

# Luigi Bouchard

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6153021/publications.pdf>

Version: 2024-02-01

84  
papers

3,857  
citations

136740

32  
h-index

133063

59  
g-index

85  
all docs

85  
docs citations

85  
times ranked

6098  
citing authors

#	ARTICLE	IF	CITATIONS
1	Family planning decisional needs assessment for recessive hereditary disorders: Insights from carrier couples and professionals. <i>Patient Education and Counseling</i> , 2022, 105, 2537-2545.	1.0	1
2	Human plasma pregnancy-associated miRNAs and their temporal variation within the first trimester of pregnancy. <i>Reproductive Biology and Endocrinology</i> , 2022, 20, 14.	1.4	17
3	Maternal Glycemic Dysregulation During Pregnancy and Neonatal Blood DNA Methylation: Meta-analyses of Epigenome-Wide Association Studies. <i>Diabetes Care</i> , 2022, 45, 614-623.	4.3	19
4	Multi-ancestry genome-wide association study of gestational diabetes mellitus highlights genetic links with type 2 diabetes. <i>Human Molecular Genetics</i> , 2022, 31, 3377-3391.	1.4	47
5	First trimester plasma microRNAs levels predict Matsuda Index-estimated insulin sensitivity between 24th and 29th week of pregnancy. <i>BMJ Open Diabetes Research and Care</i> , 2022, 10, e002703.	1.2	6
6	The Genetic and Molecular Analyses of RAD51C and RAD51D Identifies Rare Variants Implicated in Hereditary Ovarian Cancer from a Genetically Unique Population. <i>Cancers</i> , 2022, 14, 2251.	1.7	4
7	Time-course full profiling of circulating miRNAs in neurologically deceased organ donors: a proof of concept study to understand the onset of the cytokine storm. <i>Epigenetics</i> , 2022, 17, 1546-1561.	1.3	0
8	Epigenome-wide association study of maternal hemoglobin A1c in pregnancy and cord blood DNA methylation. <i>Epigenomics</i> , 2021, 13, 203-218.	1.0	5
9	Study protocol for the Sino-Canadian Healthy Life Trajectories Initiative (SCHeLTI): a multicentre, cluster-randomised, parallel-group, superiority trial of a multifaceted community-family-mother-child intervention to prevent childhood overweight and obesity. <i>BMJ Open</i> , 2021, 11, e045192.	0.8	9
10	Detecting cord blood cell type-specific epigenetic associations with gestational diabetes mellitus and early childhood growth. <i>Clinical Epigenetics</i> , 2021, 13, 131.	1.8	5
11	HDL-enriched miR-30a-5p is associated with HDL-cholesterol levels and glucose metabolism in healthy men and women. <i>Epigenomics</i> , 2021, 13, 985-994.	1.0	4
12	Placental DNA methylation signatures of maternal smoking during pregnancy and potential impacts on fetal growth. <i>Nature Communications</i> , 2021, 12, 5095.	5.8	41
13	Individuals with self-determined motivation for eating have better overall diet quality: Results from the PREDISE study. <i>Appetite</i> , 2021, 165, 105426.	1.8	10
14	Associations of maternal insulin resistance during pregnancy and offspring inflammation at birth and at 5Åyears of age: A prospective study in the Gen3G cohort. <i>Cytokine</i> , 2021, 146, 155636.	1.4	1
15	Associations between an integrated component of maternal glycemic regulation in pregnancy and cord blood DNA methylation. <i>Epigenomics</i> , 2021, 13, 1459-1472.	1.0	3
16	miR profile in pagetic osteoclasts: from large-scale sequencing to gene expression study. <i>Journal of Molecular Medicine</i> , 2021, 99, 1771-1781.	1.7	4
17	DNA methylation at <i>LRP1</i> gene locus mediates the association between maternal total cholesterol changes in pregnancy and cord blood leptin levels. <i>Journal of Developmental Origins of Health and Disease</i> , 2020, 11, 369-378.	0.7	8
18	Placental Epigenome-Wide Association Study Identified Loci Associated with Childhood Adiposity at 3 Years of Age. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7201.	1.8	9

#	ARTICLE	IF	CITATIONS
19	Gut Microbiome Composition Is Associated with Blood Pressure in Mother-Child Pairs 5 Years After Birth. <i>Current Developments in Nutrition</i> , 2020, 4, nzaa062_012.	0.1	1
20	DNA methylation at the <i>DMPK</i> gene locus is associated with cognitive functions in myotonic dystrophy type 1. <i>Epigenomics</i> , 2020, 12, 2051-2064.	1.0	11
21	Osteoclast signaling-targeting miR-146a-3p and miR-155-5p are downregulated in Paget's disease of bone. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2020, 1866, 165852.	1.8	11
22	Interplay of Placental DNA Methylation and Maternal Insulin Sensitivity in Pregnancy. <i>Diabetes</i> , 2020, 69, 484-492.	0.3	34
23	Mediation Analysis Supports a Causal Relationship between Maternal Hyperglycemia and Placental DNA Methylation Variations at the Leptin Gene Locus and Cord Blood Leptin Levels. <i>International Journal of Molecular Sciences</i> , 2020, 21, 329.	1.8	19
24	Human high-density lipoprotein microtranscriptome is unique and suggests an extended role in lipid metabolism. <i>Epigenomics</i> , 2019, 11, 917-934.	1.0	8
25	Prenatal determinants of childhood obesity: a review of risk factors. <i>Canadian Journal of Physiology and Pharmacology</i> , 2019, 97, 147-154.	0.7	26
26	Meta-analysis of epigenome-wide association studies in neonates reveals widespread differential DNA methylation associated with birthweight. <i>Nature Communications</i> , 2019, 10, 1893.	5.8	140
27	Allele length of the DMPK CTG repeat is a predictor of progressive myotonic dystrophy type 1 phenotypes. <i>Human Molecular Genetics</i> , 2019, 28, 2245-2254.	1.4	41
28	DMPK gene DNA methylation levels are associated with muscular and respiratory profiles in DM1. <i>Neurology: Genetics</i> , 2019, 5, e338.	0.9	19
29	Maternal lipid profile differs by gestational diabetes physiologic subtype. <i>Metabolism: Clinical and Experimental</i> , 2019, 91, 39-42.	1.5	35
30	An analytic approach for interpretable predictive models in high-dimensional data in the presence of interactions with exposures. <i>Genetic Epidemiology</i> , 2018, 42, 233-249.	0.6	8
31	DNA methylation of a PLPP3 MIR transposon-based enhancer promotes an osteogenic programme in calcific aortic valve disease. <i>Cardiovascular Research</i> , 2018, 114, 1525-1535.	1.8	27
32	Cohort Profile: Pregnancy And Childhood Epigenetics (PACE) Consortium. <i>International Journal of Epidemiology</i> , 2018, 47, 22-23u.	0.9	105
33	Effect of gestational diabetes and insulin resistance on offspring's myocardial relaxation kinetics at three years of age. <i>PLoS ONE</i> , 2018, 13, e0207632.	1.1	3
34	Poor Adherence to Dietary Guidelines Among French-Speaking Adults in the Province of Quebec, Canada: The PREDISE Study. <i>Canadian Journal of Cardiology</i> , 2018, 34, 1665-1673.	0.8	29
35	Genetic Determinants of Glycemic Traits and the Risk of Gestational Diabetes Mellitus. <i>Diabetes</i> , 2018, 67, 2703-2709.	0.3	30
36	Placental DNA Methylation Adaptation to Maternal Glycemic Response in Pregnancy. <i>Diabetes</i> , 2018, 67, 1673-1683.	0.3	42

#	ARTICLE	IF	CITATIONS
37	Changes in high-density lipoprotein-carried miRNA contribution to the plasmatic pool after consumption of dietarytransfat in healthy men. <i>Epigenomics</i> , 2017, 9, 669-688.	1.0	21
38	Placental lipoprotein lipase DNA methylation alterations are associated with gestational diabetes and body composition at 5Åyears of age. <i>Epigenetics</i> , 2017, 12, 616-625.	1.3	38
39	MicroRNAs in Pregnancy and Gestational Diabetes Mellitus: Emerging Role in Maternal Metabolic Regulation. <i>Current Diabetes Reports</i> , 2017, 17, 35.	1.7	58
40	Genetic determinants of adiponectin regulation revealed by pregnancy. <i>Obesity</i> , 2017, 25, 935-944.	1.5	10
41	microRNAs in lipoprotein and lipid metabolism: from biological function to clinical application. <i>Clinical Chemistry and Laboratory Medicine</i> , 2017, 55, 667-686.	1.4	36
42	PACE4 Undergoes an Oncogenic Alternative Splicing Switch in Cancer. <i>Cancer Research</i> , 2017, 77, 6863-6879.	0.4	58
43	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.	1.4	211
44	Timing of Excessive Weight Gain During Pregnancy Modulates Newborn Anthropometry. <i>Journal of Obstetrics and Gynaecology Canada</i> , 2016, 38, 108-117.	0.3	20
45	Variations in HDL-carried miR-223 and miR-135a concentrations after consumption of dietary trans fat are associated with changes in blood lipid and inflammatory markers in healthy men - an exploratory study. <i>Epigenetics</i> , 2016, 11, 438-448.	1.3	29
46	PPARGC1± gene DNA methylation variations in human placenta mediate the link between maternal hyperglycemia and leptin levels in newborns. <i>Clinical Epigenetics</i> , 2016, 8, 72.	1.8	66
47	Altered DNA Methylation of Long Noncoding RNA <i>H19</i> in Calcific Aortic Valve Disease Promotes Mineralization by Silencing <i>NOTCH1</i>. <i>Circulation</i> , 2016, 134, 1848-1862.	1.6	182
48	Genetics of Glucose regulation in Gestation and Growth (Gen3G): a prospective prebirth cohort of motherâ€child pairs in Sherbrooke, Canada. <i>BMJ Open</i> , 2016, 6, e010031.	0.8	67
49	funtooNorm: an R package for normalization of DNA methylation data when there are multiple cell or tissue types. <i>Bioinformatics</i> , 2016, 32, 593-595.	1.8	22
50	Genetic Evidence for Causal Relationships Between Maternal Obesity-Related Traits and Birth Weight. <i>JAMA - Journal of the American Medical Association</i> , 2016, 315, 1129.	3.8	220
51	Epigenetic and genetic variations at the <i>TNNT1</i> gene locus are associated with HDL-C levels and coronary artery disease. <i>Epigenomics</i> , 2016, 8, 359-371.	1.0	26
52	DNA methylation signature of interleukin 1 receptor type II in asthma. <i>Clinical Epigenetics</i> , 2015, 7, 80.	1.8	12
53	A study in familial hypercholesterolemia suggests reduced methylomic plasticity in men with coronary artery disease. <i>Epigenomics</i> , 2015, 7, 17-34.	1.0	17
54	Layered genetic control of DNA methylation and gene expression: a locus of multiple sclerosis in healthy individuals. <i>Human Molecular Genetics</i> , 2015, 24, 5733-5745.	1.4	26

#	ARTICLE	IF	CITATIONS
55	Prenatal exposure to cigarette smoke interacts with <i>OPRM1</i> to modulate dietary preference for fat. <i>Journal of Psychiatry and Neuroscience</i> , 2015, 40, 38-45.	1.4	20
56	Leptin and adiponectin DNA methylation levels in adipose tissues and blood cells are associated with BMI, waist girth and LDL-cholesterol levels in severely obese men and women. <i>BMC Medical Genetics</i> , 2015, 16, 29.	2.1	96
57	<i>LRP1B</i> , <i>BRD2</i> and <i>CACNA1D</i> : new candidate genes in fetal metabolic programming of newborns exposed to maternal hyperglycemia. <i>Epigenomics</i> , 2015, 7, 1111-1122.	1.0	24
58	Abstract 16338: Dna Hypomethylation in Long Non-coding Rna Promoter During Calcific Aortic Valve Stenosis: Implication for the Notch Pathway. <i>Circulation</i> , 2015, 132, .	1.6	0
59	Epipolymorphisms within lipoprotein genes contribute independently to plasma lipid levels in familial hypercholesterolemia. <i>Epigenetics</i> , 2014, 9, 718-729.	1.3	57
60	Cross-tissue comparisons of leptin and adiponectin. <i>Adipocyte</i> , 2014, 3, 132-140.	1.3	30
61	Glycation of Fetal Hemoglobin Reflects Hyperglycemia Exposure In Utero. <i>Diabetes Care</i> , 2014, 37, 2830-2833.	4.3	3
62	Epigenetic dysregulation of the IGF system in placenta of newborns exposed to maternal impaired glucose tolerance. <i>Epigenomics</i> , 2014, 6, 193-207.	1.0	37
63	<i>ADRB3</i> gene promoter DNA methylation in blood and visceral adipose tissue is associated with metabolic disturbances in men. <i>Epigenomics</i> , 2014, 6, 33-43.	1.0	41
64	Early Infant Nutrition and Metabolic Programming: What Are the Potential Molecular Mechanisms?. <i>Current Nutrition Reports</i> , 2014, 3, 281-288.	2.1	16
65	Acetylsalicylic acid, aging and coronary artery disease are associated with ABCA1 DNA methylation in men. <i>Clinical Epigenetics</i> , 2014, 6, 14.	1.8	67
66	Maternal Nutrition and Epigenetics in Early Life. <i>Current Nutrition Reports</i> , 2013, 2, 216-224.	2.1	1
67	Epigenetics and Fetal Metabolic Programming: A Call for Integrated Research on Larger Cohorts. <i>Diabetes</i> , 2013, 62, 1026-1028.	0.3	22
68	Epigenetic programming of obesity and diabetes by in utero exposure to gestational diabetes mellitus. <i>Nutrition Reviews</i> , 2013, 71, S88-S94.	2.6	101
69	Adaptations of placental and cord blood <i>ABCA1</i> DNA methylation profile to maternal metabolic status. <i>Epigenetics</i> , 2013, 8, 1289-1302.	1.3	86
70	Gestational diabetes mellitus epigenetically affects genes predominantly involved in metabolic diseases. <i>Epigenetics</i> , 2013, 8, 935-943.	1.3	217
71	Fetal epigenetic programming of adipokines. <i>Adipocyte</i> , 2013, 2, 41-46.	1.3	40
72	DUSP1 gene polymorphisms are associated with obesity-related metabolic complications and gene methylation levels in severely obese patients. <i>FASEB Journal</i> , 2013, 27, 226.1.	0.2	0

#	ARTICLE	IF	CITATIONS
73	Epigenome-wide analysis in familial hypercholesterolemia identified new loci associated with high-density lipoprotein cholesterol concentration. <i>Epigenomics</i> , 2012, 4, 623-639.	1.0	44
74	<i>ABCA1</i> gene promoter DNA methylation is associated with HDL particle profile and coronary artery disease in familial hypercholesterolemia. <i>Epigenetics</i> , 2012, 7, 464-472.	1.3	114
75	IGF2 DNA methylation is a modulator of newborn's fetal growth and development. <i>Epigenetics</i> , 2012, 7, 1125-1132.	1.3	131
76	Placental Adiponectin Gene DNA Methylation Levels Are Associated With Mothers' Blood Glucose Concentration. <i>Diabetes</i> , 2012, 61, 1272-1280.	0.3	188
77	<i>DPP4</i> Gene DNA Methylation in the Omentum is Associated With Its Gene Expression and Plasma Lipid Profile in Severe Obesity. <i>Obesity</i> , 2011, 19, 388-395.	1.5	52
78	Contribution of Genetic and Metabolic Syndrome to Omental Adipose Tissue PAI-1 Gene mRNA and Plasma Levels in Obesity. <i>Obesity Surgery</i> , 2010, 20, 492-499.	1.1	21
79	Differential epigenomic and transcriptomic responses in subcutaneous adipose tissue between low and high responders to caloric restriction. <i>American Journal of Clinical Nutrition</i> , 2010, 91, 309-320.	2.2	193
80	Leptin Gene Epigenetic Adaptation to Impaired Glucose Metabolism During Pregnancy. <i>Diabetes Care</i> , 2010, 33, 2436-2441.	4.3	218
81	Visceral adipose tissue DNA methylation at dipeptidyl peptidase-4 gene locus is associated with gene expression and plasma lipid levels in severe obesity. <i>FASEB Journal</i> , 2010, 24, .	0.2	0
82	Comprehensive genetic analysis of the dipeptidyl peptidase-4 gene and cardiovascular disease risk factors in obese individuals. <i>Acta Diabetologica</i> , 2009, 46, 13-21.	1.2	49
83	Association of <i>OSBPL11</i> Gene Polymorphisms With Cardiovascular Disease Risk Factors in Obesity. <i>Obesity</i> , 2009, 17, 1466-1472.	1.5	31
84	ZFP36: a Promising Candidate Gene for Obesity-Related Metabolic Complications Identified by Converging Genomics. <i>Obesity Surgery</i> , 2007, 17, 372-382.	1.1	57