

# Syed Murtuza Baker

## List of Publications by Year in descending order

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18  
papers

437  
citations

759233

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1058476

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docs citations

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times ranked

853  
citing authors

#	ARTICLE	IF	CITATIONS
1	In vivo labeling reveals continuous trafficking of TCF-1+ T cells between tumor and lymphoid tissue. <i>Journal of Experimental Medicine</i> , 2022, 219, .	8.5	42
2	Foxm1 regulates neural progenitor fate during spinal cord regeneration. <i>EMBO Reports</i> , 2021, 22, e50932.	4.5	9
3	Reciprocal transcription factor networks govern tissue-resident ILC3 subset function and identity. <i>Nature Immunology</i> , 2021, 22, 1245-1255.	14.5	49
4	Complexities in the role of acetylation dynamics in modifying inducible gene activation parameters. <i>Nucleic Acids Research</i> , 2021, 49, 12744-12756.	14.5	0
5	Chronic myelomonocytic leukaemia stem cell transcriptomes anticipate disease morphology and outcome. <i>EBioMedicine</i> , 2020, 58, 102904.	6.1	16
6	A living biobank of ovarian cancer ex vivo models reveals profound mitotic heterogeneity. <i>Nature Communications</i> , 2020, 11, 822.	12.8	62
7	HOX paralogs selectively convert binding of ubiquitous transcription factors into tissue-specific patterns of enhancer activation. <i>PLoS Genetics</i> , 2020, 16, e1009162.	3.5	23
8	ZIC3 Controls the Transition from Naive to Primed Pluripotency. <i>Cell Reports</i> , 2019, 27, 3215-3227.e6.	6.4	47
9	Classifying cells with Scasat, a single-cell ATAC-seq analysis tool. <i>Nucleic Acids Research</i> , 2019, 47, e10-e10.	14.5	60
10	Targeting the IL33â€“NLRP3 axis improves therapy for experimental cerebral malaria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 7404-7409.	7.1	37
11	Respectful Modeling: Addressing Uncertainty in Dynamic System Models for Molecular Biology. <i>Trends in Biotechnology</i> , 2017, 35, 518-529.	9.3	19
12	A unified framework for estimating parameters of kinetic biological models. <i>BMC Bioinformatics</i> , 2015, 16, 104.	2.6	19
13	An improved constraint filtering technique for inferring hidden states and parameters of a biological model. <i>Bioinformatics</i> , 2013, 29, 1052-1059.	4.1	13
14	Unscented Kalman filter with parameter identifiability analysis for the estimation of multiple parameters in kinetic models. <i>Eurasip Journal on Bioinformatics and Systems Biology</i> , 2011, 2011, 7.	1.4	7
15	Comparison of different algorithms for simultaneous estimation of multiple parameters in kinetic metabolic models. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, .	1.5	29
16	Predicting Protein-protein Interaction Using Amino Acid Sequence Information: A Computational Approach. <i>Plant Tissue Culture and Biotechnology</i> , 2010, 20, 37-45.	0.2	0
17	Nuclear receptor profiling predicts chemical disruptors as risk factors for developing breast cancer. <i>Endocrine Abstracts</i> , 0, , .	0.0	0
18	Single cell RNA-seq reveals complex processing of glucocorticoid controlled transcriptional programmes. <i>Endocrine Abstracts</i> , 0, , .	0.0	0