

# Pierre Cauchy

## List of Publications by Year in descending order

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Version: 2024-02-01

44  
papers

2,362  
citations

279701

23  
h-index

276775

41  
g-index

47  
all docs

47  
docs citations

47  
times ranked

4702  
citing authors

#	ARTICLE	IF	CITATIONS
1	Multilayer omics analysis reveals a non-classical retinoic acid signaling axis that regulates hematopoietic stem cell identity. <i>Cell Stem Cell</i> , 2022, 29, 131-148.e10.	5.2	40
2	Sequences to Differences in Gene Expression: Analysis of RNA-Seq Data. <i>Methods in Molecular Biology</i> , 2022, , 279-318.	0.4	2
3	ZFP451-mediated SUMOylation of SATB2 drives embryonic stem cell differentiation. <i>Genes and Development</i> , 2021, 35, 1142-1160.	2.7	9
4	Interactions between lineage-associated transcription factors govern haematopoietic progenitor states. <i>EMBO Journal</i> , 2020, 39, e104983.	3.5	20
5	Repetitive Elements Trigger RIG-I-like Receptor Signaling that Regulates the Emergence of Hematopoietic Stem and Progenitor Cells. <i>Immunity</i> , 2020, 53, 934-951.e9.	6.6	43
6	ERBB2b mRNA isoform encodes a nuclear variant of the ERBB2 oncogene in breast cancer. <i>Journal of Cellular Biochemistry</i> , 2020, 121, 4870-4886.	1.2	0
7	EBF1-deficient bone marrow stroma elicits persistent changes in HSC potential. <i>Nature Immunology</i> , 2020, 21, 261-273.	7.0	30
8	High WBP5 expression correlates with elevation of HOX genes levels and is associated with inferior survival in patients with acute myeloid leukaemia. <i>Scientific Reports</i> , 2020, 10, 3505.	1.6	10
9	Subtype-specific regulatory network rewiring in acute myeloid leukemia. <i>Nature Genetics</i> , 2019, 51, 151-162.	9.4	140
10	Global long terminal repeat activation participates in establishing the unique gene expression programme of classical Hodgkin lymphoma. <i>Leukemia</i> , 2019, 33, 1463-1474.	3.3	19
11	Dependence on Myb expression is attenuated in myeloid leukaemia with N-terminal CEBPA mutations. <i>Life Science Alliance</i> , 2019, 2, e201800207.	1.3	6
12	2HybridTools, a handy software to facilitate clone identification and mutation mapping from yeast two-hybrid screening. <i>PeerJ</i> , 2019, 7, e7245.	0.9	0
13	Dynamic EBF1 occupancy directs sequential epigenetic and transcriptional events in B-cell programming. <i>Genes and Development</i> , 2018, 32, 96-111.	2.7	76
14	A metabolic interplay coordinated by HLX regulates myeloid differentiation and AML through partly overlapping pathways. <i>Nature Communications</i> , 2018, 9, 3090.	5.8	21
15	Fine-Tuning Mybl2 Is Required for Proper Mesenchymal-to-Epithelial Transition during Somatic Reprogramming. <i>Cell Reports</i> , 2018, 24, 1496-1511.e8.	2.9	18
16	Two possible modes of pioneering associated with combinations of H2A.Z and p300/CBP at nucleosome-occupied enhancers. <i>Transcription</i> , 2017, 8, 179-184.	1.7	7
17	RUNX1-ETO and RUNX1-EVI1 Differentially Reprogram the Chromatin Landscape in t(8;21) and t(3;21) AML. <i>Cell Reports</i> , 2017, 19, 1654-1668.	2.9	46
18	Chromatin priming elements establish immunological memory in T cells without activating transcription. <i>BioEssays</i> , 2017, 39, 1600184.	1.2	25

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19	Integration of Kinase and Calcium Signaling at the Level of Chromatin Underlies Inducible Gene Activation in T Cells. <i>Journal of Immunology</i> , 2017, 199, 2652-2667.	0.4	51
20	Prognostic significance of high GFI1 expression in AML of normal karyotype and its association with a FLT3-ITD signature. <i>Scientific Reports</i> , 2017, 7, 11148.	1.6	16
21	T Cell Receptor and Cytokine Signaling Can Function at Different Stages to Establish and Maintain Transcriptional Memory and Enable T Helper Cell Differentiation. <i>Frontiers in Immunology</i> , 2017, 8, 204.	2.2	25
22	LMO2 is required for TAL1 DNA binding activity and initiation of definitive haematopoiesis at the haemangioblast stage. <i>Nucleic Acids Research</i> , 2017, 45, 9874-9888.	6.5	22
23	Cooperative binding of AP-1 and TEAD4 modulates the balance between vascular smooth muscle and hemogenic cell fate. <i>Development (Cambridge)</i> , 2016, 143, 4324-4340.	1.2	43
24	A threshold level of NFATc1 activity facilitates thymocyte differentiation and opposes notch-driven leukaemia development. <i>Nature Communications</i> , 2016, 7, 11841.	5.8	23
25	Pasha: a versatile R package for piling chromatin HTS data. <i>Bioinformatics</i> , 2016, 32, 2528-2530.	1.8	21
26	Inducible chromatin priming is associated with the establishment of immunological memory in T cells. <i>EMBO Journal</i> , 2016, 35, 515-535.	3.5	92
27	Dynamic Gene Regulatory Networks Drive Hematopoietic Specification and Differentiation. <i>Developmental Cell</i> , 2016, 36, 572-587.	3.1	213
28	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, 3567-3585.	6.5	39
29	Wellington-bootstrap: differential DNase-seq footprinting identifies cell-type determining transcription factors. <i>BMC Genomics</i> , 2015, 16, 1000.	1.2	49
30	Cytokine and proinflammatory gene expression in classical Hodgkin lymphoma: Its more than NF- $\kappa$ B!. <i>Cytokine</i> , 2015, 72, 115-117.	1.4	0
31	The RUNX1-PU.1 axis in the control of hematopoiesis. <i>International Journal of Hematology</i> , 2015, 101, 319-329.	0.7	78
32	Transcription-Dependent Generation of a Specialized Chromatin Structure at the TCR $\beta$ Locus. <i>Journal of Immunology</i> , 2015, 194, 3432-3443.	0.4	10
33	Chronic FLT3-ITD Signaling in Acute Myeloid Leukemia Is Connected to a Specific Chromatin Signature. <i>Cell Reports</i> , 2015, 12, 821-836.	2.9	63
34	Polycomb Protein EED is Required for Silencing of Pluripotency Genes upon ESC Differentiation. <i>Stem Cell Reviews and Reports</i> , 2015, 11, 50-61.	5.6	31
35	A multi-centre phase 2 study of azacitidine in chronic myelomonocytic leukaemia. <i>Leukemia</i> , 2014, 28, 1570-1572.	3.3	34
36	Wellington: a novel method for the accurate identification of digital genomic footprints from DNase-seq data. <i>Nucleic Acids Research</i> , 2014, 42, 11272-11272.	6.5	3

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37	Identification of a Dynamic Core Transcriptional Network in t(8;21) AML that Regulates Differentiation Block and Self-Renewal. <i>Cell Reports</i> , 2014, 8, 1974-1988.	2.9	106
38	Mapping of transcription factor motifs in active chromatin identifies IRF5 as key regulator in classical Hodgkin lymphoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4513-22.	3.3	53
39	Wellington: a novel method for the accurate identification of digital genomic footprints from DNase-seq data. <i>Nucleic Acids Research</i> , 2013, 41, e201-e201.	6.5	196
40	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
41	Depletion of RUNX1/ETO in t(8;21) AML cells leads to genome-wide changes in chromatin structure and transcription factor binding. <i>Leukemia</i> , 2012, 26, 1829-1841.	3.3	161
42	Processing CHIP-Chip Data: From the Scanner to the Browser. <i>Methods in Molecular Biology</i> , 2011, 719, 251-268.	0.4	2
43	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
44	CoCAS: a ChIP-on-chip analysis suite. <i>Bioinformatics</i> , 2009, 25, 954-955.	1.8	25