Mark F Rogers

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1382488/publications.pdf

Version: 2024-02-01

		1040056	940533	
15	1,112	9	16	
papers	citations	h-index	g-index	
16	16	16	2863	
all docs	docs citations	times ranked	citing authors	

#	Article	IF	CITATIONS
1	High-resolution breakpoint junction mapping of proximally extended D4Z4 deletions in FSHD1 reveals evidence for a founder effect. Human Molecular Genetics, 2022, 31, 748-760.	2.9	8
2	Prediction of driver variants in the cancer genome via machine learning methodologies. Briefings in Bioinformatics, $2021, 22, \ldots$	6.5	13
3	Corticosterone pattern-dependent glucocorticoid receptor binding and transcriptional regulation within the liver. PLoS Genetics, 2021, 17, e1009737.	3.5	10
4	Nucleotide diversity of functionally different groups of immune response genes in Old World camels based on newly annotated and reference-guided assemblies. BMC Genomics, 2020, 21, 606.	2.8	15
5	<i>CScape-somatic</i> : distinguishing driver and passenger point mutations in the cancer genome. Bioinformatics, 2020, 36, 3637-3644.	4.1	19
6	Estimating the Frequency of Single Point Driver Mutations across Common Solid Tumours. Scientific Reports, 2019, 9, 13452.	3.3	6
7	Seasonal adaptations of the hypothalamo-neurohypophyseal system of the dromedary camel. PLoS ONE, 2019, 14, e0216679.	2.5	10
8	Glucocorticoid Receptor–Tethered Mineralocorticoid Receptors Increase Glucocorticoid-Induced Transcriptional Responses. Endocrinology, 2019, 160, 1044-1056.	2.8	35
9	Improving Illumina assemblies with Hi and long reads: An example with the North African dromedary. Molecular Ecology Resources, 2019, 19, 1015-1026.	4.8	67
10	FATHMM-XF: accurate prediction of pathogenic point mutations via extended features. Bioinformatics, 2018, 34, 511-513.	4.1	296
11	Recognition memory-induced gene expression in the perirhinal cortex: A transcriptomic analysis. Behavioural Brain Research, 2017, 328, 1-12.	2.2	7
12	CScape: a tool for predicting oncogenic single-point mutations in the cancer genome. Scientific Reports, 2017, 7, 11597.	3.3	52
13	RNA sequencing analysis of human podocytes reveals glucocorticoid regulated gene networks targeting non-immune pathways. Scientific Reports, 2016, 6, 35671.	3.3	25
14	iCLIP identifies novel roles for SAFB1 in regulating RNA processing and neuronal function. BMC Biology, 2015, 13, 111.	3.8	23
15	An integrative approach to predicting the functional effects of non-coding and coding sequence variation. Bioinformatics, 2015, 31, 1536-1543.	4.1	524