

Matthew L Baker

List of Publications by Year in descending order

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Version: 2024-02-01

40
papers

6,864
citations

257450

24
h-index

315739

38
g-index

47
all docs

47
docs citations

47
times ranked

10212
citing authors

#	ARTICLE	IF	CITATIONS
1	Macromolecular structure determination using X-rays, neutrons and electrons: recent developments in <i>Phenix</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 861-877.	2.3	4,060
2	Common Ancestry of Herpesviruses and Tailed DNA Bacteriophages. <i>Journal of Virology</i> , 2005, 79, 14967-14970.	3.4	245
3	EMDataBank unified data resource for 3DEM. <i>Nucleic Acids Research</i> , 2016, 44, D396-D403.	14.5	230
4	Gating machinery of InsP3R channels revealed by electron cryomicroscopy. <i>Nature</i> , 2015, 527, 336-341.	27.8	199
5	Identification of Secondary Structure Elements in Intermediate-Resolution Density Maps. <i>Structure</i> , 2007, 15, 7-19.	3.3	188
6	Locoregional delivery of CAR T cells to the cerebrospinal fluid for treatment of metastatic medulloblastoma and ependymoma. <i>Nature Medicine</i> , 2020, 26, 720-731.	30.7	141
7	Electron cryomicroscopy and bioinformatics suggest protein fold models for rice dwarf virus. <i>Nature Structural Biology</i> , 2001, 8, 868-873.	9.7	125
8	TEM8/ANTXR1-Specific CAR T Cells as a Targeted Therapy for Triple-Negative Breast Cancer. <i>Cancer Research</i> , 2018, 78, 489-500.	0.9	122
9	CAR T-cells that target acute B-lineage leukemia irrespective of CD19 expression. <i>Leukemia</i> , 2021, 35, 75-89.	7.2	107
10	An atomic model of brome mosaic virus using direct electron detection and real-space optimization. <i>Nature Communications</i> , 2014, 5, 4808.	12.8	105
11	Modeling protein structure at near atomic resolutions with Gorgon. <i>Journal of Structural Biology</i> , 2011, 174, 360-373.	2.8	86
12	Cryo-EM of macromolecular assemblies at near-atomic resolution. <i>Nature Protocols</i> , 2010, 5, 1697-1708.	12.0	79
13	Cryo-EM model validation recommendations based on outcomes of the 2019 EMDataResource challenge. <i>Nature Methods</i> , 2021, 18, 156-164.	19.0	73
14	Validated near-atomic resolution structure of bacteriophage epsilon15 derived from cryo-EM and modeling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 12301-12306.	7.1	68
15	De Novo modeling in cryo-EM density maps with Pathwalking. <i>Journal of Structural Biology</i> , 2016, 196, 289-298.	2.8	68
16	The skeletal muscle Ca ²⁺ release channel has an oxidoreductase-like domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 12155-12160.	7.1	60
17	Ab Initio Modeling of the Herpesvirus VP26 Core Domain Assessed by CryoEM Density. <i>PLoS Computational Biology</i> , 2006, 2, e146.	3.2	54
18	Cryo-EM reveals ligand induced allostery underlying InsP3R channel gating. <i>Cell Research</i> , 2018, 28, 1158-1170.	12.0	48

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19	Automated segmentation of molecular subunits in electron cryomicroscopy density maps. <i>Journal of Structural Biology</i> , 2006, 156, 432-441.	2.8	47
20	Gorgon and pathwalking: Macromolecular modeling tools for subnanometer resolution density maps. <i>Biopolymers</i> , 2012, 97, 655-668.	2.4	45
21	Rotavirus Cell Entry. <i>Current Topics in Microbiology and Immunology</i> , 2010, 343, 121-148.	1.1	37
22	A homing system targets therapeutic T cells to brain cancer. <i>Nature</i> , 2018, 561, 331-337.	27.8	36
23	Architecture of the Herpes Simplex Virus Major Capsid Protein Derived from Structural Bioinformatics. <i>Journal of Molecular Biology</i> , 2003, 331, 447-456.	4.2	30
24	In situ structure of the AcrAB-TolC efflux pump at subnanometer resolution. <i>Structure</i> , 2022, 30, 107-113.e3.	3.3	28
25	Analyses of Subnanometer Resolution Cryo-EM Density Maps. <i>Methods in Enzymology</i> , 2010, 483, 1-29.	1.0	22
26	Protruding knob-like proteins violate local symmetries in an icosahedral marine virus. <i>Nature Communications</i> , 2014, 5, 4278.	12.8	21
27	Domain Organization and Conformational Plasticity of the G Protein Effector, PDE6. <i>Journal of Biological Chemistry</i> , 2015, 290, 12833-12843.	3.4	18
28	Adaptive thermogenesis enhances the life-threatening response to heat in mice with an Ryr1 mutation. <i>Nature Communications</i> , 2020, 11, 5099.	12.8	16
29	Flexible Fitting of Atomic Models into Cryo-EM Density Maps Guided by Helix Correspondences. <i>Biophysical Journal</i> , 2017, 112, 2479-2493.	0.5	13
30	Automation and assessment of de novo modeling with Pathwalking in near atomic resolution cryoEM density maps. <i>Journal of Structural Biology</i> , 2018, 204, 555-563.	2.8	13
31	AlphaFold2 and CryoEM: Revisiting CryoEM modeling in near-atomic resolution density maps. <i>IScience</i> , 2022, 25, 104496.	4.1	13
32	Targeting CD19-negative relapsed B-acute lymphoblastic leukemia using trivalent CAR T cells. <i>Journal of Clinical Oncology</i> , 2018, 36, 121-121.	1.6	8
33	Beyond the Backbone: The Next Generation of Pathwalking Utilities for Model Building in CryoEM Density Maps. <i>Biomolecules</i> , 2022, 12, 773.	4.0	6
34	Graph-based deformable matching of 3D line with application in protein fitting. <i>Visual Computer</i> , 2015, 31, 967-977.	3.5	5
35	Building and Validating Atomic Models for Cryo-EM Density Maps. <i>Microscopy and Microanalysis</i> , 2016, 22, 2080-2081.	0.4	1
36	Cryo-EM and Mass Spectrometry Based Investigations of Viral Capsid Morphogenesis. <i>Microscopy and Microanalysis</i> , 2004, 10, 226-227.	0.4	0

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37	Modeling Protein Structure in Macromolecular Assemblies at Near Atomic Resolutions. <i>Microscopy and Microanalysis</i> , 2015, 21, 541-542.	0.4	0
38	IP3R1 - Assessing Map Interpretability at Near Atomic Resolution. <i>Microscopy and Microanalysis</i> , 2015, 21, 543-544.	0.4	0
39	Rocking Motion of the Equatorial Domains of a Group II Chaperonin between Two Biochemical States Revealed by Single-Particle Cryo-EM at Near-atomic and Subnanometer Resolutions. <i>FASEB Journal</i> , 2009, 23, 673.12.	0.5	0
40	4.0 Å... Resolution Cryo-EM Structure of the Mammalian Chaperonin TRiC/CCT Reveals its Unique Subunit Arrangement. <i>FASEB Journal</i> , 2010, 24, 684.5.	0.5	0