

Jae Hoon Sul

List of Publications by Year in descending order

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Version: 2024-02-01

24
papers

1,607
citations

686830

13
h-index

713013

21
g-index

25
all docs

25
docs citations

25
times ranked

4922
citing authors

#	ARTICLE	IF	CITATIONS
1	Accurate diagnosis of atopic dermatitis by combining transcriptome and microbiota data with supervised machine learning. <i>Scientific Reports</i> , 2022, 12, 290.	1.6	12
2	xGAP: a python based efficient, modular, extensible and fault tolerant genomic analysis pipeline for variant discovery. <i>Bioinformatics</i> , 2021, 37, 9-16.	1.8	0
3	Purifying selection on noncoding deletions of human regulatory loci detected using their cellular pleiotropy. <i>Genome Research</i> , 2021, 31, 935-946.	2.4	5
4	Rare variants regulate expression of nearby individual genes in multiple tissues. <i>PLoS Genetics</i> , 2021, 17, e1009596.	1.5	6
5	Rare variants in the endocytic pathway are associated with Alzheimer's disease, its related phenotypes, and functional consequences. <i>PLoS Genetics</i> , 2021, 17, e1009772.	1.5	1
6	Contribution of common and rare variants to bipolar disorder susceptibility in extended pedigrees from population isolates. <i>Translational Psychiatry</i> , 2020, 10, 74.	2.4	25
7	Variant calling and quality control of large-scale human genome sequencing data. <i>Emerging Topics in Life Sciences</i> , 2019, 3, 399-409.	1.1	1
8	Interrogating the Genetic Determinants of Tourette's Syndrome and Other Tic Disorders Through Genome-Wide Association Studies. <i>American Journal of Psychiatry</i> , 2019, 176, 217-227.	4.0	242
9	ForestQC: Quality control on genetic variants from next-generation sequencing data using random forest. <i>PLoS Computational Biology</i> , 2019, 15, e1007556.	1.5	17
10	Leveraging allelic imbalance to refine fine-mapping for eQTL studies. <i>PLoS Genetics</i> , 2019, 15, e1008481.	1.5	20
11	Multiethnic Meta-Analysis Identifies <i>RAI1</i> as a Possible Obstructive Sleep Apnea-related Quantitative Trait Locus in Men. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2018, 58, 391-401.	1.4	65
12	Population structure in genetic studies: Confounding factors and mixed models. <i>PLoS Genetics</i> , 2018, 14, e1007309.	1.5	164
13	Understanding the Hidden Complexity of Latin American Population Isolates. <i>American Journal of Human Genetics</i> , 2018, 103, 707-726.	2.6	48
14	Negative selection in humans and fruit flies involves synergistic epistasis. <i>Science</i> , 2017, 356, 539-542.	6.0	103
15	Rare Copy Number Variants in <i>NRXN1</i> and <i>CNTN6</i> Increase Risk for Tourette Syndrome. <i>Neuron</i> , 2017, 94, 1101-1111.e7.	3.8	137
16	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
17	Accounting for Population Structure in Gene-by-Environment Interactions in Genome-Wide Association Studies Using Mixed Models. <i>PLoS Genetics</i> , 2016, 12, e1005849.	1.5	61
18	A genome-wide association analysis of chromosomal aberrations and Hirschsprung disease. <i>Translational Research</i> , 2016, 177, 31-40.e6.	2.2	10

#	ARTICLE	IF	CITATIONS
19	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
20	Increasing Generality and Power of Rare-Variant Tests by Utilizing Extended Pedigrees. <i>American Journal of Human Genetics</i> , 2016, 99, 846-859.	2.6	26
21	Colocalization of GWAS and eQTL Signals Detects Target Genes. <i>American Journal of Human Genetics</i> , 2016, 99, 1245-1260.	2.6	569
22	An efficient linear mixed model framework for meta-analytic association studies across multiple contexts. <i>Leibniz International Proceedings in Informatics, LIPIcs</i> , 2016, 2016, .	0.0	0
23	Accurate and Fast Multiple-Testing Correction in eQTL Studies. <i>American Journal of Human Genetics</i> , 2015, 96, 857-868.	2.6	25
24	Gene-Gene Interactions Detection Using a Two-stage Model. <i>Journal of Computational Biology</i> , 2015, 22, 563-576.	0.8	5