

Kimberly D Siegmund

List of Publications by Citations

Source: <https://exaly.com/author-pdf/1244635/kimberly-d-siegmund-publications-by-citations.pdf>
Version: 2024-04-09

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.
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	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
109	A Big Bang model of human colorectal tumor growth. <i>Nature Genetics</i> , 2015 , 47, 209-16	36.3	646
108	Low-level processing of Illumina Infinium DNA Methylation BeadArrays. <i>Nucleic Acids Research</i> , 2013 , 41, e90	20.1	393
107	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
106	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
105	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
104	Recommendations for the design and analysis of epigenome-wide association studies. <i>Nature Methods</i> , 2013 , 10, 949-55	21.6	276
103	Environmental epigenetics: prospects for studying epigenetic mediation of exposure-response relationships. <i>Human Genetics</i> , 2012 , 131, 1565-89	6.3	258
102	Widespread epigenetic abnormalities suggest a broad DNA methylation erasure defect in abnormal human sperm. <i>PLoS ONE</i> , 2007 , 2, e1289	3.7	215
101	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
100	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
99	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
98	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
97	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
96	Characterizing the genetic basis of methylome diversity in histologically normal human lung tissue. <i>Nature Communications</i> , 2014 , 5, 3365	17.4	103
95	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
94	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

93	Prenatal tobacco smoke exposure is associated with childhood DNA CpG methylation. <i>PLoS ONE</i> , 2014 , 9, e99716	3.7	94
92	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
91	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
90	DNA methylation changes in atypical adenomatous hyperplasia, adenocarcinoma in situ, and lung adenocarcinoma. <i>PLoS ONE</i> , 2011 , 6, e21443	3.7	77
89	Particulate matter, DNA methylation in nitric oxide synthase, and childhood respiratory disease. <i>Environmental Health Perspectives</i> , 2012 , 120, 1320-6	8.4	76
88	A comparison of cluster analysis methods using DNA methylation data. <i>Bioinformatics</i> , 2004 , 20, 1896-904	4.2	76
87	Testing linkage disequilibrium in sibships. <i>American Journal of Human Genetics</i> , 2000 , 67, 244-8	11	68
86	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
85	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
84	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
83	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
82	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
81	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
80	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
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	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
77	Statistical approaches for the analysis of DNA methylation microarray data. <i>Human Genetics</i> , 2011 , 129, 585-95	6.3	50
76	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

75	Factors associated with corneal scarring in the Collaborative Longitudinal Evaluation of Keratoconus (CLEK) Study. <i>Cornea</i> , 2000 , 19, 501-7	3.1	49
74	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
73	Genome-scale screen for DNA methylation-based detection markers for ovarian cancer. <i>PLoS ONE</i> , 2011 , 6, e28141	3.7	45
72	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
71	Integrated transcriptomic and epigenomic analysis of primary human lung epithelial cell differentiation. <i>PLoS Genetics</i> , 2013 , 9, e1003513	6	41
70	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
69	An evaluation of processing methods for HumanMethylation450 BeadChip data. <i>BMC Genomics</i> , 2016 , 17, 469	4.5	36
68	Gene-environment interaction and affected sib pair linkage analysis. <i>Human Heredity</i> , 2001 , 52, 34-46	1.1	35
67	Identifying aggressive prostate cancer foci using a DNA methylation classifier. <i>Genome Biology</i> , 2017 , 18, 3	18.3	31
66	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
65	Hormone therapy, DNA methylation and colon cancer. <i>Carcinogenesis</i> , 2010 , 31, 1060-7	4.6	28
64	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
63	A case-control study of cyclin D1 CCND1 870A-->G polymorphism and bladder cancer. <i>Carcinogenesis</i> , 2003 , 24, 1645-50	4.6	27
62	Many colorectal cancers are "flat" clonal expansions. <i>Cell Cycle</i> , 2009 , 8, 2187-93	4.7	24
61	Diet, cancer and aging in DNA mismatch repair deficient mice. <i>Carcinogenesis</i> , 2002 , 23, 1807-10	4.6	23
60	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
59	Association of internal smoking dose with blood DNA methylation in three racial/ethnic populations. <i>Clinical Epigenetics</i> , 2018 , 10, 110	7.7	22
58	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

57	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
56	Identification of DNA Methylation-Independent Epigenetic Events Underlying Clear Cell Renal Cell Carcinoma. <i>Cancer Research</i> , 2016 , 76, 1954-64	10.1	21
55	Distinct, genome-wide, gene-specific selectivity patterns of four glucocorticoid receptor coregulators. <i>Nuclear Receptor Signaling</i> , 2014 , 12, e002	1	19
54	Particulate matter, the newborn methylome, and cardio-respiratory health outcomes in childhood. <i>Environmental Epigenetics</i> , 2016 , 2, dvw005	2.4	19
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 regulation of and risk of childhood asthma symptoms. <i>Clinical Epigenetics</i> , 2017 , 9, 121	7.7	17
51	Modeling hazard functions in families. <i>Genetic Epidemiology</i> , 1998 , 15, 147-71	2.6	17
50	Inferring relative numbers of human leucocyte genome replications. <i>British Journal of Haematology</i> , 2008 , 141, 862-71	4.5	15
49	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
48	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
47	Identifying differential transcription factor binding in ChIP-seq. <i>Frontiers in Genetics</i> , 2015 , 6, 169	4.5	13
46	Improving needle biopsy accuracy in small renal mass using tumor-specific DNA methylation markers. <i>Oncotarget</i> , 2017 , 8, 5439-5448	3.3	13
45	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
44	Non-specific filtering of beta-distributed data. <i>BMC Bioinformatics</i> , 2014 , 15, 199	3.6	11
43	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
42	Epigenetic Heterogeneity in Human Colorectal Tumors Reveals Preferential Conservation And Evidence of Immune Surveillance. <i>Scientific Reports</i> , 2018 , 8, 17292	4.9	11
41	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
40	Using DNA methylation patterns to infer tumor ancestry. <i>PLoS ONE</i> , 2010 , 5, e12002	3.7	10

39	Ascertainment bias in family-based case-control studies. <i>American Journal of Epidemiology</i> , 2002 , 155, 875-80	3.8	9
38	Inter-individual variability in structural brain development from late childhood to young adulthood. <i>NeuroImage</i> , 2021 , 242, 118450	7.9	9
37	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
36	At least two well-spaced samples are needed to genotype a solid tumor. <i>BMC Cancer</i> , 2016 , 16, 250	4.8	8
35	Older individuals appear to acquire mitotically older colorectal cancers. <i>Journal of Pathology</i> , 2009 , 217, 483-8	9.4	7
34	Cluster analysis for DNA methylation profiles having a detection threshold. <i>BMC Bioinformatics</i> , 2006 , 7, 361	3.6	7
33	Testing association and linkage using affected-sib-parent study designs. <i>Genetic Epidemiology</i> , 2005 , 29, 225-33	2.6	7
32	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
31	Stratified case sampling and the use of family controls. <i>Genetic Epidemiology</i> , 2001 , 20, 316-27	2.6	7
30	Linkage analysis for diseases with variable age of onset. <i>Human Heredity</i> , 2000 , 50, 205-10	1.1	7
29	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
28	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
27	Ancestral inference in tumors: how much can we know?. <i>Journal of Theoretical Biology</i> , 2014 , 359, 136-45	2.3	6
26	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
25	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
24	Combined linkage and association analysis in pedigrees. <i>Genetic Epidemiology</i> , 2001 , 21 Suppl 1, S358-63	2.6	6
23	Beta regression improves the detection of differential DNA methylation for epigenetic epidemiology		6
22	Transcriptomic Profiling of Primary Alveolar Epithelial Cell Differentiation in Human and Rat. <i>Genomics Data</i> , 2014 , 2, 105-109		5

21	Modeling exposures for DNA methylation profiles. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2006 , 15, 567-72	4	5
20	Association tests in nuclear families. <i>Human Heredity</i> , 2001 , 52, 66-76	1.1	5
19	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
18	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
17	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
16	HiLDA: a statistical approach to investigate differences in mutational signatures. <i>PeerJ</i> , 2019 , 7, e7557	3.1	4
15	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
14	Association between promoter methylation and lung function growth during adolescence. <i>Epigenetics</i> , 2018 , 13, 1027-1038	5.7	4
13	DNA Methylation Profiles of Vegans and Non-Vegetarians in the Adventist Health Study-2 Cohort. <i>Nutrients</i> , 2020 , 12,	6.7	3
12	Total Outflow Facility in Live C57BL/6 Mice of Different Age. <i>Biomedicine Hub</i> , 2017 , 2, 1-10	1.3	3
11	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
10	Mutational signatures in colon cancer. <i>BMC Research Notes</i> , 2019 , 12, 788	2.3	2
9	Genetic complexity at expression quantitative trait loci. <i>BMC Proceedings</i> , 2016 , 10, 85-89	2.3	1
8	Association tests using unaffected-sibling versus pseudo-sibling controls. <i>Genetic Epidemiology</i> , 1999 , 17 Suppl 1, S731-6	2.6	1
7	Early mutation bursts in colorectal tumors. <i>PLoS ONE</i> , 2017 , 12, e0172516	3.7	1
6	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
5	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
4	Functional human genes typically exhibit epigenetic conservation. <i>PLoS ONE</i> , 2021 , 16, e0253250	3.7	0

- 3 Cell-free DNA (cfDNA) whole genome bisulfite sequencing in patients with muscle-invasive bladder cancer patient treated with cystectomy with curative intent.. *Journal of Clinical Oncology*, **2019**, 37, 359-359
- 2 Epigenomic profiling of plasma cell-free DNA (cfDNA) to predict bladder cancer recurrence after radical cystectomy.. *Journal of Clinical Oncology*, **2019**, 37, e14525-e14525 2.2
- 1 DNA Methylation **2019**, 933-948