

Billy K Poon

List of Publications by Year in descending order

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Version: 2024-02-01

25
papers

7,844
citations

623188

14
h-index

676716

22
g-index

26
all docs

26
docs citations

26
times ranked

12283
citing authors

#	ARTICLE	IF	CITATIONS
1	Sizes of pure and doped helium droplets from single shot x-ray imaging. <i>Journal of Chemical Physics</i> , 2022, 156, 041102.	1.2	3
2	Integration of software tools for integrative modeling of biomolecular systems. <i>Journal of Structural Biology</i> , 2022, 214, 107841.	1.3	7
3	<i>CERES</i> : a cryo-EM re-refinement system for continuous improvement of deposited models. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 48-61.	1.1	14
4	Cryo_fit: Democratization of flexible fitting for cryo-EM. <i>Journal of Structural Biology</i> , 2019, 208, 1-6.	1.3	30
5	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.	1.1	46
6	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
7	Interactive comparison and remediation of collections of macromolecular structures. <i>Protein Science</i> , 2018, 27, 182-194.	3.1	13
8	Free-electron laser data for multiple-particle fluctuation scattering analysis. <i>Scientific Data</i> , 2018, 5, 180201.	2.4	6
9	Real-space refinement in <i>PHENIX</i> for cryo-EM and crystallography. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 531-544.	1.1	2,065
10	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.	1.1	575
11	Polder maps: improving OMIT maps for ligand building and validation. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2018, 74, a308-a308.	0.0	0
12	Polder maps: improving OMIT maps for ligand building and validation. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2017, 73, C48-C48.	0.0	0
13	Polder maps: improving OMIT maps by excluding bulk solvent. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 148-157.	1.1	500
14	Video tutorials for the <i>Phenix</i> software suite. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2017, 73, C1134-C1134.	0.0	0
15	Shapes and vorticities of superfluid helium nanodroplets. <i>Science</i> , 2014, 345, 906-909.	6.0	197
16	Three-dimensional single-particle imaging using angular correlations from X-ray laser data. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2013, 69, 365-373.	0.3	45
17	Computation of fluctuation scattering profiles via three-dimensional Zernike polynomials. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2012, 68, 561-567.	0.3	13
18	Structure determination of Pt-coated Au dumbbells via fluctuation X-ray scattering. <i>Journal of Synchrotron Radiation</i> , 2012, 19, 695-700.	1.0	23

#	ARTICLE	IF	CITATIONS
19	Autoindexing with outlier rejection and identification of superimposed lattices. <i>Journal of Applied Crystallography</i> , 2010, 43, 611-616.	1.9	24
20	Detection and correction of underassigned rotational symmetry prior to structure deposition. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 503-513.	2.5	13
21	Structural improvement of unliganded simian immunodeficiency virus gp120 core by normal-mode-based X-ray crystallographic refinement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 339-347.	2.5	15
22	Application of normal-mode refinement to X-ray crystal structures at the lower resolution limit. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 633-643.	2.5	12
23	Normal mode refinement of anisotropic thermal parameters for a supramolecular complex at 3.42-Å crystallographic resolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 7869-7874.	3.3	56
24	Normal-Mode Refinement of Anisotropic Thermal Parameters for Potassium Channel KcsA at 3.2 Å... Crystallographic Resolution. <i>Structure</i> , 2007, 15, 955-962.	1.6	29
25	A New Method for Coarse-Grained Elastic Normal-Mode Analysis. <i>Journal of Chemical Theory and Computation</i> , 2006, 2, 464-471.	2.3	81