

# 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  | 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         |
| 2  | 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        |
| 3  | 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         |
| 4  | Functional human genes typically exhibit epigenetic conservation. <i>PLoS ONE</i> , 2021, 16, e0253250.   | 1.1 | 1         |
| 5  | Inter-individual variability in structural brain development from late childhood to young adulthood. <i>NeuroImage</i> , 2021, 242, 118450.   | 2.1 | 64        |
| 6  | 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        |
| 7  | DNA Methylation Profiles of Vegans and Non-Vegetarians in the Adventist Health Study-2 Cohort. <i>Nutrients</i> , 2020, 12, 3697.   | 1.7 | 9         |
| 8  | 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         |
| 9  | 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        |
| 10 | 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        |
| 11 | 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        |
| 12 | Mutational signatures in colon cancer. <i>BMC Research Notes</i> , 2019, 12, 788.   | 0.6 | 3         |
| 13 | HiLDA: a statistical approach to investigate differences in mutational signatures. <i>PeerJ</i> , 2019, 7, e7557.   | 0.9 | 5         |
| 14 | 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         |
| 15 | 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.                                     | 0.8 | 0         |
| 16 | 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         |
| 17 | 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        |
| 18 | Epigenetic Heterogeneity in Human Colorectal Tumors Reveals Preferential Conservation And Evidence of Immune Surveillance. <i>Scientific Reports</i> , 2018, 8, 17292.  | 1.6 | 17        |

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|----|--|-----|-----------|
| 19 | Total Outflow Facility in Live C57BL/6 Mice of Different Age. <i>Biomedicine Hub</i> , 2018, 2, 1-10.  | 0.4 | 5         |
| 20 | Association between <i>AXL</i> promoter methylation and lung function growth during adolescence. <i>Epigenetics</i> , 2018, 13, 1027-1038.   | 1.3 | 6         |
| 21 | 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        |
| 22 | Association of internal smoking dose with blood DNA methylation in three racial/ethnic populations. <i>Clinical Epigenetics</i> , 2018, 10, 110.   | 1.8 | 34        |
| 23 | Identifying aggressive prostate cancer foci using a DNA methylation classifier. <i>Genome Biology</i> , 2017, 18, 3.   | 3.8 | 43        |
| 24 | 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        |
| 25 | Epigenetic regulation of <i>AXL</i> and risk of childhood asthma symptoms. <i>Clinical Epigenetics</i> , 2017, 9, 121.   | 1.8 | 22        |
| 26 | Early mutation bursts in colorectal tumors. <i>PLoS ONE</i> , 2017, 12, e0172516.  | 1.1 | 1         |
| 27 | Improving needle biopsy accuracy in small renal mass using tumor-specific DNA methylation markers. <i>Oncotarget</i> , 2017, 8, 5439-5448.   | 0.8 | 17        |
| 28 | Particulate matter, the newborn methylome, and cardio-respiratory health outcomes in childhood. <i>Environmental Epigenetics</i> , 2016, 2, dvw005.  | 0.9 | 26        |
| 29 | 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        |
| 30 | An evaluation of processing methods for HumanMethylation450 BeadChip data. <i>BMC Genomics</i> , 2016, 17, 469.  | 1.2 | 54        |
| 31 | Genetic complexity at expression quantitative trait loci. <i>BMC Proceedings</i> , 2016, 10, 85-89.  | 1.8 | 1         |
| 32 | At least two well-spaced samples are needed to genotype a solid tumor. <i>BMC Cancer</i> , 2016, 16, 250.  | 1.1 | 11        |
| 33 | Identification of DNA Methylation-Independent Epigenetic Events Underlying Clear Cell Renal Cell Carcinoma. <i>Cancer Research</i> , 2016, 76, 1954-1964.  | 0.4 | 28        |
| 34 | 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        |
| 35 | Identifying differential transcription factor binding in ChIP-seq. <i>Frontiers in Genetics</i> , 2015, 6, 169.  | 1.1 | 29        |
| 36 | A Big Bang model of human colorectal tumor growth. <i>Nature Genetics</i> , 2015, 47, 209-216.   | 9.4 | 867       |

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|----|--|-----|-----------|
| 37 | 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        |
| 38 | Prenatal Tobacco Smoke Exposure Is Associated with Childhood DNA CpG Methylation. <i>PLoS ONE</i> , 2014, 9, e99716.   | 1.1 | 105       |
| 39 | Distinct, Genome-Wide, Gene-Specific Selectivity Patterns of Four Glucocorticoid Receptor Coregulators. <i>Nuclear Receptor Signaling</i> , 2014, 12, nrs.12002.   | 1.0 | 26        |
| 40 | Non-specific filtering of beta-distributed data. <i>BMC Bioinformatics</i> , 2014, 15, 199.  | 1.2 | 15        |
| 41 | Characterizing the genetic basis of methylome diversity in histologically normal human lung tissue. <i>Nature Communications</i> , 2014, 5, 3365.  | 5.8 | 123       |
| 42 | 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        |
| 43 | Transcriptomic profiling of primary alveolar epithelial cell differentiation in human and rat. <i>Genomics Data</i> , 2014, 2, 105-109.  | 1.3 | 6         |
| 44 | Ancestral inference in tumors: How much can we know?. <i>Journal of Theoretical Biology</i> , 2014, 359, 136-145.  | 0.8 | 9         |
| 45 | 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        |
| 46 | Recommendations for the design and analysis of epigenome-wide association studies. <i>Nature Methods</i> , 2013, 10, 949-955.  | 9.0 | 345       |
| 47 | Integrated Transcriptomic and Epigenomic Analysis of Primary Human Lung Epithelial Cell Differentiation. <i>PLoS Genetics</i> , 2013, 9, e1003513.   | 1.5 | 46        |
| 48 | Low-level processing of Illumina Infinium DNA Methylation BeadArrays. <i>Nucleic Acids Research</i> , 2013, 41, e90-e90.   | 6.5 | 647       |
| 49 | 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        |
| 50 | 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        |
| 51 | 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       |
| 52 | 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        |
| 53 | C9a 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       |
| 54 | Environmental epigenetics: prospects for studying epigenetic mediation of exposure-response relationships. <i>Human Genetics</i> , 2012, 131, 1565-1589.   | 1.8 | 294       |

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|----|--|-----|-----------|
| 55 | Particulate Matter, DNA Methylation in Nitric Oxide Synthase, and Childhood Respiratory Disease. <i>Environmental Health Perspectives</i> , 2012, 120, 1320-1326.  | 2.8 | 81        |
| 56 | 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        |
| 57 | 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         |
| 58 | High DNA Methylation Pattern Intratumoral Diversity Implies Weak Selection in Many Human Colorectal Cancers. <i>PLoS ONE</i> , 2011, 6, e21657.  | 1.1 | 18        |
| 59 | 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        |
| 60 | Genome-Scale Screen for DNA Methylation-Based Detection Markers for Ovarian Cancer. <i>PLoS ONE</i> , 2011, 6, e28141.   | 1.1 | 65        |
| 61 | Statistical approaches for the analysis of DNA methylation microarray data. <i>Human Genetics</i> , 2011, 129, 585-595.  | 1.8 | 53        |
| 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 | DNA Methylation Changes in Atypical Adenomatous Hyperplasia, Adenocarcinoma In Situ, and Lung Adenocarcinoma. <i>PLoS ONE</i> , 2011, 6, e21443.   | 1.1 | 98        |
| 64 | Identification and functional relevance of de novo DNA methylation in cancerous B cell populations. <i>Journal of Cellular Biochemistry</i> , 2010, 109, 818-827.  | 1.2 | 11        |
| 65 | Using DNA Methylation Patterns to Infer Tumor Ancestry. <i>PLoS ONE</i> , 2010, 5, e12002.   | 1.1 | 10        |
| 66 | 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        |
| 67 | 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       |
| 68 | 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       |
| 69 | Hormone therapy, DNA methylation and colon cancer. <i>Carcinogenesis</i> , 2010, 31, 1060-1067.  | 1.3 | 30        |
| 70 | 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       |
| 71 | 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       |
| 72 | Many colorectal cancers are clonal expansions. <i>Cell Cycle</i> , 2009, 8, 2187-2193.   | 1.3 | 29        |

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|----|---|-----|-----------|
| 73 | 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        |
| 74 | Older individuals appear to acquire mitotically older colorectal cancers. <i>Journal of Pathology</i> , 2009, 217, 483-488.   | 2.1 | 7         |
| 75 | 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       |
| 76 | Inferring relative numbers of human leucocyte genome replications. <i>British Journal of Haematology</i> , 2008, 141, 862-871.  | 1.2 | 17        |
| 77 | 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        |
| 78 | 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        |
| 79 | 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         |
| 80 | 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       |
| 81 | Widespread Epigenetic Abnormalities Suggest a Broad DNA Methylation Erasure Defect in Abnormal Human Sperm. <i>PLoS ONE</i> , 2007, 2, e1289.   | 1.1 | 254       |
| 82 | 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     |
| 83 | Cluster analysis for DNA methylation profiles having a detection threshold. <i>BMC Bioinformatics</i> , 2006, 7, 361.   | 1.2 | 7         |
| 84 | Modeling Exposures for DNA Methylation Profiles. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2006, 15, 567-572.  | 1.1 | 5         |
| 85 | Testing association and linkage using affected-sib-parent study designs. <i>Genetic Epidemiology</i> , 2005, 29, 225-233.   | 0.6 | 7         |
| 86 | 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         |
| 87 | 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       |
| 88 | A comparison of cluster analysis methods using DNA methylation data. <i>Bioinformatics</i> , 2004, 20, 1896-1904.   | 1.8 | 102       |
| 89 | 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       |
| 90 | A case-control study of cyclin D1 CCND1 870A->G polymorphism and bladder cancer. <i>Carcinogenesis</i> , 2003, 24, 1645-1650.   | 1.3 | 30        |

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| 91  | Ascertainment Bias in Family-based Case-Control Studies. <i>American Journal of Epidemiology</i> , 2002, 155, 875-880.  | 1.6 | 10        |
| 92  | Diet, cancer and aging in DNA mismatch repair deficient mice. <i>Carcinogenesis</i> , 2002, 23, 1807-1810.  | 1.3 | 26        |
| 93  | Gene-Environment Interaction and Affected Sib Pair Linkage Analysis. <i>Human Heredity</i> , 2001, 52, 34-46.   | 0.4 | 39        |
| 94  | Association Tests in Nuclear Families. <i>Human Heredity</i> , 2001, 52, 66-76.   | 0.4 | 7         |
| 95  | Should We Consider Gene-Environment Interaction in the Hunt for Quantitative Trait Loci?. <i>Genetic Epidemiology</i> , 2001, 21, S831-S836.  | 0.6 | 9         |
| 96  | Combined Linkage and Association Analysis in Pedigrees. <i>Genetic Epidemiology</i> , 2001, 21, S358-S363.  | 0.6 | 6         |
| 97  | Stratified case sampling and the use of family controls. <i>Genetic Epidemiology</i> , 2001, 20, 316-327.   | 0.6 | 11        |
| 98  | Corneal Scarring and Vision in Keratoconus. <i>Cornea</i> , 2000, 19, 804-812.  | 0.9 | 56        |
| 99  | Factors Associated with Corneal Scarring in the Collaborative Longitudinal Evaluation of Keratoconus (CLEK) Study. <i>Cornea</i> , 2000, 19, 501-507.   | 0.9 | 55        |
| 100 | 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        |
| 101 | Linkage Analysis for Diseases with Variable Age of Onset. <i>Human Heredity</i> , 2000, 50, 205-210.  | 0.4 | 7         |
| 102 | Testing Linkage Disequilibrium in Sibships. <i>American Journal of Human Genetics</i> , 2000, 67, 244-248.  | 2.6 | 73        |
| 103 | Association tests using unaffected-sibling versus pseudo-sibling controls. <i>Genetic Epidemiology</i> , 1999, 17, S731-S736.   | 0.6 | 2         |
| 104 | A frailty approach for modelling diseases with variable age of onset in families: the NHLBI family heart study. , 1999, 18, 1517-1528.  |     | 7         |
| 105 | A joint test of linkage and gene-environment interaction, with affected sib pairs. <i>Genetic Epidemiology</i> , 1999, 17, S563-S568.   | 0.6 | 8         |
| 106 | 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        |
| 107 | Modeling hazard functions in families. , 1998, 15, 147-171.   |     | 26        |
| 108 | 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        |

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| 109 | A study of reproductive function in patients with seminoma treated with radiotherapy and orchidectomy: (SWOG-8711). International Journal of Radiation Oncology Biology Physics, 1997, 38, 83-94. | 0.4 | 69        |