

# Lucas A Salas

## List of Publications by Citations

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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	DNA Methylation in Newborns and Maternal Smoking in Pregnancy: Genome-wide Consortium Meta-analysis. <i>American Journal of Human Genetics</i> , <b>2016</b> , 98, 680-96	11	489
49	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> , <b>2017</b> , 26, 4067-4085	5.6	151
48	Overview of Disinfection By-products and Associated Health Effects. <i>Current Environmental Health Reports</i> , <b>2015</b> , 2, 107-15	6.5	140
47	An optimized library for reference-based deconvolution of whole-blood biospecimens assayed using the Illumina HumanMethylationEPIC BeadArray. <i>Genome Biology</i> , <b>2018</b> , 19, 64	18.3	95
46	Cell-type deconvolution from DNA methylation: a review of recent applications. <i>Human Molecular Genetics</i> , <b>2017</b> , 26, R216-R224	5.6	81
45	Meta-analysis of epigenome-wide association studies in neonates reveals widespread differential DNA methylation associated with birthweight. <i>Nature Communications</i> , <b>2019</b> , 10, 1893	17.4	79
44	IMMU-07. IMMUNE PROFILES IN THE SAN FRANCISCO ADULT GLIOMA STUDY (AGS) USING IMMUNOMETHYLOMICS. <i>Neuro-Oncology</i> , <b>2018</b> , 20, vi122-vi122	1	78
43	expression in mesencephalic neurons and characterization of a rare polymorphism associated with decreased risk of Parkinson's disease. <i>Npj Parkinson's Disease</i> , <b>2018</b> , 4, 24	9.7	65
42	Genome-wide DNA methylation study in human placenta identifies novel loci associated with maternal smoking during pregnancy. <i>International Journal of Epidemiology</i> , <b>2016</b> , 45, 1644-1655	7.8	55
41	Maternal Gestational Diabetes Mellitus and Newborn DNA Methylation: Findings From the Pregnancy and Childhood Epigenetics Consortium. <i>Diabetes Care</i> , <b>2020</b> , 43, 98-105	14.6	45
40	Systematic evaluation and validation of reference and library selection methods for deconvolution of cord blood DNA methylation data. <i>Clinical Epigenetics</i> , <b>2019</b> , 11, 125	7.7	44
39	Immunomethylomic approach to explore the blood neutrophil lymphocyte ratio (NLR) in glioma survival. <i>Clinical Epigenetics</i> , <b>2017</b> , 9, 10	7.7	38
38	Epigenome-wide meta-analysis of blood DNA methylation in newborns and children identifies numerous loci related to gestational age. <i>Genome Medicine</i> , <b>2020</b> , 12, 25	14.4	37
37	Newborn DNA-methylation, childhood lung function, and the risks of asthma and COPD across the life course. <i>European Respiratory Journal</i> , <b>2019</b> , 53,	13.6	32
36	Identification of a new locus and validation of previously reported loci showing differential methylation associated with smoking. The REGICOR study. <i>Epigenetics</i> , <b>2015</b> , 10, 1156-65	5.7	30
35	MethylNet: an automated and modular deep learning approach for DNA methylation analysis. <i>BMC Bioinformatics</i> , <b>2020</b> , 21, 108	3.6	23
34	LINE-1 methylation in granulocyte DNA and trihalomethane exposure is associated with bladder cancer risk. <i>Epigenetics</i> , <b>2014</b> , 9, 1532-9	5.7	21

33	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> , <b>2012</b> , 31, 476-84	4.1	20
32	DNA methylation levels and long-term trihalomethane exposure in drinking water: an epigenome-wide association study. <i>Epigenetics</i> , <b>2015</b> , 10, 650-61	5.7	19
31	Biological and statistical approaches for modeling exposure to specific trihalomethanes and bladder cancer risk. <i>American Journal of Epidemiology</i> , <b>2013</b> , 178, 652-60	3.8	16
30	Integrative epigenetic and genetic pan-cancer somatic alteration portraits. <i>Epigenetics</i> , <b>2017</b> , 12, 561-574	5.7	15
29	Tracing human stem cell lineage during development using DNA methylation. <i>Genome Research</i> , <b>2018</b> , 28, 1285-1295	9.7	15
28	DNA methylation and body mass index from birth to adolescence: meta-analyses of epigenome-wide association studies. <i>Genome Medicine</i> , <b>2020</b> , 12, 105	14.4	15
27	Prenatal exposure to mixtures of xenoestrogens and genome-wide DNA methylation in human placenta. <i>Epigenomics</i> , <b>2016</b> , 8, 43-54	4.4	13
26	Genome-wide DNA methylation profiling shows a distinct epigenetic signature associated with lung macrophages in cystic fibrosis. <i>Clinical Epigenetics</i> , <b>2018</b> , 10, 152	7.7	13
25	MicroRNA-Related Genetic Variants Associated with Survival of Head and Neck Squamous Cell Carcinoma. <i>Cancer Epidemiology Biomarkers and Prevention</i> , <b>2019</b> , 28, 127-136	4	12
24	Use of urinary trichloroacetic acid as an exposure biomarker of disinfection by-products in cancer studies. <i>Environmental Research</i> , <b>2014</b> , 135, 276-84	7.9	11
23	Enhanced cell deconvolution of peripheral blood using DNA methylation for high-resolution immune profiling.. <i>Nature Communications</i> , <b>2022</b> , 13, 761	17.4	11
22	Enrichment of CpG island shore region hypermethylation in epigenetic breast field cancerization. <i>Epigenetics</i> , <b>2020</b> , 15, 1093-1106	5.7	7
21	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> , <b>2020</b> , 12, 60	7.7	6
20	PyMethylProcess-convenient high-throughput preprocessing workflow for DNA methylation data. <i>Bioinformatics</i> , <b>2019</b> , 35, 5379-5381	7.2	6
19	Newborn and childhood differential DNA methylation and liver fat in school-age children. <i>Clinical Epigenetics</i> , <b>2019</b> , 12, 3	7.7	6
18	Prediagnostic breast milk DNA methylation alterations in women who develop breast cancer. <i>Human Molecular Genetics</i> , <b>2020</b> , 29, 662-673	5.6	5
17	A transdisciplinary approach to understand the epigenetic basis of race/ethnicity health disparities. <i>Epigenomics</i> , <b>2021</b> , 13, 1761-1770	4.4	5
16	Maternal swimming pool exposure during pregnancy in relation to birth outcomes and cord blood DNA methylation among private well users. <i>Environment International</i> , <b>2019</b> , 123, 459-466	12.9	5

15	Gene expression changes in blood RNA after swimming in a chlorinated pool. <i>Journal of Environmental Sciences</i> , <b>2017</b> , 58, 250-261	6.4	4
14	Absence of an embryonic stem cell DNA methylation signature in human cancer. <i>BMC Cancer</i> , <b>2019</b> , 19, 711	4.8	4
13	Enhanced cell deconvolution of peripheral blood using DNA methylation for high-resolution immune profiling		4
12	Methylation-derived inflammatory measures and lung cancer risk and survival.. <i>Clinical Epigenetics</i> , <b>2021</b> , 13, 222	7.7	4
11	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> , <b>2019</b> , 21, 14	8.3	3
10	Immune profiles and DNA methylation alterations related with non-muscle-invasive bladder cancer outcomes.. <i>Clinical Epigenetics</i> , <b>2022</b> , 14, 14	7.7	1
9	Maternal BMI at the start of pregnancy and offspring epigenome-wide DNA methylation: Findings from the Pregnancy and Childhood Epigenetics (PACE) consortium		1
8	Systematic evaluation and validation of reference and library selection methods for deconvolution of cord blood DNA methylation data		1
7	Altered immune phenotype and DNA methylation in panic disorder. <i>Clinical Epigenetics</i> , <b>2020</b> , 12, 177	7.7	1
6	Navigating the hydroxymethylome: experimental biases and quality control tools for the tandem bisulfite and oxidative bisulfite Illumina microarrays.. <i>Epigenomics</i> , <b>2022</b> , 14, 139-152	4.4	0
5	MethylSPWNet and MethylCapsNet: Biologically Motivated Organization of DNAm Neural Networks, Inspired by Capsule Networks. <i>Npj Systems Biology and Applications</i> , <b>2021</b> , 7, 33	5	0
4	DNA 5-hydroxymethylcytosine in pediatric central nervous system tumors may impact tumor classification and is a positive prognostic marker. <i>Clinical Epigenetics</i> , <b>2021</b> , 13, 176	7.7	0
3	A core of differentially methylated CpG loci in gMDSCs isolated from neonatal and adult sources.. <i>Clinical Epigenetics</i> , <b>2022</b> , 14, 27	7.7	0
2	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> , <b>2022</b> , 2, 1-9		
1	Identification of a foetal epigenetic compartment in adult human kidney. <i>Epigenetics</i> , <b>2021</b> , 1-21	5.7	