Adam Frankish

List of Publications by Year
in descending order

31 papers	16,774 citations	279798 23 h-index	434195 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. Genome Research, 2012, 22, 1760-1774.	5.5	4,217
2	Ensembl 2018. Nucleic Acids Research, 2018, 46, D754-D761.	14.5	2,710
3	GENCODE reference annotation for the human and mouse genomes. Nucleic Acids Research, 2019, 47, D766-D773.	14.5	2,350
4	Ensembl 2021. Nucleic Acids Research, 2021, 49, D884-D891.	14.5	1,231
5	Ensembl 2022. Nucleic Acids Research, 2022, 50, D988-D995.	14.5	1,103
6	Ensembl 2020. Nucleic Acids Research, 2020, 48, D682-D688.	14.5	1,076
7	Ensembl 2019. Nucleic Acids Research, 2019, 47, D745-D751.	14.5	879
8	GENCODE 2021. Nucleic Acids Research, 2021, 49, D916-D923.	14.5	633
9	GENCODE: producing a reference annotation for ENCODE. Genome Biology, 2006, 7, S4.	9.6	533
10	Towards a complete map of the human long non-coding RNA transcriptome. Nature Reviews Genetics, 2018, 19, 535-548.	16.3	451
11	The GENCODE pseudogene resource. Genome Biology, 2012, 13, R51.	9.6	273
12	High-throughput annotation of full-length long noncoding RNAs with capture long-read sequencing. Nature Genetics, 2017, 49, 1731-1740.	21.4	227
13	Sixteen diverse laboratory mouse reference genomes define strain-specific haplotypes and novel functional loci. Nature Genetics, 2018, 50, 1574-1583.	21.4	169
14	A joint NCBI and EMBL-EBI transcript set for clinical genomics and research. Nature, 2022, 604, 310-315.	27.8	162
15	Perspectives on ENCODE. Nature, 2020, 583, 693-698.	27.8	123
16	A spatially resolved brain region- and cell type-specific isoform atlas of the postnatal mouse brain. Nature Communications, 2021, 12, 463.	12.8	109
17	Consensus coding sequence (CCDS) database: a standardized set of human and mouse protein-coding regions supported by expert curation. Nucleic Acids Research, 2018, 46, D221-D228.	14.5	97
18	Comparative analysis of pseudogenes across three phyla. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 13361-13366.	7.1	72

#	Article	IF	Citations
19	Discovery of high-confidence human protein-coding genes and exons by whole-genome PhyloCSF helps elucidate 118 GWAS loci. Genome Research, 2019, 29, 2073-2087.	5.5	52
20	Combining RT-PCR-seq and RNA-seq to catalog all genic elements encoded in the human genome. Genome Research, 2012, 22, 1698-1710.	5.5	50
21	Integrative transcriptomic analysis suggests new autoregulatory splicing events coupled with nonsense-mediated mRNA decay. Nucleic Acids Research, 2019, 47, 5293-5306.	14.5	49
22	Getting the Entire Message: Progress in Isoform Sequencing. Frontiers in Genetics, 2019, 10, 709.	2.3	39
23	Expert curation of the human and mouse olfactory receptor gene repertoires identifies conserved coding regions split across two exons. BMC Genomics, 2020, 21, 196.	2.8	28
24	Re-annotation of 191 developmental and epileptic encephalopathy-associated genes unmasks de novo variants in SCN1A. Npj Genomic Medicine, 2019, 4, 31.	3.8	27
25	Genomeâ€wide association study: Exploring the genetic basis for responsiveness to ketogenic dietary therapies for drugâ€resistant epilepsy. Epilepsia, 2018, 59, 1557-1566.	5.1	23
26	Progress, Challenges, and Surprises in Annotating the Human Genome. Annual Review of Genomics and Human Genetics, 2020, 21, 55-79.	6.2	20
27	Transcriptional activity and strain-specific history of mouse pseudogenes. Nature Communications, 2020, 11, 3695.	12.8	17
28	Nonâ€coding regulatory elements: Potential roles in disease and the case of epilepsy. Neuropathology and Applied Neurobiology, 2022, 48, .	3.2	14
29	The Ensembl COVID-19 resource: ongoing integration of public SARS-CoV-2 data. Nucleic Acids Research, 2022, 50, D765-D770.	14.5	10
30	The value of primary transcripts to the clinical and nonâ€clinical genomics community: Survey results and roadmap for improvements. Molecular Genetics & Genomic Medicine, 2021, 9, e1786.	1.2	5
31	SCN1A overexpression, associated with a genomic region marked by a risk variant for a common epilepsy, raises seizure susceptibility. Acta Neuropathologica, 2022, 144, 107-127.	7.7	3