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List of Publications by Year in descending order

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Version: 2024-02-01

28
papers

2,399
citations

361413

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501196

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docs citations

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times ranked

3795
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.	14.5	671
2	Validation of Structures in the Protein Data Bank. <i>Structure</i> , 2017, 25, 1916-1927.	3.3	210
3	SIFTS: updated Structure Integration with Function, Taxonomy and Sequences resource allows 40-fold increase in coverage of structure-based annotations for proteins. <i>Nucleic Acids Research</i> , 2019, 47, D482-D489.	14.5	165
4	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. <i>Structure</i> , 2015, 23, 1156-1167.	3.3	159
5	PDBe: Protein Data Bank in Europe. <i>Nucleic Acids Research</i> , 2014, 42, D285-D291.	14.5	133
6	PDBe: improved accessibility of macromolecular structure data from PDB and EMDB. <i>Nucleic Acids Research</i> , 2016, 44, D385-D395.	14.5	131
7	OneDep: Unified wwPDB System for Deposition, Biocuration, and Validation of Macromolecular Structures in the PDB Archive. <i>Structure</i> , 2017, 25, 536-545.	3.3	130
8	PDBe-KB: a community-driven resource for structural and functional annotations. <i>Nucleic Acids Research</i> , 2020, 48, D344-D353.	14.5	87
9	PDBe: improved findability of macromolecular structure data in the PDB. <i>Nucleic Acids Research</i> , 2020, 48, D335-D343.	14.5	86
10	PDBe: towards reusable data delivery infrastructure at protein data bank in Europe. <i>Nucleic Acids Research</i> , 2018, 46, D486-D492.	14.5	76
11	Blind Testing of Routine, Fully Automated Determination of Protein Structures from NMR Data. <i>Structure</i> , 2012, 20, 227-236.	3.3	75
12	PDBe: Protein Data Bank in Europe. <i>Nucleic Acids Research</i> , 2011, 39, D402-D410.	14.5	64
13	A novel strategy for NMR resonance assignment and protein structure determination. <i>Journal of Biomolecular NMR</i> , 2011, 49, 27-38.	2.8	46
14	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.	2.3	46
15	Worldwide Protein Data Bank biocuration supporting open access to high-quality 3D structural biology data. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	3.0	45
16	Solution NMR in structural genomics. <i>Current Opinion in Structural Biology</i> , 2006, 16, 611-617.	5.7	43
17	Three-way decomposition of a complete 3D 15N-NOESY-HSQC. <i>Journal of Biomolecular NMR</i> , 2002, 24, 191-201.	2.8	40
18	NMR Exchange Format: a unified and open standard for representation of NMR restraint data. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 433-434.	8.2	40

#	ARTICLE	IF	CITATIONS
19	An overview of tools for the validation of protein NMR structures. <i>Journal of Biomolecular NMR</i> , 2014, 58, 259-285.	2.8	34
20	Specific DNA recognition by the Antp homeodomain: MD simulations of specific and nonspecific complexes. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 57, 772-782.	2.6	20
21	The role of structural bioinformatics resources in the era of integrative structural biology. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 710-721.	2.5	17
22	Accuracy and robustness of three-way decomposition applied to NMR data. <i>Journal of Magnetic Resonance</i> , 2005, 174, 188-199.	2.1	15
23	Accurate relaxation parameters for large proteins. <i>Journal of Magnetic Resonance</i> , 2004, 167, 107-113.	2.1	13
24	Vivaldi: Visualization and validation of biomacromolecular NMR structures from the PDB. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 583-591.	2.6	13
25	PDBe aggregated API: programmatic access to an integrative knowledge graph of molecular structure data. <i>Bioinformatics</i> , 2021, 37, 3950-3952.	4.1	12
26	An intrinsically disordered proteins community for ELIXIR. <i>F1000Research</i> , 2019, 8, 1753.	1.6	12
27	Structural Characterization of a Flexible Two-Domain Protein in Solution Using Small Angle X-Ray Scattering and NMR Data. <i>Structure</i> , 2014, 22, 1862-1874.	3.3	9
28	Straightforward and complete deposition of NMR data to the PDBe. <i>Journal of Biomolecular NMR</i> , 2010, 48, 85-92.	2.8	7