

# Lee Makowski

## List of Publications by Year in descending order

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Version: 2024-02-01

57  
papers

1,894  
citations

279798  
23  
h-index

265206  
42  
g-index

59  
all docs

59  
docs citations

59  
times ranked

2755  
citing authors

#	ARTICLE	IF	CITATIONS
1	Screening of a library of phage-displayed peptides identifies human Bcl-2 as a taxol-binding protein 1 Edited by I. A. Wilson. Journal of Molecular Biology, 1999, 285, 197-203.	4.2	231
2	Multidomain assembled states of Hck tyrosine kinase in solution. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 15757-15762.	7.1	195
3	A Rapid Coarse Residue-Based Computational Method for X-Ray Solution Scattering Characterization of Protein Folds and Multiple Conformational States of Large Protein Complexes. Biophysical Journal, 2009, 96, 4449-4463.	0.5	117
4	Simulated x-ray scattering of protein solutions using explicit-solvent models. Journal of Chemical Physics, 2009, 130, 134114.	3.0	113
5	RELIC – A bioinformatics server for combinatorial peptide analysis and identification of protein–ligand interaction sites. Proteomics, 2004, 4, 1439-1460.	2.2	109
6	Molecular Crowding Inhibits Intramolecular Breathing Motions in Proteins. Journal of Molecular Biology, 2008, 375, 529-546.	4.2	86
7	Differential Enzyme Flexibility Probed Using Solid-State Nanopores. ACS Nano, 2018, 12, 4494-4502.	14.6	83
8	Biological and Clinical Consequences of Integrin Binding via a Rogue RGD Motif in the SARS CoV-2 Spike Protein. Viruses, 2021, 13, 146.	3.3	74
9	The Structure of the Catalytic Domain of a Plant Cellulose Synthase and Its Assembly into Dimers. Plant Cell, 2014, 26, 2996-3009.	6.6	61
10	SoftWAXS: a computational tool for modeling wide-angle X-ray solution scattering from biomolecules. Journal of Applied Crystallography, 2009, 42, 932-943.	4.5	60
11	High-resolution wide-angle X-ray scattering of protein solutions: effect of beam dose on protein integrity. Journal of Synchrotron Radiation, 2003, 10, 398-404.	2.4	57
12	Amyloid structure exhibits polymorphism on multiple length scales in human brain tissue. Scientific Reports, 2016, 6, 33079.	3.3	48
13	Characterization of proteins with wide-angle X-ray solution scattering (WAXS). Journal of Structural and Functional Genomics, 2010, 11, 9-19.	1.2	47
14	Multi-scale processes of beech wood disintegration and pretreatment with 1-ethyl-3-methylimidazolium acetate/water mixtures. Biotechnology for Biofuels, 2016, 9, 7.	6.2	42
15	Phage Display Reveals Multiple Contact Sites between FhuA, an Outer Membrane Receptor of Escherichia coli, and TonB. Journal of Molecular Biology, 2006, 357, 236-251.	4.2	40
16	The impact of alterations in lignin deposition on cellulose organization of the plant cell wall. Biotechnology for Biofuels, 2016, 9, 126.	6.2	40
17	Raf promotes dimerization of the Ras G-domain with increased allosteric connections. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	39
18	Characterization of Protein Fold by Wide-Angle X-ray Solution Scattering. Journal of Molecular Biology, 2008, 383, 731-744.	4.2	38

#	ARTICLE	IF	CITATIONS
19	Overcoming cellulose recalcitrance in woody biomass for the lignin-first biorefinery. <i>Biotechnology for Biofuels</i> , 2019, 12, 171.	6.2	37
20	Large-scale motions in the adenylate kinase solution ensemble: Coarse-grained simulations and comparison with solution X-ray scattering. <i>Chemical Physics</i> , 2012, 396, 84-91.	1.9	32
21	X-ray solution scattering studies of the structural diversity intrinsic to protein ensembles. <i>Biopolymers</i> , 2011, 95, 531-542.	2.4	30
22	Multiscale deconstruction of molecular architecture in corn stover. <i>Scientific Reports</i> , 2014, 4, 3756.	3.3	30
23	The Structural Basis of the Farnesylated and Methylated KRas4B Interaction with Calmodulin. <i>Structure</i> , 2019, 27, 1647-1659.e4.	3.3	30
24	Myelin Organization in the Nodal, Paranodal, and Juxtaparanodal Regions Revealed by Scanning X-Ray Microdiffraction. <i>PLoS ONE</i> , 2014, 9, e100592.	2.5	24
25	Enhanced rates of enzymatic saccharification and catalytic synthesis of biofuel substrates in gelatinized cellulose generated by trifluoroacetic acid. <i>Biotechnology for Biofuels</i> , 2017, 10, 310.	6.2	23
26	Wide-Angle X-Ray Solution Scattering for Protein-Ligand Binding: Multivariate Curve Resolution with Bayesian Confidence Intervals. <i>Biophysical Journal</i> , 2013, 104, 873-883.	0.5	21
27	Cell wall targeted <i>in planta</i> iron accumulation enhances biomass conversion and seed iron concentration in <i>Arabidopsis</i> and rice. <i>Plant Biotechnology Journal</i> , 2016, 14, 1998-2009.	8.3	19
28	Utility of Solution X-Ray Scattering for the Development of Antibody Biopharmaceuticals. <i>Journal of Pharmaceutical Sciences</i> , 2016, 105, 3278-3289.	3.3	17
29	Fine structure of conformational ensembles in adenylate kinase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 332-343.	2.6	14
30	Effects of Catalytic Action and Ligand Binding on Conformational Ensembles of Adenylate Kinase. <i>Biochemistry</i> , 2017, 56, 4559-4567.	2.5	13
31	Detection of Functional Ligand-Binding Events Using Synchrotron X-Ray Scattering. <i>Journal of Biomolecular Screening</i> , 2007, 12, 994-998.	2.6	12
32	Flow-aligned, single-shot fiber diffraction using a femtosecond X-ray free-electron laser. <i>Cytoskeleton</i> , 2017, 74, 472-481.	2.0	12
33	Diffraction pattern simulation of cellulose fibrils using distributed and quantized pair distances. <i>Journal of Applied Crystallography</i> , 2016, 49, 2244-2248.	4.5	11
34	Constrained Maximum Likelihood Estimation of Relative Abundances of Protein Conformation in a Heterogeneous Mixture From Small Angle X-Ray Scattering Intensity Measurements. <i>IEEE Transactions on Signal Processing</i> , 2015, 63, 5383-5394.	5.3	10
35	The Structural Basis of Amyloid Strains in Alzheimer's Disease. <i>ACS Biomaterials Science and Engineering</i> , 2020, 6, 2498-2505.	5.2	9
36	Breakdown of hierarchical architecture in cellulose during dilute acid pretreatments. <i>Cellulose</i> , 2015, 22, 1495-1504.	4.9	8

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37	c-Abl Tyrosine Kinase Adopts Multiple Active Conformational States in Solution. <i>Biochemistry</i> , 2016, 55, 3251-3260.	2.5	8
38	Calculation of the cross-sectional shape of a fibril from equatorial scattering. <i>Journal of Structural Biology</i> , 2017, 200, 248-257.	2.8	7
39	A Central Region of NF- $\kappa$ B Essential Modulator Is Required for IKK $\beta$ -Induced Conformational Change and for Signal Propagation. <i>Biochemistry</i> , 2019, 58, 2906-2920.	2.5	7
40	Learning Environments and Evidence-Based Practices in Bioengineering and Biomedical Engineering. <i>Biomedical Engineering Education</i> , 2022, 2, 1-16.	0.7	6
41	Modulation of HIV protease flexibility by the T80N mutation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 1929-1939.	2.6	5
42	Visualizing global properties of a molecular dynamics trajectory. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 82-91.	2.6	5
43	What Can We Learn from Wide-Angle Solution Scattering?. <i>Advances in Experimental Medicine and Biology</i> , 2017, 1009, 131-147.	1.6	5
44	Probing remote residues important for catalysis in Escherichia coli ornithine transcarbamoylase. <i>PLoS ONE</i> , 2020, 15, e0228487.	2.5	4
45	Scanning x-ray microdiffraction: In situ molecular imaging of tissue and materials. <i>Current Opinion in Structural Biology</i> , 2022, 75, 102421.	5.7	4
46	Predicting X-ray solution scattering from flexible macromolecules. <i>Protein Science</i> , 2018, 27, 2023-2036.	7.6	3
47	Glycine substitution in SH3-SH2 connector of Hck tyrosine kinase causes population shift from assembled to disassembled state. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2020, 1864, 129604.	2.4	3
48	Fast simulation of X-ray diffraction patterns from cellulose fibrils using GPUs. , 2014, , .		1
49	A framework to optimize protein structure from solution scattering using ADMM and an elastic subdomain network. , 2016, , .		1
50	Cover Image, Volume 86, Issue 3. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, C1.	2.6	1
51	Dirichlet Priors for MAP Inference of Protein Conformation Abundances from SAXS. <i>Journal of Signal Processing Systems</i> , 2018, 90, 167-174.	2.1	1
52	A new pre-processing method for scanning X-ray microdiffraction patterns. , 2015, , .		0
53	FiXR: a framework to reconstruct fiber cross-sections from X-ray fiber diffraction experiments. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 102-117.	2.3	0
54	A Simplified Adult Expiratory Support Device: First Clinical Cases in a Low-Resource Setting. <i>Annals of Thoracic Surgery</i> , 2022, 113, 1021-1025.	1.3	0

#	ARTICLE	IF	CITATIONS
55	Tailoring Biomass for Biochemical, Chemical or Thermochemical Catalytic Conversion. FASEB Journal, 2015, 29, 485.3.	0.5	0
56	Wideâ€Angle Xâ€ray Solution Scattering Studies of Slow Correlated Motions in Proteins. FASEB Journal, 2015, 29, 712.17.	0.5	0
57	Characterizing Conformational Ensemble of Hâ€, Kâ€, and Nâ€Ras Using Accelerated Molecular Dynamics and Wideâ€Angle Xâ€ray Solution Scattering (WAXS). FASEB Journal, 2016, 30, 1116.4.	0.5	0