Sang Hong Lee

List of Publications by Year in Descending Order

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	Sex-Dependent Shared and Nonshared Genetic Architecture Across Mood and Psychotic Disorders. *Biological Psychiatry*, **2022**, 91, 102-117	7.9	11
119	Lifestyle Modifies the Diabetes-Related Metabolic Risk, Conditional on Individual Genetic Differences.. *Frontiers in Genetics*, **2022**, 13, 759309	4.5	0
118	An integrative analysis of genomic and exposomic data for complex traits and phenotypic prediction. *Scientific Reports*, **2021**, 11, 21495	4.9	5
117	A Comparison of Ten Polygenic Score Methods for Psychiatric Disorders Applied Across Multiple Cohorts. *Biological Psychiatry*, **2021**, 90, 611-620	7.9	17
116	GxEsum: a novel approach to estimate the phenotypic variance explained by genome-wide GxE interaction based on GWAS summary statistics for biobank-scale data. *Genome Biology*, **2021**, 22, 183	18.3	2
115	Contextualizing genetic risk score for disease screening and rare variant discovery. *Nature Communications*, **2021**, 12, 4418	17.4	2
114	Adiposity and cancer: a Mendelian randomization analysis in the UK biobank. *International Journal of Obesity*, **2021**, 45, 2657-2665	5.5	0
113	Investigating Shared Genetic Basis Across Tourette Syndrome and Comorbid Neurodevelopmental Disorders Along the Impulsivity-Compulsivity Spectrum. *Biological Psychiatry*, **2021**, 90, 317-327	7.9	12
112	THI Modulation of Genetic and Non-genetic Variance Components for Carcass Traits in Hanwoo Cattle. *Frontiers in Genetics*, **2020**, 11, 576377	4.5	0
111	Detecting Genotype-Population Interaction Effects by Ancestry Principal Components. *Frontiers in Genetics*, **2020**, 11, 379	4.5	2
110	Efficient polygenic risk scores for biobank scale data by exploiting phenotypes from inferred relatives. *Nature Communications*, **2020**, 11, 3074	17.4	14
109	CORE GREML for estimating covariance between random effects in linear mixed models for complex trait analyses. *Nature Communications*, **2020**, 11, 4208	17.4	10
108	RICOPILI: Rapid Imputation for COnsortias PIpeLIne. *Bioinformatics*, **2020**, 36, 930-933	7.2	72
107	Whole-Genome Approach Discovers Novel Genetic and Nongenetic Variance Components Modulated by Lifestyle for Cardiovascular Health. *Journal of the American Heart Association*, **2020**, 9, e015661	6	5
106	Effect of selection and selective genotyping for creation of reference on bias and accuracy of genomic prediction. *Journal of Animal Breeding and Genetics*, **2019**, 136, 390-407	2.9	8
105	Genetic correlations of polygenic disease traits: from theory to practice. *Nature Reviews Genetics*, **2019**, 20, 567-581	30.1	98
104	Genotype-covariate correlation and interaction disentangled by a whole-genome multivariate reaction norm model. *Nature Communications*, **2019**, 10, 2239	17.4	23

103	Population-based identity-by-descent mapping combined with exome sequencing to detect rare risk variants for schizophrenia. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2019**, 180, 223-231	3.5	2
102	The genetic relationship between female reproductive traits and six psychiatric disorders. *Scientific Reports*, **2019**, 9, 12041	4.9	4
101	Using imputed whole-genome sequence data to improve the accuracy of genomic prediction for parasite resistance in Australian sheep. *Genetics Selection Evolution*, **2019**, 51, 32	4.9	14
100	Detection of genomic regions underlying resistance to gastrointestinal parasites in Australian sheep. *Genetics Selection Evolution*, **2019**, 51, 37	4.9	16
99	The Impact of Genomic and Traditional Selection on the Contribution of Mutational Variance to Long-Term Selection Response and Genetic Variance. *Genetics*, **2019**, 213, 361-378	4	4
98	Improving genetic prediction by leveraging genetic correlations among human diseases and traits. *Nature Communications*, **2018**, 9, 989	17.4	76
97	Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. *Cell*, **2018**, 173, 1705-1715.e16	56.2	360
96	A Genetic Investigation of Sex Bias in the Prevalence of Attention-Deficit/Hyperactivity Disorder. *Biological Psychiatry*, **2018**, 83, 1044-1053	7.9	93
95	Estimation of Genetic Correlation via Linkage Disequilibrium Score Regression and Genomic Restricted Maximum Likelihood. *American Journal of Human Genetics*, **2018**, 102, 1185-1194	11	55
94	Age at first birth in women is genetically associated with increased risk of schizophrenia. *Scientific Reports*, **2018**, 8, 10168	4.9	11
93	Genome-wide Association for Major Depression Through Age at Onset Stratification: Major Depressive Disorder Working Group of the Psychiatric Genomics Consortium. *Biological Psychiatry*, **2017**, 81, 325-335	7.9	129
92	Using information of relatives in genomic prediction to apply effective stratified medicine. *Scientific Reports*, **2017**, 7, 42091	4.9	31
91	Identification of genetic variants associated with Huntington's disease progression: a genome-wide association study. *Lancet Neurology, The*, **2017**, 16, 701-711	24.1	161
90	Performance of risk prediction for inflammatory bowel disease based on genotyping platform and genomic risk score method. *BMC Medical Genetics*, **2017**, 18, 94	2.1	20
89	Hidden heritability due to heterogeneity across seven populations. *Nature Human Behaviour*, **2017**, 1, 757-765	12.8	94
88	Genotype-environment interaction on human cognitive function conditioned on the status of breastfeeding and maternal smoking around birth. *Scientific Reports*, **2017**, 7, 6087	4.9	8
87	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. *Nature Genetics*, **2017**, 49, 27-35	36.3	530
86	Estimation of genomic prediction accuracy from reference populations with varying degrees of relationship. *PLoS ONE*, **2017**, 12, e0189775	3.7	38

85	Genetic Biomarkers for Endometriosis **2017**, 83-93		1
84	GCTA-GREML accounts for linkage disequilibrium when estimating genetic variance from genome-wide SNPs. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, E4579-80	11.5	25
83	Genome-wide association study reveals greater polygenic loading for schizophrenia in cases with a family history of illness. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2016** , 171B, 276-89	3.5	23
82	MTG2: an efficient algorithm for multivariate linear mixed model analysis based on genomic information. *Bioinformatics*, **2016**, 32, 1420-2	7.2	93
81	Evidence for Genetic Overlap Between Schizophrenia and Age at First Birth in Women. *JAMA Psychiatry*, **2016**, 73, 497-505	14.5	40
80	Across-cohort QC analyses of GWAS summary statistics from complex traits. *European Journal of Human Genetics*, **2016**, 25, 137-146	5.3	13
79	EigenGWAS: finding loci under selection through genome-wide association studies of eigenvectors in structured populations. *Heredity*, **2016**, 117, 51-61	3.6	54
78	Psychiatric genome-wide association study analyses implicate neuronal, immune and histone pathways. *Nature Neuroscience*, **2015**, 18, 199-209	25.5	572
77	Simultaneous discovery, estimation and prediction analysis of complex traits using a bayesian mixture model. *PLoS Genetics*, **2015**, 11, e1004969	6	206
76	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. *American Journal of Human Genetics*, **2015**, 97, 576-92	11	649
75	Contrasting genetic architectures of schizophrenia and other complex diseases using fast variance-components analysis. *Nature Genetics*, **2015**, 47, 1385-92	36.3	299
74	Shared genetics underlying epidemiological association between endometriosis and ovarian cancer. *Human Molecular Genetics*, **2015**, 24, 5955-64	5.6	48
73	Heterogeneity of genetic architecture of body size traits in a free-living population. *Molecular Ecology*, **2015**, 24, 1810-30	5.7	55
72	Implications of simplified linkage equilibrium SNP simulation. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, E5449-51	11.5	6
71	Genetic variance estimation with imputed variants finds negligible missing heritability for human height and body mass index. *Nature Genetics*, **2015**, 47, 1114-20	36.3	522
70	New data and an old puzzle: the negative association between schizophrenia and rheumatoid arthritis. *International Journal of Epidemiology*, **2015**, 44, 1706-21	7.8	43
69	The association between lower educational attainment and depression owing to shared genetic effects? Results in ~25,000 subjects. *Molecular Psychiatry*, **2015**, 20, 735-43	15.1	39
68	Dominance genetic variation contributes little to the missing heritability for human complex traits. *American Journal of Human Genetics*, **2015**, 96, 377-85	11	138

67	Joint analysis of psychiatric disorders increases accuracy of risk prediction for schizophrenia, bipolar disorder, and major depressive disorder. *American Journal of Human Genetics*, **2015**, 96, 283-94	11	161
66	LD Score regression distinguishes confounding from polygenicity in genome-wide association studies. *Nature Genetics*, **2015**, 47, 291-5	36.3	2096
65	Partitioning heritability of regulatory and cell-type-specific variants across 11 common diseases. *American Journal of Human Genetics*, **2014**, 95, 535-52	11	411
64	Biological insights from 108 schizophrenia-associated genetic loci. *Nature*, **2014**, 511, 421-7	50.4	5249
63	Research review: Polygenic methods and their application to psychiatric traits. *Journal of Child Psychology and Psychiatry and Allied Disciplines*, **2014**, 55, 1068-87	7.9	410
62	Estimation and partitioning of (co)heritability of inflammatory bowel disease from GWAS and immunochip data. *Human Molecular Genetics*, **2014**, 23, 4710-20	5.6	73
61	Statistical power to detect genetic (co)variance of complex traits using SNP data in unrelated samples. *PLoS Genetics*, **2014**, 10, e1004269	6	236
60	Genome-wide association analysis identifies 13 new risk loci for schizophrenia. *Nature Genetics*, **2013**, 45, 1150-9	36.3	1153
59	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. *Nature Genetics*, **2013**, 45, 984-94	36.3	1628
58	Estimation and partitioning of polygenic variation captured by common SNPs for Alzheimer's disease, multiple sclerosis and endometriosis. *Human Molecular Genetics*, **2013**, 22, 832-41	5.6	147
57	Estimation of SNP heritability from dense genotype data. *American Journal of Human Genetics*, **2013**, 93, 1151-5	11	85
56	Additive genetic variation in schizophrenia risk is shared by populations of African and European descent. *American Journal of Human Genetics*, **2013**, 93, 463-70	11	55
55	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. *Nature Genetics*, **2013**, 45, 501-12	36.3	437
54	GWAS of 126,559 individuals identifies genetic variants associated with educational attainment. *Science*, **2013**, 340, 1467-71	33.3	563
53	Polygenic transmission and complex neuro developmental network for attention deficit hyperactivity disorder: genome-wide association study of both common and rare variants. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2013**, 162B, 419-430	3.5	125
52	Genome-wide complex trait analysis (GCTA): methods, data analyses, and interpretations. *Methods in Molecular Biology*, **2013**, 1019, 215-36	1.4	153
51	Partitioning the heritability of Tourette syndrome and obsessive compulsive disorder reveals differences in genetic architecture. *PLoS Genetics*, **2013**, 9, e1003864	6	189
50	Novel genetic analysis for case-control genome-wide association studies: quantification of power and genomic prediction accuracy. *PLoS ONE*, **2013**, 8, e71494	3.7	30

49	Genome wide QTL mapping to identify candidate genes for carcass traits in Hanwoo (Korean Cattle). *Genes and Genomics*, **2012**, 34, 43-49	2.1	13
48	Multivariate genetic analyses of cognition and academic achievement from two population samples of 174,000 and 166,000 school children. *Behavior Genetics*, **2012**, 42, 699-710	3.2	54
47	Estimating the proportion of variation in susceptibility to schizophrenia captured by common SNPs. *Nature Genetics*, **2012**, 44, 247-50	36.3	471
46	A better coefficient of determination for genetic profile analysis. *Genetic Epidemiology*, **2012**, 36, 214-24	2.6	158
45	Runs of homozygosity implicate autozygosity as a schizophrenia risk factor. *PLoS Genetics*, **2012**, 8, e1002656	8.6	91
44	Common SNPs explain some of the variation in the personality dimensions of neuroticism and extraversion. *Translational Psychiatry*, **2012**, 2, e102	8.6	137
43	Impact of diagnostic misclassification on estimation of genetic correlations using genome-wide genotypes. *European Journal of Human Genetics*, **2012**, 20, 668-74	5.3	51
42	Estimation of pleiotropy between complex diseases using single-nucleotide polymorphism-derived genomic relationships and restricted maximum likelihood. *Bioinformatics*, **2012**, 28, 2540-2	7.2	414
41	Educational attainment: a genome wide association study in 9538 Australians. *PLoS ONE*, **2011**, 6, e20128	3.7	16
40	Genome-wide association study identifies a locus at 7p15.2 associated with endometriosis. *Nature Genetics*, **2011**, 43, 51-4	36.3	227
39	GCTA: a tool for genome-wide complex trait analysis. *American Journal of Human Genetics*, **2011**, 88, 76-82	11	3838
38	Estimating missing heritability for disease from genome-wide association studies. *American Journal of Human Genetics*, **2011**, 88, 294-305	11	737
37	Response to Browning and Browning. *American Journal of Human Genetics*, **2011**, 89, 193-195	11	22
36	QTL and gene expression analyses identify genes affecting carcass weight and marbling on BTA14 in Hanwoo (Korean Cattle). *Mammalian Genome*, **2011**, 22, 589-601	3.2	12
35	Genetic polymorphisms of the bovine fatty acid binding protein 4 gene are significantly associated with marbling and carcass weight in Hanwoo (Korean Cattle). *Animal Genetics*, **2010**, 41, 442-4	2.5	22
34	Geographical genomics of human leukocyte gene expression variation in southern Morocco. *Nature Genetics*, **2010**, 42, 62-7	36.3	117
33	A simple and fast two-locus quality control test to detect false positives due to batch effects in genome-wide association studies. *Genetic Epidemiology*, **2010**, 34, 854-62	2.6	30
32	Using the realized relationship matrix to disentangle confounding factors for the estimation of genetic variance components of complex traits. *Genetics Selection Evolution*, **2010**, 42, 22	4.9	52

31	Genetic mapping of quantitative trait loci for resistance to Haemonchus contortus in sheep. *Animal Genetics*, **2009**, 40, 262-72	2.5	45
30	Simultaneous fine mapping of closely linked epistatic quantitative trait loci using combined linkage disequilibrium and linkage with a general pedigree. *Genetics Selection Evolution*, **2008**, 40, 265-78	4.9	1
29	Using an evolutionary algorithm and parallel computing for haplotyping in a general complex pedigree with multiple marker loci. *BMC Bioinformatics*, **2008**, 9, 189	3.6	3
28	Predicting unobserved phenotypes for complex traits from whole-genome SNP data. *PLoS Genetics*, **2008**, 4, e1000231	6	147
27	Simultaneous fine mapping of closely linked epistatic quantitative trait loci using combined linkage disequilibrium and linkage with a general pedigree. *Genetics Selection Evolution*, **2008**, 40, 265-278	4.9	2
26	Evidence for multiple alleles effecting muscling and fatness at the ovine GDF8 locus. *BMC Genetics*, **2007**, 8, 80	2.6	66
25	Methods and experimental designs for detection of QTL in sheep and goats. *Small Ruminant Research*, **2007**, 70, 21-31	1.7	17
24	Fine mapping of multiple interacting quantitative trait loci using combined linkage disequilibrium and linkage information. *Journal of Zhejiang University: Science B*, **2007**, 8, 787-91	4.5	2
23	An efficient variance component approach implementing an average information REML suitable for combined LD and linkage mapping with a general complex pedigree. *Genetics Selection Evolution*, **2006**, 38, 25-43	4.9	42
22	Using dominance relationship coefficients based on linkage disequilibrium and linkage with a general complex pedigree to increase mapping resolution. *Genetics*, **2006**, 174, 1009-16	4	15
21	Simultaneous fine mapping of multiple closely linked quantitative trait Loci using combined linkage disequilibrium and linkage with a general pedigree. *Genetics*, **2006**, 173, 2329-37	4	13
20	The role of pedigree information in combined linkage disequilibrium and linkage mapping of quantitative trait loci in a general complex pedigree. *Genetics*, **2005**, 169, 455-66	4	15
19	Combining the meiosis Gibbs sampler with the random walk approach for linkage and association studies with a general complex pedigree and multimarker loci. *Genetics*, **2005**, 171, 2063-72	4	10
18	The efficiency of designs for fine-mapping of quantitative trait loci using combined linkage disequilibrium and linkage. *Genetics Selection Evolution*, **2004**, 36, 145-61	4.9	22
17	Lifestyle modifies the diabetes-related metabolic risk, conditional on individual genetic differences		2
16	Effect of selection on bias and accuracy in genomic prediction of breeding values		1
15	A Whole-Genome Approach Discovers Novel Genetic and Non-Genetic Variance Components Modulated by Lifestyle for Cardiovascular Health		1
14	Regulatory variants explain much more heritability than coding variants across 11 common diseases		5

13	Contrasting regional architectures of schizophrenia and other complex diseases using fast variance components analysis	6
12	Commentary on "Limitations of GCTA as a solution to the missing heritability problem"	11
11	Subtle stratification confounds estimates of heritability from rare variants	14
10	Mega-analysis of 31,396 individuals from 6 countries uncovers strong gene-environment interaction for human fertility	7
9	Estimation of genomic prediction accuracy from reference populations with varying degrees of relationship	1
8	A genetic investigation of sex bias in the prevalence of attention deficit hyperactivity disorder	3
7	Estimation of genetic correlation using linkage disequilibrium score regression and genomic restricted maximum likelihood	6
6	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
5	An integrative analysis of genomic and exposomic data for complex traits and phenotypic prediction	3
4	Genotype-covariate correlation and interaction disentangled by a whole-genome multivariate reaction norm model	3
3	Detecting genotype-population interaction effects by ancestry principal components	1
2	Cross-disorder GWAS meta-analysis for Attention Deficit/Hyperactivity Disorder, Autism Spectrum Disorder, Obsessive Compulsive Disorder, and Tourette Syndrome	2
1	Age at first birth in women is genetically associated with increased risk of schizophrenia	1