

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	AlphaFold illuminates half of the dark human proteins. <i>Current Opinion in Structural Biology</i> , 2022, 74, 102372.	2.6	45
2	California condor microbiomes: Bacterial variety and functional properties in captive-bred individuals. <i>PLoS ONE</i> , 2019, 14, e0225858.	1.1	11
3	California Condor Microbiomes. <i>Biophysical Journal</i> , 2017, 112, 283a-284a.	0.2	0
4	Constructing Rigorous and Broad Biosurveillance Networks for Detecting Emerging Zoonotic Outbreaks. <i>PLoS ONE</i> , 2015, 10, e0124037.	1.1	7
5	Rapid phylogenetic and functional classification of short genomic fragments with signature peptides. <i>BMC Research Notes</i> , 2012, 5, 460.	0.6	24
6	A unified model of protein dynamics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 5129-5134.	3.3	662
7	Crystal Structure of $\hat{1}^2$ -d-Xylosidase from <i>Thermoanaerobacterium saccharolyticum</i> , a Family 39 Glycoside Hydrolase. <i>Journal of Molecular Biology</i> , 2004, 335, 155-165.	2.0	69
8	The TB structural genomics consortium: a resource for <i>Mycobacterium tuberculosis</i> biology. <i>Tuberculosis</i> , 2003, 83, 223-249.	0.8	95
9	Automatic Solution of Heavy-Atom Substructures. <i>Methods in Enzymology</i> , 2003, 374, 37-83.	0.4	34
10	The TB Structural Genomics Consortium: Providing a Structural Foundation for Drug Discovery. <i>Current Drug Targets Infectious Disorders</i> , 2002, 2, 121-141.	2.1	66
11	Engineering soluble proteins for structural genomics. <i>Nature Biotechnology</i> , 2002, 20, 927-932.	9.4	174
12	Crystal structure and functional analysis of the SurE protein identify a novel phosphatase family. <i>Nature Structural Biology</i> , 2001, 8, 789-794.	9.7	199
13	Structure of a ligand-binding intermediate in wild-type carbonmonoxy myoglobin. <i>Nature</i> , 2000, 403, 921-923.	13.7	245
14	Structural alterations for proton translocation in the M state of wild-type bacteriorhodopsin. <i>Nature</i> , 2000, 406, 649-653.	13.7	335
15	The role of cavities in protein dynamics: Crystal structure of a photolytic intermediate of a mutant myoglobin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 2058-2063.	3.3	143
16	The Catalytic Pathway of Cytochrome P450cam at Atomic Resolution. <i>Science</i> , 2000, 287, 1615-1622.	6.0	1,298
17	Discrimination of solvent from protein regions in native Fourier as a means of evaluating heavy-atom solutions in the MIR and MAD methods. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 501-505.	2.5	46
18	Automated MAD and MIR structure solution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 849-861.	2.5	2,855

#	ARTICLE	IF	CITATIONS
19	Evaluation of macromolecular electron-density map quality using the correlation of local r.m.s. density. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 1872-1877.	2.5	53
20	Rapid protein-folding assay using green fluorescent protein. <i>Nature Biotechnology</i> , 1999, 17, 691-695.	9.4	840
21	Exploring structure space. A protein structure initiative. , 1999, 106, 141-147.		7
22	Crystal Structures of Myoglobin-Ligand Complexes at Near-Atomic Resolution. <i>Biophysical Journal</i> , 1999, 77, 2153-2174.	0.2	533
23	Structure of translation initiation factor 5A from <i>Pyrobaculum aerophilum</i> at 1.75 Å resolution. <i>Structure</i> , 1998, 6, 1207-1214.	1.6	109
24	Class-directed structure determination: Foundation for a protein structure initiative. <i>Protein Science</i> , 1998, 7, 1851-1856.	3.1	89
25	Out of the blue: the photocycle of the photoactive yellow protein. <i>Structure</i> , 1997, 5, 735-739.	1.6	14
26	Bayesian Correlated MAD Phasing. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1997, 53, 571-579.	2.5	63
27	Correlated Phasing of Multiple Isomorphous Replacement Data. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1996, 52, 749-757.	2.5	58
28	Bayesian Weighting for Macromolecular Crystallographic Refinement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1996, 52, 743-748.	2.5	23
29	Bayesian Difference Refinement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1996, 52, 1004-1011.	2.5	39
30	Difference refinement: obtaining differences between two related structures. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1995, 51, 609-618.	2.5	36
31	Crystal structure of photolysed carbonmonoxy-myoglobin. <i>Nature</i> , 1994, 371, 808-812.	13.7	354
32	Ligand binding to heme proteins: connection between dynamics and function. <i>Biochemistry</i> , 1991, 30, 3988-4001.	1.2	392
33	Temperature-derivative spectroscopy: a tool for protein dynamics.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1990, 87, 1-5.	3.3	174
34	Ligand binding to synthetic mutant myoglobin (His-E7→Gly): role of the distal histidine.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1988, 85, 8497-8501.	3.3	78
35	Rebinding and relaxation in the myoglobin pocket. <i>Biophysical Chemistry</i> , 1987, 26, 337-355.	1.5	372
36	Protein states and proteinquakes.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1985, 82, 5000-5004.	3.3	805

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37	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