Hyun Min Kang

List of Publications by Year
in descending order

66 papers	31,498 citations	109321 35 h-index	98798 67 g-index
80 all docs	80 docs citations	80 times ranked	53393 citing authors

#	Article	IF	Citations
1	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	27.8	13,998
2	A reference panel of 64,976 haplotypes for genotype imputation. Nature Genetics, 2016, 48, 1279-1283.	21.4	2,421
3	Variance component model to account for sample structure in genome-wide association studies. Nature Genetics, 2010, 42, 348-354.	21.4	2,287
4	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. Nature Genetics, 2012, 44, 981-990.	21.4	1,748
5	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
6	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	27.8	952
7	Loss-of-Function Mutations inAPOC3,Triglycerides, and Coronary Disease. New England Journal of Medicine, 2014, 371, 22-31.	27.0	936
8	Efficiently controlling for case-control imbalance and sample relatedness in large-scale genetic association studies. Nature Genetics, 2018, 50, 1335-1341.	21.4	896
9	Multiplexed droplet single-cell RNA-sequencing using natural genetic variation. Nature Biotechnology, 2018, 36, 89-94.	17.5	745
10	Biobank-driven genomic discovery yields new insight into atrial fibrillation biology. Nature Genetics, 2018, 50, 1234-1239.	21.4	547
11	Detecting and Estimating Contamination of Human DNA Samples in Sequencing and Array-Based Genotype Data. American Journal of Human Genetics, 2012, 91, 839-848.	6.2	441
12	Discovery of common and rare genetic risk variants for colorectal cancer. Nature Genetics, 2019, 51, 76-87.	21.4	377
13	Unified representation of genetic variants. Bioinformatics, 2015, 31, 2202-2204.	4.1	357
14	Single-Cell RNA Sequencing Resolves Molecular Relationships Among Individual Plant Cells. Plant Physiology, 2019, 179, 1444-1456.	4.8	348
15	Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. Science, 2013, 342, 1235587.	12.6	341
16	Rare coding variants in ten genes confer substantial risk for schizophrenia. Nature, 2022, 604, 509-516.	27.8	326
17	An efficient and scalable analysis framework for variant extraction and refinement from population-scale DNA sequence data. Genome Research, 2015, 25, 918-925.	5.5	308
18	Large scale meta-analysis characterizes genetic architecture for common psoriasis associated variants. Nature Communications, 2017, 8, 15382.	12.8	251

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19	Exome sequencing of 20,791Âcases of type 2 diabetes and 24,440Âcontrols. Nature, 2019, 570, 71-76.	27.8	248
20	Genome-wide Association Analysis of Psoriatic Arthritis and Cutaneous Psoriasis Reveals Differences in Their Genetic Architecture. American Journal of Human Genetics, 2015, 97, 816-836.	6.2	245
21	Microscopic examination of spatial transcriptome using Seq-Scope. Cell, 2021, 184, 3559-3572.e22.	28.9	233
22	Genome sequencing elucidates Sardinian genetic architecture and augments association analyses for lipid and blood inflammatory markers. Nature Genetics, 2015, 47, 1272-1281.	21.4	193
23	Hydro-Seq enables contamination-free high-throughput single-cell RNA-sequencing for circulating tumor cells. Nature Communications, 2019, 10, 2163.	12.8	172
24	A Central Role for GRB10 in Regulation of Islet Function in Man. PLoS Genetics, 2014, 10, e1004235.	3.5	164
25	Enhanced meta-analysis and replication studies identify five new psoriasis susceptibility loci. Nature Communications, 2015, 6, 7001.	12.8	156
26	Ancestry estimation and control of population stratification for sequence-based association studies. Nature Genetics, 2014, 46, 409-415.	21.4	136
27	Type 2 and interferon inflammation regulate SARS-CoV-2 entry factor expression in the airway epithelium. Nature Communications, 2020, 11, 5139.	12.8	131
28	Sequencing of 640,000 exomes identifies GPR75 variants associated with protection from obesity. Science, 2021, 373, .	12.6	130
29	Assessing Mitochondrial DNA Variation and Copy Number in Lymphocytes of ~2,000 Sardinians Using Tailored Sequencing Analysis Tools. PLoS Genetics, 2015, 11, e1005306.	3.5	123
30	Genetic signature to provide robust risk assessment of psoriatic arthritis development in psoriasis patients. Nature Communications, 2018, 9, 4178.	12.8	95
31	Rare variant genotype imputation with thousands of study-specific whole-genome sequences: implications for cost-effective study designs. European Journal of Human Genetics, 2015, 23, 975-983.	2.8	92
32	Genome-wide Study of Atrial Fibrillation Identifies Seven Risk Loci and Highlights Biological Pathways and Regulatory Elements Involved in Cardiac Development. American Journal of Human Genetics, 2018, 102, 103-115.	6.2	86
33	Sex-specific and pleiotropic effects underlying kidney function identified from GWAS meta-analysis. Nature Communications, 2019, 10, 1847.	12.8	55
34	Ancestry-agnostic estimation of DNA sample contamination from sequence reads. Genome Research, 2020, 30, 185-194.	5.5	51
35	Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes. Nature Communications, 2021, 12, 3505.	12.8	49
36	A Low-Frequency Inactivating AKT2 Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. Diabetes, 2017, 66, 2019-2032.	0.6	47

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37	Genetic architectures of proximal and distal colorectal cancer are partly distinct. Gut, 2021, 70, 1325-1334.	12.1	44
38	Using Population Genetics to Interrogate the Monogenic Nephrotic Syndrome Diagnosis in a Case Cohort. Journal of the American Society of Nephrology: JASN, 2016, 27, 1970-1983.	6.1	41
39	Single-Cell Transcriptome Analysis of Colon Cancer Cell Response to 5-Fluorouracil-Induced DNA Damage. Cell Reports, 2020, 32, 108077.	6.4	40
40	Correcting for Sample Contamination in Genotype Calling of DNA Sequence Data. American Journal of Human Genetics, 2015, 97, 284-290.	6.2	39
41	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. Nature Communications, 2020, 11, 6417.	12.8	39
42	Imputation-Aware Tag SNP Selection To Improve Power for Large-Scale, Multi-ethnic Association Studies. G3: Genes, Genomes, Genetics, 2018, 8, 3255-3267.	1.8	36
43	Nonsynonymous Variants in PAX4 and GLP1R Are Associated With Type 2 Diabetes in an East Asian Population. Diabetes, 2018, 67, 1892-1902.	0.6	36
44	Identifying Novel Susceptibility Genes for Colorectal Cancer Risk From a Transcriptome-Wide Association Study of 125,478 Subjects. Gastroenterology, 2021, 160, 1164-1178.e6.	1.3	36
45	Improving power of association tests using multiple sets of imputed genotypes from distributed reference panels. Genetic Epidemiology, 2017, 41, 744-755.	1.3	27
46	MEPE loss-of-function variant associates with decreased bone mineral density and increased fracture risk. Nature Communications, 2020, 11, 4093.	12.8	24
47	Rare coding variants in 35 genes associate with circulating lipid levelsâ€"A multi-ancestry analysis of 170,000 exomes. American Journal of Human Genetics, 2022, 109, 81-96.	6.2	24
48	Nasal airway transcriptome-wide association study of asthma reveals genetically driven mucus pathobiology. Nature Communications, 2022, 13, 1632.	12.8	24
49	QPLOT: A Quality Assessment Tool for Next Generation Sequencing Data. BioMed Research International, 2013, 2013, 1-4.	1.9	17
50	Holistic characterization of single-hepatocyte transcriptome responses to high-fat diet. American Journal of Physiology - Endocrinology and Metabolism, 2021, 320, E244-E258.	3.5	17
51	Mapping the 17q12â€"21.1 Locus for Variants Associated with Early-Onset Asthma in African Americans. American Journal of Respiratory and Critical Care Medicine, 2021, 203, 424-436.	5.6	16
52	Asthma and its relationship to mitochondrial copy number: Results from the Asthma Translational Genomics Collaborative (ATGC) of the Trans-Omics for Precision Medicine (TOPMed) program. PLoS ONE, 2020, 15, e0242364.	2.5	16
53	emeraLD: rapid linkage disequilibrium estimation with massive datasets. Bioinformatics, 2019, 35, 164-166.	4.1	15
54	Investigating rare pathogenic/likely pathogenic exonic variation in bipolar disorder. Molecular Psychiatry, 2021, 26, 5239-5250.	7.9	15

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55	FIVEx: an interactive eQTL browser across public datasets. Bioinformatics, 2022, 38, 559-561.	4.1	14
56	Lung Function in African American Children with Asthma Is Associated with Novel Regulatory Variants of the KIT LigandKITLG/SCFand Gene-By-Air-Pollution Interaction. Genetics, 2020, 215, 869-886.	2.9	11
57	Whole-Genome Sequencing Identifies Novel Functional Loci Associated with Lung Function in Puerto Rican Youth. American Journal of Respiratory and Critical Care Medicine, 2020, 202, 962-972.	5.6	11
58	Integrating comprehensive functional annotations to boost power and accuracy in gene-based association analysis. PLoS Genetics, 2020, 16, e1009060.	3.5	11
59	GeneVetter: a web tool for quantitative monogenic assessment of rare diseases. Bioinformatics, 2015, 31, 3682-3684.	4.1	7
60	muCNV: genotyping structural variants for population-level sequencing. Bioinformatics, 2021, 37, 2055-2057.	4.1	7
61	Robust, flexible, and scalable tests for Hardyâ€“Weinberg equilibrium across diverse ancestries. Genetics, 2021, 218, .	2.9	6
62	Identification of CFTR variants in Latino patients with cystic fibrosis from the Dominican Republic and Puerto Rico. Pediatric Pulmonology, 2020, 55, 533-540.	2.0	5
63	Sparse allele vectors and the savvy software suite. Bioinformatics, 2021, 37, 4248-4250.	4.1	3
64	Meta-imputation of transcriptome from genotypes across multiple datasets by leveraging publicly available summary-level data. PLoS Genetics, 2022, 18, e1009571.	3.5	3
65	tarSVM: Improving the accuracy of variant calls derived from microfluidic PCR-based targeted next generation sequencing using a support vector machine. BMC Bioinformatics, 2016, 17, 233.	2.6	2
66	FASTQuick: rapid and comprehensive quality assessment of raw sequence reads. GigaScience, 2021, 10, .	6.4	1