Susan K Murphy

List of Publications by Year
in descending order

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242 papers	14,560 citations	22548 61 h-index	26792 111 g-index
250 all docs	250 docs citations	250 times ranked	21774 citing authors

#	Article	IF	Citations
1	A taxonomy of riskâ€associated alternative health practices: A Delphi study. Health and Social Care in the Community, 2022, 30, 1163-1181.	0.7	6
2	Developmental nicotine exposure and masculinization of the rat preoptic area. NeuroToxicology, 2022, 89, 41-54.	1.4	2
3	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
4	Maternal tobacco smoke exposure is associated with increased DNA methylation at human metastable epialleles in infant cord blood. Environmental Epigenetics, 2022, 8, dvac005.	0.9	2
5	Neighborhood Deprivation is Associated with Increased Risk of Prenatal Smoke Exposure. Prevention Science, 2022, , 1.	1.5	5
6	Alterations in DNA methylation associate with fatty liver and metabolic abnormalities in a multi-ethnic cohort of pre-teenage children. Epigenetics, 2022, 17, 1446-1461.	1.3	4
7	Sex-specific DNA methylation and associations with in utero tobacco smoke exposure at nuclear-encoded mitochondrial genes. Epigenetics, 2022, 17, 1573-1589.	1.3	3
8	Informing women about the risks of exposing babies to tobacco smoke: outreach and education efforts using Facebook â€œboost postsâ€• Translational Behavioral Medicine, 2022, 12, 714-720.	1.2	4
9	Extended Human Papillomavirus Genotyping to Predict Progression to High-Grade Cervical Precancer: A Prospective Cohort Study in the Southeastern United States. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 1564-1571.	1.1	3
10	Cannabis alters DNA methylation at maternally imprinted and autism candidate genes in spermatogenic cells. Systems Biology in Reproductive Medicine, 2022, 68, 357-369.	1.0	11
11	CIPHERS: Effects of male marijuana use on sperm health and potential risks to future children. , 2022, 3, 100047.		0
12	Targeting Dormant Ovarian Cancer CellsIn Vitroand in anIn VivoMouse Model of Platinum Resistance. Molecular Cancer Therapeutics, 2021, 20, 85-95.	1.9	6
13	Male obesity impacts DNA methylation reprogramming in sperm. Clinical Epigenetics, 2021, 13, 17.	1.8	20
14	Epigenetic Regulation of Claudin-1 in the Development of Ovarian Cancer Recurrence and Drug Resistance. Frontiers in Oncology, 2021, 11, 620873.	1.3	13
15	Cell-Type Specific Changes in DNA Methylation of SNCA Intron 1 in Synucleinopathy Brains. Frontiers in Neuroscience, 2021, 15, 652226.	1.4	11
16	Opposing Epigenetic Signatures in Human Sperm by Intake of Fast Food Versus Healthy Food. Frontiers in Endocrinology, 2021, 12, 625204.	1.5	14
17	DNA Methylation in Babies Born to Nonsmoking Mothers Exposed to Secondhand Smoke during Pregnancy: An Epigenome-Wide Association Study. Environmental Health Perspectives, 2021, 129, 57010.	2.8	15
18	Smoke-Free Home Rules and Association with Child Secondhand Smoke Exposure among Motherâ€“Child Dyad Relationships. International Journal of Environmental Research and Public Health, 2021, 18, 5256.	1.2	2

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19	Association between PEG3 DNA methylation and high-grade cervical intraepithelial neoplasia. Infectious Agents and Cancer, 2021, 16, 42.	1.2	3
20	Periconceptional Maternal Diet Characterized by High Glycemic Loading Is Associated with Offspring Behavior in NEST. Nutrients, 2021, 13, 3180.	1.7	2
21	Refraining from use diminishes cannabis-associated epigenetic changes in human sperm. Environmental Epigenetics, 2021, 7, dvab009.	0.9	41
22	Association of maternal prenatal selenium concentration and preterm birth: a multicountry meta-analysis. BMJ Global Health, 2021, 6, e005856.	2.0	13
23	Associations between maternal obesity, gestational cytokine levels and child obesity in the <scp>NEST</scp> cohort. Pediatric Obesity, 2021, 16, e12763.	1.4	15
24	Identifying the Best Questions for Rapid Screening of Secondhand Smoke Exposure Among Children. Nicotine and Tobacco Research, 2021, 23, 1217-1223.	1.4	4
25	Direct comparisons of bisulfite pyrosequencing versus targeted bisulfite sequencing. MicroPublication Biology, 2021, 2021, .	0.1	0
26	Effect of Prenatal Smoke Exposure on Birth Weight: The Moderating Role of Maternal Depressive Symptoms. Nicotine and Tobacco Research, 2020, 22, 40-47.	1.4	6
27	Cannabis use is associated with potentially heritable widespread changes in autism candidate gene DLGAP2 DNA methylation in sperm. Epigenetics, 2020, 15, 161-173.	1.3	61
28	A TAZâ€“ANGPTL4â€“NOX2 Axis Regulates Ferroptotic Cell Death and Chemoresistance in Epithelial Ovarian Cancer. Molecular Cancer Research, 2020, 18, 79-90.	1.5	188
29	Sperm DNA methylation altered by THC and nicotine: Vulnerability of neurodevelopmental genes with bivalent chromatin. Scientific Reports, 2020, 10, 16022.	1.6	33
30	Paternal cannabis extract exposure in rats: Preconception timing effects on neurodevelopmental behavior in offspring. NeuroToxicology, 2020, 81, 180-188.	1.4	11
31	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
32	Association between DNA methylation and ADHD symptoms from birth to school age: a prospective meta-analysis. Translational Psychiatry, 2020, 10, 398.	2.4	54
33	Epigenetic alterations in cytochrome P450 oxidoreductase (Por) in sperm of rats exposed to tetrahydrocannabinol (THC). Scientific Reports, 2020, 10, 12251.	1.6	5
34	Replicated umbilical cord blood DNA methylation loci associated with gestational age at birth. Epigenetics, 2020, 15, 1243-1258.	1.3	10
35	Associations between attention deficit hyperactivity disorder symptoms and eating behaviors in early childhood. Pediatric Obesity, 2020, 15, e12631.	1.4	14
36	Cannabis use and the sperm epigenome: a budding concern?. Environmental Epigenetics, 2020, 6, dvaa002.	0.9	23

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37	Paternal factors in neurodevelopmental toxicology: THC exposure of male rats causes long-lasting neurobehavioral effects in their offspring. NeuroToxicology, 2020, 78, 57-63.	1.4	23
38	Paternal THC exposure in rats causes long-lasting neurobehavioral effects in the offspring. Neurotoxicology and Teratology, 2019, 74, 106806.	1.2	61
39	Snacking frequency and dietary intake in toddlers and preschool children. Appetite, 2019, 142, 104369.	1.8	16
40	Acquisition of a side population fraction augments malignant phenotype in ovarian cancer. Scientific Reports, 2019, 9, 14215.	1.6	11
41	Cadmium exposure and MEG3 methylation differences between Whites and African Americans in the NEST Cohort. Environmental Epigenetics, 2019, 5, dvz014.	0.9	12
42	Comparison of smoking-related DNA methylation between newborns from prenatal exposure and adults from personal smoking. Epigenomics, 2019, 11, 1487-1500.	1.0	64
43	Epigenome-wide meta-analysis of DNA methylation and childhood asthma. Journal of Allergy and Clinical Immunology, 2019, 143, 2062-2074.	1.5	147
44	Paternal nicotine exposure in rats produces long-lasting neurobehavioral effects in the offspring. Neurotoxicology and Teratology, 2019, 74, 106808.	1.2	25
45	Role of Î²â€3 adrenergic receptor polymorphism in overactive bladder. Neurourology and Urodynamics, 2019, 38, 1261-1265.	0.8	6
46	MTAP Loss Promotes Stemness in Glioblastoma and Confers Unique Susceptibility to Purine Starvation. Cancer Research, 2019, 79, 3383-3394.	0.4	30
47	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
48	Pre-Pregnancy Weight and Symptoms of Attention Deficit Hyperactivity Disorder and Executive Functioning Behaviors in Preschool Children. International Journal of Environmental Research and Public Health, 2019, 16, 667.	1.2	20
49	Lentiviral Vector Platform for the Efficient Delivery of Epigenome-editing Tools into Human Induced Pluripotent Stem Cell-derived Disease Models. Journal of Visualized Experiments, 2019, , .	0.2	9
50	Maternal pre-pregnancy obesity, offspring cord blood DNA methylation, and offspring cardiometabolic health in early childhood: an epigenome-wide association study. Epigenetics, 2019, 14, 325-340.	1.3	59
51	Urine RNA Processing in a Clinical Setting: Comparison of 3 Protocols. Female Pelvic Medicine and Reconstructive Surgery, 2019, 25, 247-251.	0.6	9
52	Early prenatal vitamin D concentrations and social-emotional development in infants. Journal of Maternal-Fetal and Neonatal Medicine, 2019, 32, 1441-1448.	0.7	24
53	Cadmium exposure increases the risk of juvenile obesity: a human and zebrafish comparative study. International Journal of Obesity, 2018, 42, 1285-1295.	1.6	54
54	DNA methylation of imprinted gene control regions in the regression of lowâ€grade cervical lesions. International Journal of Cancer, 2018, 143, 552-560.	2.3	9

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55	Folic acid throughout pregnancy: too much?. American Journal of Clinical Nutrition, 2018, 107, 497-498.	2.2	6
56	Associations between maternal cytokine levels during gestation and measures of child cognitive abilities and executive functioning. Brain, Behavior, and Immunity, 2018, 70, 390-397.	2.0	30
57	A genomeâ€scale DNA methylation study in women with interstitial cystitis/bladder pain syndrome. Neurourology and Urodynamics, 2018, 37, 1485-1493.	0.8	13
58	Maternal vitamin D, DNA methylation at imprint regulatory regions and offspring weight at birth, 1 year and 3 years. International Journal of Obesity, 2018, 42, 587-593.	1.6	13
59	Cohort Profile: Pregnancy And Childhood Epigenetics (PACE) Consortium. International Journal of Epidemiology, 2018, 47, 22-23u.	0.9	105
60	Cannabinoid exposure and altered DNA methylation in rat and human sperm. Epigenetics, 2018, 13, 1208-1221.	1.3	160
61	Branched chain amino acid transaminase 1 (BCAT1) is overexpressed and hypomethylated in patients with non-alcoholic fatty liver disease who experience adverse clinical events: A pilot study. PLoS ONE, 2018, 13, e0204308.	1.1	17
62	Periconceptional Maternal Mediterranean Diet Is Associated With Favorable Offspring Behaviors and Altered CpG Methylation of Imprinted Genes. Frontiers in Cell and Developmental Biology, 2018, 6, 107.	1.8	43
63	Downregulation of SNCA Expression by Targeted Editing of DNA Methylation: A Potential Strategy for Precision Therapy in PD. Molecular Therapy, 2018, 26, 2638-2649.	3.7	127
64	DNA methylation of imprinted genes in Mexicanâ€“American newborn children with prenatal phthalate exposure. Epigenomics, 2018, 10, 1011-1026.	1.0	33
65	DNA methylation of imprinted genes at birth is associated with child weight status at birth, 1Âyear, and 3Âyears. Clinical Epigenetics, 2018, 10, 90.	1.8	27
66	Impact of Smoking Ban on Passive Smoke Exposure in Pregnant Non-Smokers in the Southeastern United States. International Journal of Environmental Research and Public Health, 2018, 15, 83.	1.2	15
67	Self-reported prenatal tobacco smoke exposure, AXL gene-body methylation, and childhood asthma phenotypes. Clinical Epigenetics, 2018, 10, 98.	1.8	15
68	Temporal Trends in Exposure to Organophosphate Flame Retardants in the United States. Environmental Science and Technology Letters, 2017, 4, 112-118.	3.9	142
69	Histone H3.3K27M Represses p16 to Accelerate Gliomagenesis in a Murine Model of DIPG. Molecular Cancer Research, 2017, 15, 1243-1254.	1.5	120
70	Differential DNA Methylation in Whole Blood Reflects that in Liver and Distinguishes Patients with Advanced NAFLD Fibrosis from Those with Normal Histology: A Potential Non-Invasive Tool. Gastroenterology, 2017, 152, S1069-S1070.	0.6	0
71	NAFLD is associated with methylation shifts with relevance for the expression of genes involved in lipoprotein particle composition. Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids, 2017, 1862, 314-323.	1.2	17
72	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

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73	Blood monocyte transcriptome and epigenome analyses reveal loci associated with human atherosclerosis. Nature Communications, 2017, 8, 393.	5.8	51
74	Maternal inflammatory diet and adverse pregnancy outcomes: Circulating cytokines and genomic imprinting as potential regulators?. Epigenetics, 2017, 12, 688-697.	1.3	68
75	Maternal blood cadmium, lead and arsenic levels, nutrient combinations, and offspring birthweight. BMC Public Health, 2017, 17, 354.	1.2	69
76	Human exposure to flame-retardants is associated with aberrant DNA methylation at imprinted genes in sperm. Environmental Epigenetics, 2017, 3, dvx003.	0.9	42
77	Low maternal adherence to a Mediterranean diet is associated with increase in methylation at the MEG3-IG differentially methylated region in female infants. Environmental Epigenetics, 2017, 3, dvx007.	0.9	30
78	Disparities in Cervical Cancer Incidence and Mortality. Advances in Cancer Research, 2017, 133, 129-156.	1.9	12
79	Epigenetic regulation of AXL and risk of childhood asthma symptoms. Clinical Epigenetics, 2017, 9, 121.	1.8	22
80	Small-Magnitude Effect Sizes in Epigenetic End Points are Important in Childrenâ€™s Environmental Health Studies: The Childrenâ€™s Environmental Health and Disease Prevention Research Centerâ€™s Epigenetics Working Group. Environmental Health Perspectives, 2017, 125, 511-526.	2.8	243
81	Abstract 1991: Enhanced role of the extracellular matrix in ovarian cancer recurrence. , 2017, , .		0
82	Lead Exposure during Early Human Development and DNA Methylation of Imprinted Gene Regulatory Elements in Adulthood. Environmental Health Perspectives, 2016, 124, 666-673.	2.8	61
83	Distinct Epigenetic Effects of Tobacco Smoking in Whole Blood and among Leukocyte Subtypes. PLoS ONE, 2016, 11, e0166486.	1.1	113
84	A targeted analysis reveals relevant shifts in the methylation and transcription of genes responsible for bile acid homeostasis and drug metabolism in non-alcoholic fatty liver disease. BMC Genomics, 2016, 17, 462.	1.2	21
85	Association between Prepregnancy Body Mass Index and Gestational Weight Gain with Size, Tempo, and Velocity of Infant Growth: Analysis of the Newborn Epigenetic Study Cohort. Childhood Obesity, 2016, 12, 210-218.	0.8	22
86	Effects of Environmentally Acquired Heavy Metals and Nutrients on the Epigenome and Phenotype. Molecular and Integrative Toxicology, 2016, , 139-169.	0.5	1
87	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
88	Obesity-related DNA methylation at imprinted genes in human sperm: Results from the TIEGER study. Clinical Epigenetics, 2016, 8, 51.	1.8	151
89	Maternal blood lead concentrations, DNA methylation of MEG3 DMR regulating the DLK1/MEG3 imprinted domain and early growth in a multiethnic cohort. Environmental Epigenetics, 2016, 2, .	0.9	38
90	DNA Methylation of Regulatory Regions of Imprinted Genes at Birth and Its Relation to Infant Temperament. Genetics & Epigenetics, 2016, 8, GEG.S40538.	2.5	71

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91	Neighborhood and Family Environment of Expectant Mothers May Influence Prenatal Programming of Adult Cancer Risk: Discussion and an Illustrative DNA Methylation Example. Biodemography and Social Biology, 2016, 62, 87-104.	0.4	28
92	Maternal B vitamins: effects on offspring weight and DNA methylation at genomically imprinted domains. Clinical Epigenetics, 2016, 8, 8.	1.8	47
93	The BMP signaling pathway leads to enhanced proliferation in serous ovarian cancer-A potential therapeutic target. Molecular Carcinogenesis, 2016, 55, 335-345.	1.3	33
94	Effects of Pubertal Exposure to Dietary Soy on Estrogen Receptor Activity in the Breast of Cynomolgus Macaques. Cancer Prevention Research, 2016, 9, 385-395.	0.7	10
95	Establishment of a Novel Histopathological Classification of High-Grade Serous Ovarian Carcinoma Correlated with Prognostically Distinct Gene Expression Subtypes. American Journal of Pathology, 2016, 186, 1103-1113.	1.9	71
96	Suppression of ABHD2, identified through a functional genomics screen, causes anoikis resistance, chemoresistance and poor prognosis in ovarian cancer. Oncotarget, 2016, 7, 47620-47636.	0.8	28
97	Abstract A38: Identification through functional genomics screening of factors whose downregulation enhances the side population in ovarian cancer.. , 2016, , .		1
98	Abstract B63: Expression of VEGF in ovarian cancer suppresses tumor immunity through recruitment of myeloid derived suppressor cells.. , 2016, , .		0
99	BCAT1 Is Associated with Clinical Decompensation in Nonalcoholic Fatty Liver Disease: a Pilot Study. American Journal of Gastroenterology, 2016, 111, S381.	0.2	0
100	Epigenetic Regulation of GDF2 Suppresses Anoikis in Ovarian and Breast Epithelia. Neoplasia, 2015, 17, 826-838.	2.3	20
101	Geographic clustering of elevated blood heavy metal levels in pregnant women. BMC Public Health, 2015, 15, 1035.	1.2	30
102	Hepatocyte nuclear factorâ€•1Î² (HNFâ€•1Î²) promotes glucose uptake and glycolytic activity in ovarian clear cell carcinoma. Molecular Carcinogenesis, 2015, 54, 35-49.	1.3	57
103	Genotype-Epigenotype Interaction at the IGF2 DMR. Genes, 2015, 6, 777-789.	1.0	3
104	ACLY and ACC1 Regulate Hypoxia-Induced Apoptosis by Modulating ETV4 via Î±-ketoglutarate. PLoS Genetics, 2015, 11, e1005599.	1.5	36
105	Ascites Increases Expression/Function of Multidrug Resistance Proteins in Ovarian Cancer Cells. PLoS ONE, 2015, 10, e0131579.	1.1	36
106	Associations between prenatal physical activity, birth weight, and DNA methylation at genomically imprinted domains in a multiethnic newborn cohort. Epigenetics, 2015, 10, 597-606.	1.3	37
107	Invasion of uterine cervical squamous cell carcinoma cells is facilitated by locoregional interaction with cancer-associated fibroblasts via activating transforming growth factor-beta. Gynecologic Oncology, 2015, 136, 104-111.	0.6	21
108	In vitro lead exposure changes DNA methylation and expression of IGF2 and PEG1/MEST. Toxicology in Vitro, 2015, 29, 544-550.	1.1	21

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109	Alterations of a Cellular Cholesterol Metabolism Network Are a Molecular Feature of Obesity-Related Type 2 Diabetes and Cardiovascular Disease. Diabetes, 2015, 64, 3464-3474.	0.3	82
110	Comprehensive Profiling of Amino Acid Response Uncovers Unique Methionine-Deprived Response Dependent on Intact Creatine Biosynthesis. PLoS Genetics, 2015, 11, e1005158.	1.5	79
111	Epigenetic regulation of Newbornsâ€™ imprinted genes related to gestational growth: patterning by parental race/ethnicity and maternal socioeconomic status. Journal of Epidemiology and Community Health, 2015, 69, 639-647.	2.0	66
112	IL-10, IL-15, IL-17, and GMCSF levels in cervical cancer tissue of Tanzanian women infected with HPV16/18 vs. non-HPV16/18 genotypes. Infectious Agents and Cancer, 2015, 10, 10.	1.2	15
113	Maternal cadmium, iron and zinc levels, DNA methylation and birth weight. BMC Pharmacology & Toxicology, 2015, 16, 20.	1.0	95
114	Epigenetic silencing of Kruppel like factor-3 increases expression of pro-metastatic miR-182. Cancer Letters, 2015, 369, 202-211.	3.2	19
115	Mitochondrial Superoxide Dismutase Has a Protumorigenic Role in Ovarian Clear Cell Carcinoma. Cancer Research, 2015, 75, 4973-4984.	0.4	57
116	Chemotherapy Induces Programmed Cell Death-Ligand 1 Overexpression via the Nuclear Factor-ÎºB to Foster an Immunosuppressive Tumor Microenvironment in Ovarian Cancer. Cancer Research, 2015, 75, 5034-5045.	0.4	439
117	Newborns of obese parents have altered DNA methylation patterns at imprinted genes. International Journal of Obesity, 2015, 39, 650-657.	1.6	265
118	Menstrual cyclic change of metastin/GPR54 in endometrium. Medical Molecular Morphology, 2015, 48, 76-84.	0.4	20
119	Abstract 2236: Emergence of epigenetic regulation of tight junction genes in recurrent serous epithelial ovarian cancer. , 2015, , .		1
120	Abstract 3912: GDF2 promotes anoikis susceptibility in ovarian and breast epithelia. , 2015, , .		0
121	Abstract POSTER-BIOL-1319: Temporal shifts in the epigenetic regulation of tight junctions from primary to recurrent ovarian cancer. , 2015, , .		0
122	Optimizing Urine Processing Protocols for Protein and Metabolite Detection. Journal of Proteomics and Bioinformatics, 2015, 2015, .	0.4	1
123	Imprinted Genes and the Environment: Links to the Toxic Metals Arsenic, Cadmium and Lead. Genes, 2014, 5, 477-496.	1.0	22
124	Differential Angiogenic Gene Expression in TP53 Wild-Type and Mutant Ovarian Cancer Cell Lines. Frontiers in Oncology, 2014, 4, 163.	1.3	8
125	Epigenetic determinants of ovarian clear cell carcinoma biology. International Journal of Cancer, 2014, 135, 585-597.	2.3	40
126	A paternal environmental legacy: Evidence for epigenetic inheritance through the male germ line. BioEssays, 2014, 36, 359-371.	1.2	293

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127	Investigating Epigenetic Effects of Prenatal Exposure to Toxic Metals in Newborns: Challenges and Benefits. Medical Epigenetics, 2014, 2, 53-59.	262.3	23
128	Dasatinib (BMS-35482) Interacts Synergistically With Docetaxel, Gemcitabine, Topotecan, and Doxorubicin in Ovarian Cancer Cells With High SRC Pathway Activation and Protein Expression. International Journal of Gynecological Cancer, 2014, 24, 218-225.	1.2	6
129	PEG1/MEST and IGF2 DNA methylation in CIN and in cervical cancer. Clinical and Translational Oncology, 2014, 16, 266-272.	1.2	46
130	Hepatic gene expression profiles differentiate presymptomatic patients with mild versus severe nonalcoholic fatty liver disease. Hepatology, 2014, 59, 471-482.	3.6	256
131	Erythrocyte folate concentrations, CpG methylation at genomically imprinted domains, and birth weight in a multiethnic newborn cohort. Epigenetics, 2014, 9, 1120-1130.	1.3	73
132	STAT1 Drives Tumor Progression in Serous Papillary Endometrial Cancer. Cancer Research, 2014, 74, 6519-6530.	0.4	66
133	HPV genotypes and cervical intraepithelial neoplasia in a multiethnic cohort in the southeastern USA. Cancer Causes and Control, 2014, 25, 1055-1062.	0.8	62
134	Paternal obesityâ€"a risk factor for autism?. Nature Reviews Endocrinology, 2014, 10, 389-390.	4.3	7
135	Maternal Stress, Preterm Birth, and DNA Methylation at Imprint Regulatory Sequences in Humans. Genetics & Epigenetics, 2014, 6, GEG.S18067.	2.5	93
136	Epigenetic and genetic dispositions of ovarian carcinomas. Oncoscience, 2014, 1, 574-579.	0.9	13
137	Abstract 4570: Role of ERRalpha in ovarian cancer. , 2014, , .		0
138	Abstract LB-123: Novel function of STAT1 pathway as a modulator of tumor progression in serous papillary endometrial cancer. , 2014, , .		2
139	Abstract B22: Altered methylation profiles of imprinted genes in response to prenatal exposure to cigarette smoke in the Newborn Epigenetic STudy (NEST) cohort. , 2014, , .		0
140	Methylation-Specific PCR. Methods in Molecular Biology, 2013, 1049, 75-82.	0.4	20
141	Paternal obesity is associated with IGF2hypomethylation in newborns: results from a Newborn Epigenetics Study (NEST) cohort. BMC Medicine, 2013, 11, 29.	2.3	286
142	Bisulfite Sequencing of Cloned Alleles. Methods in Molecular Biology, 2013, 1049, 83-94.	0.4	8
143	Relationship Between Methylome and Transcriptome in Patients With Nonalcoholic Fatty Liver Disease. Gastroenterology, 2013, 145, 1076-1087.	0.6	340
144	Validation of ovarian cancer gene expression signatures for survival and subtype in formalin fixed paraffin embedded tissues. Gynecologic Oncology, 2013, 129, 159-164.	0.6	24

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145	Sculpting Our Future: Environmental Nudging of the Imprintome. Epigenetics and Human Health, 2013, , 51-73.	0.2	2
146	Utilization of genomic signatures to identify highâ€efficacy candidate drugs for chemorefractory endometrial cancers. International Journal of Cancer, 2013, 133, 2234-2244.	2.3	11
147	DNA methylation at imprint regulatory regions in preterm birth and infection. American Journal of Obstetrics and Gynecology, 2013, 208, 395.e1-395.e7.	0.7	62
148	75: DNA methylation at imprinted regulatory regions in preterm birth and infection. American Journal of Obstetrics and Gynecology, 2013, 208, S45.	0.7	0
149	Bisulfite Pyrosequencing. Methods in Molecular Biology, 2013, 1049, 95-107.	0.4	25
150	Stress: A Possible Link between Genetics, Epigenetics, and Childhood Asthma. American Journal of Respiratory and Critical Care Medicine, 2013, 187, 563-564.	2.5	8
151	TP53 Status is Associated with Thrombospondin1 Expression In vitro. Frontiers in Oncology, 2013, 3, 269.	1.3	6
152	Maternal BMI, IGF-I Levels, and Birth Weight in African American and White Infants. International Journal of Pediatrics (United Kingdom), 2013, 2013, 1-7.	0.2	27
153	Associations between antibiotic exposure during pregnancy, birth weight and aberrant methylation at imprinted genes among offspring. International Journal of Obesity, 2013, 37, 907-913.	1.6	118
154	Associations between Methylation of Paternally Expressed Gene 3 (PEG3), Cervical Intraepithelial Neoplasia and Invasive Cervical Cancer. PLoS ONE, 2013, 8, e56325.	1.1	73
155	Increased Intragenic IGF2 Methylation is Associated with Repression of Insulator Activity and Elevated Expression in Serous Ovarian Carcinoma. Frontiers in Oncology, 2013, 3, 131.	1.3	7
156	Main Principles and Outcomes of DNA Methylation Analysis. Methods in Molecular Biology, 2013, 1049, 67-74.	0.4	3
157	Abstract 3647: Dose-dependent alteration of CpG methylation inAHRRandGFI1in mononuclear cell DNA of smokers.. , 2013, , .		1
158	Prenatal sensitization of a postnatal trigger for metabolic disease. Journal of Clinical Investigation, 2013, 123, 2786-2788.	3.9	1
159	Abstract 4767: Preclinical mouse model of recurrent epithelial ovarian cancer.. , 2013, , .		0
160	Abstract PR08: HNF1Î² confers resistance to oxidative stress of ovarian clear cell carcinoma. , 2013, , .		0
161	Abstract B19: Functional genomics approach links anchorage-independence with tumor dormancy in ovarian cancer. , 2013, , .		0
162	Abstract A83: Induction of PD-L1 expression by cytotoxic agents through activation of NF-kB signal. , 2013, , .		0

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163	Associations between birth and one year anthropometric measurements and IGF2 and IGF2R genetic variants in African American and Caucasian American infants. Journal of Pediatric Genetics, 2013, 2, .	0.3	1
164	450K Epigenome-Wide Scan Identifies Differential DNA Methylation in Newborns Related to Maternal Smoking during Pregnancy. Environmental Health Perspectives, 2012, 120, 1425-1431.	2.8	654
165	Depression in pregnancy, infant birth weight and DNA methylation of imprint regulatory elements. Epigenetics, 2012, 7, 735-746.	1.3	175
166	Targeting the epigenome in ovarian cancer. Future Oncology, 2012, 8, 151-164.	1.1	15
167	The Human Imprintome: Regulatory Mechanisms, Methods of Ascertainment, and Roles in Disease Susceptibility. ILAR Journal, 2012, 53, 341-358.	1.8	76
168	DNA profiling analysis of endometrial and ovarian cell lines reveals misidentification, redundancy and contamination. Gynecologic Oncology, 2012, 127, 241-248.	0.6	213
169	Gender-specific methylation differences in relation to prenatal exposure to cigarette smoke. Gene, 2012, 494, 36-43.	1.0	201
170	Convergent and divergent evolution of genomic imprinting in the marsupial Monodelphis domestica. BMC Genomics, 2012, 13, 394.	1.2	24
171	Differentially Methylated Regions of Imprinted Genes in Prenatal, Perinatal and Postnatal Human Tissues. PLoS ONE, 2012, 7, e40924.	1.1	143
172	IGF2RGenetic Variants, Circulating IGF2 Concentrations and Colon Cancer Risk in African Americans and Whites. Disease Markers, 2012, 32, 133-141.	0.6	16
173	Association of cord blood methylation fractions at imprinted insulin-like growth factor 2 (IGF2), plasma IGF2, and birth weight. Cancer Causes and Control, 2012, 23, 635-645.	0.8	102
174	Insulin-Like Growth Factor 2/H19 Methylation at Birth and Risk of Overweight and Obesity in Children. Journal of Pediatrics, 2012, 161, 31-39.	0.9	123
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