

# Sang Hong Lee

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

120  
papers

24,905  
citations

50  
h-index

142  
g-index

142  
ext. papers

32,224  
ext. citations

10.6  
avg, IF

7.88  
L-index

#	Paper	IF	Citations
120	Biological insights from 108 schizophrenia-associated genetic loci. <i>Nature</i> , <b>2014</b> , 511, 421-7	50.4	5249
119	GCTA: a tool for genome-wide complex trait analysis. <i>American Journal of Human Genetics</i> , <b>2011</b> , 88, 76-82	36.3	3838
118	LD Score regression distinguishes confounding from polygenicity in genome-wide association studies. <i>Nature Genetics</i> , <b>2015</b> , 47, 291-5	36.3	2096
117	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. <i>Nature Genetics</i> , <b>2013</b> , 45, 984-94	36.3	1628
116	Genome-wide association analysis identifies 13 new risk loci for schizophrenia. <i>Nature Genetics</i> , <b>2013</b> , 45, 1150-9	36.3	1153
115	Estimating missing heritability for disease from genome-wide association studies. <i>American Journal of Human Genetics</i> , <b>2011</b> , 88, 294-305	11	737
114	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. <i>American Journal of Human Genetics</i> , <b>2015</b> , 97, 576-92	11	649
113	Psychiatric genome-wide association study analyses implicate neuronal, immune and histone pathways. <i>Nature Neuroscience</i> , <b>2015</b> , 18, 199-209	25.5	572
112	GWAS of 126,559 individuals identifies genetic variants associated with educational attainment. <i>Science</i> , <b>2013</b> , 340, 1467-71	33.3	563
111	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. <i>Nature Genetics</i> , <b>2017</b> , 49, 27-35	36.3	530
110	Genetic variance estimation with imputed variants finds negligible missing heritability for human height and body mass index. <i>Nature Genetics</i> , <b>2015</b> , 47, 1114-20	36.3	522
109	Estimating the proportion of variation in susceptibility to schizophrenia captured by common SNPs. <i>Nature Genetics</i> , <b>2012</b> , 44, 247-50	36.3	471
108	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. <i>Nature Genetics</i> , <b>2013</b> , 45, 501-12	36.3	437
107	Estimation of pleiotropy between complex diseases using single-nucleotide polymorphism-derived genomic relationships and restricted maximum likelihood. <i>Bioinformatics</i> , <b>2012</b> , 28, 2540-2	7.2	414
106	Partitioning heritability of regulatory and cell-type-specific variants across 11 common diseases. <i>American Journal of Human Genetics</i> , <b>2014</b> , 95, 535-52	11	411
105	Research review: Polygenic methods and their application to psychiatric traits. <i>Journal of Child Psychology and Psychiatry and Allied Disciplines</i> , <b>2014</b> , 55, 1068-87	7.9	410
104	Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. <i>Cell</i> , <b>2018</b> , 173, 1705-1715.e16	56.2	360

103	Contrasting genetic architectures of schizophrenia and other complex diseases using fast variance-components analysis. <i>Nature Genetics</i> , <b>2015</b> , 47, 1385-92	36.3	299
102	Statistical power to detect genetic (co)variance of complex traits using SNP data in unrelated samples. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004269	6	236
101	Genome-wide association study identifies a locus at 7p15.2 associated with endometriosis. <i>Nature Genetics</i> , <b>2011</b> , 43, 51-4	36.3	227
100	Simultaneous discovery, estimation and prediction analysis of complex traits using a bayesian mixture model. <i>PLoS Genetics</i> , <b>2015</b> , 11, e1004969	6	206
99	Partitioning the heritability of Tourette syndrome and obsessive compulsive disorder reveals differences in genetic architecture. <i>PLoS Genetics</i> , <b>2013</b> , 9, e1003864	6	189
98	Identification of genetic variants associated with Huntington's disease progression: a genome-wide association study. <i>Lancet Neurology</i> , <b>2017</b> , 16, 701-711	24.1	161
97	Joint analysis of psychiatric disorders increases accuracy of risk prediction for schizophrenia, bipolar disorder, and major depressive disorder. <i>American Journal of Human Genetics</i> , <b>2015</b> , 96, 283-94	11	161
96	A better coefficient of determination for genetic profile analysis. <i>Genetic Epidemiology</i> , <b>2012</b> , 36, 214-242.6	15.8	
95	Genome-wide complex trait analysis (GCTA): methods, data analyses, and interpretations. <i>Methods in Molecular Biology</i> , <b>2013</b> , 1019, 215-36	1.4	153
94	Estimation and partitioning of polygenic variation captured by common SNPs for Alzheimer's disease, multiple sclerosis and endometriosis. <i>Human Molecular Genetics</i> , <b>2013</b> , 22, 832-41	5.6	147
93	Predicting unobserved phenotypes for complex traits from whole-genome SNP data. <i>PLoS Genetics</i> , <b>2008</b> , 4, e1000231	6	147
92	Dominance genetic variation contributes little to the missing heritability for human complex traits. <i>American Journal of Human Genetics</i> , <b>2015</b> , 96, 377-85	11	138
91	Common SNPs explain some of the variation in the personality dimensions of neuroticism and extraversion. <i>Translational Psychiatry</i> , <b>2012</b> , 2, e102	8.6	137
90	Genome-wide Association for Major Depression Through Age at Onset Stratification: Major Depressive Disorder Working Group of the Psychiatric Genomics Consortium. <i>Biological Psychiatry</i> , <b>2017</b> , 81, 325-335	7.9	129
89	Polygenic transmission and complex neuro developmental network for attention deficit hyperactivity disorder: genome-wide association study of both common and rare variants. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , <b>2013</b> , 162B, 419-430	3.5	125
88	Geographical genomics of human leukocyte gene expression variation in southern Morocco. <i>Nature Genetics</i> , <b>2010</b> , 42, 62-7	36.3	117
87	Genetic correlations of polygenic disease traits: from theory to practice. <i>Nature Reviews Genetics</i> , <b>2019</b> , 20, 567-581	30.1	98
86	Hidden heritability due to heterogeneity across seven populations. <i>Nature Human Behaviour</i> , <b>2017</b> , 1, 757-765	12.8	94

85	MTG2: an efficient algorithm for multivariate linear mixed model analysis based on genomic information. <i>Bioinformatics</i> , <b>2016</b> , 32, 1420-2	7.2	93
84	A Genetic Investigation of Sex Bias in the Prevalence of Attention-Deficit/Hyperactivity Disorder. <i>Biological Psychiatry</i> , <b>2018</b> , 83, 1044-1053	7.9	93
83	Runs of homozygosity implicate autozygosity as a schizophrenia risk factor. <i>PLoS Genetics</i> , <b>2012</b> , 8, e1002656	9.1	
82	Estimation of SNP heritability from dense genotype data. <i>American Journal of Human Genetics</i> , <b>2013</b> , 93, 1151-5	11	85
81	Improving genetic prediction by leveraging genetic correlations among human diseases and traits. <i>Nature Communications</i> , <b>2018</b> , 9, 989	17.4	76
80	Estimation and partitioning of (co)heritability of inflammatory bowel disease from GWAS and immuno-chip data. <i>Human Molecular Genetics</i> , <b>2014</b> , 23, 4710-20	5.6	73
79	RICOPILI: Rapid Imputation for COnsortias PIpeLIne. <i>Bioinformatics</i> , <b>2020</b> , 36, 930-933	7.2	72
78	Evidence for multiple alleles effecting muscling and fatness at the ovine GDF8 locus. <i>BMC Genetics</i> , <b>2007</b> , 8, 80	2.6	66
77	Heterogeneity of genetic architecture of body size traits in a free-living population. <i>Molecular Ecology</i> , <b>2015</b> , 24, 1810-30	5.7	55
76	Additive genetic variation in schizophrenia risk is shared by populations of African and European descent. <i>American Journal of Human Genetics</i> , <b>2013</b> , 93, 463-70	11	55
75	Estimation of Genetic Correlation via Linkage Disequilibrium Score Regression and Genomic Restricted Maximum Likelihood. <i>American Journal of Human Genetics</i> , <b>2018</b> , 102, 1185-1194	11	55
74	Multivariate genetic analyses of cognition and academic achievement from two population samples of 174,000 and 166,000 school children. <i>Behavior Genetics</i> , <b>2012</b> , 42, 699-710	3.2	54
73	EigenGWAS: finding loci under selection through genome-wide association studies of eigenvectors in structured populations. <i>Heredity</i> , <b>2016</b> , 117, 51-61	3.6	54
72	Using the realized relationship matrix to disentangle confounding factors for the estimation of genetic variance components of complex traits. <i>Genetics Selection Evolution</i> , <b>2010</b> , 42, 22	4.9	52
71	Impact of diagnostic misclassification on estimation of genetic correlations using genome-wide genotypes. <i>European Journal of Human Genetics</i> , <b>2012</b> , 20, 668-74	5.3	51
70	Shared genetics underlying epidemiological association between endometriosis and ovarian cancer. <i>Human Molecular Genetics</i> , <b>2015</b> , 24, 5955-64	5.6	48
69	Genetic mapping of quantitative trait loci for resistance to <i>Haemonchus contortus</i> in sheep. <i>Animal Genetics</i> , <b>2009</b> , 40, 262-72	2.5	45
68	New data and an old puzzle: the negative association between schizophrenia and rheumatoid arthritis. <i>International Journal of Epidemiology</i> , <b>2015</b> , 44, 1706-21	7.8	43

67	An efficient variance component approach implementing an average information REML suitable for combined LD and linkage mapping with a general complex pedigree. <i>Genetics Selection Evolution</i> , <b>2006</b> , 38, 25-43	4.9	42
66	Evidence for Genetic Overlap Between Schizophrenia and Age at First Birth in Women. <i>JAMA Psychiatry</i> , <b>2016</b> , 73, 497-505	14.5	40
65	The association between lower educational attainment and depression owing to shared genetic effects? Results in ~25,000 subjects. <i>Molecular Psychiatry</i> , <b>2015</b> , 20, 735-43	15.1	39
64	Estimation of genomic prediction accuracy from reference populations with varying degrees of relationship. <i>PLoS ONE</i> , <b>2017</b> , 12, e0189775	3.7	38
63	Using information of relatives in genomic prediction to apply effective stratified medicine. <i>Scientific Reports</i> , <b>2017</b> , 7, 42091	4.9	31
62	A simple and fast two-locus quality control test to detect false positives due to batch effects in genome-wide association studies. <i>Genetic Epidemiology</i> , <b>2010</b> , 34, 854-62	2.6	30
61	Novel genetic analysis for case-control genome-wide association studies: quantification of power and genomic prediction accuracy. <i>PLoS ONE</i> , <b>2013</b> , 8, e71494	3.7	30
60	GCTA-GREML accounts for linkage disequilibrium when estimating genetic variance from genome-wide SNPs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, E4579-80	11.5	25
59	Genotype-covariate correlation and interaction disentangled by a whole-genome multivariate reaction norm model. <i>Nature Communications</i> , <b>2019</b> , 10, 2239	17.4	23
58	Genome-wide association study reveals greater polygenic loading for schizophrenia in cases with a family history of illness. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , <b>2016</b> , 171B, 276-89	3.5	23
57	Response to Browning and Browning. <i>American Journal of Human Genetics</i> , <b>2011</b> , 89, 193-195	11	22
56	Genetic polymorphisms of the bovine fatty acid binding protein 4 gene are significantly associated with marbling and carcass weight in Hanwoo (Korean Cattle). <i>Animal Genetics</i> , <b>2010</b> , 41, 442-4	2.5	22
55	The efficiency of designs for fine-mapping of quantitative trait loci using combined linkage disequilibrium and linkage. <i>Genetics Selection Evolution</i> , <b>2004</b> , 36, 145-61	4.9	22
54	Performance of risk prediction for inflammatory bowel disease based on genotyping platform and genomic risk score method. <i>BMC Medical Genetics</i> , <b>2017</b> , 18, 94	2.1	20
53	Methods and experimental designs for detection of QTL in sheep and goats. <i>Small Ruminant Research</i> , <b>2007</b> , 70, 21-31	1.7	17
52	A Comparison of Ten Polygenic Score Methods for Psychiatric Disorders Applied Across Multiple Cohorts. <i>Biological Psychiatry</i> , <b>2021</b> , 90, 611-620	7.9	17
51	Detection of genomic regions underlying resistance to gastrointestinal parasites in Australian sheep. <i>Genetics Selection Evolution</i> , <b>2019</b> , 51, 37	4.9	16
50	Educational attainment: a genome wide association study in 9538 Australians. <i>PLoS ONE</i> , <b>2011</b> , 6, e20128.7	16	16

49	Using dominance relationship coefficients based on linkage disequilibrium and linkage with a general complex pedigree to increase mapping resolution. <i>Genetics</i> , <b>2006</b> , 174, 1009-16	4	15
48	The role of pedigree information in combined linkage disequilibrium and linkage mapping of quantitative trait loci in a general complex pedigree. <i>Genetics</i> , <b>2005</b> , 169, 455-66	4	15
47	Efficient polygenic risk scores for biobank scale data by exploiting phenotypes from inferred relatives. <i>Nature Communications</i> , <b>2020</b> , 11, 3074	17.4	14
46	Using imputed whole-genome sequence data to improve the accuracy of genomic prediction for parasite resistance in Australian sheep. <i>Genetics Selection Evolution</i> , <b>2019</b> , 51, 32	4.9	14
45	Subtle stratification confounds estimates of heritability from rare variants		14
44	Genome wide QTL mapping to identify candidate genes for carcass traits in Hanwoo (Korean Cattle). <i>Genes and Genomics</i> , <b>2012</b> , 34, 43-49	2.1	13
43	Across-cohort QC analyses of GWAS summary statistics from complex traits. <i>European Journal of Human Genetics</i> , <b>2016</b> , 25, 137-146	5.3	13
42	Simultaneous fine mapping of multiple closely linked quantitative trait Loci using combined linkage disequilibrium and linkage with a general pedigree. <i>Genetics</i> , <b>2006</b> , 173, 2329-37	4	13
41	QTL and gene expression analyses identify genes affecting carcass weight and marbling on BTA14 in Hanwoo (Korean Cattle). <i>Mammalian Genome</i> , <b>2011</b> , 22, 589-601	3.2	12
40	Investigating Shared Genetic Basis Across Tourette Syndrome and Comorbid Neurodevelopmental Disorders Along the Impulsivity-Compulsivity Spectrum. <i>Biological Psychiatry</i> , <b>2021</b> , 90, 317-327	7.9	12
39	Commentary on "Limitations of GCTA as a solution to the missing heritability problem"		11
38	Sex-Dependent Shared and Nonshared Genetic Architecture Across Mood and Psychotic Disorders. <i>Biological Psychiatry</i> , <b>2022</b> , 91, 102-117	7.9	11
37	Age at first birth in women is genetically associated with increased risk of schizophrenia. <i>Scientific Reports</i> , <b>2018</b> , 8, 10168	4.9	11
36	Combining the meiosis Gibbs sampler with the random walk approach for linkage and association studies with a general complex pedigree and multimarker loci. <i>Genetics</i> , <b>2005</b> , 171, 2063-72	4	10
35	CORE GREML for estimating covariance between random effects in linear mixed models for complex trait analyses. <i>Nature Communications</i> , <b>2020</b> , 11, 4208	17.4	10
34	Effect of selection and selective genotyping for creation of reference on bias and accuracy of genomic prediction. <i>Journal of Animal Breeding and Genetics</i> , <b>2019</b> , 136, 390-407	2.9	8
33	Genotype-environment interaction on human cognitive function conditioned on the status of breastfeeding and maternal smoking around birth. <i>Scientific Reports</i> , <b>2017</b> , 7, 6087	4.9	8
32	Mega-analysis of 31,396 individuals from 6 countries uncovers strong gene-environment interaction for human fertility		7

31	Implications of simplified linkage equilibrium SNP simulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2015</b> , 112, E5449-51	11.5	6
30	Contrasting regional architectures of schizophrenia and other complex diseases using fast variance components analysis		6
29	Estimation of genetic correlation using linkage disequilibrium score regression and genomic restricted maximum likelihood		6
28	An integrative analysis of genomic and exposomic data for complex traits and phenotypic prediction. <i>Scientific Reports</i> , <b>2021</b> , 11, 21495	4.9	5
27	Regulatory variants explain much more heritability than coding variants across 11 common diseases		5
26	Whole-Genome Approach Discovers Novel Genetic and Nongenetic Variance Components Modulated by Lifestyle for Cardiovascular Health. <i>Journal of the American Heart Association</i> , <b>2020</b> , 9, e015661	6	5
25	The genetic relationship between female reproductive traits and six psychiatric disorders. <i>Scientific Reports</i> , <b>2019</b> , 9, 12041	4.9	4
24	The Impact of Genomic and Traditional Selection on the Contribution of Mutational Variance to Long-Term Selection Response and Genetic Variance. <i>Genetics</i> , <b>2019</b> , 213, 361-378	4	4
23	Using an evolutionary algorithm and parallel computing for haplotyping in a general complex pedigree with multiple marker loci. <i>BMC Bioinformatics</i> , <b>2008</b> , 9, 189	3.6	3
22	A genetic investigation of sex bias in the prevalence of attention deficit hyperactivity disorder		3
21	GxEsum: a novel approach to estimate the phenotypic variance explained by genome-wide GxE interaction based on GWAS summary statistics for biobank-scale data		3
20	An integrative analysis of genomic and exposomic data for complex traits and phenotypic prediction		3
19	Genotype-covariate correlation and interaction disentangled by a whole-genome multivariate reaction norm model		3
18	Population-based identity-by-descent mapping combined with exome sequencing to detect rare risk variants for schizophrenia. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , <b>2019</b> , 180, 223-231	3.5	2
17	Detecting Genotype-Population Interaction Effects by Ancestry Principal Components. <i>Frontiers in Genetics</i> , <b>2020</b> , 11, 379	4.5	2
16	Fine mapping of multiple interacting quantitative trait loci using combined linkage disequilibrium and linkage information. <i>Journal of Zhejiang University: Science B</i> , <b>2007</b> , 8, 787-91	4.5	2
15	Lifestyle modifies the diabetes-related metabolic risk, conditional on individual genetic differences		2
14	Simultaneous fine mapping of closely linked epistatic quantitative trait loci using combined linkage disequilibrium and linkage with a general pedigree. <i>Genetics Selection Evolution</i> , <b>2008</b> , 40, 265-278	4.9	2

13	Cross-disorder GWAS meta-analysis for Attention Deficit/Hyperactivity Disorder, Autism Spectrum Disorder, Obsessive Compulsive Disorder, and Tourette Syndrome		2
12	GxEsum: a novel approach to estimate the phenotypic variance explained by genome-wide GxE interaction based on GWAS summary statistics for biobank-scale data. <i>Genome Biology</i> , <b>2021</b> , 22, 183	18.3	2
11	Contextualizing genetic risk score for disease screening and rare variant discovery. <i>Nature Communications</i> , <b>2021</b> , 12, 4418	17.4	2
10	Simultaneous fine mapping of closely linked epistatic quantitative trait loci using combined linkage disequilibrium and linkage with a general pedigree. <i>Genetics Selection Evolution</i> , <b>2008</b> , 40, 265-78	4.9	1
9	Effect of selection on bias and accuracy in genomic prediction of breeding values		1
8	A Whole-Genome Approach Discovers Novel Genetic and Non-Genetic Variance Components Modulated by Lifestyle for Cardiovascular Health		1
7	Estimation of genomic prediction accuracy from reference populations with varying degrees of relationship		1
6	Detecting genotype-population interaction effects by ancestry principal components		1
5	Genetic Biomarkers for Endometriosis <b>2017</b> , 83-93		1
4	Age at first birth in women is genetically associated with increased risk of schizophrenia		1
3	THI Modulation of Genetic and Non-genetic Variance Components for Carcass Traits in Hanwoo Cattle. <i>Frontiers in Genetics</i> , <b>2020</b> , 11, 576377	4.5	0
2	Adiposity and cancer: a Mendelian randomization analysis in the UK biobank. <i>International Journal of Obesity</i> , <b>2021</b> , 45, 2657-2665	5.5	0
1	Lifestyle Modifies the Diabetes-Related Metabolic Risk, Conditional on Individual Genetic Differences.. <i>Frontiers in Genetics</i> , <b>2022</b> , 13, 759309	4.5	0