

Golnaz Vahedi

List of Publications by Year in descending order

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Version: 2024-02-01

62
papers

7,861
citations

109311

35
h-index

114455

63
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69
all docs

69
docs citations

69
times ranked

14337
citing authors

#	ARTICLE	IF	CITATIONS
1	Single-cell multi-omics analysis of human pancreatic islets reveals novel cellular states in type 1 diabetes. <i>Nature Metabolism</i> , 2022, 4, 284-299.	11.9	52
2	Stripenn detects architectural stripes from chromatin conformation data using computer vision. <i>Nature Communications</i> , 2022, 13, 1602.	12.8	23
3	Topologically associating domains are disrupted by evolutionary genome rearrangements forming species-specific enhancer connections in mice and humans. <i>Cell Reports</i> , 2022, 39, 110769.	6.4	12
4	± Cell dysfunction in islets from nondiabetic, glutamic acid decarboxylase autoantibody± positive individuals. <i>Journal of Clinical Investigation</i> , 2022, 132, .	8.2	24
5	TCF-1 promotes chromatin interactions across topologically associating domains in T cell progenitors. <i>Nature Immunology</i> , 2022, 23, 1052-1062.	14.5	25
6	Exome-wide evaluation of rare coding variants using electronic health records identifies new gene± phenotype associations. <i>Nature Medicine</i> , 2021, 27, 66-72.	30.7	44
7	Epigenetic scarring of exhausted T cells hinders memory differentiation upon eliminating chronic antigenic stimulation. <i>Nature Immunology</i> , 2021, 22, 1008-1019.	14.5	116
8	BET bromodomain protein inhibition reverses chimeric antigen receptor extinction and reinvigorates exhausted T cells in chronic lymphocytic leukemia. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	45
9	Remodeling the chromatin landscape in T lymphocytes by a division of labor among transcription factors. <i>Immunological Reviews</i> , 2021, 300, 167-180.	6.0	7
10	BRD4 orchestrates genome folding to promote neural crest differentiation. <i>Nature Genetics</i> , 2021, 53, 1480-1492.	21.4	48
11	Transcription factors combine to paint the methylation landscape. <i>Trends in Immunology</i> , 2021, 42, 1060-1062.	6.8	1
12	Foxp3 Re-distributes Its Heavy Lifting. <i>Immunity</i> , 2020, 53, 895-897.	14.3	2
13	SARS-CoV-2 Cell Entry Factors ACE2 and TMPRSS2 Are Expressed in the Microvasculature and Ducts of Human Pancreas but Are Not Enriched in ± Cells. <i>Cell Metabolism</i> , 2020, 32, 1028-1040.e4.	16.2	148
14	The Identity of Human Tissue-Emigrant CD8+ T Cells. <i>Cell</i> , 2020, 183, 1946-1961.e15.	28.9	58
15	Joint profiling of chromatin accessibility and CAR-T integration site analysis at population and single-cell levels. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 5442-5452.	7.1	34
16	TooManyCells identifies and visualizes relationships of single-cell clades. <i>Nature Methods</i> , 2020, 17, 405-413.	19.0	57
17	Genetic Variation in Type 1 Diabetes Reconfigures the 3D Chromatin Organization of T Cells and Alters Gene Expression. <i>Immunity</i> , 2020, 52, 257-274.e11.	14.3	42
18	A Thpok-Directed Transcriptional Circuitry Promotes Bcl6 and Maf Expression to Orchestrate T Follicular Helper Differentiation. <i>Immunity</i> , 2019, 51, 465-478.e6.	14.3	30

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19	TCF-1-Centered Transcriptional Network Drives an Effector versus Exhausted CD8 ⁺ Cell-Fate Decision. <i>Immunity</i> , 2019, 51, 840-855.e5.	14.3	409
20	A mass spectrometry-based assay using metabolic labeling to rapidly monitor chromatin accessibility of modified histone proteins. <i>Scientific Reports</i> , 2019, 9, 13613.	3.3	32
21	Oncogenic Notch Promotes Long-Range Regulatory Interactions within Hyperconnected 3D Cliques. <i>Molecular Cell</i> , 2019, 73, 1174-1190.e12.	9.7	83
22	Lineage-Determining Transcription Factor TCF-1 Initiates the Epigenetic Identity of T Cells. <i>Immunity</i> , 2018, 48, 243-257.e10.	14.3	164
23	Do Memory CD4 T Cells Keep Their Cell-Type Programming: Plasticity versus Fate Commitment?. <i>Cold Spring Harbor Perspectives in Biology</i> , 2018, 10, a028779.	5.5	7
24	A Cosine Similarity-Based Method to Infer Variability of Chromatin Accessibility at the Single-Cell Level. <i>Frontiers in Genetics</i> , 2018, 9, 319.	2.3	16
25	Long genes linked to autism spectrum disorders harbor broad enhancer-like chromatin domains. <i>Genome Research</i> , 2018, 28, 933-942.	5.5	40
26	Identification and characterization of HIV-specific resident memory CD8 ⁺ T cells in human lymphoid tissue. <i>Science Immunology</i> , 2018, 3, .	11.9	116
27	Biotin tagging of MeCP2 in mice reveals contextual insights into the Rett syndrome transcriptome. <i>Nature Medicine</i> , 2017, 23, 1203-1214.	30.7	102
28	GR Extinguishes Inflamed Chromatin, and NF- κ B Evacuates. <i>Immunity</i> , 2017, 47, 214-216.	14.3	4
29	Targeted genomic analysis reveals widespread autoimmune disease association with regulatory variants in the TNF superfamily cytokine signalling network. <i>Genome Medicine</i> , 2016, 8, 76.	8.2	17
30	Epigenetic stability of exhausted T cells limits durability of reinvigoration by PD-1 blockade. <i>Science</i> , 2016, 354, 1160-1165.	12.6	939
31	Interleukin-23-Induced Transcription Factor Blimp-1 Promotes Pathogenicity of T Helper 17 Cells. <i>Immunity</i> , 2016, 44, 131-142.	14.3	131
32	IL-10 induces a STAT3-dependent autoregulatory loop in T _H 2 cells that promotes Blimp-1 restriction of cell expansion via antagonism of STAT5 target genes. <i>Science Immunology</i> , 2016, 1, .	11.9	26
33	EZH2 is crucial for both differentiation of regulatory T cells and T effector cell expansion. <i>Scientific Reports</i> , 2015, 5, 10643.	3.3	129
34	Enhancing our understanding of enhancers in T _H helper cells. <i>European Journal of Immunology</i> , 2015, 45, 2998-3001.	2.9	2
35	Super-enhancers delineate disease-associated regulatory nodes in T cells. <i>Nature</i> , 2015, 520, 558-562.	27.8	323
36	Asymmetric Action of STAT Transcription Factors Drives Transcriptional Outputs and Cytokine Specificity. <i>Immunity</i> , 2015, 42, 877-889.	14.3	137

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37	Super-enhancers: Asset management in immune cell genomes. <i>Trends in Immunology</i> , 2015, 36, 519-526.	6.8	36
38	A mouse model of HIES reveals pro- and anti-inflammatory functions of STAT3. <i>Blood</i> , 2014, 123, 2978-2987.	1.4	71
39	Type I IFN Induces Binding of STAT1 to Bcl6: Divergent Roles of STAT Family Transcription Factors in the T Follicular Helper Cell Genetic Program. <i>Journal of Immunology</i> , 2014, 192, 2156-2166.	0.8	95
40	BRD4 assists elongation of both coding and enhancer RNAs by interacting with acetylated histones. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 1047-1057.	8.2	247
41	Enhancing the understanding of asthma. <i>Nature Immunology</i> , 2014, 15, 701-703.	14.5	10
42	Transcriptional and epigenetic networks of helper T and innate lymphoid cells. <i>Immunological Reviews</i> , 2014, 261, 23-49.	6.0	76
43	BACH2 represses effector programs to stabilize Treg-mediated immune homeostasis. <i>Nature</i> , 2013, 498, 506-510.	27.8	332
44	Helper T cell identity and evolution of differential transcriptomes and epigenomes. <i>Immunological Reviews</i> , 2013, 252, 24-40.	6.0	90
45	Mechanisms underlying helper T-cell plasticity: Implications for immune-mediated disease. <i>Journal of Allergy and Clinical Immunology</i> , 2013, 131, 1276-1287.	2.9	138
46	Transcription factors and CD4 T cells seeking identity: masters, minions, setters and spikers. <i>Immunology</i> , 2013, 139, 294-298.	4.4	25
47	Tissue Inhibitor of Metalloproteinase 1 Is Preferentially Expressed in Th1 and Th17 T-Helper Cell Subsets and Is a Direct Stat Target Gene. <i>PLoS ONE</i> , 2013, 8, e59367.	2.5	15
48	STATs Shape the Active Enhancer Landscape of T Cell Populations. <i>Cell</i> , 2012, 151, 981-993.	28.9	325
49	Distinct requirements for T-bet in gut innate lymphoid cells. <i>Journal of Experimental Medicine</i> , 2012, 209, 2331-2338.	8.5	160
50	Interleukin-27 Priming of T Cells Controls IL-17 Production In trans via Induction of the Ligand PD-L1. <i>Immunity</i> , 2012, 36, 1017-1030.	14.3	229
51	Transcriptional and Epigenetic Control of T Helper Cell Specification: Molecular Mechanisms Underlying Commitment and Plasticity. <i>Annual Review of Immunology</i> , 2012, 30, 707-731.	21.8	296
52	Early Th1 Cell Differentiation Is Marked by a Tfh Cell-like Transition. <i>Immunity</i> , 2011, 35, 919-931.	14.3	364
53	Helper T-cell differentiation and plasticity: insights from epigenetics. <i>Immunology</i> , 2011, 134, 235-245.	4.4	96
54	Opposing regulation of the locus encoding IL-17 through direct, reciprocal actions of STAT3 and STAT5. <i>Nature Immunology</i> , 2011, 12, 247-254.	14.5	522

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55	Genomic views of STAT function in CD4+ T helper cell differentiation. <i>Nature Reviews Immunology</i> , 2011, 11, 239-250.	22.7	251
56	Diverse Targets of the Transcription Factor STAT3 Contribute to T Cell Pathogenicity and Homeostasis. <i>Immunity</i> , 2010, 32, 605-615.	14.3	605
57	Discrete Roles of STAT4 and STAT6 Transcription Factors in Tuning Epigenetic Modifications and Transcription during T Helper Cell Differentiation. <i>Immunity</i> , 2010, 32, 840-851.	14.3	290
58	Sampling-rate-dependent probabilistic Boolean networks. <i>Journal of Theoretical Biology</i> , 2009, 261, 540-547.	1.7	4
59	Recent Advances in Intervention in Markovian Regulatory Networks. <i>Current Genomics</i> , 2009, 10, 463-477.	1.6	16
60	Intervention in Gene Regulatory Networks via a Stationary Mean-First-Passage-Time Control Policy. <i>IEEE Transactions on Biomedical Engineering</i> , 2008, 55, 2319-2331.	4.2	46
61	Optimal Intervention in Asynchronous Genetic Regulatory Networks. <i>IEEE Journal on Selected Topics in Signal Processing</i> , 2008, 2, 412-423.	10.8	40
62	An integrated method for mutation detection using on-chip sample preparation, single-stranded conformation polymorphism, and heteroduplex analysis. <i>Electrophoresis</i> , 2004, 25, 2346-2356.	2.4	28