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List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2206732/publications.pdf>

Version: 2024-02-01

14
papers

319
citations

1307594

7
h-index

1125743

13
g-index

17
all docs

17
docs citations

17
times ranked

601
citing authors

#	ARTICLE	IF	CITATIONS
1	shinyheatmap: Ultra fast low memory heatmap web interface for big data genomics. PLoS ONE, 2017, 12, e0176334.	2.5	112
2	HeatmapGenerator: high performance RNAseq and microarray visualization software suite to examine differential gene expression levels using an R and C++ hybrid computational pipeline. Source Code for Biology and Medicine, 2014, 9, 30.	1.7	50
3	Enhanced single-cell RNA-seq workflow reveals coronary artery disease cellular cross-talk and candidate drug targets. Atherosclerosis, 2022, 340, 12-22.	0.8	35
4	Ischemic Preconditioning Confers Epigenetic Repression of <i>Mtor</i> and Induction of Autophagy Through G9a-Dependent H3K9 Dimethylation. Journal of the American Heart Association, 2016, 5, .	3.7	32
5	Dysregulation of the histone demethylase KDM6B in alcohol dependence is associated with epigenetic regulation of inflammatory signaling pathways. Addiction Biology, 2021, 26, e12816.	2.6	28
6	Cardioinformatics: the nexus of bioinformatics and precision cardiology. Briefings in Bioinformatics, 2020, 21, 2031-2051.	6.5	15
7	MicroScope: ChIP-seq and RNA-seq software analysis suite for gene expression heatmaps. BMC Bioinformatics, 2016, 17, 390.	2.6	13
8	HeartBioPortal. Circulation Genomic and Precision Medicine, 2019, 12, e002426.	3.6	8
9	HeartBioPortal2.0: new developments and updates for genetic ancestry and cardiometabolic quantitative traits in diverse human populations. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	3.0	5
10	Targeting the cytoskeleton and extracellular matrix in cardiovascular disease drug discovery. Expert Opinion on Drug Discovery, 2022, 17, 443-460.	5.0	5
11	Gaussian-Distributed Codon Frequencies of Genomes. G3: Genes, Genomes, Genetics, 2019, 9, 1449-1456.	1.8	4
12	How the strengths of Lisp-family languages facilitate building complex and flexible bioinformatics applications. Briefings in Bioinformatics, 2016, 19, bbw130.	6.5	3
13	NERO: a biomedical named-entity (recognition) ontology with a large, annotated corpus reveals meaningful associations through text embedding. Npj Systems Biology and Applications, 2021, 7, 38.	3.0	3
14	Optimized functional annotation of ChIP-seq data. F1000Research, 0, 8, 612.	1.6	0