

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	<scp>RCSB</scp> Protein Data Bank: Celebrating 50 years of the <scp>PDB</scp> with new tools for understanding and visualizing biological macromolecules in <scp>3D</scp>. Protein Science, 2022, 31, 187-208.	7.6	84
2	Simplified quality assessment for small-molecule ligands in the Protein Data Bank. Structure, 2022, 30, 252-262.e4.	3.3	12
3	PDBx/mmCIF Ecosystem: Foundational Semantic Tools for Structural Biology. Journal of Molecular Biology, 2022, 434, 167599.	4.2	39
4	Modernized uniform representation of carbohydrate molecules in the Protein Data Bank. Glycobiology, 2021, 31, 1204-1218.	2.5	17
5	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. Nucleic Acids Research, 2021, 49, D437-D451.	14.5	918
6	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
7	Protein Data Bank: the single global archive for 3D macromolecular structure data. Nucleic Acids Research, 2019, 47, D520-D528.	14.5	671
8	RCSB Protein Data Bank: biological macromolecular structures enabling research and education in fundamental biology, biomedicine, biotechnology and energy. Nucleic Acids Research, 2019, 47, D464-D474.	14.5	918
9	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, .	3.0	45
10	OUP accepted manuscript. Nucleic Acids Research, 2017, 45, D271-D281.	14.5	619
11	OneDep: Unified wwPDB System for Deposition, Biocuration, and Validation of Macromolecular Structures in the PDB Archive. Structure, 2017, 25, 536-545.	3.3	130
12	Validation of Structures in the Protein Data Bank. Structure, 2017, 25, 1916-1927.	3.3	210
13	<i>DCC</i>: a Swiss army knife for structure factor analysis and validation. Journal of Applied Crystallography, 2016, 49, 1081-1084.	4.5	22
14	Small molecule annotation for the Protein Data Bank. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau116-bau116.	3.0	26
15	Trendspotting in the Protein Data Bank. FEBS Letters, 2013, 587, 1036-1045.	2.8	74
16	Chemical annotation of small and peptide-like molecules at the Protein Data Bank. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat079.	3.0	14
17	Structural Biology Knowledgebase: a biologists resource for protein structure and sample information. FASEB Journal, 2012, 26, lb194.	0.5	0
18	Engineering Encodable Lanthanide-Binding Tags into Loop Regions of Proteins. Journal of the American Chemical Society, 2011, 133, 808-819.	13.7	132

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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	Analysis of the Structural Determinants Underlying Discrimination between Substrate and Solvent in Î²-Phosphoglucomutase Catalysis. <i>Biochemistry</i> , 2009, 48, 1984-1995.	2.5	35
21	The X-ray crystallographic structure and activity analysis of a <i>Pseudomonas</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
22	Multiple Solvent Crystal Structures: Probing Binding Sites, Plasticity and Hydration. <i>Journal of Molecular Biology</i> , 2006, 357, 1471-1482.	4.2	138
23	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
24	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
25	Constraints for Zinc Finger Linker Design as Inferred from X-ray Crystal Structure of Tandem Zif268-DNA Complexes. <i>Journal of Molecular Biology</i> , 2003, 330, 1-7.	4.2	34
26	Design and Selection of Novel Cys2His2Zinc Finger Proteins. <i>Annual Review of Biochemistry</i> , 2001, 70, 313-340.	11.1	700
27	Crystal Structure of the Proenzyme Domain of Plasminogen. <i>Biochemistry</i> , 1999, 38, 11180-11188.	2.5	40