

Aron Marchler-Bauer

List of Publications by Year in descending order

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67
papers

30,277
citations

76196

40
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128067

60
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70
all docs

70
docs citations

70
times ranked

43103
citing authors

#	ARTICLE	IF	CITATIONS
1	CDD: NCBI's conserved domain database. <i>Nucleic Acids Research</i> , 2015, 43, D222-D226.	6.5	3,022
2	CDD: a Conserved Domain Database for the functional annotation of proteins. <i>Nucleic Acids Research</i> , 2011, 39, D225-D229.	6.5	2,727
3	CDD/SPARCLE: functional classification of proteins via subfamily domain architectures. <i>Nucleic Acids Research</i> , 2017, 45, D200-D203.	6.5	2,402
4	CDD/SPARCLE: the conserved domain database in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D265-D268.	6.5	1,878
5	CD-Search: protein domain annotations on the fly. <i>Nucleic Acids Research</i> , 2004, 32, W327-W331.	6.5	1,785
6	The InterPro protein families and domains database: 20 years on. <i>Nucleic Acids Research</i> , 2021, 49, D344-D354.	6.5	1,385
7	InterPro in 2017â€”beyond protein family and domain annotations. <i>Nucleic Acids Research</i> , 2017, 45, D190-D199.	6.5	1,358
8	Database resources of the National Center for Biotechnology Information. <i>Nucleic Acids Research</i> , 2018, 46, D8-D13.	6.5	1,291
9	InterPro in 2019: improving coverage, classification and access to protein sequence annotations. <i>Nucleic Acids Research</i> , 2019, 47, D351-D360.	6.5	1,291
10	CDD: a Conserved Domain Database for protein classification. <i>Nucleic Acids Research</i> , 2004, 33, D192-D196.	6.5	976
11	CDD: specific functional annotation with the Conserved Domain Database. <i>Nucleic Acids Research</i> , 2009, 37, D205-D210.	6.5	935
12	Database resources of the national center for biotechnology information. <i>Nucleic Acids Research</i> , 2022, 50, D20-D26.	6.5	887
13	CDD: conserved domains and protein three-dimensional structure. <i>Nucleic Acids Research</i> , 2012, 41, D348-D352.	6.5	766
14	Database Resources of the National Center for Biotechnology Information. <i>Nucleic Acids Research</i> , 2017, 45, D12-D17.	6.5	764
15	RefSeq: an update on prokaryotic genome annotation and curation. <i>Nucleic Acids Research</i> , 2018, 46, D851-D860.	6.5	749
16	CDD: a conserved domain database for interactive domain family analysis. <i>Nucleic Acids Research</i> , 2007, 35, D237-D240.	6.5	744
17	The NCBI BioSystems database. <i>Nucleic Acids Research</i> , 2010, 38, D492-D496.	6.5	706
18	CDD: a curated Entrez database of conserved domain alignments. <i>Nucleic Acids Research</i> , 2003, 31, 383-387.	6.5	673

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19	CDD: a database of conserved domain alignments with links to domain three-dimensional structure. <i>Nucleic Acids Research</i> , 2002, 30, 281-283.	6.5	609
20	Database resources of the National Center for Biotechnology Information. <i>Nucleic Acids Research</i> , 2011, 39, D38-D51.	6.5	582
21	Database resources of the National Center for Biotechnology Information. <i>Nucleic Acids Research</i> , 2021, 49, D10-D17.	6.5	545
22	RefSeq: expanding the Prokaryotic Genome Annotation Pipeline reach with protein family model curation. <i>Nucleic Acids Research</i> , 2021, 49, D1020-D1028.	6.5	519
23	Database resources of the National Center for Biotechnology Information. <i>Nucleic Acids Research</i> , 2012, 40, D13-D25.	6.5	510
24	Database resources of the National Center for Biotechnology Information. <i>Nucleic Acids Research</i> , 2019, 47, D23-D28.	6.5	502
25	Database resources of the National Center for Biotechnology Information. <i>Nucleic Acids Research</i> , 2010, 38, D5-D16.	6.5	417
26	Database resources of the National Center for Biotechnology Information. <i>Nucleic Acids Research</i> , 2014, 42, D7-D17.	6.5	349
27	MMDB and VAST+: tracking structural similarities between macromolecular complexes. <i>Nucleic Acids Research</i> , 2014, 42, D297-D303.	6.5	278
28	MMDB: Entrez's 3D-structure database. <i>Nucleic Acids Research</i> , 2003, 31, 474-477.	6.5	137
29	NCBI's Conserved Domain Database and Tools for Protein Domain Analysis. <i>Current Protocols in Bioinformatics</i> , 2020, 69, e90.	25.8	136
30	Combination of threading potentials and sequence profiles improves fold recognition 1 Edited by B. Honig. <i>Journal of Molecular Biology</i> , 2000, 296, 1319-1331.	2.0	116
31	iCn3D, a web-based 3D viewer for sharing 1D/2D/3D representations of biomolecular structures. <i>Bioinformatics</i> , 2020, 36, 131-135.	1.8	113
32	MMDB: 3D structures and macromolecular interactions. <i>Nucleic Acids Research</i> , 2012, 40, D461-D464.	6.5	96
33	MMDB: annotating protein sequences with Entrez's 3D-structure database. <i>Nucleic Acids Research</i> , 2007, 35, D298-D300.	6.5	92
34	IBIS (Inferred Biomolecular Interaction Server) reports, predicts and integrates multiple types of conserved interactions for proteins. <i>Nucleic Acids Research</i> , 2012, 40, D834-D840.	6.5	88
35	MMDB: Entrez's 3D-structure database. <i>Nucleic Acids Research</i> , 2002, 30, 249-252.	6.5	87
36	Identification of a Subunit of a Novel Kleisin- \hat{I}^2 /SMC Complex as a Potential Substrate of Protein Phosphatase 2A. <i>Current Biology</i> , 2003, 13, 2058-2064.	1.8	84

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37	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-D524.	6.5	75
38	Threading with explicit models for evolutionary conservation of structure and sequence. , 1999, 37, 133-140.		53
39	An improved pair potential to recognize native protein folds. <i>Proteins: Structure, Function and Bioinformatics</i> , 1994, 18, 254-261.	1.5	47
40	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.	1.0	44
41	MMDB: Entrez's 3D structure database. <i>Nucleic Acids Research</i> , 1999, 27, 240-243.	6.5	43
42	MMDB: 3D structure data in Entrez. <i>Nucleic Acids Research</i> , 2000, 28, 243-245.	6.5	43
43	A measure of success in fold recognition. <i>Trends in Biochemical Sciences</i> , 1997, 22, 236-240.	3.7	37
44	A measure of progress in fold recognition?. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 37, 218-225.	1.5	37
45	Measures of threading specificity and accuracy. , 1997, 29, 74-82.		35
46	Comparison of sequence and structure alignments for protein domains. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 48, 439-446.	1.5	34
47	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, 301-308.	2.4	33
48	A retrospective analysis of CASP2 threading predictions. , 1997, 29, 83-91.		28
49	Protein subfamily assignment using the Conserved Domain Database. <i>BMC Research Notes</i> , 2008, 1, 114.	0.6	26
50	iCn3D: From Web-Based 3D Viewer to Structural Analysis Tool in Batch Mode. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 831740.	1.6	26
51	Annotation of functional sites with the Conserved Domain Database. <i>Database: the Journal of Biological Databases and Curation</i> , 2012, 2012, bar058-bar058.	1.4	20
52	Improving the consistency of domain annotation within the Conserved Domain Database. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, .	1.4	16
53	Knowledge-based expert systems and a proof-of-concept case study for multiple sequence alignment construction and analysis. <i>Briefings in Bioinformatics</i> , 2008, 10, 11-23.	3.2	15
54	AlexSys: a knowledge-based expert system for multiple sequence alignment construction and analysis. <i>Nucleic Acids Research</i> , 2010, 38, 6338-6349.	6.5	12

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55	Automated hierarchical classification of protein domain subfamilies based on functionally-divergent residue signatures. BMC Bioinformatics, 2012, 13, 144.	1.2	11
56	Biological Assembly Comparison with VAST+. Methods in Molecular Biology, 2020, 2112, 175-186.	0.4	11
57	PubMed Text Similarity Model and its application to curation efforts in the Conserved Domain Database. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	10
58	CORAL: aligning conserved core regions across domain families. Bioinformatics, 2009, 25, 1862-1868.	1.8	4
59	cddApp: a Cytoscape app for accessing the NCBI conserved domain database. Bioinformatics, 2015, 31, 134-136.	1.8	4
60	Obtaining extremely large and accurate protein multiple sequence alignments from curated hierarchical alignments. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	1.4	4
61	Automatic annotation of experimentally derived, evolutionarily conserved post-translational modifications onto multiple genomes. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar019-bar019.	1.4	3
62	Abstract 95: Phylogenetic classification, structural evolution, and functional divergence of the ABC-type transporters: Inferences derived from CDTree/Cn3D software applications. , 2010, , .		2
63	The combinatorics and extreme value statistics of protein threading. Annals of Combinatorics, 1999, 3, 81-93.	0.3	1
64	Abstract 2900: Phylogenetic classification, structural evolution, and functional divergence of the Ras superfamily of GTPases as tracked by the Conserved Domain Database (CDD)... , 2013, , .		0
65	Abstract 1090: Evolutionary, structural, and functional insights into the seven-transmembrane GPCR superfamily through NCBI's Conserved Domain Database. , 2015, , .		0
66	Abstract 556: CDD: functional insights into orphan GPCRs via subfamily domain architectures. , 2017, , .		0
67	Quantifying the immunological distinctiveness of emerging SARS-CoV-2 variants in the context of prior regional herd exposure. , 0, , .		0