

Hao Chen

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7766889/publications.pdf>

Version: 2024-02-01

14
papers

3,152
citations

759233

12
h-index

1125743

13
g-index

15
all docs

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docs citations

15
times ranked

6349
citing authors

#	ARTICLE	IF	CITATIONS
1	The TREM2-APOE Pathway Drives the Transcriptional Phenotype of Dysfunctional Microglia in Neurodegenerative Diseases. <i>Immunity</i> , 2017, 47, 566-581.e9.	14.3	1,741
2	Unexpected role of interferon- β in regulating neuronal connectivity and social behaviour. <i>Nature</i> , 2016, 535, 425-429.	27.8	507
3	The Reference Genome of the Halophytic Plant <i>Eutrema salsugineum</i> . <i>Frontiers in Plant Science</i> , 2013, 4, 46.	3.6	198
4	Identification of piRNA Binding Sites Reveals the Argonaute Regulatory Landscape of the <i>C.Âelegans</i> Germline. <i>Cell</i> , 2018, 172, 937-951.e18.	28.9	189
5	Temporal patterns of gene expression in developing maize endosperm identified through transcriptome sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 7582-7587.	7.1	146
6	Dynamic Expression of Imprinted Genes Associates with Maternally Controlled Nutrient Allocation during Maize Endosperm Development. <i>Plant Cell</i> , 2013, 25, 3212-3227.	6.6	97
7	ZNFX-1 Functions within Perinuclear Nuage to Balance Epigenetic Signals. <i>Molecular Cell</i> , 2018, 70, 639-649.e6.	9.7	84
8	The prediction of protein-protein interaction networks in rice blast fungus. <i>BMC Genomics</i> , 2008, 9, 519.	2.8	77
9	pirScan: a webserver to predict piRNA targeting sites and to avoid transgene silencing in <i>C. elegans</i> . <i>Nucleic Acids Research</i> , 2018, 46, W43-W48.	14.5	41
10	CrusView: A Java-Based Visualization Platform for Comparative Genomics Analyses in Brassicaceae Species. <i>Plant Physiology</i> , 2013, 163, 354-362.	4.8	33
11	A systems level approach to temporal expression dynamics in <i>Drosophila</i> reveals clusters of long term memory genes. <i>PLoS Genetics</i> , 2017, 13, e1007054.	3.5	26
12	KGBassembler: a karyotype-based genome assembler for Brassicaceae species. <i>Bioinformatics</i> , 2012, 28, 3141-3143.	4.1	12
13	HiVis: a portable, scalable tool for hierarchical visualization and analysis of biological networks. <i>Applied Informatics</i> , 2018, 5, .	0.5	1
14	ZNFX-1 Engages Argonaute Proteins to Promote the Stable Inheritance of Epigenetic States in <i>C. Elegans</i> . <i>SSRN Electronic Journal</i> , 0, , .	0.4	0