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List of Publications by Year in descending order

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78
papers

24,513
citations

71102

41
h-index

62596

80
g-index

89
all docs

89
docs citations

89
times ranked

32291
citing authors

#	ARTICLE	IF	CITATIONS
1	The IntAct database: efficient access to fine-grained molecular interaction data. Nucleic Acids Research, 2022, 50, D648-D653.	14.5	89
2	The Quest for Orthologs orthology benchmark service in 2022. Nucleic Acids Research, 2022, 50, W623-W632.	14.5	29
3	Profiling the Human Phosphoproteome to Estimate the True Extent of Protein Phosphorylation. Journal of Proteome Research, 2022, 21, 1510-1524.	3.7	15
4	Method for Independent Estimation of the False Localization Rate for Phosphoproteomics. Journal of Proteome Research, 2022, 21, 1603-1615.	3.7	14
5	SLPred: a multi-view subcellular localization prediction tool for multi-location human proteins. Bioinformatics, 2022, 38, 4226-4229.	4.1	3
6	MDeePred: novel multi-channel protein featurization for deep learning-based binding affinity prediction in drug discovery. Bioinformatics, 2021, 37, 693-704.	4.1	61
7	UniProt: the universal protein knowledgebase in 2021. Nucleic Acids Research, 2021, 49, D480-D489.	14.5	4,709
8	CROssBAR: comprehensive resource of biomedical relations with knowledge graph representations. Nucleic Acids Research, 2021, 49, e96-e96.	14.5	19
9	Enhancing the interoperability of glycan data flow between ChEBI, PubChem, and GlyGen. Glycobiology, 2021, , .	2.5	2
10	The Enzyme Portal: an integrative tool for enzyme information and analysis. FEBS Journal, 2021, , .	4.7	2
11	The Gene Ontology resource: enriching a GOld mine. Nucleic Acids Research, 2021, 49, D325-D334.	14.5	2,416
12	A GO catalogue of human DNA-binding transcription factors. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2021, 1864, 194765.	1.9	15
13	Protein domain-based prediction of drug/compoundâ€target interactions and experimental validation on LIM kinases. PLoS Computational Biology, 2021, 17, e1009171.	3.2	13
14	GlyGen: Computational and Informatics Resources for Glycoscience. Glycobiology, 2020, 30, 72-73.	2.5	123
15	DEEPScreen: high performance drugâ€target interaction prediction with convolutional neural networks using 2-D structural compound representations. Chemical Science, 2020, 11, 2531-2557.	7.4	131
16	Effect of sequence padding on the performance of deep learning models in archaeal protein functional prediction. Scientific Reports, 2020, 10, 14634.	3.3	21
17	Gene Ontology Curation of Neuroinflammation Biology Improves the Interpretation of Alzheimerâ€™s Disease Gene Expression Data. Journal of Alzheimer's Disease, 2020, 75, 1417-1435.	2.6	18
18	UniRule: a unified rule resource for automatic annotation in the UniProt Knowledgebase. Bioinformatics, 2020, 36, 4643-4648.	4.1	42

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19	The Quest for Orthologs benchmark service and consensus calls in 2020. Nucleic Acids Research, 2020, 48, W538-W545.	14.5	41
20	GlyGen data model and processing workflow. Bioinformatics, 2020, 36, 3941-3943.	4.1	22
21	Recent applications of deep learning and machine intelligence on in silico drug discovery: methods, tools and databases. Briefings in Bioinformatics, 2019, 20, 1878-1912.	6.5	310
22	FAIR adoption, assessment and challenges at UniProt. Scientific Data, 2019, 6, 175.	5.3	11
23	DEEPred: Automated Protein Function Prediction with Multi-task Feed-forward Deep Neural Networks. Scientific Reports, 2019, 9, 7344.	3.3	80
24	UniProt genomic mapping for deciphering functional effects of missense variants. Human Mutation, 2019, 40, 694-705.	2.5	29
25	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. Genome Biology, 2019, 20, 244.	8.8	261
26	SIFTS: updated Structure Integration with Function, Taxonomy and Sequences resource allows 40-fold increase in coverage of structure-based annotations for proteins. Nucleic Acids Research, 2019, 47, D482-D489.	14.5	165
27	ProForma: A Standard Proteoform Notation. Journal of Proteome Research, 2018, 17, 1321-1325.	3.7	35
28	Large-scale automated function prediction of protein sequences and an experimental case study validation on PTEN transcript variants. Proteins: Structure, Function and Bioinformatics, 2018, 86, 135-151.	2.6	13
29	Improving the Gene Ontology Resource to Facilitate More Informative Analysis and Interpretation of Alzheimer's Disease Data. Genes, 2018, 9, 593.	2.4	15
30	ECPred: a tool for the prediction of the enzymatic functions of protein sequences based on the EC nomenclature. BMC Bioinformatics, 2018, 19, 334.	2.6	99
31	Gearing up to handle the mosaic nature of life in the quest for orthologs. Bioinformatics, 2018, 34, 323-329.	4.1	36
32	Expanding the horizons of microRNA bioinformatics. Rna, 2018, 24, 1005-1017.	3.5	27
33	Uniclust databases of clustered and deeply annotated protein sequences and alignments. Nucleic Acids Research, 2017, 45, D170-D176.	14.5	520
34	The Proteins API: accessing key integrated protein and genome information. Nucleic Acids Research, 2017, 45, W539-W544.	14.5	69
35	ProtVista: visualization of protein sequence annotations. Bioinformatics, 2017, 33, 2040-2041.	4.1	58
36	UniProt Protein Knowledgebase. Methods in Molecular Biology, 2017, 1558, 41-55.	0.9	263

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37	Identifiers for the 21st century: How to design, provision, and reuse persistent identifiers to maximize utility and impact of life science data. PLoS Biology, 2017, 15, e2001414.	5.6	97
38	UniProt Tools. Current Protocols in Bioinformatics, 2016, 53, 1.29.1-1.29.15.	25.8	150
39	From data repositories to submission portals: rethinking the role of domain-specific databases in CollecTF. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw055.	3.0	20
40	Standardized benchmarking in the quest for orthologs. Nature Methods, 2016, 13, 425-430.	19.0	198
41	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. Genome Biology, 2016, 17, 184.	8.8	308
42	UniProt-DAAC: domain architecture alignment and classification, a new method for automatic functional annotation in UniProtKB. Bioinformatics, 2016, 32, 2264-2271.	4.1	37
43	Minimizing proteome redundancy in the UniProt Knowledgebase. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw139.	3.0	24
44	Prediction of Metabolic Pathway Involvement in Prokaryotic UniProtKB Data by Association Rule Mining. PLoS ONE, 2016, 11, e0158896.	2.5	13
45	Searching and Navigating UniProt Databases. Current Protocols in Bioinformatics, 2015, 50, 1.27.1-1.27.10.	25.8	72
46	The GOA database: Gene Ontology annotation updates for 2015. Nucleic Acids Research, 2015, 43, D1057-D1063.	14.5	493
47	Analysis of the Protein Domain and Domain Architecture Content in Fungi and Its Application in the Search of New Antifungal Targets. PLoS Computational Biology, 2014, 10, e1003733.	3.2	25
48	Big data and other challenges in the quest for orthologs. Bioinformatics, 2014, 30, 2993-2998.	4.1	109
49	Understanding how and why the Gene Ontology and its annotations evolve: the GO within UniProt. GigaScience, 2014, 3, 4.	6.4	70
50	FeatureViewer, a BioJS component for visualization of position-based annotations in protein sequences. F1000Research, 2014, 3, 47.	1.6	11
51	FeatureViewer, a BioJS component for visualization of position-based annotations in protein sequences. F1000Research, 2014, 3, 47.	1.6	8
52	BioJS: an open source JavaScript framework for biological data visualization. Bioinformatics, 2013, 29, 1103-1104.	4.1	110
53	The COMBREX Project: Design, Methodology, and Initial Results. PLoS Biology, 2013, 11, e1001638.	5.6	54
54	The EBI enzyme portal. Nucleic Acids Research, 2013, 41, D773-D780.	14.5	19

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55	Use of Gene Ontology Annotation to understand the peroxisome proteome in humans. Database: the Journal of Biological Databases and Curation, 2013, 2013, bas062.	3.0	17
56	HAMAP in 2013, new developments in the protein family classification and annotation system. Nucleic Acids Research, 2013, 41, D584-D589.	14.5	57
57	Reorganizing the protein space at the Universal Protein Resource (UniProt). Nucleic Acids Research, 2012, 40, D71-D75.	14.5	1,196
58	Update on activities at the Universal Protein Resource (UniProt) in 2013. Nucleic Acids Research, 2012, 41, D43-D47.	14.5	620
59	The Gene Ontology: enhancements for 2011. Nucleic Acids Research, 2012, 40, D559-D564.	14.5	191
60	AntiFam: a tool to help identify spurious ORFs in protein annotation. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas003-bas003.	3.0	38
61	SIFTS: Structure Integration with Function, Taxonomy and Sequences resource. Nucleic Acids Research, 2012, 41, D483-D489.	14.5	238
62	Gene Ontology Annotations and Resources. Nucleic Acids Research, 2012, 41, D530-D535.	14.5	456
63	The UniProt-GO Annotation database in 2011. Nucleic Acids Research, 2012, 40, D565-D570.	14.5	349
64	MyDas, an Extensible Java DAS Server. PLoS ONE, 2012, 7, e44180.	2.5	2
65	The Impact of Focused Gene Ontology Curation of Specific Mammalian Systems. PLoS ONE, 2011, 6, e27541.	2.5	23
66	Dasty3, a WEB framework for DAS. Bioinformatics, 2011, 27, 2616-2617.	4.1	14
67	Infrastructure for the life sciences: design and implementation of the UniProt website. BMC Bioinformatics, 2009, 10, 136.	2.6	405
68	UniProtJAPI: a remote API for accessing UniProt data. Bioinformatics, 2008, 24, 1321-1322.	4.1	56
69	The Universal Protein Resource (UniProt): an expanding universe of protein information. Nucleic Acids Research, 2006, 34, D187-D191.	14.5	961
70	The Universal Protein Resource (UniProt). Nucleic Acids Research, 2004, 33, D154-D159.	14.5	1,681
71	UniProt: the Universal Protein knowledgebase. Nucleic Acids Research, 2004, 32, 115D-119.	14.5	2,994
72	Protein Sequence Database Methods. , 2004, , 13-17.		0

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73	The SWISS-PROT protein knowledgebase and its supplement TrEMBL in 2003. Nucleic Acids Research, 2003, 31, 365-370.	14.5	3,096
74	Comparing Bacterial Genomes Through Conservation Profiles. Genome Research, 2003, 13, 991-998.	5.5	26
75	The European Bioinformatics Institute's data resources. Nucleic Acids Research, 2003, 31, 43-50.	14.5	56
76	Managing core resources for genomics and proteomics. Pharmacogenomics, 2003, 4, 343-350.	1.3	4
77	High-quality protein knowledge resource: SWISS-PROT and TrEMBL. Briefings in Bioinformatics, 2002, 3, 275-284.	6.5	273
78	The role SWISS-PROT and TrEMBL play in the genome research environment. Journal of Biotechnology, 2000, 78, 221-234.	3.8	23