## Yun Ju Sung

List of Publications by Year in descending order

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VUN LU SUNC

#	Article	IF	CITATIONS
1	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
2	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	21.4	1,818
3	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	27.8	1,328
4	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. PLoS Genetics, 2015, 11, e1005378.	3.5	331
5	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. Nature Communications, 2016, 7, 10495.	12.8	245
6	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. Nature Communications, 2017, 8, 14977.	12.8	169
7	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. Nature Communications, 2016, 7, 10494.	12.8	153
8	Genomic atlas of the proteome from brain, CSF and plasma prioritizes proteins implicated in neurological disorders. Nature Neuroscience, 2021, 24, 1302-1312.	14.8	105
9	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357.	12.8	74
10	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	12.8	64
11	Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. Nature Communications, 2019, 10, 5121.	12.8	62
12	A multi-ancestry genome-wide study incorporating gene–smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. Human Molecular Genetics, 2019, 28, 2615-2633.	2.9	31
13	Methods for Collapsing Multiple Rare Variants in Wholeâ€Genome Sequence Data. Genetic Epidemiology, 2014, 38, S13-20.	1.3	18
14	Influence of Smoking Status and Intensity on Discovery of Blood Pressure Loci Through Gene moking Interactions. Genetic Epidemiology, 2015, 39, 480-488.	1.3	17
15	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. Molecular Psychiatry, 2020, 26, 2111-2125.	7.9	17
16	GEM: scalable and flexible gene–environment interaction analysis in millions of samples. Bioinformatics, 2021, 37, 3514-3520.	4.1	17
17	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
18	Efficient gene–environment interaction tests for large biobankâ€scale sequencing studies. Genetic Epidemiology, 2020, 44, 908-923.	1.3	15

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19	Genomic and transcriptomic predictors of triglyceride response to regular exercise. British Journal of Sports Medicine, 2015, 49, 1524-1531.	6.7	14
20	Multi-ancestry genome-wide gene–sleep interactions identify novel loci for blood pressure. Molecular Psychiatry, 2021, 26, 6293-6304.	7.9	13
21	Leveraging large multi-center cohorts of Alzheimer disease endophenotypes to understand the role of Klotho heterozygosity on disease risk. PLoS ONE, 2022, 17, e0267298.	2.5	9
22	Comparison between single-marker analysis using Merlin and multi-marker analysis using LASSO for Framingham simulated data. BMC Proceedings, 2009, 3, S27.	1.6	7
23	Identifying blood pressure loci whose effects are modulated by multiple lifestyle exposures. Genetic Epidemiology, 2020, 44, 629-641.	1.3	6
24	Application of collapsing methods for continuous traits to the Genetic Analysis Workshop 17 exome sequence data. BMC Proceedings, 2011, 5, S121.	1.6	5
25	Modelâ€based linkage analysis with imprinting for quantitative traits: ignoring imprinting effects can severely jeopardize detection of linkage. Genetic Epidemiology, 2008, 32, 487-496.	1.3	4
26	Three Approaches to Modeling Geneâ€Environment Interactions in Longitudinal Family Data: Geneâ€Smoking Interactions in Blood Pressure. Genetic Epidemiology, 2016, 40, 73-80.	1.3	2
27	The Promise of Selecting Individuals from the Extremes of Exposure in the Analysis of Gene-Physical Activity Interactions. Human Heredity, 2018, 83, 315-332.	0.8	2
28	Multi-ancestry genome-wide association study accounting for gene-psychosocial factor interactions identifies novel loci for blood pressure traits. Human Genetics and Genomics Advances, 2021, 2, 100013.	1.7	2
29	Lifestyle Risk Score: handling missingness of individual lifestyle components in meta-analysis of gene-by-lifestyle interactions. European Journal of Human Genetics, 2021, 29, 839-850.	2.8	0