

Salvatore Spicuglia

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

64

papers

3,057

citations

28

h-index

55

g-index

93

ext. papers

3,760

ext. citations

10.7

avg, IF

4.56

L-index

#	Paper	IF	Citations
64	Epromoters function as a hub to recruit key transcription factors required for the inflammatory response. <i>Nature Communications</i> , 2021 , 12, 6660	17.4	2
63	Epigenetic analysis of patients with T-ALL identifies poor outcomes and a hypomethylating agent-responsive subgroup. <i>Science Translational Medicine</i> , 2021 , 13,	17.5	3
62	Dynamic of broad H3K4me3 domains uncover an epigenetic switch between cell identity and cancer-related genes. <i>Genome Research</i> , 2021 ,	9.7	3
61	PRC2 loss of function confers a targetable vulnerability to BET proteins in T-ALL. <i>Blood</i> , 2021 , 138, 1855-1869	18.69	8
60	Low level CpG island promoter methylation predicts a poor outcome in adult T-cell acute lymphoblastic leukemia. <i>Haematologica</i> , 2020 , 105, 1575-1581	6.6	7
59	Integration of high-throughput reporter assays identify a critical enhancer of the Ikzf1 gene. <i>PLoS ONE</i> , 2020 , 15, e0233191	3.7	2
58	IL-12 Signaling Contributes to the Reprogramming of Neonatal CD8 T Cells. <i>Frontiers in Immunology</i> , 2020 , 11, 1089	8.4	3
57	Alternative Enhancer Usage and Targeted Polycomb Marking Hallmark Promoter Choice during T Cell Differentiation. <i>Cell Reports</i> , 2020 , 32, 108048	10.6	3
56	Blueprint of human thymopoiesis reveals molecular mechanisms of stage-specific TCR enhancer activation. <i>Journal of Experimental Medicine</i> , 2020 , 217,	16.6	6
55	Epigenetic Silencing Affects L-Asparaginase Sensitivity and Predicts Outcome in T-ALL. <i>Clinical Cancer Research</i> , 2019 , 25, 2483-2493	12.9	15
54	Cooperation between T cell receptor and Toll-like receptor 5 signaling for CD4 T cell activation. <i>Science Signaling</i> , 2019 , 12,	8.8	19
53	A critical regulator of Bcl2 revealed by systematic transcript discovery of lncRNAs associated with T-cell differentiation. <i>Scientific Reports</i> , 2019 , 9, 4707	4.9	6
52	Protein complexes associated with Eatenin differentially influence the differentiation profile of neonatal and adult CD8 T cells. <i>Journal of Cellular Physiology</i> , 2019 , 234, 18639-18652	7	1
51	A comprehensive catalog of lncRNAs expressed in T-cell acute lymphoblastic leukemia. <i>Leukemia and Lymphoma</i> , 2019 , 60, 2002-2014	1.9	2
50	Widespread Enhancer Activity from Core Promoters. <i>Trends in Biochemical Sciences</i> , 2018 , 43, 452-468	10.3	35
49	Transcriptional regulation by promoters with enhancer function. <i>Transcription</i> , 2018 , 9, 307-314	4.8	19
48	Genome-wide characterization of mammalian promoters with distal enhancer functions. <i>Nature Genetics</i> , 2017 , 49, 1073-1081	36.3	143

47	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	2.2	89
46	Homeobox protein TLX3 activates miR-125b expression to promote T-cell acute lymphoblastic leukemia. <i>Blood Advances</i> , 2017 , 1, 733-747	7.8	19
45	Recent advances in high-throughput approaches to dissect enhancer function. <i>F1000Research</i> , 2017 , 6, 939	3.6	23
44	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016 , 167, 1145-1149	56.2	232
43	CD8 T Cells from Human Neonates Are Biased toward an Innate Immune Response. <i>Cell Reports</i> , 2016 , 17, 2151-2160	10.6	34
42	Triggering the TCR Developmental Checkpoint Activates a Therapeutically Targetable Tumor Suppressive Pathway in T-cell Leukemia. <i>Cancer Discovery</i> , 2016 , 6, 972-85	24.4	24
41	Dynamic recruitment of Ets1 to both nucleosome-occupied and -depleted enhancer regions mediates a transcriptional program switch during early T-cell differentiation. <i>Nucleic Acids Research</i> , 2016 , 44, 3567-85	20.1	31
40	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. <i>Haematologica</i> , 2016 , 101, 732-40	6.6	36
39	Integrative analysis of public CHIP-seq experiments reveals a complex multi-cell regulatory landscape. <i>Nucleic Acids Research</i> , 2015 , 43, e27	20.1	95
38	High-throughput and quantitative assessment of enhancer activity in mammals by CapStarr-seq. <i>Nature Communications</i> , 2015 , 6, 6905	17.4	93
37	Transcription-dependent generation of a specialized chromatin structure at the TCR β locus. <i>Journal of Immunology</i> , 2015 , 194, 3432-43	5.3	9
36	Reversal of microRNA-150 silencing disadvantages crizotinib-resistant NPM-ALK(+) cell growth. <i>Journal of Clinical Investigation</i> , 2015 , 125, 3505-18	15.9	28
35	RUNX1-dependent RAG1 deposition instigates human TCR β locus rearrangement. <i>Journal of Experimental Medicine</i> , 2014 , 211, 1821-32	16.6	16
34	Cryptic XPO1-MLLT10 translocation is associated with HOXA locus deregulation in T-ALL. <i>Blood</i> , 2014 , 124, 3023-5	2.2	16
33	Candidate luminal B breast cancer genes identified by genome, gene expression and DNA methylation profiling. <i>PLoS ONE</i> , 2014 , 9, e81843	3.7	42
32	RUNX1-dependent RAG1 deposition instigates human TCR β locus rearrangement. <i>Journal of Experimental Medicine</i> , 2014 , 211, 2681-2681	16.6	78
31	Divergent transcription is associated with promoters of transcriptional regulators. <i>BMC Genomics</i> , 2013 , 14, 914	4.5	83
30	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	4.6	8

29	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 signaling. <i>Journal of Immunology</i> , 2013 , 191, 3712-24	5.3	39
28	Extensive molecular mapping of TCR β and TCR α involved chromosomal translocations reveals distinct mechanisms of oncogene activation in T-ALL. <i>Blood</i> , 2012 , 120, 3298-309	2.2	20
27	CpG islands and GC content dictate nucleosome depletion in a transcription-independent manner at mammalian promoters. <i>Genome Research</i> , 2012 , 22, 2399-408	9.7	152
26	Chromatin signatures of active enhancers. <i>Nucleus</i> , 2012 , 3, 126-31	3.9	37
25	TLX homeodomain oncogenes mediate T cell maturation arrest in T-ALL via interaction with ETS1 and suppression of TCR β gene expression. <i>Cancer Cell</i> , 2012 , 21, 563-76	24.3	72
24	BLUEPRINT to decode the epigenetic signature written in blood. <i>Nature Biotechnology</i> , 2012 , 30, 224-6	44.5	261
23	The Role of Epigenetics in Cancer: From Molecular Function to High-Throughput Assays 2012 , 137-152		
22	H3K4 tri-methylation provides an epigenetic signature of active enhancers. <i>EMBO Journal</i> , 2011 , 30, 4198-210	22.2	
21	Transcription initiation platforms and GTF recruitment at tissue-specific enhancers and promoters. <i>Nature Structural and Molecular Biology</i> , 2011 , 18, 956-63	17.6	227
20	Characterisation of genome-wide PLZF/RARA target genes. <i>PLoS ONE</i> , 2011 , 6, e24176	3.7	19
19	TCR beta allelic exclusion in dynamical models of V(D)J recombination based on allele independence. <i>Journal of Immunology</i> , 2010 , 185, 1622-32	5.3	7
18	Epigenetic control of Tcrb gene rearrangement. <i>Seminars in Immunology</i> , 2010 , 22, 330-6	10.7	16
17	A unique H3K4me2 profile marks tissue-specific gene regulation. <i>Genome Research</i> , 2010 , 20, 1493-502	9.7	91
16	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	2.3	17
15	Epigenetic regulation of antigen receptor gene rearrangement. <i>F1000 Biology Reports</i> , 2010 , 2,		6
14	Duality of enhancer functioning mode revealed in a reduced TCR beta gene enhancer knockin mouse model. <i>Journal of Immunology</i> , 2009 , 183, 7939-48	5.3	12
13	CoCAS: a ChIP-on-chip analysis suite. <i>Bioinformatics</i> , 2009 , 25, 954-5	7.2	23
12	Molecular genetics at the T-cell receptor beta locus: insights into the regulation of V(D)J recombination. <i>Advances in Experimental Medicine and Biology</i> , 2009 , 650, 116-32	3.6	10

11	In vivo reinsertion of excised episomes by the V(D)J recombinase: a potential threat to genomic stability. <i>PLoS Biology</i> , 2007 , 5, e43	9.7	29
10	Regulation of V(D)J recombination. <i>Current Opinion in Immunology</i> , 2006 , 18, 158-63	7.8	26
9	Uncleaved TFIIA is a substrate for taspase 1 and active in transcription. <i>Molecular and Cellular Biology</i> , 2006 , 26, 2728-35	4.8	61
8	Characterization of lysine 56 of histone H3 as an acetylation site in <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2005 , 280, 25949-52	5.4	97
7	Potassium permanganate as a probe to map DNA-protein interactions in vivo. <i>Journal of Proteomics</i> , 2004 , 59, 189-94		4
6	Assessing the role of the T cell receptor beta gene enhancer in regulating coding joint formation during V(D)J recombination. <i>Journal of Biological Chemistry</i> , 2003 , 278, 18101-9	5.4	22
5	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, 1944-51	20.1	15
4	Promoter activation by enhancer-dependent and -independent loading of activator and coactivator complexes. <i>Molecular Cell</i> , 2002 , 10, 1479-87	17.6	77
3	Novel CD28-responsive enhancer activated by CREB/ATF and AP-1 families in the human interleukin-2 receptor alpha-chain locus. <i>Molecular and Cellular Biology</i> , 2001 , 21, 4515-27	4.8	28
2	Definition of a T-cell receptor beta gene core enhancer of V(D)J recombination by transgenic mapping. <i>Molecular and Cellular Biology</i> , 2000 , 20, 42-53	4.8	36
1	Chromatin remodeling by the T cell receptor (TCR)-beta gene enhancer during early T cell development: Implications for the control of TCR-beta locus recombination. <i>Journal of Experimental Medicine</i> , 2000 , 192, 625-36	16.6	144