

Ardan Patwardhan

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

3,811
citations

331259

21
h-index

433756

31
g-index

37
all docs

37
docs citations

37
times ranked

5548
citing authors

#	ARTICLE	IF	CITATIONS
1	Protein Data Bank: the single global archive for 3D macromolecular structure data. <i>Nucleic Acids Research</i> , 2019, 47, D520-D528.	6.5	671
2	Single-particle electron cryo-microscopy: towards atomic resolution. <i>Quarterly Reviews of Biophysics</i> , 2000, 33, 307-369.	2.4	535
3	OMERO: flexible, model-driven data management for experimental biology. <i>Nature Methods</i> , 2012, 9, 245-253.	9.0	478
4	EMPIAR: a public archive for raw electron microscopy image data. <i>Nature Methods</i> , 2016, 13, 387-388.	9.0	298
5	EMDataBank unified data resource for 3DEM. <i>Nucleic Acids Research</i> , 2016, 44, D396-D403.	6.5	230
6	Validation of Structures in the Protein Data Bank. <i>Structure</i> , 2017, 25, 1916-1927.	1.6	210
7	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. <i>Structure</i> , 2015, 23, 1156-1167.	1.6	159
8	PDBe: Protein Data Bank in Europe. <i>Nucleic Acids Research</i> , 2014, 42, D285-D291.	6.5	133
9	PDBe: improved accessibility of macromolecular structure data from PDB and EMDB. <i>Nucleic Acids Research</i> , 2016, 44, D385-D395.	6.5	131
10	OneDep: Unified wwPDB System for Deposition, Biocuration, and Validation of Macromolecular Structures in the PDB Archive. <i>Structure</i> , 2017, 25, 536-545.	1.6	130
11	A call for public archives for biological image data. <i>Nature Methods</i> , 2018, 15, 849-854.	9.0	99
12	Collaborative Computational Project for Electron cryo-Microscopy. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 123-126.	2.5	84
13	Trends in the Electron Microscopy Data Bank (EMDB). <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 503-508.	1.1	79
14	Cryo-EM model validation recommendations based on outcomes of the 2019 EMDataResource challenge. <i>Nature Methods</i> , 2021, 18, 156-164.	9.0	73
15	REMBI: Recommended Metadata for Biological Images enabling reuse of microscopy data in biology. <i>Nature Methods</i> , 2021, 18, 1418-1422.	9.0	63
16	Improved metrics for comparing structures of macromolecular assemblies determined by 3D electron-microscopy. <i>Journal of Structural Biology</i> , 2017, 199, 12-26.	1.3	56
17	Data management challenges in three-dimensional EM. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1203-1207.	3.6	49
18	A 3D cellular context for the macromolecular world. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 841-845.	3.6	47

#	ARTICLE	IF	CITATIONS
19	Worldwide Protein Data Bank biocuration supporting open access to high-quality 3D structural biology data. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	45
20	The BioImage Archive â€œ Building a Home for Life-Sciences Microscopy Data. Journal of Molecular Biology, 2022, 434, 167505.	2.0	45
21	Web-based visualisation and analysis of 3D electron-microscopy data from EMDB and PDB. Journal of Structural Biology, 2013, 184, 173-181.	1.3	34
22	Comparing Cryo-EM Reconstructions and Validating Atomic Model Fit Using Difference Maps. Journal of Chemical Information and Modeling, 2020, 60, 2552-2560.	2.5	29
23	EMDB Web Resources. Current Protocols in Bioinformatics, 2018, 61, 5.10.1-5.10.12.	25.8	21
24	The role of structural bioinformatics resources in the era of integrative structural biology. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 710-721.	2.5	17
25	The first single particle analysis Map Challenge: A summary of the assessments. Journal of Structural Biology, 2018, 204, 291-300.	1.3	17
26	Web-based volume slicer for 3D electron-microscopy data from EMDB. Journal of Structural Biology, 2016, 194, 164-170.	1.3	13
27	The Electron Microscopy eXchange (EMX) initiative. Journal of Structural Biology, 2016, 194, 156-163.	1.3	12
28	Structural biology data archiving â€œ where we are and what lies ahead. FEBS Letters, 2018, 592, 2153-2167.	1.3	11
29	Validation analysis of EMDB entries. Acta Crystallographica Section D: Structural Biology, 2022, 78, 542-552.	1.1	9
30	Data-deposition protocols for correlative soft X-ray tomography and super-resolution structured illumination microscopy applications. STAR Protocols, 2021, 2, 100253.	0.5	7