

Salvatore Spicuglia

List of Publications by Year in descending order

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Version: 2024-02-01

65
papers

4,050
citations

159525

30
h-index

128225

60
g-index

93
all docs

93
docs citations

93
times ranked

8653
citing authors

#	ARTICLE	IF	CITATIONS
1	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016, 167, 1145-1149.	13.5	404
2	BLUEPRINT to decode the epigenetic signature written in blood. <i>Nature Biotechnology</i> , 2012, 30, 224-226.	9.4	323
3	Transcription initiation platforms and GTF recruitment at tissue-specific enhancers and promoters. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 956-963.	3.6	296
4	H3K4 tri-methylation provides an epigenetic signature of active enhancers. <i>EMBO Journal</i> , 2011, 30, 4198-4210.	3.5	265
5	Genome-wide characterization of mammalian promoters with distal enhancer functions. <i>Nature Genetics</i> , 2017, 49, 1073-1081.	9.4	222
6	CpG islands and GC content dictate nucleosome depletion in a transcription-independent manner at mammalian promoters. <i>Genome Research</i> , 2012, 22, 2399-2408.	2.4	197
7	Chromatin Remodeling by the T Cell Receptor (Tcr)- \hat{I}^2 Gene Enhancer during Early T Cell Development. <i>Journal of Experimental Medicine</i> , 2000, 192, 625-636.	4.2	153
8	High-throughput and quantitative assessment of enhancer activity in mammals by CapStarr-seq. <i>Nature Communications</i> , 2015, 6, 6905.	5.8	138
9	Early Response-Based Therapy Stratification Improves Survival in Adult Early Thymic Precursor Acute Lymphoblastic Leukemia: A Group for Research on Adult Acute Lymphoblastic Leukemia Study. <i>Journal of Clinical Oncology</i> , 2017, 35, 2683-2691.	0.8	134
10	A unique H3K4me2 profile marks tissue-specific gene regulation. <i>Genome Research</i> , 2010, 20, 1493-1502.	2.4	117
11	Integrative analysis of public ChIP-seq experiments reveals a complex multi-cell regulatory landscape. <i>Nucleic Acids Research</i> , 2015, 43, e27-e27.	6.5	113
12	Characterization of Lysine 56 of Histone H3 as an Acetylation Site in <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2005, 280, 25949-25952.	1.6	105
13	Divergent transcription is associated with promoters of transcriptional regulators. <i>BMC Genomics</i> , 2013, 14, 914.	1.2	95
14	Promoter Activation by Enhancer-Dependent and -Independent Loading of Activator and Coactivator Complexes. <i>Molecular Cell</i> , 2002, 10, 1479-1487.	4.5	82
15	TLX Homeodomain Oncogenes Mediate T Cell Maturation Arrest in T-ALL via Interaction with ETS1 and Suppression of TCR \hat{I} Gene Expression. <i>Cancer Cell</i> , 2012, 21, 563-576.	7.7	81
16	Chromatin signatures of active enhancers. <i>Nucleus</i> , 2012, 3, 126-131.	0.6	70
17	Uncleaved TFIIA Is a Substrate for Taspase 1 and Active in Transcription. <i>Molecular and Cellular Biology</i> , 2006, 26, 2728-2735.	1.1	67
18	CD8 + T Cells from Human Neonates Are Biased toward an Innate Immune Response. <i>Cell Reports</i> , 2016, 17, 2151-2160.	2.9	64

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19	Widespread Enhancer Activity from Core Promoters. Trends in Biochemical Sciences, 2018, 43, 452-468.	3.7	54
20	Candidate Luminal B Breast Cancer Genes Identified by Genome, Gene Expression and DNA Methylation Profiling. PLoS ONE, 2014, 9, e81843.	1.1	53
21	An early thymic precursor phenotype predicts outcome exclusively in HOXA-overexpressing adult T-cell acute lymphoblastic leukemia: a Group for Research in Adult Acute Lymphoblastic Leukemia study. Haematologica, 2016, 101, 732-740.	1.7	53
22	Active STAT5 Regulates T-bet and Eomesodermin Expression in CD8 T Cells and Imprints a T-bet-Dependent Tc1 Program with Repressed IL-6/TGF- β 1 Signaling. Journal of Immunology, 2013, 191, 3712-3724.	0.4	49
23	Recent advances in high-throughput approaches to dissect enhancer function. F1000Research, 2017, 6, 939.	0.8	44
24	Transcriptional regulation by promoters with enhancer function. Transcription, 2018, 9, 307-314.	1.7	43
25	Definition of a T-Cell Receptor β Gene Core Enhancer of V(D)J Recombination by Transgenic Mapping. Molecular and Cellular Biology, 2000, 20, 42-53.	1.1	40
26	Dynamic recruitment of Ets1 to both nucleosome-occupied and -depleted enhancer regions mediates a transcriptional program switch during early T-cell differentiation. Nucleic Acids Research, 2016, 44, 3567-3585.	6.5	39
27	Cooperation between T cell receptor and Toll-like receptor 5 signaling for CD4 ⁺ T cell activation. Science Signaling, 2019, 12, .	1.6	38
28	Triggering the TCR Developmental Checkpoint Activates a Therapeutically Targetable Tumor Suppressive Pathway in T-cell Leukemia. Cancer Discovery, 2016, 6, 972-985.	7.7	33
29	Novel CD28-Responsive Enhancer Activated by CREB/ATF and AP-1 Families in the Human Interleukin-2 Receptor β -Chain Locus. Molecular and Cellular Biology, 2001, 21, 4515-4527.	1.1	32
30	Reversal of microRNA-150 silencing disadvantages crizotinib-resistant NPM-ALK(+) cell growth. Journal of Clinical Investigation, 2015, 125, 3505-3518.	3.9	32
31	In Vivo Reinsertion of Excised Episomes by the V(D)J Recombinase: A Potential Threat to Genomic Stability. PLoS Biology, 2007, 5, e43.	2.6	31
32	Extensive molecular mapping of TCR β - and TCR γ -involved chromosomal translocations reveals distinct mechanisms of oncogene activation in T-ALL. Blood, 2012, 120, 3298-3309.	0.6	31
33	Homeobox protein TLX3 activates miR-125b expression to promote T-cell acute lymphoblastic leukemia. Blood Advances, 2017, 1, 733-747.	2.5	31
34	Regulation of V(D)J recombination. Current Opinion in Immunology, 2006, 18, 158-163.	2.4	30
35	CoCAS: a ChIP-on-chip analysis suite. Bioinformatics, 2009, 25, 954-955.	1.8	25
36	Epigenetic Silencing Affects Asparaginase Sensitivity and Predicts Outcome in T-ALL. Clinical Cancer Research, 2019, 25, 2483-2493.	3.2	25

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37	Assessing the Role of the T Cell Receptor \hat{I}^2 Gene Enhancer in Regulating Coding Joint Formation during V(D)J Recombination. <i>Journal of Biological Chemistry</i> , 2003, 278, 18101-18109.	1.6	24
38	PRC2 loss of function confers a targetable vulnerability to BET proteins in T-ALL. <i>Blood</i> , 2021, 138, 1855-1869.	0.6	23
39	Characterisation of Genome-Wide PLZF/RARA Target Genes. <i>PLoS ONE</i> , 2011, 6, e24176.	1.1	22
40	Cryptic XPO1-MLLT10 translocation is associated with HOXA locus deregulation in T-ALL. <i>Blood</i> , 2014, 124, 3023-3025.	0.6	21
41	Epromoters function as a hub to recruit key transcription factors required for the inflammatory response. <i>Nature Communications</i> , 2021, 12, 6660.	5.8	20
42	Epigenetic control of Tcrb gene rearrangement. <i>Seminars in Immunology</i> , 2010, 22, 330-336.	2.7	19
43	RUNX1-dependent RAG1 deposition instigates human TCR \hat{I} locus rearrangement. <i>Journal of Experimental Medicine</i> , 2014, 211, 1821-1832.	4.2	19
44	Control of IL-2Ralpha gene expression: structural changes within the proximal enhancer/core promoter during T-cell development. <i>Nucleic Acids Research</i> , 2002, 30, 1944-1951.	6.5	17
45	Assessing the efficiency and significance of Methylated DNA Immunoprecipitation (MeDIP) assays in using in vitro methylated genomic DNA. <i>BMC Research Notes</i> , 2010, 3, 240.	0.6	17
46	A critical regulator of Bcl2 revealed by systematic transcript discovery of lncRNAs associated with T-cell differentiation. <i>Scientific Reports</i> , 2019, 9, 4707.	1.6	17
47	Blueprint of human thymopoiesis reveals molecular mechanisms of stage-specific TCR enhancer activation. <i>Journal of Experimental Medicine</i> , 2020, 217, .	4.2	15
48	Dynamics of broad H3K4me3 domains uncover an epigenetic switch between cell identity and cancer-related genes. <i>Genome Research</i> , 2022, 32, 1328-1342.	2.4	14
49	Duality of Enhancer Functioning Mode Revealed in a Reduced TCR \hat{I}^2 Gene Enhancer Knockin Mouse Model. <i>Journal of Immunology</i> , 2009, 183, 7939-7948.	0.4	13
50	Alternative Enhancer Usage and Targeted Polycomb Marking Hallmark Promoter Choice during T Cell Differentiation. <i>Cell Reports</i> , 2020, 32, 108048.	2.9	13
51	Epigenetic analysis of patients with T-ALL identifies poor outcomes and a hypomethylating agent-responsive subgroup. <i>Science Translational Medicine</i> , 2021, 13, .	5.8	13
52	An update on recent methods applied for deciphering the diversity of the noncoding RNA genome structure and function. <i>Methods</i> , 2013, 63, 3-17.	1.9	11
53	Molecular Genetics at the T-Cell Receptor \hat{I}^2 Locus: Insights into the Regulation of V(D)J Recombination. <i>Advances in Experimental Medicine and Biology</i> , 2009, 650, 116-132.	0.8	11
54	Transcription-Dependent Generation of a Specialized Chromatin Structure at the TCR \hat{I}^2 Locus. <i>Journal of Immunology</i> , 2015, 194, 3432-3443.	0.4	10

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55	Low level CpG island promoter methylation predicts a poor outcome in adult T-cell acute lymphoblastic leukemia. <i>Haematologica</i> , 2020, 105, 1575-1581.	1.7	10
56	Identification of ATP2B4 Regulatory Element Containing Functional Genetic Variants Associated with Severe Malaria. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4849.	1.8	9
57	TCR β Allelic Exclusion in Dynamical Models of V(D)J Recombination Based on Allele Independence. <i>Journal of Immunology</i> , 2010, 185, 1622-1632.	0.4	8
58	Epigenomic translocation of H3K4me3 broad domains over oncogenes following hijacking of super-enhancers. <i>Genome Research</i> , 2022, 32, 1343-1354.	2.4	8
59	Epigenetic regulation of antigen receptor gene rearrangement. <i>F1000 Biology Reports</i> , 2010, 2, .	4.0	7
60	Potassium permanganate as a probe to map DNA-protein interactions in vivo. <i>Journal of Proteomics</i> , 2004, 59, 189-194.	2.4	6
61	IL-12 Signaling Contributes to the Reprogramming of Neonatal CD8+ T Cells. <i>Frontiers in Immunology</i> , 2020, 11, 1089.	2.2	5
62	A comprehensive catalog of LncRNAs expressed in T-cell acute lymphoblastic leukemia. <i>Leukemia and Lymphoma</i> , 2019, 60, 2002-2014.	0.6	4
63	Integration of high-throughput reporter assays identify a critical enhancer of the <i>Ikzf1</i> gene. <i>PLoS ONE</i> , 2020, 15, e0233191.	1.1	4
64	Protein complexes associated with β -catenin differentially influence the differentiation profile of neonatal and adult CD8 + T cells. <i>Journal of Cellular Physiology</i> , 2019, 234, 18639-18652.	2.0	2
65	The Role of Epigenetics in Cancer: From Molecular Function to High-Throughput Assays. , 2012, , 137-152.		0