## Lin Tong

## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7746398/publications.pdf

Version: 2024-02-01

		687363	839539	
18	1,595	13	18	
papers	citations	h-index	g-index	
19	19	19	4497	
all docs	docs citations	times ranked	citing authors	

#	Article	IF	CITATIONS
1	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. Nature Genetics, 2021, 53, 1300-1310.	21.4	590
2	Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation. Nature Genetics, 2015, 47, 1282-1293.	21.4	294
3	Determinants of telomere length across human tissues. Science, 2020, 369, .	12.6	257
4	Mediation Analysis Demonstrates That Trans-eQTLs Are Often Explained by Cis-Mediation: A Genome-Wide Analysis among 1,800 South Asians. PLoS Genetics, 2014, 10, e1004818.	3.5	88
5	Determinants and Consequences of Arsenic Metabolism Efficiency among 4,794 Individuals: Demographics, Lifestyle, Genetics, and Toxicity. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 381-390.	2.5	67
6	Co-occurring expression and methylation QTLs allow detection of common causal variants and shared biological mechanisms. Nature Communications, 2018, 9, 804.	12.8	66
7	Arsenic exposure, telomere length, and expression of telomere-related genes among Bangladeshi individuals. Environmental Research, 2015, 136, 462-469.	7.5	40
8	Association of Arsenic Exposure with Whole Blood DNA Methylation: An Epigenome-Wide Study of Bangladeshi Adults. Environmental Health Perspectives, 2019, 127, 57011.	6.0	40
9	Genome-wide association study of telomere length among South Asians identifies a second RTEL1 association signal. Journal of Medical Genetics, 2018, 55, 64-71.	3.2	33
10	The contribution of parent-to-offspring transmission of telomeres to the heritability of telomere length in humans. Human Genetics, 2019, 138, 49-60.	3.8	24
11	Identification of genetic effects underlying type 2 diabetes in South Asian and European populations. Communications Biology, 2022, 5, 329.	4.4	21
12	A missense variant in FTCD is associated with arsenic metabolism and toxicity phenotypes in Bangladesh. PLoS Genetics, 2019, 15, e1007984.	3.5	19
13	Genetic Determinants of Reduced Arsenic Metabolism Efficiency in the 10q24.32 Region Are Associated With Reduced <i>AS3MT</i> Expression in Multiple Human Tissue Types. Toxicological Sciences, 2020, 176, 382-395.	3.1	14
14	The association between telomere length and mortality in Bangladesh. Aging, 2017, 9, 1537-1551.	3.1	12
15	The effect of age on DNA methylation in whole blood among Bangladeshi men and women. BMC Genomics, 2019, 20, 704.	2.8	10
16	Rare, Protein-Altering Variants in <i>AS3MT</i> and Arsenic Metabolism Efficiency: A Multi-Population Association Study. Environmental Health Perspectives, 2021, 129, 47007.	6.0	9
17	Screening for gene–environment (G×E) interaction using omics data from exposed individuals: an application to gene-arsenic interaction. Mammalian Genome, 2018, 29, 101-111.	2.2	7
18	Assessing the impact of arsenic metabolism efficiency on DNA methylation using Mendelian randomization. Environmental Epidemiology, 2020, 4, e083.	3.0	4