

# Cy Mj Jeffries

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9578836/publications.pdf>

Version: 2024-02-01

77  
papers

4,266  
citations

147566

31  
h-index

123241

61  
g-index

83  
all docs

83  
docs citations

83  
times ranked

5785  
citing authors

#	ARTICLE	IF	CITATIONS
1	<scp>EFAMIX</scp>, a tool to decompose inline chromatography <scp>SAXS</scp> data from partially overlapping components. Protein Science, 2022, 31, 269-282.	3.1	16
2	Recombinant AcnB, NrdR and RibD of Acinetobacter baumannii and their potential interaction with DNA adenine methyltransferase AamA. Protein Expression and Purification, 2022, 199, 106134.	0.6	1
3	<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
4	Comment on the Optimal Parameters to Derive Intrinsically Disordered Protein Conformational Ensembles from Small-Angle X-ray Scattering Data Using the Ensemble Optimization Method. Journal of Chemical Theory and Computation, 2021, 17, 2014-2021.	2.3	13
5	ASAXS measurements on ferritin and apoferritin at the bioSAXS beamline P12 (PETRA III, DESY). Journal of Applied Crystallography, 2021, 54, 830-838.	1.9	6
6	Order from disorder in the sarcomere: FATZ forms a fuzzy but tight complex and phase-separated condensates with $\hat{\pm}$ -actinin. Science Advances, 2021, 7, .	4.7	15
7	pUL21 is a viral phosphatase adaptor that promotes herpes simplex virus replication and spread. PLoS Pathogens, 2021, 17, e1009824.	2.1	19
8	Small-angle X-ray and neutron scattering. Nature Reviews Methods Primers, 2021, 1, .	11.8	77
9	SASBDB: Towards an automatically curated and validated repository for biological scattering data. Protein Science, 2020, 29, 66-75.	3.1	158
10	Structural basis for DNA recognition and allosteric control of the retinoic acid receptors RAR $\hat{\alpha}$ -RXR. Nucleic Acids Research, 2020, 48, 9969-9985.	6.5	17
11	Structure-Based Identification and Functional Characterization of a Lipocalin in the Malaria Parasite Plasmodium falciparum. Cell Reports, 2020, 31, 107817.	2.9	23
12	The basics of small-angle neutron scattering (SANS for new users of structural biology). EPJ Web of Conferences, 2020, 236, 03001.	0.1	3
13	Anomeric Selectivity of Trehalose Transferase with Rare <scp>l</scp>-Sugars. ACS Catalysis, 2020, 10, 8835-8839.	5.5	1
14	RovC - a novel type of hexameric transcriptional activator promoting type VI secretion gene expression. PLoS Pathogens, 2020, 16, e1008552.	2.1	6
15	Structure of a collagen VI $\hat{\pm}$ 3 chain VWA domain array: adaptability and functional implications of myopathy causing mutations. Journal of Biological Chemistry, 2020, 295, 12755-12771.	1.6	7
16	Adding Size Exclusion Chromatography (SEC) and Light Scattering (LS) Devices to Obtain High-Quality Small Angle X-Ray Scattering (SAXS) Data. Crystals, 2020, 10, 975.	1.0	48
17	Selection, biophysical and structural analysis of synthetic nanobodies that effectively neutralize SARS-CoV-2. Nature Communications, 2020, 11, 5588.	5.8	132
18	Hydration in aqueous osmolyte solutions: the case of TMAO and urea. Physical Chemistry Chemical Physics, 2020, 22, 11614-11624.	1.3	11

#	ARTICLE	IF	CITATIONS
19	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
20	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
21	Insights into herpesvirus assembly from the structure of the pUL7:pUL51 complex. <i>ELife</i> , 2020, 9, .	2.8	27
22	The quaternary structure of insulin glargine and glulisine under formulation conditions. <i>Biophysical Chemistry</i> , 2019, 253, 106226.	1.5	9
23	The dimeric ectodomain of the alkali-sensing insulin receptor-related receptor (ectolRR) has a droplike shape. <i>Journal of Biological Chemistry</i> , 2019, 294, 17790-17798.	1.6	10
24	An intrinsically disordered proteins community for ELIXIR. <i>F1000Research</i> , 2019, 8, 1753.	0.8	12
25	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
26	Hydration in aqueous solutions of ectoine and hydroxyectoine. <i>Physical Chemistry Chemical Physics</i> , 2018, 20, 27917-27923.	1.3	16
27	Recombinant production of AIS_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
28	Consensus Bayesian assessment of protein molecular mass from solution X-ray scattering data. <i>Scientific Reports</i> , 2018, 8, 7204.	1.6	154
29	Machine Learning Methods for X-Ray Scattering Data Analysis from Biomacromolecular Solutions. <i>Biophysical Journal</i> , 2018, 114, 2485-2492.	0.2	71
30	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
31	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.	1.6	16
32	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
33	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
34	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
35	Sample and Buffer Preparation for SAXS. <i>Advances in Experimental Medicine and Biology</i> , 2017, 1009, 11-30.	0.8	13
36	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

#	ARTICLE	IF	CITATIONS
37	Preparing monodisperse macromolecular samples for successful biological small-angle X-ray and neutron-scattering experiments. <i>Nature Protocols</i> , 2016, 11, 2122-2153.	5.5	142
38	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
39	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
40	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
41	SASBDB, a repository for biological small-angle scattering data. <i>Nucleic Acids Research</i> , 2015, 43, D357-D363.	6.5	279
42	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
43	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, 273-279.	1.0	112
44	Automated Pipeline for Purification, Biophysical and X-Ray Analysis of Biomacromolecular Solutions. <i>Scientific Reports</i> , 2015, 5, 10734.	1.6	99
45	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.	1.9	508
46	Correlation Map, a goodness-of-fit test for one-dimensional X-ray scattering spectra. <i>Nature Methods</i> , 2015, 12, 419-422.	9.0	195
47	Cooperative folding of intrinsically disordered domains drives assembly of a strong elongated protein. <i>Nature Communications</i> , 2015, 6, 7271.	5.8	52
48	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
49	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
50	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
51	Structural Analysis of Influenza A Virus Matrix Protein M1 and Its Self-Assemblies at Low pH. <i>PLoS ONE</i> , 2013, 8, e82431.	1.1	60
52	The Motif of Human Cardiac Myosin-binding Protein C Is Required for Its Ca <sup>2+</sup> -dependent Interaction with Calmodulin. <i>Journal of Biological Chemistry</i> , 2012, 287, 31596-31607.	1.6	19
53	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
54	Solution structure studies of monomeric human TIP47/perilipin <sup>3</sup> reveal a highly extended conformation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 2046-2055.	1.5	15

#	ARTICLE	IF	CITATIONS
55	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
56	Effects of Macromolecular Crowding on an Intrinsically Disordered Protein Characterized by Small-Angle Neutron Scattering with Contrast Matching. <i>Biophysical Journal</i> , 2011, 100, 1120-1128.	0.2	71
57	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
58	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
59	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
60	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
61	Invited review: Probing the structures of muscle regulatory proteins using small-angle solution scattering. <i>Biopolymers</i> , 2011, 95, 505-516.	1.2	5
62	Activation of the Retroviral Budding Factor ALIX. <i>Journal of Virology</i> , 2011, 85, 9222-9226.	1.5	47
63	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
64	The Macromolecular Architecture of Extracellular Domain of $\beta$ -NRXN1: Domain Organization, Flexibility, and Insights into Trans-Synaptic Disposition. <i>Structure</i> , 2010, 18, 1044-1053.	1.6	30
65	LIM Domain Binding Proteins 1 and 2 Have Different Oligomeric States. <i>Journal of Molecular Biology</i> , 2010, 399, 133-144.	2.0	38
66	Calmodulin Disrupts the Structure of the HIV-1 MA Protein. <i>Journal of Molecular Biology</i> , 2010, 400, 702-714.	2.0	18
67	A picornaviral loop-to-loop replication complex. <i>Journal of Structural Biology</i> , 2009, 166, 251-262.	1.3	21
68	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, 1186-1199.	2.0	56
69	Histidine Kinase Regulation by a Cyclophilin-like Inhibitor. <i>Journal of Molecular Biology</i> , 2008, 384, 422-435.	2.0	29
70	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, 18360-18365.	3.3	107
71	Competition between LIM-binding domains. <i>Biochemical Society Transactions</i> , 2008, 36, 1393-1397.	1.6	33
72	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

#	ARTICLE	IF	CITATIONS
73	Stabilization of a binary protein complex by intein-mediated cyclization. <i>Protein Science</i> , 2006, 15, 2612-2618.	3.1	29
74	MICREDOX <sup>®</sup> 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, 524-532.	5.3	79
75	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
76	Of barn owls and bankers: a lush variety of $\beta$ hydrolases. <i>Structure</i> , 1999, 7, R141-R146.	1.6	220
77	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