Yeunjoo E Song

List of Publications by Year
in descending order

51 papers	1,504 citations	759233 12 h-index	395702 33 g-index
62 all docs	62 docs citations	62 times ranked	1788 citing authors

#	Article	IF	Citations
1	New insights into the genetic etiology of Alzheimer's disease and related dementias. Nature Genetics, 2022, 54, 412-436.	21.4	700
2	Genome-wide analyses identify 68 new loci associated with intraocular pressure and improve risk prediction for primary open-angle glaucoma. Nature Genetics, 2018, 50, 778-782.	21.4	214
3	Genome-wide association analysis identifies TXNRD2, ATXN2 and FOXC1 as susceptibility loci for primary open-angle glaucoma. Nature Genetics, 2016, 48, 189-194.	21.4	211
4	A Common Variant in <i>MIR182</i> Is Associated With Primary Open-Angle Glaucoma in the NEIGHBORHOOD Consortium. , 2016, 57, 4528.		42
5	Structural equation model-based genome scan for the metabolic syndrome. BMC Genetics, 2003, 4, S99.	2.7	34
6	Defining genetic determinants of the Metabolic Syndrome in the Framingham Heart Study using association and structural equation modeling methods. BMC Proceedings, 2009, 3, S50.	1.6	27
7	ONETOOL for the analysis of family-based big data. Bioinformatics, 2018, 34, 2851-2853.	4.1	25
8	Association Between Germline Mutation in <i>VSIG10L</i> and Familial Barrett Neoplasia. JAMA Oncology, 2016, 2, 1333.	7.1	23
9	Assessing the impact of global versus local ancestry in association studies. BMC Proceedings, 2009, 3, S107.	1.6	21
10	Multivariate Analysis of Anthropometric Traits Using Summary Statistics of Genome-Wide Association Studies from GIANT Consortium. PLoS ONE, 2016, 11, e0163912.	2.5	19
11	Genetic correlations between intraocular pressure, blood pressure and primary open-angle glaucoma: a multi-cohort analysis. European Journal of Human Genetics, 2017, 25, 1261-1267.	2.8	18
12	AMISH EYE STUDY. Retina, 2019, 39, 1540-1550.	1.7	17
13	Testosterone Pathway Genetic Polymorphisms in Relation to Primary Open-Angle Glaucoma: An Analysis in Two Large Datasets. , 2018, 59, 629.		14
14	The effect of multiple genetic variants in predicting the risk of type 2 diabetes. BMC Proceedings, 2009, 3, S49.	1.6	13
15	Genetic Correlations Between Diabetes and Glaucoma: An Analysis of Continuous and Dichotomous Phenotypes. American Journal of Ophthalmology, 2019, 206, 245-255.	3.3	12
16	Multivariate association analysis of the components of metabolic syndrome from the Framingham Heart Study. BMC Proceedings, 2009, 3, S42.	1.6	11
17	Structural equation modeling with latent variables for longitudinal blood pressure traits using general pedigrees. BMC Proceedings, 2016, 10, 303-307.	1.6	9
18	An autosome-wide search using longitudinal data for loci linked to type 2 diabetes progression. BMC Genetics, 2003, 4, S8.	2.7	8

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19	Lower Levels of Education Are Associated with Cognitive Impairment in the Old Order Amish. Journal of Alzheimer's Disease, 2021, 79, 451-458.	2.6	8
20	A method to correct for population structure using a segregation model. BMC Proceedings, 2009, 3, S104.	1.6	7
21	Interval Estimation of Familial Correlations from Pedigrees. Statistical Applications in Genetics and Molecular Biology, 2011, 10, Article 11.	0.6	7
22	Rare variants and loci for age-related macular degeneration in the Ohio and Indiana Amish. Human Genetics, 2019, 138, 1171-1182.	3.8	7
23	strum: an R package for structural modeling of latent variables for general pedigrees. BMC Genetics, 2015, 16, 35.	2.7	6
24	Age at natural menopause genetic risk score in relation to age at natural menopause and primary open-angle glaucoma in a US-based sample. Menopause, 2017, 24, 150-156.	2.0	6
25	Interaction of gender and body mass index (BMI) reveals evidence of linkage for hypertension in the Framingham Heart Study. BMC Genetics, 2003, 4, S45.	2.7	5
26	Linkage analysis of alcohol dependence using both affected and discordant sib pairs. BMC Genetics, 2005, 6, S36.	2.7	5
27	Prediction of Empirical p Values from Asymptotic p Values for Conditional Logistic Affected Relative Pair Linkage Analysis. Human Heredity, 2006, 61, 45-54.	0.8	4
28	Genetic variants in the *SHISA6* gene are associated with delayed cognitive impairment in two family datasets. Alzheimer's and Dementia, 2023, 19, 611-620.	0.8	4
29	Using Overall Allele-Sharing to Detect the Presence of Large-Scale Data Errors and Parameter Misspecification in Sib-Pair Linkage Studies. Human Heredity, 2004, 58, 49-54.	0.8	3
30	Effect of genotyping error in model-free linkage analysis using microsatellite or single-nucleotide polymorphism marker maps. BMC Genetics, 2005, 6, S153.	2.7	3
31	Comparison of univariate and multivariate linkage analysis of traits related to hypertension. BMC Proceedings, 2009, 3, S99.	1.6	3
32	PedWiz: a web-based tool for pedigree informatics. Frontiers in Genetics, 2013, 4, 189.	2.3	3
33	Model-Based Linkage Analysis of a Quantitative Trait. Methods in Molecular Biology, 2017, 1666, 283-310.	0.9	3
34	Familial Segregation of Venous Thromboembolism in Sweden: A Nationwide Family Study of Heritability and Complex Segregation Analysis. Journal of the American Heart Association, 2021, 10, e020323.	3.7	3
35	Comparison of a unified analysis approach for family and unrelated samples with the transmission-disequilibrium test to study associations of hypertension in the Framingham Heart Study. BMC Proceedings, 2009, 3, S22.	1.6	2
36	A method to detect single-nucleotide polymorphisms accounting for a linkage signal using covariate-based affected relative pair linkage analysis. BMC Proceedings, 2011, 5, S84.	1.6	2

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37	The null distribution of likelihood-ratio statistics in the conditional-logistic linkage model. Frontiers in Genetics, 2013, 4, 244.	2.3	2
38	Optimizing the evidence for linkage by permuting marker order. BMC Genetics, 2005, 6, S61.	2.7	1
39	Studying genetic determinants of natural variation in human gene expression using Bayesian ANOVA. BMC Proceedings, 2007, 1, S115.	1.6	1
40	The genetic architecture of Alzheimer disease risk in the Ohio and Indiana Amish. Human Genetics and Genomics Advances, 2022, 3, 100114.	1.7	1
41	Longitudinal assessment of cognitive decline in the Amish. Alzheimer's and Dementia, 2020, 16, e043440.	0.8	0
42	Search for protective genetic variants in Alzheimer disease in the U.S. Midwestern Amish. Alzheimer's and Dementia, 2020, 16, e045350.	0.8	0
43	Joint linkage and association mapping of preserved cognition in the old‐order Amish. Alzheimer's and Dementia, 2020, 16, e046416.	0.8	0
44	The GGLEAM Study: Understanding Glaucoma in the Ohio Amish. International Journal of Environmental Research and Public Health, 2021, 18, 1551.	2.6	0
45	Algorithm to Estimate the Extended Turnaround Time Including Outpatient Waiting Time for Blood Specimen Collection when a Stand-alone Queue Ticket System not Connectable to Laboratory Information System Is Used. Annals of Clinical and Laboratory Science, 2018, 48, 726-735.	0.2	0
46	Association of a locus on chromosome 17 with earlier age at onset of cognitive impairment in a familial Amish dataset. Alzheimer's and Dementia, 2021, 17, e056288.	0.8	0
47	Genome‐wide association for protective variants in Alzheimer's disease in the Midwestern Amish. Alzheimer's and Dementia, 2021, 17, e056363.	0.8	0
48	Preferential preservation of constructional praxis delayed recall compared to word list delayed recall in the Amish. Alzheimer's and Dementia, 2021, 17, e056386.	0.8	0
49	Genetic risk score for Alzheimer's disease in the Amish highlights differences in the genetic architecture compared to other European ancestry populations.. Alzheimer's and Dementia, 2021, 17 Suppl 3, e053304.	0.8	0
50	Suggestive linkage and association of preserved cognition to chromosome 18 in genetically at-risk Amish.. Alzheimer's and Dementia, 2021, 17 Suppl 3, e056306.	0.8	0
51	Genome-wide association study of cognitive status and decline in the Amish.. Alzheimer's and Dementia, 2021, 17 Suppl 3, e056525.	0.8	0