

Skirmantas Kriaucionis

List of Publications by Year in descending order

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Version: 2024-02-01

37
papers

5,298
citations

331538

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times ranked

7577
citing authors

#	ARTICLE	IF	CITATIONS
1	Decitabine increases neoantigen and cancer testis antigen expression to enhance T-cell-mediated toxicity against glioblastoma. <i>Neuro-Oncology</i> , 2022, 24, 2093-2106.	0.6	18
2	Neuronal non-CG methylation is an essential target for MeCP2 function. <i>Molecular Cell</i> , 2021, 81, 1260-1275.e12.	4.5	24
3	Epigenetic nucleotides enhance therapy. <i>Science</i> , 2021, 372, 127-128.	6.0	0
4	Endonuclease enrichment TAPS for cost-effective genome-wide base-resolution DNA methylation detection. <i>Nucleic Acids Research</i> , 2021, 49, e76-e76.	6.5	8
5	LKB1 cooperates with Sox17 to drive metastasis. <i>Nature Cell Biology</i> , 2021, 23, 816-817.	4.6	3
6	Repressed Chromatin Drives Leukaemogenesis in Mutant IDH2 Acute Myeloid Leukaemia Via Inhibition of Granulocyte Differentiation and Cell Cycle Progression. <i>Blood</i> , 2021, 138, 3467-3467.	0.6	0
7	Distinct contributions of DNA methylation and histone acetylation to the genomic occupancy of transcription factors. <i>Genome Research</i> , 2020, 30, 1393-1406.	2.4	41
8	ATACing DNA Methylation during Differentiation. <i>Molecular Cell</i> , 2020, 77, 1159-1161.	4.5	4
9	How m6A sneaks into DNA. <i>Nature Chemical Biology</i> , 2020, 16, 604-605.	3.9	3
10	The polymorphic variant rs1800734 influences methylation acquisition and allele-specific TFAP4 binding in the MLH1 promoter leading to differential mRNA expression. <i>Scientific Reports</i> , 2019, 9, 13463.	1.6	6
11	Capturing the dynamics of genome replication on individual ultra-long nanopore sequence reads. <i>Nature Methods</i> , 2019, 16, 429-436.	9.0	82
12	The non-canonical SMC protein SmcHD1 antagonises TAD formation and compartmentalisation on the inactive X chromosome. <i>Nature Communications</i> , 2019, 10, 30.	5.8	87
13	Telomere length and genetics are independent colorectal tumour risk factors in an evaluation of biomarkers in normal bowel. <i>British Journal of Cancer</i> , 2018, 118, 727-732.	2.9	11
14	DNA Replication and associated repair pathways are involved in the mutagenesis of methylated cytosine. <i>DNA Repair</i> , 2018, 62, 1-7.	1.3	25
15	Identification of UHRF2 as a novel DNA interstrand crosslink sensor protein. <i>PLoS Genetics</i> , 2018, 14, e1007643.	1.5	17
16	Mutational signature distribution varies with DNA replication timing and strand asymmetry. <i>Genome Biology</i> , 2018, 19, 129.	3.8	99
17	Molecular and Functional Sex Differences of Noradrenergic Neurons in the Mouse Locus Coeruleus. <i>Cell Reports</i> , 2018, 23, 2225-2235.	2.9	74
18	The SET1 Complex Selects Actively Transcribed Target Genes via Multivalent Interaction with CpG Island Chromatin. <i>Cell Reports</i> , 2017, 20, 2313-2327.	2.9	86

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19	MicroRNAs of the miR-290/295 Family Maintain Bivalency in Mouse Embryonic Stem Cells. <i>Stem Cell Reports</i> , 2016, 6, 635-642.	2.3	24
20	Expression of Idh1R132H in the Murine Subventricular Zone Stem Cell Niche Recapitulates Features of Early Gliomagenesis. <i>Cancer Cell</i> , 2016, 30, 578-594.	7.7	122
21	5-hydroxymethylcytosine marks regions with reduced mutation frequency in human DNA. <i>ELife</i> , 2016, 5, .	2.8	28
22	A simple modification to the luminometric methylation assay to control for the effects of DNA fragmentation. <i>BioTechniques</i> , 2015, 58, 262-4.	0.8	4
23	CDA directs metabolism of epigenetic nucleosides revealing a therapeutic window in cancer. <i>Nature</i> , 2015, 524, 114-118.	13.7	79
24	Structural insights into how 5-hydroxymethylation influences transcription factor binding. <i>Chemical Communications</i> , 2014, 50, 1794-1796.	2.2	71
25	Another stable base in DNA. <i>Nature Chemistry</i> , 2014, 6, 1031-1033.	6.6	7
26	Expanding the Epigenetic Landscape: Novel Modifications of Cytosine in Genomic DNA. <i>Cold Spring Harbor Perspectives in Biology</i> , 2014, 6, a018630-a018630.	2.3	42
27	Different Roles for Tet1 and Tet2 Proteins in Reprogramming-Mediated Erasure of Imprints Induced by EGC Fusion. <i>Molecular Cell</i> , 2013, 49, 1023-1033.	4.5	86
28	Covering the bases: loss of 5-hydroxymethylcytosine in melanoma. <i>Pigment Cell and Melanoma Research</i> , 2013, 26, 159-161.	1.5	0
29	Fate Mapping for Activation-Induced Cytidine Deaminase (AID) Marks Non-Lymphoid Cells During Mouse Development. <i>PLoS ONE</i> , 2013, 8, e69208.	1.1	28
30	Bio-CAP: a versatile and highly sensitive technique to purify and characterise regions of non-methylated DNA. <i>Nucleic Acids Research</i> , 2012, 40, e32-e32.	6.5	27
31	MeCP2 Binds to 5hmC Enriched within Active Genes and Accessible Chromatin in the Nervous System. <i>Cell</i> , 2012, 151, 1417-1430.	13.5	837
32	The Nuclear DNA Base 5-Hydroxymethylcytosine Is Present in Purkinje Neurons and the Brain. <i>Science</i> , 2009, 324, 929-930.	6.0	2,433
33	Interaction between chromatin proteins MECP2 and ATRX is disrupted by mutations that cause inherited mental retardation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 2709-2714.	3.3	231
34	Gene Expression Analysis Exposes Mitochondrial Abnormalities in a Mouse Model of Rett Syndrome. <i>Molecular and Cellular Biology</i> , 2006, 26, 5033-5042.	1.1	182
35	Up-regulation of glucocorticoid-regulated genes in a mouse model of Rett syndrome. <i>Human Molecular Genetics</i> , 2005, 14, 2247-2256.	1.4	174
36	The major form of MeCP2 has a novel N-terminus generated by alternative splicing. <i>Nucleic Acids Research</i> , 2004, 32, 1818-1823.	6.5	217

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37	DNA methylation and Rett syndrome. Human Molecular Genetics, 2003, 12, R221-R227.	1.4	106