

# Kimberly D Siegmund

## List of Publications by Year in descending order

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Version: 2024-02-01

109  
papers

9,411  
citations

66315

42  
h-index

40954

93  
g-index

114  
all docs

114  
docs citations

114  
times ranked

16391  
citing authors

#	ARTICLE	IF	CITATIONS
1	CpG island methylator phenotype underlies sporadic microsatellite instability and is tightly associated with BRAF mutation in colorectal cancer. <i>Nature Genetics</i> , 2006, 38, 787-793.	9.4	1,715
2	A Big Bang model of human colorectal tumor growth. <i>Nature Genetics</i> , 2015, 47, 209-216.	9.4	867
3	Low-level processing of Illumina Infinium DNA Methylation BeadArrays. <i>Nucleic Acids Research</i> , 2013, 41, e90-e90.	6.5	647
4	Genome-scale analysis of DNA methylation in lung adenocarcinoma and integration with mRNA expression. <i>Genome Research</i> , 2012, 22, 1197-1211.	2.4	461
5	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.	1.1	375
6	Recommendations for the design and analysis of epigenome-wide association studies. <i>Nature Methods</i> , 2013, 10, 949-955.	9.0	345
7	Association of Breast Cancer DNA Methylation Profiles with Hormone Receptor Status and Response to Tamoxifen. <i>Cancer Research</i> , 2004, 64, 3807-3813.	0.4	304
8	Environmental epigenetics: prospects for studying epigenetic mediation of exposureâ€“response relationships. <i>Human Genetics</i> , 2012, 131, 1565-1589.	1.8	294
9	Widespread Epigenetic Abnormalities Suggest a Broad DNA Methylation Erasure Defect in Abnormal Human Sperm. <i>PLoS ONE</i> , 2007, 2, e1289.	1.1	254
10	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.	1.5	252
11	Epigenetic profiling of somatic tissues from human autopsy specimens identifies tissue- and individual-specific DNA methylation patterns. <i>Human Molecular Genetics</i> , 2009, 18, 4808-4817.	1.4	230
12	Detection of Methylated Apoptosis-Associated Genes in Urine Sediments of Bladder Cancer Patients. <i>Clinical Cancer Research</i> , 2004, 10, 7457-7465.	3.2	202
13	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, 8169-8178.	0.4	148
14	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, 4828-4833.	3.3	134
15	Characterizing the genetic basis of methylome diversity in histologically normal human lung tissue. <i>Nature Communications</i> , 2014, 5, 3365.	5.8	123
16	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, 19673-19678.	3.3	119
17	Associations between Smoking, Alcohol Consumption, and Colorectal Cancer, Overall and by Tumor Microsatellite Instability Status. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2009, 18, 2745-2750.	1.1	109
18	Prenatal Tobacco Smoke Exposure Is Associated with Childhood DNA CpG Methylation. <i>PLoS ONE</i> , 2014, 9, e99716.	1.1	105

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19	A comparison of cluster analysis methods using DNA methylation data. <i>Bioinformatics</i> , 2004, 20, 1896-1904.	1.8	102
20	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, 4000-4013.	1.6	98
21	DNA Methylation Changes in Atypical Adenomatous Hyperplasia, Adenocarcinoma In Situ, and Lung Adenocarcinoma. <i>PLoS ONE</i> , 2011, 6, e21443.	1.1	98
22	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, 11128-11132.	0.4	87
23	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.	2.8	83
24	Particulate Matter, DNA Methylation in Nitric Oxide Synthase, and Childhood Respiratory Disease. <i>Environmental Health Perspectives</i> , 2012, 120, 1320-1326.	2.8	81
25	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.	1.2	78
26	A Panel of Three Markers Hyper- and Hypomethylated in Urine Sediments Accurately Predicts Bladder Cancer Recurrence. <i>Clinical Cancer Research</i> , 2014, 20, 1978-1989.	3.2	77
27	Testing Linkage Disequilibrium in Sibships. <i>American Journal of Human Genetics</i> , 2000, 67, 244-248.	2.6	73
28	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.	1.1	71
29	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, 3167-3173.	1.1	70
30	A study of reproductive function in patients with seminoma treated with radiotherapy and orchidectomy: (SWOG-8711). <i>International Journal of Radiation Oncology Biology Physics</i> , 1997, 38, 83-94.	0.4	69
31	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, 1192-1196.	0.7	68
32	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, 1086-1089.	0.7	68
33	Genome-Scale Screen for DNA Methylation-Based Detection Markers for Ovarian Cancer. <i>PLoS ONE</i> , 2011, 6, e28141.	1.1	65
34	Inter-individual variability in structural brain development from late childhood to young adulthood. <i>NeuroImage</i> , 2021, 242, 118450.	2.1	64
35	Red meat and poultry intake, polymorphisms in the nucleotide excision repair and mismatch repair pathways and colorectal cancer risk. <i>Carcinogenesis</i> , 2009, 30, 472-479.	1.3	63
36	Testicular germ cell tumor susceptibility associated with the UCK2 locus on chromosome 1q23. <i>Human Molecular Genetics</i> , 2013, 22, 2748-2753.	1.4	59

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37	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, 738.	1.8	58
38	Corneal Scarring and Vision in Keratoconus. <i>Cornea</i> , 2000, 19, 804-812.	0.9	56
39	Factors Associated with Corneal Scarring in the Collaborative Longitudinal Evaluation of Keratoconus (CLEK) Study. <i>Cornea</i> , 2000, 19, 501-507.	0.9	55
40	An evaluation of processing methods for HumanMethylation450 BeadChip data. <i>BMC Genomics</i> , 2016, 17, 469.	1.2	54
41	Statistical approaches for the analysis of DNA methylation microarray data. <i>Human Genetics</i> , 2011, 129, 585-595.	1.8	53
42	Carcinogen metabolism genes, red meat and poultry intake, and colorectal cancer risk. <i>International Journal of Cancer</i> , 2012, 130, 1898-1907.	2.3	47
43	Integrated Transcriptomic and Epigenomic Analysis of Primary Human Lung Epithelial Cell Differentiation. <i>PLoS Genetics</i> , 2013, 9, e1003513.	1.5	46
44	Identifying aggressive prostate cancer foci using a DNA methylation classifier. <i>Genome Biology</i> , 2017, 18, 3.	3.8	43
45	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.	3.3	43
46	Gene-Environment Interaction and Affected Sib Pair Linkage Analysis. <i>Human Heredity</i> , 2001, 52, 34-46.	0.4	39
47	Association of internal smoking dose with blood DNA methylation in three racial/ethnic populations. <i>Clinical Epigenetics</i> , 2018, 10, 110.	1.8	34
48	Lipoprotein(a) interactions with lipid and non-lipid risk factors in patients with early onset coronary artery disease. <i>Atherosclerosis</i> , 1998, 141, 333-345.	0.4	33
49	The genome-wide impact of trisomy 21 on DNA methylation and its implications for hematopoiesis. <i>Nature Communications</i> , 2021, 12, 821.	5.8	32
50	A case-control study of cyclin D1 CCND1 870A->G polymorphism and bladder cancer. <i>Carcinogenesis</i> , 2003, 24, 1645-1650.	1.3	30
51	Hormone therapy, DNA methylation and colon cancer. <i>Carcinogenesis</i> , 2010, 31, 1060-1067.	1.3	30
52	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-E399.	1.8	30
53	Many private mutations originate from the first few divisions of a human colorectal adenoma. <i>Journal of Pathology</i> , 2015, 237, 355-362.	2.1	30
54	Many colorectal cancers are clonal expansions. <i>Cell Cycle</i> , 2009, 8, 2187-2193.	1.3	29

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55	Identifying differential transcription factor binding in CHIP-seq. <i>Frontiers in Genetics</i> , 2015, 6, 169.	1.1	29
56	Identification of DNA Methylation-Independent Epigenetic Events Underlying Clear Cell Renal Cell Carcinoma. <i>Cancer Research</i> , 2016, 76, 1954-1964.	0.4	28
57	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.	1.4	27
58	Modeling hazard functions in families. , 1998, 15, 147-171.		26
59	Diet, cancer and aging in DNA mismatch repair deficient mice. <i>Carcinogenesis</i> , 2002, 23, 1807-1810.	1.3	26
60	Distinct, Genome-Wide, Gene-Specific Selectivity Patterns of Four Glucocorticoid Receptor Coregulators. <i>Nuclear Receptor Signaling</i> , 2014, 12, nrs.12002.	1.0	26
61	Particulate matter, the newborn methylome, and cardio-respiratory health outcomes in childhood. <i>Environmental Epigenetics</i> , 2016, 2, dvw005.	0.9	26
62	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, 1238-1243.	1.3	24
63	Epigenetic regulation of AXL and risk of childhood asthma symptoms. <i>Clinical Epigenetics</i> , 2017, 9, 121.	1.8	22
64	High DNA Methylation Pattern Intratumoral Diversity Implies Weak Selection in Many Human Colorectal Cancers. <i>PLoS ONE</i> , 2011, 6, e21657.	1.1	18
65	Inferring relative numbers of human leucocyte genome replications. <i>British Journal of Haematology</i> , 2008, 141, 862-871.	1.2	17
66	Epigenetic Heterogeneity in Human Colorectal Tumors Reveals Preferential Conservation And Evidence of Immune Surveillance. <i>Scientific Reports</i> , 2018, 8, 17292.	1.6	17
67	Improving needle biopsy accuracy in small renal mass using tumor-specific DNA methylation markers. <i>Oncotarget</i> , 2017, 8, 5439-5448.	0.8	17
68	A novel role for vaping in mitochondrial gene dysregulation and inflammation fundamental to disease development. <i>Scientific Reports</i> , 2021, 11, 22773.	1.6	16
69	Modeling DNA Methylation in a Population of Cancer Cells. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2008, 7, Article 18.	0.2	15
70	Non-specific filtering of beta-distributed data. <i>BMC Bioinformatics</i> , 2014, 15, 199.	1.2	15
71	Systematic Review and Meta-analysis of Testicular Germ Cell Tumors Following In Utero Exposure to Diethylstilbestrol. <i>JNCI Cancer Spectrum</i> , 2019, 3, pkz045.	1.4	15
72	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, 1240-1245.	1.6	14

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73	Stratified case sampling and the use of family controls. <i>Genetic Epidemiology</i> , 2001, 20, 316-327.	0.6	11
74	Identification and functional relevance of de novo DNA methylation in cancerous B&#x2014;cell populations. <i>Journal of Cellular Biochemistry</i> , 2010, 109, 818-827.	1.2	11
75	At least two well-spaced samples are needed to genotype a solid tumor. <i>BMC Cancer</i> , 2016, 16, 250.	1.1	11
76	Ascertainment Bias in Family-based Case-Control Studies. <i>American Journal of Epidemiology</i> , 2002, 155, 875-880.	1.6	10
77	Using DNA Methylation Patterns to Infer Tumor Ancestry. <i>PLoS ONE</i> , 2010, 5, e12002.	1.1	10
78	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.	1.1	10
79	Epigenetic plasticity potentiates a rapid cyclical shift to and from an aggressive cancer phenotype. <i>International Journal of Cancer</i> , 2020, 146, 3065-3076.	2.3	10
80	Should We Consider Gene&#x2014;Environment Interaction in the Hunt for Quantitative Trait Loci?. <i>Genetic Epidemiology</i> , 2001, 21, S831-S836.	0.6	9
81	Ancestral inference in tumors: How much can we know?. <i>Journal of Theoretical Biology</i> , 2014, 359, 136-145.	0.8	9
82	DNA Methylation Profiles of Vegans and Non-Vegetarians in the Adventist Health Study-2 Cohort. <i>Nutrients</i> , 2020, 12, 3697.	1.7	9
83	A joint test of linkage and gene&#x2014;environment interaction, with affected sib pairs. <i>Genetic Epidemiology</i> , 1999, 17, S563-S568.	0.6	8
84	Identifying susceptibility genes by using joint tests of association and linkage and accounting for epistasis. <i>BMC Genetics</i> , 2005, 6, S147.	2.7	8
85	A frailty approach for modelling diseases with variable age of onset in families: the NHLBI family heart study. , 1999, 18, 1517-1528.		7
86	Linkage Analysis for Diseases with Variable Age of Onset. <i>Human Heredity</i> , 2000, 50, 205-210.	0.4	7
87	Association Tests in Nuclear Families. <i>Human Heredity</i> , 2001, 52, 66-76.	0.4	7
88	Testing association and linkage using affected-sib-parent study designs. <i>Genetic Epidemiology</i> , 2005, 29, 225-233.	0.6	7
89	Cluster analysis for DNA methylation profiles having a detection threshold. <i>BMC Bioinformatics</i> , 2006, 7, 361.	1.2	7
90	Older individuals appear to acquire mitotically older colorectal cancers. <i>Journal of Pathology</i> , 2009, 217, 483-488.	2.1	7

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91	Repeated assessment by high-throughput assay demonstrates that sperm DNA methylation levels are highly reproducible. <i>Fertility and Sterility</i> , 2011, 96, 1325-1330.	0.5	7
92	Combined Linkage and Association Analysis in Pedigrees. <i>Genetic Epidemiology</i> , 2001, 21, S358-S363.	0.6	6
93	Transcriptomic profiling of primary alveolar epithelial cell differentiation in human and rat. <i>Genomics Data</i> , 2014, 2, 105-109.	1.3	6
94	Association between <i>AXL</i> promoter methylation and lung function growth during adolescence. <i>Epigenetics</i> , 2018, 13, 1027-1038.	1.3	6
95	Modeling Exposures for DNA Methylation Profiles. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2006, 15, 567-572.	1.1	5
96	Total Outflow Facility in Live C57BL/6 Mice of Different Age. <i>Biomedicine Hub</i> , 2018, 2, 1-10.	0.4	5
97	A Novel DNA Methylation Signature as an Independent Prognostic Factor in Muscle-Invasive Bladder Cancer. <i>Frontiers in Oncology</i> , 2021, 11, 614927.	1.3	5
98	HiLDA: a statistical approach to investigate differences in mutational signatures. <i>PeerJ</i> , 2019, 7, e7557.	0.9	5
99	Statistical Methods for Evaluating DNA Methylation as a Marker for Early Detection or Prognosis. <i>Disease Markers</i> , 2007, 23, 113-120.	0.6	4
100	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.	1.0	4
101	Mutational signatures in colon cancer. <i>BMC Research Notes</i> , 2019, 12, 788.	0.6	3
102	Cell-free DNA methylation as a predictive biomarker of response to neoadjuvant chemotherapy for patients with muscle-invasive bladder cancer in SWOG S1314. <i>Journal of Clinical Oncology</i> , 2022, 40, 4506-4506.	0.8	3
103	Association tests using unaffected-sibling versus pseudo-sibling controls. <i>Genetic Epidemiology</i> , 1999, 17, S731-S736.	0.6	2
104	The Genome-Wide Impact of Trisomy 21 on DNA Methylation and Its Implications for Hematologic Malignancies. <i>Blood</i> , 2019, 134, 2510-2510.	0.6	2
105	Genetic complexity at expression quantitative trait loci. <i>BMC Proceedings</i> , 2016, 10, 85-89.	1.8	1
106	Functional human genes typically exhibit epigenetic conservation. <i>PLoS ONE</i> , 2021, 16, e0253250.	1.1	1
107	Early mutation bursts in colorectal tumors. <i>PLoS ONE</i> , 2017, 12, e0172516.	1.1	1
108	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.	0.8	0

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109	Epigenomic profiling of plasma cell-free DNA (cfDNA) to predict bladder cancer recurrence after radical cystectomy.. Journal of Clinical Oncology, 2019, 37, e14525-e14525.	0.8	0