

# Michael Corces

## List of Publications by Year in descending order

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Version: 2024-02-01

44  
papers

12,071  
citations

147801

31  
h-index

289244

40  
g-index

60  
all docs

60  
docs citations

60  
times ranked

19843  
citing authors

#	ARTICLE	IF	CITATIONS
1	A long noncoding RNA maintains active chromatin to coordinate homeotic gene expression. <i>Nature</i> , 2011, 472, 120-124.	27.8	1,760
2	An improved ATAC-seq protocol reduces background and enables interrogation of frozen tissues. <i>Nature Methods</i> , 2017, 14, 959-962.	19.0	1,653
3	Lineage-specific and single-cell chromatin accessibility charts human hematopoiesis and leukemia evolution. <i>Nature Genetics</i> , 2016, 48, 1193-1203.	21.4	952
4	The chromatin accessibility landscape of primary human cancers. <i>Science</i> , 2018, 362, .	12.6	781
5	Clonal Evolution of Preleukemic Hematopoietic Stem Cells Precedes Human Acute Myeloid Leukemia. <i>Science Translational Medicine</i> , 2012, 4, 149ra118.	12.4	630
6	Preleukemic mutations in human acute myeloid leukemia affect epigenetic regulators and persist in remission. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 2548-2553.	7.1	628
7	Massively parallel single-cell chromatin landscapes of human immune cell development and intratumoral T cell exhaustion. <i>Nature Biotechnology</i> , 2019, 37, 925-936.	17.5	622
8	ArchR is a scalable software package for integrative single-cell chromatin accessibility analysis. <i>Nature Genetics</i> , 2021, 53, 403-411.	21.4	610
9	Integrated Single-Cell Analysis Maps the Continuous Regulatory Landscape of Human Hematopoietic Differentiation. <i>Cell</i> , 2018, 173, 1535-1548.e16.	28.9	545
10	Isocitrate dehydrogenase 1 and 2 mutations induce BCL-2 dependence in acute myeloid leukemia. <i>Nature Medicine</i> , 2015, 21, 178-184.	30.7	459
11	Enhancer connectome in primary human cells identifies target genes of disease-associated DNA elements. <i>Nature Genetics</i> , 2017, 49, 1602-1612.	21.4	419
12	Circular ecDNA promotes accessible chromatin and high oncogene expression. <i>Nature</i> , 2019, 575, 699-703.	27.8	343
13	Single-cell multiomic analysis identifies regulatory programs in mixed-phenotype acute leukemia. <i>Nature Biotechnology</i> , 2019, 37, 1458-1465.	17.5	321
14	Insulin Signaling and Dietary Restriction Differentially Influence the Decline of Learning and Memory with Age. <i>PLoS Biology</i> , 2010, 8, e1000372.	5.6	223
15	Single-cell epigenomic analyses implicate candidate causal variants at inherited risk loci for Alzheimer's and Parkinson's diseases. <i>Nature Genetics</i> , 2020, 52, 1158-1168.	21.4	217
16	A humanized bone marrow ossicle xenotransplantation model enables improved engraftment of healthy and leukemic human hematopoietic cells. <i>Nature Medicine</i> , 2016, 22, 812-821.	30.7	181
17	Leukemia-Associated Cohesin Mutants Dominantly Enforce Stem Cell Programs and Impair Human Hematopoietic Progenitor Differentiation. <i>Cell Stem Cell</i> , 2015, 17, 675-688.	11.1	177
18	Transcript-indexed ATAC-seq for precision immune profiling. <i>Nature Medicine</i> , 2018, 24, 580-590.	30.7	124

#	ARTICLE	IF	CITATIONS
19	ecDNA hubs drive cooperative intermolecular oncogene expression. <i>Nature</i> , 2021, 600, 731-736.	27.8	123
20	Rapid Chromatin Switch in the Direct Reprogramming of Fibroblasts to Neurons. <i>Cell Reports</i> , 2017, 20, 3236-3247.	6.4	121
21	Pre-leukemic evolution of hematopoietic stem cells: the importance of early mutations in leukemogenesis. <i>Leukemia</i> , 2014, 28, 2276-2282.	7.2	116
22	Superenhancer Analysis Defines Novel Epigenomic Subtypes of Non-APL AML, Including an RAR $\alpha$ Dependency Targetable by SY-1425, a Potent and Selective RAR $\alpha$ Agonist. <i>Cancer Discovery</i> , 2017, 7, 1136-1153.	9.4	110
23	Chromatin accessibility profiling by ATAC-seq. <i>Nature Protocols</i> , 2022, 17, 1518-1552.	12.0	105
24	Human AML-iPSCs Reacquire Leukemic Properties after Differentiation and Model Clonal Variation of Disease. <i>Cell Stem Cell</i> , 2017, 20, 329-344.e7.	11.1	101
25	Single-cell lineage tracing by endogenous mutations enriched in transposase accessible mitochondrial DNA. <i>ELife</i> , 2019, 8, .	6.0	93
26	The three-dimensional cancer genome. <i>Current Opinion in Genetics and Development</i> , 2016, 36, 1-7.	3.3	72
27	HiChIRP reveals RNA-associated chromosome conformation. <i>Nature Methods</i> , 2019, 16, 489-492.	19.0	70
28	Single-cell mutational profiling enhances the clinical evaluation of AML MRD. <i>Blood Advances</i> , 2020, 4, 943-952.	5.2	63
29	Complement factor C1q mediates sleep spindle loss and epileptic spikes after mild brain injury. <i>Science</i> , 2021, 373, eabj2685.	12.6	55
30	Mutant WT1 is associated with DNA hypermethylation of PRC2 targets in AML and responds to EZH2 inhibition. <i>Blood</i> , 2015, 125, 316-326.	1.4	45
31	Preleukemic Hematopoietic Stem Cells in Human Acute Myeloid Leukemia. <i>Frontiers in Oncology</i> , 2017, 7, 263.	2.8	39
32	Epigenomic priming of immune genes implicates oligodendroglia in multiple sclerosis susceptibility. <i>Neuron</i> , 2022, 110, 1193-1210.e13.	8.1	36
33	PEPATAC: an optimized pipeline for ATAC-seq data analysis with serial alignments. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab101.	3.2	34
34	Polycomb-mediated genome architecture enables long-range spreading of H3K27 methylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	33
35	LKB1 inactivation modulates chromatin accessibility to drive metastatic progression. <i>Nature Cell Biology</i> , 2021, 23, 915-924.	10.3	26
36	Monocytic Differentiation and AHR Signaling as Primary Nodes of BET Inhibitor Response in Acute Myeloid Leukemia. <i>Blood Cancer Discovery</i> , 2021, 2, 518-531.	5.0	23

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37	The Cell Type-Specific 5hmC Landscape and Dynamics of Healthy Human Hematopoiesis and TET2-Mutant Preleukemia. <i>Blood Cancer Discovery</i> , 2022, 3, 346-367.	5.0	16
38	GATM and GAMT synthesize creatine locally throughout the mammalian body and within oligodendrocytes of the brain. <i>Brain Research</i> , 2021, 1770, 147627.	2.2	13
39	HiChIRP: RNA-centric chromatin conformation. <i>Protocol Exchange</i> , 0, , .	0.3	1
40	Chromatin Accessibility Analysis Reveals Epigenetic Evolution Is a Common Mechanism of Relapse in Acute Myeloid Leukemia. <i>Blood</i> , 2021, 138, 677-677.	1.4	1
41	Multi-Omic Analysis Identifies Epigenetic Evolution in Relapsed Acute Myeloid Leukemia. <i>Blood</i> , 2020, 136, 13-14.	1.4	1
42	Abstract 3303: Clonal evolution of pre-leukemic hematopoietic stem cells precedes human acute myeloid leukemia. , 2012, , .		0
43	Pluripotent Reprogramming of Human AML Resets Leukemic Behavior and Models Therapeutic Targeting of Subclones. <i>Blood</i> , 2016, 128, 575-575.	1.4	0
44	Single-Cell Mutational Profiling of Clonal Evolution in De Novo AML during Therapy and Relapse. <i>Blood</i> , 2018, 132, 1469-1469.	1.4	0