Adam Frankish

List of Publications by Citations

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31 papers	9,282 citations	20 h-index	37 g-index
37 ext. papers	13,910 ext. citations	17.7 avg, IF	5.07 L-index

#	Paper	IF	Citations
31	GENCODE: the reference human genome annotation for The ENCODE Project. *Genome Research*, **2012**, 22, 1760-74	9.7	3142
30	Ensembl 2018. *Nucleic Acids Research*, **2018**, 46, D754-D761	20.1	1822
29	GENCODE reference annotation for the human and mouse genomes. *Nucleic Acids Research*, **2019**, 47, D766-D773	20.1	1140
28	Ensembl 2020. *Nucleic Acids Research*, **2020**, 48, D682-D688	20.1	645
27	Ensembl 2019. *Nucleic Acids Research*, **2019**, 47, D745-D751	20.1	554
26	GENCODE: producing a reference annotation for ENCODE. *Genome Biology*, **2006**, 7 Suppl 1, S4.1-9	18.3	434
25	Ensembl 2021. *Nucleic Acids Research*, **2021**, 49, D884-D891	20.1	324
24	Towards a complete map of the human long non-coding RNA transcriptome. *Nature Reviews Genetics*, **2018**, 19, 535-548	30.1	248
23	The GENCODE pseudogene resource. *Genome Biology*, **2012**, 13, R51	18.3	232
22	High-throughput annotation of full-length long noncoding RNAs with capture long-read sequencing. *Nature Genetics*, **2017**, 49, 1731-1740	36.3	140
21	Sixteen diverse laboratory mouse reference genomes define strain-specific haplotypes and novel functional loci. *Nature Genetics*, **2018**, 50, 1574-1583	36.3	91
20	GENCODE 2021. *Nucleic Acids Research*, **2021**, 49, D916-D923	20.1	82
19	Ensembl 2022. *Nucleic Acids Research*, **2021**,	20.1	72
18	Perspectives on ENCODE. *Nature*, **2020**, 583, 693-698	50.4	61
17	Comparative analysis of pseudogenes across three phyla. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 13361-6	11.5	54
16	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	20.1	46
15	Combining RT-PCR-seq and RNA-seq to catalog all genic elements encoded in the human genome. *Genome Research*, **2012**, 22, 1698-710	9.7	44

14	A spatially resolved brain region- and cell type-specific isoform atlas of the postnatal mouse brain. *Nature Communications*, **2021**, 12, 463	17.4	27
13	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	9.7	26
12	Integrative transcriptomic analysis suggests new autoregulatory splicing events coupled with nonsense-mediated mRNA decay. *Nucleic Acids Research*, **2019**, 47, 5293-5306	20.1	22
11	Getting the Entire Message: Progress in Isoform Sequencing. *Frontiers in Genetics*, **2019**, 10, 709	4.5	16
10	Re-annotation of 191 developmental and epileptic encephalopathy-associated genes unmasks de novo variants in. *Npj Genomic Medicine*, **2019**, 4, 31	6.2	12
9	Expert curation of the human and mouse olfactory receptor gene repertoires identifies conserved coding regions split across two exons. *BMC Genomics*, **2020**, 21, 196	4.5	10
8	Transcriptional activity and strain-specific history of mouse pseudogenes. *Nature Communications*, **2020**, 11, 3695	17.4	8
7	Progress, Challenges, and Surprises in Annotating the Human Genome. *Annual Review of Genomics and Human Genetics*, **2020**, 21, 55-79	9.7	6
6	Genome-wide association study: Exploring the genetic basis for responsiveness to ketogenic dietary therapies for drug-resistant epilepsy. *Epilepsia*, **2018**, 59, 1557-1566	6.4	6
5	A community-driven roadmap to advance research on translated open reading frames detected by Ribo-seq		4
4	High-throughput annotation of full-length long noncoding RNAs with Capture Long-Read Sequencing		3
3	The Ensembl COVID-19 resource: ongoing integration of public SARS-CoV-2 data. *Nucleic Acids Research*, **2021**,	20.1	3
2	Non-coding regulatory elements: potential roles in disease and the case of epilepsy. *Neuropathology and Applied Neurobiology*, **2021**,	5.2	2
1	The value of primary transcripts to the clinical and non-clinical genomics community: Survey results and roadmap for improvements. *Molecular Genetics & Genomic Medicine*, **2021**, e1786	2.3	2