

Harinder Singh

List of Publications by Year in descending order

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Version: 2024-02-01

63
papers

17,214
citations

147566

31
h-index

133063

59
g-index

72
all docs

72
docs citations

72
times ranked

32344
citing authors

#	ARTICLE	IF	CITATIONS
1	Simple Combinations of Lineage-Determining Transcription Factors Prime cis-Regulatory Elements Required for Macrophage and B Cell Identities. <i>Molecular Cell</i> , 2010, 38, 576-589.	4.5	10,215
2	Regulation of B Lymphocyte and Macrophage Development by Graded Expression of PU.1. <i>Science</i> , 2000, 288, 1439-1441.	6.0	627
3	Multilineage Transcriptional Priming and Determination of Alternate Hematopoietic Cell Fates. <i>Cell</i> , 2006, 126, 755-766.	13.5	572
4	Graded Expression of Interferon Regulatory Factor-4 Coordinates Isotype Switching with Plasma Cell Differentiation. <i>Immunity</i> , 2006, 25, 225-236.	6.6	480
5	Single-cell analysis of mixed-lineage states leading to a binary cell fate choice. <i>Nature</i> , 2016, 537, 698-702.	13.7	444
6	IFN Regulatory Factor-4 and -8 Govern Dendritic Cell Subset Development and Their Functional Diversity. <i>Journal of Immunology</i> , 2005, 174, 2573-2581.	0.4	390
7	Compensatory dendritic cell development mediated by BATF-IRF interactions. <i>Nature</i> , 2012, 490, 502-507.	13.7	367
8	Transcriptional Regulation of Germinal Center B and Plasma Cell Fates by Dynamical Control of IRF4. <i>Immunity</i> , 2013, 38, 918-929.	6.6	356
9	Regulation of macrophage and neutrophil cell fates by the PU.1:EBP1± ratio and granulocyte colony-stimulating factor. <i>Nature Immunology</i> , 2003, 4, 1029-1036.	7.0	347
10	A Genomic Regulatory Element That Directs Assembly and Function of Immune-Specific AP-1-IRF Complexes. <i>Science</i> , 2012, 338, 975-980.	6.0	298
11	Interferon Regulatory Factor 4 (IRF4) Interacts with NFATc2 to Modulate Interleukin 4 Gene Expression. <i>Journal of Experimental Medicine</i> , 2002, 195, 1003-1012.	4.2	293
12	Orchestrating B cell lymphopoiesis through interplay of IL-7 receptor and pre-B cell receptor signalling. <i>Nature Reviews Immunology</i> , 2014, 14, 69-80.	10.6	252
13	Cooperative and Antagonistic Interplay between PU.1 and GATA-2 in the Specification of Myeloid Cell Fates. <i>Immunity</i> , 2002, 17, 665-676.	6.6	242
14	Transcriptional programming of dendritic cells for enhanced MHC class II antigen presentation. <i>Nature Immunology</i> , 2014, 15, 161-167.	7.0	224
15	Assembly requirements of PU.1-Pip (IRF-4) activator complexes: inhibiting function in vivo using fused dimers. <i>EMBO Journal</i> , 1999, 18, 977-991.	3.5	179
16	Contingent gene regulatory networks and B cell fate specification. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 4949-4953.	3.3	173
17	A Recurrent Network Involving the Transcription Factors PU.1 and Gfi1 Orchestrates Innate and Adaptive Immune Cell Fates. <i>Immunity</i> , 2009, 31, 576-586.	6.6	159
18	Specification of type 2 innate lymphocytes by the transcriptional determinant Gfi1. <i>Nature Immunology</i> , 2013, 14, 1229-1236.	7.0	158

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19	DoubletDecon: Deconvoluting Doublets from Single-Cell RNA-Sequencing Data. Cell Reports, 2019, 29, 1718-1727.e8.	2.9	134
20	An incoherent regulatory network architecture that orchestrates B cell diversification in response to antigen signaling. Molecular Systems Biology, 2011, 7, 495.	3.2	111
21	Regulation of bifurcating B cell trajectories by mutual antagonism between transcription factors IRF4 and IRF8. Nature Immunology, 2015, 16, 1274-1281.	7.0	108
22	Nonpeptidergic neurons suppress mast cells via glutamate to maintain skin homeostasis. Cell, 2021, 184, 2151-2166.e16.	13.5	87
23	Transcriptional determinants of tolerogenic and immunogenic states during dendritic cell maturation. Journal of Cell Biology, 2017, 216, 779-792.	2.3	82
24	Gene regulatory networks in the immune system. Trends in Immunology, 2014, 35, 211-218.	2.9	73
25	TSLP signaling in CD4 ⁺ T cells programs a pathogenic T helper 2 cell state. Science Signaling, 2018, 11, .	1.6	72
26	Competition for Active TGF β 2 Cytokine Allows for Selective Retention of Antigen-Specific Tissue-Resident Memory T Cells in the Epidermal Niche. Immunity, 2021, 54, 84-98.e5.	6.6	68
27	IL-10 ⁺ producing Tfh cells accumulate with age and link inflammation with age-related immune suppression. Science Advances, 2020, 6, eabb0806.	4.7	67
28	Coupled analysis of transcriptome and BCR mutations reveals role of OXPHOS in affinity maturation. Nature Immunology, 2021, 22, 904-913.	7.0	62
29	Affinity Maturation Is Impaired by Natural Killer Cell Suppression of Germinal Centers. Cell Reports, 2018, 24, 3367-3373.e4.	2.9	59
30	Inhibiting Oxidative Phosphorylation In Vivo Restrains Th17 Effector Responses and Ameliorates Murine Colitis. Journal of Immunology, 2017, 198, 2735-2746.	0.4	56
31	Charting the cis-regulome of activated B cells by coupling structural and functional genomics. Nature Immunology, 2020, 21, 210-220.	7.0	40
32	Suppression of Inflammasome Activation by IRF8 and IRF4 in cDCs Is Critical for T Cell Priming. Cell Reports, 2020, 31, 107604.	2.9	40
33	Gimap5-dependent inactivation of GSK3 β is required for CD4 ⁺ T cell homeostasis and prevention of immune pathology. Nature Communications, 2018, 9, 430.	5.8	32
34	Gene Regulatory Networks that Orchestrate the Development of B Lymphocyte Precursors. , 2007, 596, 57-62.		30
35	Coordinated Circulating T Follicular Helper and Activated B Cell Responses Underlie the Onset of Antibody-Mediated Rejection in Kidney Transplantation. Journal of the American Society of Nephrology: JASN, 2020, 31, 2457-2474.	3.0	30
36	Genomic programming of IRF4-expressing human Langerhans cells. Nature Communications, 2020, 11, 313.	5.8	22

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37	Gene regulatory networks and the determination of lymphoid cell fates. <i>Current Opinion in Immunology</i> , 2006, 18, 116-120.	2.4	20
38	T-bet+CD27+CD21 ^{hi} B cells poised for plasma cell differentiation during antibody-mediated rejection of kidney transplants. <i>JCI Insight</i> , 2021, 6, .	2.3	20
39	Proteasomal adaptations underlying carfilzomib-resistance in human bone marrow plasma cells. <i>American Journal of Transplantation</i> , 2020, 20, 399-410.	2.6	18
40	The Molecular Choreography of IRF4 and IRF8 with Immune System Partners. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2013, 78, 101-104.	2.0	17
41	Regulated Capture of V _H Gene Topologically Associating Domains by Transcription Factories. <i>Cell Reports</i> , 2018, 24, 2443-2456.	2.9	16
42	Genetic analysis of transcription factors implicated in B lymphocyte development. <i>Immunologic Research</i> , 1994, 13, 280-290.	1.3	15
43	Crystallization and characterization of PU.1/IRF-4/DNA ternary complex. <i>Journal of Structural Biology</i> , 2002, 139, 55-59.	1.3	14
44	Cell fate dynamics and genomic programming of plasma cell precursors. <i>Immunological Reviews</i> , 2021, 303, 62-71.	2.8	11
45	People critically ill with COVID-19 exhibit peripheral immune profiles predictive of mortality and reflective of SARS-CoV-2 lung viral burden. <i>Cell Reports Medicine</i> , 2021, 2, 100476.	3.3	11
46	Antibodies targeting conserved non-canonical antigens and endemic coronaviruses associate with favorable outcomes in severe COVID-19. <i>Cell Reports</i> , 2022, 39, 111020.	2.9	11
47	Divergent COVID-19 Disease Trajectories Predicted by a DAMP-Centered Immune Network Model. <i>Frontiers in Immunology</i> , 2021, 12, 754127.	2.2	10
48	Tolerogenic and immunogenic states of Langerhans cells are orchestrated by epidermal signals acting on a core maturation gene module. <i>BioEssays</i> , 2021, 43, e2000182.	1.2	9
49	CISH attenuates homeostatic cytokine signaling to promote lung-specific macrophage programming and function. <i>Science Signaling</i> , 2021, 14, eabe5137.	1.6	9
50	SPaRTAN, a computational framework for linking cell-surface receptors to transcriptional regulators. <i>Nucleic Acids Research</i> , 2021, 49, 9633-9647.	6.5	9
51	Essential Regression: A generalizable framework for inferring causal latent factors from multi-omic datasets. <i>Patterns</i> , 2022, 3, 100473.	3.1	8
52	The independent prognostic value of global epigenetic alterations: An analysis of single-cell ATAC-seq of circulating leukocytes from trauma patients followed by validation in whole blood leukocyte transcriptomes across three etiologies of critical illness. <i>EBioMedicine</i> , 2022, 76, 103860.	2.7	7
53	PU.1, a Shared Transcriptional Regulator of Innate and Adaptive Immune Cell Fates. <i>Journal of Immunology</i> , 2008, 181, 1595-1596.	0.4	5
54	Transcriptional and epigenetic networks orchestrating immune cell development and function. <i>Immunological Reviews</i> , 2014, 261, 5-8.	2.8	5

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55	Pseudocell Tracer—A method for inferring dynamic trajectories using scRNAseq and its application to B cells undergoing immunoglobulin class switch recombination. PLoS Computational Biology, 2021, 17, e1008094.	1.5	5
56	Shedding B Cell Identity. Immunity, 2006, 24, 239-240.	6.6	1
57	Double TIP-ping. Science, 2010, 329, 914-915.	6.0	1
58	Targeting RNA polymerase II Mediator subunits in cancer therapy. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	1
59	Identification of the Origin of Eosinophils. Blood, 2015, 126, 886-886.	0.6	1
60	Regulation of B cell fate specification and V H gene rearrangements by Ikaros. FASEB Journal, 2008, 22, 844.7.	0.2	0
61	EBF restricts alternate lineage options and promotes B cell fate commitment independently of Pax5. FASEB Journal, 2008, 22, 844.4.	0.2	0
62	Molecular Mechanisms Underlying the Regulation of Alternate Macrophage and Neutrophil Gene Programs by the Egr Transcription Factors. Blood, 2008, 112, 4773-4773.	0.6	0
63	Organizational Properties of a Functional Mammalian Cis-Regulome. SSRN Electronic Journal, 0, , .	0.4	0