Nomi L Harris

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/629469/publications.pdf

Version: 2024-02-01

30 papers 13,307 citations

20 h-index 414414 32 g-index

37 all docs

37 docs citations

37 times ranked

17163 citing authors

#	Article	IF	CITATIONS
1	NSAID use and clinical outcomes in COVID-19 patients: a 38-center retrospective cohort study. Virology Journal, 2022, 19, 84.	3.4	19
2	A Simple Standard for Sharing Ontological Mappings (SSSOM). Database: the Journal of Biological Databases and Curation, 2022, 2022, .	3.0	23
3	Progress toward a universal biomedical data translator. Clinical and Translational Science, 2022, 15, 1838-1847.	3.1	17
4	The GA4GH Phenopacket schema defines a computable representation of clinical data. Nature Biotechnology, 2022, 40, 817-820.	17.5	38
5	Biolink Model: A universal schema for knowledge graphs in clinical, biomedical, and translational science. Clinical and Translational Science, 2022, 15, 1848-1855.	3.1	38
6	KG-COVID-19: A Framework to Produce Customized Knowledge Graphs for COVID-19 Response. Patterns, 2021, 2, 100155.	5.9	62
7	The Human Phenotype Ontology in 2021. Nucleic Acids Research, 2021, 49, D1207-D1217.	14.5	652
8	The Gene Ontology resource: enriching a GOld mine. Nucleic Acids Research, 2021, 49, D325-D334.	14.5	2,416
9	OBO Foundry in 2021: operationalizing open data principles to evaluate ontologies. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	3.0	77
10	The Monarch Initiative in 2019: an integrative data and analytic platform connecting phenotypes to genotypes across species. Nucleic Acids Research, 2020, 48, D704-D715.	14.5	178
11	The case for open science: rare diseases. JAMIA Open, 2020, 3, 472-486.	2.0	33
12	How many rare diseases are there?. Nature Reviews Drug Discovery, 2020, 19, 77-78.	46.4	204
13	The 21st annual Bioinformatics Open Source Conference (BOSC 2020, part of BCC2020). F1000Research, 2020, 9, 1160.	1.6	1
14	ROBOT: A Tool for Automating Ontology Workflows. BMC Bioinformatics, 2019, 20, 407.	2.6	97
15	Apollo: Democratizing genome annotation. PLoS Computational Biology, 2019, 15, e1006790.	3.2	179
16	The Pediatric Cell Atlas: Defining the Growth Phase of Human Development at Single-Cell Resolution. Developmental Cell, 2019, 49, 10-29.	7.0	57
17	Expansion of the Human Phenotype Ontology (HPO) knowledge base and resources. Nucleic Acids Research, 2019, 47, D1018-D1027.	14.5	539
18	BOSC 2019, the 20th annual Bioinformatics Open Source Conference. F1000Research, 2019, 8, 2132.	1.6	3

#	Article	IF	CITATIONS
19	Reconstruction and Analysis of Central Metabolism in Microbes. Methods in Molecular Biology, 2018, 1716, 111-129.	0.9	1
20	KBase: The United States Department of Energy Systems Biology Knowledgebase. Nature Biotechnology, 2018, 36, 566-569.	17.5	955
21	Using KBase to Assemble and Annotate Prokaryotic Genomes. Current Protocols in Microbiology, 2017, 46, 1E.13.1-1E.13.18.	6.5	22
22	The 2017 Bioinformatics Open Source Conference (BOSC). F1000Research, 2017, 6, 1858.	1.6	2
23	The 2016 Bioinformatics Open Source Conference (BOSC). F1000Research, 2016, 5, 2464.	1.6	2
24	The Bioinformatics Open Source Conference (BOSC) 2013. Bioinformatics, 2015, 31, 299-300.	4.1	3
25	The Genome Sequence of <i>Drosophila melanogaster</i> . Science, 2000, 287, 2185-2195.	12.6	5,566
26	Comparative Genomics of the Eukaryotes. Science, 2000, 287, 2204-2215.	12.6	1,573
27	Genome Annotation Assessment in Drosophila melanogaster. Genome Research, 2000, 10, 483-501.	5.5	172
28	Genotator: A Workbench for Sequence Annotation. Genome Research, 1997, 7, 754-762.	5 . 5	100
29	Four helix bundle diversity in globular proteins. Journal of Molecular Biology, 1994, 236, 1356-1368.	4.2	151
30	Distribution and consenus of branch point signals in eukaryotic genes: a computerized statistical analysis. Nucleic Acids Research, 1990, 18, 3015-3015.	14.5	81