

Fiona Cunningham

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

48
papers

19,953
citations

33
h-index

56
g-index

56
ext. papers

28,001
ext. citations

16.2
avg, IF

6.09
L-index

#	Paper	IF	Citations
48	The Ensembl Variant Effect Predictor. <i>Genome Biology</i> , 2016 , 17, 122	18.3	2595
47	Ensembl 2018. <i>Nucleic Acids Research</i> , 2018 , 46, D754-D761	20.1	1822
46	The NHGRI-EBI GWAS Catalog of published genome-wide association studies, targeted arrays and summary statistics 2019. <i>Nucleic Acids Research</i> , 2019 , 47, D1005-D1012	20.1	1422
45	The new NHGRI-EBI Catalog of published genome-wide association studies (GWAS Catalog). <i>Nucleic Acids Research</i> , 2017 , 45, D896-D901	20.1	1321
44	Deriving the consequences of genomic variants with the Ensembl API and SNP Effect Predictor. <i>Bioinformatics</i> , 2010 , 26, 2069-70	7.2	1240
43	GENCODE reference annotation for the human and mouse genomes. <i>Nucleic Acids Research</i> , 2019 , 47, D766-D773	20.1	1140
42	Ensembl 2016. <i>Nucleic Acids Research</i> , 2016 , 44, D710-6	20.1	1094
41	Ensembl 2014. <i>Nucleic Acids Research</i> , 2014 , 42, D749-55	20.1	1087
40	Ensembl 2015. <i>Nucleic Acids Research</i> , 2015 , 43, D662-9	20.1	1013
39	Ensembl 2012. <i>Nucleic Acids Research</i> , 2012 , 40, D84-90	20.1	798
38	Ensembl 2013. <i>Nucleic Acids Research</i> , 2013 , 41, D48-55	20.1	797
37	Ensembl 2020. <i>Nucleic Acids Research</i> , 2020 , 48, D682-D688	20.1	645
36	Ensembl 2011. <i>Nucleic Acids Research</i> , 2011 , 39, D800-6	20.1	590
35	Ensembl 2019. <i>Nucleic Acids Research</i> , 2019 , 47, D745-D751	20.1	554
34	WormBase: a multi-species resource for nematode biology and genomics. <i>Nucleic Acids Research</i> , 2004 , 32, D411-7	20.1	543
33	Ensembl 2017. <i>Nucleic Acids Research</i> , 2017 , 45, D635-D642	20.1	404
32	Ensembl 2021. <i>Nucleic Acids Research</i> , 2021 , 49, D884-D891	20.1	324

31	Modernizing reference genome assemblies. <i>PLoS Biology</i> , 2011 , 9, e1001091	9.7	294
30	Integrative annotation of variants from 1092 humans: application to cancer genomics. <i>Science</i> , 2013 , 342, 1235587	33.3	281
29	Integrated allelic, transcriptional, and phenomic dissection of the cardiac effects of titin truncations in health and disease. <i>Science Translational Medicine</i> , 2015 , 7, 270ra6	17.5	267
28	Ensembl 10th year. <i>Nucleic Acids Research</i> , 2010 , 38, D557-62	20.1	240
27	Ensembl variation resources. <i>Database: the Journal of Biological Databases and Curation</i> , 2018 , 2018,	5	230
26	WormBase: a comprehensive data resource for Caenorhabditis biology and genomics. <i>Nucleic Acids Research</i> , 2005 , 33, D383-9	20.1	140
25	Whole-genome sequencing of patients with rare diseases in a national health system. <i>Nature</i> , 2020 , 583, 96-102	50.4	139
24	Ensembl variation resources. <i>BMC Genomics</i> , 2010 , 11, 293	4.5	104
23	WormBase: a cross-species database for comparative genomics. <i>Nucleic Acids Research</i> , 2003 , 31, 133-7	20.1	90
22	A standardized framework for representation of ancestry data in genomics studies, with application to the NHGRI-EBI GWAS Catalog. <i>Genome Biology</i> , 2018 , 19, 21	18.3	87
21	Locus Reference Genomic sequences: an improved basis for describing human DNA variants. <i>Genome Medicine</i> , 2010 , 2, 24	14.4	86
20	GENCODE 2021. <i>Nucleic Acids Research</i> , 2021 , 49, D916-D923	20.1	82
19	A combined functional annotation score for non-synonymous variants. <i>Human Heredity</i> , 2012 , 73, 47-51	1.1	79
18	Ensembl 2022. <i>Nucleic Acids Research</i> , 2021 ,	20.1	72
17	A standard variation file format for human genome sequences. <i>Genome Biology</i> , 2010 , 11, R88	18.3	71
16	Locus Reference Genomic: reference sequences for the reporting of clinically relevant sequence variants. <i>Nucleic Acids Research</i> , 2014 , 42, D873-8	20.1	58
15	IQSEC2-related encephalopathy in males and females: a comparative study including 37 novel patients. <i>Genetics in Medicine</i> , 2019 , 21, 837-849	8.1	32
14	Paralogous annotation of disease-causing variants in long QT syndrome genes. <i>Human Mutation</i> , 2012 , 33, 1188-1191	4.7	26

13	A database and API for variation, dense genotyping and resequencing data. <i>BMC Bioinformatics</i> , 2010 , 11, 238	3.6	26
12	Flexible and scalable diagnostic filtering of genomic variants using G2P with Ensembl VEP. <i>Nature Communications</i> , 2019 , 10, 2373	17.4	22
11	Scaling up data curation using deep learning: An application to literature triage in genomic variation resources. <i>PLoS Computational Biology</i> , 2018 , 14, e1006390	5	21
10	Improving the Sequence Ontology terminology for genomic variant annotation. <i>Journal of Biomedical Semantics</i> , 2015 , 6, 32	2.2	20
9	GA4GH: International policies and standards for data sharing across genomic research and healthcare.. <i>Cell Genomics</i> , 2021 , 1, 100029-100029		20
8	TranscriptSNPView: a genome-wide catalog of mouse coding variation. <i>Nature Genetics</i> , 2006 , 38, 853	36.3	14
7	The European Variation Archive: a FAIR resource of genomic variation for all species. <i>Nucleic Acids Research</i> , 2021 ,	20.1	10
6	Haplosaurus computes protein haplotypes for use in precision drug design. <i>Nature Communications</i> , 2018 , 9, 4128	17.4	8
5	The Gene Curation Coalition: A global effort to harmonize gene-disease evidence resources.. <i>Genetics in Medicine</i> , 2022 ,	8.1	4
4	DECIPHER: Supporting the interpretation and sharing of rare disease phenotype-linked variant data to advance diagnosis and research.. <i>Human Mutation</i> , 2022 ,	4.7	2
3	A standardized framework for representation of ancestry data in genomics studies, with application to the NHGRI-EBI GWAS Catalog		2
2	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 , e1786	2.3	2
1	Annotation and curation of human genomic variations: an ELIXIR Implementation Study. <i>F1000Research</i> , 9, 1207	3.6	