Mudassar Iqbal

List of Publications by Year
in descending order

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27	724	623574	677027
papers	citations	14 h-index	22 g-index

34	34	34	1309
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	HNF4A modulates glucocorticoid action in the liver. Cell Reports, 2022, 39, 110697.	2.9	10
2	Circadian control of hepatitis B virus replication. Nature Communications, 2021, 12, 1658.	5.8	28
3	PEGS: An efficient tool for gene set enrichment within defined sets of genomic intervals. F1000Research, 2021, 10, 570.	0.8	5
4	Adipocyte NR1D1 dictates adipose tissue expansion during obesity. ELife, 2021, 10, .	2.8	24
5	Nuclear receptor REVERBÎ± is a state-dependent regulator of liver energy metabolism. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 25869-25879.	3.3	34
6	The clock gene Bmal1 inhibits macrophage motility, phagocytosis, and impairs defense against pneumonia. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 1543-1551.	3.3	89
7	Glucocorticoids rapidly inhibit cell migration through a novel, non-transcriptional HDAC6 pathway. Journal of Cell Science, 2020, 133, .	1.2	5
8	ZIC3 Controls the Transition from Naive to Primed Pluripotency. Cell Reports, 2019, 27, 3215-3227.e6.	2.9	47
9	REVERBa couples the circadian clock to hepatic glucocorticoid action. Journal of Clinical Investigation, 2018, 128, 4454-4471.	3.9	70
10	Efficient inference for sparse latent variable models of transcriptional regulation. Bioinformatics, 2017, 33, 3776-3783.	1.8	3
11	A non-transcriptional role for the glucocorticoid receptor in mediating the cell stress response. Scientific Reports, 2017, 7, 12101.	1.6	0
12	Reconstructing promoter activity from Lux bioluminescent reporters. PLoS Computational Biology, 2017, 13, e1005731.	1.5	14
13	Predicting stimulation-dependent enhancer-promoter interactions from ChIP-Seq time course data. PeerJ, 2017, 5, e3742.	0.9	12
14	PP2A-3 interacts with ACR4 and regulates formative cell division in the Arabidopsis root. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 1447-1452.	3.3	43
15	The dynamic balance of import and export of zinc in Escherichia coli suggests a heterogeneous population response to stress. Journal of the Royal Society Interface, 2015, 12, 20150069.	1.5	19
16	Analysis of Occludin Trafficking, Demonstrating Continuous Endocytosis, Degradation, Recycling and Biosynthetic Secretory Trafficking. PLoS ONE, 2014, 9, e111176.	1.1	17
17	Computational Prediction of Domain-domain Interactions: Factor-graph Based Modelling and Inference. Current Chemical Biology, 2014, 7, 234-240.	0.2	0
18	Extracting regulator activity profiles by integration of de novo motifs and expression data: characterizing key regulators of nutrient depletion responses in Streptomyces coelicolor. Nucleic Acids Research, 2012, 40, 5227-5239.	6.5	24

#	Article	IF	Citations
19	Inferring the Brassica rapa Interactome Using Proteinâ€“Protein Interaction Data from Arabidopsis thaliana. Frontiers in Plant Science, 2012, 3, 297.	1.7	25
20	The dynamic architecture of the metabolic switch in Streptomyces coelicolor. BMC Genomics, 2010, 11, 10.	1.2	171
21	A Hybrid Rule-Induction/Likelihood-Ratio Based Approach for Predicting Protein-Protein Interactions. Intelligent Systems Reference Library, 2009, , 623-637.	1.0	3
22	Message-passing algorithms for the prediction of protein domain interactions from proteinâ€“protein interaction data. Bioinformatics, 2008, 24, 2064-2070.	1.8	13
23	Protein Interaction Inference Using Particle Swarm Optimization Algorithm. , 2008, , 61-70.		2
24	Codon Usage Domains over Bacterial Chromosomes. PLoS Computational Biology, 2006, 2, e37.	1.5	38
25	An Estimation of Distribution Particle Swarm Optimization Algorithm. Lecture Notes in Computer Science, 2006, , 72-83.	1.0	24
26	Glucocorticoids rapidly inhibit cell migration through a novel, non-transcriptional pathway involving HDAC6. Endocrine Abstracts, 0, , .	0.0	0
27	PEGS: An efficient tool for gene set enrichment within defined sets of genomic intervals. F1000Research, 0, 10, 570.	0.8	4