

Christine Ladd-Acosta

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.

57 papers	8,822 citations	28 h-index	63 g-index
63 ext. papers	10,798 ext. citations	8.9 avg, IF	5.62 L-index

#	Paper	IF	Citations
57	Maternal tobacco smoking and offspring autism spectrum disorder or traits in ECHO cohorts.. <i>Autism Research</i> , 2022 ,	5.1	1
56	Individual and Combined Association Between Prenatal Polysubstance Exposure and Childhood Risk of Attention-Deficit/Hyperactivity Disorder.. <i>JAMA Network Open</i> , 2022 , 5, e221957	10.4	2
55	Association between pica and gastrointestinal symptoms in preschoolers with and without autism spectrum disorder: Study to Explore Early Development. <i>Disability and Health Journal</i> , 2021 , 14, 101052	4.2	1
54	Autism-Associated DNA Methylation at Birth From Multiple Tissues Is Enriched for Autism Genes in the Early Autism Risk Longitudinal Investigation.. <i>Frontiers in Molecular Neuroscience</i> , 2021 , 14, 775390	6.1	1
53	Distributional Properties and Criterion Validity of a Shortened Version of the Social Responsiveness Scale: Results from the ECHO Program and Implications for Social Communication Research. <i>Journal of Autism and Developmental Disorders</i> , 2021 , 51, 2241-2253	4.6	2
52	Cerebral cortex and blood transcriptome changes in mouse neonates prenatally exposed to air pollution particulate matter. <i>Journal of Neurodevelopmental Disorders</i> , 2021 , 13, 30	4.6	0
51	Maternal Psychiatric Conditions, Treatment With Selective Serotonin Reuptake Inhibitors, and Neurodevelopmental Disorders. <i>Biological Psychiatry</i> , 2021 , 90, 253-262	7.9	4
50	Epigenome-wide association study of serum urate reveals insights into urate co-regulation and the SLC2A9 locus. <i>Nature Communications</i> , 2021 , 12, 7173	17.4	1
49	Interaction of Cigarette Smoking and Polygenic Risk Score on Reduced Lung Function.. <i>JAMA Network Open</i> , 2021 , 4, e2139525	10.4	3
48	Early developmental exposure to air pollution increases the risk of Alzheimers disease and amyloid production: Studies in mouse and Caenorhabditis elegans. <i>Alzheimers and Dementia</i> , 2020 , 16, e043846	1.2	
47	Cadmium, Smoking, and Human Blood DNA Methylation Profiles in Adults from the Strong Heart Study. <i>Environmental Health Perspectives</i> , 2020 , 128, 67005	8.4	22
46	Beyond the looking glass: recent advances in understanding the impact of environmental exposures on neuropsychiatric disease. <i>Neuropsychopharmacology</i> , 2020 , 45, 1086-1096	8.7	27
45	Adult mouse hippocampal transcriptome changes associated with long-term behavioral and metabolic effects of gestational air pollution toxicity. <i>Translational Psychiatry</i> , 2020 , 10, 218	8.6	12
44	The Association Between Parental Age and Autism-Related Outcomes in Children at High Familial Risk for Autism. <i>Autism Research</i> , 2020 , 13, 998-1010	5.1	4
43	Familial confounding of the association between maternal smoking in pregnancy and autism spectrum disorder in offspring. <i>Autism Research</i> , 2020 , 13, 134-144	5.1	11
42	Early Life Exposure to Air Pollution and Autism Spectrum Disorder: Findings from a Multisite Case-Control Study. <i>Epidemiology</i> , 2020 , 31, 103-114	3.1	21
41	Interaction between Maternal Immune Activation and Antibiotic Use during Pregnancy and Child Risk of Autism Spectrum Disorder. <i>Autism Research</i> , 2020 , 13, 2230-2241	5.1	9

40	Genome, Environment, Microbiome and Metabolome in Autism (GEMMA) Study Design: Biomarkers Identification for Precision Treatment and Primary Prevention of Autism Spectrum Disorders by an Integrated Multi-Omics Systems Biology Approach. <i>Brain Sciences</i> , 2020 , 10,	3.4	6
39	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
38	The Evolving Field of Genetic Epidemiology: From Familial Aggregation to Genomic Sequencing. <i>American Journal of Epidemiology</i> , 2019 , 188, 2069-2077	3.8	3
37	DNA methylation signatures as biomarkers of prior environmental exposures. <i>Current Epidemiology Reports</i> , 2019 , 6, 1-13	2.9	14
36	Epigenetic marks of prenatal air pollution exposure found in multiple tissues relevant for child health. <i>Environment International</i> , 2019 , 126, 363-376	12.9	31
35	Variable DNA methylation in neonates mediates the association between prenatal smoking and birth weight. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019 , 374, 20180120	5.8	28
34	Invited Commentary: Is DNA Methylation an Actionable Mediator of Prenatal Exposure Effects on Child Health?. <i>American Journal of Epidemiology</i> , 2019 , 188, 1887-1889	3.8	3
33	A meta-analysis of two high-risk prospective cohort studies reveals autism-specific transcriptional changes to chromatin, autoimmune, and environmental response genes in umbilical cord blood. <i>Molecular Autism</i> , 2019 , 10, 36	6.5	8
32	The role of epigenetics in respiratory health in urban populations in low and middle-income countries. <i>Global Health, Epidemiology and Genomics</i> , 2019 , 4, e8	2.9	
31	epigenetics of metal exposure and subclinical atherosclerosis in middle aged men: pilot results from the Aragon Workers Health Study. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2018 , 373,	5.8	10
30	Genome-wide DNA methylation associations with spontaneous preterm birth in US blacks: findings in maternal and cord blood samples. <i>Epigenetics</i> , 2018 , 13, 163-172	5.7	30
29	Cohort Profile: Pregnancy And Childhood Epigenetics (PACE) Consortium. <i>International Journal of Epidemiology</i> , 2018 , 47, 22-23u	7.8	62
28	Case-control meta-analysis of blood DNA methylation and autism spectrum disorder. <i>Molecular Autism</i> , 2018 , 9, 40	6.5	48
27	Elevated polygenic burden for autism is associated with differential DNA methylation at birth. <i>Genome Medicine</i> , 2018 , 10, 19	14.4	58
26	The Changing Epidemiology of Autism Spectrum Disorders. <i>Annual Review of Public Health</i> , 2017 , 38, 81-102	20.6	404
25	Opportunities and Challenges for Environmental Exposure Assessment in Population-Based Studies. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017 , 26, 1370-1380	4	17
24	Prenatal exposure to fever is associated with autism spectrum disorder in the boston birth cohort. <i>Autism Research</i> , 2017 , 10, 1878-1890	5.1	35
23	Cross-tissue integration of genetic and epigenetic data offers insight into autism spectrum disorder. <i>Nature Communications</i> , 2017 , 8, 1011	17.4	44

22	Patients with a Kabuki syndrome phenotype demonstrate DNA methylation abnormalities. <i>European Journal of Human Genetics</i> , 2017 , 25, 1335-1344	5.3	33
21	"Gap hunting" to characterize clustered probe signals in Illumina methylation array data. <i>Epigenetics and Chromatin</i> , 2016 , 9, 56	5.8	34
20	The role of epigenetics in genetic and environmental epidemiology. <i>Epigenomics</i> , 2016 , 8, 271-83	4.4	90
19	Presence of an epigenetic signature of prenatal cigarette smoke exposure in childhood. <i>Environmental Research</i> , 2016 , 144, 139-148	7.9	75
18	Pleiotropic Mechanisms Indicated for Sex Differences in Autism. <i>PLoS Genetics</i> , 2016 , 12, e1006425	6	45
17	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
16	Epigenetic Signatures as Biomarkers of Exposure. <i>Current Environmental Health Reports</i> , 2015 , 2, 117-256.5	6.5	63
15	Minfi: a flexible and comprehensive Bioconductor package for the analysis of Infinium DNA methylation microarrays. <i>Bioinformatics</i> , 2014 , 30, 1363-9	7.2	1941
14	Accurate genome-scale percentage DNA methylation estimates from microarray data. <i>Biostatistics</i> , 2011 , 12, 197-210	3.7	62
13	Parent-of-origin effects in autism identified through genome-wide linkage analysis of 16,000 SNPs. <i>PLoS ONE</i> , 2010 , 5, e12513	3.7	28
12	Prognostic and predictive gene signature for adjuvant chemotherapy in resected non-small-cell lung cancer. <i>Journal of Clinical Oncology</i> , 2010 , 28, 4417-24	2.2	350
11	The human colon cancer methylome shows similar hypo- and hypermethylation at conserved tissue-specific CpG island shores. <i>Nature Genetics</i> , 2009 , 41, 178-186	36.3	1681
10	Differential methylation of tissue- and cancer-specific CpG island shores distinguishes human induced pluripotent stem cells, embryonic stem cells and fibroblasts. <i>Nature Genetics</i> , 2009 , 41, 1350-3	36.3	936
9	Gene expression-based survival prediction in lung adenocarcinoma: a multi-site, blinded validation study. <i>Nature Medicine</i> , 2008 , 14, 822-7	50.5	835
8	An erythroid differentiation signature predicts response to lenalidomide in myelodysplastic syndrome. <i>PLoS Medicine</i> , 2008 , 5, e35	11.6	132
7	Comprehensive high-throughput arrays for relative methylation (CHARM). <i>Genome Research</i> , 2008 , 18, 780-90	9.7	350
6	DNA methylation signatures within the human brain. <i>American Journal of Human Genetics</i> , 2007 , 81, 1304-15	15	228
5	An Erythroid Differentiation Gene Expression Signature Predicts Response to Lenalidomide in Myelodysplasia.. <i>Blood</i> , 2006 , 108, 2668-2668	2.2	1

4	An oncogenic KRAS2 expression signature identified by cross-species gene-expression analysis. <i>Nature Genetics</i> , 2005 , 37, 48-55	36.3	361
3	Interlaboratory comparability study of cancer gene expression analysis using oligonucleotide microarrays. <i>Clinical Cancer Research</i> , 2005 , 11, 565-72	12.9	116
2	A meta-analysis of two high-risk prospective cohort studies reveals autism-specific transcriptional changes to chromatin, autoimmune, and environmental response genes in umbilical cord blood		2
1	Placenta DNA methylation at ZNF300 is associated with fetal sex and placental morphology		2