

Hae Kyung Im

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Polygenic transcriptome risk scores (PTRS) can improve portability of polygenic risk scores across ancestries.. <i>Genome Biology</i> , 2022 , 23, 23	18.3	3
87	Protein prediction for trait mapping in diverse populations.. <i>PLoS ONE</i> , 2022 , 17, e0264341	3.7	0
86	Transcriptome prediction performance across machine learning models and diverse ancestries. <i>Human Genetics and Genomics Advances</i> , 2021 , 2, 100019-100019	0.8	4
85	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. <i>Cell</i> , 2021 , 184, 2633-2648.e19	56.2	20
84	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, 100042-100042	0.8	0
83	Probabilistic colocalization of genetic variants from complex and molecular traits: promise and limitations. <i>American Journal of Human Genetics</i> , 2021 , 108, 25-35	11	13
82	Exploiting the GTEx resources to decipher the mechanisms at GWAS loci. <i>Genome Biology</i> , 2021 , 22, 49	18.3	38
81	A scalable unified framework of total and allele-specific counts for cis-QTL, fine-mapping, and prediction. <i>Nature Communications</i> , 2021 , 12, 1424	17.4	2
80	Fine-mapping and QTL tissue-sharing information improves the reliability of causal gene identification. <i>Genetic Epidemiology</i> , 2020 , 44, 854	2.6	9
79	Analysis of Genetically Regulated Gene Expression Identifies a Prefrontal PTSD Gene, SNRNP35, Specific to Military Cohorts. <i>Cell Reports</i> , 2020 , 31, 107716	10.6	21
78	Transcriptomic signatures across human tissues identify functional rare genetic variation. <i>Science</i> , 2020 , 369,	33.3	36
77	Cell type-specific genetic regulation of gene expression across human tissues. <i>Science</i> , 2020 , 369,	33.3	68
76	The impact of sex on gene expression across human tissues. <i>Science</i> , 2020 , 369,	33.3	100
75	PTWAS: investigating tissue-relevant causal molecular mechanisms of complex traits using probabilistic TWAS analysis. <i>Genome Biology</i> , 2020 , 21, 232	18.3	11
74	PhenomeXcan: Mapping the genome to the phenome through the transcriptome. <i>Science Advances</i> , 2020 , 6,	14.3	24
73	Impact of admixture and ancestry on eQTL analysis and GWAS colocalization in GTEx. <i>Genome Biology</i> , 2020 , 21, 233	18.3	19
72	A vast resource of allelic expression data spanning human tissues. <i>Genome Biology</i> , 2020 , 21, 234	18.3	18

71	sn-sPMF: matrix factorization informs tissue-specific genetic regulation of gene expression. <i>Genome Biology</i> , 2020 , 21, 235	18.3	6
70	CORE GREML for estimating covariance between random effects in linear mixed models for complex trait analyses. <i>Nature Communications</i> , 2020 , 11, 4208	17.4	10
69	Integrating predicted transcriptome from multiple tissues improves association detection. <i>PLoS Genetics</i> , 2019 , 15, e1007889	6	100
68	A -Ethnic Genome-Wide Association Study of Uterine Fibroids. <i>Frontiers in Genetics</i> , 2019 , 10, 511	4.5	10
67	Gene expression imputation across multiple brain regions provides insights into schizophrenia risk. <i>Nature Genetics</i> , 2019 , 51, 659-674	36.3	99
66	Opportunities and challenges for transcriptome-wide association studies. <i>Nature Genetics</i> , 2019 , 51, 592-599	36.3	266
65	Imputed gene associations identify replicable trans-acting genes enriched in transcription pathways and complex traits. <i>Genetic Epidemiology</i> , 2019 , 43, 596-608	2.6	12
64	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	35.1	111
63	Genetic regulatory variation in populations informs transcriptome analysis in rare disease. <i>Science</i> , 2019 , 366, 351-356	33.3	42
62	ukbREST: efficient and streamlined data access for reproducible research in large biobanks. <i>Bioinformatics</i> , 2019 , 35, 1971-1973	7.2	4
61	Functionally oriented analysis of cardiometabolic traits in a trans-ethnic sample. <i>Human Molecular Genetics</i> , 2019 , 28, 1212-1224	5.6	5
60	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	10.1	32
59	Exploring the phenotypic consequences of tissue specific gene expression variation inferred from GWAS summary statistics. <i>Nature Communications</i> , 2018 , 9, 1825	17.4	367
58	Genetic architecture of gene expression traits across diverse populations. <i>PLoS Genetics</i> , 2018 , 14, e1007586	5.8	57
57	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function. <i>Nature Communications</i> , 2018 , 9, 2976	17.4	45
56	Annotation-free quantification of RNA splicing using LeafCutter. <i>Nature Genetics</i> , 2018 , 50, 151-158	36.3	234
55	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	36.3	257
54	A Low-Frequency Inactivating Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. <i>Diabetes</i> , 2017 , 66, 2019-2032	0.9	29

53	Trans-ethnic predicted expression genome-wide association analysis identifies a gene for estrogen receptor-negative breast cancer. <i>PLoS Genetics</i> , 2017 , 13, e1006727	6	6
52	A multi-stage genome-wide association study of uterine fibroids in African Americans. <i>Human Genetics</i> , 2017 , 136, 1363-1373	6.3	17
51	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. <i>Scientific Data</i> , 2017 , 4, 170179	8.2	22
50	<i>C. elegans</i> and mutants with chronic nicotine exposure as a novel model of cancer phenotype. <i>Cancer Biology and Therapy</i> , 2016 , 17, 91-103	4.6	3
49	Survey of the Heritability and Sparse Architecture of Gene Expression Traits across Human Tissues. <i>PLoS Genetics</i> , 2016 , 12, e1006423	6	99
48	The genetic architecture of type 2 diabetes. <i>Nature</i> , 2016 , 536, 41-47	50.4	704
47	Imputing Gene Expression in Uncollected Tissues Within and Beyond GTEx. <i>American Journal of Human Genetics</i> , 2016 , 98, 697-708	11	25
46	MicroRNA biogenesis and cellular proliferation. <i>Translational Research</i> , 2015 , 166, 145-51	11	16
45	Human genomics. The Genotype-Tissue Expression (GTEx) pilot analysis: multitissue gene regulation in humans. <i>Science</i> , 2015 , 348, 648-60	33.3	3242
44	Human genomics. Effect of predicted protein-truncating genetic variants on the human transcriptome. <i>Science</i> , 2015 , 348, 666-9	33.3	170
43	A gene-based association method for mapping traits using reference transcriptome data. <i>Nature Genetics</i> , 2015 , 47, 1091-8	36.3	850
42	Poly-omic prediction of complex traits: OmicKriging. <i>Genetic Epidemiology</i> , 2014 , 38, 402-15	2.6	34
41	The Genotype-Tissue Expression (GTEx) project. <i>Nature Genetics</i> , 2013 , 45, 580-5	36.3	4179
40	Functional consequences of PRPF39 on distant genes and cisplatin sensitivity. <i>Human Molecular Genetics</i> , 2012 , 21, 4348-55	5.6	6
39	Identification of novel germline polymorphisms governing capecitabine sensitivity. <i>Cancer</i> , 2012 , 118, 4063-73	6.4	23
38	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, 591-8	11	61
37	Genetic architecture of microRNA expression: implications for the transcriptome and complex traits. <i>American Journal of Human Genetics</i> , 2012 , 90, 1046-63	11	80
36	Mixed effects modeling of proliferation rates in cell-based models: consequence for pharmacogenomics and cancer. <i>PLoS Genetics</i> , 2012 , 8, e1002525	6	24

35	An eQTL-based method identifies CTTN and ZMAT3 as pemetrexed susceptibility markers. <i>Human Molecular Genetics</i> , 2012 , 21, 1470-80	5.6	12
34	Genetic variation that predicts platinum sensitivity reveals the role of miR-193b* in chemotherapeutic susceptibility. <i>Molecular Cancer Therapeutics</i> , 2012 , 11, 2054-61	6.1	33
33	Whole-genome studies identify solute carrier transporters in cellular susceptibility to paclitaxel. <i>Pharmacogenetics and Genomics</i> , 2012 , 22, 498-507	1.9	21
32	Germline polymorphisms discovered via a cell-based, genome-wide approach predict platinum response in head and neck cancers. <i>Translational Research</i> , 2011 , 157, 265-72	11	37
31	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, 5490-500	12.9	55
30	Population differences in microRNA expression and biological implications. <i>RNA Biology</i> , 2011 , 8, 692-704	1.8	115
29	Targeting the urokinase plasminogen activator receptor inhibits ovarian cancer metastasis. <i>Clinical Cancer Research</i> , 2011 , 17, 459-71	12.9	61
28	Comprehensive evaluation of the contribution of X chromosome genes to platinum sensitivity. <i>Molecular Cancer Therapeutics</i> , 2011 , 10, 472-80	6.1	4
27	Exprtarget: an integrative approach to predicting human microRNA targets. <i>PLoS ONE</i> , 2010 , 5, e13534	3.7	65
26	Space-time modeling of 20 years of daily air temperature in the Chicago metropolitan region. <i>Environmetrics</i> , 2009 , 20, 494-511	1.3	7
25	Accounting for animal movement in estimation of resource selection functions: sampling and data analysis. <i>Ecology</i> , 2009 , 90, 3554-65	4.6	219
24	Semiparametric Estimation of Spectral Density With Irregular Observations. <i>Journal of the American Statistical Association</i> , 2007 , 102, 726-735	2.8	20
23	Proximity effect of thin films on superconducting substrates. <i>Physical Review B</i> , 1994 , 50, 10117-10121	3.3	1
22	Fine-mapping and QTL tissue-sharing information improve causal gene identification and transcriptome prediction performance		2
21	Shared and Distinct Genetic Risk Factors for Childhood Onset and Adult Onset Asthma: Genome- and Transcriptome-wide Studies		1
20	Investigating tissue-relevant causal molecular mechanisms of complex traits using probabilistic TWAS analysis		1
19	LeafCutter: annotation-free quantification of RNA splicing		18
18	Exploring the phenotypic consequences of tissue specific gene expression variation inferred from GWAS summary statistics		30

17	Integrative cross tissue analysis of gene expression identifies novel type 2 diabetes genes	7
16	Probabilistic Colocalization of Genetic Variants from Complex and Molecular Traits: Promise and Limitations	1
15	Polygenic transcriptome risk scores improve portability of polygenic risk scores across ancestries	4
14	Transcriptome-wide association studies: opportunities and challenges	12
13	Gene expression imputation across multiple brain regions reveals schizophrenia risk throughout development	6
12	Transcriptomic Imputation of Bipolar Disorder and Bipolar subtypes reveals 29 novel associated genes	9
11	Identifying tissues implicated in Anorexia Nervosa using Transcriptomic Imputation	1
10	Integrating Predicted Transcriptome From Multiple Tissues Improves Association Detection	1
9	Analysis of Genetically Regulated Gene Expression identifies a trauma type specific PTSD gene, SNRNP35	1
8	Diverse transcriptomic signatures across human tissues identify functional rare genetic variation	13
7	The GTEx Consortium atlas of genetic regulatory effects across human tissues	81
6	Cell type specific genetic regulation of gene expression across human tissues	7
5	Exploiting the GTEx resources to decipher the mechanisms at GWAS loci	21
4	PhenomeXcan: Mapping the genome to the phenome through the transcriptome	6
3	PrediXcan: Trait Mapping Using Human Transcriptome Regulation	4
2	Survey of the Heritability and Sparse Architecture of Gene Expression Traits Across Human Tissues	2
1	Genomic analyses for age at menarche identify 389 independent signals and indicate BMI-independent effects of puberty timing on cancer susceptibility	1