

Thomas M Keane

List of Publications by Year in descending order

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Version: 2024-02-01

39
papers

23,226
citations

236925
25
h-index

289244
40
g-index

44
all docs

44
docs citations

44
times ranked

42413
citing authors

#	ARTICLE	IF	CITATIONS
1	A global reference for human genetic variation. <i>Nature</i> , 2015, 526, 68-74.	27.8	13,998
2	Twelve years of SAMtools and BCFtools. <i>GigaScience</i> , 2021, 10, .	6.4	4,546
3	Mouse genomic variation and its effect on phenotypes and gene regulation. <i>Nature</i> , 2011, 477, 289-294.	27.8	1,461
4	The UK10K project identifies rare variants in health and disease. <i>Nature</i> , 2015, 526, 82-90.	27.8	1,014
5	Sequence-based characterization of structural variation in the mouse genome. <i>Nature</i> , 2011, 477, 326-329.	27.8	299
6	HTSlib: C library for reading/writing high-throughput sequencing data. <i>GigaScience</i> , 2021, 10, .	6.4	191
7	Sixteen diverse laboratory mouse reference genomes define strain-specific haplotypes and novel functional loci. <i>Nature Genetics</i> , 2018, 50, 1574-1583.	21.4	169
8	The European Nucleotide Archive in 2018. <i>Nucleic Acids Research</i> , 2019, 47, D84-D88.	14.5	103
9	Repeat associated mechanisms of genome evolution and function revealed by the <i>Mus caroli</i> and <i>Mus pahari</i> genomes. <i>Genome Research</i> , 2018, 28, 448-459.	5.5	99
10	The European Nucleotide Archive in 2019. <i>Nucleic Acids Research</i> , 2020, 48, D70-D76.	14.5	95
11	Chromosome assembly of large and complex genomes using multiple references. <i>Genome Research</i> , 2018, 28, 1720-1732.	5.5	94
12	GA4GH: International policies and standards for data sharing across genomic research and healthcare. <i>Cell Genomics</i> , 2021, 1, 100029.	6.5	94
13	Comparative Annotation Toolkit (CAT) simultaneous clade and personal genome annotation. <i>Genome Research</i> , 2018, 28, 1029-1038.	5.5	86
14	Variation in olfactory neuron repertoires is genetically controlled and environmentally modulated. <i>ELife</i> , 2017, 6, .	6.0	86
15	Genomic and Proteomic Dissection of the Ubiquitous Plant Pathogen, <i>Armillaria mellea</i> : Toward a New Infection Model System. <i>Journal of Proteome Research</i> , 2013, 12, 2552-2570.	3.7	85
16	The European Nucleotide Archive in 2017. <i>Nucleic Acids Research</i> , 2018, 46, D36-D40.	14.5	79
17	Similarities and differences in patterns of germline mutation between mice and humans. <i>Nature Communications</i> , 2019, 10, 4053.	12.8	79
18	Deep genome sequencing and variation analysis of 13 inbred mouse strains defines candidate phenotypic alleles, private variation and homozygous truncating mutations. <i>Genome Biology</i> , 2016, 17, 167.	8.8	70

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19	Leveraging European infrastructures to access 1 million human genomes by 2022. <i>Nature Reviews Genetics</i> , 2019, 20, 693-701.	16.3	69
20	The European Genome-phenome Archive in 2021. <i>Nucleic Acids Research</i> , 2022, 50, D980-D987.	14.5	55
21	Next-generation sequencing of experimental mouse strains. <i>Mammalian Genome</i> , 2012, 23, 490-498.	2.2	53
22	Structural Variation Shapes the Landscape of Recombination in Mouse. <i>Genetics</i> , 2017, 206, 603-619.	2.9	51
23	The European Variation Archive: a FAIR resource of genomic variation for all species. <i>Nucleic Acids Research</i> , 2022, 50, D1216-D1220.	14.5	50
24	Interplay between Gliotoxin Resistance, Secretion, and the Methyl/Methionine Cycle in <i>Aspergillus fumigatus</i> . <i>Eukaryotic Cell</i> , 2015, 14, 941-957.	3.4	48
25	The fine-scale architecture of structural variants in 17 mouse genomes. <i>Genome Biology</i> , 2012, 13, R18.	9.6	47
26	htsget: a protocol for securely streaming genomic data. <i>Bioinformatics</i> , 2019, 35, 119-121.	4.1	23
27	Identification of structural variation in mouse genomes. <i>Frontiers in Genetics</i> , 2014, 5, 192.	2.3	19
28	Using reference-free compressed data structures to analyze sequencing reads from thousands of human genomes. <i>Genome Research</i> , 2017, 27, 300-309.	5.5	19
29	ELIXIRâ€™EXCELERATE: establishing Europe’s data infrastructure for the life science research of the future. <i>EMBO Journal</i> , 2021, 40, e107409.	7.8	18
30	Transcriptional activity and strain-specific history of mouse pseudogenes. <i>Nature Communications</i> , 2020, 11, 3695.	12.8	17
31	The growing need for controlled data access models in clinical proteomics and metabolomics. <i>Nature Communications</i> , 2021, 12, 5787.	12.8	17
32	An improved approach to mate-paired library preparation for Illumina sequencing. <i>Methods in Next Generation Sequencing</i> , 2013, 1, .	1.5	13
33	Proteomic Characterization of <i>Armillaria mellea</i> Reveals Oxidative Stress Response Mechanisms and Altered Secondary Metabolism Profiles. <i>Microorganisms</i> , 2017, 5, 60.	3.6	12
34	Mouse protein coding diversity: Whatâ€™s left to discover?. <i>PLoS Genetics</i> , 2019, 15, e1008446.	3.5	11
35	Integration of genomics, metagenomics, and metabolomics to identify interplay between susceptibility alleles and microbiota in adenoma initiation. <i>BMC Cancer</i> , 2020, 20, 600.	2.6	11
36	Refget: standardized access to reference sequences. <i>Bioinformatics</i> , 2021, 38, 299-300.	4.1	8

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37	Crypt4GH: a file format standard enabling native access to encrypted data. Bioinformatics, 2021, 37, 2753-2754.	4.1	7
38	A Requirement for Zic2 in the Regulation of Nodal Expression Underlies the Establishment of Left-Sided Identity. Scientific Reports, 2018, 8, 10439.	3.3	6
39	The ELIXIR Human Copy Number Variations Community: building bioinformatics infrastructure for research. F1000Research, 2020, 9, 1229.	1.6	5