

Eun Yong Kang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11607979/publications.pdf>

Version: 2024-02-01

21
papers

1,406
citations

623188

14
h-index

713013

21
g-index

23
all docs

23
docs citations

23
times ranked

4292
citing authors

#	ARTICLE	IF	CITATIONS
1	Profiling allele-specific gene expression in brains from individuals with autism spectrum disorder reveals preferential minor allele usage. <i>Nature Neuroscience</i> , 2019, 22, 1521-1532.	7.1	28
2	An ancestry-based approach for detecting interactions. <i>Genetic Epidemiology</i> , 2018, 42, 49-63.	0.6	17
3	An Association Mapping Framework To Account for Potential Sex Difference in Genetic Architectures. <i>Genetics</i> , 2018, 209, 685-698.	1.2	5
4	Multidimensional Genetic Analysis of Repeated Seizures in the Hybrid Mouse Diversity Panel Reveals a Novel Epileptogenesis Susceptibility Locus. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2545-2558.	0.8	13
5	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
6	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
7	The Genetic Basis of Host Preference and Resting Behavior in the Major African Malaria Vector, <i>Anopheles arabiensis</i> . <i>PLoS Genetics</i> , 2016, 12, e1006303.	1.5	76
8	Efficient and Accurate Multiple-Phenotype Regression Method for High Dimensional Data Considering Population Structure. <i>Genetics</i> , 2016, 204, 1379-1390.	1.2	26
9	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
10	Imputing Phenotypes for Genome-wide Association Studies. <i>American Journal of Human Genetics</i> , 2016, 99, 89-103.	2.6	40
11	Genetic and environmental control of host-gut microbiota interactions. <i>Genome Research</i> , 2015, 25, 1558-1569.	2.4	288
12	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
13	Genome-Wide Association Study for Age-Related Hearing Loss (AHL) in the Mouse: A Meta-Analysis. <i>JARO - Journal of the Association for Research in Otolaryngology</i> , 2014, 15, 335-352.	0.9	31
14	Identifying Causal Variants at Loci with Multiple Signals of Association. <i>Genetics</i> , 2014, 198, 497-508.	1.2	400
15	The benefits of selecting phenotype-specific variants for applications of mixed models in genomics. <i>Scientific Reports</i> , 2013, 3, 1815.	1.6	43
16	A powerful and efficient set test for genetic markers that handles confounders. <i>Bioinformatics</i> , 2013, 29, 1526-1533.	1.8	72
17	Hybrid mouse diversity panel: a panel of inbred mouse strains suitable for analysis of complex genetic traits. <i>Mammalian Genome</i> , 2012, 23, 680-692.	1.0	134
18	Increasing Association Mapping Power and Resolution in Mouse Genetic Studies Through the Use of Meta-Analysis for Structured Populations. <i>Genetics</i> , 2012, 191, 959-967.	1.2	14

#	ARTICLE	IF	CITATIONS
19	Fine Mapping in 94 Inbred Mouse Strains Using a High-Density Haplotype Resource. <i>Genetics</i> , 2010, 185, 1081-1095.	1.2	95
20	Detecting the Presence and Absence of Causal Relationships between Expression of Yeast Genes with Very Few Samples. <i>Journal of Computational Biology</i> , 2010, 17, 533-546.	0.8	8
21	Detecting the Presence and Absence of Causal Relationships between Expression of Yeast Genes with Very Few Samples. <i>Lecture Notes in Computer Science</i> , 2009, , 466-481.	1.0	2