Yeunjoo E Song

List of Publications by Year
in descending order

51	1,504	759233	395702
papers	citations	12 h-index	33 g-index

62	62	62	1788
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	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
2	New insights into the genetic etiology of Alzheimerâ€™s disease and related dementias. Nature Genetics, 2022, 54, 412-436.	21.4	700
3	The genetic architecture of Alzheimer disease risk in the Ohio and Indiana Amish. Human Genetics and Genomics Advances, 2022, 3, 100114.	1.7	1
4	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
5	The GGLEAM Study: Understanding Glaucoma in the Ohio Amish. International Journal of Environmental Research and Public Health, 2021, 18, 1551.	2.6	0
6	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
7	Genomeâ€wide association for protective variants in Alzheimerâ€™s disease in the Midwestern Amish. Alzheimer's and Dementia, 2021, 17, e056363.	0.8	0
8	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
9	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
10	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
11	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
12	Genome-wide association study of cognitive status and decline in the Amish.. Alzheimer's and Dementia, 2021, 17 Suppl 3, e056525.	0.8	0
13	Longitudinal assessment of cognitive decline in the Amish. Alzheimer's and Dementia, 2020, 16, e043440.	0.8	0
14	Search for protective genetic variants in Alzheimer disease in the U.S. Midwestern Amish. Alzheimer's and Dementia, 2020, 16, e045350.	0.8	0
15	Joint linkage and association mapping of preserved cognition in the oldâ€order Amish. Alzheimer's and Dementia, 2020, 16, e046416.	0.8	0
16	AMISH EYE STUDY. Retina, 2019, 39, 1540-1550.	1.7	17
17	Rare variants and loci for age-related macular degeneration in the Ohio and Indiana Amish. Human Genetics, 2019, 138, 1171-1182.	3.8	7
18	Genetic Correlations Between Diabetes and Glaucoma: An Analysis of Continuous and Dichotomous Phenotypes. American Journal of Ophthalmology, 2019, 206, 245-255.	3.3	12

#	Article	IF	Citations
19	ONETOOL for the analysis of family-based big data. Bioinformatics, 2018, 34, 2851-2853.	4.1	25
20	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
21	Testosterone Pathway Genetic Polymorphisms in Relation to Primary Open-Angle Glaucoma: An Analysis in Two Large Datasets. , 2018, 59, 629.		14
22	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
23	Model-Based Linkage Analysis of a Quantitative Trait. Methods in Molecular Biology, 2017, 1666, 283-310.	0.9	3
24	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
25	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
26	A Common Variant in MIR182 Is Associated With Primary Open-Angle Glaucoma in the NEIGHBORHOOD Consortium. , 2016, 57, 4528.		42
27	Association Between Germline Mutation inVSIG10Land Familial Barrett Neoplasia. JAMA Oncology, 2016, 2, 1333.	7.1	23
28	Structural equation modeling with latent variables for longitudinal blood pressure traits using general pedigrees. BMC Proceedings, 2016, 10, 303-307.	1.6	9
29	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
30	Multivariate Analysis of Anthropometric Traits Using Summary Statistics of Genome-Wide Association Studies from GIANT Consortium. PLoS ONE, 2016, 11, e0163912.	2.5	19
31	strum: an R package for structural modeling of latent variables for general pedigrees. BMC Genetics, 2015, 16, 35.	2.7	6
32	PedWiz: a web-based tool for pedigree informatics. Frontiers in Genetics, 2013, 4, 189.	2.3	3
33	The null distribution of likelihood-ratio statistics in the conditional-logistic linkage model. Frontiers in Genetics, 2013, 4, 244.	2.3	2
34	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
35	Interval Estimation of Familial Correlations from Pedigrees. Statistical Applications in Genetics and Molecular Biology, 2011, 10, Article 11.	0.6	7
36	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

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37	A method to correct for population structure using a segregation model. BMC Proceedings, 2009, 3, S104.	1.6	7
38	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
39	Comparison of univariate and multivariate linkage analysis of traits related to hypertension. BMC Proceedings, 2009, 3, S99.	1.6	3
40	The effect of multiple genetic variants in predicting the risk of type 2 diabetes. BMC Proceedings, 2009, 3, S49.	1.6	13
41	Assessing the impact of global versus local ancestry in association studies. BMC Proceedings, 2009, 3, S107.	1.6	21
42	Multivariate association analysis of the components of metabolic syndrome from the Framingham Heart Study. BMC Proceedings, 2009, 3, S42.	1.6	11
43	Studying genetic determinants of natural variation in human gene expression using Bayesian ANOVA. BMC Proceedings, 2007, 1, S115.	1.6	1
44	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
45	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
46	Linkage analysis of alcohol dependence using both affected and discordant sib pairs. BMC Genetics, 2005, 6, S36.	2.7	5
47	Optimizing the evidence for linkage by permuting marker order. BMC Genetics, 2005, 6, S61.	2.7	1
48	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
49	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
50	An autosome-wide search using longitudinal data for loci linked to type 2 diabetes progression. BMC Genetics, 2003, 4, S8.	2.7	8
51	Structural equation model-based genome scan for the metabolic syndrome. BMC Genetics, 2003, 4, S99.	2.7	34