

Vincent B Chen

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8374637/publications.pdf>

Version: 2024-02-01

12
papers

23,184
citations

840119

11
h-index

1199166

12
g-index

13
all docs

13
docs citations

13
times ranked

33384
citing authors

#	ARTICLE	IF	CITATIONS
1	Improving SARS-CoV-2 structures: Peer review by early coordinate release. <i>Biophysical Journal</i> , 2021, 120, 1085-1096.	0.2	21
2	<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
3	New tools in MolProbity validation: CaBLAM for CryoEM backbone, UnDowser to rethink "waters," and NGL Viewer to recapture online 3D graphics. <i>Protein Science</i> , 2020, 29, 315-329.	3.1	104
4	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
5	Model validation: local diagnosis, correction and when to quit. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 132-142.	1.1	29
6	MolProbity: More and better reference data for improved all-atom structure validation. <i>Protein Science</i> , 2018, 27, 293-315.	3.1	2,776
7	Assessment of detailed conformations suggests strategies for improving cryoEM models: Helix at lower resolution, ensembles, pre-refinement fixups, and validation at multi-residue length scale. <i>Journal of Structural Biology</i> , 2018, 204, 301-312.	1.3	22
8	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
9	<i>MolProbity</i> : all-atom structure validation for macromolecular crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 12-21.	2.5	12,318
10	KING (Kinemage, Next Generation): A versatile interactive molecular and scientific visualization program. <i>Protein Science</i> , 2009, 18, 2403-2409.	3.1	146
11	KinImmerse: Macromolecular VR for NMR ensembles. <i>Source Code for Biology and Medicine</i> , 2009, 4, 3.	1.7	19
12	MolProbity: all-atom contacts and structure validation for proteins and nucleic acids. <i>Nucleic Acids Research</i> , 2007, 35, W375-W383.	6.5	3,443