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 g-index
49 all docs	49 docs citations	49 times ranked	18194 citing authors

#	Article	IF	Citations
1	Atlas of the Radical SAM Superfamily: Divergent Evolution of Function Using a â€œPlug and Playâ€• Domain. Methods in Enzymology, 2018, 606, 1-71.	0.4	99
2	Prediction of Functionally Important Phospho-Regulatory Events in Xenopus laevis Oocytes. PLoS Computational Biology, 2015, 11, e1004362.	1.5	14
3	ModBase, a database of annotated comparative protein structure models and associated resources. Nucleic Acids Research, 2014, 42, D336-D346.	6.5	275
4	Coordinating the impact of structural genomics on the human Î±-helical transmembrane proteome. Nature Structural and Molecular Biology, 2013, 20, 135-138.	3.6	64
5	A Role for Matrix Metalloproteinases in Regulating Mammary Stem Cell Function via the Wnt Signaling Pathway. Cell Stem Cell, 2013, 13, 300-313.	5.2	123
6	Structure, Dynamics, Evolution, and Function of a Major Scaffold Component in the Nuclear Pore Complex. Structure, 2013, 21, 560-571.	1.6	53
7	Target Prediction for an Open Access Set of Compounds Active against Mycobacterium tuberculosis. PLoS Computational Biology, 2013, 9, e1003253.	1.5	51
8	Consequences of domain insertion on sequence-structure divergence in a superfold. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E3381-7.	3.3	25
9	Biochemical characterization and structural modeling of human cathepsin E variant 2 in comparison to the wild-type protein. Biological Chemistry, 2012, 393, 177-186.	1.2	3
10	SALIGN: a web server for alignment of multiple protein sequences and structures. Bioinformatics, 2012, 28, 2072-2073.	1.8	72
11	Atomic structure of the nuclear pore complex targeting domain of a Nup116 homologue from the yeast, Candida glabrata. Proteins: Structure, Function and Bioinformatics, 2012, 80, 2110-2116.	1.5	7
12	Facile backbone structure determination of human membrane proteins by NMR spectroscopy. Nature Methods, 2012, 9, 834-839.	9.0	83
13	Structure of the Câ€terminal domain of Saccharomyces cerevisiae Nup133, a component of the nuclear pore complex. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1672-1677.	1.5	16
14	Response to â€œPredictable difficulty or difficulty to predictâ€• Protein Science, 2011, 20, 4-5.	3.1	0
15	A Conserved Coatomer-related Complex Containing Sec13 and Seh1 Dynamically Associates With the Vacuole in Saccharomyces cerevisiae. Molecular and Cellular Proteomics, 2011, 10, M110.006478.	2.5	115
16	ModBase, a database of annotated comparative protein structure models, and associated resources. Nucleic Acids Research, 2011, 39, D465-D474.	6.5	506
17	Comparison of human solute carriers. Protein Science, 2010, 19, 412-428.	3.1	99
18	Functional hot spots in human ATPâ€binding cassette transporter nucleotide binding domains. Protein Science, 2010, 19, 2110-2121.	3.1	19

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19	Structures of the autoproteolytic domain from the Saccharomyces cerevisiae nuclear pore complex component, Nup145. Proteins: Structure, Function and Bioinformatics, 2010, 78, 1992-1998.	1.5	13
20	Structure of a putative BenFâ€‰ke porin from Pseudomonas fluorescens Pfâ€‰5 at 2.6 Ã... resolution. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3056-3062.	1.5	17
21	Prediction of protease substrates using sequence and structure features. Bioinformatics, 2010, 26, 1714-1722.	1.8	61
22	MODBASE, a database of annotated comparative protein structure models and associated resources. Nucleic Acids Research, 2009, 37, D347-D354.	6.5	154
23	A Kernel for Open Source Drug Discovery in Tropical Diseases. PLoS Neglected Tropical Diseases, 2009, 3, e418.	1.3	23
24	Carbanion or Amide? First Charge Density Study of Parent 2â€‰Picolyllithium. Angewandte Chemie - International Edition, 2009, 48, 2978-2982.	7.2	51
25	Target selection and annotation for the structural genomics of the amidohydrolase and enolase superfamilies. Journal of Structural and Functional Genomics, 2009, 10, 107-125.	1.2	25
26	A survey of integral Î±-helical membrane proteins. Journal of Structural and Functional Genomics, 2009, 10, 269-280.	1.2	12
27	A kernel for the Tropical Disease Initiative. Nature Biotechnology, 2009, 27, 320-321.	9.4	7
28	Selecting Optimum Eukaryotic Integral Membrane Proteins for Structure Determination by Rapid Expression and Solubilization Screening. Journal of Molecular Biology, 2009, 385, 820-830.	2.0	53
29	Genomic-scale prioritization of drug targets: the TDR Targets database. Nature Reviews Drug Discovery, 2008, 7, 900-907.	21.5	282
30	DBAli tools: mining the protein structure space. Nucleic Acids Research, 2007, 35, W393-W397.	6.5	25
31	The AnnoLite and AnnoLyze programs for comparative annotation of protein structures. BMC Bioinformatics, 2007, 8, S4.	1.2	36
32	Comparative Protein Structure Modeling Using MODELLER. Current Protocols in Protein Science, 2007, 50, Unit 2.9.	2.8	1,056
33	Comparative Protein Structure Modeling Using Modeller. Current Protocols in Bioinformatics, 2006, 15, Unit-5.6.	25.8	2,858
34	Protein complex compositions predicted by structural similarity. Nucleic Acids Research, 2006, 34, 2943-2952.	6.5	56
35	MODBASE: a database of annotated comparative protein structure models and associated resources. Nucleic Acids Research, 2006, 34, D291-D295.	6.5	265
36	Comparative Protein Structure Modeling. , 2005, , 831-860.		15

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37	LS-SNP: large-scale annotation of coding non-synonymous SNPs based on multiple information sources. Bioinformatics, 2005, 21, 2814-2820.	1.8	202
38	High-Throughput Computational and Experimental Techniques in Structural Genomics. Genome Research, 2004, 14, 2145-2154.	2.4	59
39	MODBASE, a database of annotated comparative protein structure models, and associated resources. Nucleic Acids Research, 2004, 32, 217D-222.	6.5	256
40	Modeling Protein Structure from its Sequence. Current Protocols in Bioinformatics, 2003, 3, 5.1.1.	25.8	6
41	Tools for comparative protein structure modeling and analysis. Nucleic Acids Research, 2003, 31, 3375-3380.	6.5	406
42	ModView, visualization of multiple protein sequences and structures. Bioinformatics, 2003, 19, 165-166.	1.8	18
43	MODBASE, a database of annotated comparative protein structure models. Nucleic Acids Research, 2002, 30, 255-259.	6.5	114
44	Structural genomics: A pipeline for providing structures for the biologist. Protein Science, 2002, 11, 723-738.	3.1	168
45	Homology-based annotation yields 1,042 new candidate genes in the Drosophila melanogaster genome. Nature Genetics, 2001, 27, 337-340.	9.4	58
46	Protein structure modeling for structural genomics. Nature Structural Biology, 2000, 7, 986-990.	9.7	199
47	Structural features of halophilicity derived from the crystal structure of dihydrofolate reductase from the Dead Sea halophilic archaeon, Haloferax volcanii. Structure, 1998, 6, 75-88.	1.6	96
48	Structural evidence for the evolutionary divergence of mycoplasma from Gram-positive bacteria: the histidine-containing phosphocarrier protein. Structure, 1995, 3, 781-790.	1.6	22
49	Syntheses and x-ray structures of (diphenylpyridylmethyl)lithium, -sodium, and -potassium in comparison with the triphenylmethyl derivatives. Organometallics, 1993, 12, 1201-1206.	1.1	68