# Hae Kyung Im

List of Publications by Year
in descending order

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|---|---|---|---|
| 69<br>papers | 20,740<br>citations | 101543<br>36<br>h-index | 88630<br>70<br>g-index |
| 107<br>all docs | 107<br>docs citations | 107<br>times ranked | 37982<br>citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Polygenic transcriptome risk scores (PTRS) can improve portability of polygenic risk scores across ancestries. Genome Biology, 2022, 23, 23. | 8.8 | 42 |
| 2 | Protein prediction for trait mapping in diverse populations. PLoS ONE, 2022, 17, e0264341. | 2.5 | 13 |
| 3 | Polygenic transcriptome risk scores for COPD and lung function improve cross-ethnic portability of prediction in the NHLBI TOPMed program. American Journal of Human Genetics, 2022, 109, 857-870. | 6.2 | 7 |
| 4 | Fine-mapping studies distinguish genetic risks for childhood- and adult-onset asthma in the HLA region. Genome Medicine, 2022, 14, . | 8.2 | 2 |
| 5 | Probabilistic colocalization of genetic variants from complex and molecular traits: promise and limitations. American Journal of Human Genetics, 2021, 108, 25-35. | 6.2 | 67 |
| 6 | Exploiting the GTEx resources to decipher the mechanisms at GWAS loci. Genome Biology, 2021, 22, 49. | 8.8 | 150 |
| 7 | A scalable unified framework of total and allele-specific counts for cis-QTL, fine-mapping, and prediction. Nature Communications, 2021, 12, 1424. | 12.8 | 23 |
| 8 | Transcriptome prediction performance across machine learning models and diverse ancestries. Human Genetics and Genomics Advances, 2021, 2, 100019. | 1.7 | 14 |
| 9 | Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. Cell, 2021, 184, 2633-2648.e19. | 28.9 | 94 |
| 10 | 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. | 1.7 | 6 |
| 11 | Fineâ€mapping and QTL tissueâ€sharing information improves the reliability of causal gene identification. Genetic Epidemiology, 2020, 44, 854-867. | 1.3 | 28 |
| 12 | Analysis of Genetically Regulated Gene Expression Identifies a Prefrontal PTSD Gene, SNRNP35, Specific to Military Cohorts. Cell Reports, 2020, 31, 107716. | 6.4 | 44 |
| 13 | Transcriptomic signatures across human tissues identify functional rare genetic variation. Science, 2020, 369, . | 12.6 | 89 |
| 14 | Cell typeâ€“specific genetic regulation of gene expression across human tissues. Science, 2020, 369, . | 12.6 | 210 |
| 15 | The impact of sex on gene expression across human tissues. Science, 2020, 369, . | 12.6 | 329 |
| 16 | PTWAS: investigating tissue-relevant causal molecular mechanisms of complex traits using probabilistic TWAS analysis. Genome Biology, 2020, 21, 232. | 8.8 | 46 |
| 17 | PhenomeXcan: Mapping the genome to the phenome through the transcriptome. Science Advances, 2020, 6, . | 10.3 | 83 |
| 18 | Impact of admixture and ancestry on eQTL analysis and GWAS colocalization in GTEx. Genome Biology, 2020, 21, 233. | 8.8 | 64 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | A vast resource of allelic expression data spanning human tissues. Genome Biology, 2020, 21, 234. | 8.8 | 68 |
| 20 | sn-spMF: matrix factorization informs tissue-specific genetic regulation of gene expression. Genome Biology, 2020, 21, 235. | 8.8 | 18 |
| 21 | CORE GREML for estimating covariance between random effects in linear mixed models for complex trait analyses. Nature Communications, 2020, 11, 4208. | 12.8 | 23 |
| 22 | 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. | 10.7 | 238 |
| 23 | Genetic regulatory variation in populations informs transcriptome analysis in rare disease. Science, 2019, 366, 351-356. | 12.6 | 99 |
| 24 | Integrating predicted transcriptome from multiple tissues improves association detection. PLoS Genetics, 2019, 15, e1007889. | 3.5 | 239 |
| 25 | A Trans-Ethnic Genome-Wide Association Study of Uterine Fibroids. Frontiers in Genetics, 2019, 10, 511. | 2.3 | 32 |
| 26 | Gene expression imputation across multiple brain regions provides insights into schizophrenia risk. Nature Genetics, 2019, 51, 659-674. | 21.4 | 154 |
| 27 | Opportunities and challenges for transcriptome-wide association studies. Nature Genetics, 2019, 51, 592-599. | 21.4 | 592 |
| 28 | Imputed gene associations identify replicable transâ€acting genes enriched in transcription pathways and complex traits. Genetic Epidemiology, 2019, 43, 596-608. | 1.3 | 19 |
| 29 | ukbREST: efficient and streamlined data access for reproducible research in large biobanks. Bioinformatics, 2019, 35, 1971-1973. | 4.1 | 6 |
| 30 | Functionally oriented analysis of cardiometabolic traits in a trans-ethnic sample. Human Molecular Genetics, 2019, 28, 1212-1224. | 2.9 | 12 |
| 31 | Annotation-free quantification of RNA splicing using LeafCutter. Nature Genetics, 2018, 50, 151-158. | 21.4 | 520 |
| 32 | 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. | 0.9 | 54 |
| 33 | Exploring the phenotypic consequences of tissue specific gene expression variation inferred from GWAS summary statistics. Nature Communications, 2018, 9, 1825. | 12.8 | 748 |
| 34 | Genetic architecture of gene expression traits across diverse populations. PLoS Genetics, 2018, 14, e1007586. | 3.5 | 117 |
| 35 | Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function. Nature Communications, 2018, 9, 2976. | 12.8 | 85 |
| 36 | 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. | 21.4 | 426 |

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|---|---|---|---|
| 37 | 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 |
| 38 | A multi-stage genome-wide association study of uterine fibroids in African Americans. Human Genetics, 2017, 136, 1363-1373. | 3.8 | 39 |
| 39 | Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179. | 5.3 | 31 |
| 40 | Trans-ethnic predicted expression genome-wide association analysis identifies a gene for estrogen receptor-negative breast cancer. PLoS Genetics, 2017, 13, e1006727. | 3.5 | 14 |
| 41 | Survey of the Heritability and Sparse Architecture of Gene Expression Traits across Human Tissues. PLoS Genetics, 2016, 12, e1006423. | 3.5 | 143 |
| 42 | The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47. | 27.8 | 952 |
| 43 | Imputing Gene Expression in Uncollected Tissues Within and Beyond GTEx. American Journal of Human Genetics, 2016, 98, 697-708. | 6.2 | 51 |
| 44 | C. elegansand mutants with chronic nicotine exposure as a novel model of cancer phenotype. Cancer Biology and Therapy, 2016, 17, 91-103. | 3.4 | 3 |
| 45 | MicroRNA biogenesis and cellular proliferation. Translational Research, 2015, 166, 145-151. | 5.0 | 18 |
| 46 | The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. Science, 2015, 348, 648-660. | 12.6 | 4,659 |
| 47 | Effect of predicted protein-truncating genetic variants on the human transcriptome. Science, 2015, 348, 666-669. | 12.6 | 252 |
| 48 | A gene-based association method for mapping traits using reference transcriptome data. Nature Genetics, 2015, 47, 1091-1098. | 21.4 | 1,473 |
| 49 | Poly-Omic Prediction of Complex Traits: OmicKriging. Genetic Epidemiology, 2014, 38, 402-415. | 1.3 | 41 |
| 50 | The Genotype-Tissue Expression (GTEx) project. Nature Genetics, 2013, 45, 580-585. | 21.4 | 6,815 |
| 51 | Mixed Effects Modeling of Proliferation Rates in Cell-Based Models: Consequence for Pharmacogenomics and Cancer. PLoS Genetics, 2012, 8, e1002525. | 3.5 | 26 |
| 52 | An eQTL-based method identifies CTTN and ZMAT3 as pemetrexed susceptibility markers. Human Molecular Genetics, 2012, 21, 1470-1480. | 2.9 | 16 |
| 53 | Genetic Variation That Predicts Platinum Sensitivity Reveals the Role of miR-193b* in Chemotherapeutic Susceptibility. Molecular Cancer Therapeutics, 2012, 11, 2054-2061. | 4.1 | 35 |
| 54 | Whole-genome studies identify solute carrier transporters in cellular susceptibility to paclitaxel. Pharmacogenetics and Genomics, 2012, 22, 498-507. | 1.5 | 28 |

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|---|---|---|---|
| 55 | Functional consequences of PRPF39 on distant genes and cisplatin sensitivity. Human Molecular Genetics, 2012, 21, 4348-4355. | 2.9 | 7 |
| 56 | Identification of novel germline polymorphisms governing capecitabine sensitivity. Cancer, 2012, 118, 4063-4073. | 4.1 | 25 |
| 57 | 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, 591-598. | 6.2 | 87 |
| 58 | Genetic Architecture of MicroRNA Expression: Implications for the Transcriptome and Complex Traits. American Journal of Human Genetics, 2012, 90, 1046-1063. | 6.2 | 92 |
| 59 | Germline polymorphisms discovered via a cell-based, genome-wide approach predict platinum response in head and neck cancers. Translational Research, 2011, 157, 265-272. | 5.0 | 42 |
| 60 | Platinum Sensitivityâ€“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, 5490-5500. | 7.0 | 57 |
| 61 | Population differences in microRNA expression and biological implications. RNA Biology, 2011, 8, 692-701. | 3.1 | 138 |
| 62 | Targeting the Urokinase Plasminogen Activator Receptor Inhibits Ovarian Cancer Metastasis. Clinical Cancer Research, 2011, 17, 459-471. | 7.0 | 69 |
| 63 | Comprehensive Evaluation of the Contribution of X Chromosome Genes to Platinum Sensitivity. Molecular Cancer Therapeutics, 2011, 10, 472-480. | 4.1 | 5 |
| 64 | ExprTarget: An Integrative Approach to Predicting Human MicroRNA Targets. PLoS ONE, 2010, 5, e13534. | 2.5 | 80 |
| 65 | Spaceâ€“time modeling of 20 years of daily air temperature in the Chicago metropolitan region. Environmetrics, 2009, 20, 494-511. | 1.4 | 12 |
| 66 | Accounting for animal movement in estimation of resource selection functions: sampling and data analysis. Ecology, 2009, 90, 3554-3565. | 3.2 | 295 |
| 67 | Semiparametric Estimation of Spectral Density With Irregular Observations. Journal of the American Statistical Association, 2007, 102, 726-735. | 3.1 | 26 |
| 68 | Proximity effect of thin films on superconducting substrates. Physical Review B, 1994, 50, 10117-10121. | 3.2 | 1 |
| 69 | Analysis of Genetically Regulated Gene Expression Identifies a Trauma Type Specific PTSD Gene, SNRNP35. SSRN Electronic Journal, 0, , . | 0.4 | 0 |