

Hae Kyung Im

List of Publications by Year in descending order

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Version: 2024-02-01

69
papers

20,740
citations

101543

36
h-index

88630

70
g-index

107
all docs

107
docs citations

107
times ranked

37982
citing authors

#	ARTICLE	IF	CITATIONS
1	The Genotype-Tissue Expression (GTEx) project. <i>Nature Genetics</i> , 2013, 45, 580-585.	21.4	6,815
2	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. <i>Science</i> , 2015, 348, 648-660.	12.6	4,659
3	A gene-based association method for mapping traits using reference transcriptome data. <i>Nature Genetics</i> , 2015, 47, 1091-1098.	21.4	1,473
4	The genetic architecture of type 2 diabetes. <i>Nature</i> , 2016, 536, 41-47.	27.8	952
5	Exploring the phenotypic consequences of tissue specific gene expression variation inferred from GWAS summary statistics. <i>Nature Communications</i> , 2018, 9, 1825.	12.8	748
6	Opportunities and challenges for transcriptome-wide association studies. <i>Nature Genetics</i> , 2019, 51, 592-599.	21.4	592
7	Annotation-free quantification of RNA splicing using LeafCutter. <i>Nature Genetics</i> , 2018, 50, 151-158.	21.4	520
8	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. <i>Nature Genetics</i> , 2017, 49, 834-841.	21.4	426
9	The impact of sex on gene expression across human tissues. <i>Science</i> , 2020, 369, .	12.6	329
10	Accounting for animal movement in estimation of resource selection functions: sampling and data analysis. <i>Ecology</i> , 2009, 90, 3554-3565.	3.2	295
11	Effect of predicted protein-truncating genetic variants on the human transcriptome. <i>Science</i> , 2015, 348, 666-669.	12.6	252
12	Integrating predicted transcriptome from multiple tissues improves association detection. <i>PLoS Genetics</i> , 2019, 15, e1007889.	3.5	239
13	Shared and distinct genetic risk factors for childhood-onset and adult-onset asthma: genome-wide and transcriptome-wide studies. <i>Lancet Respiratory Medicine</i> , 2019, 7, 509-522.	10.7	238
14	Cell type-specific genetic regulation of gene expression across human tissues. <i>Science</i> , 2020, 369, .	12.6	210
15	Gene expression imputation across multiple brain regions provides insights into schizophrenia risk. <i>Nature Genetics</i> , 2019, 51, 659-674.	21.4	154
16	Exploiting the GTEx resources to decipher the mechanisms at GWAS loci. <i>Genome Biology</i> , 2021, 22, 49.	8.8	150
17	Survey of the Heritability and Sparse Architecture of Gene Expression Traits across Human Tissues. <i>PLoS Genetics</i> , 2016, 12, e1006423.	3.5	143
18	Population differences in microRNA expression and biological implications. <i>RNA Biology</i> , 2011, 8, 692-701.	3.1	138

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19	Genetic architecture of gene expression traits across diverse populations. <i>PLoS Genetics</i> , 2018, 14, e1007586.	3.5	117
20	Genetic regulatory variation in populations informs transcriptome analysis in rare disease. <i>Science</i> , 2019, 366, 351-356.	12.6	99
21	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. <i>Cell</i> , 2021, 184, 2633-2648.e19.	28.9	94
22	Genetic Architecture of MicroRNA Expression: Implications for the Transcriptome and Complex Traits. <i>American Journal of Human Genetics</i> , 2012, 90, 1046-1063.	6.2	92
23	Transcriptomic signatures across human tissues identify functional rare genetic variation. <i>Science</i> , 2020, 369, .	12.6	89
24	On Sharing Quantitative Trait GWAS Results in an Era of Multiple-omics Data and the Limits of Genomic Privacy. <i>American Journal of Human Genetics</i> , 2012, 90, 591-598.	6.2	87
25	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function. <i>Nature Communications</i> , 2018, 9, 2976.	12.8	85
26	PhenomeXcan: Mapping the genome to the phenome through the transcriptome. <i>Science Advances</i> , 2020, 6, .	10.3	83
27	ExprTarget: An Integrative Approach to Predicting Human MicroRNA Targets. <i>PLoS ONE</i> , 2010, 5, e13534.	2.5	80
28	Targeting the Urokinase Plasminogen Activator Receptor Inhibits Ovarian Cancer Metastasis. <i>Clinical Cancer Research</i> , 2011, 17, 459-471.	7.0	69
29	A vast resource of allelic expression data spanning human tissues. <i>Genome Biology</i> , 2020, 21, 234.	8.8	68
30	Probabilistic colocalization of genetic variants from complex and molecular traits: promise and limitations. <i>American Journal of Human Genetics</i> , 2021, 108, 25-35.	6.2	67
31	Impact of admixture and ancestry on eQTL analysis and GWAS colocalization in GTEx. <i>Genome Biology</i> , 2020, 21, 233.	8.8	64
32	Platinum Sensitivity-Related Germline Polymorphism Discovered via a Cell-Based Approach and Analysis of Its Association with Outcome in Ovarian Cancer Patients. <i>Clinical Cancer Research</i> , 2011, 17, 5490-5500.	7.0	57
33	A Transcriptome-Wide Association Study Among 97,898 Women to Identify Candidate Susceptibility Genes for Epithelial Ovarian Cancer Risk. <i>Cancer Research</i> , 2018, 78, 5419-5430.	0.9	54
34	Imputing Gene Expression in Uncollected Tissues Within and Beyond GTEx. <i>American Journal of Human Genetics</i> , 2016, 98, 697-708.	6.2	51
35	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.	0.6	47
36	PTWAS: investigating tissue-relevant causal molecular mechanisms of complex traits using probabilistic TWAS analysis. <i>Genome Biology</i> , 2020, 21, 232.	8.8	46

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37	Analysis of Genetically Regulated Gene Expression Identifies a Prefrontal PTSD Gene, SNRNP35, Specific to Military Cohorts. <i>Cell Reports</i> , 2020, 31, 107716.	6.4	44
38	Germline polymorphisms discovered via a cell-based, genome-wide approach predict platinum response in head and neck cancers. <i>Translational Research</i> , 2011, 157, 265-272.	5.0	42
39	Polygenic transcriptome risk scores (PTRS) can improve portability of polygenic risk scores across ancestries. <i>Genome Biology</i> , 2022, 23, 23.	8.8	42
40	Poly-Omic Prediction of Complex Traits: OmicKriging. <i>Genetic Epidemiology</i> , 2014, 38, 402-415.	1.3	41
41	A multi-stage genome-wide association study of uterine fibroids in African Americans. <i>Human Genetics</i> , 2017, 136, 1363-1373.	3.8	39
42	Genetic Variation That Predicts Platinum Sensitivity Reveals the Role of miR-193b* in Chemotherapeutic Susceptibility. <i>Molecular Cancer Therapeutics</i> , 2012, 11, 2054-2061.	4.1	35
43	A Trans-Ethnic Genome-Wide Association Study of Uterine Fibroids. <i>Frontiers in Genetics</i> , 2019, 10, 511.	2.3	32
44	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. <i>Scientific Data</i> , 2017, 4, 170179.	5.3	31
45	Whole-genome studies identify solute carrier transporters in cellular susceptibility to paclitaxel. <i>Pharmacogenetics and Genomics</i> , 2012, 22, 498-507.	1.5	28
46	Fine-mapping and QTL tissue-sharing information improves the reliability of causal gene identification. <i>Genetic Epidemiology</i> , 2020, 44, 854-867.	1.3	28
47	Semiparametric Estimation of Spectral Density With Irregular Observations. <i>Journal of the American Statistical Association</i> , 2007, 102, 726-735.	3.1	26
48	Mixed Effects Modeling of Proliferation Rates in Cell-Based Models: Consequence for Pharmacogenomics and Cancer. <i>PLoS Genetics</i> , 2012, 8, e1002525.	3.5	26
49	Identification of novel germline polymorphisms governing capecitabine sensitivity. <i>Cancer</i> , 2012, 118, 4063-4073.	4.1	25
50	CORE GREML for estimating covariance between random effects in linear mixed models for complex trait analyses. <i>Nature Communications</i> , 2020, 11, 4208.	12.8	23
51	A scalable unified framework of total and allele-specific counts for cis-QTL, fine-mapping, and prediction. <i>Nature Communications</i> , 2021, 12, 1424.	12.8	23
52	Imputed gene associations identify replicable trans-acting genes enriched in transcription pathways and complex traits. <i>Genetic Epidemiology</i> , 2019, 43, 596-608.	1.3	19
53	MicroRNA biogenesis and cellular proliferation. <i>Translational Research</i> , 2015, 166, 145-151.	5.0	18
54	sn-spMF: matrix factorization informs tissue-specific genetic regulation of gene expression. <i>Genome Biology</i> , 2020, 21, 235.	8.8	18

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55	An eQTL-based method identifies CTTN and ZMAT3 as pemetrexed susceptibility markers. <i>Human Molecular Genetics</i> , 2012, 21, 1470-1480.	2.9	16
56	Trans-ethnic predicted expression genome-wide association analysis identifies a gene for estrogen receptor-negative breast cancer. <i>PLoS Genetics</i> , 2017, 13, e1006727.	3.5	14
57	Transcriptome prediction performance across machine learning models and diverse ancestries. <i>Human Genetics and Genomics Advances</i> , 2021, 2, 100019.	1.7	14
58	Protein prediction for trait mapping in diverse populations. <i>PLoS ONE</i> , 2022, 17, e0264341.	2.5	13
59	Space-time modeling of 20 years of daily air temperature in the Chicago metropolitan region. <i>Environmetrics</i> , 2009, 20, 494-511.	1.4	12
60	Functionally oriented analysis of cardiometabolic traits in a trans-ethnic sample. <i>Human Molecular Genetics</i> , 2019, 28, 1212-1224.	2.9	12
61	Functional consequences of PRPF39 on distant genes and cisplatin sensitivity. <i>Human Molecular Genetics</i> , 2012, 21, 4348-4355.	2.9	7
62	Polygenic transcriptome risk scores for COPD and lung function improve cross-ethnic portability of prediction in the NHLBI TOPMed program. <i>American Journal of Human Genetics</i> , 2022, 109, 857-870.	6.2	7
63	ukbREST: efficient and streamlined data access for reproducible research in large biobanks. <i>Bioinformatics</i> , 2019, 35, 1971-1973.	4.1	6
64	Pleiotropy-guided transcriptome imputation from normal and tumor tissues identifies candidate susceptibility genes for breast and ovarian cancer. <i>Human Genetics and Genomics Advances</i> , 2021, 2, 100042.	1.7	6
65	Comprehensive Evaluation of the Contribution of X Chromosome Genes to Platinum Sensitivity. <i>Molecular Cancer Therapeutics</i> , 2011, 10, 472-480.	4.1	5
66	<i>C. elegans</i> mutants with chronic nicotine exposure as a novel model of cancer phenotype. <i>Cancer Biology and Therapy</i> , 2016, 17, 91-103.	3.4	3
67	Fine-mapping studies distinguish genetic risks for childhood- and adult-onset asthma in the HLA region. <i>Genome Medicine</i> , 2022, 14, .	8.2	2
68	Proximity effect of thin films on superconducting substrates. <i>Physical Review B</i> , 1994, 50, 10117-10121.	3.2	1
69	Analysis of Genetically Regulated Gene Expression Identifies a Trauma Type Specific PTSD Gene, SNRNP35. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0