Sang Hong Lee

List of Publications by Year
in descending order

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108 papers	36,321 citations	34016 52 h-index	24915 109 g-index
144 all docs	144 docs citations	144 times ranked	38096 citing authors

#	Article	IF	Citations
1	Sex-Dependent Shared and Nonshared Genetic Architecture Across Mood and Psychotic Disorders. Biological Psychiatry, 2022, 91, 102-117.	0.7	61
2	Interaction Testing and Polygenic Risk Scoring to Estimate the Association of Common Genetic Variants With Treatment Resistance in Schizophrenia. JAMA Psychiatry, 2022, 79, 260.	6.0	44
3	Lifestyle Modifies the Diabetes-Related Metabolic Risk, Conditional on Individual Genetic Differences. Frontiers in Genetics, 2022, 13, 759309.	1.1	4
4	Exploring polygenicâ€environment and residualâ€environment interactions for depressive symptoms within the UK Biobank. Genetic Epidemiology, 2022, 46, 219-233.	0.6	4
5	Considering hormone-sensitive cancers as a single disease in the UK biobank reveals shared aetiology. Communications Biology, 2022, 5, .	2.0	3
6	A Comparison of Ten Polygenic Score Methods for Psychiatric Disorders Applied Across Multiple Cohorts. Biological Psychiatry, 2021, 90, 611-620.	0.7	103
7	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.	3.8	14
8	An opportunity for primary prevention research in psychotic disorders. Schizophrenia Research, 2021, , .	1.1	1
9	Contextualizing genetic risk score for disease screening and rare variant discovery. Nature Communications, 2021, 12, 4418.	5.8	11
10	Adiposity and cancer: a Mendelian randomization analysis in the UK biobank. International Journal of Obesity, 2021, 45, 2657-2665.	1.6	20
11	Investigating Shared Genetic Basis Across Tourette Syndrome and Comorbid Neurodevelopmental Disorders Along the Impulsivity-Compulsivity Spectrum. Biological Psychiatry, 2021, 90, 317-327.	0.7	49
12	An integrative analysis of genomic and exposomic data for complex traits and phenotypic prediction. Scientific Reports, 2021, 11, 21495.	1.6	8
13	RICOPILI: Rapid Imputation for COnsortias PIpeLIne. Bioinformatics, 2020, 36, 930-933.	1.8	201
14	CORE GREML for estimating covariance between random effects in linear mixed models for complex trait analyses. Nature Communications, 2020, 11, 4208.	5.8	23
15	THI Modulation of Genetic and Non-genetic Variance Components for Carcass Traits in Hanwoo Cattle. Frontiers in Genetics, 2020, 11, 576377.	1.1	1
16	Detecting Genotype-Population Interaction Effects by Ancestry Principal Components. Frontiers in Genetics, 2020, 11, 379.	1.1	2
17	Efficient polygenic risk scores for biobank scale data by exploiting phenotypes from inferred relatives. Nature Communications, 2020, 11, 3074.	5.8	24
18	Wholeâ€Genome Approach Discovers Novel Genetic and Nongenetic Variance Components Modulated by Lifestyle for Cardiovascular Health. Journal of the American Heart Association, 2020, 9, e015661.	1.6	12

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19	The genetic relationship between female reproductive traits and six psychiatric disorders. Scientific Reports, 2019, 9, 12041.	1.6	18
20	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.	1.2	28
21	Detection of genomic regions underlying resistance to gastrointestinal parasites in Australian sheep. Genetics Selection Evolution, 2019, 51, 37.	1.2	36
22	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.	1.2	8
23	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.	0.8	26
24	Genetic correlations of polygenic disease traits: from theory to practice. Nature Reviews Genetics, 2019, 20, 567-581.	7.7	236
25	Genotypeâ€"covariate correlation and interaction disentangled by a whole-genome multivariate reaction norm model. Nature Communications, 2019, 10, 2239.	5.8	45
26	Populationâ€based identityâ€byâ€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.	1.1	2
27	Improving genetic prediction by leveraging genetic correlations among human diseases and traits. Nature Communications, 2018, 9, 989.	5.8	136
28	A Genetic Investigation of Sex Bias in the Prevalence of Attention-Deficit/Hyperactivity Disorder. Biological Psychiatry, 2018, 83, 1044-1053.	0.7	146
29	Estimation of Genetic Correlation via Linkage Disequilibrium Score Regression and Genomic Restricted Maximum Likelihood. American Journal of Human Genetics, 2018, 102, 1185-1194.	2.6	119
30	Age at first birth in women is genetically associated with increased risk of schizophrenia. Scientific Reports, 2018, 8, 10168.	1.6	17
31	Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. Cell, 2018, 173, 1705-1715.e16.	13.5	623
32	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.	0.7	175
33	Using information of relatives in genomic prediction to apply effective stratified medicine. Scientific Reports, 2017, 7, 42091.	1.6	38
34	Identification of genetic variants associated with Huntington's disease progression: a genome-wide association study. Lancet Neurology, The, 2017, 16, 701-711.	4.9	248
35	Hidden heritability due to heterogeneity across seven populations. Nature Human Behaviour, 2017, 1, 757-765.	6.2	137
36	Genotype-environment interaction on human cognitive function conditioned on the status of breastfeeding and maternal smoking around birth. Scientific Reports, 2017, 7, 6087.	1.6	9

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37	Across-cohort QC analyses of GWAS summary statistics from complex traits. European Journal of Human Genetics, 2017, 25, 137-146.	1.4	18
38	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. Nature Genetics, 2017, 49, 27-35.	9.4	838
39	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	36
40	Estimation of genomic prediction accuracy from reference populations with varying degrees of relationship. PLoS ONE, 2017, 12, e0189775.	1.1	58
41	Genetic Biomarkers for Endometriosis. , 2017, , 83-93.		2
42	EigenGWAS: finding loci under selection through genome-wide association studies of eigenvectors in structured populations. Heredity, 2016, 117, 51-61.	1.2	69
43	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.	3.3	45
44	Genomeâ€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, 171, 276-289.	1.1	28
45	MTG2: an efficient algorithm for multivariate linear mixed model analysis based on genomic information. Bioinformatics, 2016, 32, 1420-1422.	1.8	178
46	Evidence for Genetic Overlap Between Schizophrenia and Age at First Birth in Women. JAMA Psychiatry, 2016, 73, 497.	6.0	51
47	The association between lower educational attainment and depression owing to shared genetic effects? Results in ~25â€‰000 subjects. Molecular Psychiatry, 2015, 20, 735-743.	4.1	59
48	Dominance Genetic Variation Contributes Little to the Missing Heritability for Human Complex Traits. American Journal of Human Genetics, 2015, 96, 377-385.	2.6	191
49	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, 283-294.	2.6	225
50	LD Score regression distinguishes confounding from polygenicity in genome-wide association studies. Nature Genetics, 2015, 47, 291-295.	9.4	3,905
51	Psychiatric genome-wide association study analyses implicate neuronal, immune and histone pathways. Nature Neuroscience, 2015, 18, 199-209.	7.1	701
52	Simultaneous Discovery, Estimation and Prediction Analysis of Complex Traits Using a Bayesian Mixture Model. PLoS Genetics, 2015, 11, e1004969.	1.5	339
53	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	2.6	1,098
54	Contrasting genetic architectures of schizophrenia and other complex diseases using fast variance-components analysis. Nature Genetics, 2015, 47, 1385-1392.	9.4	431

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55	Shared genetics underlying epidemiological association between endometriosis and ovarian cancer. Human Molecular Genetics, 2015, 24, 5955-5964.	1.4	68
56	Heterogeneity of genetic architecture of body size traits in a freeâ€living population. Molecular Ecology, 2015, 24, 1810-1830.	2.0	72
57	Implications of simplified linkage equilibrium SNP simulation. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E5449-51.	3.3	7
58	Genetic variance estimation with imputed variants finds negligible missing heritability for human height and body mass index. Nature Genetics, 2015, 47, 1114-1120.	9.4	709
59	New data and an old puzzle: the negative association between schizophrenia and rheumatoid arthritis. International Journal of Epidemiology, 2015, 44, 1706-1721.	0.9	53
60	Estimation and partitioning of (co)heritability of inflammatory bowel disease from GWAS and immunochip data. Human Molecular Genetics, 2014, 23, 4710-4720.	1.4	110
61	Statistical Power to Detect Genetic (Co)Variance of Complex Traits Using SNP Data in Unrelated Samples. PLoS Genetics, 2014, 10, e1004269.	1.5	303
62	Partitioning Heritability of Regulatory and Cell-Type-Specific Variants across 11 Common Diseases. American Journal of Human Genetics, 2014, 95, 535-552.	2.6	569
63	Biological insights from 108 schizophrenia-associated genetic loci. Nature, 2014, 511, 421-427.	13.7	6,934
64	Research Review: Polygenic methods and their application to psychiatric traits. Journal of Child Psychology and Psychiatry and Allied Disciplines, 2014, 55, 1068-1087.	3.1	578
65	Genome-wide association analysis identifies 13 new risk loci for schizophrenia. Nature Genetics, 2013, 45, 1150-1159.	9.4	1,395
66	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. Nature Genetics, 2013, 45, 984-994.	9.4	2,067
67	Estimation and partitioning of polygenic variation captured by common SNPs for Alzheimer's disease, multiple sclerosis and endometriosis. Human Molecular Genetics, 2013, 22, 832-841.	1.4	186
68	Estimation of SNP Heritability from Dense Genotype Data. American Journal of Human Genetics, 2013, 93, 1151-1155.	2.6	103
69	Additive Genetic Variation in Schizophrenia Risk Is Shared by Populations of African and European Descent. American Journal of Human Genetics, 2013, 93, 463-470.	2.6	72
70	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	9.4	578
71	GWAS of 126,559 Individuals Identifies Genetic Variants Associated with Educational Attainment. Science, 2013, 340, 1467-1471.	6.0	750
72	Polygenic transmission and complex neuro developmental network for attention deficit hyperactivity disorder: Genomeâ€wide association study of both common and rare variants. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2013, 162, 419-430.	1.1	157

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73	Genome-Wide Complex Trait Analysis (GCTA): Methods, Data Analyses, and Interpretations. Methods in Molecular Biology, 2013, 1019, 215-236.	0.4	200
74	Partitioning the Heritability of Tourette Syndrome and Obsessive Compulsive Disorder Reveals Differences in Genetic Architecture. PLoS Genetics, 2013, 9, e1003864.	1.5	241
75	Novel Genetic Analysis for Case-Control Genome-Wide Association Studies: Quantification of Power and Genomic Prediction Accuracy. PLoS ONE, 2013, 8, e71494.	1.1	34
76	Runs of Homozygosity Implicate Autozygosity as a Schizophrenia Risk Factor. PLoS Genetics, 2012, 8, e1002656.	1.5	109
77	Common SNPs explain some of the variation in the personality dimensions of neuroticism and extraversion. Translational Psychiatry, 2012, 2, e102-e102.	2.4	156
78	Impact of diagnostic misclassification on estimation of genetic correlations using genome-wide genotypes. European Journal of Human Genetics, 2012, 20, 668-674.	1.4	65
79	Estimation of pleiotropy between complex diseases using single-nucleotide polymorphism-derived genomic relationships and restricted maximum likelihood. Bioinformatics, 2012, 28, 2540-2542.	1.8	564
80	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.	1.4	62
81	Estimating the proportion of variation in susceptibility to schizophrenia captured by common SNPs. Nature Genetics, 2012, 44, 247-250.	9.4	578
82	A Better Coefficient of Determination for Genetic Profile Analysis. Genetic Epidemiology, 2012, 36, 214-224.	0.6	274
83	Genome wide QTL mapping to identify candidate genes for carcass traits in Hanwoo (Korean Cattle). Genes and Genomics, 2012, 34, 43-49.	0.5	16
84	Educational Attainment: A Genome Wide Association Study in 9538 Australians. PLoS ONE, 2011, 6, e20128.	1.1	18
85	Genome-Wide Association Study Identifies a Locus at 7p15.2 Associated With Endometriosis. Obstetrical and Gynecological Survey, 2011, 66, 214-216.	0.2	0
86	Genome-wide association study identifies a locus at 7p15.2 associated with endometriosis. Nature Genetics, 2011, 43, 51-54.	9.4	261
87	GCTA: A Tool for Genome-wide Complex Trait Analysis. American Journal of Human Genetics, 2011, 88, 76-82.	2.6	6,212
88	Estimating Missing Heritability for Disease from Genome-wide Association Studies. American Journal of Human Genetics, 2011, 88, 294-305.	2.6	949
89	Response to Browning and Browning. American Journal of Human Genetics, 2011, 89, 193-195.	2.6	27
90	QTL and gene expression analyses identify genes affecting carcass weight and marbling on BTA14 in Hanwoo (Korean Cattle). Mammalian Genome, 2011, 22, 589-601.	1.0	15

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91	A simple and fast twoâ€locus quality control test to detect false positives due to batch effects in genomeâ€wide association studies. Genetic Epidemiology, 2010, 34, 854-862.	0.6	33
92	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.	1.2	58
93	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, 442-444.	0.6	38
94	Geographical genomics of human leukocyte gene expression variation in southern Morocco. Nature Genetics, 2010, 42, 62-67.	9.4	142
95	Genetic mapping of quantitative trait loci for resistance to Haemonchus contortus in sheep. Animal Genetics, 2009, 40, 262-272.	0.6	56
96	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.	1.2	1
97	Using an evolutionary algorithm and parallel computing for haplotyping in a general complex pedigree with multiple marker loci. BMC Bioinformatics, 2008, 9, 189.	1.2	3
98	Predicting Unobserved Phenotypes for Complex Traits from Whole-Genome SNP Data. PLoS Genetics, 2008, 4, e1000231.	1.5	175
99	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.	1.2	2
100	Evidence for multiple alleles effecting muscling and fatness at the Ovine GDF8 locus. BMC Genetics, 2007, 8, 80.	2.7	88
101	Methods and experimental designs for detection of QTL in sheep and goats. Small Ruminant Research, 2007, 70, 21-31.	0.6	20
102	Fine mapping of multiple interacting quantitative trait loci using combined linkage disequilibrium and linkage information. Journal of Zhejiang University: Science B, 2007, 8, 787-791.	1.3	2
103	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.	1.2	57
104	Using Dominance Relationship Coefficients Based on Linkage Disequilibrium and Linkage With a General Complex Pedigree to Increase Mapping Resolution. Genetics, 2006, 174, 1009-1016.	1.2	22
105	Simultaneous Fine Mapping of Multiple Closely Linked Quantitative Trait Loci Using Combined Linkage Disequilibrium and Linkage With a General Pedigree. Genetics, 2006, 173, 2329-2337.	1.2	16
106	The Role of Pedigree Information in Combined Linkage Disequilibrium and Linkage Mapping of Quantitative Trait Loci in a General Complex Pedigree. Genetics, 2005, 169, 455-466.	1.2	19
107	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, 2063-2072.	1.2	12
108	The efficiency of designs for fine-mapping of quantitative trait loci using combined linkage disequilibrium and linkage. Genetics Selection Evolution, 2004, 36, 145-61.	1.2	26