Hae Kyung Im

List of Publications by Citations

88 papers	12,518 citations	32 h-index	107 g-index
107 ext. papers	17,683 ext. citations	14.3 avg, IF	5.41 L-index

#	Paper	IF	Citations
88	The Genotype-Tissue Expression (GTEx) project. *Nature Genetics*, **2013**, 45, 580-5	36.3	4179
87	Human genomics. The Genotype-Tissue Expression (GTEx) pilot analysis: multitissue gene regulation in humans. *Science*, **2015**, 348, 648-60	33.3	3242
86	A gene-based association method for mapping traits using reference transcriptome data. *Nature Genetics*, **2015**, 47, 1091-8	36.3	850
85	The genetic architecture of type 2 diabetes. *Nature*, **2016**, 536, 41-47	50.4	704
84	Exploring the phenotypic consequences of tissue specific gene expression variation inferred from GWAS summary statistics. *Nature Communications*, **2018**, 9, 1825	17.4	367
83	Opportunities and challenges for transcriptome-wide association studies. *Nature Genetics*, **2019**, 51, 592-599	36.3	266
82	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. *Nature Genetics*, **2017**, 49, 834-841	36.3	257
81	Annotation-free quantification of RNA splicing using LeafCutter. *Nature Genetics*, **2018**, 50, 151-158	36.3	234
80	Accounting for animal movement in estimation of resource selection functions: sampling and data analysis. *Ecology*, **2009**, 90, 3554-65	4.6	219
79	Human genomics. Effect of predicted protein-truncating genetic variants on the human transcriptome. *Science*, **2015**, 348, 666-9	33.3	170
78	Population differences in microRNA expression and biological implications. *RNA Biology*, **2011**, 8, 692-701	4.8	115
77	Shared and distinct genetic risk factors for childhood-onset and adult-onset asthma: genome-wide and transcriptome-wide studies. *Lancet Respiratory Medicine,the*, **2019**, 7, 509-522	35.1	111
76	Integrating predicted transcriptome from multiple tissues improves association detection. *PLoS Genetics*, **2019**, 15, e1007889	6	100
75	The impact of sex on gene expression across human tissues. *Science*, **2020**, 369,	33.3	100
74	Gene expression imputation across multiple brain regions provides insights into schizophrenia risk. *Nature Genetics*, **2019**, 51, 659-674	36.3	99
73	Survey of the Heritability and Sparse Architecture of Gene Expression Traits across Human Tissues. *PLoS Genetics*, **2016**, 12, e1006423	6	99
72	The GTEx Consortium atlas of genetic regulatory effects across human tissues		81

71	Genetic architecture of microRNA expression: implications for the transcriptome and complex traits. *American Journal of Human Genetics*, **2012**, 90, 1046-63	11	80
70	Cell type-specific genetic regulation of gene expression across human tissues. *Science*, **2020**, 369,	33.3	68
69	Exprtarget: an integrative approach to predicting human microRNA targets. *PLoS ONE*, **2010**, 5, e13534	3.7	65
68	On sharing quantitative trait GWAS results in an era of multiple-omics data and the limits of genomic privacy. *American Journal of Human Genetics*, **2012**, 90, 591-8	11	61
67	Targeting the urokinase plasminogen activator receptor inhibits ovarian cancer metastasis. *Clinical Cancer Research*, **2011**, 17, 459-71	12.9	61
66	Genetic architecture of gene expression traits across diverse populations. *PLoS Genetics*, **2018**, 14, e1007586	7	57
65	Platinum sensitivity-related germline polymorphism discovered via a cell-based approach and analysis of its association with outcome in ovarian cancer patients. *Clinical Cancer Research*, **2011**, 17, 5490-500	12.9	55
64	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function. *Nature Communications*, **2018**, 9, 2976	17.4	45
63	Genetic regulatory variation in populations informs transcriptome analysis in rare disease. *Science*, **2019**, 366, 351-356	33.3	42
62	Exploiting the GTEx resources to decipher the mechanisms at GWAS loci. *Genome Biology*, **2021**, 22, 49	18.3	38
61	Germline polymorphisms discovered via a cell-based, genome-wide approach predict platinum response in head and neck cancers. *Translational Research*, **2011**, 157, 265-72	11	37
60	Transcriptomic signatures across human tissues identify functional rare genetic variation. *Science*, **2020**, 369,	33.3	36
59	Poly-omic prediction of complex traits: OmicKriging. *Genetic Epidemiology*, **2014**, 38, 402-15	2.6	34
58	Genetic variation that predicts platinum sensitivity reveals the role of miR-193b* in chemotherapeutic susceptibility. *Molecular Cancer Therapeutics*, **2012**, 11, 2054-61	6.1	33
57	A Transcriptome-Wide Association Study Among 97,898 Women to Identify Candidate Susceptibility Genes for Epithelial Ovarian Cancer Risk. *Cancer Research*, **2018**, 78, 5419-5430	10.1	32
56	Exploring the phenotypic consequences of tissue specific gene expression variation inferred from GWAS summary statistics		30
55	A Low-Frequency Inactivating Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. *Diabetes*, **2017**, 66, 2019-2032	0.9	29
54	Imputing Gene Expression in Uncollected Tissues Within and Beyond GTEx. *American Journal of Human Genetics*, **2016**, 98, 697-708	11	25

53	Mixed effects modeling of proliferation rates in cell-based models: consequence for pharmacogenomics and cancer. *PLoS Genetics*, **2012**, 8, e1002525	6	24
52	PhenomeXcan: Mapping the genome to the phenome through the transcriptome. *Science Advances*, **2020**, 6,	14.3	24
51	Identification of novel germline polymorphisms governing capecitabine sensitivity. *Cancer*, **2012**, 118, 4063-73	6.4	23
50	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. *Scientific Data*, **2017**, 4, 170179	8.2	22
49	Whole-genome studies identify solute carrier transporters in cellular susceptibility to paclitaxel. *Pharmacogenetics and Genomics*, **2012**, 22, 498-507	1.9	21
48	Exploiting the GTEx resources to decipher the mechanisms at GWAS loci		21
47	Analysis of Genetically Regulated Gene Expression Identifies a Prefrontal PTSD Gene, SNRNP35, Specific to Military Cohorts. *Cell Reports*, **2020**, 31, 107716	10.6	21
46	Semiparametric Estimation of Spectral Density With Irregular Observations. *Journal of the American Statistical Association*, **2007**, 102, 726-735	2.8	20
45	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. *Cell*, **2021**, 184, 2633-2648.e19	56.2	20
44	Impact of admixture and ancestry on eQTL analysis and GWAS colocalization in GTEx. *Genome Biology*, **2020**, 21, 233	18.3	19
43	LeafCutter: annotation-free quantification of RNA splicing		18
42	A vast resource of allelic expression data spanning human tissues. *Genome Biology*, **2020**, 21, 234	18.3	18
41	A multi-stage genome-wide association study of uterine fibroids in African Americans. *Human Genetics*, **2017**, 136, 1363-1373	6.3	17
40	MicroRNA biogenesis and cellular proliferation. *Translational Research*, **2015**, 166, 145-51	11	16
39	Diverse transcriptomic signatures across human tissues identify functional rare genetic variation		13
38	Probabilistic colocalization of genetic variants from complex and molecular traits: promise and limitations. *American Journal of Human Genetics*, **2021**, 108, 25-35	11	13
37	Imputed gene associations identify replicable trans-acting genes enriched in transcription pathways and complex traits. *Genetic Epidemiology*, **2019**, 43, 596-608	2.6	12
36	An eQTL-based method identifies CTTN and ZMAT3 as pemetrexed susceptibility markers. *Human Molecular Genetics*, **2012**, 21, 1470-80	5.6	12

17	Transcriptome prediction performance across machine learning models and diverse ancestries. *Human Genetics and Genomics Advances*, **2021**, 2, 100019-100019	0.8	4
16	ukbREST: efficient and streamlined data access for reproducible research in large biobanks. *Bioinformatics*, **2019**, 35, 1971-1973	7.2	4
15	C. elegans and mutants with chronic nicotine exposure as a novel model of cancer phenotype. *Cancer Biology and Therapy*, **2016**, 17, 91-103	4.6	3
14	Polygenic transcriptome risk scores (PTRS) can improve portability of polygenic risk scores across ancestries.. *Genome Biology*, **2022**, 23, 23	18.3	3
13	Fine-mapping and QTL tissue-sharing information improve causal gene identification and transcriptome prediction performance		2
12	Survey of the Heritability and Sparse Architecture of Gene Expression Traits Across Human Tissues		2
11	Pleiotropy-guided transcriptome imputation from normal and tumor tissues identifies candidate susceptibility genes for breast and ovarian cancer. *Human Genetics and Genomics Advances*, **2021**, 2, 100042-100042	0.8	2
10	A scalable unified framework of total and allele-specific counts for cis-QTL, fine-mapping, and prediction. *Nature Communications*, **2021**, 12, 1424	17.4	2
9	Proximity effect of thin films on superconducting substrates. *Physical Review B*, **1994**, 50, 10117-10121	3.3	1
8	Shared and Distinct Genetic Risk Factors for Childhood Onset and Adult Onset Asthma: Genome- and Transcriptome-wide Studies		1
7	Investigating tissue-relevant causal molecular mechanisms of complex traits using probabilistic TWAS analysis		1
6	Probabilistic Colocalization of Genetic Variants from Complex and Molecular Traits: Promise and Limitations		1
5	Identifying tissues implicated in Anorexia Nervosa using Transcriptomic Imputation		1
4	Integrating Predicted Transcriptome From Multiple Tissues Improves Association Detection		1
3	Analysis of Genetically Regulated Gene Expression identifies a trauma type specific PTSD gene, SNRNP35		1
2	Genomic analyses for age at menarche identify 389 independent signals and indicate BMI-independent effects of puberty timing on cancer susceptibility		1
1	Protein prediction for trait mapping in diverse populations.. *PLoS ONE*, **2022**, 17, e0264341	3.7	0