

Maya A Kappil

List of Publications by Year in descending order

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Version: 2024-02-01

48
papers

1,660
citations

279487

23
h-index

288905

40
g-index

49
all docs

49
docs citations

49
times ranked

3396
citing authors

#	ARTICLE	IF	CITATIONS
1	Variation in placental microRNA expression associates with maternal family history of cardiovascular disease. <i>Journal of Developmental Origins of Health and Disease</i> , 2023, 14, 132-139.	0.7	0
2	Potential roles of imprinted genes in the teratogenic effects of alcohol on the placenta, somatic growth, and the developing brain. <i>Experimental Neurology</i> , 2022, 347, 113919.	2.0	7
3	PM2.5 exposure during pregnancy is associated with altered placental expression of lipid metabolic genes in a US birth cohort. <i>Environmental Research</i> , 2022, 211, 113066.	3.7	7
4	Placental microRNA expression associates with birthweight through control of adipokines: results from two independent cohorts. <i>Epigenetics</i> , 2021, 16, 770-782.	1.3	12
5	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
6	Sex-Specific Influence of Gestational PM2.5 Exposure on Placental Metabolic Gene Expression within the Rhode Island Child Health Study (RICHs). <i>ISEE Conference Abstracts</i> , 2021, 2021, .	0.0	0
7	Placental gene networks at the interface between maternal PM2.5 exposure early in gestation and reduced infant birthweight. <i>Environmental Research</i> , 2021, 199, 111342.	3.7	24
8	Placental gene network modules are associated with maternal stress during pregnancy and infant temperament. <i>FASEB Journal</i> , 2021, 35, e21922.	0.2	4
9	In-depth characterization of the placental imprintome reveals novel differentially methylated regions across birth weight categories. <i>Epigenetics</i> , 2020, 15, 47-60.	1.3	11
10	Differences in Placental Imprinted Gene Expression across Preeclamptic and Non-Preeclamptic Pregnancies. <i>Genes</i> , 2020, 11, 1146.	1.0	3
11	Seasonally variant gene expression in full-term human placenta. <i>FASEB Journal</i> , 2020, 34, 10431-10442.	0.2	9
12	Placental lncRNA expression associated with placental cadmium concentrations and birth weight. <i>Environmental Epigenetics</i> , 2020, 6, dvaa003.	0.9	17
13	Moderate prenatal stress may buffer the impact of Superstorm Sandy on placental genes: Stress in Pregnancy (SIP) Study. <i>PLoS ONE</i> , 2020, 15, e0226605.	1.1	7
14	Maternal stress in relation to sex-specific expression of placental genes involved in nutrient transport, oxygen tension, immune response, and the glucocorticoid barrier. <i>Placenta</i> , 2020, 96, 19-26.	0.7	17
15	Placental Expression of Imprinted Genes, Overall and in Sex-Specific Patterns, Associated with Placental Cadmium Concentrations and Birth Size. <i>Environmental Health Perspectives</i> , 2019, 127, 57005.	2.8	24
16	Maternal circadian disruption is associated with variation in placental DNA methylation. <i>PLoS ONE</i> , 2019, 14, e0215745.	1.1	22
17	DNA Methylation as a Biomarker in Environmental Epidemiology. , 2019, , 173-189.		1
18	Prenatal exposure to maternal depression and anxiety on imprinted gene expression in placenta and infant neurodevelopment and growth. <i>Pediatric Research</i> , 2018, 83, 1075-1083.	1.1	15

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19	Genetic regulation of the placental transcriptome underlies birth weight and risk of childhood obesity. <i>PLoS Genetics</i> , 2018, 14, e1007799.	1.5	38
20	Intrauterine multi-metal exposure is associated with reduced fetal growth through modulation of the placental gene network. <i>Environment International</i> , 2018, 120, 373-381.	4.8	46
21	Alcohol-Related Alterations in Placental Imprinted Gene Expression in Humans Mediate Effects of Prenatal Alcohol Exposure on Postnatal Growth. <i>Alcoholism: Clinical and Experimental Research</i> , 2018, 42, 1431-1443.	1.4	20
22	Placental imprinting variation associated with assisted reproductive technologies and subfertility. <i>Epigenetics</i> , 2017, 12, 653-661.	1.3	42
23	Maternal residential air pollution and placental imprinted gene expression. <i>Environment International</i> , 2017, 108, 204-211.	4.8	26
24	Expression quantitative trait loci (eQTLs) in human placentas suggest developmental origins of complex diseases. <i>Human Molecular Genetics</i> , 2017, 26, 3432-3441.	1.4	58
25	Expression of placental regulatory genes is associated with fetal growth. <i>Journal of Perinatal Medicine</i> , 2017, 45, 887-893.	0.6	13
26	Whole-transcriptome analysis delineates the human placenta gene network and its associations with fetal growth. <i>BMC Genomics</i> , 2017, 18, 520.	1.2	53
27	Developmental Origins of Common Disease: Epigenetic Contributions to Obesity. <i>Annual Review of Genomics and Human Genetics</i> , 2016, 17, 177-192.	2.5	18
28	In utero exposures to environmental organic pollutants disrupt epigenetic marks linked to fetoplacental development. <i>Environmental Epigenetics</i> , 2016, 2, dvv013.	0.9	44
29	Mismatch Repair Polymorphisms as Markers of Breast Cancer Prevalence in the Breast Cancer Family Registry. <i>Anticancer Research</i> , 2016, 36, 4437-4442.	0.5	24
30	DNA Repair Gene Expression Levels as Indicators of Breast Cancer in the Breast Cancer Family Registry. <i>Anticancer Research</i> , 2016, 36, 4039-44.	0.5	8
31	Placental expression profile of imprinted genes impacts birth weight. <i>Epigenetics</i> , 2015, 10, 842-849.	1.3	79
32	Expression of imprinted genes in placenta is associated with infant neurobehavioral development. <i>Epigenetics</i> , 2015, 10, 834-841.	1.3	59
33	Environmental Influences on Genomic Imprinting. <i>Current Environmental Health Reports</i> , 2015, 2, 155-162.	3.2	33
34	Exploring the associations between microRNA expression profiles and environmental pollutants in human placenta from the National Children's Study (NCS). <i>Epigenetics</i> , 2015, 10, 793-802.	1.3	91
35	Correlation of DNA methylation levels in blood and saliva DNA in young girls of the LEGACY Girls study. <i>Epigenetics</i> , 2014, 9, 929-933.	1.3	32
36	Environmental exposures in utero and microRNA. <i>Current Opinion in Pediatrics</i> , 2014, 26, 243-251.	1.0	12

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37	Global DNA methylation levels in white blood cell DNA from sisters discordant for breast cancer from the New York site of the Breast Cancer Family Registry. <i>Epigenetics</i> , 2012, 7, 868-874.	1.3	40
38	Genome-wide aberrant DNA methylation of microRNA host genes in hepatocellular carcinoma. <i>Epigenetics</i> , 2012, 7, 1230-1237.	1.3	59
39	White blood cell global methylation and IL-6 promoter methylation in association with diet and lifestyle risk factors in a cancer-free population. <i>Epigenetics</i> , 2012, 7, 606-614.	1.3	80
40	Genome-wide DNA methylation profiles in hepatocellular carcinoma. <i>Hepatology</i> , 2012, 55, 1799-1808.	3.6	178
41	Biologic and epigenetic impact of commuting to work by car or using public transportation: A case-control study. <i>Preventive Medicine</i> , 2012, 54, 229-233.	1.6	22
42	Global DNA methylation levels in girls with and without a family history of breast cancer. <i>Epigenetics</i> , 2011, 6, 29-33.	1.3	31
43	Global methylation profiles in DNA from different blood cell types. <i>Epigenetics</i> , 2011, 6, 76-85.	1.3	128
44	Serum Oxidized Protein and Prostate Cancer Risk within the Prostate Cancer Prevention Trial. <i>Cancer Prevention Research</i> , 2010, 3, 478-483.	0.7	12
45	Association between Arsenic Exposure from Drinking Water and Plasma Levels of Soluble Cell Adhesion Molecules. <i>Environmental Health Perspectives</i> , 2007, 115, 1415-1420.	2.8	65
46	Acetaminophen attenuates peroxynitrite-activated matrix metalloproteinase-2-mediated troponin I cleavage in the isolated guinea pig myocardium. <i>Journal of Molecular and Cellular Cardiology</i> , 2006, 40, 553-561.	0.9	27
47	Tissue Inhibitor of Metalloproteinases-1 Stimulates Gene Expression in MDA-MB-435 Human Breast Cancer Cells by Means of its Ability to Inhibit Metalloproteinases. <i>Breast Cancer Research and Treatment</i> , 2005, 94, 185-193.	1.1	12
48	Enhanced cell surface CD44 variant (v6, v9) expression by osteopontin in breast cancer epithelial cells facilitates tumor cell migration: Novel post-transcriptional, post-translational regulation. <i>Clinical and Experimental Metastasis</i> , 2005, 22, 663-673.	1.7	89