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List of Publications by Year in descending order

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Version: 2024-02-01

12
papers

209
citations

1478505

6
h-index

1281871

11
g-index

14
all docs

14
docs citations

14
times ranked

350
citing authors

#	ARTICLE	IF	CITATIONS
1	Deconvolution of transcriptional networks identifies TCF4 as a master regulator in schizophrenia. <i>Science Advances</i> , 2019, 5, eaau4139.	10.3	59
2	Next-generation sequencing in drug development: target identification and genetically stratified clinical trials. <i>Drug Discovery Today</i> , 2018, 23, 1776-1783.	6.4	46
3	A hybrid fuzzy-ontology based intelligent system to determine level of severity and treatment recommendation for Benign Prostatic Hyperplasia. <i>Computer Methods and Programs in Biomedicine</i> , 2014, 113, 301-313.	4.7	29
4	Alpha-plane based automatic general type-2 fuzzy clustering based on simulated annealing meta-heuristic algorithm for analyzing gene expression data. <i>Computers in Biology and Medicine</i> , 2015, 64, 347-359.	7.0	24
5	The proteome and its dynamics: A missing piece for integrative multi-omics in schizophrenia. <i>Schizophrenia Research</i> , 2020, 217, 148-161.	2.0	16
6	Integrated analysis on transcriptome and behaviors defines HTT repeat-dependent network modules in Huntington's disease. <i>Genes and Diseases</i> , 2022, 9, 479-493.	3.4	9
7	Transcriptional network analysis on brains reveals a potential regulatory role of PPP1R3F in autism spectrum disorders. <i>BMC Research Notes</i> , 2018, 11, 489.	1.4	7
8	Sparse Pathway-Induced Dynamic Network Biomarker Discovery for Early Warning Signal Detection in Complex Diseases. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1028-1034.	3.0	6
9	Cell-Type-Specific Proteogenomic Signal Diffusion for Integrating Multi-Omics Data Predicts Novel Schizophrenia Risk Genes. <i>Patterns</i> , 2020, 1, 100091.	5.9	5
10	A computational method for direct imputation of cell type-specific expression profiles and cellular compositions from bulk-tissue RNA-Seq in brain disorders. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab056.	3.2	5
11	Cell Type-Specific Annotation and Fine Mapping of Variants Associated With Brain Disorders. <i>Frontiers in Genetics</i> , 2020, 11, 575928.	2.3	2
12	A two-stage meta-heuristic approach to general type-ii fuzzy clustering for microarray data analysis. , 2014, , .		1