

# Wei Shi

## List of Publications by Year in descending order

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41  
papers

55,932  
citations

147801

31  
h-index

289244

40  
g-index

43  
all docs

43  
docs citations

43  
times ranked

91434  
citing authors

#	ARTICLE	IF	CITATIONS
1	limma powers differential expression analyses for RNA-sequencing and microarray studies. <i>Nucleic Acids Research</i> , 2015, 43, e47-e47.	14.5	26,032
2	featureCounts: an efficient general purpose program for assigning sequence reads to genomic features. <i>Bioinformatics</i> , 2014, 30, 923-930.	4.1	16,839
3	voom: precision weights unlock linear model analysis tools for RNA-seq read counts. <i>Genome Biology</i> , 2014, 15, R29.	9.6	4,603
4	The Subread aligner: fast, accurate and scalable read mapping by seed-and-vote. <i>Nucleic Acids Research</i> , 2013, 41, e108-e108.	14.5	2,389
5	The R package Rsubread is easier, faster, cheaper and better for alignment and quantification of RNA sequencing reads. <i>Nucleic Acids Research</i> , 2019, 47, e47-e47.	14.5	1,744
6	Hobit and Blimp1 instruct a universal transcriptional program of tissue residency in lymphocytes. <i>Science</i> , 2016, 352, 459-463.	12.6	721
7	The transcriptional regulators IRF4, BATF and IL-33 orchestrate development and maintenance of adipose tissue-resident regulatory T cells. <i>Nature Immunology</i> , 2015, 16, 276-285.	14.5	442
8	Transcription Factor IRF4 Promotes CD8+ T Cell Exhaustion and Limits the Development of Memory-like T Cells during Chronic Infection. <i>Immunity</i> , 2017, 47, 1129-1141.e5.	14.3	335
9	Transcriptional profiling of mouse B cell terminal differentiation defines a signature for antibody-secreting plasma cells. <i>Nature Immunology</i> , 2015, 16, 663-673.	14.5	332
10	Complementarity and redundancy of IL-22-producing innate lymphoid cells. <i>Nature Immunology</i> , 2016, 17, 179-186.	14.5	211
11	Blocking IL-6 trans-Signaling Prevents High-Fat Diet-Induced Adipose Tissue Macrophage Recruitment but Does Not Improve Insulin Resistance. <i>Cell Metabolism</i> , 2015, 21, 403-416.	16.2	208
12	Early precursor T cells establish and propagate T cell exhaustion in chronic infection. <i>Nature Immunology</i> , 2020, 21, 1256-1266.	14.5	160
13	A molecular threshold for effector CD8+ T cell differentiation controlled by transcription factors Blimp-1 and T-bet. <i>Nature Immunology</i> , 2016, 17, 422-432.	14.5	145
14	c-Maf-dependent Treg cell control of intestinal TH17 cells and IgA establishes host-microbiota homeostasis. <i>Nature Immunology</i> , 2019, 20, 471-481.	14.5	138
15	Deciphering the Innate Lymphoid Cell Transcriptional Program. <i>Cell Reports</i> , 2016, 17, 436-447.	6.4	131
16	The transcription factors IRF8 and PU.1 negatively regulate plasma cell differentiation. <i>Journal of Experimental Medicine</i> , 2014, 211, 2169-2181.	8.5	126
17	Assessing technical performance in differential gene expression experiments with external spike-in RNA control ratio mixtures. <i>Nature Communications</i> , 2014, 5, 5125.	12.8	122
18	Global Changes in the Mammary Epigenome Are Induced by Hormonal Cues and Coordinated by Ezh2. <i>Cell Reports</i> , 2013, 3, 411-426.	6.4	117

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19	The TNF Receptor Superfamily-NF- $\kappa$ B Axis Is Critical to Maintain Effector Regulatory T Cells in Lymphoid and Non-lymphoid Tissues. <i>Cell Reports</i> , 2017, 20, 2906-2920.	6.4	115
20	Haemopedia RNA-seq: a database of gene expression during haematopoiesis in mice and humans. <i>Nucleic Acids Research</i> , 2019, 47, D780-D785.	14.5	104
21	The Helix-Loop-Helix Protein ID2 Governs NK Cell Fate by Tuning Their Sensitivity to Interleukin-15. <i>Immunity</i> , 2016, 44, 103-115.	14.3	101
22	Transforming growth factor- $\beta$ 2 and Notch ligands act as opposing environmental cues in regulating the plasticity of type 3 innate lymphoid cells. <i>Science Signaling</i> , 2016, 9, ra46.	3.6	88
23	Effector Regulatory T Cell Differentiation and Immune Homeostasis Depend on the Transcription Factor Myb. <i>Immunity</i> , 2017, 46, 78-91.	14.3	83
24	Transforming growth factor- $\beta$ 2-regulated mTOR activity preserves cellular metabolism to maintain long-term T cell responses in chronic infection. <i>Immunity</i> , 2021, 54, 1698-1714.e5.	14.3	82
25	Pax5 loss imposes a reversible differentiation block in B-progenitor acute lymphoblastic leukemia. <i>Genes and Development</i> , 2014, 28, 1337-1350.	5.9	73
26	Peripheral natural killer cell maturation depends on the transcription factor Aiolos. <i>EMBO Journal</i> , 2014, 33, 2721-2734.	7.8	67
27	Dynamic changes in Id3 and E-protein activity orchestrate germinal center and plasma cell development. <i>Journal of Experimental Medicine</i> , 2016, 213, 1095-1111.	8.5	53
28	A lineage of diploid platelet-forming cells precedes polyploid megakaryocyte formation in the mouse embryo. <i>Blood</i> , 2014, 124, 2725-2729.	1.4	52
29	TCF-1 limits the formation of Tc17 cells via repression of the MAF-ROR $\gamma$ t axis. <i>Journal of Experimental Medicine</i> , 2019, 216, 1682-1699.	8.5	48
30	IRF4 Activity Is Required in Established Plasma Cells to Regulate Gene Transcription and Mitochondrial Homeostasis. <i>Cell Reports</i> , 2019, 29, 2634-2645.e5.	6.4	47
31	The transcription factor Nerfin-1 prevents reversion of neurons into neural stem cells. <i>Genes and Development</i> , 2015, 29, 129-143.	5.9	40
32	A crucial role for the homeodomain transcription factor Hhex in lymphopoiesis. <i>Blood</i> , 2015, 125, 803-814.	1.4	39
33	Transcription Factor T-bet in B Cells Modulates Germinal Center Polarization and Antibody Affinity Maturation in Response to Malaria. <i>Cell Reports</i> , 2019, 29, 2257-2269.e6.	6.4	36
34	Acute myeloid leukemia requires Hhex to enable PRC2-mediated epigenetic repression of <i>Cdkn2a</i> . <i>Genes and Development</i> , 2016, 30, 78-91.	5.9	30
35	Oct2 and Obf1 as Facilitators of B:T Cell Collaboration during a Humoral Immune Response. <i>Frontiers in Immunology</i> , 2014, 5, 108.	4.8	25
36	Read trimming is not required for mapping and quantification of RNA-seq reads at the gene level. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa068.	3.2	22

#	ARTICLE	IF	CITATIONS
37	Molecular profiling reveals features of clinical immunity and immunosuppression in asymptomatic <i>P. falciparum</i> malaria. <i>Molecular Systems Biology</i> , 2022, 18, e10824.	7.2	9
38	Impact of gene annotation choice on the quantification of RNA-seq data. <i>BMC Bioinformatics</i> , 2022, 23, 107.	2.6	8
39	IL-36G promotes cancer-cell intrinsic hallmarks in human gastric cancer cells. <i>Cytokine</i> , 2022, 155, 155887.	3.2	6
40	Whole transcriptome analysis for T cell receptor-affinity and IRF4-regulated clonal expansion of T cells. <i>Genomics Data</i> , 2014, 2, 396-398.	1.3	4
41	The NUP98-HOXD13 Fusion Oncogene Induces Thymocyte Self-Renewal Via Lmo2/Lyl1. <i>Blood</i> , 2018, 132, 2614-2614.	1.4	0