

Aron Marchler-Bauer

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

64
papers

20,283
citations

38
h-index

70
g-index

70
ext. papers

26,328
ext. citations

14.1
avg, IF

6.82
L-index

#	Paper	IF	Citations
64	iCn3D: From Web-Based 3D Viewer to Structural Analysis Tool in Batch Mode.. <i>Frontiers in Molecular Biosciences</i> , 2022 , 9, 831740	5.6	3
63	Database resources of the national center for biotechnology information. <i>Nucleic Acids Research</i> , 2021 ,	20.1	55
62	The InterPro protein families and domains database: 20 years on. <i>Nucleic Acids Research</i> , 2021 , 49, D344-D354	20.1	358
61	RefSeq: expanding the Prokaryotic Genome Annotation Pipeline reach with protein family model curation. <i>Nucleic Acids Research</i> , 2021 , 49, D1020-D1028	20.1	110
60	Database resources of the National Center for Biotechnology Information. <i>Nucleic Acids Research</i> , 2021 , 49, D10-D17	20.1	143
59	Obtaining extremely large and accurate protein multiple sequence alignments from curated hierarchical alignments. <i>Database: the Journal of Biological Databases and Curation</i> , 2020 , 2020,	5	1
58	NCBI's Conserved Domain Database and Tools for Protein Domain Analysis. <i>Current Protocols in Bioinformatics</i> , 2020 , 69, e90	24.2	34
57	CDD/SPARCLE: the conserved domain database in 2020. <i>Nucleic Acids Research</i> , 2020 , 48, D265-D268	20.1	652
56	iCn3D, a web-based 3D viewer for sharing 1D/2D/3D representations of biomolecular structures. <i>Bioinformatics</i> , 2020 , 36, 131-135	7.2	50
55	Biological Assembly Comparison with VAST. <i>Methods in Molecular Biology</i> , 2020 , 2112, 175-186	1.4	3
54	PubMed Text Similarity Model and its application to curation efforts in the Conserved Domain Database. <i>Database: the Journal of Biological Databases and Curation</i> , 2019 , 2019,	5	8
53	Database resources of the National Center for Biotechnology Information. <i>Nucleic Acids Research</i> , 2019 , 47, D23-D28	20.1	301
52	InterPro in 2019: improving coverage, classification and access to protein sequence annotations. <i>Nucleic Acids Research</i> , 2019 , 47, D351-D360	20.1	835
51	Database resources of the National Center for Biotechnology Information. <i>Nucleic Acids Research</i> , 2018 , 46, D8-D13	20.1	746
50	RefSeq: an update on prokaryotic genome annotation and curation. <i>Nucleic Acids Research</i> , 2018 , 46, D851-D860	20.1	428
49	Database Resources of the National Center for Biotechnology Information. <i>Nucleic Acids Research</i> , 2017 , 45, D12-D17	20.1	608
48	InterPro in 2017-beyond protein family and domain annotations. <i>Nucleic Acids Research</i> , 2017 , 45, D190-D199	20.1	970

47	CDD/SPARCLE: functional classification of proteins via subfamily domain architectures. <i>Nucleic Acids Research</i> , 2017 , 45, D200-D203	20.1	1514
46	cddApp: a Cytoscape app for accessing the NCBI conserved domain database. <i>Bioinformatics</i> , 2015 , 31, 134-6	7.2	3
45	Improving the consistency of domain annotation within the Conserved Domain Database. <i>Database: the Journal of Biological Databases and Curation</i> , 2015 , 2015,	5	12
44	CDD: NCBI's conserved domain database. <i>Nucleic Acids Research</i> , 2015 , 43, D222-6	20.1	2149
43	Database resources of the National Center for Biotechnology Information. <i>Nucleic Acids Research</i> , 2014 , 42, D7-17	20.1	313
42	MMDB and VAST+: tracking structural similarities between macromolecular complexes. <i>Nucleic Acids Research</i> , 2014 , 42, D297-303	20.1	194
41	CDD: conserved domains and protein three-dimensional structure. <i>Nucleic Acids Research</i> , 2013 , 41, D348-52	20.1	665
40	Automated hierarchical classification of protein domain subfamilies based on functionally-divergent residue signatures. <i>BMC Bioinformatics</i> , 2012 , 13, 144	3.6	9
39	MMDB: 3D structures and macromolecular interactions. <i>Nucleic Acids Research</i> , 2012 , 40, D461-4	20.1	85
38	Annotation of functional sites with the Conserved Domain Database. <i>Database: the Journal of Biological Databases and Curation</i> , 2012 , 2012, bar058	5	16
37	IBIS (Inferred Biomolecular Interaction Server) reports, predicts and integrates multiple types of conserved interactions for proteins. <i>Nucleic Acids Research</i> , 2012 , 40, D834-40	20.1	75
36	Database resources of the National Center for Biotechnology Information. <i>Nucleic Acids Research</i> , 2012 , 40, D13-25	20.1	458
35	CDD: a Conserved Domain Database for the functional annotation of proteins. <i>Nucleic Acids Research</i> , 2011 , 39, D225-9	20.1	2249
34	Database resources of the National Center for Biotechnology Information. <i>Nucleic Acids Research</i> , 2011 , 39, D38-51	20.1	510
33	Automatic annotation of experimentally derived, evolutionarily conserved post-translational modifications onto multiple genomes. <i>Database: the Journal of Biological Databases and Curation</i> , 2011 , 2011, bar019	5	3
32	AlexSys: a knowledge-based expert system for multiple sequence alignment construction and analysis. <i>Nucleic Acids Research</i> , 2010 , 38, 6338-49	20.1	10
31	Inferred Biomolecular Interaction Server--a web server to analyze and predict protein interacting partners and binding sites. <i>Nucleic Acids Research</i> , 2010 , 38, D518-24	20.1	66
30	The NCBI BioSystems database. <i>Nucleic Acids Research</i> , 2010 , 38, D492-6	20.1	526

29	Database resources of the National Center for Biotechnology Information. <i>Nucleic Acids Research</i> , 2010 , 38, D5-16	20.1	374
28	CDD: specific functional annotation with the Conserved Domain Database. <i>Nucleic Acids Research</i> , 2009 , 37, D205-10	20.1	864
27	CORAL: aligning conserved core regions across domain families. <i>Bioinformatics</i> , 2009 , 25, 1862-8	7.2	4
26	Knowledge-based expert systems and a proof-of-concept case study for multiple sequence alignment construction and analysis. <i>Briefings in Bioinformatics</i> , 2009 , 10, 11-23	13.4	12
25	Protein subfamily assignment using the Conserved Domain Database. <i>BMC Research Notes</i> , 2008 , 1, 114	2.3	22
24	MMDB: annotating protein sequences with Entrez's 3D-structure database. <i>Nucleic Acids Research</i> , 2007 , 35, D298-300	20.1	86
23	CDD: a conserved domain database for interactive domain family analysis. <i>Nucleic Acids Research</i> , 2007 , 35, D237-40	20.1	664
22	CDD: a Conserved Domain Database for protein classification. <i>Nucleic Acids Research</i> , 2005 , 33, D192-6	20.1	880
21	CD-Search: protein domain annotations on the fly. <i>Nucleic Acids Research</i> , 2004 , 32, W327-31	20.1	1369
20	Identification of a subunit of a novel Kleisin-beta/SMC complex as a potential substrate of protein phosphatase 2A. <i>Current Biology</i> , 2003 , 13, 2058-64	6.3	79
19	CDD: a curated Entrez database of conserved domain alignments. <i>Nucleic Acids Research</i> , 2003 , 31, 383-7	20.1	620
18	MMDB: Entrez's 3D-structure database. <i>Nucleic Acids Research</i> , 2003 , 31, 474-7	20.1	128
17	Comparison of sequence and structure alignments for protein domains. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002 , 48, 439-46	4.2	32
16	MMDB: Entrez's 3D-structure database. <i>Nucleic Acids Research</i> , 2002 , 30, 249-52	20.1	27
15	CDD: a database of conserved domain alignments with links to domain three-dimensional structure. <i>Nucleic Acids Research</i> , 2002 , 30, 281-3	20.1	513
14	MMDB: 3D structure data in Entrez. <i>Nucleic Acids Research</i> , 2000 , 28, 243-5	20.1	31
13	Characterization of p40/GPR69A as a peripheral membrane protein related to the lantibiotic synthetase component C. <i>Biochemical and Biophysical Research Communications</i> , 2000 , 275, 69-74	3.4	38
12	Combination of threading potentials and sequence profiles improves fold recognition. <i>Journal of Molecular Biology</i> , 2000 , 296, 1319-31	6.5	110

11	MMDB: Entrez's 3D structure database. <i>Nucleic Acids Research</i> , 1999 , 27, 240-3	20.1	41
10	The combinatorics and extreme value statistics of protein threading. <i>Annals of Combinatorics</i> , 1999 , 3, 81-93	0.7	1
9	Threading with explicit models for evolutionary conservation of structure and sequence 1999 , 37, 133-140		42
8	A measure of progress in fold recognition?. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999 , 37, 218-225	4.2	33
7	Isolation, molecular characterization, and tissue-specific expression of a novel putative G protein-coupled receptor. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1998 , 1395, 301-8		29
6	A measure of success in fold recognition. <i>Trends in Biochemical Sciences</i> , 1997 , 22, 236-40	10.3	33
5	Measures of threading specificity and accuracy 1997 , 29, 74-82		28
4	A retrospective analysis of CASP2 threading predictions 1997 , 29, 83-91		21
3	A retrospective analysis of CASP2 threading predictions. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997 , 29, 83-91	4.2	1
2	An improved pair potential to recognize native protein folds. <i>Proteins: Structure, Function and Bioinformatics</i> , 1994 , 18, 254-61	4.2	37
1	iCn3D, a Web-based 3D Viewer for Sharing 1D/2D/3D Representations of Biomolecular Structures		1