

Ravi K Patel

List of Publications by Year in descending order

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Version: 2024-02-01

18
papers

4,452
citations

840776

11
h-index

940533

16
g-index

21
all docs

21
docs citations

21
times ranked

6970
citing authors

#	ARTICLE	IF	CITATIONS
1	NGS QC Toolkit: A Toolkit for Quality Control of Next Generation Sequencing Data. PLoS ONE, 2012, 7, e30619.	2.5	2,732
2	De Novo Assembly of Chickpea Transcriptome Using Short Reads for Gene Discovery and Marker Identification. DNA Research, 2011, 18, 53-63.	3.4	406
3	Base-pair-resolution genome-wide mapping of active RNA polymerases using precision nuclear run-on (PRO-seq). Nature Protocols, 2016, 11, 1455-1476.	12.0	392
4	A draft genome sequence of the pulse crop chickpea (<i>Cicer arietinum</i>). Plant Journal, 2013, 74, 715-729.	5.7	382
5	Gene Discovery and Tissue-Specific Transcriptome Analysis in Chickpea with Massively Parallel Pyrosequencing and Web Resource Development. Plant Physiology, 2011, 156, 1661-1678.	4.8	213
6	Developmental Origin Governs CD8+ T Cell Fate Decisions during Infection. Cell, 2018, 174, 117-130.e14.	28.9	132
7	A widespread sequence-specific mRNA decay pathway mediated by hnRNPs A1 and A2/B1. Genes and Development, 2016, 30, 1070-1085.	5.9	46
8	CTDB: An Integrated Chickpea Transcriptome Database for Functional and Applied Genomics. PLoS ONE, 2015, 10, e0136880.	2.5	45
9	The Notch signaling pathway promotes basophil responses during helminth-induced type 2 inflammation. Journal of Experimental Medicine, 2019, 216, 1268-1279.	8.5	26
10	Robust partitioning of microRNA targets from downstream regulatory changes. Nucleic Acids Research, 2020, 48, 9724-9746.	14.5	18
11	CDK2 kinase activity is a regulator of male germ cell fate. Development (Cambridge), 2019, 146, .	2.5	15
12	Reproductive Long Intergenic Noncoding RNAs Exhibit Male Gamete Specificity and Polycomb Repressive Complex 2-Mediated Repression. Plant Physiology, 2018, 177, 1198-1217.	4.8	14
13	Inhibition of MET Signaling with Ficlatusumab in Combination with Chemotherapy in Refractory AML: Clinical Outcomes and High-Dimensional Analysis. Blood Cancer Discovery, 2021, 2, 434-449.	5.0	7
14	PlantRGS: A Web Server for the Identification of Most Suitable Candidate Reference Genes for Quantitative Gene Expression Studies in Plants. DNA Research, 2011, 18, 463-470.	3.4	6
15	NGS QC Toolkit: A Platform for Quality Control of Next-Generation Sequencing Data. , 2015, , 544-548.		6
16	MiR-146a wild-type 3' UTR sequence identity is dispensable for proper innate immune function in vivo. Life Science Alliance, 2019, 2, e201800249.	2.8	5
17	MicroRNA-29 specifies age-related differences in the CD8+ T cell immune response. Cell Reports, 2021, 37, 109969.	6.4	3
18	NGS QC Toolkit: A Platform for Quality Control of Next-Generation Sequencing Data. , 2013, , 1-5.		2