# Billy K Poon

List of Publications by Year
in descending order



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|---|---|---|---|
| 25 papers | 7,844 citations | 623734 14 h-index | 677142 22 g-index |
| 26 all docs | 26 docs citations | 26 times ranked | 12283 citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | 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 |
| 2 | Real-space refinement inPHENIXfor cryo-EM and crystallography. Acta Crystallographica Section D: Structural Biology, 2018, 74, 531-544. | 2.3 | 2,065 |
| 3 | New tools for the analysis and validation of cryo-EM maps and atomic models. Acta Crystallographica Section D: Structural Biology, 2018, 74, 814-840. | 2.3 | 575 |
| 4 | Polder maps: improving OMIT maps by excluding bulk solvent. Acta Crystallographica Section D: Structural Biology, 2017, 73, 148-157. | 2.3 | 500 |
| 5 | Shapes and vorticities of superfluid helium nanodroplets. Science, 2014, 345, 906-909. | 12.6 | 197 |
| 6 | A New Method for Coarse-Grained Elastic Normal-Mode Analysis. Journal of Chemical Theory and Computation, 2006, 2, 464-471. | 5.3 | 81 |
| 7 | Normal mode refinement of anisotropic thermal parameters for a supramolecular complex at 3.42-A crystallographic resolution. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 7869-7874. | 7.1 | 56 |
| 8 | Announcing mandatory submission of PDBx/mmCIF format files for crystallographic depositions to the Protein Data Bank (PDB). Acta Crystallographica Section D: Structural Biology, 2019, 75, 451-454. | 2.3 | 46 |
| 9 | Three-dimensional single-particle imaging using angular correlations from X-ray laser data. Acta Crystallographica Section A: Foundations and Advances, 2013, 69, 365-373. | 0.3 | 45 |
| 10 | Cryo_fit: Democratization of flexible fitting for cryo-EM. Journal of Structural Biology, 2019, 208, 1-6. | 2.8 | 30 |
| 11 | Normal-Mode Refinement of Anisotropic Thermal Parameters for Potassium Channel KcsA at 3.2 Ã… Crystallographic Resolution. Structure, 2007, 15, 955-962. | 3.3 | 29 |
| 12 | Autoindexing with outlier rejection and identification of superimposed lattices. Journal of Applied Crystallography, 2010, 43, 611-616. | 4.5 | 24 |
| 13 | Structure determination of Pt-coated Au dumbbellsviafluctuation X-ray scattering. Journal of Synchrotron Radiation, 2012, 19, 695-700. | 2.4 | 23 |
| 14 | Structural improvement of unliganded simian immunodeficiency virus gp120 core by normal-mode-based X-ray crystallographic refinement. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 339-347. | 2.5 | 15 |
| 15 | CERES: a cryo-EM re-refinement system for continuous improvement of deposited models. Acta Crystallographica Section D: Structural Biology, 2021, 77, 48-61. | 2.3 | 14 |
| 16 | Detection and correction of underassigned rotational symmetry prior to structure deposition. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 503-513. | 2.5 | 13 |
| 17 | Computation of fluctuation scattering profilesviathree-dimensional Zernike polynomials. Acta Crystallographica Section A: Foundations and Advances, 2012, 68, 561-567. | 0.3 | 13 |
| 18 | Interactive comparison and remediation of collections of macromolecular structures. Protein Science, 2018, 27, 182-194. | 7.6 | 13 |

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|---|---|---|---|
| 19 | Application of normal-mode refinement to X-ray crystal structures at the lower resolution limit. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 633-643. | 2.5 | 12 |
| 20 | Integration of software tools for integrative modeling of biomolecular systems. Journal of Structural Biology, 2022, 214, 107841. | 2.8 | 7 |
| 21 | Free-electron laser data for multiple-particle fluctuation scattering analysis. Scientific Data, 2018, 5, 180201. | 5.3 | 6 |
| 22 | Sizes of pure and doped helium droplets from single shot x-ray imaging. Journal of Chemical Physics, 2022, 156, 041102. | 3.0 | 3 |
| 23 | Polder maps: improving OMIT maps for ligand building and validation. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, C48-C48. | 0.1 | 0 |
| 24 | Video tutorials for the Phenix software suite. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, C1134-C1134. | 0.1 | 0 |
| 25 | Polder maps: improving OMIT maps for ligand building and validation. Acta Crystallographica Section A: Foundations and Advances, 2018, 74, a308-a308. | 0.1 | 0 |