

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	Rare transmission of commensal and pathogenic bacteria in the gut microbiome of hospitalized adults. <i>Nature Communications</i> , 2022, 13, 586.	12.8	21
2	Expanding human variation at PLOS Genetics. <i>PLoS Genetics</i> , 2022, 18, e1010070.	3.5	0
3	Robust identification of temporal biomarkers in longitudinal omics studies. <i>Bioinformatics</i> , 2022, 38, 3802-3811.	4.1	10
4	RobNorm: model-based robust normalization method for labeled quantitative mass spectrometry proteomics data. <i>Bioinformatics</i> , 2021, 37, 815-821.	4.1	3
5	Functional and structural basis of extreme conservation in vertebrate 5' untranslated regions. <i>Nature Genetics</i> , 2021, 53, 729-741.	21.4	17
6	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
7	Identification of putative causal loci in whole-genome sequencing data via knockoff statistics. <i>Nature Communications</i> , 2021, 12, 3152.	12.8	17
8	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
9	Advances and challenges in quantitative delineation of the genetic architecture of complex traits. <i>Quantitative Biology</i> , 2021, 9, 168-184.	0.5	0
10	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
11	The Polygenic and Monogenic Basis of Blood Traits and Diseases. <i>Cell</i> , 2020, 182, 1214-1231.e11.	28.9	388
12	Detecting fitness epistasis in recently admixed populations with genome-wide data. <i>BMC Genomics</i> , 2020, 21, 476.	2.8	4
13	A Quantitative Proteome Map of the Human Body. <i>Cell</i> , 2020, 183, 269-283.e19.	28.9	243
14	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
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	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. <i>Nature Communications</i> , 2019, 10, 376.	12.8	64
17	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
18	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

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19	Evaluating the strength of genetic results: Risks and responsibilities. <i>PLoS Genetics</i> , 2019, 15, e1008437.	3.5	1
20	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
21	Doubling down on forensic twin studies. <i>PLoS Genetics</i> , 2018, 14, e1007831.	3.5	0
22	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
23	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
24	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
25	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
26	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
27	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
28	Exome-wide association study of plasma lipids in ~300,000 individuals. <i>Nature Genetics</i> , 2017, 49, 1758-1766.	21.4	470
29	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
30	Trans-ancestry Fine Mapping and Molecular Assays Identify Regulatory Variants at the ANGPTL8 HDL-C GWAS Locus. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3217-3227.	1.8	19
31	Joint genotype and ancestry-based genome-wide association studies in admixed populations. <i>Genetic Epidemiology</i> , 2017, 41, 555-566.	1.3	11
32	Skin color variation in Africa. <i>Science</i> , 2017, 358, 867-868.	12.6	8
33	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
34	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
35	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
36	Gene by Environment Investigation of Incident Lung Cancer Risk in African-Americans. <i>EBioMedicine</i> , 2016, 4, 153-161.	6.1	12

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37	PREMIX: PRivacy-preserving EstiMation of Individual admIXture. AMIA ... Annual Symposium proceedings, 2016, 2016, 1747-1755.	0.2	11
38	GENETIC STRUCTURE OF HUMAN POPULATION. , 2015, , 937-960.		0
39	Variants for HDL-C, LDL-C, and Triglycerides Identified from Admixture Mapping and Fine-Mapping Analysis in African American Families. Circulation: Cardiovascular Genetics, 2015, 8, 106-113.	5.1	18
40	Leveraging Multi-ethnic Evidence for Mapping Complex Traits in Minority Populations: An Empirical Bayes Approach. American Journal of Human Genetics, 2015, 96, 740-752.	6.2	22
41	Integrative analysis of RNA, translation, and protein levels reveals distinct regulatory variation across humans. Genome Research, 2015, 25, 1610-1621.	5.5	157
42	Characterizing Race/Ethnicity and Genetic Ancestry for 100,000 Subjects in the Genetic Epidemiology Research on Adult Health and Aging (GERA) Cohort. Genetics, 2015, 200, 1285-1295.	2.9	273
43	PLOS Genetics Data Sharing Policy: In Pursuit of Functional Utility. PLoS Genetics, 2015, 11, e1005716.	3.5	10
44	The Association of the Vanin-1 N131S Variant with Blood Pressure Is Mediated by Endoplasmic Reticulum-Associated Degradation and Loss of Function. PLoS Genetics, 2014, 10, e1004641.	3.5	16
45	Modeling 3D Facial Shape from DNA. PLoS Genetics, 2014, 10, e1004224.	3.5	190
46	Genome-wide association and admixture analysis of glaucoma in the Women's Health Initiative. Human Molecular Genetics, 2014, 23, 6634-6643.	2.9	22
47	Leveraging population admixture to characterize the heritability of complex traits. Nature Genetics, 2014, 46, 1356-1362.	21.4	69
48	Trans-ethnic meta-analysis of white blood cell phenotypes. Human Molecular Genetics, 2014, 23, 6944-6960.	2.9	60
49	Genome-wide Association Analysis of Blood-Pressure Traits in African-Ancestry Individuals Reveals Common Associated Genes in African and Non-African Populations. American Journal of Human Genetics, 2013, 93, 545-554.	6.2	189
50	Genome-wide Characterization of Shared and Distinct Genetic Components that Influence Blood Lipid Levels in Ethnically Diverse Human Populations. American Journal of Human Genetics, 2013, 92, 904-916.	6.2	113
51	Variation and genetic control of protein abundance in humans. Nature, 2013, 499, 79-82.	27.8	343
52	Genetic Architecture of Skin and Eye Color in an African-European Admixed Population. PLoS Genetics, 2013, 9, e1003372.	3.5	137
53	Identification Of The Disease-Causing Mutation In Autosomal Dominant Familial Immune Thrombocytopenia By Genome-Wide Linkage Analysis and Whole Genome Sequencing. Blood, 2013, 122, 565-565.	1.4	0
54	Personal Omics Profiling Reveals Dynamic Molecular and Medical Phenotypes. Cell, 2012, 148, 1293-1307.	28.9	1,134

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55	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
56	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
57	Ancestral Components of Admixed Genomes in a Mexican Cohort. <i>PLoS Genetics</i> , 2011, 7, e1002410.	3.5	109
58	Joint testing of genotype and ancestry association in admixed families. <i>Genetic Epidemiology</i> , 2010, 34, 783-791.	1.3	43
59	Response—How the Gray Wolf Got Its Color. <i>Science</i> , 2009, 325, 34-34.	12.6	3
60	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
61	Characterizing the admixed African ancestry of African Americans. <i>Genome Biology</i> , 2009, 10, R141.	9.6	145
62	Worldwide Human Relationships Inferred from Genome-Wide Patterns of Variation. <i>Science</i> , 2008, 319, 1100-1104.	12.6	1,774
63	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
64	Recent Genetic Selection in the Ancestral Admixture of Puerto Ricans. <i>American Journal of Human Genetics</i> , 2007, 81, 626-633.	6.2	168
65	Controlling for false positive findings of trans-hubs in expression quantitative trait loci mapping. <i>BMC Proceedings</i> , 2007, 1, S157.	1.6	6
66	Combining multiple family-based association studies. <i>BMC Proceedings</i> , 2007, 1, S162.	1.6	3
67	Reconstructing Genetic Ancestry Blocks in Admixed Individuals. <i>American Journal of Human Genetics</i> , 2006, 79, 1-12.	6.2	240
68	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
69	Estimation of individual admixture: Analytical and study design considerations. <i>Genetic Epidemiology</i> , 2005, 28, 289-301.	1.3	571
70	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
71	Frequentist Estimation of Coalescence Times From Nucleotide Sequence Data Using a Tree-Based Partition. <i>Genetics</i> , 2002, 161, 447-459.	2.9	76
72	Locating Regions of Differential Variability in DNA and Protein Sequences. <i>Genetics</i> , 1999, 153, 485-495.	2.9	43