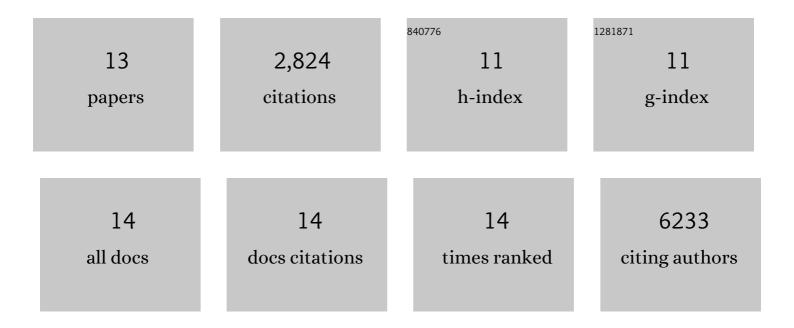
Susan Fairley

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2119506/publications.pdf Version: 2024-02-01



SUSAN FAIDLEY

#	Article	IF	CITATIONS
1	The Ensembl gene annotation system. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw093.	3.0	912
2	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	12.8	636
3	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. Science, 2021, 372, .	12.6	358
4	The International Genome Sample Resource (IGSR) collection of open human genomic variation resources. Nucleic Acids Research, 2020, 48, D941-D947.	14.5	221
5	The international Genome sample resource (IGSR): A worldwide collection of genome variation incorporating the 1000 Genomes Project data. Nucleic Acids Research, 2017, 45, D854-D859.	14.5	215
6	GA4GH: International policies and standards for data sharing across genomic research and healthcare. Cell Genomics, 2021, 1, 100029.	6.5	94
7	Variant calling on the GRCh38 assembly with the data from phase three of the 1000 Genomes Project. Wellcome Open Research, 2019, 4, 50.	1.8	73
8	European Nucleotide Archive in 2016. Nucleic Acids Research, 2017, 45, D32-D36.	14.5	68
9	Alignment of 1000 Genomes Project reads to reference assembly CRCh38. GigaScience, 2017, 6, 1-8.	6.4	49
10	Genome Wide Association Mapping of Grain and Straw Biomass Traits in the Rice Bengal and Assam Aus Panel (BAAP) Grown Under Alternate Wetting and Drying and Permanently Flooded Irrigation. Frontiers in Plant Science, 2018, 9, 1223.	3.6	41
11	Variant calling on the GRCh38 assembly with the data from phase three of the 1000 Genomes Project. Wellcome Open Research, 2019, 4, 50.	1.8	26
12	Variant calling across 505 openly consented samples from four Gambian populations on GRCh38. Wellcome Open Research, 0, 6, 239.	1.8	1
13	Mapping Affymetrix Microarray Probes to the Rat Genome via a Persistent Index. International Journal of Knowledge Discovery in Bioinformatics, 2010, 1, 48-65.	0.8	0