

Joel Berendzen

List of Publications by Year in descending order

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37
papers

10,382
citations

159358

30
h-index

344852

36
g-index

39
all docs

39
docs citations

39
times ranked

9336
citing authors

#	ARTICLE	IF	CITATIONS
1	Automated MAD and MIR structure solution. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 849-861.	2.5	2,855
2	The Catalytic Pathway of Cytochrome P450cam at Atomic Resolution. Science, 2000, 287, 1615-1622.	6.0	1,298
3	Rapid protein-folding assay using green fluorescent protein. Nature Biotechnology, 1999, 17, 691-695.	9.4	840
4	Protein states and proteinquakes.. Proceedings of the National Academy of Sciences of the United States of America, 1985, 82, 5000-5004.	3.3	805
5	A unified model of protein dynamics. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 5129-5134.	3.3	662
6	Crystal Structures of Myoglobin-Ligand Complexes at Near-Atomic Resolution. Biophysical Journal, 1999, 77, 2153-2174.	0.2	533
7	Ligand binding to heme proteins: connection between dynamics and function. Biochemistry, 1991, 30, 3988-4001.	1.2	392
8	Rebinding and relaxation in the myoglobin pocket. Biophysical Chemistry, 1987, 26, 337-355.	1.5	372
9	Crystal structure of photolysed carbonmonoxy-myoglobin. Nature, 1994, 371, 808-812.	13.7	354
10	Structural alterations for proton translocation in the M state of wild-type bacteriorhodopsin. Nature, 2000, 406, 649-653.	13.7	335
11	Structure of a ligand-binding intermediate in wild-type carbonmonoxy myoglobin. Nature, 2000, 403, 921-923.	13.7	245
12	Crystal structure and functional analysis of the SurE protein identify a novel phosphatase family. Nature Structural Biology, 2001, 8, 789-794.	9.7	199
13	Temperature-derivative spectroscopy: a tool for protein dynamics.. Proceedings of the National Academy of Sciences of the United States of America, 1990, 87, 1-5.	3.3	174
14	Engineering soluble proteins for structural genomics. Nature Biotechnology, 2002, 20, 927-932.	9.4	174
15	The role of cavities in protein dynamics: Crystal structure of a photolytic intermediate of a mutant myoglobin. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 2058-2063.	3.3	143
16	Structure of translation initiation factor 5A from Pyrobaculum aerophilum at 1.75 Å resolution. Structure, 1998, 6, 1207-1214.	1.6	109
17	The TB structural genomics consortium: a resource for Mycobacterium tuberculosis biology. Tuberculosis, 2003, 83, 223-249.	0.8	95
18	Class-directed structure determination: Foundation for a protein structure initiative. Protein Science, 1998, 7, 1851-1856.	3.1	89

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19	Ligand binding to synthetic mutant myoglobin (His-E7→Gly): role of the distal histidine.. Proceedings of the National Academy of Sciences of the United States of America, 1988, 85, 8497-8501.	3.3	78
20	Crystal Structure of Î²-d-Xylosidase from Thermoanaerobacterium saccharolyticum, a Family 39 Glycoside Hydrolase. Journal of Molecular Biology, 2004, 335, 155-165.	2.0	69
21	The TB Structural Genomics Consortium: Providing a Structural Foundation for Drug Discovery. Current Drug Targets Infectious Disorders, 2002, 2, 121-141.	2.1	66
22	Bayesian Correlated MAD Phasing. Acta Crystallographica Section D: Biological Crystallography, 1997, 53, 571-579.	2.5	63
23	Correlated Phasing of Multiple Isomorphous Replacement Data. Acta Crystallographica Section D: Biological Crystallography, 1996, 52, 749-757.	2.5	58
24	Evaluation of macromolecular electron-density map quality using the correlation of local r.m.s. density. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 1872-1877.	2.5	53
25	Discrimination of solvent from protein regions in native Fouriers as a means of evaluating heavy-atom solutions in the MIR and MAD methods. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 501-505.	2.5	46
26	AlphaFold illuminates half of the dark human proteins. Current Opinion in Structural Biology, 2022, 74, 102372.	2.6	45
27	Bayesian Difference Refinement. Acta Crystallographica Section D: Biological Crystallography, 1996, 52, 1004-1011.	2.5	39
28	Difference refinement: obtaining differences between two related structures. Acta Crystallographica Section D: Biological Crystallography, 1995, 51, 609-618.	2.5	36
29	Automatic Solution of Heavy-Atom Substructures. Methods in Enzymology, 2003, 374, 37-83.	0.4	34
30	Comparison of the magnetic properties of deoxy- and photodissociated myoglobin.. Proceedings of the National Academy of Sciences of the United States of America, 1984, 81, 2359-2363.	3.3	33
31	Rapid phylogenetic and functional classification of short genomic fragments with signature peptides. BMC Research Notes, 2012, 5, 460.	0.6	24
32	Bayesian Weighting for Macromolecular Crystallographic Refinement. Acta Crystallographica Section D: Biological Crystallography, 1996, 52, 743-748.	2.5	23
33	Out of the blue: the photocycle of the photoactive yellow protein. Structure, 1997, 5, 735-739.	1.6	14
34	California condor microbiomes: Bacterial variety and functional properties in captive-bred individuals. PLoS ONE, 2019, 14, e0225858.	1.1	11
35	Exploring structure space. A protein structure initiative. , 1999, 106, 141-147.		7
36	Constructing Rigorous and Broad Biosurveillance Networks for Detecting Emerging Zoonotic Outbreaks. PLoS ONE, 2015, 10, e0124037.	1.1	7

#	ARTICLE	IF	CITATIONS
37	California Condor Microbiomes. Biophysical Journal, 2017, 112, 283a-284a.	0.2	0