Ilene Karsch-Mizrachi

List of Publications by Year
in descending order

35 papers	**8,449** citations	279487 **23** h-index	344852 **36** g-index
38 all docs	**38** docs citations	**38** times ranked	**13733** citing authors

#	Article	IF	Citations
1	GenBank. Nucleic Acids Research, 2022, 50, D161-D164.	6.5	119
2	Using GenBank and SRA. Methods in Molecular Biology, 2022, 2443, 1-25.	0.4	12
3	Rapid automated validation, annotation and publication of SARS-CoV-2 sequences to GenBank. Database: the Journal of Biological Databases and Curation, 2022, 2022, .	1.4	4
4	Future-proofing and maximizing the utility of metadata: The PHA4GE SARS-CoV-2 contextual data specification package. GigaScience, 2022, 11, .	3.3	18
5	Multilateral benefit-sharing from digital sequence information will support both science and biodiversity conservation. Nature Communications, 2022, 13, 1086.	5.8	34
6	GenBank. Nucleic Acids Research, 2021, 49, D92-D96.	6.5	199
7	Ribovore: ribosomal RNA sequence analysis for GenBank submissions and database curation. BMC Bioinformatics, 2021, 22, 400.	1.2	3
8	The international nucleotide sequence database collaboration. Nucleic Acids Research, 2021, 49, D121-D124.	6.5	135
9	GenBank. Nucleic Acids Research, 2020, 48, D84-D86.	6.5	269
10	NCBI Taxonomy: a comprehensive update on curation, resources and tools. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	1.4	925
11	VADR: validation and annotation of virus sequence submissions to GenBank. BMC Bioinformatics, 2020, 21, 211.	1.2	46
12	COVID-19 pandemic reveals the peril of ignoring metadata standards. Scientific Data, 2020, 7, 188.	2.4	56
13	Minimum Information about an Uncultivated Virus Genome (MIUViG). Nature Biotechnology, 2019, 37, 29-37.	9.4	414
14	GenBank. Nucleic Acids Research, 2019, 47, D94-D99.	6.5	373
15	GenBank. Nucleic Acids Research, 2018, 46, D41-D47.	6.5	607
16	VecScreen_plus_taxonomy: imposing a tax(onomy) increase on vector contamination screening. Bioinformatics, 2018, 34, 755-759.	1.8	23
17	The international nucleotide sequence database collaboration. Nucleic Acids Research, 2018, 46, D48-D51.	6.5	146
18	The NCBI BioCollections Database. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	43

#	Article	IF	Citations
19	GenBank. Nucleic Acids Research, 2017, 45, D37-D42.	6.5	466
20	Managing Sequence Data. Methods in Molecular Biology, 2017, 1525, 79-106.	0.4	3
21	Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. Nature Biotechnology, 2017, 35, 725-731.	9.4	1,512
22	Plant specimen contextual data consensus. GigaScience, 2016, 5, 1-4.	3.3	8
23	The International Nucleotide Sequence Database Collaboration. Nucleic Acids Research, 2016, 44, D48-D50.	6.5	166
24	GenBank. Nucleic Acids Research, 2016, 44, D67-D72.	6.5	1,132
25	Using GenBank. Methods in Molecular Biology, 2016, 1374, 1-22.	0.4	5
26	GenBank. Nucleic Acids Research, 2015, 43, D30-D35.	6.5	371
27	Standardized Metadata for Human Pathogen/Vector Genomic Sequences. PLoS ONE, 2014, 9, e99979.	1.1	34
28	Toward richer metadata for microbial sequences: replacing strain-level NCBI taxonomy taxids with BioProject, BioSample and Assembly records. Standards in Genomic Sciences, 2014, 9, 1275-1277.	1.5	38
29	Genomic Standards Consortium Projects. Standards in Genomic Sciences, 2014, 9, 599-601.	1.5	26
30	Genomic Standards Consortium Projects. Standards in Genomic Sciences, 2014, 9, 599-601.	1.5	29
31	BioProject and BioSample databases at NCBI: facilitating capture and organization of metadata. Nucleic Acids Research, 2012, 40, D57-D63.	6.5	268
32	The International Nucleotide Sequence Database Collaboration. Nucleic Acids Research, 2012, 40, D33-D37.	6.5	327
33	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIxS) specifications. Nature Biotechnology, 2011, 29, 415-420.	9.4	608
34	Managing Sequence Data. Methods in Molecular Biology, 2008, 452, 3-27.	0.4	2
35	The GenBank Sequence. Methods of Biochemical Analysis, 2002, , 45-63.	0.2	13