

Ursula Pieper

List of Publications by Year in descending order

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49
papers

8,305
citations

147566

31
h-index

214527

47
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49
all docs

49
docs citations

49
times ranked

18194
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparative Protein Structure Modeling Using Modeller. <i>Current Protocols in Bioinformatics</i> , 2006, 15, Unit-5.6.	25.8	2,858
2	Comparative Protein Structure Modeling Using MODELLER. <i>Current Protocols in Protein Science</i> , 2007, 50, Unit 2.9.	2.8	1,056
3	ModBase, a database of annotated comparative protein structure models, and associated resources. <i>Nucleic Acids Research</i> , 2011, 39, D465-D474.	6.5	506
4	Tools for comparative protein structure modeling and analysis. <i>Nucleic Acids Research</i> , 2003, 31, 3375-3380.	6.5	406
5	Genomic-scale prioritization of drug targets: the TDR Targets database. <i>Nature Reviews Drug Discovery</i> , 2008, 7, 900-907.	21.5	282
6	ModBase, a database of annotated comparative protein structure models and associated resources. <i>Nucleic Acids Research</i> , 2014, 42, D336-D346.	6.5	275
7	MODBASE: a database of annotated comparative protein structure models and associated resources. <i>Nucleic Acids Research</i> , 2006, 34, D291-D295.	6.5	265
8	MODBASE, a database of annotated comparative protein structure models, and associated resources. <i>Nucleic Acids Research</i> , 2004, 32, 217D-222.	6.5	256
9	LS-SNP: large-scale annotation of coding non-synonymous SNPs based on multiple information sources. <i>Bioinformatics</i> , 2005, 21, 2814-2820.	1.8	202
10	Protein structure modeling for structural genomics. <i>Nature Structural Biology</i> , 2000, 7, 986-990.	9.7	199
11	Structural genomics: A pipeline for providing structures for the biologist. <i>Protein Science</i> , 2002, 11, 723-738.	3.1	168
12	MODBASE, a database of annotated comparative protein structure models and associated resources. <i>Nucleic Acids Research</i> , 2009, 37, D347-D354.	6.5	154
13	A Role for Matrix Metalloproteinases in Regulating Mammary Stem Cell Function via the Wnt Signaling Pathway. <i>Cell Stem Cell</i> , 2013, 13, 300-313.	5.2	123
14	A Conserved Coatmer-related Complex Containing Sec13 and Seh1 Dynamically Associates With the Vacuole in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.006478.	2.5	115
15	MODBASE, a database of annotated comparative protein structure models. <i>Nucleic Acids Research</i> , 2002, 30, 255-259.	6.5	114
16	Comparison of human solute carriers. <i>Protein Science</i> , 2010, 19, 412-428.	3.1	99
17	Atlas of the Radical SAM Superfamily: Divergent Evolution of Function Using a "Plug and Play" Domain. <i>Methods in Enzymology</i> , 2018, 606, 1-71.	0.4	99
18	Structural features of halophilicity derived from the crystal structure of dihydrofolate reductase from the Dead Sea halophilic archaeon, <i>Haloferax volcanii</i> . <i>Structure</i> , 1998, 6, 75-88.	1.6	96

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19	Facile backbone structure determination of human membrane proteins by NMR spectroscopy. <i>Nature Methods</i> , 2012, 9, 834-839.	9.0	83
20	SALIGN: a web server for alignment of multiple protein sequences and structures. <i>Bioinformatics</i> , 2012, 28, 2072-2073.	1.8	72
21	Syntheses and x-ray structures of (diphenylpyridylmethyl)lithium, -sodium, and -potassium in comparison with the triphenylmethyl derivatives. <i>Organometallics</i> , 1993, 12, 1201-1206.	1.1	68
22	Coordinating the impact of structural genomics on the human α -helical transmembrane proteome. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 135-138.	3.6	64
23	Prediction of protease substrates using sequence and structure features. <i>Bioinformatics</i> , 2010, 26, 1714-1722.	1.8	61
24	High-Throughput Computational and Experimental Techniques in Structural Genomics. <i>Genome Research</i> , 2004, 14, 2145-2154.	2.4	59
25	Homology-based annotation yields 1,042 new candidate genes in the <i>Drosophila melanogaster</i> genome. <i>Nature Genetics</i> , 2001, 27, 337-340.	9.4	58
26	Protein complex compositions predicted by structural similarity. <i>Nucleic Acids Research</i> , 2006, 34, 2943-2952.	6.5	56
27	Selecting Optimum Eukaryotic Integral Membrane Proteins for Structure Determination by Rapid Expression and Solubilization Screening. <i>Journal of Molecular Biology</i> , 2009, 385, 820-830.	2.0	53
28	Structure, Dynamics, Evolution, and Function of a Major Scaffold Component in the Nuclear Pore Complex. <i>Structure</i> , 2013, 21, 560-571.	1.6	53
29	Carbanion or Amide? First Charge Density Study of Parent β -Picolyllithium. <i>Angewandte Chemie - International Edition</i> , 2009, 48, 2978-2982.	7.2	51
30	Target Prediction for an Open Access Set of Compounds Active against <i>Mycobacterium tuberculosis</i> . <i>PLoS Computational Biology</i> , 2013, 9, e1003253.	1.5	51
31	The AnnoLite and AnnoLyze programs for comparative annotation of protein structures. <i>BMC Bioinformatics</i> , 2007, 8, S4.	1.2	36
32	DBAli tools: mining the protein structure space. <i>Nucleic Acids Research</i> , 2007, 35, W393-W397.	6.5	25
33	Target selection and annotation for the structural genomics of the amidohydrolase and enolase superfamilies. <i>Journal of Structural and Functional Genomics</i> , 2009, 10, 107-125.	1.2	25
34	Consequences of domain insertion on sequence-structure divergence in a superfold. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E3381-7.	3.3	25
35	A Kernel for Open Source Drug Discovery in Tropical Diseases. <i>PLoS Neglected Tropical Diseases</i> , 2009, 3, e418.	1.3	23
36	Structural evidence for the evolutionary divergence of mycoplasma from Gram-positive bacteria: the histidine-containing phosphocarrier protein. <i>Structure</i> , 1995, 3, 781-790.	1.6	22

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37	Functional hot spots in human ATP-binding cassette transporter nucleotide binding domains. <i>Protein Science</i> , 2010, 19, 2110-2121.	3.1	19
38	ModView, visualization of multiple protein sequences and structures. <i>Bioinformatics</i> , 2003, 19, 165-166.	1.8	18
39	Structure of a putative BenF-like porin from <i>Pseudomonas fluorescens</i> Pf5 at 2.6 Å... resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 3056-3062.	1.5	17
40	Structure of the C-terminal domain of <i>Saccharomyces cerevisiae</i> Nup133, a component of the nuclear pore complex. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 1672-1677.	1.5	16
41	Comparative Protein Structure Modeling. , 2005, , 831-860.		15
42	Prediction of Functionally Important Phospho-Regulatory Events in <i>Xenopus laevis</i> Oocytes. <i>PLoS Computational Biology</i> , 2015, 11, e1004362.	1.5	14
43	Structures of the autoproteolytic domain from the <i>Saccharomyces cerevisiae</i> nuclear pore complex component, Nup145. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 1992-1998.	1.5	13
44	A survey of integral α -helical membrane proteins. <i>Journal of Structural and Functional Genomics</i> , 2009, 10, 269-280.	1.2	12
45	A kernel for the Tropical Disease Initiative. <i>Nature Biotechnology</i> , 2009, 27, 320-321.	9.4	7
46	Atomic structure of the nuclear pore complex targeting domain of a Nup116 homologue from the yeast, <i>Candida glabrata</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 2110-2116.	1.5	7
47	Modeling Protein Structure from its Sequence. <i>Current Protocols in Bioinformatics</i> , 2003, 3, 5.1.1.	25.8	6
48	Biochemical characterization and structural modeling of human cathepsin E variant 2 in comparison to the wild-type protein. <i>Biological Chemistry</i> , 2012, 393, 177-186.	1.2	3
49	Response to "Predictable difficulty or difficulty to predict". <i>Protein Science</i> , 2011, 20, 4-5.	3.1	0