

Lucas A Salas

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

50
papers

1,728
citations

19
h-index

41
g-index

77
ext. papers

2,442
ext. citations

7.2
avg, IF

4.28
L-index

#	Paper	IF	Citations
50	Phase I Study of High-Dose L-methylfolate in Combination with Temozolomide and Bevacizumab in Recurrent IDH wild-type High-Grade Glioma.. <i>Cancer Research Communications</i> , 2022 , 2, 1-9		
49	Immune profiles and DNA methylation alterations related with non-muscle-invasive bladder cancer outcomes.. <i>Clinical Epigenetics</i> , 2022 , 14, 14	7.7	1
48	Navigating the hydroxymethylome: experimental biases and quality control tools for the tandem bisulfite and oxidative bisulfite Illumina microarrays.. <i>Epigenomics</i> , 2022 , 14, 139-152	4.4	0
47	Enhanced cell deconvolution of peripheral blood using DNA methylation for high-resolution immune profiling.. <i>Nature Communications</i> , 2022 , 13, 761	17.4	11
46	A core of differentially methylated CpG loci in gMDSs isolated from neonatal and adult sources.. <i>Clinical Epigenetics</i> , 2022 , 14, 27	7.7	0
45	Identification of a foetal epigenetic compartment in adult human kidney. <i>Epigenetics</i> , 2021 , 1-21	5.7	
44	A transdisciplinary approach to understand the epigenetic basis of race/ethnicity health disparities. <i>Epigenomics</i> , 2021 , 13, 1761-1770	4.4	5
43	MethylSPWNet and MethylCapsNet: Biologically Motivated Organization of DNAm Neural Networks, Inspired by Capsule Networks. <i>Npj Systems Biology and Applications</i> , 2021 , 7, 33	5	0
42	DNA 5-hydroxymethylcytosine in pediatric central nervous system tumors may impact tumor classification and is a positive prognostic marker. <i>Clinical Epigenetics</i> , 2021 , 13, 176	7.7	0
41	Methylation-derived inflammatory measures and lung cancer risk and survival.. <i>Clinical Epigenetics</i> , 2021 , 13, 222	7.7	4
40	Cord blood DNA methylation reflects cord blood C-reactive protein levels but not maternal levels: a longitudinal study and meta-analysis. <i>Clinical Epigenetics</i> , 2020 , 12, 60	7.7	6
39	MethylNet: an automated and modular deep learning approach for DNA methylation analysis. <i>BMC Bioinformatics</i> , 2020 , 21, 108	3.6	23
38	Epigenome-wide meta-analysis of blood DNA methylation in newborns and children identifies numerous loci related to gestational age. <i>Genome Medicine</i> , 2020 , 12, 25	14.4	37
37	Prediagnostic breast milk DNA methylation alterations in women who develop breast cancer. <i>Human Molecular Genetics</i> , 2020 , 29, 662-673	5.6	5
36	Enrichment of CpG island shore region hypermethylation in epigenetic breast field cancerization. <i>Epigenetics</i> , 2020 , 15, 1093-1106	5.7	7
35	Altered immune phenotype and DNA methylation in panic disorder. <i>Clinical Epigenetics</i> , 2020 , 12, 177	7.7	1
34	DNA methylation and body mass index from birth to adolescence: meta-analyses of epigenome-wide association studies. <i>Genome Medicine</i> , 2020 , 12, 105	14.4	15

33	Maternal Gestational Diabetes Mellitus and Newborn DNA Methylation: Findings From the Pregnancy and Childhood Epigenetics Consortium. <i>Diabetes Care</i> , 2020 , 43, 98-105	14.6	45
32	Systematic evaluation and validation of reference and library selection methods for deconvolution of cord blood DNA methylation data. <i>Clinical Epigenetics</i> , 2019 , 11, 125	7.7	44
31	Molecular and epigenetic profiles of BRCA1-like hormone-receptor-positive breast tumors identified with development and application of a copy-number-based classifier. <i>Breast Cancer Research</i> , 2019 , 21, 14	8.3	3
30	Meta-analysis of epigenome-wide association studies in neonates reveals widespread differential DNA methylation associated with birthweight. <i>Nature Communications</i> , 2019 , 10, 1893	17.4	79
29	Newborn DNA-methylation, childhood lung function, and the risks of asthma and COPD across the life course. <i>European Respiratory Journal</i> , 2019 , 53,	13.6	32
28	MicroRNA-Related Genetic Variants Associated with Survival of Head and Neck Squamous Cell Carcinoma. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019 , 28, 127-136	4	12
27	PyMethylProcess-convenient high-throughput preprocessing workflow for DNA methylation data. <i>Bioinformatics</i> , 2019 , 35, 5379-5381	7.2	6
26	Absence of an embryonic stem cell DNA methylation signature in human cancer. <i>BMC Cancer</i> , 2019 , 19, 711	4.8	4
25	Newborn and childhood differential DNA methylation and liver fat in school-age children. <i>Clinical Epigenetics</i> , 2019 , 12, 3	7.7	6
24	Maternal swimming pool exposure during pregnancy in relation to birth outcomes and cord blood DNA methylation among private well users. <i>Environment International</i> , 2019 , 123, 459-466	12.9	5
23	Tracing human stem cell lineage during development using DNA methylation. <i>Genome Research</i> , 2018 , 28, 1285-1295	9.7	15
22	An optimized library for reference-based deconvolution of whole-blood biospecimens assayed using the Illumina HumanMethylationEPIC BeadArray. <i>Genome Biology</i> , 2018 , 19, 64	18.3	95
21	expression in mesencephalic neurons and characterization of a rare polymorphism associated with decreased risk of Parkinson's disease. <i>Npj Parkinson's Disease</i> , 2018 , 4, 24	9.7	65
20	IMMU-07. IMMUNE PROFILES IN THE SAN FRANCISCO ADULT GLIOMA STUDY (AGS) USING IMMUNOMETHYLOMICS. <i>Neuro-Oncology</i> , 2018 , 20, vi122-vi122	1	78
19	Genome-wide DNA methylation profiling shows a distinct epigenetic signature associated with lung macrophages in cystic fibrosis. <i>Clinical Epigenetics</i> , 2018 , 10, 152	7.7	13
18	Immunomethylomic approach to explore the blood neutrophil lymphocyte ratio (NLR) in glioma survival. <i>Clinical Epigenetics</i> , 2017 , 9, 10	7.7	38
17	Integrative epigenetic and genetic pan-cancer somatic alteration portraits. <i>Epigenetics</i> , 2017 , 12, 561-574	4.7	15
16	Gene expression changes in blood RNA after swimming in a chlorinated pool. <i>Journal of Environmental Sciences</i> , 2017 , 58, 250-261	6.4	4

15	Maternal BMI at the start of pregnancy and offspring epigenome-wide DNA methylation: findings from the pregnancy and childhood epigenetics (PACE) consortium. <i>Human Molecular Genetics</i> , 2017 , 26, 4067-4085	5.6	151
14	Cell-type deconvolution from DNA methylation: a review of recent applications. <i>Human Molecular Genetics</i> , 2017 , 26, R216-R224	5.6	81
13	Prenatal exposure to mixtures of xenoestrogens and genome-wide DNA methylation in human placenta. <i>Epigenomics</i> , 2016 , 8, 43-54	4.4	13
12	DNA Methylation in Newborns and Maternal Smoking in Pregnancy: Genome-wide Consortium Meta-analysis. <i>American Journal of Human Genetics</i> , 2016 , 98, 680-96	11	489
11	Genome-wide DNA methylation study in human placenta identifies novel loci associated with maternal smoking during pregnancy. <i>International Journal of Epidemiology</i> , 2016 , 45, 1644-1655	7.8	55
10	Overview of Disinfection By-products and Associated Health Effects. <i>Current Environmental Health Reports</i> , 2015 , 2, 107-15	6.5	140
9	DNA methylation levels and long-term trihalomethane exposure in drinking water: an epigenome-wide association study. <i>Epigenetics</i> , 2015 , 10, 650-61	5.7	19
8	Identification of a new locus and validation of previously reported loci showing differential methylation associated with smoking. The REGICOR study. <i>Epigenetics</i> , 2015 , 10, 1156-65	5.7	30
7	Use of urinary trichloroacetic acid as an exposure biomarker of disinfection by-products in cancer studies. <i>Environmental Research</i> , 2014 , 135, 276-84	7.9	11
6	LINE-1 methylation in granulocyte DNA and trihalomethane exposure is associated with bladder cancer risk. <i>Epigenetics</i> , 2014 , 9, 1532-9	5.7	21
5	Biological and statistical approaches for modeling exposure to specific trihalomethanes and bladder cancer risk. <i>American Journal of Epidemiology</i> , 2013 , 178, 652-60	3.8	16
4	A cluster-randomized controlled trial of handrubs for prevention of infectious diseases among children in Colombia. <i>Revista Panamericana De Salud Publica/Pan American Journal of Public Health</i> , 2012 , 31, 476-84	4.1	20
3	Maternal BMI at the start of pregnancy and offspring epigenome-wide DNA methylation: Findings from the Pregnancy and Childhood Epigenetics (PACE) consortium		1
2	Systematic evaluation and validation of reference and library selection methods for deconvolution of cord blood DNA methylation data		1
1	Enhanced cell deconvolution of peripheral blood using DNA methylation for high-resolution immune profiling		4