

# Hyun Min Kang

## List of Publications by Year in descending order

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Version: 2024-02-01

66  
papers

31,498  
citations

125106

35  
h-index

111975

67  
g-index

80  
all docs

80  
docs citations

80  
times ranked

58359  
citing authors

#	ARTICLE	IF	CITATIONS
1	FIVEx: an interactive eQTL browser across public datasets. <i>Bioinformatics</i> , 2022, 38, 559-561.	1.8	14
2	Meta-imputation of transcriptome from genotypes across multiple datasets by leveraging publicly available summary-level data. <i>PLoS Genetics</i> , 2022, 18, e1009571.	1.5	3
3	Rare coding variants in 35 genes associate with circulating lipid levels—A multi-ancestry analysis of 170,000 exomes. <i>American Journal of Human Genetics</i> , 2022, 109, 81-96.	2.6	24
4	Nasal airway transcriptome-wide association study of asthma reveals genetically driven mucus pathobiology. <i>Nature Communications</i> , 2022, 13, 1632.	5.8	24
5	Rare coding variants in ten genes confer substantial risk for schizophrenia. <i>Nature</i> , 2022, 604, 509-516.	13.7	326
6	Mapping the 17q12—21.1 Locus for Variants Associated with Early-Onset Asthma in African Americans. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2021, 203, 424-436.	2.5	16
7	Identifying Novel Susceptibility Genes for Colorectal Cancer Risk From a Transcriptome-Wide Association Study of 125,478 Subjects. <i>Gastroenterology</i> , 2021, 160, 1164-1178.e6.	0.6	36
8	Holistic characterization of single-hepatocyte transcriptome responses to high-fat diet. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2021, 320, E244-E258.	1.8	17
9	FASTQuick: rapid and comprehensive quality assessment of raw sequence reads. <i>GigaScience</i> , 2021, 10, .	3.3	1
10	Genetic architectures of proximal and distal colorectal cancer are partly distinct. <i>Gut</i> , 2021, 70, 1325-1334.	6.1	44
11	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. <i>Nature</i> , 2021, 590, 290-299.	13.7	1,069
12	muCNV: genotyping structural variants for population-level sequencing. <i>Bioinformatics</i> , 2021, 37, 2055-2057.	1.8	7
13	Robust, flexible, and scalable tests for Hardy—Weinberg equilibrium across diverse ancestries. <i>Genetics</i> , 2021, 218, .	1.2	6
14	Sparse allele vectors and the savvy software suite. <i>Bioinformatics</i> , 2021, 37, 4248-4250.	1.8	3
15	Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes. <i>Nature Communications</i> , 2021, 12, 3505.	5.8	49
16	Microscopic examination of spatial transcriptome using Seq-Scope. <i>Cell</i> , 2021, 184, 3559-3572.e22.	13.5	233
17	Sequencing of 640,000 exomes identifies <i>GPR75</i> variants associated with protection from obesity. <i>Science</i> , 2021, 373, .	6.0	130
18	Investigating rare pathogenic/likely pathogenic exonic variation in bipolar disorder. <i>Molecular Psychiatry</i> , 2021, 26, 5239-5250.	4.1	15

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19	Identification of CFTR variants in Latino patients with cystic fibrosis from the Dominican Republic and Puerto Rico. <i>Pediatric Pulmonology</i> , 2020, 55, 533-540.	1.0	5
20	Single-Cell Transcriptome Analysis of Colon Cancer Cell Response to 5-Fluorouracil-Induced DNA Damage. <i>Cell Reports</i> , 2020, 32, 108077.	2.9	40
21	Type 2 and interferon inflammation regulate SARS-CoV-2 entry factor expression in the airway epithelium. <i>Nature Communications</i> , 2020, 11, 5139.	5.8	131
22	MEPE loss-of-function variant associates with decreased bone mineral density and increased fracture risk. <i>Nature Communications</i> , 2020, 11, 4093.	5.8	24
23	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. <i>Nature Communications</i> , 2020, 11, 6417.	5.8	39
24	Lung Function in African American Children with Asthma Is Associated with Novel Regulatory Variants of the KIT Ligand <i>KITLG/SCF</i> and Gene-By-Air-Pollution Interaction. <i>Genetics</i> , 2020, 215, 869-886.	1.2	11
25	Whole-Genome Sequencing Identifies Novel Functional Loci Associated with Lung Function in Puerto Rican Youth. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2020, 202, 962-972.	2.5	11
26	Ancestry-agnostic estimation of DNA sample contamination from sequence reads. <i>Genome Research</i> , 2020, 30, 185-194.	2.4	51
27	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. <i>PLoS ONE</i> , 2020, 15, e0242364.	1.1	16
28	Integrating comprehensive functional annotations to boost power and accuracy in gene-based association analysis. <i>PLoS Genetics</i> , 2020, 16, e1009060.	1.5	11
29	emeraldD: rapid linkage disequilibrium estimation with massive datasets. <i>Bioinformatics</i> , 2019, 35, 164-166.	1.8	15
30	Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls. <i>Nature</i> , 2019, 570, 71-76.	13.7	248
31	Hydro-Seq enables contamination-free high-throughput single-cell RNA-sequencing for circulating tumor cells. <i>Nature Communications</i> , 2019, 10, 2163.	5.8	172
32	Sex-specific and pleiotropic effects underlying kidney function identified from GWAS meta-analysis. <i>Nature Communications</i> , 2019, 10, 1847.	5.8	55
33	Single-Cell RNA Sequencing Resolves Molecular Relationships Among Individual Plant Cells. <i>Plant Physiology</i> , 2019, 179, 1444-1456.	2.3	348
34	Discovery of common and rare genetic risk variants for colorectal cancer. <i>Nature Genetics</i> , 2019, 51, 76-87.	9.4	377
35	Genome-wide Study of Atrial Fibrillation Identifies Seven Risk Loci and Highlights Biological Pathways and Regulatory Elements Involved in Cardiac Development. <i>American Journal of Human Genetics</i> , 2018, 102, 103-115.	2.6	86
36	Multiplexed droplet single-cell RNA-sequencing using natural genetic variation. <i>Nature Biotechnology</i> , 2018, 36, 89-94.	9.4	745

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37	Imputation-Aware Tag SNP Selection To Improve Power for Large-Scale, Multi-ethnic Association Studies. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3255-3267.	0.8	36
38	Genetic signature to provide robust risk assessment of psoriatic arthritis development in psoriasis patients. <i>Nature Communications</i> , 2018, 9, 4178.	5.8	95
39	Nonsynonymous Variants in <i>PAX4</i> and <i>GLP1R</i> Are Associated With Type 2 Diabetes in an East Asian Population. <i>Diabetes</i> , 2018, 67, 1892-1902.	0.3	36
40	Biobank-driven genomic discovery yields new insight into atrial fibrillation biology. <i>Nature Genetics</i> , 2018, 50, 1234-1239.	9.4	547
41	Efficiently controlling for case-control imbalance and sample relatedness in large-scale genetic association studies. <i>Nature Genetics</i> , 2018, 50, 1335-1341.	9.4	896
42	Large scale meta-analysis characterizes genetic architecture for common psoriasis associated variants. <i>Nature Communications</i> , 2017, 8, 15382.	5.8	251
43	A Low-Frequency Inactivating <i>AKT2</i> Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. <i>Diabetes</i> , 2017, 66, 2019-2032.	0.3	47
44	Improving power of association tests using multiple sets of imputed genotypes from distributed reference panels. <i>Genetic Epidemiology</i> , 2017, 41, 744-755.	0.6	27
45	tarSVM: Improving the accuracy of variant calls derived from microfluidic PCR-based targeted next generation sequencing using a support vector machine. <i>BMC Bioinformatics</i> , 2016, 17, 233.	1.2	2
46	The genetic architecture of type 2 diabetes. <i>Nature</i> , 2016, 536, 41-47.	13.7	952
47	A reference panel of 64,976 haplotypes for genotype imputation. <i>Nature Genetics</i> , 2016, 48, 1279-1283.	9.4	2,421
48	Using Population Genetics to Interrogate the Monogenic Nephrotic Syndrome Diagnosis in a Case Cohort. <i>Journal of the American Society of Nephrology: JASN</i> , 2016, 27, 1970-1983.	3.0	41
49	Assessing Mitochondrial DNA Variation and Copy Number in Lymphocytes of ~2,000 Sardinians Using Tailored Sequencing Analysis Tools. <i>PLoS Genetics</i> , 2015, 11, e1005306.	1.5	123
50	Enhanced meta-analysis and replication studies identify five new psoriasis susceptibility loci. <i>Nature Communications</i> , 2015, 6, 7001.	5.8	156
51	Unified representation of genetic variants. <i>Bioinformatics</i> , 2015, 31, 2202-2204.	1.8	357
52	Correcting for Sample Contamination in Genotype Calling of DNA Sequence Data. <i>American Journal of Human Genetics</i> , 2015, 97, 284-290.	2.6	39
53	An efficient and scalable analysis framework for variant extraction and refinement from population-scale DNA sequence data. <i>Genome Research</i> , 2015, 25, 918-925.	2.4	308
54	A global reference for human genetic variation. <i>Nature</i> , 2015, 526, 68-74.	13.7	13,998

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55	GeneVetter: a web tool for quantitative monogenic assessment of rare diseases. <i>Bioinformatics</i> , 2015, 31, 3682-3684.	1.8	7
56	Genome sequencing elucidates Sardinian genetic architecture and augments association analyses for lipid and blood inflammatory markers. <i>Nature Genetics</i> , 2015, 47, 1272-1281.	9.4	193
57	Genome-wide Association Analysis of Psoriatic Arthritis and Cutaneous Psoriasis Reveals Differences in Their Genetic Architecture. <i>American Journal of Human Genetics</i> , 2015, 97, 816-836.	2.6	245
58	Rare variant genotype imputation with thousands of study-specific whole-genome sequences: implications for cost-effective study designs. <i>European Journal of Human Genetics</i> , 2015, 23, 975-983.	1.4	92
59	A Central Role for GRB10 in Regulation of Islet Function in Man. <i>PLoS Genetics</i> , 2014, 10, e1004235.	1.5	164
60	Ancestry estimation and control of population stratification for sequence-based association studies. <i>Nature Genetics</i> , 2014, 46, 409-415.	9.4	136
61	Loss-of-Function Mutations in <i>APOC3</i> , Triglycerides, and Coronary Disease. <i>New England Journal of Medicine</i> , 2014, 371, 22-31.	13.9	936
62	Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. <i>Science</i> , 2013, 342, 1235-1237.	6.0	341
63	QPLOT: A Quality Assessment Tool for Next Generation Sequencing Data. <i>BioMed Research International</i> , 2013, 2013, 1-4.	0.9	17
64	Detecting and Estimating Contamination of Human DNA Samples in Sequencing and Array-Based Genotype Data. <i>American Journal of Human Genetics</i> , 2012, 91, 839-848.	2.6	441
65	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. <i>Nature Genetics</i> , 2012, 44, 981-990.	9.4	1,748
66	Variance component model to account for sample structure in genome-wide association studies. <i>Nature Genetics</i> , 2010, 42, 348-354.	9.4	2,287