Airlie J Mccoy

List of Publications by Year
in descending order

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65 papers	56,697 citations	94433 37 h-index	110387 64 g-index
68 all docs	68 docs citations	68 times ranked	51897 citing authors

#	Article	IF	Citations
1	PHENIX: a comprehensive Python-based system for macromolecular structure solution. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 213-221.	2.5	20,564
2	Phasercrystallographic software. Journal of Applied Crystallography, 2007, 40, 658-674.	4.5	17,782
3	Macromolecular structure determination using X-rays, neutrons and electrons: recent developments in Phenix. Acta Crystallographica Section D: Structural Biology, 2019, 75, 861-877.	2.3	4,060
4	PHENIX: building new software for automated crystallographic structure determination. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 1948-1954.	2.5	3,979
5	Likelihood-enhanced fast translation functions. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 458-464.	2.5	1,560
6	Solving structures of protein complexes by molecular replacement withPhaser. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 32-41.	2.5	1,452
7	Likelihood-enhanced fast rotation functions. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 432-438.	2.5	1,074
8	Decision-making in structure solution using Bayesian estimates of map quality: thePHENIX AutoSolwizard. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 582-601.	2.5	804
9	The Phenix software for automated determination of macromolecular structures. Methods, 2011, 55, 94-106.	3.8	764
10	Molecular Architecture and Functional Model of the Endocytic AP2 Complex. Cell, 2002, 109, 523-535.	28.9	522
11	Automated Structure Solution with the PHENIX Suite. Methods in Molecular Biology, 2008, 426, 419-435.	0.9	492
12	Recent developments in thePHENIXsoftware for automated crystallographic structure determination. Journal of Synchrotron Radiation, 2004, 11, 53-55.	2.4	319
13	A Large-Scale Conformational Change Couples Membrane Recruitment to Cargo Binding in the AP2 Clathrin Adaptor Complex. Cell, 2010, 141, 1220-1229.	28.9	305
14	High-resolution structure prediction and the crystallographic phase problem. Nature, 2007, 450, 259-264.	27.8	296
15	A structural explanation for the binding of endocytic dileucine motifs by the AP2 complex. Nature, 2008, 456, 976-979.	27.8	280
16	Phaser.MRage: automated molecular replacement. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2276-2286.	2.5	216
17	Structural basis for molecular recognition between nuclear transport factor 2 (NTF2) and the GDP-bound form of the ras-family GTPase ran 1 1Edited by I. B. Holland. Journal of Molecular Biology, 1998, 277, 635-646.	4.2	152
18	Graphical tools for macromolecular crystallography inPHENIX. Journal of Applied Crystallography, 2012, 45, 581-586.	4.5	139

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19	Structure of Î²-Antithrombin and the Effect of Glycosylation on Antithrombin's Heparin Affinity and Activity. Journal of Molecular Biology, 2003, 326, 823-833.	4.2	121
20	A SNAREâ€“adaptor interaction is a new mode of cargo recognition in clathrin-coated vesicles. Nature, 2007, 450, 570-574.	27.8	114
21	VARP Is Recruited on to Endosomes by Direct Interaction with Retromer, Where Together They Function in Export to the Cell Surface. Developmental Cell, 2014, 29, 591-606.	7.0	110
22	Using SAD data inPhaser. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 338-344.	2.5	105
23	Simple algorithm for a maximum-likelihood SAD function. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 1220-1228.	2.5	101
24	Transient Fcho1/2â‹…Eps15/Râ‹…AP-2 Nanoclusters Prime the AP-2 Clathrin Adaptor for Cargo Binding. Developmental Cell, 2016, 37, 428-443.	7.0	92
25	scFv multimers of the anti-neuraminidase antibody NC10: length of the linker between VH and VL domains dictates precisely the transition between diabodies and triabodies. Protein Engineering, Design and Selection, 1999, 12, 597-604.	2.1	84
26	Crystal Structure of Rab11 in Complex with Rab11 Family Interacting Protein 2. Structure, 2006, 14, 1273-1283.	3.3	82
27	ScFv multimers of the anti-neuraminidase antibody NC10: shortening of the linker in single-chain Fv fragment assembled in VL to VH orientation drives the formation of dimers, trimers, tetramers and higher molecular mass multimers. Protein Engineering, Design and Selection, 2000, 13, 565-574.	2.1	73
28	Nuclear protein import is decreased by engineered mutants of nuclear transport factor 2 (NTF2) that do not bind GDP-Ran. Journal of Molecular Biology, 1997, 272, 716-730.	4.2	70
29	The structure of the Q69L mutant of GDP-ran shows a major conformational change in the switch II loop that accounts for its failure to bind nuclear transport factor 2 (NTF2) 1 1Edited by I. B. Holland. Journal of Molecular Biology, 1998, 284, 1517-1527.	4.2	66
30	Implications of AlphaFold2 for crystallographic phasing by molecular replacement. Acta Crystallographica Section D: Structural Biology, 2022, 78, 1-13.	2.3	65
31	A log-likelihood-gain intensity target for crystallographic phasing that accounts for experimental error. Acta Crystallographica Section D: Structural Biology, 2016, 72, 375-387.	2.3	58
32	Structural basis for dimerization of the Dictyostelium gelation factor (ABP120) rod. Nature Structural Biology, 1999, 6, 836-841.	9.7	57
33	Ab initio solution of macromolecular crystal structures without direct methods. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 3637-3641.	7.1	47
34	Assessing the utility of <scp>CASP14</scp> models for molecular replacement. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1752-1769.	2.6	47
35	Acknowledging Errors: Advanced Molecular Replacement with Phaser. Methods in Molecular Biology, 2017, 1607, 421-453.	0.9	46
36	Experimental phasing: best practice and pitfalls. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 458-469.	2.5	45

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37	Intensity statistics in the presence of translational noncrystallographic symmetry. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 176-183.	2.5	43
38	Automating crystallographic structure solution and refinement of proteinâ€“ligand complexes. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 144-154.	2.5	43
39	Improved estimates of coordinate error for molecular replacement. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2209-2215.	2.5	42
40	Automated identification of elemental ions in macromolecular crystal structures. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1104-1114.	2.5	40
41	Temporal Ordering in Endocytic Clathrin-Coated Vesicle Formation via AP2 Phosphorylation. Developmental Cell, 2019, 50, 494-508.e11.	7.0	40
42	On the application of the expected log-likelihood gain to decision making in molecular replacement. Acta Crystallographica Section D: Structural Biology, 2018, 74, 245-255.	2.3	40
43	Three-dimensional structures of single-chain Fv-neuraminidase complexes. Journal of Molecular Biology, 1998, 279, 901-910.	4.2	32
44	Macromolecular X-ray structure determination using weak, single-wavelength anomalous data. Nature Methods, 2015, 12, 127-130.	19.0	31
45	Exploiting distant homologues for phasing through the generation of compact fragments, local fold refinement and partial solution combination. Acta Crystallographica Section D: Structural Biology, 2018, 74, 290-304.	2.3	30
46	Liking likelihood. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 2169-2183.	2.5	28
47	Likelihood-based molecular-replacement solution for a highly pathological crystal with tetartohedral twinning and sevenfold translational noncrystallographic symmetry. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 471-480.	2.5	24
48	X-ray structure determination using low-resolution electron microscopy maps for molecular replacement. Nature Protocols, 2015, 10, 1275-1284.	12.0	22
49	Engineered mutants in the switch II loop of ran define the contribution made by key residues to the interaction with nuclear transport factor 2 (NTF2) and the role of this interaction in nuclear protein import. Journal of Molecular Biology, 1999, 289, 565-577.	4.2	18
50	SCEDS: protein fragments for molecular replacement inPhaser. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2216-2225.	2.5	16
51	ANS complex of St John's wort PR-10 protein with 28 copies in the asymmetric unit: a fiendish combination of pseudosymmetry with tetartohedral twinning. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 829-843.	2.5	15
52	Gyreandgimble: a maximum-likelihood replacement for Patterson correlation refinement. Acta Crystallographica Section D: Structural Biology, 2018, 74, 279-289.	2.3	14
53	Phasertng: directed acyclic graphs for crystallographic phasing. Acta Crystallographica Section D: Structural Biology, 2021, 77, 1-10.	2.3	10
54	Structure and evolution of <scp>ENTH</scp> and <scp>VHS</scp>/<scp>ENTH</scp>â€like domains in tepsin. Traffic, 2017, 18, 590-603.	2.7	9

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55	Structure of the Human Cation-Independent Mannose 6-Phosphate/IGF2 Receptor Domains 7â€“11ÂUncovers the Mannose 6-Phosphate Binding Site of Domain 9. Structure, 2020, 28, 1300-1312.e5.	3.3	8
56	New applications of maximum likelihood and Bayesian statistics in macromolecular crystallography. Current Opinion in Structural Biology, 2002, 12, 670-673.	5.7	6
57	Factors influencing estimates of coordinate error for molecular replacement. Acta Crystallographica Section D: Structural Biology, 2020, 76, 19-27.	2.3	6
58	Crystallization and Preliminary X-Ray Diffraction Characterization of a Dimerizing Fragment of the Rod Domain of theDictyosteliumGelation Factor (ABP-120). Journal of Structural Biology, 1997, 120, 192-195.	2.8	5
59	Detection of translational noncrystallographic symmetry in Patterson functions. Acta Crystallographica Section D: Structural Biology, 2021, 77, 131-141.	2.3	5
60	Maximum-likelihood determination of anomalous substructures. Acta Crystallographica Section D: Structural Biology, 2018, 74, 98-105.	2.3	4
61	Automated structure determination with phenix. NATO Science Series Series II, Mathematics, Physics and Chemistry, 2007, , 101-109.	0.1	4
62	Measuring and using information gained by observing diffraction data. Acta Crystallographica Section D: Structural Biology, 2020, 76, 238-247.	2.3	3
63	The suppressor of copper sensitivity protein C from Caulobacter crescentus is a trimeric disulfide isomerase that binds copper(I) with subpicomolar affinity. Acta Crystallographica Section D: Structural Biology, 2022, 78, 337-352.	2.3	3
64	Likelihood-based estimation of substructure content from single-wavelength anomalous diffraction (SAD) intensity data. Acta Crystallographica Section D: Structural Biology, 2021, 77, 880-893.	2.3	1
65	Extending the Reach of Molecular Replacement. NATO Science for Peace and Security Series A: Chemistry and Biology, 2013, , 113-122.	0.5	0