Buhm Han

List of Publications by Year
in descending order

71 papers	5,981 citations	136950 32 h-index	95266 68 g-index
77 all docs	77 docs citations	77 times ranked	14652 citing authors

#	Article	IF	Citations
1	Analysis of five chronic inflammatory diseases identifies 27 new associations and highlights disease-specific patterns at shared loci. Nature Genetics, 2016, 48, 510-518.	21.4	617
2	Chromatin marks identify critical cell types for fine mapping complex trait variants. Nature Genetics, 2013, 45, 124-130.	21.4	553
3	Imputing Amino Acid Polymorphisms in Human Leukocyte Antigens. PLoS ONE, 2013, 8, e64683.	2.5	538
4	Random-Effects Model Aimed at Discovering Associations in Meta-Analysis of Genome-wide Association Studies. American Journal of Human Genetics, 2011, 88, 586-598.	6.2	515
5	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.	21.4	235
6	Loci associated with ischaemic stroke and its subtypes (SiGN): a genome-wide association study. Lancet Neurology, The, 2016, 15, 174-184.	10.2	217
7	Exosomal PD-L1 promotes tumor growth through immune escape in non-small cell lung cancer. Experimental and Molecular Medicine, 2019, 51, 1-13.	7.7	194
8	Fine Mapping Major Histocompatibility Complex Associations in Psoriasis and Its Clinical Subtypes. American Journal of Human Genetics, 2014, 95, 162-172.	6.2	182
9	Interpreting Meta-Analyses of Genome-Wide Association Studies. PLoS Genetics, 2012, 8, e1002555.	3.5	171
10	Widespread non-additive and interaction effects within HLA loci modulate the risk of autoimmune diseases. Nature Genetics, 2015, 47, 1085-1090.	21.4	164
11	Rapid and Accurate Multiple Testing Correction and Power Estimation for Millions of Correlated Markers. PLoS Genetics, 2009, 5, e1000456.	3.5	157
12	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.	6.2	156
13	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.	8.4	150
14	Comparison of Two Meta-Analysis Methods: Inverse-Variance-Weighted Average and Weighted Sum of Z-Scores. Genomics and Informatics, 2016, 14, 173.	0.8	147
15	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.	7.1	139
16	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.	2.9	135
17	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.	6.2	122
18	Association of HLA-DRB1 Haplotypes With Rheumatoid Arthritis Severity, Mortality, and Treatment Response. JAMA - Journal of the American Medical Association, 2015, 313, 1645.	7.4	119

#	Article	IF	Citations
19	Effectively Identifying eQTLs from Multiple Tissues by Combining Mixed Model and Meta-analytic Approaches. PLoS Genetics, 2013, 9, e1003491.	3.5	109
20	Fine Mapping in 94 Inbred Mouse Strains Using a High-Density Haplotype Resource. Genetics, 2010, 185, 1081-1095.	2.9	95
21	Variation at HLA-DRB1 is associated with resistance to enteric fever. Nature Genetics, 2014, 46, 1333-1336.	21.4	85
22	The HLA-DRÎ²1 amino acid positions 11â€“13â€“26 explain the majority of SLEâ€“MHC associations. Nature Communications, 2014, 5, 5902.	12.8	80
23	Multiple testing correction in linear mixed models. Genome Biology, 2016, 17, 62.	8.8	72
24	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.	21.4	69
25	Cross-disorder analysis of schizophrenia and 19 immune-mediated diseases identifies shared genetic risk. Human Molecular Genetics, 2019, 28, 3498-3513.	2.9	65
26	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.	21.4	62
27	A weighted genetic risk score using all known susceptibility variants to estimate rheumatoid arthritis risk. Annals of the Rheumatic Diseases, 2015, 74, 170-176.	0.9	55
28	Meta-Analysis Identifies Gene-by-Environment Interactions as Demonstrated in a Study of 4,965 Mice. PLoS Genetics, 2014, 10, e1004022.	3.5	46
29	Generation and molecular characterization of pancreatic cancer patient-derived xenografts reveals their heterologous nature. Oncotarget, 2016, 7, 62533-62546.	1.8	46
30	An Optimal Weighted Aggregated Association Test for Identification of Rare Variants Involved in Common Diseases. Genetics, 2011, 188, 181-188.	2.9	43
31	A general framework for meta-analyzing dependent studies with overlapping subjects in association mapping. Human Molecular Genetics, 2016, 25, 1857-1866.	2.9	42
32	Imputing Phenotypes for Genome-wide Association Studies. American Journal of Human Genetics, 2016, 99, 89-103.	6.2	40
33	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.	1.3	38
34	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.	3.3	36
35	Structural Alignment of Pseudoknotted RNA. Journal of Computational Biology, 2008, 15, 489-504.	1.6	32
36	ForestPMPlot: A Flexible Tool for Visualizing Heterogeneity Between Studies in Meta-analysis. G3: Genes, Genomes, Genetics, 2016, 6, 1793-1798.	1.8	30

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37	Identification of Loci at 1q21 and 16q23 That Affect Susceptibility to Inflammatory Bowel Disease in Koreans. Gastroenterology, 2016, 151, 1096-1099.e4.	1.3	30
38	Accurate and Fast Multiple-Testing Correction in eQTL Studies. American Journal of Human Genetics, 2015, 96, 857-868.	6.2	25
39	PLEIO: a method to map and interpret pleiotropic loci with GWAS summary statistics. American Journal of Human Genetics, 2021, 108, 36-48.	6.2	22
40	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.	4.1	21
41	Accurate imputation of human leukocyte antigens with CookHLA. Nature Communications, 2021, 12, 1264.	12.8	21
42	Postassociation cleaning using linkage disequilibrium information. Genetic Epidemiology, 2011, 35, 1-10.	1.3	20
43	Amino acid position 37 of HLA-DRÎ²1 affects susceptibility to Crohnâ€™s disease in Asians. Human Molecular Genetics, 2018, 27, 3901-3910.	2.9	19
44	Hap-seq: An Optimal Algorithm for Haplotype Phasing with Imputation Using Sequencing Data. Journal of Computational Biology, 2013, 20, 80-92.	1.6	18
45	Discovering Single Nucleotide Polymorphisms Regulating Human Gene Expression Using Allele Specific Expression from RNA-seq Data. Genetics, 2016, 204, 1057-1064.	2.9	17
46	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.	7.1	16
47	Clinically Applicable Deep Learning Algorithm Using Quantitative Proteomic Data. Journal of Proteome Research, 2019, 18, 3195-3202.	3.7	16
48	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.	2.3	15
49	Increasing Power of Groupwise Association Test with Likelihood Ratio Test. Journal of Computational Biology, 2011, 18, 1611-1624.	1.6	14
50	Using genomic annotations increases statistical power to detect eGenes. Bioinformatics, 2016, 32, i156-i163.	4.1	14
51	Association of HLA Genotype and Fulminant Type 1 Diabetes in Koreans. Genomics and Informatics, 2015, 13, 126.	0.8	14
52	Rare Variant Association Testing Under Low-Coverage Sequencing. Genetics, 2013, 194, 769-779.	2.9	13
53	IPED: Inheritance Path-based Pedigree Reconstruction Algorithm Using Genotype Data. Journal of Computational Biology, 2013, 20, 780-791.	1.6	13
54	HATK: HLA analysis toolkit. Bioinformatics, 2021, 37, 416-418.	4.1	13

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55	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.	1.3	13
56	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.	1.3	12
57	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.	1.3	9
58	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.	14.5	8
59	Association of CDKN2A/CDKN2B with inflammatory bowel disease in Koreans. Journal of Gastroenterology and Hepatology (Australia), 2018, 33, 887-893.	2.8	7
60	Rare variants regulate expression of nearby individual genes in multiple tissues. PLoS Genetics, 2021, 17, e1009596.	3.5	6
61	Fast pairwise IBD association testing in genome-wide association studies. Bioinformatics, 2014, 30, 206-213.	4.1	5
62	An Association Mapping Framework To Account for Potential Sex Difference in Genetic Architectures. Genetics, 2018, 209, 685-698.	2.9	5
63	MergeReference: A Tool for Merging Reference Panels for HLA Imputation. Genomics and Informatics, 2017, 15, 108-111.	0.8	5
64	Identification of shared loci associated with both Crohnâ€™s disease and leprosy in East Asians. Human Molecular Genetics, 2022, 31, 3934-3944.	2.9	5
65	Genomic GPS: using genetic distance from individuals to public data for genomic analysis without disclosing personal genomes. Genome Biology, 2019, 20, 175.	8.8	4
66	FOLD: a method to optimize power in meta-analysis of genetic association studies with overlapping subjects. Bioinformatics, 2017, 33, 3947-3954.	4.1	3
67	Effects of smoking on the association of human leukocyte antigen with ulcerative colitis. Journal of Gastroenterology and Hepatology (Australia), 2019, 34, 1777-1783.	2.8	2
68	Phenome-wide association study of the major histocompatibility complex region in the Korean population identifies novel association signals. Human Molecular Genetics, 2022, , .	2.9	1
69	A theory-based practical solution to correct for sex-differential participation bias. Genome Biology, 2022, 23, .	8.8	1
70	Analysis of differences in human leukocyte antigen between the two Wellcome Trust Case Control Consortium control datasets. Genomics and Informatics, 2019, 17, e29.	0.8	0
71	Exploration of errors in variance caused by using the first-order approximation in Mendelian randomization. Genomics and Informatics, 2022, 20, e9.	0.8	0