

Cy Mj Jeffries

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77
papers

2,793
citations

29
h-index

52
g-index

83
ext. papers

3,619
ext. citations

6.4
avg, IF

5.3
L-index

#	Paper	IF	Citations
77	Versatile sample environments and automation for biological solution X-ray scattering experiments at the P12 beamline (PETRA III, DESY). <i>Journal of Applied Crystallography</i> , 2015 , 48, 431-443	3.8	350
76	SASBDB, a repository for biological small-angle scattering data. <i>Nucleic Acids Research</i> , 2015 , 43, D357-63	10.1	211
75	Of barn owls and bankers: a lush variety of alpha/beta hydrolases. <i>Structure</i> , 1999 , 7, R141-6	5.2	205
74	Correlation Map, a goodness-of-fit test for one-dimensional X-ray scattering spectra. <i>Nature Methods</i> , 2015 , 12, 419-22	21.6	141
73	: expanded functionality and new tools for small-angle scattering data analysis. <i>Journal of Applied Crystallography</i> , 2021 , 54, 343-355	3.8	120
72	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
71	Preparing monodisperse macromolecular samples for successful biological small-angle X-ray and neutron-scattering experiments. <i>Nature Protocols</i> , 2016 , 11, 2122-2153	18.8	98
70	Limiting radiation damage for high-brilliance biological solution scattering: practical experience at the EMBL P12 beamline PETRAIII. <i>Journal of Synchrotron Radiation</i> , 2015 , 22, 273-9	2.4	92
69	Consensus Bayesian assessment of protein molecular mass from solution X-ray scattering data. <i>Scientific Reports</i> , 2018 , 8, 7204	4.9	82
68	Automated pipeline for purification, biophysical and x-ray analysis of biomacromolecular solutions. <i>Scientific Reports</i> , 2015 , 5, 10734	4.9	77
67	Selection, biophysical and structural analysis of synthetic nanobodies that effectively neutralize SARS-CoV-2. <i>Nature Communications</i> , 2020 , 11, 5588	17.4	73
66	MICREDOX--development of a ferricyanide-mediated rapid biochemical oxygen demand method using an immobilised <i>Proteus vulgaris</i> biocomponent. <i>Biosensors and Bioelectronics</i> , 2004 , 20, 524-32	11.8	68
65	SASBDB: Towards an automatically curated and validated repository for biological scattering data. <i>Protein Science</i> , 2020 , 29, 66-75	6.3	65
64	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
63	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
62	Structural analysis of influenza A virus matrix protein M1 and its self-assemblies at low pH. <i>PLoS ONE</i> , 2013 , 8, e82431	3.7	46
61	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

60	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
59	Domain-swap polymerization drives the self-assembly of the bacterial flagellar motor. <i>Nature Structural and Molecular Biology</i> , 2016 , 23, 197-203	17.6	42
58	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, 171-8	11.8	39
57	Cooperative folding of intrinsically disordered domains drives assembly of a strong elongated protein. <i>Nature Communications</i> , 2015 , 6, 7271	17.4	38
56	Activation of the retroviral budding factor ALIX. <i>Journal of Virology</i> , 2011 , 85, 9222-6	6.6	38
55	Evaluation of a thermophile enzyme for a carbon paste amperometric biosensor: L-glutamate dehydrogenase. <i>Biosensors and Bioelectronics</i> , 1997 , 12, 225-232	11.8	36
54	The CD27L and CTP1L endolysins targeting Clostridia contain a built-in trigger and release factor. <i>PLoS Pathogens</i> , 2014 , 10, e1004228	7.6	34
53	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
52	Machine Learning Methods for X-Ray Scattering Data Analysis from Biomacromolecular Solutions. <i>Biophysical Journal</i> , 2018 , 114, 2485-2492	2.9	33
51	LIM domain binding proteins 1 and 2 have different oligomeric states. <i>Journal of Molecular Biology</i> , 2010 , 399, 133-44	6.5	33
50	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
49	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
48	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, 908-13	6.5	29
47	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
46	Histidine kinase regulation by a cyclophilin-like inhibitor. <i>Journal of Molecular Biology</i> , 2008 , 384, 422-356.5	6.5	26
45	Stabilization of a binary protein complex by intein-mediated cyclization. <i>Protein Science</i> , 2006 , 15, 2612-8.3	6.3	26
44	Competition between LIM-binding domains. <i>Biochemical Society Transactions</i> , 2008 , 36, 1393-7	5.1	24
43	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

42	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	2.4	19
41	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	4.9	17
40	Calmodulin disrupts the structure of the HIV-1 MA protein. <i>Journal of Molecular Biology</i> , 2010 , 400, 702-715	1.5	17
39	A picornaviral loop-to-loop replication complex. <i>Journal of Structural Biology</i> , 2009 , 166, 251-62	3.4	16
38	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	2.3	15
37	Small-angle X-ray and neutron scattering. <i>Nature Reviews Methods Primers</i> , 2021 , 1,		15
36	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
35	The modular structure of haemagglutinin/adhesin regions in gingipains of <i>Porphyromonas gingivalis</i> . <i>Molecular Microbiology</i> , 2011 , 81, 1358-73	4.1	13
34	Insights into herpesvirus assembly from the structure of the pUL7:pUL51 complex. <i>ELife</i> , 2020 , 9,	8.9	13
33	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
32	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	4.6	11
31	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
30	The <i>Shigella</i> 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	5.4	10
29	Structure-Based Identification and Functional Characterization of a Lipocalin in the Malaria Parasite <i>Plasmodium falciparum</i> . <i>Cell Reports</i> , 2020 , 31, 107817	10.6	9
28	Hydration in aqueous solutions of ectoine and hydroxyectoine. <i>Physical Chemistry Chemical Physics</i> , 2018 , 20, 27917-27923	3.6	9
27	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	5.4	8
26	Sample and Buffer Preparation for SAXS. <i>Advances in Experimental Medicine and Biology</i> , 2017 , 1009, 11-30	3.6	8
25	Rapid screening of 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	3.8	8

24	EFAMIX, a tool to decompose inline chromatography SAXS data from partially overlapping components. <i>Protein Science</i> , 2021 ,	6.3	8
23	Expression, purification and crystallization of human kynurenine aminotransferase 2 exploiting a highly optimized codon set. <i>Protein Expression and Purification</i> , 2016 , 121, 41-5	2	7
22	An intrinsically disordered proteins community for ELIXIR. <i>F1000Research</i> , 2019 , 8,	3.6	7
21	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
20	Structural basis for DNA recognition and allosteric control of the retinoic acid receptors RAR-RXR. <i>Nucleic Acids Research</i> , 2020 , 48, 9969-9985	20.1	7
19	The quaternary structure of insulin glargine and glulisine under formulation conditions. <i>Biophysical Chemistry</i> , 2019 , 253, 106226	3.5	6
18	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	1.4	6
17	Hydration in aqueous osmolyte solutions: the case of TMAO and urea. <i>Physical Chemistry Chemical Physics</i> , 2020 , 22, 11614-11624	3.6	5
16	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	2	5
15	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	1.2	4
14	Invited review: probing the structures of muscle regulatory proteins using small-angle solution scattering. <i>Biopolymers</i> , 2011 , 95, 505-16	2.2	4
13	ASAXS measurements on ferritin and apoferritin at the bioSAXS beamline P12 (PETRA III, DESY). <i>Journal of Applied Crystallography</i> , 2021 , 54, 830-838	3.8	4
12	pUL21 is a viral phosphatase adaptor that promotes herpes simplex virus replication and spread. <i>PLoS Pathogens</i> , 2021 , 17, e1009824	7.6	4
11	Small-angle X-Ray analysis of macromolecular structure: the structure of protein NS2 (NEP) in solution. <i>Crystallography Reports</i> , 2017 , 62, 894-902	0.6	3
10	RovC - a novel type of hexameric transcriptional activator promoting type VI secretion gene expression. <i>PLoS Pathogens</i> , 2020 , 16, e1008552	7.6	3
9	Structure of a collagen VI B chain VWA domain array: adaptability and functional implications of myopathy causing mutations. <i>Journal of Biological Chemistry</i> , 2020 , 295, 12755-12771	5.4	3
8	Tetrameric Structures of Inorganic CBS-Pyrophosphatases from Various Bacterial Species Revealed by Small-Angle X-ray Scattering in Solution. <i>Biomolecules</i> , 2020 , 10,	5.9	2
7	Interactions between LHX3- and ISL1-family LIM-homeodomain transcription factors are conserved in <i>Caenorhabditis elegans</i> . <i>Scientific Reports</i> , 2017 , 7, 4579	4.9	2

6	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	6.4	2
5	X-Ray Solution Scattering Study of Four Escherichia coli Enzymes Involved in Stationary-Phase Metabolism. <i>PLoS ONE</i> , 2016 , 11, e0156105	3.7	2
4	The basics of small-angle neutron scattering (SANS for new users of structural biology). <i>EPJ Web of Conferences</i> , 2020 , 236, 03001	0.3	1
3	Anomeric Selectivity of Trehalose Transferase with Rare l-Sugars. <i>ACS Catalysis</i> , 2020 , 10, 8835-8839	13.1	1
2	pUL21 is a viral phosphatase adaptor that promotes herpes simplex virus replication and spread		1
1	Order from disorder in the sarcomere: FATZ forms a fuzzy but tight complex and phase-separated condensates with F-actinin. <i>Science Advances</i> , 2021 , 7,	14.3	1