Pierre Cauchy

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/2710327/publications.pdf

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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	Transcription initiation platforms and GTF recruitment at tissue-specific enhancers and promoters. Nature Structural and Molecular Biology, 2011, 18, 956-963.	3.6	296
2	Dynamic Gene Regulatory Networks Drive Hematopoietic Specification and Differentiation. Developmental Cell, 2016, 36, 572-587.	3.1	213
3	CpG islands and GC content dictate nucleosome depletion in a transcription-independent manner at mammalian promoters. Genome Research, 2012, 22, 2399-2408.	2.4	197
4	Wellington: a novel method for the accurate identification of digital genomic footprints from DNase-seq data. Nucleic Acids Research, 2013, 41, e201-e201.	6.5	196
5	Depletion of RUNX1/ETO in t(8;21) AML cells leads to genome-wide changes in chromatin structure and transcription factor binding. Leukemia, 2012, 26, 1829-1841.	3.3	161
6	Subtype-specific regulatory network rewiring in acute myeloid leukemia. Nature Genetics, 2019, 51, 151-162.	9.4	140
7	Identification of a Dynamic Core Transcriptional Network in t(8;21) AML that Regulates Differentiation Block and Self-Renewal. Cell Reports, 2014, 8, 1974-1988.	2.9	106
8	Inducible chromatin priming is associated with the establishment of immunological memory in T cells. EMBO Journal, 2016, 35, 515-535.	3.5	92
9	The RUNX1â€“PU.1 axis in the control of hematopoiesis. International Journal of Hematology, 2015, 101, 319-329.	0.7	78
10	Dynamic EBF1 occupancy directs sequential epigenetic and transcriptional events in B-cell programming. Genes and Development, 2018, 32, 96-111.	2.7	76
11	Chronic FLT3-ITD Signaling in Acute Myeloid Leukemia Is Connected to a Specific Chromatin Signature. Cell Reports, 2015, 12, 821-836.	2.9	63
12	Mapping of transcription factor motifs in active chromatin identifies IRF5 as key regulator in classical Hodgkin lymphoma. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E4513-22.	3.3	53
13	Integration of Kinase and Calcium Signaling at the Level of Chromatin Underlies Inducible Gene Activation in T Cells. Journal of Immunology, 2017, 199, 2652-2667.	0.4	51
14	Wellington-bootstrap: differential DNase-seq footprinting identifies cell-type determining transcription factors. BMC Genomics, 2015, 16, 1000.	1.2	49
15	RUNX1-ETO and RUNX1-EVI1 Differentially Reprogram the Chromatin Landscape in t(8;21) and t(3;21) AML. Cell Reports, 2017, 19, 1654-1668.	2.9	46
16	Cooperative binding of AP-1 and TEAD4 modulates the balance between vascular smooth muscle and hemogenic cell fate. Development (Cambridge), 2016, 143, 4324-4340.	1.2	43
17	Repetitive Elements Trigger RIG-I-like Receptor Signaling that Regulates the Emergence of Hematopoietic Stem and Progenitor Cells. Immunity, 2020, 53, 934-951.e9.	6.6	43
18	Multilayer omics analysis reveals a non-classical retinoic acid signaling axis that regulates hematopoietic stem cell identity. Cell Stem Cell, 2022, 29, 131-148.e10.	5.2	40

#	Article	IF	Citations
19	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
20	A multi-centre phase 2 study of azacitidine in chronic myelomonocytic leukaemia. Leukemia, 2014, 28, 1570-1572.	3.3	34
21	Polycomb Protein EED is Required for Silencing of Pluripotency Genes upon ESC Differentiation. Stem Cell Reviews and Reports, 2015, 11, 50-61.	5.6	31
22	EBF1-deficient bone marrow stroma elicits persistent changes in HSC potential. Nature Immunology, 2020, 21, 261-273.	7.0	30
23	CoCAS: a ChIP-on-chip analysis suite. Bioinformatics, 2009, 25, 954-955.	1.8	25
24	Chromatin priming elements establish immunological memory in T cells without activating transcription. BioEssays, 2017, 39, 1600184.	1.2	25
25	T Cell Receptor and Cytokine Signaling Can Function at Different Stages to Establish and Maintain Transcriptional Memory and Enable T Helper Cell Differentiation. Frontiers in Immunology, 2017, 8, 204.	2.2	25
26	A threshold level of NFATc1 activity facilitates thymocyte differentiation and opposes notch-driven leukaemia development. Nature Communications, 2016, 7, 11841.	5.8	23
27	LMO2 is required for TAL1 DNA binding activity and initiation of definitive haematopoiesis at the haemangioblast stage. Nucleic Acids Research, 2017, 45, 9874-9888.	6.5	22
28	Pasha: a versatile R package for piling chromatin HTS data. Bioinformatics, 2016, 32, 2528-2530.	1.8	21
29	A metabolic interplay coordinated by HLX regulates myeloid differentiation and AML through partly overlapping pathways. Nature Communications, 2018, 9, 3090.	5.8	21
30	Interactions between lineageâ€associated transcription factors govern haematopoietic progenitor states. EMBO Journal, 2020, 39, e104983.	3.5	20
31	Global long terminal repeat activation participates in establishing the unique gene expression programme of classical Hodgkin lymphoma. Leukemia, 2019, 33, 1463-1474.	3.3	19
32	Fine-Tuning Mybl2 Is Required for Proper Mesenchymal-to-Epithelial Transition during Somatic Reprogramming. Cell Reports, 2018, 24, 1496-1511.e8.	2.9	18
33	Prognostic significance of high GFI1 expression in AML of normal karyotype and its association with a FLT3-ITD signature. Scientific Reports, 2017, 7, 11148.	1.6	16
34	Transcription-Dependent Generation of a Specialized Chromatin Structure at the TCRÎ² Locus. Journal of Immunology, 2015, 194, 3432-3443.	0.4	10
35	High WBP5 expression correlates with elevation of HOX genes levels and is associated with inferior survival in patients with acute myeloid leukaemia. Scientific Reports, 2020, 10, 3505.	1.6	10
36	ZFP451-mediated SUMOylation of SATB2 drives embryonic stem cell differentiation. Genes and Development, 2021, 35, 1142-1160.	2.7	9

#	ARTICLE	IF	CITATIONS
37	Two possible modes of pioneering associated with combinations of H2A.Z and p300/CBP at nucleosome-occupied enhancers. Transcription, 2017, 8, 179-184.	1.7	7
38	Dependence on Myb expression is attenuated in myeloid leukaemia with N-terminal CEBPA mutations. Life Science Alliance, 2019, 2, e201800207.	1.3	6
39	Wellington: a novel method for the accurate identification of digital genomic footprints from DNase-seq data. Nucleic Acids Research, 2014, 42, 11272-11272.	6.5	3
40	Processing ChIP-Chip Data: From the Scanner to the Browser. Methods in Molecular Biology, 2011, 719, 251-268.	0.4	2
41	Sequences to Differences in Gene Expression: Analysis of RNA-Seq Data. Methods in Molecular Biology, 2022, , 279-318.	0.4	2
42	Cytokine and proinflammatory gene expression in classical Hodgkin lymphoma: Its more than NF-Îº B!. Cytokine, 2015, 72, 115-117.	1.4	0
43	ERBB2b mRNA isoform encodes a nuclear variant of the ERBB2 oncogene in breast cancer. Journal of Cellular Biochemistry, 2020, 121, 4870-4886.	1.2	0
44	2HybridTools, a handy software to facilitate clone identification and mutation mapping from yeast two-hybrid screening. PeerJ, 2019, 7, e7245.	0.9	0