## Lin Tong

## List of Publications by Year in descending order

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

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		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	Identification of genetic effects underlying type 2 diabetes in South Asian and European populations. Communications Biology, 2022, 5, 329.	4.4	21
2	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
3	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
4	Determinants of telomere length across human tissues. Science, 2020, 369, .	12.6	257
5	Assessing the impact of arsenic metabolism efficiency on DNA methylation using Mendelian randomization. Environmental Epidemiology, 2020, 4, e083.	3.0	4
6	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
7	The effect of age on DNA methylation in whole blood among Bangladeshi men and women. BMC Genomics, 2019, 20, 704.	2.8	10
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	A missense variant in FTCD is associated with arsenic metabolism and toxicity phenotypes in Bangladesh. PLoS Genetics, 2019, 15, e1007984.	3.5	19
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	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
12	Co-occurring expression and methylation QTLs allow detection of common causal variants and shared biological mechanisms. Nature Communications, 2018, 9, 804.	12.8	66
13	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
14	The association between telomere length and mortality in Bangladesh. Aging, 2017, 9, 1537-1551.	3.1	12
15	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
16	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
17	Arsenic exposure, telomere length, and expression of telomere-related genes among Bangladeshi individuals. Environmental Research, 2015, 136, 462-469.	7.5	40
18	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 <b>.</b> 5	88