

Lee Makowski

List of Publications by Year in descending order

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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	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
2	Learning Environments and Evidence-Based Practices in Bioengineering and Biomedical Engineering. <i>Biomedical Engineering Education</i> , 2022, 2, 1-16.	0.7	6
3	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
4	Biological and Clinical Consequences of Integrin Binding via a Rogue RGD Motif in the SARS CoV-2 Spike Protein. <i>Viruses</i> , 2021, 13, 146.	3.3	74
5	Raf promotes dimerization of the Ras G-domain with increased allosteric connections. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	39
6	The Structural Basis of Amyloid Strains in Alzheimer's Disease. <i>ACS Biomaterials Science and Engineering</i> , 2020, 6, 2498-2505.	5.2	9
7	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
8	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
9	Probing remote residues important for catalysis in Escherichia coli ornithine transcarbamoylase. <i>PLoS ONE</i> , 2020, 15, e0228487.	2.5	4
10	Overcoming cellulose recalcitrance in woody biomass for the lignin-first biorefinery. <i>Biotechnology for Biofuels</i> , 2019, 12, 171.	6.2	37
11	The Structural Basis of the Farnesylated and Methylated KRas4B Interaction with Calmodulin. <i>Structure</i> , 2019, 27, 1647-1659.e4.	3.3	30
12	A Central Region of NF- κ B Essential Modulator Is Required for IKK β -Induced Conformational Change and for Signal Propagation. <i>Biochemistry</i> , 2019, 58, 2906-2920.	2.5	7
13	Differential Enzyme Flexibility Probed Using Solid-State Nanopores. <i>ACS Nano</i> , 2018, 12, 4494-4502.	14.6	83
14	Fine structure of conformational ensembles in adenylate kinase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 332-343.	2.6	14
15	Cover Image, Volume 86, Issue 3. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, C1.	2.6	1
16	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
17	Predicting X-ray solution scattering from flexible macromolecules. <i>Protein Science</i> , 2018, 27, 2023-2036.	7.6	3
18	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

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19	Flow-aligned, single-shot fiber diffraction using a femtosecond X-ray free-electron laser. <i>Cytoskeleton</i> , 2017, 74, 472-481.	2.0	12
20	Effects of Catalytic Action and Ligand Binding on Conformational Ensembles of Adenylate Kinase. <i>Biochemistry</i> , 2017, 56, 4559-4567.	2.5	13
21	What Can We Learn from Wide-Angle Solution Scattering?. <i>Advances in Experimental Medicine and Biology</i> , 2017, 1009, 131-147.	1.6	5
22	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
23	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
24	Amyloid structure exhibits polymorphism on multiple length scales in human brain tissue. <i>Scientific Reports</i> , 2016, 6, 33079.	3.3	48
25	Cell wall targeted 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
26	Visualizing global properties of a molecular dynamics trajectory. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 82-91.	2.6	5
27	The impact of alterations in lignin deposition on cellulose organization of the plant cell wall. <i>Biotechnology for Biofuels</i> , 2016, 9, 126.	6.2	40
28	A framework to optimize protein structure from solution scattering using ADMM and an elastic subdomain network. , 2016, , .		1
29	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
30	c-Abl Tyrosine Kinase Adopts Multiple Active Conformational States in Solution. <i>Biochemistry</i> , 2016, 55, 3251-3260.	2.5	8
31	Multi-scale processes of beech wood disintegration and pretreatment with 1-ethyl-3-methylimidazolium acetate/water mixtures. <i>Biotechnology for Biofuels</i> , 2016, 9, 7.	6.2	42
32	Characterizing Conformational Ensemble of H α , K α , and N α Ras Using Accelerated Molecular Dynamics and Wide-Angle X-ray Solution Scattering (WAXS). <i>FASEB Journal</i> , 2016, 30, 1116.4.	0.5	0
33	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
34	A new pre-processing method for scanning X-ray microdiffraction patterns. , 2015, , .		0
35	Breakdown of hierarchical architecture in cellulose during dilute acid pretreatments. <i>Cellulose</i> , 2015, 22, 1495-1504.	4.9	8
36	Modulation of HIV protease flexibility by the T80N mutation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 1929-1939.	2.6	5

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37	Tailoring Biomass for Biochemical, Chemical or Thermochemical Catalytic Conversion. FASEB Journal, 2015, 29, 485.3.	0.5	0
38	Wide-Angle X-Ray Solution Scattering Studies of Slow Correlated Motions in Proteins. FASEB Journal, 2015, 29, 712.17.	0.5	0
39	Myelin Organization in the Nodal, Paranodal, and Juxtaparanodal Regions Revealed by Scanning X-Ray Microdiffraction. PLoS ONE, 2014, 9, e100592.	2.5	24
40	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
41	Fast simulation of X-ray diffraction patterns from cellulose fibrils using GPUs. , 2014, , .		1
42	Multiscale deconstruction of molecular architecture in corn stover. Scientific Reports, 2014, 4, 3756.	3.3	30
43	Wide-Angle X-Ray Solution Scattering for Protein-Ligand Binding: Multivariate Curve Resolution with Bayesian Confidence Intervals. Biophysical Journal, 2013, 104, 873-883.	0.5	21
44	Large-scale motions in the adenylate kinase solution ensemble: Coarse-grained simulations and comparison with solution X-ray scattering. Chemical Physics, 2012, 396, 84-91.	1.9	32
45	X-ray solution scattering studies of the structural diversity intrinsic to protein ensembles. Biopolymers, 2011, 95, 531-542.	2.4	30
46	Characterization of proteins with wide-angle X-ray solution scattering (WAXS). Journal of Structural and Functional Genomics, 2010, 11, 9-19.	1.2	47
47	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
48	Simulated x-ray scattering of protein solutions using explicit-solvent models. Journal of Chemical Physics, 2009, 130, 134114.	3.0	113
49	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
50	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
51	Molecular Crowding Inhibits Intramolecular Breathing Motions in Proteins. Journal of Molecular Biology, 2008, 375, 529-546.	4.2	86
52	Characterization of Protein Fold by Wide-Angle X-ray Solution Scattering. Journal of Molecular Biology, 2008, 383, 731-744.	4.2	38
53	Detection of Functional Ligand-Binding Events Using Synchrotron X-Ray Scattering. Journal of Biomolecular Screening, 2007, 12, 994-998.	2.6	12
54	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

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55	RELIC – A bioinformatics server for combinatorial peptide analysis and identification of protein–ligand interaction sites. <i>Proteomics</i> , 2004, 4, 1439-1460.	2.2	109
56	High-resolution wide-angle X-ray scattering of protein solutions: effect of beam dose on protein integrity. <i>Journal of Synchrotron Radiation</i> , 2003, 10, 398-404.	2.4	57
57	Screening of a library of phage-displayed peptides identifies human Bcl-2 as a taxol-binding protein 1 Edited by I. A. Wilson. <i>Journal of Molecular Biology</i> , 1999, 285, 197-203.	4.2	231