

# Salvatore Spicuglia

## List of Publications by Citations

**Source:** <https://exaly.com/author-pdf/6272362/salvatore-spicuglia-publications-by-citations.pdf>

**Version:** 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	BLUEPRINT to decode the epigenetic signature written in blood. <i>Nature Biotechnology</i> , <b>2012</b> , 30, 224-6	44.5	261
63	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , <b>2016</b> , 167, 1145-1149	56.2	232
62	Transcription initiation platforms and GTF recruitment at tissue-specific enhancers and promoters. <i>Nature Structural and Molecular Biology</i> , <b>2011</b> , 18, 956-63	17.6	227
61	H3K4 tri-methylation provides an epigenetic signature of active enhancers. <i>EMBO Journal</i> , <b>2011</b> , 30, 4198-210	21.0	222
60	CpG islands and GC content dictate nucleosome depletion in a transcription-independent manner at mammalian promoters. <i>Genome Research</i> , <b>2012</b> , 22, 2399-408	9.7	152
59	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> , <b>2000</b> , 192, 625-36	16.6	144
58	Genome-wide characterization of mammalian promoters with distal enhancer functions. <i>Nature Genetics</i> , <b>2017</b> , 49, 1073-1081	36.3	143
57	Characterization of lysine 56 of histone H3 as an acetylation site in <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , <b>2005</b> , 280, 25949-52	5.4	97
56	Integrative analysis of public ChIP-seq experiments reveals a complex multi-cell regulatory landscape. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, e27	20.1	95
55	High-throughput and quantitative assessment of enhancer activity in mammals by CapStarr-seq. <i>Nature Communications</i> , <b>2015</b> , 6, 6905	17.4	93
54	A unique H3K4me2 profile marks tissue-specific gene regulation. <i>Genome Research</i> , <b>2010</b> , 20, 1493-502	9.7	91
53	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> , <b>2017</b> , 35, 2683-2691	2.2	89
52	Divergent transcription is associated with promoters of transcriptional regulators. <i>BMC Genomics</i> , <b>2013</b> , 14, 914	4.5	83
51	RUNX1-dependent RAG1 deposition instigates human TCR- $\beta$ locus rearrangement. <i>Journal of Experimental Medicine</i> , <b>2014</b> , 211, 2681-2681	16.6	78
50	Promoter activation by enhancer-dependent and -independent loading of activator and coactivator complexes. <i>Molecular Cell</i> , <b>2002</b> , 10, 1479-87	17.6	77
49	TLX homeodomain oncogenes mediate T cell maturation arrest in T-ALL via interaction with ETS1 and suppression of TCR $\beta$ gene expression. <i>Cancer Cell</i> , <b>2012</b> , 21, 563-76	24.3	72
48	Uncleaved TFIIA is a substrate for caspase 1 and active in transcription. <i>Molecular and Cellular Biology</i> , <b>2006</b> , 26, 2728-35	4.8	61

47	Candidate luminal B breast cancer genes identified by genome, gene expression and DNA methylation profiling. <i>PLoS ONE</i> , <b>2014</b> , 9, e81843	3.7	42
46	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- $\beta$ signaling. <i>Journal of Immunology</i> , <b>2013</b> , 191, 3712-24	5.3	39
45	Chromatin signatures of active enhancers. <i>Nucleus</i> , <b>2012</b> , 3, 126-31	3.9	37
44	Definition of a T-cell receptor beta gene core enhancer of V(D)J recombination by transgenic mapping. <i>Molecular and Cellular Biology</i> , <b>2000</b> , 20, 42-53	4.8	36
43	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> , <b>2016</b> , 101, 732-40	6.6	36
42	Widespread Enhancer Activity from Core Promoters. <i>Trends in Biochemical Sciences</i> , <b>2018</b> , 43, 452-468	10.3	35
41	CD8 T Cells from Human Neonates Are Biased toward an Innate Immune Response. <i>Cell Reports</i> , <b>2016</b> , 17, 2151-2160	10.6	34
40	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> , <b>2016</b> , 44, 3567-85	20.1	31
39	In vivo reinsertion of excised episomes by the V(D)J recombinase: a potential threat to genomic stability. <i>PLoS Biology</i> , <b>2007</b> , 5, e43	9.7	29
38	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> , <b>2001</b> , 21, 4515-27	4.8	28
37	Reversal of microRNA-150 silencing disadvantages crizotinib-resistant NPM-ALK(+) cell growth. <i>Journal of Clinical Investigation</i> , <b>2015</b> , 125, 3505-18	15.9	28
36	Regulation of V(D)J recombination. <i>Current Opinion in Immunology</i> , <b>2006</b> , 18, 158-63	7.8	26
35	Triggering the TCR Developmental Checkpoint Activates a Therapeutically Targetable Tumor Suppressive Pathway in T-cell Leukemia. <i>Cancer Discovery</i> , <b>2016</b> , 6, 972-85	24.4	24
34	CoCAS: a ChIP-on-chip analysis suite. <i>Bioinformatics</i> , <b>2009</b> , 25, 954-5	7.2	23
33	Recent advances in high-throughput approaches to dissect enhancer function. <i>F1000Research</i> , <b>2017</b> , 6, 939	3.6	23
32	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> , <b>2003</b> , 278, 18101-9	5.4	22
31	Extensive molecular mapping of TCR $\beta$ and TCR $\alpha$ involved chromosomal translocations reveals distinct mechanisms of oncogene activation in T-ALL. <i>Blood</i> , <b>2012</b> , 120, 3298-309	2.2	20
30	Cooperation between T cell receptor and Toll-like receptor 5 signaling for CD4 T cell activation. <i>Science Signaling</i> , <b>2019</b> , 12,	8.8	19

29	Transcriptional regulation by promoters with enhancer function. <i>Transcription</i> , <b>2018</b> , 9, 307-314	4.8	19
28	Homeobox protein TLX3 activates miR-125b expression to promote T-cell acute lymphoblastic leukemia. <i>Blood Advances</i> , <b>2017</b> , 1, 733-747	7.8	19
27	Characterisation of genome-wide PLZF/RARA target genes. <i>PLoS ONE</i> , <b>2011</b> , 6, e24176	3.7	19
26	Assessing the efficiency and significance of Methylated DNA Immunoprecipitation (MeDIP) assays in using in vitro methylated genomic DNA. <i>BMC Research Notes</i> , <b>2010</b> , 3, 240	2.3	17
25	RUNX1-dependent RAG1 deposition instigates human TCR- $\beta$ locus rearrangement. <i>Journal of Experimental Medicine</i> , <b>2014</b> , 211, 1821-32	16.6	16
24	Cryptic XPO1-MLLT10 translocation is associated with HOXA locus deregulation in T-ALL. <i>Blood</i> , <b>2014</b> , 124, 3023-5	2.2	16
23	Epigenetic control of Tcrb gene rearrangement. <i>Seminars in Immunology</i> , <b>2010</b> , 22, 330-6	10.7	16
22	Epigenetic Silencing Affects L-Asparaginase Sensitivity and Predicts Outcome in T-ALL. <i>Clinical Cancer Research</i> , <b>2019</b> , 25, 2483-2493	12.9	15
21	Control of IL-2Ralpha gene expression: structural changes within the proximal enhancer/core promoter during T-cell development. <i>Nucleic Acids Research</i> , <b>2002</b> , 30, 1944-51	20.1	15
20	Duality of enhancer functioning mode revealed in a reduced TCR beta gene enhancer knockin mouse model. <i>Journal of Immunology</i> , <b>2009</b> , 183, 7939-48	5.3	12
19	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> , <b>2009</b> , 650, 116-32	3.6	10
18	Transcription-dependent generation of a specialized chromatin structure at the TCR $\beta$ locus. <i>Journal of Immunology</i> , <b>2015</b> , 194, 3432-43	5.3	9
17	An update on recent methods applied for deciphering the diversity of the noncoding RNA genome structure and function. <i>Methods</i> , <b>2013</b> , 63, 3-17	4.6	8
16	PRC2 loss of function confers a targetable vulnerability to BET proteins in T-ALL. <i>Blood</i> , <b>2021</b> , 138, 1855-1869	18.69	8
15	Low level CpG island promoter methylation predicts a poor outcome in adult T-cell acute lymphoblastic leukemia. <i>Haematologica</i> , <b>2020</b> , 105, 1575-1581	6.6	7
14	TCR beta allelic exclusion in dynamical models of V(D)J recombination based on allele independence. <i>Journal of Immunology</i> , <b>2010</b> , 185, 1622-32	5.3	7
13	A critical regulator of Bcl2 revealed by systematic transcript discovery of lncRNAs associated with T-cell differentiation. <i>Scientific Reports</i> , <b>2019</b> , 9, 4707	4.9	6
12	Epigenetic regulation of antigen receptor gene rearrangement. <i>F1000 Biology Reports</i> , <b>2010</b> , 2,		6

11	Blueprint of human thymopoiesis reveals molecular mechanisms of stage-specific TCR enhancer activation. <i>Journal of Experimental Medicine</i> , <b>2020</b> , 217,	16.6	6
10	Potassium permanganate as a probe to map DNA-protein interactions in vivo. <i>Journal of Proteomics</i> , <b>2004</b> , 59, 189-94		4
9	IL-12 Signaling Contributes to the Reprogramming of Neonatal CD8 T Cells. <i>Frontiers in Immunology</i> , <b>2020</b> , 11, 1089	8.4	3
8	Alternative Enhancer Usage and Targeted Polycomb Marking Hallmark Promoter Choice during T Cell Differentiation. <i>Cell Reports</i> , <b>2020</b> , 32, 108048	10.6	3
7	Epigenetic analysis of patients with T-ALL identifies poor outcomes and a hypomethylating agent-responsive subgroup. <i>Science Translational Medicine</i> , <b>2021</b> , 13,	17.5	3
6	Dynamic of broad H3K4me3 domains uncover an epigenetic switch between cell identity and cancer-related genes. <i>Genome Research</i> , <b>2021</b> ,	9.7	3
5	Integration of high-throughput reporter assays identify a critical enhancer of the Ikzf1 gene. <i>PLoS ONE</i> , <b>2020</b> , 15, e0233191	3.7	2
4	Epromoters function as a hub to recruit key transcription factors required for the inflammatory response. <i>Nature Communications</i> , <b>2021</b> , 12, 6660	17.4	2
3	A comprehensive catalog of LncRNAs expressed in T-cell acute lymphoblastic leukemia. <i>Leukemia and Lymphoma</i> , <b>2019</b> , 60, 2002-2014	1.9	2
2	Protein complexes associated with Ecatenin differentially influence the differentiation profile of neonatal and adult CD8 T cells. <i>Journal of Cellular Physiology</i> , <b>2019</b> , 234, 18639-18652	7	1
1	The Role of Epigenetics in Cancer: From Molecular Function to High-Throughput Assays <b>2012</b> , 137-152		