Ursula Pieper

List of Publications by Year
in descending order

49	8,305	147801	214800
papers	citations	31	47
		h-index	g-index

49	49	49	18194
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Comparative Protein Structure Modeling Using Modeller. Current Protocols in Bioinformatics, 2006, 15, Unit-5.6.	25.8	2,858
2	Comparative Protein Structure Modeling Using MODELLER. Current Protocols in Protein Science, 2007, 50, Unit 2.9.	2.8	1,056
3	ModBase, a database of annotated comparative protein structure models, and associated resources. Nucleic Acids Research, 2011, 39, D465-D474.	14.5	506
4	Tools for comparative protein structure modeling and analysis. Nucleic Acids Research, 2003, 31, 3375-3380.	14.5	406
5	Genomic-scale prioritization of drug targets: the TDR Targets database. Nature Reviews Drug Discovery, 2008, 7, 900-907.	46.4	282
6	ModBase, a database of annotated comparative protein structure models and associated resources. Nucleic Acids Research, 2014, 42, D336-D346.	14.5	275
7	MODBASE: a database of annotated comparative protein structure models and associated resources. Nucleic Acids Research, 2006, 34, D291-D295.	14.5	265
8	MODBASE, a database of annotated comparative protein structure models, and associated resources. Nucleic Acids Research, 2004, 32, 217D-222.	14.5	256
9	LS-SNP: large-scale annotation of coding non-synonymous SNPs based on multiple information sources. Bioinformatics, 2005, 21, 2814-2820.	4.1	202
10	Protein structure modeling for structural genomics. Nature Structural Biology, 2000, 7, 986-990.	9.7	199
11	Structural genomics: A pipeline for providing structures for the biologist. Protein Science, 2002, 11, 723-738.	7.6	168
12	MODBASE, a database of annotated comparative protein structure models and associated resources. Nucleic Acids Research, 2009, 37, D347-D354.	14.5	154
13	A Role for Matrix Metalloproteinases in Regulating Mammary Stem Cell Function via the Wnt Signaling Pathway. Cell Stem Cell, 2013, 13, 300-313.	11.1	123
14	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.	3.8	115
15	MODBASE, a database of annotated comparative protein structure models. Nucleic Acids Research, 2002, 30, 255-259.	14.5	114
16	Comparison of human solute carriers. Protein Science, 2010, 19, 412-428.	7.6	99
17	Atlas of the Radical SAM Superfamily: Divergent Evolution of Function Using a â€œPlug and Playâ€• Domain. Methods in Enzymology, 2018, 606, 1-71.	1.0	99
18	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.	3.3	96

#	ARTICLE	IF	CITATIONS
19	Facile backbone structure determination of human membrane proteins by NMR spectroscopy. Nature Methods, 2012, 9, 834-839.	19.0	83
20	SALIGN: a web server for alignment of multiple protein sequences and structures. Bioinformatics, 2012, 28, 2072-2073.	4.1	72
21	Syntheses and x-ray structures of (diphenylpyridylmethyl)lithium, -sodium, and -potassium in comparison with the triphenylmethyl derivatives. Organometallics, 1993, 12, 1201-1206.	2.3	68
22	Coordinating the impact of structural genomics on the human α-helical transmembrane proteome. Nature Structural and Molecular Biology, 2013, 20, 135-138.	8.2	64
23	Prediction of protease substrates using sequence and structure features. Bioinformatics, 2010, 26, 1714-1722.	4.1	61
24	High-Throughput Computational and Experimental Techniques in Structural Genomics. Genome Research, 2004, 14, 2145-2154.	5.5	59
25	Homology-based annotation yields 1,042 new candidate genes in the Drosophila melanogaster genome. Nature Genetics, 2001, 27, 337-340.	21.4	58
26	Protein complex compositions predicted by structural similarity. Nucleic Acids Research, 2006, 34, 2943-2952.	14.5	56
27	Selecting Optimum Eukaryotic Integral Membrane Proteins for Structure Determination by Rapid Expression and Solubilization Screening. Journal of Molecular Biology, 2009, 385, 820-830.	4.2	53
28	Structure, Dynamics, Evolution, and Function of a Major Scaffold Component in the Nuclear Pore Complex. Structure, 2013, 21, 560-571.	3.3	53
29	Carbanion or Amide? First Charge Density Study of Parent 2-Picolyllithium. Angewandte Chemie - International Edition, 2009, 48, 2978-2982.	13.8	51
30	Target Prediction for an Open Access Set of Compounds Active against Mycobacterium tuberculosis. PLoS Computational Biology, 2013, 9, e1003253.	3.2	51
31	The AnnoLite and AnnoLyze programs for comparative annotation of protein structures. BMC Bioinformatics, 2007, 8, S4.	2.6	36
32	DBAli tools: mining the protein structure space. Nucleic Acids Research, 2007, 35, W393-W397.	14.5	25
33	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
34	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.	7.1	25
35	A Kernel for Open Source Drug Discovery in Tropical Diseases. PLoS Neglected Tropical Diseases, 2009, 3, e418.	3.0	23
36	Structural evidence for the evolutionary divergence of mycoplasma from Gram-positive bacteria: the histidine-containing phosphocarrier protein. Structure, 1995, 3, 781-790.	3.3	22

#	Article	IF	Citations
37	Functional hot spots in human ATPâ€binding cassette transporter nucleotide binding domains. Protein Science, 2010, 19, 2110-2121.	7.6	19
38	ModView, visualization of multiple protein sequences and structures. Bioinformatics, 2003, 19, 165-166.	4.1	18
39	Structure of a putative BenFâ€like porin from <i>Pseudomonas fluorescens</i> Pfâ€5 at 2.6 Ã… resolution. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3056-3062.	2.6	17
40	Structure of the Câ€terminal domain of <i>Saccharomyces cerevisiae</i> Nup133, a component of the nuclear pore complex. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1672-1677.	2.6	16
41	Comparative Protein Structure Modeling. , 2005, , 831-860.		15
42	Prediction of Functionally Important Phospho-Regulatory Events in Xenopus laevis Oocytes. PLoS Computational Biology, 2015, 11, e1004362.	3.2	14
43	Structures of the autoproteolytic domain from the <i>Saccharomyces cerevisiae</i> nuclear pore complex component, Nup145. Proteins: Structure, Function and Bioinformatics, 2010, 78, 1992-1998.	2.6	13
44	A survey of integral Î±-helical membrane proteins. Journal of Structural and Functional Genomics, 2009, 10, 269-280.	1.2	12
45	A kernel for the Tropical Disease Initiative. Nature Biotechnology, 2009, 27, 320-321.	17.5	7
46	Atomic structure of the nuclear pore complex targeting domain of a Nup116 homologue from the yeast, <i>Candida glabrata</i>. Proteins: Structure, Function and Bioinformatics, 2012, 80, 2110-2116.	2.6	7
47	Modeling Protein Structure from its Sequence. Current Protocols in Bioinformatics, 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. Biological Chemistry, 2012, 393, 177-186.	2.5	3
49	Response to â€œPredictable difficulty or difficulty to predictâ€. Protein Science, 2011, 20, 4-5.	7.6	0