

Ezra Peisach

List of Publications by Year in descending order

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Version: 2024-02-01

27
papers

5,195
citations

331670

21
h-index

526287

27
g-index

28
all docs

28
docs citations

28
times ranked

7341
citing authors

#	ARTICLE	IF	CITATIONS
1	RCSB Protein Data Bank: biological macromolecular structures enabling research and education in fundamental biology, biomedicine, biotechnology and energy. <i>Nucleic Acids Research</i> , 2019, 47, D464-D474.	14.5	918
2	RCSB Protein Data Bank: powerful new tools for exploring 3D structures of biological macromolecules for basic and applied research and education in fundamental biology, biomedicine, biotechnology, bioengineering and energy sciences. <i>Nucleic Acids Research</i> , 2021, 49, D437-D451.	14.5	918
3	Design and Selection of Novel Cys2His2Zinc Finger Proteins. <i>Annual Review of Biochemistry</i> , 2001, 70, 313-340.	11.1	700
4	Protein Data Bank: the single global archive for 3D macromolecular structure data. <i>Nucleic Acids Research</i> , 2019, 47, D520-D528.	14.5	671
5	OUP accepted manuscript. <i>Nucleic Acids Research</i> , 2017, 45, D271-D281.	14.5	619
6	Validation of Structures in the Protein Data Bank. <i>Structure</i> , 2017, 25, 1916-1927.	3.3	210
7	Structural Origin of the High Affinity of a Chemically Evolved Lanthanide-Binding Peptide. <i>Angewandte Chemie - International Edition</i> , 2004, 43, 3682-3685.	13.8	158
8	Multiple Solvent Crystal Structures: Probing Binding Sites, Plasticity and Hydration. <i>Journal of Molecular Biology</i> , 2006, 357, 1471-1482.	4.2	138
9	Engineering Encodable Lanthanide-Binding Tags into Loop Regions of Proteins. <i>Journal of the American Chemical Society</i> , 2011, 133, 808-819.	13.7	132
10	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
11	<sc>RCSB</sc> Protein Data Bank: Celebrating 50 years of the <sc>PDB</sc> with new tools for understanding and visualizing biological macromolecules in <sc>3D</sc>. <i>Protein Science</i> , 2022, 31, 187-208.	7.6	84
12	Trendspotting in the Protein Data Bank. <i>FEBS Letters</i> , 2013, 587, 1036-1045.	2.8	74
13	X-ray Crystal Structure of the Hypothetical Phosphotyrosine Phosphatase MDP-1 of the Haloacid Dehalogenase Superfamily. <i>Biochemistry</i> , 2004, 43, 12770-12779.	2.5	47
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	Crystal Structure of the Proenzyme Domain of Plasminogen. <i>Biochemistry</i> , 1999, 38, 11180-11188.	2.5	40
17	PDBx/mmCIF Ecosystem: Foundational Semantic Tools for Structural Biology. <i>Journal of Molecular Biology</i> , 2022, 434, 167599.	4.2	39
18	Analysis of the Structural Determinants Underlying Discrimination between Substrate and Solvent in $\hat{1}$ -Phosphoglucomutase Catalysis. <i>Biochemistry</i> , 2009, 48, 1984-1995.	2.5	35

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19	Structural Determinants of Substrate Recognition in the HAD Superfamily Member d-glycero-d-manno-Heptose-1,7-bisphosphate Phosphatase (GmhB),. <i>Biochemistry</i> , 2010, 49, 1082-1092.	2.5	35
20	Constraints for Zinc Finger Linker Design as Inferred from X-ray Crystal Structure of Tandem Zif268â€“DNA Complexes. <i>Journal of Molecular Biology</i> , 2003, 330, 1-7.	4.2	34
21	Small molecule annotation for the Protein Data Bank. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau116-bau116.	3.0	26
22	<i>DCC</i>: a Swiss army knife for structure factor analysis and validation. <i>Journal of Applied Crystallography</i> , 2016, 49, 1081-1084.	4.5	22
23	Modernized uniform representation of carbohydrate molecules in the Protein Data Bank. <i>Glycobiology</i> , 2021, 31, 1204-1218.	2.5	17
24	Chemical annotation of small and peptide-like molecules at the Protein Data Bank. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat079.	3.0	14
25	Simplified quality assessment for small-molecule ligands in the Protein Data Bank. <i>Structure</i> , 2022, 30, 252-262.e4.	3.3	12
26	The Xâ€“ray crystallographic structure and activity analysis of a <i>Pseudomonasâ€“</i> specific subfamily of the HAD enzyme superfamily evidences a novel biochemical function. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 197-207.	2.6	5
27	Structural Biology Knowledgebase: a biologists resource for protein structure and sample information. <i>FASEB Journal</i> , 2012, 26, lb194.	0.5	0