Syed Murtuza Baker

List of Publications by Year
in descending order

18 papers	437 citations	759233 12 h-index	1058476 14 g-index
21 all docs	21 docs citations	21 times ranked	853 citing authors

#	Article	IF	Citations
1	A living biobank of ovarian cancer ex vivo models reveals profound mitotic heterogeneity. Nature Communications, 2020, 11, 822.	12.8	62
2	Classifying cells with Scasat, a single-cell ATAC-seq analysis tool. Nucleic Acids Research, 2019, 47, e10-e10.	14.5	60
3	Reciprocal transcription factor networks govern tissue-resident ILC3 subset function and identity. Nature Immunology, 2021, 22, 1245-1255.	14.5	49
4	ZIC3 Controls the Transition from Naive to Primed Pluripotency. Cell Reports, 2019, 27, 3215-3227.e6.	6.4	47
5	In vivo labeling reveals continuous trafficking of TCF-1+ T cells between tumor and lymphoid tissue. Journal of Experimental Medicine, 2022, 219, .	8.5	42
6	Targeting the IL33–NLRP3 axis improves therapy for experimental cerebral malaria. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 7404-7409.	7.1	37
7	Comparison of different algorithms for simultaneous estimation of multiple parameters in kinetic metabolic models. Journal of Integrative Bioinformatics, 2010, 7, .	1.5	29
8	HOX paralogs selectively convert binding of ubiquitous transcription factors into tissue-specific patterns of enhancer activation. PLoS Genetics, 2020, 16, e1009162.	3.5	23
9	A unified framework for estimating parameters of kinetic biological models. BMC Bioinformatics, 2015, 16, 104.	2.6	19
10	Respectful Modeling: Addressing Uncertainty in Dynamic System Models for Molecular Biology. Trends in Biotechnology, 2017, 35, 518-529.	9.3	19
11	Chronic myelomonocytic leukaemia stem cell transcriptomes anticipate disease morphology and outcome. EBioMedicine, 2020, 58, 102904.	6.1	16
12	An improved constraint filtering technique for inferring hidden states and parameters of a biological model. Bioinformatics, 2013, 29, 1052-1059.	4.1	13
13	Foxm1 regulates neural progenitor fate during spinal cord regeneration. EMBO Reports, 2021, 22, e50932.	4.5	9
14	Unscented Kalman filter with parameter identifiability analysis for the estimation of multiple parameters in kinetic models. Eurasip Journal on Bioinformatics and Systems Biology, 2011, 2011, 7.	1.4	7
15	Predicting Protein-protein Interaction Using Amino Acid Sequence Information: A Computational Approach. Plant Tissue Culture and Biotechnology, 2010, 20, 37-45.	0.2	0
16	Nuclear receptor profiling predicts chemical disruptors as risk factors for developing breast cancer. Endocrine Abstracts, 0, , .	0.0	0
17	Single cell RNA-seq reveals complex processing of glucocorticoid controlled transcriptional programmes. Endocrine Abstracts, 0, , .	0.0	0
18	Complexities in the role of acetylation dynamics in modifying inducible gene activation parameters. Nucleic Acids Research, 2021, 49, 12744-12756.	14.5	0