Duncan Sproul

List of Publications by Year
in descending order

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	Cluster mean-field theory accurately predicts statistical properties of large-scale DNA methylation patterns. Journal of the Royal Society Interface, 2022, 19, 20210707.	1.5	0
2	*In Vivo* Modeling of Patient Genetic Heterogeneity Identifies New Ways to Target Cholangiocarcinoma. Cancer Research, 2022, 82, 1548-1559.	0.4	8
3	An epigenetic predictor of death captures multi-modal measures of brain health. Molecular Psychiatry, 2021, 26, 3806-3816.	4.1	77
4	Glioblastomas acquire myeloid-affiliated transcriptional programs via epigenetic immunoediting to elicit immune evasion. Cell, 2021, 184, 2454-2470.e26.	13.5	165
5	De novo DNA methyltransferase activity in colorectal cancer is directed towards H3K36me3 marked CpG islands. Nature Communications, 2021, 12, 694.	5.8	24
6	cGAS-mediated induction of type I interferon due to inborn errors of histone pre-mRNA processing. Nature Genetics, 2020, 52, 1364-1372.	9.4	105
7	Transition to naïve human pluripotency mirrors pan-cancer DNA hypermethylation. Nature Communications, 2020, 11, 3671.	5.8	17
8	Activation of transcription factor circuity in 2i-induced ground state pluripotency is independent of repressive global epigenetic landscapes. Nucleic Acids Research, 2020, 48, 7748-7766.	6.5	5
9	Age-related clonal haemopoiesis is associated with increased epigenetic age. Current Biology, 2019, 29, R786-R787.	1.8	37
10	Parent of origin genetic effects on methylation in humans are common and influence complex trait variation. Nature Communications, 2019, 10, 1383.	5.8	37
11	Gain-of-function DNMT3A mutations cause microcephalic dwarfism and hypermethylation of Polycomb-regulated regions. Nature Genetics, 2019, 51, 96-105.	9.4	110
12	Variable outcome and methylation status according to *CEBPA* mutant type in double-mutated acute myeloid leukemia patients and the possible implications for treatment. Haematologica, 2018, 103, 91-100.	1.7	9
13	Genotype effects contribute to variation in longitudinal methylome patterns in older people. Genome Medicine, 2018, 10, 75.	3.6	37
14	Elevated FOXG1 and SOX2 in glioblastoma enforces neural stem cell identity through transcriptional control of cell cycle and epigenetic regulators. Genes and Development, 2017, 31, 757-773.	2.7	102
15	Diverse interventions that extend mouse lifespan suppress shared age-associated epigenetic changes at critical gene regulatory regions. Genome Biology, 2017, 18, 58.	3.8	147
16	Estrogen-induced chromatin decondensation and nuclear re-organization linked to regional epigenetic regulation in breast cancer. Genome Biology, 2015, 16, 145.	3.8	49
17	Transcription factor binding predicts histone modifications in human cell lines. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 13367-13372.	3.3	109
18	DNA methylation reprogramming in cancer: Does it act by reâ€‚configuring the binding landscape of Polycomb repressive complexes?. BioEssays, 2014, 36, 134-140.	1.2	36

#	ARTICLE	IF	CITATIONS
19	The Use of DNA Methylation Profiling to Assess the Significance of Different Types of Mutations in CEBPA-Mutated AML. Blood, 2014, 124, 2328-2328.	0.6	0
20	Genomic insights into cancer-associated aberrant CpG island hypermethylation. Briefings in Functional Genomics, 2013, 12, 174-190.	1.3	105
21	Expression of a large LINE-1-driven antisense RNA is linked to epigenetic silencing of the metastasis suppressor gene TFPI-2 in cancer. Nucleic Acids Research, 2013, 41, 6857-6869.	6.5	54
22	Lactate, a product of glycolytic metabolism, inhibits histone deacetylase activity and promotes changes in gene expression. Nucleic Acids Research, 2012, 40, 4794-4803.	6.5	249
23	Tissue of origin determines cancer-associated CpG island promoter hypermethylation patterns. Genome Biology, 2012, 13, R84.	13.9	140
24	Tissue type is a major modifier of the 5-hydroxymethylcytosine content of human genes. Genome Research, 2012, 22, 467-477.	2.4	348
25	Diversity of Matriptase Expression Level and Function in Breast Cancer. PLoS ONE, 2012, 7, e34182.	1.1	21
26	Targeting of Rac GTPases blocks the spread of intact human breast cancer. Oncotarget, 2012, 3, 608-619.	0.8	57
27	Modelling genetic and clinical heterogeneity in epithelial ovarian cancers. Carcinogenesis, 2011, 32, 1540-1549.	1.3	36
28	Transcriptionally repressed genes become aberrantly methylated and distinguish tumors of different lineages in breast cancer. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4364-4369.	3.3	144
29	Ring1B Compacts Chromatin Structure and Represses Gene Expression Independent of Histone Ubiquitination. Molecular Cell, 2010, 38, 452-464.	4.5	485
30	Analysis of Active and Inactive X Chromosome Architecture Reveals the Independent Organization ofÂ30Ânm and Large-Scale Chromatin Structures. Molecular Cell, 2010, 40, 397-409.	4.5	73
31	Recruitment to the Nuclear Periphery Can Alter Expression of Genes in Human Cells. PLoS Genetics, 2008, 4, e1000039.	1.5	494
32	The role of chromatin structure in regulating the expression of clustered genes. Nature Reviews Genetics, 2005, 6, 775-781.	7.7	263