

Duncan Sproul

List of Publications by Year in descending order

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Version: 2024-02-01

32
papers

3,543
citations

279487

23
h-index

454577

30
g-index

36
all docs

36
docs citations

36
times ranked

7372
citing authors

#	ARTICLE	IF	CITATIONS
1	Recruitment to the Nuclear Periphery Can Alter Expression of Genes in Human Cells. <i>PLoS Genetics</i> , 2008, 4, e1000039.	1.5	494
2	Ring1B Compacts Chromatin Structure and Represses Gene Expression Independent of Histone Ubiquitination. <i>Molecular Cell</i> , 2010, 38, 452-464.	4.5	485
3	Tissue type is a major modifier of the 5-hydroxymethylcytosine content of human genes. <i>Genome Research</i> , 2012, 22, 467-477.	2.4	348
4	The role of chromatin structure in regulating the expression of clustered genes. <i>Nature Reviews Genetics</i> , 2005, 6, 775-781.	7.7	263
5	Lactate, a product of glycolytic metabolism, inhibits histone deacetylase activity and promotes changes in gene expression. <i>Nucleic Acids Research</i> , 2012, 40, 4794-4803.	6.5	249
6	Glioblastomas acquire myeloid-affiliated transcriptional programs via epigenetic immunoediting to elicit immune evasion. <i>Cell</i> , 2021, 184, 2454-2470.e26.	13.5	165
7	Diverse interventions that extend mouse lifespan suppress shared age-associated epigenetic changes at critical gene regulatory regions. <i>Genome Biology</i> , 2017, 18, 58.	3.8	147
8	Transcriptionally repressed genes become aberrantly methylated and distinguish tumors of different lineages in breast cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 4364-4369.	3.3	144
9	Tissue of origin determines cancer-associated CpG island promoter hypermethylation patterns. <i>Genome Biology</i> , 2012, 13, R84.	13.9	140
10	Gain-of-function DNMT3A mutations cause microcephalic dwarfism and hypermethylation of Polycomb-regulated regions. <i>Nature Genetics</i> , 2019, 51, 96-105.	9.4	110
11	Transcription factor binding predicts histone modifications in human cell lines. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 13367-13372.	3.3	109
12	Genomic insights into cancer-associated aberrant CpG island hypermethylation. <i>Briefings in Functional Genomics</i> , 2013, 12, 174-190.	1.3	105
13	cGAS-mediated induction of type I interferon due to inborn errors of histone pre-mRNA processing. <i>Nature Genetics</i> , 2020, 52, 1364-1372.	9.4	105
14	Elevated FOXG1 and SOX2 in glioblastoma enforces neural stem cell identity through transcriptional control of cell cycle and epigenetic regulators. <i>Genes and Development</i> , 2017, 31, 757-773.	2.7	102
15	An epigenetic predictor of death captures multi-modal measures of brain health. <i>Molecular Psychiatry</i> , 2021, 26, 3806-3816.	4.1	77
16	Analysis of Active and Inactive X Chromosome Architecture Reveals the Independent Organization of 30nm and Large-Scale Chromatin Structures. <i>Molecular Cell</i> , 2010, 40, 397-409.	4.5	73
17	Targeting of Rac GTPases blocks the spread of intact human breast cancer. <i>Oncotarget</i> , 2012, 3, 608-619.	0.8	57
18	Expression of a large LINE-1-driven antisense RNA is linked to epigenetic silencing of the metastasis suppressor gene TFPI-2 in cancer. <i>Nucleic Acids Research</i> , 2013, 41, 6857-6869.	6.5	54

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19	Estrogen-induced chromatin decondensation and nuclear re-organization linked to regional epigenetic regulation in breast cancer. <i>Genome Biology</i> , 2015, 16, 145.	3.8	49
20	Genotype effects contribute to variation in longitudinal methylome patterns in older people. <i>Genome Medicine</i> , 2018, 10, 75.	3.6	37
21	Age-related clonal haemopoiesis is associated with increased epigenetic age. <i>Current Biology</i> , 2019, 29, R786-R787.	1.8	37
22	Parent of origin genetic effects on methylation in humans are common and influence complex trait variation. <i>Nature Communications</i> , 2019, 10, 1383.	5.8	37
23	Modelling genetic and clinical heterogeneity in epithelial ovarian cancers. <i>Carcinogenesis</i> , 2011, 32, 1540-1549.	1.3	36
24	<sc>DNA</sc> methylation reprogramming in cancer: Does it act by reconfiguring the binding landscape of Polycomb repressive complexes?. <i>BioEssays</i> , 2014, 36, 134-140.	1.2	36
25	De novo DNA methyltransferase activity in colorectal cancer is directed towards H3K36me3 marked CpG islands. <i>Nature Communications</i> , 2021, 12, 694.	5.8	24
26	Diversity of Matriptase Expression Level and Function in Breast Cancer. <i>PLoS ONE</i> , 2012, 7, e34182.	1.1	21
27	Transition to naïve human pluripotency mirrors pan-cancer DNA hypermethylation. <i>Nature Communications</i> , 2020, 11, 3671.	5.8	17
28	Variable outcome and methylation status according to <i>CEBPA</i> mutant type in double-mutated acute myeloid leukemia patients and the possible implications for treatment. <i>Haematologica</i> , 2018, 103, 91-100.	1.7	9
29	<i>In Vivo</i> Modeling of Patient Genetic Heterogeneity Identifies New Ways to Target Cholangiocarcinoma. <i>Cancer Research</i> , 2022, 82, 1548-1559.	0.4	8
30	Activation of transcription factor circuitry in 2i-induced ground state pluripotency is independent of repressive global epigenetic landscapes. <i>Nucleic Acids Research</i> , 2020, 48, 7748-7766.	6.5	5
31	The Use of DNA Methylation Profiling to Assess the Significance of Different Types of Mutations in CEBPA-Mutated AML. <i>Blood</i> , 2014, 124, 2328-2328.	0.6	0
32	Cluster mean-field theory accurately predicts statistical properties of large-scale DNA methylation patterns. <i>Journal of the Royal Society Interface</i> , 2022, 19, 20210707.	1.5	0