

Yun Ju Sung

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6234045/publications.pdf>

Version: 2024-02-01

29
papers

8,369
citations

643344

15
h-index

563245

28
g-index

31
all docs

31
docs citations

31
times ranked

17832
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	13.7	3,823
2	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014, 46, 1173-1186.	9.4	1,818
3	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015, 518, 187-196.	13.7	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. <i>PLoS Genetics</i> , 2015, 11, e1005378.	1.5	331
5	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. <i>Nature Communications</i> , 2016, 7, 10495.	5.8	245
6	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. <i>Nature Communications</i> , 2017, 8, 14977.	5.8	169
7	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. <i>Nature Communications</i> , 2016, 7, 10494.	5.8	153
8	Genomic atlas of the proteome from brain, CSF and plasma prioritizes proteins implicated in neurological disorders. <i>Nature Neuroscience</i> , 2021, 24, 1302-1312.	7.1	105
9	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. <i>Nature Communications</i> , 2016, 7, 13357.	5.8	74
10	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. <i>Nature Communications</i> , 2019, 10, 376.	5.8	64
11	Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. <i>Nature Communications</i> , 2019, 10, 5121.	5.8	62
12	A multi-ancestry genome-wide study incorporating gene \times smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. <i>Human Molecular Genetics</i> , 2019, 28, 2615-2633.	1.4	31
13	Methods for Collapsing Multiple Rare Variants in Whole \times Genome Sequence Data. <i>Genetic Epidemiology</i> , 2014, 38, S13-20.	0.6	18
14	Influence of Smoking Status and Intensity on Discovery of Blood Pressure Loci Through Gene \times Smoking Interactions. <i>Genetic Epidemiology</i> , 2015, 39, 480-488.	0.6	17
15	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. <i>Molecular Psychiatry</i> , 2020, 26, 2111-2125.	4.1	17
16	GEM: scalable and flexible gene \times environment interaction analysis in millions of samples. <i>Bioinformatics</i> , 2021, 37, 3514-3520.	1.8	17
17	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.	1.5	16
18	Efficient gene \times environment interaction tests for large biobank \times scale sequencing studies. <i>Genetic Epidemiology</i> , 2020, 44, 908-923.	0.6	15

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19	Genomic and transcriptomic predictors of triglyceride response to regular exercise. <i>British Journal of Sports Medicine</i> , 2015, 49, 1524-1531.	3.1	14
20	Multi-ancestry genome-wide gene×sleep interactions identify novel loci for blood pressure. <i>Molecular Psychiatry</i> , 2021, 26, 6293-6304.	4.1	13
21	Leveraging large multi-center cohorts of Alzheimer disease endophenotypes to understand the role of Klotho heterozygosity on disease risk. <i>PLoS ONE</i> , 2022, 17, e0267298.	1.1	9
22	Comparison between single-marker analysis using Merlin and multi-marker analysis using LASSO for Framingham simulated data. <i>BMC Proceedings</i> , 2009, 3, S27.	1.8	7
23	Identifying blood pressure loci whose effects are modulated by multiple lifestyle exposures. <i>Genetic Epidemiology</i> , 2020, 44, 629-641.	0.6	6
24	Application of collapsing methods for continuous traits to the Genetic Analysis Workshop 17 exome sequence data. <i>BMC Proceedings</i> , 2011, 5, S121.	1.8	5
25	Model-based linkage analysis with imprinting for quantitative traits: ignoring imprinting effects can severely jeopardize detection of linkage. <i>Genetic Epidemiology</i> , 2008, 32, 487-496.	0.6	4
26	Three Approaches to Modeling Gene×Environment Interactions in Longitudinal Family Data: Gene×Smoking Interactions in Blood Pressure. <i>Genetic Epidemiology</i> , 2016, 40, 73-80.	0.6	2
27	The Promise of Selecting Individuals from the Extremes of Exposure in the Analysis of Gene-Physical Activity Interactions. <i>Human Heredity</i> , 2018, 83, 315-332.	0.4	2
28	Multi-ancestry genome-wide association study accounting for gene-psychosocial factor interactions identifies novel loci for blood pressure traits. <i>Human Genetics and Genomics Advances</i> , 2021, 2, 100013.	1.0	2
29	Lifestyle Risk Score: handling missingness of individual lifestyle components in meta-analysis of gene-by-lifestyle interactions. <i>European Journal of Human Genetics</i> , 2021, 29, 839-850.	1.4	0