Fiona Cunningham

List of Publications by Year
in descending order

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49 papers	32,718 citations	81743 39 h-index	189595 50 g-index
56 all docs	56 docs citations	56 times ranked	62040 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	Ensembl 2022. Nucleic Acids Research, 2022, 50, D988-D995.	6.5	1,103
3	DECIPHER: Supporting the interpretation and sharing of rare disease phenotypeâ€linked variant data to advance diagnosis and research. Human Mutation, 2022, , .	1.1	10
4	A joint NCBI and EMBL-EBI transcript set for clinical genomics and research. Nature, 2022, 604, 310-315.	13.7	162
5	Annotating and prioritizing genomic variants using the Ensembl Variant Effect Predictorâ€”A tutorial. Human Mutation, 2022, 43, 986-997.	1.1	30
6	The Gene Curation Coalition: A global effort to harmonize geneâ€“disease evidence resources. Genetics in Medicine, 2022, 24, 1732-1742.	1.1	56
7	Ensembl 2021. Nucleic Acids Research, 2021, 49, D884-D891.	6.5	1,231
8	GENCODE 2021. Nucleic Acids Research, 2021, 49, D916-D923.	6.5	633
9	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.	0.6	5
10	GA4GH: International policies and standards for data sharing across genomic research and healthcare. Cell Genomics, 2021, 1, 100029.	3.0	94
11	Ensembl 2020. Nucleic Acids Research, 2020, 48, D682-D688.	6.5	1,076
12	Whole-genome sequencing of patients with rare diseases in a national health system. Nature, 2020, 583, 96-102.	13.7	338
13	Flexible and scalable diagnostic filtering of genomic variants using G2P with Ensembl VEP. Nature Communications, 2019, 10, 2373.	5.8	86
14	IQSEC2-related encephalopathy in males and females: a comparative study including 37 novel patients. Genetics in Medicine, 2019, 21, 837-849.	1.1	47
15	The NHGRI-EBI GWAS Catalog of published genome-wide association studies, targeted arrays and summary statistics 2019. Nucleic Acids Research, 2019, 47, D1005-D1012.	6.5	3,179
16	GENCODE reference annotation for the human and mouse genomes. Nucleic Acids Research, 2019, 47, D766-D773.	6.5	2,350
17	Ensembl 2019. Nucleic Acids Research, 2019, 47, D745-D751.	6.5	879
18	Ensembl 2018. Nucleic Acids Research, 2018, 46, D754-D761.	6.5	2,710

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19	Ensembl variation resources. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	377
20	Haplosaurus computes protein haplotypes for use in precision drug design. Nature Communications, 2018, 9, 4128.	5.8	21
21	A standardized framework for representation of ancestry data in genomics studies, with application to the NHGRI-EBI GWAS Catalog. Genome Biology, 2018, 19, 21.	3.8	159
22	Scaling up data curation using deep learning: An application to literature triage in genomic variation resources. PLoS Computational Biology, 2018, 14, e1006390.	1.5	33
23	Ensembl 2017. Nucleic Acids Research, 2017, 45, D635-D642.	6.5	535
24	The new NHGRI-EBI Catalog of published genome-wide association studies (GWAS Catalog). Nucleic Acids Research, 2017, 45, D896-D901.	6.5	1,932
25	The Ensembl Variant Effect Predictor. Genome Biology, 2016, 17, 122.	3.8	5,181
26	Ensembl 2016. Nucleic Acids Research, 2016, 44, D710-D716.	6.5	1,372
27	Improving the Sequence Ontology terminology for genomic variant annotation. Journal of Biomedical Semantics, 2015, 6, 32.	0.9	23
28	Integrated allelic, transcriptional, and phenomic dissection of the cardiac effects of titin truncations in health and disease. Science Translational Medicine, 2015, 7, 270ra6.	5.8	375
29	Ensembl 2015. Nucleic Acids Research, 2015, 43, D662-D669.	6.5	1,145
30	Ensembl 2014. Nucleic Acids Research, 2014, 42, D749-D755.	6.5	1,211
31	Locus Reference Genomic: reference sequences for the reporting of clinically relevant sequence variants. Nucleic Acids Research, 2014, 42, D873-D878.	6.5	73
32	Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. Science, 2013, 342, 1235587.	6.0	341
33	A Combined Functional Annotation Score for Non-Synonymous Variants. Human Heredity, 2012, 73, 47-51.	0.4	90
34	Ensembl 2012. Nucleic Acids Research, 2012, 40, D84-D90.	6.5	840
35	Ensembl 2013. Nucleic Acids Research, 2012, 41, D48-D55.	6.5	856
36	Paralogous annotation of disease-causing variants in long QT syndrome genes. Human Mutation, 2012, 33, 1188-1191.	1.1	44

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37	Ensembl 2011. Nucleic Acids Research, 2011, 39, D800-D806.	6.5	630
38	Modernizing Reference Genome Assemblies. PLoS Biology, 2011, 9, e1001091.	2.6	458
39	A database and API for variation, dense genotyping and resequencing data. BMC Bioinformatics, 2010, 11, 238.	1.2	33
40	Ensembl variation resources. BMC Genomics, 2010, 11, 293.	1.2	124
41	Ensembl's 10th year. Nucleic Acids Research, 2010, 38, D557-D562.	6.5	251
42	Deriving the consequences of genomic variants with the Ensembl API and SNP Effect Predictor. Bioinformatics, 2010, 26, 2069-2070.	1.8	1,461
43	A standard variation file format for human genome sequences. Genome Biology, 2010, 11, R88.	13.9	79
44	Locus Reference Genomic sequences: an improved basis for describing human DNA variants. Genome Medicine, 2010, 2, 24.	3.6	100
45	TranscriptSNPView: a genome-wide catalog of mouse coding variation. Nature Genetics, 2006, 38, 853-853.	9.4	14
46	WormBase: a comprehensive data resource for Caenorhabditis biology and genomics. Nucleic Acids Research, 2004, 33, D383-D389.	6.5	155
47	WormBase: a multi-species resource for nematode biology and genomics. Nucleic Acids Research, 2004, 32, 411D-417.	6.5	610
48	WormBase: a cross-species database for comparative genomics. Nucleic Acids Research, 2003, 31, 133-137.	6.5	107
49	Annotation and curation of human genomic variations: an ELIXIR Implementation Study. F1000Research, 0, 9, 1207.	0.8	0