Donghyung Lee

List of Publications by Year in descending order

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1163117 1125743 13 309 8 13 citations h-index g-index papers 14 14 14 1155 docs citations times ranked citing authors all docs

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