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List of Publications by Year in descending order

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39 papers	23,226 citations	236612 25 h-index	288905 40 g-index
44 all docs	44 docs citations	44 times ranked	42413 citing authors

#	Article	IF	Citations
1	The European Variation Archive: a FAIR resource of genomic variation for all species. Nucleic Acids Research, 2022, 50, D1216-D1220.	6.5	50
2	The European Genome-phenome Archive in 2021. Nucleic Acids Research, 2022, 50, D980-D987.	6.5	55
3	HTSlib: C library for reading/writing high-throughput sequencing data. GigaScience, 2021, 10, .	3.3	191
4	Crypt4GH: a file format standard enabling native access to encrypted data. Bioinformatics, 2021, 37, 2753-2754.	1.8	7
5	ELIXIRâ€EXCELERATE: establishing Europe's data infrastructure for the life science research of the future. EMBO Journal, 2021, 40, e107409.	3.5	18
6	Refget: standardized access to reference sequences. Bioinformatics, 2021, 38, 299-300.	1.8	8
7	The growing need for controlled data access models in clinical proteomics and metabolomics. Nature Communications, 2021, 12, 5787.	5.8	17
8	Twelve years of SAMtools and BCFtools. GigaScience, 2021, 10, .	3.3	4,546
9	GA4GH: International policies and standards for data sharing across genomic research and healthcare. Cell Genomics, 2021, 1, 100029.	3.0	94
10	The European Nucleotide Archive in 2019. Nucleic Acids Research, 2020, 48, D70-D76.	6.5	95
11	Transcriptional activity and strain-specific history of mouse pseudogenes. Nature Communications, 2020, 11, 3695.	5.8	17
12	Integration of genomics, metagenomics, and metabolomics to identify interplay between susceptibility alleles and microbiota in adenoma initiation. BMC Cancer, 2020, 20, 600.	1.1	11
13	The ELIXIR Human Copy Number Variations Community: building bioinformatics infrastructure for research. F1000Research, 2020, 9, 1229.	0.8	5
14	htsget: a protocol for securely streaming genomic data. Bioinformatics, 2019, 35, 119-121.	1.8	23
15	Mouse protein coding diversity: Whatâ€™s left to discover?. PLoS Genetics, 2019, 15, e1008446.	1.5	11
16	Leveraging European infrastructures to access 1 million human genomes by 2022. Nature Reviews Genetics, 2019, 20, 693-701.	7.7	69
17	Similarities and differences in patterns of germline mutation between mice and humans. Nature Communications, 2019, 10, 4053.	5.8	79
18	The European Nucleotide Archive in 2018. Nucleic Acids Research, 2019, 47, D84-D88.	6.5	103

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19	The European Nucleotide Archive in 2017. Nucleic Acids Research, 2018, 46, D36-D40.	6.5	79
20	Repeat associated mechanisms of genome evolution and function revealed by the Mus caroli and Mus pahari genomes. Genome Research, 2018, 28, 448-459.	2.4	99
21	Sixteen diverse laboratory mouse reference genomes define strain-specific haplotypes and novel functional loci. Nature Genetics, 2018, 50, 1574-1583.	9.4	169
22	Chromosome assembly of large and complex genomes using multiple references. Genome Research, 2018, 28, 1720-1732.	2.4	94
23	A Requirement for Zic2 in the Regulation of Nodal Expression Underlies the Establishment of Left-Sided Identity. Scientific Reports, 2018, 8, 10439.	1.6	6
24	Comparative Annotation Toolkit (CAT)â€"simultaneous clade and personal genome annotation. Genome Research, 2018, 28, 1029-1038.	2.4	86
25	Structural Variation Shapes the Landscape of Recombination in Mouse. Genetics, 2017, 206, 603-619.	1.2	51
26	Using reference-free compressed data structures to analyze sequencing reads from thousands of human genomes. Genome Research, 2017, 27, 300-309.	2.4	19
27	Proteomic Characterization of Armillaria mellea Reveals Oxidative Stress Response Mechanisms and Altered Secondary Metabolism Profiles. Microorganisms, 2017, 5, 60.	1.6	12
28	Variation in olfactory neuron repertoires is genetically controlled and environmentally modulated. ELife, 2017, 6, .	2.8	86
29	Deep genome sequencing and variation analysis of 13 inbred mouse strains defines candidate phenotypic alleles, private variation and homozygous truncating mutations. Genome Biology, 2016, 17, 167.	3.8	70
30	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	13.7	13,998
31	Interplay between Gliotoxin Resistance, Secretion, and the Methyl/Methionine Cycle in Aspergillus fumigatus. Eukaryotic Cell, 2015, 14, 941-957.	3.4	48
32	The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90.	13.7	1,014
33	Identification of structural variation in mouse genomes. Frontiers in Genetics, 2014, 5, 192.	1.1	19
34	Genomic and Proteomic Dissection of the Ubiquitous Plant Pathogen, Armillaria mellea: Toward a New Infection Model System. Journal of Proteome Research, 2013, 12, 2552-2570.	1.8	85
35	An improved approach to mate-paired library preparation for Illumina sequencing. Methods in Next Generation Sequencing, 2013, 1, .	1.5	13
36	The fine-scale architecture of structural variants in 17 mouse genomes. Genome Biology, 2012, 13, R18.	13.9	47

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37	Next-generation sequencing of experimental mouse strains. Mammalian Genome, 2012, 23, 490-498.	1.0	53
38	Mouse genomic variation and its effect on phenotypes and gene regulation. Nature, 2011, 477, 289-294.	13.7	1,461
39	Sequence-based characterization of structural variation in the mouse genome. Nature, 2011, 477, 326-329.	13.7	299