

Nigel W Moriarty

List of Publications by Year in descending order

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76
papers

45,342
citations

101543

36
h-index

98798

67
g-index

82
all docs

82
docs citations

82
times ranked

47385
citing authors

#	ARTICLE	IF	CITATIONS
1	A radical approach to radicals. <i>Acta Crystallographica Section D: Structural Biology</i> , 2022, 78, 43-51.	2.3	0
2	XFEL serial crystallography reveals the room temperature structure of methyl-coenzyme M reductase. <i>Journal of Inorganic Biochemistry</i> , 2022, 230, 111768.	3.5	6
3	PDBx/mmCIF Ecosystem: Foundational Semantic Tools for Structural Biology. <i>Journal of Molecular Biology</i> , 2022, 434, 167599.	4.2	39
4	Reply to Wang et al.: Clear evidence of binding of O _x to the oxygen-evolving complex of photosystem II is best observed in the omit map. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, e2102342118.	7.1	7
5	Macromolecular refinement of X-ray and cryoelectron microscopy structures with Phenix/OPLS3e for improved structure and ligand quality. <i>Structure</i> , 2021, 29, 913-921.e4.	3.3	29
6	Cryo-EM structure of the <i>Rhodospirillum rubrum</i> RC-LH1 complex at 2.5 Å. <i>Biochemical Journal</i> , 2021, 478, 3253-3263.	3.7	23
7	CERES: a cryo-EM re-refinement system for continuous improvement of deposited models. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 48-61.	2.3	14
8	Room temperature XFEL crystallography reveals asymmetry in the vicinity of the two phylloquinones in photosystem I. <i>Scientific Reports</i> , 2021, 11, 21787.	3.3	11
9	Structural dynamics in the water and proton channels of photosystem II during the S ₂ to S ₃ transition. <i>Nature Communications</i> , 2021, 12, 6531.	12.8	73
10	A Global Ramachandran Score Identifies Protein Structures with Unlikely Stereochemistry. <i>Structure</i> , 2020, 28, 1249-1258.e2.	3.3	86
11	What are the current limits on determination of protonation state using neutron macromolecular crystallography?. <i>Methods in Enzymology</i> , 2020, 634, 225-255.	1.0	0
12	Untangling the sequence of events during the S ₂ → S ₃ transition in photosystem II and implications for the water oxidation mechanism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 12624-12635.	7.1	149
13	Including crystallographic symmetry in quantum-based refinement: Q R ² . <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 41-50.	2.3	13
14	Improved chemistry restraints for crystallographic refinement by integrating the Amber force field into Phenix. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 51-62.	2.3	29
15	Real-space quantum-based refinement for cryo-EM: Q R ³ . <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 1184-1191.	2.3	7
16	Arginine off-kilter: guanidinium is not as planar as restraints denote. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 1159-1166.	2.3	7
17	Cryo_fit: Democratization of flexible fitting for cryo-EM. <i>Journal of Structural Biology</i> , 2019, 208, 1-6.	2.8	30
18	Announcing mandatory submission of PDBx/mmCIF format files for crystallographic depositions to the Protein Data Bank (PDB). <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 451-454.	2.3	46

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19	Iron–sulfur clusters have no right angles. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 16-20.	2.3	16
20	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
21	Updated validation and deposition tools in the <i>Phenix</i> GUI. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2019, 75, a339-a339.	0.1	0
22	Accurate geometries for “Mountain pass” regions of the Ramachandran plot using quantum chemical calculations. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 273-278.	2.6	7
23	<i>DiSCaMB</i> : a software library for aspherical atom model X-ray scattering factor calculations with CPUs and GPUs. <i>Journal of Applied Crystallography</i> , 2018, 51, 193-199.	4.5	24
24	Interactive comparison and remediation of collections of macromolecular structures. <i>Protein Science</i> , 2018, 27, 182-194.	7.6	13
25	MolProbity: More and better reference data for improved all-atom structure validation. <i>Protein Science</i> , 2018, 27, 293-315.	7.6	2,776
26	Structures of the intermediates of Kok’s photosynthetic water oxidation clock. <i>Nature</i> , 2018, 563, 421-425.	27.8	386
27	Improved chemistry restraints for crystallographic refinement by integrating Amber molecular mechanics in <i>Phenix</i> . <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2018, 74, a145-a145.	0.1	2
28	Evaluation of models determined by neutron diffraction and proposed improvements to their validation and deposition. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 800-813.	2.3	15
29	New tools for the analysis and validation of cryo-EM maps and atomic models. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 814-840.	2.3	575
30	Polder maps: improving OMIT maps for ligand building and validation. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2018, 74, a308-a308.	0.1	0
31	High-throughput protein–ligand complex structure solution with <i>Phenix</i> . <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2018, 74, a445-a445.	0.1	0
32	Polder maps: improving OMIT maps for ligand building and validation. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2017, 73, C48-C48.	0.1	0
33	Polder maps: improving OMIT maps by excluding bulk solvent. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 148-157.	2.3	500
34	Solving the scalability issue in quantum-based refinement: Q R#1. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 1020-1028.	2.3	20
35	An editor for the generation and customization of geometry restraints. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 123-130.	2.3	27
36	Video tutorials for the <i>Phenix</i> software suite. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2017, 73, C1134-C1134.	0.1	0

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37	Structure of photosystem II and substrate binding at room temperature. <i>Nature</i> , 2016, 540, 453-457.	27.8	323
38	A new default restraint library for the protein backbone in <i>Phenix</i> : a conformation-dependent geometry goes mainstream. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 176-179.	2.3	39
39	Improved ligand geometries in crystallographic refinement using <i>AFITT</i> in <i>PHENIX</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 1062-1072.	2.3	29
40	FEM: feature-enhanced map. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 646-666.	2.5	157
41	Azasugar inhibitors as pharmacological chaperones for Krabbe disease. <i>Chemical Science</i> , 2015, 6, 3075-3086.	7.4	42
42	Structural and Biochemical Studies of Actin in Complex with Synthetic Macrolide Tail Analogues. <i>ChemMedChem</i> , 2014, 9, 2286-2293.	3.2	20
43	Conformation-dependent backbone geometry restraints set a new standard for protein crystallographic refinement. <i>FEBS Journal</i> , 2014, 281, 4061-4071.	4.7	36
44	Automating crystallographic structure solution and refinement of protein-ligand complexes. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 144-154.	2.5	43
45	Ligand placement based on prior structures: the guided ligand-replacement method. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 134-143.	2.5	11
46	Flexible torsion-angle noncrystallographic symmetry restraints for improved macromolecular structure refinement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1346-1356.	2.5	19
47	New tools for automated model completion and refinement. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2014, 70, C327-C327.	0.1	0
48	Graphical tools for macromolecular crystallography in <i>PHENIX</i> . <i>Journal of Applied Crystallography</i> , 2012, 45, 581-586.	4.5	139
49	Use of knowledge-based restraints in <i>phenix.refine</i> to improve macromolecular refinement at low resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 381-390.	2.5	230
50	Towards automated crystallographic structure refinement with <i>phenix.refine</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 352-367.	2.5	4,573
51	The Phenix software for automated determination of macromolecular structures. <i>Methods</i> , 2011, 55, 94-106.	3.8	764
52	<i>phenix.model_vs_data</i> : a high-level tool for the calculation of crystallographic model and data statistics. <i>Journal of Applied Crystallography</i> , 2010, 43, 669-676.	4.5	112
53	<i>PHENIX</i> : a comprehensive Python-based system for macromolecular structure solution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 213-221.	2.5	20,564
54	Joint X-ray and neutron refinement with <i>phenix.refine</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 1153-1163.	2.5	259

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55	Decision-making in structure solution using Bayesian estimates of map quality: the <i>PHENIX</i> AutoSol wizard. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 582-601.	2.5	804
56	<i>electronic Ligand Builder and Optimization Workbench (eLBOW)</i> : a tool for ligand coordinate and restraint generation. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 1074-1080.	2.5	1,035
57	Torsion Angle Refinement and Dynamics as a Tool to Aid Crystallographic Structure Determination. , 2009, , .		1
58	Iterative model building, structure refinement and density modification with the <i>PHENIX</i> AutoBuild wizard. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 61-69.	2.5	1,319
59	Iterative-build OMIT maps: map improvement by iterative model building and refinement without model bias. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 515-524.	2.5	165
60	Automated Structure Solution with the PHENIX Suite. Methods in Molecular Biology, 2008, 426, 419-435.	0.9	492
61	Ligand identification using electron-density map correlations. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 101-107.	2.5	57
62	Interpretation of ensembles created by multiple iterative rebuilding of macromolecular models. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 597-610.	2.5	60
63	Automated structure determination with phenix. NATO Science Series Series II, Mathematics, Physics and Chemistry, 2007, , 101-109.	0.1	4
64	Automated ligand fitting by core-fragment fitting and extension into density. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 915-922.	2.5	98
65	Recent developments in the <i>PHENIX</i> software for automated crystallographic structure determination. Journal of Synchrotron Radiation, 2004, 11, 53-55.	2.4	319
66	Computational economy improvements in PRISM. International Journal of Chemical Kinetics, 2003, 35, 438-452.	1.6	32
67	The Computational Crystallography Toolbox: crystallographic algorithms in a reusable software framework. Journal of Applied Crystallography, 2002, 35, 126-136.	4.5	262
68	<i>PHENIX</i> : building new software for automated crystallographic structure determination. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 1948-1954.	2.5	3,979
69	A quantum Monte Carlo study of energy differences in C ₄ H ₃ and C ₄ H ₅ isomers. International Journal of Chemical Kinetics, 2001, 33, 808-820.	1.6	18
70	On unimolecular decomposition of phenyl radical. Proceedings of the Combustion Institute, 2000, 28, 1545-1555.	3.9	45
71	Ab initio study of naphthalene formation by addition of vinylacetylene to phenyl. Proceedings of the Combustion Institute, 2000, 28, 2563-2568.	3.9	35
72	Propargyl radical: an electron localization function study. Chemical Physics Letters, 1999, 314, 534-542.	2.6	38

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73	Hydrogen Migration in the Phenylethen-2-yl Radical. <i>Journal of Physical Chemistry A</i> , 1999, 103, 7127-7135.	2.5	48
74	PRISM: Piecewise Reusable Implementation of Solution Mapping. An Economical Strategy for Chemical Kinetics. <i>Israel Journal of Chemistry</i> , 1999, 39, 97-106.	2.3	95
75	Hydrogen migration in polyaromatic growth. <i>Proceedings of the Combustion Institute</i> , 1998, 27, 1655-1661.	0.3	51
76	Computational convergence of electronic structure calculations of transition metal ligand complexes. <i>Journal of Computational Chemistry</i> , 1993, 14, 961-969.	3.3	18