Yin C Lin

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/9539056/publications.pdf

Version: 2024-02-01

24 papers

12,370 citations

15 h-index 677142 22 g-index

28 all docs

 $\begin{array}{c} 28 \\ \text{docs citations} \end{array}$

28 times ranked

27251 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	A global network of transcription factors, involving E2A, EBF1 and Foxo1, that orchestrates B cell fate. Nature Immunology, 2010, 11, 635-643.	14.5	475
3	Stimulation of the XPB ATP-dependent helicase by the beta subunit of TFIIE. Nucleic Acids Research, 2005, 33, 3072-3081.	14.5	267
4	Global changes in the nuclear positioning of genes and intra- and interdomain genomic interactions that orchestrate B cell fate. Nature Immunology, 2012, 13, 1196-1204.	14.5	249
5	ICOS Coreceptor Signaling Inactivates the Transcription Factor FOXO1 to Promote Tfh Cell Differentiation. Immunity, 2015, 42, 239-251.	14.3	204
6	CCCTC-binding factor (CTCF) and cohesin influence the genomic architecture of the <i>Igh</i> locus and antisense transcription in pro-B cells. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 9566-9571.	7.1	195
7	Multilineage Priming of Enhancer Repertoires Precedes Commitment to the B and Myeloid Cell Lineages in Hematopoietic Progenitors. Immunity, 2011, 35, 413-425.	14.3	125
8	The opposing roles of the transcription factor E2A and its antagonist Id3 that orchestrate and enforce the naive fate of T cells. Nature Immunology, 2011, 12, 992-1001.	14.5	121
9	Positive intergenic feedback circuitry, involving EBF1 and FOXO1, orchestrates B-cell fate. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 21028-21033.	7.1	101
10	Active enhancer and chromatin accessibility landscapes chart the regulatory network of primary multiple myeloma. Blood, 2018, 131, 2138-2150.	1.4	77
11	TFIIH XPB mutants suggest a unified bacterial-like mechanism for promoter opening but not escape. Nature Structural and Molecular Biology, 2005, 12, 603-607.	8.2	74
12	The E-Id Protein Axis Specifies Adaptive Lymphoid Cell Identity and Suppresses Thymic Innate Lymphoid Cell Development. Immunity, 2017, 46, 818-834.e4.	14.3	73
13	Factors and networks that underpin early hematopoiesis. Seminars in Immunology, 2011, 23, 317-325.	5. 6	41
14	The transcription factor E2A activates multiple enhancers that drive <i>Rag</i> expression in developing T and B cells. Science Immunology, 2020, 5, .	11.9	41
15	Transcriptional Repression of IFN Regulatory Factor 7 by MYC Is Critical for Type I IFN Production in Human Plasmacytoid Dendritic Cells. Journal of Immunology, 2016, 197, 3348-3359.	0.8	37
16	Chromatin Accessibility Identifies Regulatory Elements Predictive of Gene Expression and Disease Outcome in Multiple Myeloma. Clinical Cancer Research, 2021, 27, 3178-3189.	7.0	15
17	CTCF Expression and Dynamic Motif Accessibility Modulates Epithelial–Mesenchymal Gene Expression. Cancers, 2022, 14, 209.	3.7	15
18	Plasma Cell Fate Is Orchestrated by Elaborate Changes in Genome Compartmentalization and Inter-chromosomal Hubs. Cell Reports, 2020, 31, 107470.	6.4	14

#	ARTICLE	IF	CITATION
19	The Schizosaccharomyces pombe Open Promoter Bubble: Mammalian-like Arrangement and Properties. Journal of Molecular Biology, 2004, 340, 981-989.	4.2	10
20	Nuclear location and the control of developmental progression. Current Opinion in Genetics and Development, 2013, 23, 104-108.	3.3	4
21	CRISPR Explorer: A fast and intuitive tool for designing guide RNA for genome editing. Journal of Biological Methods, 2016, 3, e56.	0.6	4
22	A Latent Inhibitor of Fibrin Polymerization with Ancillary Anticoagulant Activity. Thrombosis Research, 2000, 97, 375-378.	1.7	2
23	Abstract LB-B27: Novel antitumor agent GZ17-6.02 exerts discrete effects on transcriptional regulation in pancreatic cancer cells and cancer associated fibroblasts. , 2018, , .		1
24	Chromatin Accessibility Identifies Regulatory Elements Predictive of Oncogene Expression in Multiple Myeloma. Blood, 2020, 136, 31-32.	1.4	0