Fiona Cunningham

List of Publications by Year
in descending order

28 papers	11,828 citations	257450 24 h-index	477307 29 g-index
29 all docs	29 docs citations	29 times ranked	28062 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.	14.5	50
2	Ensembl 2022. Nucleic Acids Research, 2022, 50, D988-D995.	14.5	1,103
3	DECIPHER: Supporting the interpretation and sharing of rare disease phenotypeâ€linked variant data to advance diagnosis and research. Human Mutation, 2022, , .	2.5	10
4	Annotating and prioritizing genomic variants using the Ensembl Variant Effect Predictorâ€”A tutorial. Human Mutation, 2022, 43, 986-997.	2.5	30
5	â€œItâ€™s something Iâ€™ve committed to longer termâ€: The impact of an immersion program for physicians on adoption of genomic medicine. Patient Education and Counseling, 2021, 104, 480-488.	2.2	3
6	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
7	Ensembl 2020. Nucleic Acids Research, 2020, 48, D682-D688.	14.5	1,076
8	Ensembl 2019. Nucleic Acids Research, 2019, 47, D745-D751.	14.5	879
9	Ensembl variation resources. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	377
10	Ensembl 2015. Nucleic Acids Research, 2015, 43, D662-D669.	14.5	1,145
11	Ensembl 2014. Nucleic Acids Research, 2014, 42, D749-D755.	14.5	1,211
12	Policy challenges of clinical genome sequencing. BMJ, The, 2013, 347, f6845-f6845.	6.0	50
13	A Combined Functional Annotation Score for Non-Synonymous Variants. Human Heredity, 2012, 73, 47-51.	0.8	90
14	Ensembl 2012. Nucleic Acids Research, 2012, 40, D84-D90.	14.5	840
15	Ensembl 2013. Nucleic Acids Research, 2012, 41, D48-D55.	14.5	856
16	Paralogous annotation of disease-causing variants in long QT syndrome genes. Human Mutation, 2012, 33, 1188-1191.	2.5	44
17	Ensembl 2011. Nucleic Acids Research, 2011, 39, D800-D806.	14.5	630
18	Modernizing Reference Genome Assemblies. PLoS Biology, 2011, 9, e1001091.	5.6	458

#	Article	IF	Citations
19	A database and API for variation, dense genotyping and resequencing data. BMC Bioinformatics, 2010, 11, 238.	2.6	33
20	Ensembl variation resources. BMC Genomics, 2010, 11, 293.	2.8	124
21	Ensembl's 10th year. Nucleic Acids Research, 2010, 38, D557-D562.	14.5	251
22	Deriving the consequences of genomic variants with the Ensembl API and SNP Effect Predictor. Bioinformatics, 2010, 26, 2069-2070.	4.1	1,461
23	A standard variation file format for human genome sequences. Genome Biology, 2010, 11, R88.	9.6	79
24	Locus Reference Genomic sequences: an improved basis for describing human DNA variants. Genome Medicine, 2010, 2, 24.	8.2	100
25	TranscriptSNPView: a genome-wide catalog of mouse coding variation. Nature Genetics, 2006, 38, 853-853.	21.4	14
26	WormBase: a comprehensive data resource for Caenorhabditis biology and genomics. Nucleic Acids Research, 2004, 33, D383-D389.	14.5	155
27	WormBase: a multi-species resource for nematode biology and genomics. Nucleic Acids Research, 2004, 32, 411D-417.	14.5	610
28	WormBase: a cross-species database for comparative genomics. Nucleic Acids Research, 2003, 31, 133-137.	14.5	107