Ira M Hall

List of Publications by Year
in descending order

46 papers	31,464 citations	117625 34 h-index	223800 46 g-index
57 all docs	57 docs citations	57 times ranked	54076 citing authors

#	Article	IF	Citations
1	Inverting the model of genomics data sharing with the NHGRI Genomic Data Science Analysis, Visualization, and Informatics Lab-space. Cell Genomics, 2022, 2, 100085.	6.5	59
2	Genome-wide association studies of metabolites in Finnish men identify disease-relevant loci. Nature Communications, 2022, 13, 1644.	12.8	63
3	The complete sequence of a human genome. Science, 2022, 376, 44-53.	12.6	1,222
4	The Human Pangenome Project: a global resource to map genomic diversity. Nature, 2022, 604, 437-446.	27.8	192
5	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.	7.9	8
6	Association of structural variation with cardiometabolic traits in Finns. American Journal of Human Genetics, 2021, 108, 583-596.	6.2	22
7	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. Science, 2021, 372, .	12.6	358
8	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. Cell, 2021, 184, 2633-2648.e19.	28.9	94
9	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.	2.9	7
10	Structural variants are a major source of gene expression differences in humans and often affect multiple nearby genes. Genome Research, 2021, 31, 2249-2257.	5.5	48
11	Telomere-to-telomere assembly of a complete human X chromosome. Nature, 2020, 585, 79-84.	27.8	549
12	Transcriptomic signatures across human tissues identify functional rare genetic variation. Science, 2020, 369, .	12.6	89
13	Mapping and characterization of structural variation in 17,795 human genomes. Nature, 2020, 583, 83-89.	27.8	194
14	Exome sequencing of Finnish isolates enhances rare-variant association power. Nature, 2019, 572, 323-328.	27.8	161
15	svtools: population-scale analysis of structural variation. Bioinformatics, 2019, 35, 4782-4787.	4.1	51
16	Genomic Analysis in the Age of Human Genome Sequencing. Cell, 2019, 177, 70-84.	28.9	205
17	Functional equivalence of genome sequencing analysis pipelines enables harmonized variant calling across human genetics projects. Nature Communications, 2018, 9, 4038.	12.8	166
18	Identification of Drivers of Aneuploidy in Breast Tumors. Cell Reports, 2018, 23, 2758-2769.	6.4	57

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19	SVScore: an impact prediction tool for structural variation. Bioinformatics, 2017, 33, 1083-1085.	4.1	54
20	The impact of structural variation on human gene expression. Nature Genetics, 2017, 49, 692-699.	21.4	334
21	The impact of rare variation on gene expression across tissues. Nature, 2017, 550, 239-243.	27.8	229
22	The Complete Genome Sequences, Unique Mutational Spectra, and Developmental Potency of Adult Neurons Revealed by Cloning. Neuron, 2016, 89, 1223-1236.	8.1	85
23	Ploidy-Seq: inferring mutational chronology by sequencing polyploid tumor subpopulations. Genome Medicine, 2015, 7, 6.	8.2	6
24	SpeedSeq: ultra-fast personal genome analysis and interpretation. Nature Methods, 2015, 12, 966-968.	19.0	515
25	Population-based structural variation discovery with Hydra-Multi. Bioinformatics, 2015, 31, 1286-1289.	4.1	19
26	LUMPY: a probabilistic framework for structural variant discovery. Genome Biology, 2014, 15, R84.	9.6	1,199
27	Mosaic Copy Number Variation in Human Neurons. Science, 2013, 342, 632-637.	12.6	488
28	Breakpoint profiling of 64 cancer genomes reveals numerous complex rearrangements spawned by homology-independent mechanisms. Genome Research, 2013, 23, 762-776.	5.5	155
29	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.	3.4	15
30	YAHA: fast and flexible long-read alignment with optimal breakpoint detection. Bioinformatics, 2012, 28, 2417-2424.	4.1	62
31	Defining the DNA uptake specificity of naturally competent Haemophilus influenzae cells. Nucleic Acids Research, 2012, 40, 8536-8549.	14.5	46
32	Complex reorganization and predominant non-homologous repair following chromosomal breakage in karyotypically balanced germline rearrangements and transgenic integration. Nature Genetics, 2012, 44, 390-397.	21.4	229
33	GEM: crystal-clear DNA alignment. Nature Methods, 2012, 9, 1159-1160.	19.0	1
34	Characterizing complex structural variation in germline and somatic genomes. Trends in Genetics, 2012, 28, 43-53.	6.7	93
35	Whole Genome Sequencing Reveals Novel Recurring Somatic Mutations Affecting HUWE1 and DIAPH2 Genes in Multiple Myeloma. Blood, 2012, 120, 320-320.	1.4	0
36	DNA Structural Variants as Genetic Risk Factors for the Long QT Syndrome. Journal of the American College of Cardiology, 2011, 57, 48-50.	2.8	4

#	ARTICLE	IF	CITATIONS
37	Genome Sequencing of Mouse Induced Pluripotent Stem Cells Reveals Retroelement Stability and Infrequent DNA Rearrangement during Reprogramming. Cell Stem Cell, 2011, 9, 366-373.	11.1	102
38	Transformation of Natural Genetic Variation into Haemophilus Influenzae Genomes. PLoS Pathogens, 2011, 7, e1002151.	4.7	75
39	Genome-wide mapping and assembly of structural variant breakpoints in the mouse genome. Genome Research, 2010, 20, 623-635.	5.5	257
40	BEDTools: a flexible suite of utilities for comparing genomic features. Bioinformatics, 2010, 26, 841-842.	4.1	20,367
41	Recurrent DNA copy number variation in the laboratory mouse. Nature Genetics, 2007, 39, 1384-1389.	21.4	129
42	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.	7.1	55
43	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.	7.1	22
44	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.	7.1	306
45	Regulation of Heterochromatic Silencing and Histone H3 Lysine-9 Methylation by RNAi. Science, 2002, 297, 1833-1837.	12.6	1,889
46	Establishment and Maintenance of a Heterochromatin Domain. Science, 2002, 297, 2232-2237.	12.6	833