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	Deriving the consequences of genomic variants with the Ensembl API and SNP Effect Predictor. Bioinformatics, 2010, 26, 2069-2070.	4.1	1,461
2	Ensembl 2014. Nucleic Acids Research, 2014, 42, D749-D755.	14.5	1,211
3	Ensembl 2015. Nucleic Acids Research, 2015, 43, D662-D669.	14.5	1,145
4	Ensembl 2022. Nucleic Acids Research, 2022, 50, D988-D995.	14.5	1,103
5	Ensembl 2020. Nucleic Acids Research, 2020, 48, D682-D688.	14.5	1,076
6	Ensembl 2019. Nucleic Acids Research, 2019, 47, D745-D751.	14.5	879
7	Ensembl 2013. Nucleic Acids Research, 2012, 41, D48-D55.	14.5	856
8	Ensembl 2012. Nucleic Acids Research, 2012, 40, D84-D90.	14.5	840
9	Ensembl 2011. Nucleic Acids Research, 2011, 39, D800-D806.	14.5	630
10	WormBase: a multi-species resource for nematode biology and genomics. Nucleic Acids Research, 2004, 32, 411D-417.	14.5	610
11	Modernizing Reference Genome Assemblies. PLoS Biology, 2011, 9, e1001091.	5.6	458
12	Ensembl variation resources. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	377
13	Ensembl's 10th year. Nucleic Acids Research, 2010, 38, D557-D562.	14.5	251
14	WormBase: a comprehensive data resource for Caenorhabditis biology and genomics. Nucleic Acids Research, 2004, 33, D383-D389.	14.5	155
15	Ensembl variation resources. BMC Genomics, 2010, 11, 293.	2.8	124
16	WormBase: a cross-species database for comparative genomics. Nucleic Acids Research, 2003, 31, 133-137.	14.5	107
17	Locus Reference Genomic sequences: an improved basis for describing human DNA variants. Genome Medicine, 2010, 2, 24.	8.2	100
18	A Combined Functional Annotation Score for Non-Synonymous Variants. Human Heredity, 2012, 73, 47-51.	0.8	90

#	ARTICLE	IF	CITATIONS
19	A standard variation file format for human genome sequences. Genome Biology, 2010, 11, R88.	9.6	79
20	Policy challenges of clinical genome sequencing. BMJ, The, 2013, 347, f6845-f6845.	6.0	50
21	The European Variation Archive: a FAIR resource of genomic variation for all species. Nucleic Acids Research, 2022, 50, D1216-D1220.	14.5	50
22	Paralogous annotation of disease-causing variants in long QT syndrome genes. Human Mutation, 2012, 33, 1188-1191.	2.5	44
23	A database and API for variation, dense genotyping and resequencing data. BMC Bioinformatics, 2010, 11, 238.	2.6	33
24	Annotating and prioritizing genomic variants using the Ensembl Variant Effect Predictorâ€"A tutorial. Human Mutation, 2022, 43, 986-997.	2.5	30
25	TranscriptSNPView: a genome-wide catalog of mouse coding variation. Nature Genetics, 2006, 38, 853-853.	21.4	14
26	DECIPHER: Supporting the interpretation and sharing of rare disease phenotypeâ€linked variant data to advance diagnosis and research. Human Mutation, 2022, , .	2.5	10
27	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
28	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