Ira M Hall

List of Publications by Year
in descending order

46	31,464	134610 34	252626 46
papers	citations	h-index	g-index

57	57	57	59838
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	BEDTools: a flexible suite of utilities for comparing genomic features. Bioinformatics, 2010, 26, 841-842.	1.8	20,367
2	Regulation of Heterochromatic Silencing and Histone H3 Lysine-9 Methylation by RNAi. Science, 2002, 297, 1833-1837.	6.0	1,889
3	The complete sequence of a human genome. Science, 2022, 376, 44-53.	6.0	1,222
4	LUMPY: a probabilistic framework for structural variant discovery. Genome Biology, 2014, 15, R84.	13.9	1,199
5	Establishment and Maintenance of a Heterochromatin Domain. Science, 2002, 297, 2232-2237.	6.0	833
6	Telomere-to-telomere assembly of a complete human X chromosome. Nature, 2020, 585, 79-84.	13.7	549
7	SpeedSeq: ultra-fast personal genome analysis and interpretation. Nature Methods, 2015, 12, 966-968.	9.0	515
8	Mosaic Copy Number Variation in Human Neurons. Science, 2013, 342, 632-637.	6.0	488
9	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. Science, 2021, 372, .	6.0	358
10	The impact of structural variation on human gene expression. Nature Genetics, 2017, 49, 692-699.	9.4	334
11	RNA interference machinery regulates chromosome dynamics during mitosis and meiosis in fission yeast. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 193-198.	3.3	306
12	Genome-wide mapping and assembly of structural variant breakpoints in the mouse genome. Genome Research, 2010, 20, 623-635.	2.4	257
13	Complex reorganization and predominant non-homologous repair following chromosomal breakage in karyotypically balanced germline rearrangements and transgenic integration. Nature Genetics, 2012, 44, 390-397.	9.4	229
14	The impact of rare variation on gene expression across tissues. Nature, 2017, 550, 239-243.	13.7	229
15	Genomic Analysis in the Age of Human Genome Sequencing. Cell, 2019, 177, 70-84.	13.5	205
16	Mapping and characterization of structural variation in 17,795 human genomes. Nature, 2020, 583, 83-89.	13.7	194
17	The Human Pangenome Project: a global resource to map genomic diversity. Nature, 2022, 604, 437-446.	13.7	192
18	Functional equivalence of genome sequencing analysis pipelines enables harmonized variant calling across human genetics projects. Nature Communications, 2018, 9, 4038.	5.8	166

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19	Exome sequencing of Finnish isolates enhances rare-variant association power. Nature, 2019, 572, 323-328.	13.7	161
20	Breakpoint profiling of 64 cancer genomes reveals numerous complex rearrangements spawned by homology-independent mechanisms. Genome Research, 2013, 23, 762-776.	2.4	155
21	Recurrent DNA copy number variation in the laboratory mouse. Nature Genetics, 2007, 39, 1384-1389.	9.4	129
22	Genome Sequencing of Mouse Induced Pluripotent Stem Cells Reveals Retroelement Stability and Infrequent DNA Rearrangement during Reprogramming. Cell Stem Cell, 2011, 9, 366-373.	5.2	102
23	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. Cell, 2021, 184, 2633-2648.e19.	13.5	94
24	Characterizing complex structural variation in germline and somatic genomes. Trends in Genetics, 2012, 28, 43-53.	2.9	93
25	Transcriptomic signatures across human tissues identify functional rare genetic variation. Science, 2020, 369, .	6.0	89
26	The Complete Genome Sequences, Unique Mutational Spectra, and Developmental Potency of Adult Neurons Revealed by Cloning. Neuron, 2016, 89, 1223-1236.	3.8	85
27	Transformation of Natural Genetic Variation into Haemophilus Influenzae Genomes. PLoS Pathogens, 2011, 7, e1002151.	2.1	75
28	Genome-wide association studies of metabolites in Finnish men identify disease-relevant loci. Nature Communications, 2022, 13, 1644.	5.8	63
29	YAHA: fast and flexible long-read alignment with optimal breakpoint detection. Bioinformatics, 2012, 28, 2417-2424.	1.8	62
30	Inverting the model of genomics data sharing with the NHGRI Genomic Data Science Analysis, Visualization, and Informatics Lab-space. Cell Genomics, 2022, 2, 100085.	3.0	59
31	Identification of Drivers of Aneuploidy in Breast Tumors. Cell Reports, 2018, 23, 2758-2769.	2.9	57
32	Identification of alterations in DNA copy number in host stromal cells during tumor progression. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 19848-19853.	3.3	55
33	SVScore: an impact prediction tool for structural variation. Bioinformatics, 2017, 33, 1083-1085.	1.8	54
34	svtools: population-scale analysis of structural variation. Bioinformatics, 2019, 35, 4782-4787.	1.8	51
35	Structural variants are a major source of gene expression differences in humans and often affect multiple nearby genes. Genome Research, 2021, 31, 2249-2257.	2.4	48
36	Defining the DNA uptake specificity of naturally competent Haemophilus influenzae cells. Nucleic Acids Research, 2012, 40, 8536-8549.	6.5	46

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37	Mouse genomic representational oligonucleotide microarray analysis: Detection of copy number variations in normal and tumor specimens. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 11234-11239.	3.3	22
38	Association of structural variation with cardiometabolic traits in Finns. American Journal of Human Genetics, 2021, 108, 583-596.	2.6	22
39	Population-based structural variation discovery with Hydra-Multi. Bioinformatics, 2015, 31, 1286-1289.	1.8	19
40	Chromosomal structural variations during progression of a prostate epithelial cell line to a malignant metastatic state inactivate the NF2, NIPSNAP1, UGT2B17, and LPIN2 genes. Cancer Biology and Therapy, 2013, 14, 840-852.	1.5	15
41	Polygenic burden has broader impact on health, cognition, and socioeconomic outcomes than most rare and high-risk copy number variants. Molecular Psychiatry, 2021, 26, 4884-4895.	4.1	8
42	Mitochondrial genome copy number measured by DNA sequencing in human blood is strongly associated with metabolic traits via cell-type composition differences. Human Genomics, 2021, 15, 34.	1.4	7
43	Ploidy-Seq: inferring mutational chronology by sequencing polyploid tumor subpopulations. Genome Medicine, 2015, 7, 6.	3.6	6
44	DNA Structural Variants as Genetic Risk Factors for the Long QT Syndrome. Journal of the American College of Cardiology, 2011, 57, 48-50.	1.2	4
45	GEM: crystal-clear DNA alignment. Nature Methods, 2012, 9, 1159-1160.	9.0	1
46	Whole Genome Sequencing Reveals Novel Recurring Somatic Mutations Affecting HUWE1 and DIAPH2 Genes in Multiple Myeloma. Blood, 2012, 120, 320-320.	0.6	0