

Airlie J Mccoy

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/12021049/publications.pdf>

Version: 2024-02-01

65
papers

56,697
citations

108046

37
h-index

124990

64
g-index

68
all docs

68
docs citations

68
times ranked

57023
citing authors

#	ARTICLE	IF	CITATIONS
1	Implications of <i>AlphaFold</i> ² for crystallographic phasing by molecular replacement. <i>Acta Crystallographica Section D: Structural Biology</i> , 2022, 78, 1-13.	1.1	65
2	The suppressor of copper sensitivity protein C from <i>Caulobacter crescentus</i> is a trimeric disulfide isomerase that binds copper(I) with subpicomolar affinity. <i>Acta Crystallographica Section D: Structural Biology</i> , 2022, 78, 337-352.	1.1	3
3	Phasertng: directed acyclic graphs for crystallographic phasing. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 1-10.	1.1	10
4	Detection of translational noncrystallographic symmetry in Patterson functions. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 131-141.	1.1	5
5	Likelihood-based estimation of substructure content from single-wavelength anomalous diffraction (SAD) intensity data. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 880-893.	1.1	1
6	Assessing the utility of <i>CASP14</i> models for molecular replacement. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1752-1769.	1.5	47
7	Structure of the Human Cation-Independent Mannose 6-Phosphate/IGF2 Receptor Domains $\approx 11 \text{ \AA}$ Uncovers the Mannose 6-Phosphate Binding Site of Domain 9. <i>Structure</i> , 2020, 28, 1300-1312.e5.	1.6	8
8	Factors influencing estimates of coordinate error for molecular replacement. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 19-27.	1.1	6
9	Measuring and using information gained by observing diffraction data. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 238-247.	1.1	3
10	Temporal Ordering in Endocytic Clathrin-Coated Vesicle Formation via AP2 Phosphorylation. <i>Developmental Cell</i> , 2019, 50, 494-508.e11.	3.1	40
11	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.	1.1	4,060
12	Maximum-likelihood determination of anomalous substructures. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 98-105.	1.1	4
13	Exploiting distant homologues for phasing through the generation of compact fragments, local fold refinement and partial solution combination. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 290-304.	1.1	30
14	Gyreandgimble: a maximum-likelihood replacement for Patterson correlation refinement. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 279-289.	1.1	14
15	On the application of the expected log-likelihood gain to decision making in molecular replacement. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 245-255.	1.1	40
16	Ab initio solution of macromolecular crystal structures without direct methods. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 3637-3641.	3.3	47
17	Structure and evolution of <i>ENTH</i> and <i>VHS</i> / <i>ENTH</i> -like domains in tepsin. <i>Traffic</i> , 2017, 18, 590-603.	1.3	9
18	Acknowledging Errors: Advanced Molecular Replacement with Phaser. <i>Methods in Molecular Biology</i> , 2017, 1607, 421-453.	0.4	46

#	ARTICLE	IF	CITATIONS
19	A log-likelihood-gain intensity target for crystallographic phasing that accounts for experimental error. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 375-387.	1.1	58
20	Transient Fcho1/2â€¦Eps15/Râ€¦AP-2 Nanoclusters Prime the AP-2 Clathrin Adaptor for Cargo Binding. <i>Developmental Cell</i> , 2016, 37, 428-443.	3.1	92
21	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. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 829-843.	2.5	15
22	X-ray structure determination using low-resolution electron microscopy maps for molecular replacement. <i>Nature Protocols</i> , 2015, 10, 1275-1284.	5.5	22
23	Macromolecular X-ray structure determination using weak, single-wavelength anomalous data. <i>Nature Methods</i> , 2015, 12, 127-130.	9.0	31
24	Automated identification of elemental ions in macromolecular crystal structures. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1104-1114.	2.5	40
25	VARP Is Recruited on to Endosomes by Direct Interaction with Retromer, Where Together They Function in Export to the Cell Surface. <i>Developmental Cell</i> , 2014, 29, 591-606.	3.1	110
26	Likelihood-based molecular-replacement solution for a highly pathological crystal with tetartohedral twinning and sevenfold translational noncrystallographic symmetry. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 471-480.	2.5	24
27	Automating crystallographic structure solution and refinement of proteinâ€“ligand complexes. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 144-154.	2.5	43
28	Intensity statistics in the presence of translational noncrystallographic symmetry. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 176-183.	2.5	43
29	SCEDS: protein fragments for molecular replacement in <i>Phaser</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2216-2225.	2.5	16
30	<i>Phaser.MRage</i> : automated molecular replacement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2276-2286.	2.5	216
31	Improved estimates of coordinate error for molecular replacement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2209-2215.	2.5	42
32	Extending the Reach of Molecular Replacement. <i>NATO Science for Peace and Security Series A: Chemistry and Biology</i> , 2013, , 113-122.	0.5	0
33	Graphical tools for macromolecular crystallography in <i>PHENIX</i> . <i>Journal of Applied Crystallography</i> , 2012, 45, 581-586.	1.9	139
34	The Phenix software for automated determination of macromolecular structures. <i>Methods</i> , 2011, 55, 94-106.	1.9	764
35	Using SAD data in <i>Phaser</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 338-344.	2.5	105
36	<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

#	ARTICLE	IF	CITATIONS
37	Experimental phasing: best practice and pitfalls. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 458-469.	2.5	45
38	A Large-Scale Conformational Change Couples Membrane Recruitment to Cargo Binding in the AP2 Clathrin Adaptor Complex. <i>Cell</i> , 2010, 141, 1220-1229.	13.5	305
39	Decision-making in structure solution using Bayesian estimates of map quality: the PHENIX AutoSol wizard. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 582-601.	2.5	804
40	Automated Structure Solution with the PHENIX Suite. <i>Methods in Molecular Biology</i> , 2008, 426, 419-435.	0.4	492
41	A structural explanation for the binding of endocytic dileucine motifs by the AP2 complex. <i>Nature</i> , 2008, 456, 976-979.	13.7	280
42	Phaser crystallographic software. <i>Journal of Applied Crystallography</i> , 2007, 40, 658-674.	1.9	17,782
43	Solving structures of protein complexes by molecular replacement with Phaser. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 32-41.	2.5	1,452
44	High-resolution structure prediction and the crystallographic phase problem. <i>Nature</i> , 2007, 450, 259-264.	13.7	296
45	A SNARE adaptor interaction is a new mode of cargo recognition in clathrin-coated vesicles. <i>Nature</i> , 2007, 450, 570-574.	13.7	114
46	Automated structure determination with phenix. <i>NATO Science Series Series II, Mathematics, Physics and Chemistry</i> , 2007, , 101-109.	0.1	4
47	Crystal Structure of Rab11 in Complex with Rab11 Family Interacting Protein 2. <i>Structure</i> , 2006, 14, 1273-1283.	1.6	82
48	Likelihood-enhanced fast translation functions. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 458-464.	2.5	1,560
49	Recent developments in the PHENIX software for automated crystallographic structure determination. <i>Journal of Synchrotron Radiation</i> , 2004, 11, 53-55.	1.0	319
50	Likelihood-enhanced fast rotation functions. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 432-438.	2.5	1,074
51	Simple algorithm for a maximum-likelihood SAD function. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1220-1228.	2.5	101
52	Liking likelihood. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 2169-2183.	2.5	28
53	Structure of \hat{I}^2 -Antithrombin and the Effect of Glycosylation on Antithrombin's Heparin Affinity and Activity. <i>Journal of Molecular Biology</i> , 2003, 326, 823-833.	2.0	121
54	Molecular Architecture and Functional Model of the Endocytic AP2 Complex. <i>Cell</i> , 2002, 109, 523-535.	13.5	522

#	ARTICLE	IF	CITATIONS
55	New applications of maximum likelihood and Bayesian statistics in macromolecular crystallography. <i>Current Opinion in Structural Biology</i> , 2002, 12, 670-673.	2.6	6
56	PHENIX: building new software for automated crystallographic structure determination. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 1948-1954.	2.5	3,979
57	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. <i>Protein Engineering, Design and Selection</i> , 2000, 13, 565-574.	1.0	73
58	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. <i>Protein Engineering, Design and Selection</i> , 1999, 12, 597-604.	1.0	84
59	Structural basis for dimerization of the Dictyostelium gelation factor (ABP120) rod. <i>Nature Structural Biology</i> , 1999, 6, 836-841.	9.7	57
60	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. <i>Journal of Molecular Biology</i> , 1999, 289, 565-577.	2.0	18
61	Structural basis for molecular recognition between nuclear transport factor 2 (NTF2) and the GDP-bound form of the ras-family GTPase ran 1 1 Edited by I. B. Holland. <i>Journal of Molecular Biology</i> , 1998, 277, 635-646.	2.0	152
62	Three-dimensional structures of single-chain Fv-neuraminidase complexes. <i>Journal of Molecular Biology</i> , 1998, 279, 901-910.	2.0	32
63	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 1 Edited by I. B. Holland. <i>Journal of Molecular Biology</i> , 1998, 284, 1517-1527.	2.0	66
64	Nuclear protein import is decreased by engineered mutants of nuclear transport factor 2 (NTF2) that do not bind GDP-Ran. <i>Journal of Molecular Biology</i> , 1997, 272, 716-730.	2.0	70
65	Crystallization and Preliminary X-Ray Diffraction Characterization of a Dimerizing Fragment of the Rod Domain of the Dictyostelium Gelation Factor (ABP-120). <i>Journal of Structural Biology</i> , 1997, 120, 192-195.	1.3	5