids Research</i> , 2020, 48, 9969-9985.	6.5	17
48	Rapid screening of <i>in cellulo</i> grown protein crystals via a small-angle X-ray scattering/X-ray powder diffraction synergistic approach. <i>Journal of Applied Crystallography</i> , 2020, 53, 1169-1180.	1.9	17
49	The Shigella Virulence Factor IcsA Relieves N-WASP Autoinhibition by Displacing the Verprolin Homology/Cofilin/Acidic (VCA) Domain. <i>Journal of Biological Chemistry</i> , 2017, 292, 134-145.	1.6	16
50	Hydration in aqueous solutions of ectoine and hydroxyectoine. <i>Physical Chemistry Chemical Physics</i> , 2018, 20, 27917-27923.	1.3	16
51	EFAMIX, a tool to decompose inline chromatography SAXS data from partially overlapping components. <i>Protein Science</i> , 2022, 31, 269-282.	3.1	16
52	Solution structure studies of monomeric human TIP47/perilipin β reveal a highly extended conformation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 2046-2055.	1.5	15
53	Order from disorder in the sarcomere: FATZ forms a fuzzy but tight complex and phase-separated condensates with \pm -actinin. <i>Science Advances</i> , 2021, 7, .	4.7	15
54	Calmodulin Binds a Highly Extended HIV-1 MA Protein That Refolds Upon Its Release. <i>Biophysical Journal</i> , 2012, 103, 541-549.	0.2	13

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55	Sample and Buffer Preparation for SAXS. <i>Advances in Experimental Medicine and Biology</i> , 2017, 1009, 11-30.	0.8	13
56	Functional interaction of low-homology FRPs from different cyanobacteria with <i>Synechocystis</i> OCP. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2018, 1859, 382-393.	0.5	13
57	Comment on the Optimal Parameters to Derive Intrinsically Disordered Protein Conformational Ensembles from Small-Angle X-ray Scattering Data Using the Ensemble Optimization Method. <i>Journal of Chemical Theory and Computation</i> , 2021, 17, 2014-2021.	2.3	13
58	An intrinsically disordered proteins community for ELIXIR. <i>F1000Research</i> , 2019, 8, 1753.	0.8	12
59	Recombinant production of A1S_0222 from <i>Acinetobacter baumannii</i> ATCC 17978 and confirmation of its DNA-(adenine N6)-methyltransferase activity. <i>Protein Expression and Purification</i> , 2018, 151, 78-85.	0.6	11
60	Hydration in aqueous osmolyte solutions: the case of TMAO and urea. <i>Physical Chemistry Chemical Physics</i> , 2020, 22, 11614-11624.	1.3	11
61	The dimeric ectodomain of the alkali-sensing insulin receptor-related receptor (ectoIRR) has a droplike shape. <i>Journal of Biological Chemistry</i> , 2019, 294, 17790-17798.	1.6	10
62	The quaternary structure of insulin glargine and glulisine under formulation conditions. <i>Biophysical Chemistry</i> , 2019, 253, 106226.	1.5	9
63	Expression, purification and crystallization of human kynurenine aminotransferase 2 exploiting a highly optimized codon set. <i>Protein Expression and Purification</i> , 2016, 121, 41-45.	0.6	7
64	Structure of a collagen VI ± 3 chain VWA domain array: adaptability and functional implications of myopathy causing mutations. <i>Journal of Biological Chemistry</i> , 2020, 295, 12755-12771.	1.6	7
65	High-Throughput Studies of Protein Shapes and Interactions by Synchrotron Small-Angle X-Ray Scattering. <i>Methods in Molecular Biology</i> , 2015, 1261, 277-301.	0.4	7
66	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.	1.1	7
67	RovC - a novel type of hexameric transcriptional activator promoting type VI secretion gene expression. <i>PLoS Pathogens</i> , 2020, 16, e1008552.	2.1	6
68	ASAXS measurements on ferritin and apoferritin at the bioSAXS beamline P12 (PETRA III, DESY). <i>Journal of Applied Crystallography</i> , 2021, 54, 830-838.	1.9	6
69	Invited review: Probing the structures of muscle regulatory proteins using small-angle solution scattering. <i>Biopolymers</i> , 2011, 95, 505-516.	1.2	5
70	Interactions between LHX3- and ISL1-family LIM-homeodomain transcription factors are conserved in <i>Caenorhabditis elegans</i> . <i>Scientific Reports</i> , 2017, 7, 4579.	1.6	5
71	Exploring the structure of biological macromolecules in solution using Quokka, the small angle neutron scattering instrument, at ANSTO. <i>Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment</i> , 2015, 798, 44-51.	0.7	4
72	Small-angle X-Ray analysis of macromolecular structure: the structure of protein NS2 (NEP) in solution. <i>Crystallography Reports</i> , 2017, 62, 894-902.	0.1	4

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73	Tetrameric Structures of Inorganic CBS-Pyrophosphatases from Various Bacterial Species Revealed by Small-Angle X-ray Scattering in Solution. <i>Biomolecules</i> , 2020, 10, 564.	1.8	4
74	The basics of small-angle neutron scattering (SANS for new users of structural biology). <i>EPJ Web of Conferences</i> , 2020, 236, 03001.	0.1	3
75	X-Ray Solution Scattering Study of Four <i>Escherichia coli</i> Enzymes Involved in Stationary-Phase Metabolism. <i>PLoS ONE</i> , 2016, 11, e0156105.	1.1	2
76	Anomeric Selectivity of Trehalose Transferase with Rare α -Sugars. <i>ACS Catalysis</i> , 2020, 10, 8835-8839.	5.5	1
77	Recombinant AcnB, NrdR and RibD of <i>Acinetobacter baumannii</i> and their potential interaction with DNA adenine methyltransferase AamA. <i>Protein Expression and Purification</i> , 2022, 199, 106134.	0.6	1