

Majid Kazemian

List of Publications by Year in descending order

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Version: 2024-02-01

45
papers

1,971
citations

279701

23
h-index

289141

40
g-index

54
all docs

54
docs citations

54
times ranked

3689
citing authors

#	ARTICLE	IF	CITATIONS
1	Autocrine vitamin D signaling switches off pro-inflammatory programs of TH1 cells. <i>Nature Immunology</i> , 2022, 23, 62-74.	7.0	105
2	SARS-CoV-2 drives JAK1/2-dependent local complement hyperactivation. <i>Science Immunology</i> , 2021, 6, .	5.6	144
3	Host-Virus Chimeric Events in SARS-CoV-2-Infected Cells Are Infrequent and Artifactual. <i>Journal of Virology</i> , 2021, 95, e0029421.	1.5	28
4	STAT5 Represses a STAT3-Independent Th17-like Program during Th9 Cell Differentiation. <i>Journal of Immunology</i> , 2021, 207, 1265-1274.	0.4	7
5	TCF-1 controls Treg cell functions that regulate inflammation, CD8+ T cell cytotoxicity and severity of colon cancer. <i>Nature Immunology</i> , 2021, 22, 1152-1162.	7.0	42
6	Thymic stromal lymphopoietin limits primary and recall CD8+ T-cell anti-viral responses. <i>ELife</i> , 2021, 10, .	2.8	6
7	Reply to Grigoriev et al., "Sequences of SARS-CoV-2 "Hybrids" with the Human Genome: Signs of Non-coding RNA?" <i>Journal of Virology</i> , 2021, , JVI0169021.	1.5	0
8	Mitochondrial C5aR1 activity in macrophages controls IL-1 β production underlying sterile inflammation. <i>Science Immunology</i> , 2021, 6, eabf2489.	5.6	50
9	Epstein-Barr Virus Episome Physically Interacts with Active Regions of the Host Genome in Lymphoblastoid Cells. <i>Journal of Virology</i> , 2020, 94, .	1.5	26
10	Restoration of RNA helicase DDX5 suppresses hepatitis B virus (HBV) biosynthesis and Wnt signaling in HBV-related hepatocellular carcinoma. <i>Theranostics</i> , 2020, 10, 10957-10972.	4.6	31
11	Transcription factor p73 regulates Th1 differentiation. <i>Nature Communications</i> , 2020, 11, 1475.	5.8	22
12	Diapedesis-Induced Integrin Signaling via LFA-1 Facilitates Tissue Immunity by Inducing Intrinsic Complement C3 Expression in Immune Cells. <i>Immunity</i> , 2020, 52, 513-527.e8.	6.6	57
13	CDK8 Fine-Tunes IL-6 Transcriptional Activities by Limiting STAT3 Resident Time at the Gene Loci. <i>Cell Reports</i> , 2020, 33, 108545.	2.9	26
14	Granzyme A-producing T helper cells are critical for acute graft-versus-host disease. <i>JCI Insight</i> , 2020, 5, .	2.3	9
15	PBRM1 Regulates Stress Response in Epithelial Cells. <i>Science</i> , 2019, 15, 196-210.	1.9	24
16	Integrated Pan-Cancer Map of EBV-Associated Neoplasms Reveals Functional Host-Virus Interactions. <i>Cancer Research</i> , 2019, 79, 6010-6023.	0.4	43
17	IL-21/type I interferon interplay regulates neutrophil-dependent innate immune responses to <i>Staphylococcus aureus</i> . <i>ELife</i> , 2019, 8, .	2.8	14
18	CRM Discovery Beyond Model Insects. <i>Methods in Molecular Biology</i> , 2019, 1858, 117-139.	0.4	6

#	ARTICLE	IF	CITATIONS
19	Kinetics of cytokine receptor trafficking determine signaling and functional selectivity. <i>ELife</i> , 2019, 8, .	2.8	34
20	Human retinoic acid-regulated CD161+ regulatory T cells support wound repair in intestinal mucosa. <i>Nature Immunology</i> , 2018, 19, 1403-1414.	7.0	86
21	BACH2 immunodeficiency illustrates an association between super-enhancers and haploinsufficiency. <i>Nature Immunology</i> , 2017, 18, 813-823.	7.0	113
22	Critical functions for STAT5 tetramers in the maturation and survival of natural killer cells. <i>Nature Communications</i> , 2017, 8, 1320.	5.8	67
23	A TSLP-complement axis mediates neutrophil killing of methicillin-resistant <i>Staphylococcus aureus</i> . <i>Science Immunology</i> , 2016, 1, .	5.6	37
24	ZSCAN5B and primate-specific paralogs bind RNA polymerase III genes and extra-TFIIC (ETC) sites to modulate mitotic progression. <i>Oncotarget</i> , 2016, 7, 72571-72592.	0.8	5
25	Comprehensive assembly of novel transcripts from unmapped human RNA-seq data and their association with cancer. <i>Molecular Systems Biology</i> , 2015, 11, 826.	3.2	18
26	Integrating motif, DNA accessibility and gene expression data to build regulatory maps in an organism. <i>Nucleic Acids Research</i> , 2015, 43, 3998-4012.	6.5	36
27	Opposing roles of STAT1 and STAT3 in IL-21 function in CD4 ⁺ T cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 9394-9399.	3.3	108
28	Possible Human Papillomavirus 38 Contamination of Endometrial Cancer RNA Sequencing Samples in The Cancer Genome Atlas Database. <i>Journal of Virology</i> , 2015, 89, 8967-8973.	1.5	21
29	Evidence for Deep Regulatory Similarities in Early Developmental Programs across Highly Diverged Insects. <i>Genome Biology and Evolution</i> , 2014, 6, 2301-2320.	1.1	37
30	Simulations of Enhancer Evolution Provide Mechanistic Insights into Gene Regulation. <i>Molecular Biology and Evolution</i> , 2014, 31, 184-200.	3.5	25
31	Computational Identification of Diverse Mechanisms Underlying Transcription Factor-DNA Occupancy. <i>PLoS Genetics</i> , 2013, 9, e1003571.	1.5	49
32	Widespread evidence of cooperative DNA binding by transcription factors in <i>Drosophila</i> development. <i>Nucleic Acids Research</i> , 2013, 41, 8237-8252.	6.5	83
33	Global analysis of <i>Drosophila</i> Cys2-His2 zinc finger proteins reveals a multitude of novel recognition motifs and binding determinants. <i>Genome Research</i> , 2013, 23, 928-940.	2.4	70
34	Prediction of Breeding Values for Dairy Cattle Using Artificial Neural Networks and Neuro-Fuzzy Systems. <i>Computational and Mathematical Methods in Medicine</i> , 2012, 2012, 1-9.	0.7	39
35	Genome surveyor 2.0: cis-regulatory analysis in <i>Drosophila</i> . <i>Nucleic Acids Research</i> , 2011, 39, W79-W85.	6.5	11
36	Improved accuracy of supervised CRM discovery with interpolated Markov models and cross-species comparison. <i>Nucleic Acids Research</i> , 2011, 39, 9463-9472.	6.5	37

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37	FlyFactorSurvey: a database of Drosophila transcription factor binding specificities determined using the bacterial one-hybrid system. <i>Nucleic Acids Research</i> , 2011, 39, D111-D117.	6.5	202
38	Using classifier fusion techniques for protein secondary structure prediction. <i>International Journal of Computational Intelligence in Bioinformatics and Systems Biology</i> , 2010, 1, 418.	0.1	3
39	Quantitative Analysis of the Drosophila Segmentation Regulatory Network Using Pattern Generating Potentials. <i>PLoS Biology</i> , 2010, 8, e1000456.	2.6	69
40	Motif-Blind, Genome-Wide Discovery of cis-Regulatory Modules in Drosophila and Mouse. <i>Developmental Cell</i> , 2009, 17, 568-579.	3.1	60
41	Aggregation of web search engines based on users' preferences in WebFusion. <i>Knowledge-Based Systems</i> , 2007, 20, 321-328.	4.0	50
42	Swarm Clustering Based on Flowers Pollination by Artificial Bees. <i>Studies in Computational Intelligence</i> , 2006, , 191-202.	0.7	19
43	Application of OWA Based Classifier Fusion in Diagnosis and Treatment offering for Female Urinary Incontinence. <i>Lecture Notes in Computer Science</i> , 2006, , 433-442.	1.0	0
44	Protein Secondary Structure Classifiers Fusion Using OWA. <i>Lecture Notes in Computer Science</i> , 2005, , 338-345.	1.0	7
45	Distributed Data Clustering Based on Flowers Pollination by Artificial Bees. , 2005, , 959-966.		0