Ravi K Patel

List of Publications by Year
in descending order

18 papers	4,452 citations	840585 11 h-index	940416 16 g-index
21 all docs	21 docs citations	21 times ranked	6970 citing authors

#	Article	IF	Citations
1	Inhibition of MET Signaling with Ficlatuzumab in Combination with Chemotherapy in Refractory AML: Clinical Outcomes and High-Dimensional Analysis. Blood Cancer Discovery, 2021, 2, 434-449.	2.6	7
2	MicroRNA-29 specifies age-related differences in the CD8+ TÂcell immune response. Cell Reports, 2021, 37, 109969.	2.9	3
3	Robust partitioning of microRNA targets from downstream regulatory changes. Nucleic Acids Research, 2020, 48, 9724-9746.	6.5	18
4	CDK2 kinase activity is a regulator of male germ cell fate. Development (Cambridge), 2019, 146, .	1.2	15
5	The Notch signaling pathway promotes basophil responses during helminth-induced type 2 inflammation. Journal of Experimental Medicine, 2019, 216, 1268-1279.	4.2	26
6	MiR-146a wild-type 3â€² sequence identity is dispensable for proper innate immune function in vivo. Life Science Alliance, 2019, 2, e201800249.	1.3	5
7	Developmental Origin Governs CD8+ T Cell Fate Decisions during Infection. Cell, 2018, 174, 117-130.e14.	13.5	132
8	Reproductive Long Intergenic Noncoding RNAs Exhibit Male Gamete Specificity and Polycomb Repressive Complex 2-Mediated Repression. Plant Physiology, 2018, 177, 1198-1217.	2.3	14
9	A widespread sequence-specific mRNA decay pathway mediated by hnRNPs A1 and A2/B1. Genes and Development, 2016, 30, 1070-1085.	2.7	46
10	Base-pair-resolution genome-wide mapping of active RNA polymerases using precision nuclear run-on (PRO-seq). Nature Protocols, 2016, 11, 1455-1476.	5.5	392
11	NGS QC Toolkit: A Platform for Quality Control of Next-Generation Sequencing Data. , 2015, , 544-548.		6
12	CTDB: An Integrated Chickpea Transcriptome Database for Functional and Applied Genomics. PLoS ONE, 2015, 10, e0136880.	1.1	45
13	A draft genome sequence of the pulse crop chickpea (<i><scp>C</scp>icer arietinum</i>ÂL.). Plant Journal, 2013, 74, 715-729.	2.8	382
14	NGS QC Toolkit: A Platform for Quality Control of Next-Generation Sequencing Data. , 2013, , 1-5.		2
15	NGS QC Toolkit: A Toolkit for Quality Control of Next Generation Sequencing Data. PLoS ONE, 2012, 7, e30619.	1.1	2,732
16	De Novo Assembly of Chickpea Transcriptome Using Short Reads for Gene Discovery and Marker Identification. DNA Research, 2011, 18, 53-63.	1.5	406
17	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.	1.5	6
18	Gene Discovery and Tissue-Specific Transcriptome Analysis in Chickpea with Massively Parallel Pyrosequencing and Web Resource Development Â Â. Plant Physiology, 2011, 156, 1661-1678.	2.3	213