Mariona Bustamante

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7241765/publications.pdf

Version: 2024-02-01

50170 46693 9,235 138 46 89 citations h-index g-index papers 153 153 153 15015 docs citations times ranked citing authors all docs

#	Article	IF	Citations
1	Polygenic risk for ADHD and ASD and their relation with cognitive measures in school children. Psychological Medicine, 2022, 52, 1356-1364.	2.7	14
2	DNA methylation changes associated with prenatal mercury exposure: A meta-analysis of prospective cohort studies from PACE consortium. Environmental Research, 2022, 204, 112093.	3.7	11
3	Maternal haemoglobin levels in pregnancy and child DNA methylation: a study in the pregnancy and childhood epigenetics consortium. Epigenetics, 2022, 17, 19-31.	1.3	3
4	Meta-analysis of epigenome-wide association studies in newborns and children show widespread sex differences in blood DNA methylation. Mutation Research - Reviews in Mutation Research, 2022, 789, 108415.	2.4	24
5	Identification of autosomal cis expression quantitative trait methylation (cis eQTMs) in children's blood. ELife, 2022, 11, .	2.8	28
6	Maternal Mediterranean diet in pregnancy and newborn DNA methylation: a meta-analysis in the PACE Consortium. Epigenetics, 2022, 17, 1419-1431.	1.3	8
7	Short- and medium-term air pollution exposure, plasmatic protein levels and blood pressure in children. Environmental Research, 2022, 211, 113109.	3.7	5
8	The early-life exposome modulates the effect of polymorphic inversions on DNA methylation. Communications Biology, 2022, 5, 455.	2.0	6
9	Study of the Combined Effect of Maternal Tobacco Smoking and Polygenic Risk Scores on Birth Weight and Body Mass Index in Childhood. Frontiers in Genetics, 2022, 13, .	1.1	1
10	Prenatal Maternal Smoke, DNA Methylation, and Multi-omics of Tissues and Child Health. Current Environmental Health Reports, 2022, 9, 502-512.	3.2	6
11	Cell type-specific novel long non-coding RNA and circular RNA in the BLUEPRINT hematopoietic transcriptomes atlas. Haematologica, 2021, 106, 2613-2623.	1.7	12
12	<i>methylclock</i> : a Bioconductor package to estimate DNA methylation age. Bioinformatics, 2021, 37, 1759-1760.	1.8	67
13	Integration of gene expression and DNA methylation identifies epigenetically controlled modules related to PM2.5 exposure. Environment International, 2021, 146, 106248.	4.8	20
14	Urinary metabolite quantitative trait loci in children and their interaction with dietary factors. Human Molecular Genetics, 2021, 29, 3830-3844.	1.4	7
15	Shared DNA methylation signatures in childhood allergy: The MeDALL study. Journal of Allergy and Clinical Immunology, 2021, 147, 1031-1040.	1.5	24
16	Plasma MicroRNA Profiling of <i>Plasmodium falciparum</i> Biomass and Association with Severity of Malaria Disease. Emerging Infectious Diseases, 2021, 27, 430-442.	2.0	24
17	Epigenetic association studies at birth and the origin of lung function development. European Respiratory Journal, 2021, 57, 2100109.	3.1	2
18	The alternative serotonin transporter promoter P2 impacts gene function in females with irritable bowel syndrome. Journal of Cellular and Molecular Medicine, 2021, 25, 8047-8061.	1.6	5

#	Article	IF	Citations
19	Variability of multi-omics profiles in a population-based child cohort. BMC Medicine, 2021, 19, 166.	2.3	23
20	Placental DNA methylation signatures of maternal smoking during pregnancy and potential impacts on fetal growth. Nature Communications, 2021, 12, 5095.	5.8	41
21	In Utero Exposure to Mercury Is Associated With Increased Susceptibility to Liver Injury and Inflammation in Childhood. Hepatology, 2021, 74, 1546-1559.	3.6	22
22	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. Nature Genetics, 2021, 53, 1311-1321.	9.4	218
23	The early-life exposome and epigenetic age acceleration in children. Environment International, 2021, 155, 106683.	4.8	47
24	Advancing tools for human early lifecourse exposome research and translation (ATHLETE). Environmental Epidemiology, 2021, 5, e166.	1.4	24
25	Neurogenetics of dynamic connectivity patterns associated with obsessive-compulsive symptoms in healthy children. Biological Psychiatry Global Open Science, 2021, , .	1.0	2
26	Rare variant analysis in eczema identifies exonic variants in DUSP1, NOTCH4 and SLC9A4. Nature Communications, 2021, 12, 6618.	5.8	17
27	Maternal seafood consumption during pregnancy and child attention outcomes: a cohort study with gene effect modification by PUFA-related genes. International Journal of Epidemiology, 2020, 49, 559-571.	0.9	10
28	Green spaces, excess weight and obesity in Spain. International Journal of Hygiene and Environmental Health, 2020, 223, 45-55.	2.1	41
29	Dose and time effects of solarâ€simulated ultraviolet radiation on the <i>inÂvivo</i> human skin transcriptome. British Journal of Dermatology, 2020, 182, 1458-1468.	1.4	27
30	Early life tobacco exposure and children's telomere length: The HELIX project. Science of the Total Environment, 2020, 711, 135028.	3.9	17
31	Interaction between filaggrin mutations and neonatal cat exposure in atopic dermatitis. Allergy: European Journal of Allergy and Clinical Immunology, 2020, 75, 1481-1485.	2.7	5
32	Novel loci for childhood body mass index and shared heritability with adult cardiometabolic traits. PLoS Genetics, 2020, 16, e1008718.	1.5	95
33	DNA methylation and body mass index from birth to adolescence: meta-analyses of epigenome-wide association studies. Genome Medicine, 2020, 12, 105.	3.6	41
34	Association of greenspace exposure with telomere length in preschool children. Environmental Pollution, 2020, 266, 115228.	3.7	14
35	The LifeCycle Project-EU Child Cohort Network: a federated analysis infrastructure and harmonized data of more than 250,000 children and parents. European Journal of Epidemiology, 2020, 35, 709-724.	2.5	81
36	In utero and childhood exposure to tobacco smoke and multi-layer molecular signatures in children. BMC Medicine, 2020, 18, 243.	2.3	22

#	Article	IF	CITATIONS
37	Using methylome data to inform exposome-health association studies: An application to the identification of environmental drivers of child body mass index. Environment International, 2020, 138, 105622.	4.8	22
38	Epigenome-wide meta-analysis of blood DNA methylation in newborns and children identifies numerous loci related to gestational age. Genome Medicine, 2020, 12, 25.	3.6	81
39	A novel whole blood gene expression signature for asthma, dermatitis, and rhinitis multimorbidity in children and adolescents. Allergy: European Journal of Allergy and Clinical Immunology, 2020, 75, 3248-3260.	2.7	55
40	Association of Fish Consumption and Mercury Exposure During Pregnancy With Metabolic Health and Inflammatory Biomarkers in Children. JAMA Network Open, 2020, 3, e201007.	2.8	30
41	Prenatal and Childhood Traffic-Related Air Pollution Exposure and Telomere Length in European Children: The HELIX Project. Environmental Health Perspectives, 2019, 127, 87001.	2.8	32
42	A trans-ancestral meta-analysis of genome-wide association studies reveals loci associated with childhood obesity. Human Molecular Genetics, 2019, 28, 3327-3338.	1.4	76
43	Comparison of Illumina 450K and EPIC arrays in placental DNA methylation. Epigenetics, 2019, 14, 1177-1182.	1.3	15
44	Variants in the fetal genome near pro-inflammatory cytokine genes on 2q13 associate with gestational duration. Nature Communications, 2019, 10, 3927.	5.8	49
45	SU89TRAFFIC-RELATED AIR POLLUTION, APOE ε4 STATUS, AND NEURODEVELOPMENTAL OUTCOMES AMONG SCHOOL CHILDREN ENROLLED IN THE BREATHE PROJECT (CATALONIA, SPAIN). European Neuropsychopharmacology, 2019, 29, S1313.	0.3	O
46	Mendelian randomization analysis rules out disylipidaemia as colorectal cancer cause. Scientific Reports, 2019, 9, 13407.	1.6	11
47	Importance of considering circadian rhythm in the design of in vivo transcriptional studies of acute effects of environmental exposures. Environmental Research, 2019, 178, 108691.	3.7	1
48	Comparison of smoking-related DNA methylation between newborns from prenatal exposure and adults from personal smoking. Epigenomics, 2019, 11, 1487-1500.	1.0	64
49	Epigenome-wide meta-analysis of DNA methylation and childhood asthma. Journal of Allergy and Clinical Immunology, 2019, 143, 2062-2074.	1.5	147
50	Prenatal Particulate Air Pollution and DNA Methylation in Newborns: An Epigenome-Wide Meta-Analysis. Environmental Health Perspectives, 2019, 127, 57012.	2.8	111
51	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. Nature Genetics, 2019, 51, 804-814.	9.4	402
52	Meta-analysis of epigenome-wide association studies in neonates reveals widespread differential DNA methylation associated with birthweight. Nature Communications, 2019, 10, 1893.	5.8	140
53	The Early Growth Genetics (EGG) and EArly Genetics and Lifecourse Epidemiology (EAGLE) consortia: design, results and future prospects. European Journal of Epidemiology, 2019, 34, 279-300.	2.5	26
54	Newborn DNA-methylation, childhood lung function, and the risks of asthma and COPD across the life course. European Respiratory Journal, 2019, 53, 1801795.	3.1	48

#	Article	IF	Citations
55	Obesity is associated with shorter telomeres in 8 year-old children. Scientific Reports, 2019, 9, 18739.	1.6	40
56	Effect modification of <i>FADS2</i> polymorphisms on the association between breastfeeding and intelligence: results from a collaborative meta-analysis. International Journal of Epidemiology, 2019, 48, 45-57.	0.9	5
57	Is childhood asthma associated with biological aging markers?. , 2019, , .		O
58	Vitamin D status during pregnancy and wheezing and asthma during childhood. , 2019, , .		0
59	DNA methylation in childhood asthma: an epigenome-wide meta-analysis. Lancet Respiratory Medicine,the, 2018, 6, 379-388.	5.2	170
60	Validating a breast cancer score in Spanish women. The MCC-Spain study. Scientific Reports, 2018, 8, 3036.	1.6	5
61	DNA Methylome Marks of Exposure to Particulate Matter at Three Time Points in Early Life. Environmental Science & Environmental Science & Environmenta	4.6	21
62	Cohort Profile: Pregnancy And Childhood Epigenetics (PACE) Consortium. International Journal of Epidemiology, 2018, 47, 22-23u.	0.9	105
63	Maternal and fetal genetic contribution to gestational weight gain. International Journal of Obesity, 2018, 42, 775-784.	1.6	36
64	Prenatal co-exposure to neurotoxic metals and neurodevelopment in preschool children: The Environment and Childhood (INMA) Project. Science of the Total Environment, 2018, 621, 340-351.	3.9	103
65	Genetic and epigenetic regulation of YKL-40 in childhood. Journal of Allergy and Clinical Immunology, 2018, 141, 1105-1114.	1.5	27
66	Traffic-Related Air Pollution, <i>APOE</i> \hat{l} µ4 Status, and Neurodevelopmental Outcomes among School Children Enrolled in the BREATHE Project (Catalonia, Spain). Environmental Health Perspectives, 2018, 126, 087001.	2.8	53
67	Human Early Life Exposome (HELIX) study: a European population-based exposome cohort. BMJ Open, 2018, 8, e021311.	0.8	161
68	Strategies for integrated analysis in imaging genetics studies. Neuroscience and Biobehavioral Reviews, 2018, 93, 57-70.	2.9	7
69	A systemic approach to identify signaling pathways activated during short-term exposure to traffic-related urban air pollution from human blood. Environmental Science and Pollution Research, 2018, 25, 29572-29583.	2.7	1
70	Sparse multiple factor analysis to integrate genetic data, neuroimaging features, and attentionâ€deficit/hyperactivity disorder domains. International Journal of Methods in Psychiatric Research, 2018, 27, e1738.	1.1	10
71	Circulating miRNAs, isomiRs and small RNA clusters in human plasma and breast milk. PLoS ONE, 2018, 13, e0193527.	1.1	51
72	Fruit and vegetable intake and vitamin C transporter gene (SLC23A2) polymorphisms in chronic lymphocytic leukaemia. European Journal of Nutrition, 2017, 56, 1123-1133.	1.8	11

#	Article	IF	CITATIONS
73	Risk Model for Colorectal Cancer in Spanish Population Using Environmental and Genetic Factors: Results from the MCC-Spain study. Scientific Reports, 2017, 7, 43263.	1.6	41
74	CYP3A genes and the association between prenatal methylmercury exposure and neurodevelopment. Environment International, 2017, 105, 34-42.	4.8	24
75	Gene expression changes in blood RNA after swimming in a chlorinated pool. Journal of Environmental Sciences, 2017, 58, 250-261.	3.2	5
76	Interaction between airborne copper exposure and ATP7B polymorphisms on inattentiveness in scholar children. International Journal of Hygiene and Environmental Health, 2017, 220, 51-56.	2.1	14
77	The acute effects of ultraviolet radiation on the blood transcriptome are independent of plasma 250HD3. Environmental Research, 2017, 159, 239-248.	3.7	13
78	Maternal BMI at the start of pregnancy and offspring epigenome-wide DNA methylation: findings from the pregnancy and childhood epigenetics (PACE) consortium. Human Molecular Genetics, 2017, 26, 4067-4085.	1.4	211
79	Gene-wide Association Study Reveals RNF122 Ubiquitin Ligase as a Novel Susceptibility Gene for Attention Deficit Hyperactivity Disorder. Scientific Reports, 2017, 7, 5407.	1.6	11
80	The emerging landscape of dynamic DNA methylation in early childhood. BMC Genomics, 2017, 18, 25.	1.2	49
81	Epigenome-Wide Meta-Analysis of Methylation in Children Related to Prenatal NO ₂ Air Pollution Exposure. Environmental Health Perspectives, 2017, 125, 104-110.	2.8	176
82	Prenatal Ambient Air Pollution, Placental Mitochondrial DNA Content, and Birth Weight in the INMA (Spain) and ENVIR <i>ON</i> AGE (Belgium) Birth Cohorts. Environmental Health Perspectives, 2016, 124, 659-665.	2.8	105
83	A Genome-Wide Association Study of Attention Function in a Population-Based Sample of Children. PLoS ONE, 2016, 11, e0163048.	1.1	11
84	Drinking Water Disinfection By-products, Genetic Polymorphisms, and Birth Outcomes in a European Mother–Child Cohort Study. Epidemiology, 2016, 27, 903-911.	1.2	27
85	DNA Methylation in Newborns and Maternal Smoking in Pregnancy: Genome-wide Consortium Meta-analysis. American Journal of Human Genetics, 2016, 98, 680-696.	2.6	717
86	Genome-wide DNA methylation study in human placenta identifies novel loci associated with maternal smoking during pregnancy. International Journal of Epidemiology, 2016, 45, 1644-1655.	0.9	85
87	Genome-wide associations for birth weight and correlations with adult disease. Nature, 2016, 538, 248-252.	13.7	406
88	A genome-wide association meta-analysis of diarrhoeal disease in young children identifies <i>FUT2</i> locus and provides plausible biological pathways. Human Molecular Genetics, 2016, 25, 4127-4142.	1.4	35
89	Heritability and Genome-Wide Association Analyses of Sleep Duration in Children: The EAGLE Consortium. Sleep, 2016, 39, 1859-1869.	0.6	34
90	Prenatal exposure to mixtures of xenoestrogens and genome-wide DNA methylation in human placenta. Epigenomics, 2016, 8, 43-54.	1.0	15

#	Article	IF	CITATIONS
91	Ancient Haplotypes at the 15q24.2 Microdeletion Region Are Linked to Brain Expression of MAN2C1 and Children's Intelligence. PLoS ONE, 2016, 11, e0157739.	1.1	2
92	Differentially methylated genes related to gestational age are also expressed during fetal lung development. , 2016, , .		0
93	New suggestive genetic loci and biological pathways for attention function in adult attentionâ€deficit/hyperactivity disorder. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2015, 168, 459-470.	1.1	78
94	DNA methylation levels and long-term trihalomethane exposure in drinking water: an epigenome-wide association study. Epigenetics, 2015, 10, 650-661.	1.3	22
95	Population-based multicase-control study in common tumors in Spain (MCC-Spain): rationale and study design. Gaceta Sanitaria, 2015, 29, 308-315.	0.6	158
96	Multi-ancestry genome-wide association study of 21,000 cases and 95,000 controls identifies new risk loci for atopic dermatitis. Nature Genetics, 2015, 47, 1449-1456.	9.4	529
97	A novel common variant in DCST2 is associated with length in early life and height in adulthood. Human Molecular Genetics, 2015, 24, 1155-1168.	1.4	109
98	Case–Control Genome-Wide Association Study of Persistent Attention-Deficit Hyperactivity Disorder Identifies FBXO33 as a Novel Susceptibility Gene for the Disorder. Neuropsychopharmacology, 2015, 40, 915-926.	2.8	59
99	The Human Early-Life Exposome (HELIX): Project Rationale and Design. Environmental Health Perspectives, 2014, 122, 535-544.	2.8	280
100	A Common 16p11.2 Inversion Underlies the Joint Susceptibility to Asthma and Obesity. American Journal of Human Genetics, 2014, 94, 361-372.	2.6	66
101	Genome-wide association study of sexual maturation in males and females highlights a role for body mass and menarche loci in male puberty. Human Molecular Genetics, 2014, 23, 4452-4464.	1.4	82
102	Prenatal exposure to mixtures of xenoestrogens and repetitive element DNA methylation changes in human placenta. Environment International, 2014, 71, 81-87.	4.8	52
103	In utero exposure to mixtures of xenoestrogens and child neuropsychological development. Environmental Research, 2014, 134, 98-104.	3.7	16
104	Polymorphisms in ABC Transporter Genes and Concentrations of Mercury in Newborns – Evidence from Two Mediterranean Birth Cohorts. PLoS ONE, 2014, 9, e97172.	1.1	39
105	Storage conditions and stability of global DNA methylation in placental tissue. Epigenomics, 2013, 5, 341-348.	1.0	34
106	Male specific association between xenoestrogen levels in placenta and birthweight. Environment International, 2013, 51, 174-181.	4.8	28
107	New loci associated with birth weight identify genetic links between intrauterine growth and adult height and metabolism. Nature Genetics, 2013, 45, 76-82.	9.4	293
108	Gene Expression of Desaturase (FADS1 and FADS2) and Elongase (ELOVL5) Enzymes in Peripheral Blood: Association with Polyunsaturated Fatty Acid Levels and Atopic Eczema in 4-Year-Old Children. PLoS ONE, 2013, 8, e78245.	1.1	20

#	Article	IF	Citations
109	Indoor Air Pollution From Gas Cooking and Infant Neurodevelopment. Epidemiology, 2012, 23, 23-32.	1.2	59
110	DNA Hypomethylation atALOX12Is Associated with Persistent Wheezing in Childhood. American Journal of Respiratory and Critical Care Medicine, 2012, 185, 937-943.	2.5	97
111	A genome-wide association meta-analysis identifies new childhood obesity loci. Nature Genetics, 2012, 44, 526-531.	9.4	352
112	Influence of fetal glutathione S-transferase copy number variants on adverse reproductive outcomes. BJOG: an International Journal of Obstetrics and Gynaecology, 2012, 119, 1141-1146.	1.1	11
113	Dietary benzo(a)pyrene and fetal growth: Effect modification by vitamin C intake and glutathione S-transferase P1 polymorphism. Environment International, 2012, 45, 1-8.	4.8	22
114	Genetic Variants of the FADS Gene Cluster and ELOVL Gene Family, Colostrums LC-PUFA Levels, Breastfeeding, and Child Cognition. PLoS ONE, 2011, 6, e17181.	1.1	111
115	Disinfection Byproducts, Polymorphisms, and Susceptibility to Adverse Pregnancy Outcomes. Epidemiology, 2011, 22, S67-S68.	1.2	0
116	Maternal C-reactive protein levels in pregnancy are associated with wheezing and lower respiratory tract infections in the offspring. American Journal of Obstetrics and Gynecology, 2011, 204, 164.e1-164.e9.	0.7	29
117	Colorectal Cancer and Disinfection Byproducts in Italy and Spain. Epidemiology, 2011, 22, S156.	1.2	0
118	Analysis of Three Functional Polymorphisms in Relation to Osteoporosis Phenotypes: Replication in a Spanish Cohort. Calcified Tissue International, 2010, 87, 14-24.	1.5	25
119	Role of the neurotrophin network in eating disorders' subphenotypes: Body mass index and age at onset of the disease. Journal of Psychiatric Research, 2010, 44, 834-840.	1.5	10
120	Genotoxic Effects in Swimmers Exposed to Disinfection By-products in Indoor Swimming Pools. Environmental Health Perspectives, 2010, 118, 1531-1537.	2.8	126
121	Short-Term Changes in Respiratory Biomarkers after Swimming in a Chlorinated Pool. Environmental Health Perspectives, 2010, 118, 1538-1544.	2.8	94
122	Early life environment, neurodevelopment and the interrelation with atopy. Environmental Research, 2010, 110, 733-738.	3.7	8
123	Association of Early-life Exposure to Household Gas Appliances and Indoor Nitrogen Dioxide With Cognition and Attention Behavior in Preschoolers. American Journal of Epidemiology, 2009, 169, 1327-1336.	1.6	81
124	A pooling-based genome-wide analysis identifies new potential candidate genes for atopy in the European Community Respiratory Health Survey (ECRHS). BMC Medical Genetics, 2009, 10, 128.	2.1	43
125	Prenatal Exposure to Gas Cooking and Neurodevelopment at 14 Months. Epidemiology, 2009, 20, S37-S38.	1.2	0
126	A Haplotype-Based Analysis of the <i>LRP5</i> Gene in Relation to Osteoporosis Phenotypes in Spanish Postmenopausal Women. Journal of Bone and Mineral Research, 2008, 23, 1954-1963.	3.1	18

#	Article	IF	CITATIONS
127	Large-scale analysis of association between polymorphisms in the transforming growth factor beta 1 gene (TGFB1) and osteoporosis: The GENOMOS study. Bone, 2008, 42, 969-981.	1.4	91
128	Polymorphisms in the interleukin-6 receptor gene are associated with bone mineral density and body mass index in Spanish postmenopausal women. European Journal of Endocrinology, 2007, 157, 677-684.	1.9	42
129	Bone Mass of a 113-Year-Old Man. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2007, 62, 794-795.	1.7	5
130	Promoter 2 -1025 T/C Polymorphism in the RUNX2 Gene Is Associated with Femoral Neck BMD in Spanish Postmenopausal Women. Calcified Tissue International, 2007, 81, 327-332.	1.5	32
131	COL1A1, ESR1, VDR and TGFB1 polymorphisms and haplotypes in relation to BMD in Spanish postmenopausal women. Osteoporosis International, 2007, 18, 235-243.	1.3	56
132	A new SNP in a negative regulatory region of the CYP19A1 gene is associated with lumbar spine BMD in postmenopausal women. Bone, 2006, 38, 738-743.	1.4	27
133	Large-Scale Evidence for the Effect of the COLIA1 Sp1 Polymorphism on Osteoporosis Outcomes: The GENOMOS Study. PLoS Medicine, 2006, 3, e90.	3.9	160
134	The Association between Common Vitamin D Receptor Gene Variations and Osteoporosis: A Participant-Level Meta-Analysis. Annals of Internal Medicine, 2006, 145, 255.	2.0	219
135	Functional analysis of the I.3, I.6, pll and I.4 promoters of CYP19 (aromatase) gene in human osteoblasts and their role in vitamin D and dexamethasone stimulation. European Journal of Endocrinology, 2005, 153, 981-988.	1.9	34
136	In vitro functional assay of alleles and haplotypes of two -promoter SNPs. Bone, 2005, 36, 902-908.	1.4	36
137	Differential Genetic Effects of <emph type="ITAL">ESR1</emph> Gene Polymorphisms on Osteoporosis Outcomes. JAMA - Journal of the American Medical Association, 2004, 292, 2105.	3.8	265
138	Usefulness of Gadolinium-Enhanced MR Imaging in the Evaluation of the Vascularity of Scaphoid Nonunions. American Journal of Roentgenology, 2000, 174, 141-149.	1.0	138