

Kimberly D Siegmund

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.

110 papers	7,634 citations	40 h-index	87 g-index
114 ext. papers	8,698 ext. citations	5.9 avg, IF	5.43 L-index

#	Paper	IF	Citations
110	A novel role for vaping in mitochondrial gene dysregulation and inflammation fundamental to disease development. <i>Scientific Reports</i> , 2021 , 11, 22773	4.9	1
109	The genome-wide impact of trisomy 21 on DNA methylation and its implications for hematopoiesis. <i>Nature Communications</i> , 2021 , 12, 821	17.4	7
108	A Novel DNA Methylation Signature as an Independent Prognostic Factor in Muscle-Invasive Bladder Cancer. <i>Frontiers in Oncology</i> , 2021 , 11, 614927	5.3	4
107	Functional human genes typically exhibit epigenetic conservation. <i>PLoS ONE</i> , 2021 , 16, e0253250	3.7	0
106	Inter-individual variability in structural brain development from late childhood to young adulthood. <i>NeuroImage</i> , 2021 , 242, 118450	7.9	9
105	Epigenetic Conservation Is a Beacon of Function: An Analysis Using Methcon5 Software for Studying Gene Methylation. <i>JCO Clinical Cancer Informatics</i> , 2020 , 4, 100-107	5.2	2
104	Epigenetic plasticity potentiates a rapid cyclical shift to and from an aggressive cancer phenotype. <i>International Journal of Cancer</i> , 2020 , 146, 3065-3076	7.5	6
103	DNA Methylation Profiles of Vegans and Non-Vegetarians in the Adventist Health Study-2 Cohort. <i>Nutrients</i> , 2020 , 12,	6.7	3
102	Systematic Review and Meta-analysis of Testicular Germ Cell Tumors Following In Utero Exposure to Diethylstilbestrol. <i>JNCI Cancer Spectrum</i> , 2019 , 3, pkz045	4.6	8
101	Deregulation of Biologically Significant Genes and Associated Molecular Pathways in the Oral Epithelium of Electronic Cigarette Users. <i>International Journal of Molecular Sciences</i> , 2019 , 20,	6.3	37
100	HiLDA: a statistical approach to investigate differences in mutational signatures. <i>PeerJ</i> , 2019 , 7, e7557	3.1	4
99	Cell-free DNA (cfDNA) whole genome bisulfite sequencing in patients with muscle-invasive bladder cancer patient treated with cystectomy with curative intent.. <i>Journal of Clinical Oncology</i> , 2019 , 37, 359-359	3.3	3
98	Epigenomic profiling of plasma cell-free DNA (cfDNA) to predict bladder cancer recurrence after radical cystectomy.. <i>Journal of Clinical Oncology</i> , 2019 , 37, e14525-e14525	2.2	2
97	DNA Methylation 2019 , 933-948		
96	The Genome-Wide Impact of Trisomy 21 on DNA Methylation and Its Implications for Hematologic Malignancies. <i>Blood</i> , 2019 , 134, 2510-2510	2.2	1
95	Mutational signatures in colon cancer. <i>BMC Research Notes</i> , 2019 , 12, 788	2.3	2
94	Comprehensive meta-analysis reveals association between multiple imprinting disorders and conception by assisted reproductive technology. <i>Journal of Assisted Reproduction and Genetics</i> , 2018 , 35, 943-952	3.4	48

93	Association of internal smoking dose with blood DNA methylation in three racial/ethnic populations. <i>Clinical Epigenetics</i> , 2018 , 10, 110	7.7	22
92	Epigenetic Heterogeneity in Human Colorectal Tumors Reveals Preferential Conservation And Evidence of Immune Surveillance. <i>Scientific Reports</i> , 2018 , 8, 17292	4.9	11
91	Association between promoter methylation and lung function growth during adolescence. <i>Epigenetics</i> , 2018 , 13, 1027-1038	5.7	4
90	Spatial mutation patterns as markers of early colorectal tumor cell mobility. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 5774-5779	11.5	23
89	Identifying aggressive prostate cancer foci using a DNA methylation classifier. <i>Genome Biology</i> , 2017 , 18, 3	18.3	31
88	Epigenetic regulation of and risk of childhood asthma symptoms. <i>Clinical Epigenetics</i> , 2017 , 9, 121	7.7	17
87	Cross-Species Transcriptome Profiling Identifies New Alveolar Epithelial Type I Cell-Specific Genes. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2017 , 56, 310-321	5.7	14
86	Early mutation bursts in colorectal tumors. <i>PLoS ONE</i> , 2017 , 12, e0172516	3.7	1
85	Improving needle biopsy accuracy in small renal mass using tumor-specific DNA methylation markers. <i>Oncotarget</i> , 2017 , 8, 5439-5448	3.3	13
84	Total Outflow Facility in Live C57BL/6 Mice of Different Age. <i>Biomedicine Hub</i> , 2017 , 2, 1-10	1.3	3
83	Genetic complexity at expression quantitative trait loci. <i>BMC Proceedings</i> , 2016 , 10, 85-89	2.3	1
82	At least two well-spaced samples are needed to genotype a solid tumor. <i>BMC Cancer</i> , 2016 , 16, 250	4.8	8
81	Identification of DNA Methylation-Independent Epigenetic Events Underlying Clear Cell Renal Cell Carcinoma. <i>Cancer Research</i> , 2016 , 76, 1954-64	10.1	21
80	Particulate matter, the newborn methylome, and cardio-respiratory health outcomes in childhood. <i>Environmental Epigenetics</i> , 2016 , 2, dvw005	2.4	19
79	Prenatal Air Pollution Exposures, DNA Methyl Transferase Genotypes, and Associations with Newborn LINE1 and Alu Methylation and Childhood Blood Pressure and Carotid Intima-Media Thickness in the Children's Health Study. <i>Environmental Health Perspectives</i> , 2016 , 124, 1905-1912	8.4	56
78	An evaluation of processing methods for HumanMethylation450 BeadChip data. <i>BMC Genomics</i> , 2016 , 17, 469	4.5	36
77	Many private mutations originate from the first few divisions of a human colorectal adenoma. <i>Journal of Pathology</i> , 2015 , 237, 355-62	9.4	22
76	Identifying differential transcription factor binding in ChIP-seq. <i>Frontiers in Genetics</i> , 2015 , 6, 169	4.5	13

75	A Big Bang model of human colorectal tumor growth. <i>Nature Genetics</i> , 2015 , 47, 209-16	36.3	646
74	Association of the colorectal CpG island methylator phenotype with molecular features, risk factors, and family history. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015 , 24, 512-519	4	59
73	Characterizing the genetic basis of methylome diversity in histologically normal human lung tissue. <i>Nature Communications</i> , 2014 , 5, 3365	17.4	103
72	A panel of three markers hyper- and hypomethylated in urine sediments accurately predicts bladder cancer recurrence. <i>Clinical Cancer Research</i> , 2014 , 20, 1978-89	12.9	60
71	Transcriptomic Profiling of Primary Alveolar Epithelial Cell Differentiation in Human and Rat. <i>Genomics Data</i> , 2014 , 2, 105-109		5
70	Ancestral inference in tumors: how much can we know?. <i>Journal of Theoretical Biology</i> , 2014 , 359, 136-45.	2.3	6
69	Prenatal tobacco smoke exposure is associated with childhood DNA CpG methylation. <i>PLoS ONE</i> , 2014 , 9, e99716	3.7	94
68	Distinct, genome-wide, gene-specific selectivity patterns of four glucocorticoid receptor coregulators. <i>Nuclear Receptor Signaling</i> , 2014 , 12, e002	1	19
67	Non-specific filtering of beta-distributed data. <i>BMC Bioinformatics</i> , 2014 , 15, 199	3.6	11
66	Testicular germ cell tumor susceptibility associated with the UCK2 locus on chromosome 1q23. <i>Human Molecular Genetics</i> , 2013 , 22, 2748-53	5.6	53
65	Recommendations for the design and analysis of epigenome-wide association studies. <i>Nature Methods</i> , 2013 , 10, 949-55	21.6	276
64	Integrated transcriptomic and epigenomic analysis of primary human lung epithelial cell differentiation. <i>PLoS Genetics</i> , 2013 , 9, e1003513	6	41
63	Low-level processing of Illumina Infinium DNA Methylation BeadArrays. <i>Nucleic Acids Research</i> , 2013 , 41, e90	20.1	393
62	Null association between histology of first and second primary malignancies in men with bilateral testicular germ cell tumors. <i>American Journal of Epidemiology</i> , 2013 , 178, 1240-5	3.8	14
61	Carcinogen metabolism genes, red meat and poultry intake, and colorectal cancer risk. <i>International Journal of Cancer</i> , 2012 , 130, 1898-907	7.5	44
60	G9a functions as a molecular scaffold for assembly of transcriptional coactivators on a subset of glucocorticoid receptor target genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 19673-8	11.5	95
59	Environmental epigenetics: prospects for studying epigenetic mediation of exposure-response relationships. <i>Human Genetics</i> , 2012 , 131, 1565-89	6.3	258
58	Particulate matter, DNA methylation in nitric oxide synthase, and childhood respiratory disease. <i>Environmental Health Perspectives</i> , 2012 , 120, 1320-6	8.4	76

57	Shorter androgen receptor CAG repeat lengths associated with cryptorchidism risk among Hispanic white boys. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2012 , 97, E393-9	5.6	27
56	Genome-scale analysis of DNA methylation in lung adenocarcinoma and integration with mRNA expression. <i>Genome Research</i> , 2012 , 22, 1197-211	9.7	361
55	Selective roles for cAMP response element-binding protein binding protein and p300 protein as coregulators for androgen-regulated gene expression in advanced prostate cancer cells. <i>Journal of Biological Chemistry</i> , 2012 , 287, 4000-13	5.4	86
54	Repeated assessment by high-throughput assay demonstrates that sperm DNA methylation levels are highly reproducible. <i>Fertility and Sterility</i> , 2011 , 96, 1325-30	4.8	6
53	High DNA methylation pattern intratumoral diversity implies weak selection in many human colorectal cancers. <i>PLoS ONE</i> , 2011 , 6, e21657	3.7	18
52	Epigenetic subgroups of esophageal and gastric adenocarcinoma with differential GATA5 DNA methylation associated with clinical and lifestyle factors. <i>PLoS ONE</i> , 2011 , 6, e25985	3.7	10
51	Genome-scale screen for DNA methylation-based detection markers for ovarian cancer. <i>PLoS ONE</i> , 2011 , 6, e28141	3.7	45
50	Statistical approaches for the analysis of DNA methylation microarray data. <i>Human Genetics</i> , 2011 , 129, 585-95	6.3	50
49	Heterogenous effect of androgen receptor CAG tract length on testicular germ cell tumor risk: shorter repeats associated with seminoma but not other histologic types. <i>Carcinogenesis</i> , 2011 , 32, 1238-43	4.6	22
48	DNA methylation changes in atypical adenomatous hyperplasia, adenocarcinoma in situ, and lung adenocarcinoma. <i>PLoS ONE</i> , 2011 , 6, e21443	3.7	77
47	Using DNA methylation patterns to infer tumor ancestry. <i>PLoS ONE</i> , 2010 , 5, e12002	3.7	10
46	Polymorphisms in base excision repair genes as colorectal cancer risk factors and modifiers of the effect of diets high in red meat. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2010 , 19, 3167-73	4	66
45	Unique DNA methylation patterns distinguish noninvasive and invasive urothelial cancers and establish an epigenetic field defect in premalignant tissue. <i>Cancer Research</i> , 2010 , 70, 8169-78	10.1	133
44	Hypomethylation of a LINE-1 promoter activates an alternate transcript of the MET oncogene in bladders with cancer. <i>PLoS Genetics</i> , 2010 , 6, e1000917	6	210
43	Hormone therapy, DNA methylation and colon cancer. <i>Carcinogenesis</i> , 2010 , 31, 1060-7	4.6	28
42	Identification and functional relevance of de novo DNA methylation in cancerous B-cell populations. <i>Journal of Cellular Biochemistry</i> , 2010 , 109, 818-27	4.7	11
41	Inferring clonal expansion and cancer stem cell dynamics from DNA methylation patterns in colorectal cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 4828-33	11.5	108
40	Epigenetic profiling of somatic tissues from human autopsy specimens identifies tissue- and individual-specific DNA methylation patterns. <i>Human Molecular Genetics</i> , 2009 , 18, 4808-17	5.6	206

39	Many colorectal cancers are "flat" clonal expansions. <i>Cell Cycle</i> , 2009 , 8, 2187-93	4.7	24
38	Red meat and poultry intake, polymorphisms in the nucleotide excision repair and mismatch repair pathways and colorectal cancer risk. <i>Carcinogenesis</i> , 2009 , 30, 472-9	4.6	59
37	Older individuals appear to acquire mitotically older colorectal cancers. <i>Journal of Pathology</i> , 2009 , 217, 483-8	9.4	7
36	Associations between smoking, alcohol consumption, and colorectal cancer, overall and by tumor microsatellite instability status. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2009 , 18, 2745-50	4	98
35	Inferring relative numbers of human leucocyte genome replications. <i>British Journal of Haematology</i> , 2008 , 141, 862-71	4.5	15
34	Modeling DNA methylation in a population of cancer cells. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2008 , 7, Article 18	1.2	12
33	Statistical methods for evaluating DNA methylation as a marker for early detection or prognosis. <i>Disease Markers</i> , 2007 , 23, 113-20	3.2	4
32	Variants on 9p24 and 8q24 are associated with risk of colorectal cancer: results from the Colon Cancer Family Registry. <i>Cancer Research</i> , 2007 , 67, 11128-32	10.1	82
31	DNA methylation in the human cerebral cortex is dynamically regulated throughout the life span and involves differentiated neurons. <i>PLoS ONE</i> , 2007 , 2, e895	3.7	330
30	Widespread epigenetic abnormalities suggest a broad DNA methylation erasure defect in abnormal human sperm. <i>PLoS ONE</i> , 2007 , 2, e1289	3.7	215
29	Cluster analysis for DNA methylation profiles having a detection threshold. <i>BMC Bioinformatics</i> , 2006 , 7, 361	3.6	7
28	Modeling exposures for DNA methylation profiles. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2006 , 15, 567-72	4	5
27	CpG island methylator phenotype underlies sporadic microsatellite instability and is tightly associated with BRAF mutation in colorectal cancer. <i>Nature Genetics</i> , 2006 , 38, 787-93	36.3	1514
26	Testing association and linkage using affected-sib-parent study designs. <i>Genetic Epidemiology</i> , 2005 , 29, 225-33	2.6	7
25	Identifying susceptibility genes by using joint tests of association and linkage and accounting for epistasis. <i>BMC Genetics</i> , 2005 , 6 Suppl 1, S147	2.6	7
24	Association of breast cancer DNA methylation profiles with hormone receptor status and response to tamoxifen. <i>Cancer Research</i> , 2004 , 64, 3807-13	10.1	284
23	A comparison of cluster analysis methods using DNA methylation data. <i>Bioinformatics</i> , 2004 , 20, 1896-904	4.2	76
22	Detection of methylated apoptosis-associated genes in urine sediments of bladder cancer patients. <i>Clinical Cancer Research</i> , 2004 , 10, 7457-65	12.9	186

21	A case-control study of cyclin D1 CCND1 870A-->G polymorphism and bladder cancer. <i>Carcinogenesis</i> , 2003 , 24, 1645-50	4.6	27
20	Ascertainment bias in family-based case-control studies. <i>American Journal of Epidemiology</i> , 2002 , 155, 875-80	3.8	9
19	Diet, cancer and aging in DNA mismatch repair deficient mice. <i>Carcinogenesis</i> , 2002 , 23, 1807-10	4.6	23
18	Should we consider gene x environment interaction in the hunt for quantitative trait loci?. <i>Genetic Epidemiology</i> , 2001 , 21 Suppl 1, S831-6	2.6	6
17	Combined linkage and association analysis in pedigrees. <i>Genetic Epidemiology</i> , 2001 , 21 Suppl 1, S358-63	2.6	6
16	Stratified case sampling and the use of family controls. <i>Genetic Epidemiology</i> , 2001 , 20, 316-27	2.6	7
15	Gene-environment interaction and affected sib pair linkage analysis. <i>Human Heredity</i> , 2001 , 52, 34-46	1.1	35
14	Association tests in nuclear families. <i>Human Heredity</i> , 2001 , 52, 66-76	1.1	5
13	Corneal scarring and vision in keratoconus: a baseline report from the Collaborative Longitudinal Evaluation of Keratoconus (CLEK) Study. <i>Cornea</i> , 2000 , 19, 804-12	3.1	49
12	Factors associated with corneal scarring in the Collaborative Longitudinal Evaluation of Keratoconus (CLEK) Study. <i>Cornea</i> , 2000 , 19, 501-7	3.1	49
11	Hostility, social support, and carotid artery atherosclerosis in the National Heart, Lung, and Blood Institute Family Heart Study. <i>American Journal of Cardiology</i> , 2000 , 86, 1086-9	3	59
10	Linkage analysis for diseases with variable age of onset. <i>Human Heredity</i> , 2000 , 50, 205-10	1.1	7
9	Testing linkage disequilibrium in sibships. <i>American Journal of Human Genetics</i> , 2000 , 67, 244-8	1.1	68
8	Association tests using unaffected-sibling versus pseudo-sibling controls. <i>Genetic Epidemiology</i> , 1999 , 17 Suppl 1, S731-6	2.6	1
7	A frailty approach for modelling diseases with variable age of onset in families: the NHLBI Family Heart Study. <i>Statistics in Medicine</i> , 1999 , 18, 1517-28	2.3	4
6	A joint test of linkage and gene x environment interaction, with affected sib pairs. <i>Genetic Epidemiology</i> , 1999 , 17 Suppl 1, S563-8	2.6	5
5	Hostility, social support, and coronary heart disease in the National Heart, Lung, and Blood Institute Family Heart Study. <i>American Journal of Cardiology</i> , 1998 , 82, 1192-6	3	57
4	Modeling hazard functions in families. <i>Genetic Epidemiology</i> , 1998 , 15, 147-71	2.6	17

3	Lipoprotein(a) interactions with lipid and non-lipid risk factors in patients with early onset coronary artery disease: results from the NHLBI Family Heart Study. <i>Atherosclerosis</i> , 1998 , 141, 333-45	3.1	30
2	A study of reproductive function in patients with seminoma treated with radiotherapy and orchidectomy: (SWOG-8711). Southwest Oncology Group. <i>International Journal of Radiation Oncology Biology Physics</i> , 1997 , 38, 83-94	4	58
1	Beta regression improves the detection of differential DNA methylation for epigenetic epidemiology		6