

Hua Tang

List of Publications by Year in descending order

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Version: 2024-02-01

72
papers

10,018
citations

94433

37
h-index

98798

67
g-index

77
all docs

77
docs citations

77
times ranked

18007
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Worldwide Human Relationships Inferred from Genome-Wide Patterns of Variation. <i>Science</i> , 2008, 319, 1100-1104. | 12.6 | 1,774 |
| 2 | Personal Omics Profiling Reveals Dynamic Molecular and Medical Phenotypes. <i>Cell</i> , 2012, 148, 1293-1307. | 28.9 | 1,134 |
| 3 | Estimation of individual admixture: Analytical and study design considerations. <i>Genetic Epidemiology</i> , 2005, 28, 289-301. | 1.3 | 571 |
| 4 | Genetic Structure, Self-Identified Race/Ethnicity, and Confounding in Case-Control Association Studies. <i>American Journal of Human Genetics</i> , 2005, 76, 268-275. | 6.2 | 513 |
| 5 | Genetics of blood lipids among ~300,000 multi-ethnic participants of the Million Veteran Program. <i>Nature Genetics</i> , 2018, 50, 1514-1523. | 21.4 | 497 |
| 6 | Exome-wide association study of plasma lipids in >300,000 individuals. <i>Nature Genetics</i> , 2017, 49, 1758-1766. | 21.4 | 470 |
| 7 | The Polygenic and Monogenic Basis of Blood Traits and Diseases. <i>Cell</i> , 2020, 182, 1214-1231.e11. | 28.9 | 388 |
| 8 | Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. <i>Cell</i> , 2020, 182, 1198-1213.e14. | 28.9 | 353 |
| 9 | Variation and genetic control of protein abundance in humans. <i>Nature</i> , 2013, 499, 79-82. | 27.8 | 343 |
| 10 | Characterizing Race/Ethnicity and Genetic Ancestry for 100,000 Subjects in the Genetic Epidemiology Research on Adult Health and Aging (GERA) Cohort. <i>Genetics</i> , 2015, 200, 1285-1295. | 2.9 | 273 |
| 11 | A Quantitative Proteome Map of the Human Body. <i>Cell</i> , 2020, 183, 269-283.e19. | 28.9 | 243 |
| 12 | Reconstructing Genetic Ancestry Blocks in Admixed Individuals. <i>American Journal of Human Genetics</i> , 2006, 79, 1-12. | 6.2 | 240 |
| 13 | Modeling 3D Facial Shape from DNA. <i>PLoS Genetics</i> , 2014, 10, e1004224. | 3.5 | 190 |
| 14 | Genome-wide Association Analysis of Blood-Pressure Traits in African-Ancestry Individuals Reveals Common Associated Genes in African and Non-African Populations. <i>American Journal of Human Genetics</i> , 2013, 93, 545-554. | 6.2 | 189 |
| 15 | Harmonizing Genetic Ancestry and Self-identified Race/Ethnicity in Genome-wide Association Studies. <i>American Journal of Human Genetics</i> , 2019, 105, 763-772. | 6.2 | 169 |
| 16 | Recent Genetic Selection in the Ancestral Admixture of Puerto Ricans. <i>American Journal of Human Genetics</i> , 2007, 81, 626-633. | 6.2 | 168 |
| 17 | Integrative analysis of RNA, translation, and protein levels reveals distinct regulatory variation across humans. <i>Genome Research</i> , 2015, 25, 1610-1621. | 5.5 | 157 |
| 18 | Characterizing the admixed African ancestry of African Americans. <i>Genome Biology</i> , 2009, 10, R141. | 9.6 | 145 |

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|----|--|------|-----------|
| 19 | Genome-Wide Association Study Implicates Chromosome 9q21.31 as a Susceptibility Locus for Asthma in Mexican Children. <i>PLoS Genetics</i> , 2009, 5, e1000623. | 3.5 | 139 |
| 20 | Genetic Architecture of Skin and Eye Color in an African-European Admixed Population. <i>PLoS Genetics</i> , 2013, 9, e1003372. | 3.5 | 137 |
| 21 | A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. <i>American Journal of Human Genetics</i> , 2018, 102, 375-400. | 6.2 | 123 |
| 22 | Genome-wide Characterization of Shared and Distinct Genetic Components that Influence Blood Lipid Levels in Ethnically Diverse Human Populations. <i>American Journal of Human Genetics</i> , 2013, 92, 904-916. | 6.2 | 113 |
| 23 | Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. <i>Nature Genetics</i> , 2019, 51, 636-648. | 21.4 | 112 |
| 24 | Ancestral Components of Admixed Genomes in a Mexican Cohort. <i>PLoS Genetics</i> , 2011, 7, e1002410. | 3.5 | 109 |
| 25 | Genome-wide Association and Population Genetic Analysis of C-Reactive Protein in African American and Hispanic American Women. <i>American Journal of Human Genetics</i> , 2012, 91, 502-512. | 6.2 | 107 |
| 26 | Genome-Wide Association Studies of Quantitatively Measured Skin, Hair, and Eye Pigmentation in Four European Populations. <i>PLoS ONE</i> , 2012, 7, e48294. | 2.5 | 94 |
| 27 | Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. <i>PLoS ONE</i> , 2018, 13, e0198166. | 2.5 | 94 |
| 28 | Single-trait and multi-trait genome-wide association analyses identify novel loci for blood pressure in African-ancestry populations. <i>PLoS Genetics</i> , 2017, 13, e1006728. | 3.5 | 88 |
| 29 | Racial admixture and its impact on BMI and blood pressure in African and Mexican Americans. <i>Human Genetics</i> , 2006, 119, 624-633. | 3.8 | 81 |
| 30 | Frequentist Estimation of Coalescence Times From Nucleotide Sequence Data Using a Tree-Based Partition. <i>Genetics</i> , 2002, 161, 447-459. | 2.9 | 76 |
| 31 | Leveraging Multi-ethnic Evidence for Risk Assessment of Quantitative Traits in Minority Populations. <i>American Journal of Human Genetics</i> , 2017, 101, 218-226. | 6.2 | 75 |
| 32 | Leveraging population admixture to characterize the heritability of complex traits. <i>Nature Genetics</i> , 2014, 46, 1356-1362. | 21.4 | 69 |
| 33 | Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. <i>Nature Communications</i> , 2019, 10, 376. | 12.8 | 64 |
| 34 | Meta-analysis of lipid-traits in Hispanics identifies novel loci, population-specific effects and tissue-specific enrichment of eQTLs. <i>Scientific Reports</i> , 2016, 6, 19429. | 3.3 | 63 |
| 35 | Trans-ethnic meta-analysis of white blood cell phenotypes. <i>Human Molecular Genetics</i> , 2014, 23, 6944-6960. | 2.9 | 60 |
| 36 | Genome-wide Trans-ethnic Meta-analysis Identifies Seven Genetic Loci Influencing Erythrocyte Traits and a Role for RBPMS in Erythropoiesis. <i>American Journal of Human Genetics</i> , 2017, 100, 51-63. | 6.2 | 45 |

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|----|--|------|-----------|
| 37 | Joint testing of genotype and ancestry association in admixed families. <i>Genetic Epidemiology</i> , 2010, 34, 783-791. | 1.3 | 43 |
| 38 | Regulation of gene expression and RNA editing in <i>Drosophila</i> adapting to divergent microclimates. <i>Nature Communications</i> , 2017, 8, 1570. | 12.8 | 43 |
| 39 | Locating Regions of Differential Variability in DNA and Protein Sequences. <i>Genetics</i> , 1999, 153, 485-495. | 2.9 | 43 |
| 40 | Dissecting Complex Diseases in Complex Populations: Asthma in Latino Americans. <i>Proceedings of the American Thoracic Society</i> , 2007, 4, 226-233. | 3.5 | 41 |
| 41 | A multi-ancestry genome-wide study incorporating gene-smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. <i>Human Molecular Genetics</i> , 2019, 28, 2615-2633. | 2.9 | 31 |
| 42 | Inference on the Genetic Basis of Eye and Skin Color in an Admixed Population via Bayesian Linear Mixed Models. <i>Genetics</i> , 2017, 206, 1113-1126. | 2.9 | 30 |
| 43 | Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. <i>American Journal of Human Genetics</i> , 2021, 108, 874-893. | 6.2 | 28 |
| 44 | Genome-wide association and admixture analysis of glaucoma in the Women's Health Initiative. <i>Human Molecular Genetics</i> , 2014, 23, 6634-6643. | 2.9 | 22 |
| 45 | Leveraging Multi-ethnic Evidence for Mapping Complex Traits in Minority Populations: An Empirical Bayes Approach. <i>American Journal of Human Genetics</i> , 2015, 96, 740-752. | 6.2 | 22 |
| 46 | Rare transmission of commensal and pathogenic bacteria in the gut microbiome of hospitalized adults. <i>Nature Communications</i> , 2022, 13, 586. | 12.8 | 21 |
| 47 | <i>Trans</i> -ancestry Fine Mapping and Molecular Assays Identify Regulatory Variants at the <i>ANGPTL8</i> HDL-C GWAS Locus. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3217-3227. | 1.8 | 19 |
| 48 | Variants for HDL-C, LDL-C, and Triglycerides Identified from Admixture Mapping and Fine-Mapping Analysis in African American Families. <i>Circulation: Cardiovascular Genetics</i> , 2015, 8, 106-113. | 5.1 | 18 |
| 49 | Functional and structural basis of extreme conservation in vertebrate 5' untranslated regions. <i>Nature Genetics</i> , 2021, 53, 729-741. | 21.4 | 17 |
| 50 | Identification of putative causal loci in whole-genome sequencing data via knockoff statistics. <i>Nature Communications</i> , 2021, 12, 3152. | 12.8 | 17 |
| 51 | The Association of the Vanin-1 N131S Variant with Blood Pressure Is Mediated by Endoplasmic Reticulum-Associated Degradation and Loss of Function. <i>PLoS Genetics</i> , 2014, 10, e1004641. | 3.5 | 16 |
| 52 | Whole-genome sequencing in diverse subjects identifies genetic correlates of leukocyte traits: The NHLBI TOPMed program. <i>American Journal of Human Genetics</i> , 2021, 108, 1836-1851. | 6.2 | 14 |
| 53 | Gene by Environment Investigation of Incident Lung Cancer Risk in African-Americans. <i>EBioMedicine</i> , 2016, 4, 153-161. | 6.1 | 12 |
| 54 | Genome-wide analysis of common and rare variants via multiple knockoffs at biobank scale, with an application to Alzheimer disease genetics. <i>American Journal of Human Genetics</i> , 2021, 108, 2336-2353. | 6.2 | 12 |

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|----|---|------|-----------|
| 55 | Joint genotype- and ancestry-based genome-wide association studies in admixed populations. <i>Genetic Epidemiology</i> , 2017, 41, 555-566. | 1.3 | 11 |
| 56 | PREMIX: PRivacy-preserving EstiMation of Individual admiXture. <i>AMIA ... Annual Symposium proceedings</i> , 2016, 2016, 1747-1755. | 0.2 | 11 |
| 57 | PLOS Genetics Data Sharing Policy: In Pursuit of Functional Utility. <i>PLoS Genetics</i> , 2015, 11, e1005716. | 3.5 | 10 |
| 58 | Robust identification of temporal biomarkers in longitudinal omics studies. <i>Bioinformatics</i> , 2022, 38, 3802-3811. | 4.1 | 10 |
| 59 | Genome-wide survey in African Americans demonstrates potential epistasis of fitness in the human genome. <i>Genetic Epidemiology</i> , 2017, 41, 122-135. | 1.3 | 9 |
| 60 | Skin color variation in Africa. <i>Science</i> , 2017, 358, 867-868. | 12.6 | 8 |
| 61 | Controlling for false positive findings of trans-hubs in expression quantitative trait loci mapping. <i>BMC Proceedings</i> , 2007, 1, S157. | 1.6 | 6 |
| 62 | A Poisson Log-Normal Model for Constructing Gene Covariation Network Using RNA-seq Data. <i>Journal of Computational Biology</i> , 2017, 24, 721-731. | 1.6 | 4 |
| 63 | Detecting fitness epistasis in recently admixed populations with genome-wide data. <i>BMC Genomics</i> , 2020, 21, 476. | 2.8 | 4 |
| 64 | Combining multiple family-based association studies. <i>BMC Proceedings</i> , 2007, 1, S162. | 1.6 | 3 |
| 65 | Response-How the Gray Wolf Got Its Color. <i>Science</i> , 2009, 325, 34-34. | 12.6 | 3 |
| 66 | RobNorm: model-based robust normalization method for labeled quantitative mass spectrometry proteomics data. <i>Bioinformatics</i> , 2021, 37, 815-821. | 4.1 | 3 |
| 67 | Evaluating the strength of genetic results: Risks and responsibilities. <i>PLoS Genetics</i> , 2019, 15, e1008437. | 3.5 | 1 |
| 68 | GENETIC STRUCTURE OF HUMAN POPULATION. , 2015, , 937-960. | | 0 |
| 69 | Doubling down on forensic twin studies. <i>PLoS Genetics</i> , 2018, 14, e1007831. | 3.5 | 0 |
| 70 | Advances and challenges in quantitative delineation of the genetic architecture of complex traits. <i>Quantitative Biology</i> , 2021, 9, 168-184. | 0.5 | 0 |
| 71 | Identification Of The Disease-Causing Mutation In Autosomal Dominant Familial Immune Thrombocytopenia By Genome-Wide Linkage Analysis and Whole Genome Sequencing. <i>Blood</i> , 2013, 122, 565-565. | 1.4 | 0 |
| 72 | Expanding human variation at PLOS Genetics. <i>PLoS Genetics</i> , 2022, 18, e1010070. | 3.5 | 0 |