Buhm Han

List of Publications by Year
in descending order

71 papers	5,981 citations	136885 32 h-index	95218 68 g-index
77 all docs	77 docs citations	77 times ranked	14652 citing authors

#	Article	IF	Citations
1	Phenome-wide association study of the major histocompatibility complex region in the Korean population identifies novel association signals. Human Molecular Genetics, 2022, , .	1.4	1
2	MarcoPolo: a method to discover differentially expressed genes in single-cell RNA-seq data without depending on prior clustering. Nucleic Acids Research, 2022, 50, e71-e71.	6.5	8
3	Exploration of errors in variance caused by using the first-order approximation in Mendelian randomization. Genomics and Informatics, 2022, 20, e9.	0.4	0
4	Identification of shared loci associated with both Crohnâ€™s disease and leprosy in East Asians. Human Molecular Genetics, 2022, 31, 3934-3944.	1.4	5
5	A theory-based practical solution to correct for sex-differential participation bias. Genome Biology, 2022, 23, .	3.8	1
6	HATK: HLA analysis toolkit. Bioinformatics, 2021, 37, 416-418.	1.8	13
7	PLEIO: a method to map and interpret pleiotropic loci with GWAS summary statistics. American Journal of Human Genetics, 2021, 108, 36-48.	2.6	22
8	Accurate imputation of human leukocyte antigens with CookHLA. Nature Communications, 2021, 12, 1264.	5.8	21
9	Identification of Three Novel Susceptibility Loci for Inflammatory Bowel Disease in Koreans in an Extended Genome-Wide Association Study. Journal of Crohn's and Colitis, 2021, 15, 1898-1907.	0.6	13
10	Rare variants regulate expression of nearby individual genes in multiple tissues. PLoS Genetics, 2021, 17, e1009596.	1.5	6
11	A high-resolution HLA reference panel capturing global population diversity enables multi-ancestry fine-mapping in HIV host response. Nature Genetics, 2021, 53, 1504-1516.	9.4	69
12	Expression Quantitative Trait Loci (eQTL) Mapping in Korean Patients With Crohnâ€™s Disease and Identification of Potential Causal Genes Through Integration With Disease Associations. Frontiers in Genetics, 2020, 11, 486.	1.1	15
13	Exosomal PD-L1 promotes tumor growth through immune escape in non-small cell lung cancer. Experimental and Molecular Medicine, 2019, 51, 1-13.	3.2	194
14	Clinically Applicable Deep Learning Algorithm Using Quantitative Proteomic Data. Journal of Proteome Research, 2019, 18, 3195-3202.	1.8	16
15	Genomic GPS: using genetic distance from individuals to public data for genomic analysis without disclosing personal genomes. Genome Biology, 2019, 20, 175.	3.8	4
16	Cross-disorder analysis of schizophrenia and 19 immune-mediated diseases identifies shared genetic risk. Human Molecular Genetics, 2019, 28, 3498-3513.	1.4	65
17	Prognostic value of the association between MHC class I downregulation and PD-L1 upregulation in head and neck squamous cell carcinoma patients. Scientific Reports, 2019, 9, 7680.	1.6	36
18	Effects of smoking on the association of human leukocyte antigen with ulcerative colitis. Journal of Gastroenterology and Hepatology (Australia), 2019, 34, 1777-1783.	1.4	2

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19	Analysis of differences in human leukocyte antigen between the two Wellcome Trust Case Control Consortium control datasets. Genomics and Informatics, 2019, 17, e29.	0.4	0
20	Immunochip Meta-Analysis of Inflammatory Bowel Disease Identifies Three Novel Loci and Four Novel Associations in Previously Reported Loci. Journal of Crohn's and Colitis, 2018, 12, 730-741.	0.6	38
21	Association of CDKN2A/CDKN2B with inflammatory bowel disease in Koreans. Journal of Gastroenterology and Hepatology (Australia), 2018, 33, 887-893.	1.4	7
22	An Association Mapping Framework To Account for Potential Sex Difference in Genetic Architectures. Genetics, 2018, 209, 685-698.	1.2	5
23	Amino acid position 37 of HLA-DRÎ²1 affects susceptibility to Crohnâ€™s disease in Asians. Human Molecular Genetics, 2018, 27, 3901-3910.	1.4	19
24	An Intergenic Variant rs9268877 Between HLA-DRA and HLA-DRB Contributes to the Clinical Course and Long-term Outcome of Ulcerative Colitis. Journal of Crohn's and Colitis, 2018, 12, 1113-1121.	0.6	12
25	X Chromosome-wide Association Study Identifies a Susceptibility Locus for Inflammatory Bowel Disease in Koreans. Journal of Crohn's and Colitis, 2017, 11, 820-830.	0.6	9
26	FOLD: a method to optimize power in meta-analysis of genetic association studies with overlapping subjects. Bioinformatics, 2017, 33, 3947-3954.	1.8	3
27	Applying meta-analysis to genotype-tissue expression data from multiple tissues to identify eQTLs and increase the number of eGenes. Bioinformatics, 2017, 33, i67-i74.	1.8	21
28	MergeReference: A Tool for Merging Reference Panels for HLA Imputation. Genomics and Informatics, 2017, 15, 108-111.	0.4	5
29	Comparison of Two Meta-Analysis Methods: Inverse-Variance-Weighted Average and Weighted Sum of Z-Scores. Genomics and Informatics, 2016, 14, 173.	0.4	147
30	ForestPMPlot: A Flexible Tool for Visualizing Heterogeneity Between Studies in Meta-analysis. G3: Genes, Genomes, Genetics, 2016, 6, 1793-1798.	0.8	30
31	Generation and molecular characterization of pancreatic cancer patient-derived xenografts reveals their heterologous nature. Oncotarget, 2016, 7, 62533-62546.	0.8	46
32	Using genomic annotations increases statistical power to detect eGenes. Bioinformatics, 2016, 32, i156-i163.	1.8	14
33	A method to decipher pleiotropy by detecting underlying heterogeneity driven by hidden subgroups applied to autoimmune and neuropsychiatric diseases. Nature Genetics, 2016, 48, 803-810.	9.4	62
34	A general framework for meta-analyzing dependent studies with overlapping subjects in association mapping. Human Molecular Genetics, 2016, 25, 1857-1866.	1.4	42
35	Identification of Loci at 1q21 and 16q23 That Affect Susceptibility to Inflammatory Bowel Disease in Koreans. Gastroenterology, 2016, 151, 1096-1099.e4.	0.6	30
36	Discovering Single Nucleotide Polymorphisms Regulating Human Gene Expression Using Allele Specific Expression from RNA-seq Data. Genetics, 2016, 204, 1057-1064.	1.2	17

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37	Multiple testing correction in linear mixed models. Genome Biology, 2016, 17, 62.	3.8	72
38	Imputing Phenotypes for Genome-wide Association Studies. American Journal of Human Genetics, 2016, 99, 89-103.	2.6	40
39	Loci associated with ischaemic stroke and its subtypes (SiGN): a genome-wide association study. Lancet Neurology, The, 2016, 15, 174-184.	4.9	217
40	Analysis of five chronic inflammatory diseases identifies 27 new associations and highlights disease-specific patterns at shared loci. Nature Genetics, 2016, 48, 510-518.	9.4	617
41	Investigating the Causal Relationship of C-Reactive Protein with 32 Complex Somatic and Psychiatric Outcomes: A Large-Scale Cross-Consortium Mendelian Randomization Study. PLoS Medicine, 2016, 13, e1001976.	3.9	150
42	Disentangling the Effects of Colocalizing Genomic Annotations to Functionally Prioritize Non-coding Variants within Complex-Trait Loci. American Journal of Human Genetics, 2015, 97, 139-152.	2.6	122
43	Accurate and Fast Multiple-Testing Correction in eQTL Studies. American Journal of Human Genetics, 2015, 96, 857-868.	2.6	25
44	HLA-DRB1*11and variants of the MHC class II locus are strong risk factors for systemic juvenile idiopathic arthritis. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 15970-15975.	3.3	139
45	Additive and interaction effects at three amino acid positions in HLA-DQ and HLA-DR molecules drive type 1 diabetes risk. Nature Genetics, 2015, 47, 898-905.	9.4	235
46	Association of HLA-DRB1 Haplotypes With Rheumatoid Arthritis Severity, Mortality, and Treatment Response. JAMA - Journal of the American Medical Association, 2015, 313, 1645.	3.8	119
47	A weighted genetic risk score using all known susceptibility variants to estimate rheumatoid arthritis risk. Annals of the Rheumatic Diseases, 2015, 74, 170-176.	0.5	55
48	Widespread non-additive and interaction effects within HLA loci modulate the risk of autoimmune diseases. Nature Genetics, 2015, 47, 1085-1090.	9.4	164
49	Association of HLA Genotype and Fulminant Type 1 Diabetes in Koreans. Genomics and Informatics, 2015, 13, 126.	0.4	14
50	The HLA-DRÎ²1 amino acid positions 11â€“13â€“26 explain the majority of SLEâ€“MHC associations. Nature Communications, 2014, 5, 5902.	5.8	80
51	Meta-Analysis Identifies Gene-by-Environment Interactions as Demonstrated in a Study of 4,965 Mice. PLoS Genetics, 2014, 10, e1004022.	1.5	46
52	Variation at HLA-DRB1 is associated with resistance to enteric fever. Nature Genetics, 2014, 46, 1333-1336.	9.4	85
53	Risk for ACPA-positive rheumatoid arthritis is driven by shared HLA amino acid polymorphisms in Asian and European populations. Human Molecular Genetics, 2014, 23, 6916-6926.	1.4	135
54	Fine Mapping Major Histocompatibility Complex Associations in Psoriasis and Its Clinical Subtypes. American Journal of Human Genetics, 2014, 95, 162-172.	2.6	182

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55	Fine Mapping Seronegative and Seropositive Rheumatoid Arthritis to Shared and Distinct HLA Alleles by Adjusting for the Effects of Heterogeneity. American Journal of Human Genetics, 2014, 94, 522-532.	2.6	156
56	Fast pairwise IBD association testing in genome-wide association studies. Bioinformatics, 2014, 30, 206-213.	1.8	5
57	Chromatin marks identify critical cell types for fine mapping complex trait variants. Nature Genetics, 2013, 45, 124-130.	9.4	553
58	Rare Variant Association Testing Under Low-Coverage Sequencing. Genetics, 2013, 194, 769-779.	1.2	13
59	Effectively Identifying eQTLs from Multiple Tissues by Combining Mixed Model and Meta-analytic Approaches. PLoS Genetics, 2013, 9, e1003491.	1.5	109
60	IPED: Inheritance Path-based Pedigree Reconstruction Algorithm Using Genotype Data. Journal of Computational Biology, 2013, 20, 780-791.	0.8	13
61	Application of user-guided automated cytometric data analysis to large-scale immunoprofiling of invariant natural killer T cells. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 19030-19035.	3.3	16
62	Hap-seq: An Optimal Algorithm for Haplotype Phasing with Imputation Using Sequencing Data. Journal of Computational Biology, 2013, 20, 80-92.	0.8	18
63	Imputing Amino Acid Polymorphisms in Human Leukocyte Antigens. PLoS ONE, 2013, 8, e64683.	1.1	538
64	Interpreting Meta-Analyses of Genome-Wide Association Studies. PLoS Genetics, 2012, 8, e1002555.	1.5	171
65	Random-Effects Model Aimed at Discovering Associations in Meta-Analysis of Genome-wide Association Studies. American Journal of Human Genetics, 2011, 88, 586-598.	2.6	515
66	Postassociation cleaning using linkage disequilibrium information. Genetic Epidemiology, 2011, 35, 1-10.	0.6	20
67	Increasing Power of Groupwise Association Test with Likelihood Ratio Test. Journal of Computational Biology, 2011, 18, 1611-1624.	0.8	14
68	An Optimal Weighted Aggregated Association Test for Identification of Rare Variants Involved in Common Diseases. Genetics, 2011, 188, 181-188.	1.2	43
69	Fine Mapping in 94 Inbred Mouse Strains Using a High-Density Haplotype Resource. Genetics, 2010, 185, 1081-1095.	1.2	95
70	Rapid and Accurate Multiple Testing Correction and Power Estimation for Millions of Correlated Markers. PLoS Genetics, 2009, 5, e1000456.	1.5	157
71	Structural Alignment of Pseudoknotted RNA. Journal of Computational Biology, 2008, 15, 489-504.	0.8	32