Harinder Singh

List of Publications by Year
in descending order

63 papers	17,214 citations	147801 31 h-index	133252 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. Molecular Cell, 2010, 38, 576-589.	9.7	10,215
2	Regulation of B Lymphocyte and Macrophage Development by Graded Expression of PU.1. Science, 2000, 288, 1439-1441.	12.6	627
3	Multilineage Transcriptional Priming and Determination of Alternate Hematopoietic Cell Fates. Cell, 2006, 126, 755-766.	28.9	572
4	Graded Expression of Interferon Regulatory Factor-4 Coordinates Isotype Switching with Plasma Cell Differentiation. Immunity, 2006, 25, 225-236.	14.3	480
5	Single-cell analysis of mixed-lineage states leading to a binary cell fate choice. Nature, 2016, 537, 698-702.	27.8	444
6	IFN Regulatory Factor-4 and -8 Govern Dendritic Cell Subset Development and Their Functional Diversity. Journal of Immunology, 2005, 174, 2573-2581.	0.8	390
7	Compensatory dendritic cell development mediated by BATFâ€"IRF interactions. Nature, 2012, 490, 502-507.	27.8	367
8	Transcriptional Regulation of Germinal Center B and Plasma Cell Fates by Dynamical Control of IRF4. Immunity, 2013, 38, 918-929.	14.3	356
9	Regulation of macrophage and neutrophil cell fates by the PU.1:C/EBPÎ± ratio and granulocyte colony-stimulating factor. Nature Immunology, 2003, 4, 1029-1036.	14.5	347
10	A Genomic Regulatory Element That Directs Assembly and Function of Immune-Specific AP-1â€"IRF Complexes. Science, 2012, 338, 975-980.	12.6	298
11	Interferon Regulatory Factor 4 (IRF4) Interacts with NFATc2 to Modulate Interleukin 4 Gene Expression. Journal of Experimental Medicine, 2002, 195, 1003-1012.	8.5	293
12	Orchestrating B cell lymphopoiesis through interplay of IL-7 receptor and pre-B cell receptor signalling. Nature Reviews Immunology, 2014, 14, 69-80.	22.7	252
13	Cooperative and Antagonistic Interplay between PU.1 and GATA-2 in the Specification of Myeloid Cell Fates. Immunity, 2002, 17, 665-676.	14.3	242
14	Transcriptional programming of dendritic cells for enhanced MHC class II antigen presentation. Nature Immunology, 2014, 15, 161-167.	14.5	224
15	Assembly requirements of PU.1â€"Pip (IRF-4) activator complexes: inhibiting function in vivo using fused dimers. EMBO Journal, 1999, 18, 977-991.	7.8	179
16	Contingent gene regulatory networks and B cell fate specification. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 4949-4953.	7.1	173
17	A Recurrent Network Involving the Transcription Factors PU.1 and Gfi1 Orchestrates Innate and Adaptive Immune Cell Fates. Immunity, 2009, 31, 576-586.	14.3	159
18	Specification of type 2 innate lymphocytes by the transcriptional determinant Gfi1. Nature Immunology, 2013, 14, 1229-1236.	14.5	158

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19	DoubletDecon: Deconvoluting Doublets from Single-Cell RNA-Sequencing Data. Cell Reports, 2019, 29, 1718-1727.e8.	6.4	134
20	An incoherent regulatory network architecture that orchestrates B cell diversification in response to antigen signaling. Molecular Systems Biology, 2011, 7, 495.	7.2	111
21	Regulation of bifurcating B cell trajectories by mutual antagonism between transcription factors IRF4 and IRF8. Nature Immunology, 2015, 16, 1274-1281.	14.5	108
22	Nonpeptidergic neurons suppress mast cells via glutamate to maintain skin homeostasis. Cell, 2021, 184, 2151-2166.e16.	28.9	87
23	Transcriptional determinants of tolerogenic and immunogenic states during dendritic cell maturation. Journal of Cell Biology, 2017, 216, 779-792.	5.2	82
24	Gene regulatory networks in the immune system. Trends in Immunology, 2014, 35, 211-218.	6.8	73
25	TSLP signaling in CD4 ⁺ T cells programs a pathogenic T helper 2 cell state. Science Signaling, 2018, 11, .	3.6	72
26	Competition for Active TGFÎ² Cytokine Allows for Selective Retention of Antigen-Specific Tissue-Resident Memory T Cells in the Epidermal Niche. Immunity, 2021, 54, 84-98.e5.	14.3	68
27	IL-10â€“producing Tfh cells accumulate with age and link inflammation with age-related immune suppression. Science Advances, 2020, 6, eabb0806.	10.3	67
28	Coupled analysis of transcriptome and BCR mutations reveals role of OXPHOS in affinity maturation. Nature Immunology, 2021, 22, 904-913.	14.5	62
29	Affinity Maturation Is Impaired by Natural Killer Cell Suppression of Germinal Centers. Cell Reports, 2018, 24, 3367-3373.e4.	6.4	59
30	Inhibiting Oxidative Phosphorylation In Vivo Restrains Th17 Effector Responses and Ameliorates Murine Colitis. Journal of Immunology, 2017, 198, 2735-2746.	0.8	56
31	Charting the cis-regulome of activated B cells by coupling structural and functional genomics. Nature Immunology, 2020, 21, 210-220.	14.5	40
32	Suppression of Inflammasome Activation by IRF8 and IRF4 in cDCs Is Critical for T Cell Priming. Cell Reports, 2020, 31, 107604.	6.4	40
33	Gimap5-dependent inactivation of GSK3Î² is required for CD4+ T cell homeostasis and prevention of immune pathology. Nature Communications, 2018, 9, 430.	12.8	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.	6.1	30
36	Genomic programming of IRF4-expressing human Langerhans cells. Nature Communications, 2020, 11, 313.	12.8	22

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37	Gene regulatory networks and the determination of lymphoid cell fates. Current Opinion in Immunology, 2006, 18, 116-120.	5.5	20
38	T-bet+CD27+CD21â€“ B cells poised for plasma cell differentiation during antibody-mediated rejection of kidney transplants. JCI Insight, 2021, 6, .	5.0	20
39	Proteasomal adaptations underlying carfilzomib-resistance in human bone marrow plasma cells. American Journal of Transplantation, 2020, 20, 399-410.	4.7	18
40	The Molecular Choreography of IRF4 and IRF8 with Immune System Partners. Cold Spring Harbor Symposia on Quantitative Biology, 2013, 78, 101-104.	1.1	17
41	Regulated Capture of VÎº Gene Topologically Associating Domains by Transcription Factories. Cell Reports, 2018, 24, 2443-2456.	6.4	16
42	Genetic analysis of transcription factors implicated in B lymphocyte development. Immunologic Research, 1994, 13, 280-290.	2.9	15
43	Crystallization and characterization of PU.1/IRF-4/DNA ternary complex. Journal of Structural Biology, 2002, 139, 55-59.	2.8	14
44	Cell fate dynamics and genomic programming of plasma cell precursors. Immunological Reviews, 2021, 303, 62-71.	6.0	11
45	People critically ill with COVID-19 exhibit peripheral immune profiles predictive of mortality and reflective of SARS-CoV-2 lung viral burden. Cell Reports Medicine, 2021, 2, 100476.	6.5	11
46	Antibodies targeting conserved non-canonical antigens and endemic coronaviruses associate with favorable outcomes in severe COVID-19. Cell Reports, 2022, 39, 111020.	6.4	11
47	Divergent COVID-19 Disease Trajectories Predicted by a DAMP-Centered Immune Network Model. Frontiers in Immunology, 2021, 12, 754127.	4.8	10
48	Tolerogenic and immunogenic states of Langerhans cells are orchestrated by epidermal signals acting on a core maturation gene module. BioEssays, 2021, 43, e2000182.	2.5	9
49	CISH attenuates homeostatic cytokine signaling to promote lung-specific macrophage programming and function. Science Signaling, 2021, 14, eabe5137.	3.6	9
50	SPaRTAN, a computational framework for linking cell-surface receptors to transcriptional regulators. Nucleic Acids Research, 2021, 49, 9633-9647.	14.5	9
51	Essential Regression: A generalizable framework for inferring causal latent factors from multi-omic datasets. Patterns, 2022, 3, 100473.	5.9	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. EBioMedicine, 2022, 76, 103860.	6.1	7
53	PU.1, a Shared Transcriptional Regulator of Innate and Adaptive Immune Cell Fates. Journal of Immunology, 2008, 181, 1595-1596.	0.8	5
54	Transcriptional and epigenetic networks orchestrating immune cell development and function. Immunological Reviews, 2014, 261, 5-8.	6.0	5

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55	Pseudocell Tracerâ€"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.	3.2	5
56	Shedding B Cell Identity. Immunity, 2006, 24, 239-240.	14.3	1
57	Double TIP-ping. Science, 2010, 329, 914-915.	12.6	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, .	7.1	1
59	Identification of the Origin of Eosinophils. Blood, 2015, 126, 886-886.	1.4	1
60	Regulation of B cell fate specification and V H gene rearrangements by Ikaros. FASEB Journal, 2008, 22, 844.7.	0.5	0
61	EBF restricts alternate lineage options and promotes B cell fate commitment independently of Pax5. FASEB Journal, 2008, 22, 844.4.	0.5	0
62	Molecular Mechanisms Underlying the Regulation of Alternate Macrophage and Neutrophil Gene Programs by the Egr Transcription Factors. Blood, 2008, 112, 4773-4773.	1.4	0
63	Organizational Properties of a Functional Mammalian Cis-Regulome. SSRN Electronic Journal, 0, , .	0.4	0