

Donghyung Lee

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6634798/publications.pdf>

Version: 2024-02-01

13
papers

309
citations

1163117

8
h-index

1125743

13
g-index

14
all docs

14
docs citations

14
times ranked

1155
citing authors

#	ARTICLE	IF	CITATIONS
1	DIST: direct imputation of summary statistics for unmeasured SNPs. <i>Bioinformatics</i> , 2013, 29, 2925-2927.	4.1	75
2	A simple yet accurate correction for winner's curse can predict signals discovered in much larger genome scans. <i>Bioinformatics</i> , 2016, 32, 2598-2603.	4.1	44
3	Meta-analysis of Positive and Negative Symptoms Reveals Schizophrenia Modifier Genes: Table 1.. <i>Schizophrenia Bulletin</i> , 2016, 42, 279-287.	4.3	40
4	Tracing neuronal circuits in transgenic animals by transneuronal control of transcription (TRACT). <i>ELife</i> , 2017, 6, .	6.0	33
5	JEPEG: a summary statistics based tool for gene-level joint testing of functional variants. <i>Bioinformatics</i> , 2015, 31, 1176-1182.	4.1	27
6	DISTMIX: direct imputation of summary statistics for unmeasured SNPs from mixed ethnicity cohorts. <i>Bioinformatics</i> , 2015, 31, 3099-3104.	4.1	25
7	Genome-wide gene pathway analysis of psychotic illness symptom dimensions based on a new schizophrenia-specific model of the OPCRIT. <i>Schizophrenia Research</i> , 2015, 164, 181-186.	2.0	19
8	Methods to investigate the structure and connectivity of the nervous system. <i>Fly</i> , 2017, 11, 224-238.	1.7	15
9	JEPEGMIX: gene-level joint analysis of functional SNPs in cosmopolitan cohorts. <i>Bioinformatics</i> , 2016, 32, 295-297.	4.1	8
10	Detection of correlated hidden factors from single cell transcriptomes using Iteratively Adjusted-SVA (IA-SVA). <i>Scientific Reports</i> , 2018, 8, 17040.	3.3	8
11	V-SVA: an R Shiny application for detecting and annotating hidden sources of variation in single-cell RNA-seq data. <i>Bioinformatics</i> , 2020, 36, 3582-3584.	4.1	7
12	JEPEGMIX2: improved gene-level joint analysis of eQTLs in cosmopolitan cohorts. <i>Bioinformatics</i> , 2018, 34, 286-288.	4.1	6
13	Association Testing Strategy for Data from Dense Marker Panels. <i>PLoS ONE</i> , 2013, 8, e80540.	2.5	2