

Ming Wen

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11388072/publications.pdf>

Version: 2024-02-01

15
papers

2,857
citations

623734

14
h-index

996975

15
g-index

16
all docs

16
docs citations

16
times ranked

6618
citing authors

#	ARTICLE	IF	CITATIONS
1	Kidney transplantation after rescue allocationâ€”meticulous selection yields the chance for excellent outcome. <i>Nephrology Dialysis Transplantation</i> , 2021, 36, 551-560.	0.7	5
2	Interferon Regulatory Factors IRF1 and IRF7 Directly Regulate Gene Expression in Bats in Response to Viral Infection. <i>Cell Reports</i> , 2020, 33, 108345.	6.4	41
3	Dampened NLRP3-mediated inflammation in bats and implications for a special viral reservoir host. <i>Nature Microbiology</i> , 2019, 4, 789-799.	13.3	245
4	Exploring the genome and transcriptome of the cave nectar bat <i>Eonycteris spelaea</i> with PacBio long-read sequencing. <i>GigaScience</i> , 2018, 7, .	6.4	33
5	Mapping the human DC lineage through the integration of high-dimensional techniques. <i>Science</i> , 2017, 356, .	12.6	429
6	An Evolutionary View of the Biogenesis and Function of Rice Small RNAs. <i>RNA Technologies</i> , 2017, , 69-88.	0.3	0
7	Proteomic analysis of ascending colon biopsies from a paediatric inflammatory bowel disease inception cohort identifies protein biomarkers that differentiate Crohn's disease from UC. <i>Gut</i> , 2017, 66, 1573-1583.	12.1	69
8	Small RNA transcriptomes of mangroves evolve adaptively in extreme environments. <i>Scientific Reports</i> , 2016, 6, 27551.	3.3	18
9	Expression Variations of miRNAs and mRNAs in Rice (<i>Oryza sativa</i>). <i>Genome Biology and Evolution</i> , 2016, 8, 3529-3544.	2.5	32
10	MetaPro-IQ: a universal metaproteomic approach to studying human and mouse gut microbiota. <i>Microbiome</i> , 2016, 4, 31.	11.1	154
11	Bottom-Up Proteomics (2013â€“2015): Keeping up in the Era of Systems Biology. <i>Analytical Chemistry</i> , 2016, 88, 95-121.	6.5	52
12	Specific adaptation of <i>Ustilaginoidea virens</i> in occupying host florets revealed by comparative and functional genomics. <i>Nature Communications</i> , 2014, 5, 3849.	12.8	202
13	miREvo: an integrative microRNA evolutionary analysis platform for next-generation sequencing experiments. <i>BMC Bioinformatics</i> , 2012, 13, 140.	2.6	468
14	Testing hypotheses on the rate of molecular evolution in relation to gene expression using microRNAs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 15942-15947.	7.1	22
15	The sequence and de novo assembly of the giant panda genome. <i>Nature</i> , 2010, 463, 311-317.	27.8	1,058