

Buhm Han

List of Publications by Year in descending order

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Version: 2024-02-01

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	Analysis of five chronic inflammatory diseases identifies 27 new associations and highlights disease-specific patterns at shared loci. <i>Nature Genetics</i> , 2016, 48, 510-518.	9.4	617
2	Chromatin marks identify critical cell types for fine mapping complex trait variants. <i>Nature Genetics</i> , 2013, 45, 124-130.	9.4	553
3	Imputing Amino Acid Polymorphisms in Human Leukocyte Antigens. <i>PLoS ONE</i> , 2013, 8, e64683.	1.1	538
4	Random-Effects Model Aimed at Discovering Associations in Meta-Analysis of Genome-wide Association Studies. <i>American Journal of Human Genetics</i> , 2011, 88, 586-598.	2.6	515
5	Additive and interaction effects at three amino acid positions in HLA-DQ and HLA-DR molecules drive type 1 diabetes risk. <i>Nature Genetics</i> , 2015, 47, 898-905.	9.4	235
6	Loci associated with ischaemic stroke and its subtypes (SiGN): a genome-wide association study. <i>Lancet Neurology</i> , The, 2016, 15, 174-184.	4.9	217
7	Exosomal PD-L1 promotes tumor growth through immune escape in non-small cell lung cancer. <i>Experimental and Molecular Medicine</i> , 2019, 51, 1-13.	3.2	194
8	Fine Mapping Major Histocompatibility Complex Associations in Psoriasis and Its Clinical Subtypes. <i>American Journal of Human Genetics</i> , 2014, 95, 162-172.	2.6	182
9	Interpreting Meta-Analyses of Genome-Wide Association Studies. <i>PLoS Genetics</i> , 2012, 8, e1002555.	1.5	171
10	Widespread non-additive and interaction effects within HLA loci modulate the risk of autoimmune diseases. <i>Nature Genetics</i> , 2015, 47, 1085-1090.	9.4	164
11	Rapid and Accurate Multiple Testing Correction and Power Estimation for Millions of Correlated Markers. <i>PLoS Genetics</i> , 2009, 5, e1000456.	1.5	157
12	Fine Mapping Seronegative and Seropositive Rheumatoid Arthritis to Shared and Distinct HLA Alleles by Adjusting for the Effects of Heterogeneity. <i>American Journal of Human Genetics</i> , 2014, 94, 522-532.	2.6	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. <i>PLoS Medicine</i> , 2016, 13, e1001976.	3.9	150
14	Comparison of Two Meta-Analysis Methods: Inverse-Variance-Weighted Average and Weighted Sum of Z-Scores. <i>Genomics and Informatics</i> , 2016, 14, 173.	0.4	147
15	<i>H</i> LA-DRB1*11 and variants of the MHC class II locus are strong risk factors for systemic juvenile idiopathic arthritis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 15970-15975.	3.3	139
16	Risk for ACPA-positive rheumatoid arthritis is driven by shared HLA amino acid polymorphisms in Asian and European populations. <i>Human Molecular Genetics</i> , 2014, 23, 6916-6926.	1.4	135
17	Disentangling the Effects of Colocalizing Genomic Annotations to Functionally Prioritize Non-coding Variants within Complex-Trait Loci. <i>American Journal of Human Genetics</i> , 2015, 97, 139-152.	2.6	122
18	Association of HLA-DRB1 Haplotypes With Rheumatoid Arthritis Severity, Mortality, and Treatment Response. <i>JAMA - Journal of the American Medical Association</i> , 2015, 313, 1645.	3.8	119

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19	Effectively Identifying eQTLs from Multiple Tissues by Combining Mixed Model and Meta-analytic Approaches. <i>PLoS Genetics</i> , 2013, 9, e1003491.	1.5	109
20	Fine Mapping in 94 Inbred Mouse Strains Using a High-Density Haplotype Resource. <i>Genetics</i> , 2010, 185, 1081-1095.	1.2	95
21	Variation at HLA-DRB1 is associated with resistance to enteric fever. <i>Nature Genetics</i> , 2014, 46, 1333-1336.	9.4	85
22	The HLA-DR β 1 amino acid positions 11-13-26 explain the majority of SLE-MHC associations. <i>Nature Communications</i> , 2014, 5, 5902.	5.8	80
23	Multiple testing correction in linear mixed models. <i>Genome Biology</i> , 2016, 17, 62.	3.8	72
24	A high-resolution HLA reference panel capturing global population diversity enables multi-ancestry fine-mapping in HIV host response. <i>Nature Genetics</i> , 2021, 53, 1504-1516.	9.4	69
25	Cross-disorder analysis of schizophrenia and 19 immune-mediated diseases identifies shared genetic risk. <i>Human Molecular Genetics</i> , 2019, 28, 3498-3513.	1.4	65
26	A method to decipher pleiotropy by detecting underlying heterogeneity driven by hidden subgroups applied to autoimmune and neuropsychiatric diseases. <i>Nature Genetics</i> , 2016, 48, 803-810.	9.4	62
27	A weighted genetic risk score using all known susceptibility variants to estimate rheumatoid arthritis risk. <i>Annals of the Rheumatic Diseases</i> , 2015, 74, 170-176.	0.5	55
28	Meta-Analysis Identifies Gene-by-Environment Interactions as Demonstrated in a Study of 4,965 Mice. <i>PLoS Genetics</i> , 2014, 10, e1004022.	1.5	46
29	Generation and molecular characterization of pancreatic cancer patient-derived xenografts reveals their heterologous nature. <i>Oncotarget</i> , 2016, 7, 62533-62546.	0.8	46
30	An Optimal Weighted Aggregated Association Test for Identification of Rare Variants Involved in Common Diseases. <i>Genetics</i> , 2011, 188, 181-188.	1.2	43
31	A general framework for meta-analyzing dependent studies with overlapping subjects in association mapping. <i>Human Molecular Genetics</i> , 2016, 25, 1857-1866.	1.4	42
32	Imputing Phenotypes for Genome-wide Association Studies. <i>American Journal of Human Genetics</i> , 2016, 99, 89-103.	2.6	40
33	ImmunoChIP Meta-Analysis of Inflammatory Bowel Disease Identifies Three Novel Loci and Four Novel Associations in Previously Reported Loci. <i>Journal of Crohn's and Colitis</i> , 2018, 12, 730-741.	0.6	38
34	Prognostic value of the association between MHC class I downregulation and PD-L1 upregulation in head and neck squamous cell carcinoma patients. <i>Scientific Reports</i> , 2019, 9, 7680.	1.6	36
35	Structural Alignment of Pseudoknotted RNA. <i>Journal of Computational Biology</i> , 2008, 15, 489-504.	0.8	32
36	ForestPMPlot: A Flexible Tool for Visualizing Heterogeneity Between Studies in Meta-analysis. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1793-1798.	0.8	30

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37	Identification of Loci at 1q21 and 16q23 That Affect Susceptibility to Inflammatory Bowel Disease in Koreans. <i>Gastroenterology</i> , 2016, 151, 1096-1099.e4.	0.6	30
38	Accurate and Fast Multiple-Testing Correction in eQTL Studies. <i>American Journal of Human Genetics</i> , 2015, 96, 857-868.	2.6	25
39	PLEIO: a method to map and interpret pleiotropic loci with GWAS summary statistics. <i>American Journal of Human Genetics</i> , 2021, 108, 36-48.	2.6	22
40	Applying meta-analysis to genotype-tissue expression data from multiple tissues to identify eQTLs and increase the number of eGenes. <i>Bioinformatics</i> , 2017, 33, i67-i74.	1.8	21
41	Accurate imputation of human leukocyte antigens with CookHLA. <i>Nature Communications</i> , 2021, 12, 1264.	5.8	21
42	Postassociation cleaning using linkage disequilibrium information. <i>Genetic Epidemiology</i> , 2011, 35, 1-10.	0.6	20
43	Amino acid position 37 of HLA-DR ¹ affects susceptibility to Crohn's disease in Asians. <i>Human Molecular Genetics</i> , 2018, 27, 3901-3910.	1.4	19
44	Hap-seq: An Optimal Algorithm for Haplotype Phasing with Imputation Using Sequencing Data. <i>Journal of Computational Biology</i> , 2013, 20, 80-92.	0.8	18
45	Discovering Single Nucleotide Polymorphisms Regulating Human Gene Expression Using Allele Specific Expression from RNA-seq Data. <i>Genetics</i> , 2016, 204, 1057-1064.	1.2	17
46	Application of user-guided automated cytometric data analysis to large-scale immunoprofiling of invariant natural killer T cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 19030-19035.	3.3	16
47	Clinically Applicable Deep Learning Algorithm Using Quantitative Proteomic Data. <i>Journal of Proteome Research</i> , 2019, 18, 3195-3202.	1.8	16
48	Expression Quantitative Trait Loci (eQTL) Mapping in Korean Patients With Crohn's Disease and Identification of Potential Causal Genes Through Integration With Disease Associations. <i>Frontiers in Genetics</i> , 2020, 11, 486.	1.1	15
49	Increasing Power of Groupwise Association Test with Likelihood Ratio Test. <i>Journal of Computational Biology</i> , 2011, 18, 1611-1624.	0.8	14
50	Using genomic annotations increases statistical power to detect eGenes. <i>Bioinformatics</i> , 2016, 32, i156-i163.	1.8	14
51	Association of HLA Genotype and Fulminant Type 1 Diabetes in Koreans. <i>Genomics and Informatics</i> , 2015, 13, 126.	0.4	14
52	Rare Variant Association Testing Under Low-Coverage Sequencing. <i>Genetics</i> , 2013, 194, 769-779.	1.2	13
53	IPED: Inheritance Path-based Pedigree Reconstruction Algorithm Using Genotype Data. <i>Journal of Computational Biology</i> , 2013, 20, 780-791.	0.8	13
54	HATK: HLA analysis toolkit. <i>Bioinformatics</i> , 2021, 37, 416-418.	1.8	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. <i>Journal of Crohn's and Colitis</i> , 2021, 15, 1898-1907.	0.6	13
56	An Intergenic Variant rs9268877 Between HLA-DRA and HLA-DRB Contributes to the Clinical Course and Long-term Outcome of Ulcerative Colitis. <i>Journal of Crohn's and Colitis</i> , 2018, 12, 1113-1121.	0.6	12
57	X Chromosome-wide Association Study Identifies a Susceptibility Locus for Inflammatory Bowel Disease in Koreans. <i>Journal of Crohn's and Colitis</i> , 2017, 11, 820-830.	0.6	9
58	MarcoPolo: a method to discover differentially expressed genes in single-cell RNA-seq data without depending on prior clustering. <i>Nucleic Acids Research</i> , 2022, 50, e71-e71.	6.5	8
59	Association of <i>CDKN2A/CDKN2B</i> with inflammatory bowel disease in Koreans. <i>Journal of Gastroenterology and Hepatology (Australia)</i> , 2018, 33, 887-893.	1.4	7
60	Rare variants regulate expression of nearby individual genes in multiple tissues. <i>PLoS Genetics</i> , 2021, 17, e1009596.	1.5	6
61	Fast pairwise IBD association testing in genome-wide association studies. <i>Bioinformatics</i> , 2014, 30, 206-213.	1.8	5
62	An Association Mapping Framework To Account for Potential Sex Difference in Genetic Architectures. <i>Genetics</i> , 2018, 209, 685-698.	1.2	5
63	MergeReference: A Tool for Merging Reference Panels for HLA Imputation. <i>Genomics and Informatics</i> , 2017, 15, 108-111.	0.4	5
64	Identification of shared loci associated with both Crohn's disease and leprosy in East Asians. <i>Human Molecular Genetics</i> , 2022, 31, 3934-3944.	1.4	5
65	Genomic GPS: using genetic distance from individuals to public data for genomic analysis without disclosing personal genomes. <i>Genome Biology</i> , 2019, 20, 175.	3.8	4
66	FOLD: a method to optimize power in meta-analysis of genetic association studies with overlapping subjects. <i>Bioinformatics</i> , 2017, 33, 3947-3954.	1.8	3
67	Effects of smoking on the association of human leukocyte antigen with ulcerative colitis. <i>Journal of Gastroenterology and Hepatology (Australia)</i> , 2019, 34, 1777-1783.	1.4	2
68	Phenome-wide association study of the major histocompatibility complex region in the Korean population identifies novel association signals. <i>Human Molecular Genetics</i> , 2022, , .	1.4	1
69	A theory-based practical solution to correct for sex-differential participation bias. <i>Genome Biology</i> , 2022, 23, .	3.8	1
70	Analysis of differences in human leukocyte antigen between the two Wellcome Trust Case Control Consortium control datasets. <i>Genomics and Informatics</i> , 2019, 17, e29.	0.4	0
71	Exploration of errors in variance caused by using the first-order approximation in Mendelian randomization. <i>Genomics and Informatics</i> , 2022, 20, e9.	0.4	0