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List of Publications by Year in descending order

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Version: 2024-02-01

31
papers

16,774
citations

279487

23
h-index

433756

31
g-index

37
all docs

37
docs citations

37
times ranked

35197
citing authors

#	ARTICLE	IF	CITATIONS
1	GENCODE: The reference human genome annotation for The ENCODE Project. <i>Genome Research</i> , 2012, 22, 1760-1774.	2.4	4,217
2	Ensembl 2018. <i>Nucleic Acids Research</i> , 2018, 46, D754-D761.	6.5	2,710
3	GENCODE reference annotation for the human and mouse genomes. <i>Nucleic Acids Research</i> , 2019, 47, D766-D773.	6.5	2,350
4	Ensembl 2021. <i>Nucleic Acids Research</i> , 2021, 49, D884-D891.	6.5	1,231
5	Ensembl 2022. <i>Nucleic Acids Research</i> , 2022, 50, D988-D995.	6.5	1,103
6	Ensembl 2020. <i>Nucleic Acids Research</i> , 2020, 48, D682-D688.	6.5	1,076
7	Ensembl 2019. <i>Nucleic Acids Research</i> , 2019, 47, D745-D751.	6.5	879
8	GENCODE 2021. <i>Nucleic Acids Research</i> , 2021, 49, D916-D923.	6.5	633
9	GENCODE: producing a reference annotation for ENCODE. <i>Genome Biology</i> , 2006, 7, S4.	13.9	533
10	Towards a complete map of the human long non-coding RNA transcriptome. <i>Nature Reviews Genetics</i> , 2018, 19, 535-548.	7.7	451
11	The GENCODE pseudogene resource. <i>Genome Biology</i> , 2012, 13, R51.	13.9	273
12	High-throughput annotation of full-length long noncoding RNAs with capture long-read sequencing. <i>Nature Genetics</i> , 2017, 49, 1731-1740.	9.4	227
13	Sixteen diverse laboratory mouse reference genomes define strain-specific haplotypes and novel functional loci. <i>Nature Genetics</i> , 2018, 50, 1574-1583.	9.4	169
14	A joint NCBI and EMBL-EBI transcript set for clinical genomics and research. <i>Nature</i> , 2022, 604, 310-315.	13.7	162
15	Perspectives on ENCODE. <i>Nature</i> , 2020, 583, 693-698.	13.7	123
16	A spatially resolved brain region- and cell type-specific isoform atlas of the postnatal mouse brain. <i>Nature Communications</i> , 2021, 12, 463.	5.8	109
17	Consensus coding sequence (CCDS) database: a standardized set of human and mouse protein-coding regions supported by expert curation. <i>Nucleic Acids Research</i> , 2018, 46, D221-D228.	6.5	97
18	Comparative analysis of pseudogenes across three phyla. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 13361-13366.	3.3	72

#	ARTICLE	IF	CITATIONS
19	Discovery of high-confidence human protein-coding genes and exons by whole-genome PhyloCSF helps elucidate 118 GWAS loci. <i>Genome Research</i> , 2019, 29, 2073-2087.	2.4	52
20	Combining RT-PCR-seq and RNA-seq to catalog all genic elements encoded in the human genome. <i>Genome Research</i> , 2012, 22, 1698-1710.	2.4	50
21	Integrative transcriptomic analysis suggests new autoregulatory splicing events coupled with nonsense-mediated mRNA decay. <i>Nucleic Acids Research</i> , 2019, 47, 5293-5306.	6.5	49
22	Getting the Entire Message: Progress in Isoform Sequencing. <i>Frontiers in Genetics</i> , 2019, 10, 709.	1.1	39
23	Expert curation of the human and mouse olfactory receptor gene repertoires identifies conserved coding regions split across two exons. <i>BMC Genomics</i> , 2020, 21, 196.	1.2	28
24	Re-annotation of 191 developmental and epileptic encephalopathy-associated genes unmask de novo variants in SCN1A. <i>Npj Genomic Medicine</i> , 2019, 4, 31.	1.7	27
25	Genome-wide association study: Exploring the genetic basis for responsiveness to ketogenic dietary therapies for drug-resistant epilepsy. <i>Epilepsia</i> , 2018, 59, 1557-1566.	2.6	23
26	Progress, Challenges, and Surprises in Annotating the Human Genome. <i>Annual Review of Genomics and Human Genetics</i> , 2020, 21, 55-79.	2.5	20
27	Transcriptional activity and strain-specific history of mouse pseudogenes. <i>Nature Communications</i> , 2020, 11, 3695.	5.8	17
28	Non-coding regulatory elements: Potential roles in disease and the case of epilepsy. <i>Neuropathology and Applied Neurobiology</i> , 2022, 48, .	1.8	14
29	The Ensembl COVID-19 resource: ongoing integration of public SARS-CoV-2 data. <i>Nucleic Acids Research</i> , 2022, 50, D765-D770.	6.5	10
30	The value of primary transcripts to the clinical and non-clinical genomics community: Survey results and roadmap for improvements. <i>Molecular Genetics & Genomic Medicine</i> , 2021, 9, e1786.	0.6	5
31	SCN1A overexpression, associated with a genomic region marked by a risk variant for a common epilepsy, raises seizure susceptibility. <i>Acta Neuropathologica</i> , 2022, 144, 107-127.	3.9	3