

# Ira M Hall

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9308668/publications.pdf>

Version: 2024-02-01

46  
papers

31,464  
citations

134610

34  
h-index

252626

46  
g-index

57  
all docs

57  
docs citations

57  
times ranked

59838  
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. <i>Cell Genomics</i> , 2022, 2, 100085.	3.0	59
2	Genome-wide association studies of metabolites in Finnish men identify disease-relevant loci. <i>Nature Communications</i> , 2022, 13, 1644.	5.8	63
3	The complete sequence of a human genome. <i>Science</i> , 2022, 376, 44-53.	6.0	1,222
4	The Human Pangenome Project: a global resource to map genomic diversity. <i>Nature</i> , 2022, 604, 437-446.	13.7	192
5	Polygenic burden has broader impact on health, cognition, and socioeconomic outcomes than most rare and high-risk copy number variants. <i>Molecular Psychiatry</i> , 2021, 26, 4884-4895.	4.1	8
6	Association of structural variation with cardiometabolic traits in Finns. <i>American Journal of Human Genetics</i> , 2021, 108, 583-596.	2.6	22
7	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. <i>Science</i> , 2021, 372, .	6.0	358
8	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. <i>Cell</i> , 2021, 184, 2633-2648.e19.	13.5	94
9	Mitochondrial genome copy number measured by DNA sequencing in human blood is strongly associated with metabolic traits via cell-type composition differences. <i>Human Genomics</i> , 2021, 15, 34.	1.4	7
10	Structural variants are a major source of gene expression differences in humans and often affect multiple nearby genes. <i>Genome Research</i> , 2021, 31, 2249-2257.	2.4	48
11	Telomere-to-telomere assembly of a complete human X chromosome. <i>Nature</i> , 2020, 585, 79-84.	13.7	549
12	Transcriptomic signatures across human tissues identify functional rare genetic variation. <i>Science</i> , 2020, 369, .	6.0	89
13	Mapping and characterization of structural variation in 17,795 human genomes. <i>Nature</i> , 2020, 583, 83-89.	13.7	194
14	Exome sequencing of Finnish isolates enhances rare-variant association power. <i>Nature</i> , 2019, 572, 323-328.	13.7	161
15	svtools: population-scale analysis of structural variation. <i>Bioinformatics</i> , 2019, 35, 4782-4787.	1.8	51
16	Genomic Analysis in the Age of Human Genome Sequencing. <i>Cell</i> , 2019, 177, 70-84.	13.5	205
17	Functional equivalence of genome sequencing analysis pipelines enables harmonized variant calling across human genetics projects. <i>Nature Communications</i> , 2018, 9, 4038.	5.8	166
18	Identification of Drivers of Aneuploidy in Breast Tumors. <i>Cell Reports</i> , 2018, 23, 2758-2769.	2.9	57

#	ARTICLE	IF	CITATIONS
19	SVScore: an impact prediction tool for structural variation. <i>Bioinformatics</i> , 2017, 33, 1083-1085.	1.8	54
20	The impact of structural variation on human gene expression. <i>Nature Genetics</i> , 2017, 49, 692-699.	9.4	334
21	The impact of rare variation on gene expression across tissues. <i>Nature</i> , 2017, 550, 239-243.	13.7	229
22	The Complete Genome Sequences, Unique Mutational Spectra, and Developmental Potency of Adult Neurons Revealed by Cloning. <i>Neuron</i> , 2016, 89, 1223-1236.	3.8	85
23	Ploidy-Seq: inferring mutational chronology by sequencing polyploid tumor subpopulations. <i>Genome Medicine</i> , 2015, 7, 6.	3.6	6
24	SpeedSeq: ultra-fast personal genome analysis and interpretation. <i>Nature Methods</i> , 2015, 12, 966-968.	9.0	515
25	Population-based structural variation discovery with Hydra-Multi. <i>Bioinformatics</i> , 2015, 31, 1286-1289.	1.8	19
26	LUMPY: a probabilistic framework for structural variant discovery. <i>Genome Biology</i> , 2014, 15, R84.	13.9	1,199
27	Mosaic Copy Number Variation in Human Neurons. <i>Science</i> , 2013, 342, 632-637.	6.0	488
28	Breakpoint profiling of 64 cancer genomes reveals numerous complex rearrangements spawned by homology-independent mechanisms. <i>Genome Research</i> , 2013, 23, 762-776.	2.4	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. <i>Cancer Biology and Therapy</i> , 2013, 14, 840-852.	1.5	15
30	YAHA: fast and flexible long-read alignment with optimal breakpoint detection. <i>Bioinformatics</i> , 2012, 28, 2417-2424.	1.8	62
31	Defining the DNA uptake specificity of naturally competent <i>Haemophilus influenzae</i> cells. <i>Nucleic Acids Research</i> , 2012, 40, 8536-8549.	6.5	46
32	Complex reorganization and predominant non-homologous repair following chromosomal breakage in karyotypically balanced germline rearrangements and transgenic integration. <i>Nature Genetics</i> , 2012, 44, 390-397.	9.4	229
33	GEM: crystal-clear DNA alignment. <i>Nature Methods</i> , 2012, 9, 1159-1160.	9.0	1
34	Characterizing complex structural variation in germline and somatic genomes. <i>Trends in Genetics</i> , 2012, 28, 43-53.	2.9	93
35	Whole Genome Sequencing Reveals Novel Recurring Somatic Mutations Affecting HUWE1 and DIAPH2 Genes in Multiple Myeloma. <i>Blood</i> , 2012, 120, 320-320.	0.6	0
36	DNA Structural Variants as Genetic Risk Factors for the Long QT Syndrome. <i>Journal of the American College of Cardiology</i> , 2011, 57, 48-50.	1.2	4

#	ARTICLE	IF	CITATIONS
37	Genome Sequencing of Mouse Induced Pluripotent Stem Cells Reveals Retroelement Stability and Infrequent DNA Rearrangement during Reprogramming. <i>Cell Stem Cell</i> , 2011, 9, 366-373.	5.2	102
38	Transformation of Natural Genetic Variation into Haemophilus Influenzae Genomes. <i>PLoS Pathogens</i> , 2011, 7, e1002151.	2.1	75
39	Genome-wide mapping and assembly of structural variant breakpoints in the mouse genome. <i>Genome Research</i> , 2010, 20, 623-635.	2.4	257
40	BEDTools: a flexible suite of utilities for comparing genomic features. <i>Bioinformatics</i> , 2010, 26, 841-842.	1.8	20,367
41	Recurrent DNA copy number variation in the laboratory mouse. <i>Nature Genetics</i> , 2007, 39, 1384-1389.	9.4	129
42	Identification of alterations in DNA copy number in host stromal cells during tumor progression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 19848-19853.	3.3	55
43	Mouse genomic representational oligonucleotide microarray analysis: Detection of copy number variations in normal and tumor specimens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 11234-11239.	3.3	22
44	RNA interference machinery regulates chromosome dynamics during mitosis and meiosis in fission yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 193-198.	3.3	306
45	Regulation of Heterochromatic Silencing and Histone H3 Lysine-9 Methylation by RNAi. <i>Science</i> , 2002, 297, 1833-1837.	6.0	1,889
46	Establishment and Maintenance of a Heterochromatin Domain. <i>Science</i> , 2002, 297, 2232-2237.	6.0	833