

Brock C Christensen

List of Publications by Year in descending order

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85
papers

7,751
citations

147801

31
h-index

71685

76
g-index

114
all docs

114
docs citations

114
times ranked

12230
citing authors

#	ARTICLE	IF	CITATIONS
1	Interactions of Age and Blood Immune Factors and Noninvasive Prediction of Glioma Survival. <i>Journal of the National Cancer Institute</i> , 2022, 114, 446-457.	6.3	11
2	Phase I Study of High-Dose I-Methylfolate in Combination with Temozolomide and Bevacizumab in Recurrent IDH Wild-Type High-Grade Glioma. <i>Cancer Research Communications</i> , 2022, 2, 1-9.	1.7	0
3	Immune profiles and DNA methylation alterations related with non-muscle-invasive bladder cancer outcomes. <i>Clinical Epigenetics</i> , 2022, 14, 14.	4.1	13
4	Navigating the hydroxymethylome: experimental biases and quality control tools for the tandem bisulfite and oxidative bisulfite Illumina microarrays. <i>Epigenomics</i> , 2022, 14, 139-152.	2.1	3
5	Enhanced cell deconvolution of peripheral blood using DNA methylation for high-resolution immune profiling. <i>Nature Communications</i> , 2022, 13, 761.	12.8	93
6	A core of differentially methylated CpG loci in gMDSCs isolated from neonatal and adult sources. <i>Clinical Epigenetics</i> , 2022, 14, 27.	4.1	2
7	Human cytomegalovirus alters immune cell profile with potential implications for patient survival in head and neck cancer. <i>Carcinogenesis</i> , 2022, , .	2.8	0
8	Distinct cytosine modification profiles define epithelial-to-mesenchymal cell-state transitions. <i>Epigenomics</i> , 2022, 14, 519-535.	2.1	4
9	Genome-Scale DNA Methylation Analysis Identifies Repeat Element Alterations that Modulate the Genomic Stability of Melanocytic Nevi. <i>Journal of Investigative Dermatology</i> , 2022, 142, 1893-1902.e7.	0.7	14
10	Development of biologically interpretable multimodal deep learning model for cancer prognosis prediction. , 2022, , .		7
11	Widespread redundancy in -omics profiles of cancer mutation states. <i>Genome Biology</i> , 2022, 23, .	8.8	5
12	Hypermethylation and global remodelling of DNA methylation is associated with acquired cisplatin resistance in testicular germ cell tumours. <i>Epigenetics</i> , 2021, 16, 1071-1084.	2.7	21
13	A phase 1 study of combined guadecitabine and cisplatin in platinum refractory germ cell cancer. <i>Cancer Medicine</i> , 2021, 10, 156-163.	2.8	23
14	A large-scale internal validation study of unsupervised virtual trichrome staining technologies on nonalcoholic steatohepatitis liver biopsies. <i>Modern Pathology</i> , 2021, 34, 808-822.	5.5	29
15	IFAA: Robust Association Identification and Inference for Absolute Abundance in Microbiome Analyses. <i>Journal of the American Statistical Association</i> , 2021, 116, 1595-1608.	3.1	2
16	Identification of a foetal epigenetic compartment in adult human kidney. <i>Epigenetics</i> , 2021, , 1-21.	2.7	0
17	Abstract 2115: Multicomponent epigenetic profiling of intermediate epithelial-to-mesenchymal states in triple negative breast cancer identifies distinct regulatory signatures. , 2021, , .		0
18	MethylSPWNet and MethylCapsNet: Biologically Motivated Organization of DNAm Neural Networks, Inspired by Capsule Networks. <i>Npj Systems Biology and Applications</i> , 2021, 7, 33.	3.0	12

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19	DNA 5-hydroxymethylcytosine in pediatric central nervous system tumors may impact tumor classification and is a positive prognostic marker. <i>Clinical Epigenetics</i> , 2021, 13, 176.	4.1	9
20	Exposure to extracellular vesicles from <i>Pseudomonas aeruginosa</i> result in loss of DNA methylation at enhancer and DNase hypersensitive site regions in lung macrophages. <i>Epigenetics</i> , 2021, 16, 1187-1200.	2.7	11
21	Topological Feature Extraction and Visualization of Whole Slide Images using Graph Neural Networks. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2021, 26, 285-296.	0.7	5
22	Genome-wide characterization of cytosine-specific 5-hydroxymethylation in normal breast tissue. <i>Epigenetics</i> , 2020, 15, 398-418.	2.7	11
23	Altered immune phenotype and DNA methylation in panic disorder. <i>Clinical Epigenetics</i> , 2020, 12, 177.	4.1	6
24	Limiting Self-Renewal of the Basal Compartment by PKA Activation Induces Differentiation and Alters the Evolution of Mammary Tumors. <i>Developmental Cell</i> , 2020, 55, 544-557.e6.	7.0	20
25	MethylNet: an automated and modular deep learning approach for DNA methylation analysis. <i>BMC Bioinformatics</i> , 2020, 21, 108.	2.6	69
26	Silencing hepatic MCJ attenuates non-alcoholic fatty liver disease (NAFLD) by increasing mitochondrial fatty acid oxidation. <i>Nature Communications</i> , 2020, 11, 3360.	12.8	73
27	Enrichment of CpG island shore region hypermethylation in epigenetic breast field cancerization. <i>Epigenetics</i> , 2020, 15, 1093-1106.	2.7	17
28	Using Natural Language Processing and Sentiment Analysis to Augment Traditional User-Centered Design: Development and Usability Study. <i>JMIR MHealth and UHealth</i> , 2020, 8, e16862.	3.7	16
29	Extracellular Vesicles from <i>Pseudomonas aeruginosa</i> Suppress MHC-Related Molecules in Human Lung Macrophages. <i>ImmunoHorizons</i> , 2020, 4, 508-519.	1.8	19
30	Preliminary Evaluation of the Utility of Deep Generative Histopathology Image Translation at a Mid-sized NCI Cancer Center. , 2020, , .		5
31	PathFlowAI: A High-Throughput Workflow for Preprocessing, Deep Learning and Interpretation in Digital Pathology. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2020, 25, 403-414.	0.7	8
32	BIOM-13. DNA METHYLATION MARKS GLUCOCORTICOID PATHWAY RESPONSE IN DEXAMETHASONE-TREATED BRAIN TUMOR PATIENTS. <i>Neuro-Oncology</i> , 2020, 22, ii4-ii4.	1.2	0
33	EPCO-25. AN IMMUNOMETHYLOMIC PLATFORM INTEGRATING SYSTEMIC IMMUNE PROFILES AND EPIGENETIC AGE IN NEURO-ONCOLOGY. <i>Neuro-Oncology</i> , 2020, 22, ii74-ii74.	1.2	0
34	MicroRNA-Related Genetic Variants Associated with Survival of Head and Neck Squamous Cell Carcinoma. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019, 28, 127-136.	2.5	17
35	PyMethylProcessâ€”convenient high-throughput preprocessing workflow for DNA methylation data. <i>Bioinformatics</i> , 2019, 35, 5379-5381.	4.1	12
36	Absence of an embryonic stem cell DNA methylation signature in human cancer. <i>BMC Cancer</i> , 2019, 19, 711.	2.6	6

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37	Systematic evaluation and validation of reference and library selection methods for deconvolution of cord blood DNA methylation data. <i>Clinical Epigenetics</i> , 2019, 11, 125.	4.1	107
38	Molecular and epigenetic profiles of BRCA1-like hormone-receptor-positive breast tumors identified with development and application of a copy-number-based classifier. <i>Breast Cancer Research</i> , 2019, 21, 14.	5.0	5
39	DNA methylation aging clocks: challenges and recommendations. <i>Genome Biology</i> , 2019, 20, 249.	8.8	552
40	Maternal swimming pool exposure during pregnancy in relation to birth outcomes and cord blood DNA methylation among private well users. <i>Environment International</i> , 2019, 123, 459-466.	10.0	10
41	DNA Methylation Changes in Regional Lung Macrophages Are Associated with Metabolic Differences. <i>ImmunoHorizons</i> , 2019, 3, 274-281.	1.8	33
42	Genome-wide DNA methylation profiling shows a distinct epigenetic signature associated with lung macrophages in cystic fibrosis. <i>Clinical Epigenetics</i> , 2018, 10, 152.	4.1	28
43	Smoking and Other Risk Factors in Individuals With Synchronous Conventional High-Risk Adenomas and Clinically Significant Serrated Polyps. <i>American Journal of Gastroenterology</i> , 2018, 113, 1828-1835.	0.4	27
44	Tracing human stem cell lineage during development using DNA methylation. <i>Genome Research</i> , 2018, 28, 1285-1295.	5.5	27
45	An optimized library for reference-based deconvolution of whole-blood biospecimens assayed using the Illumina HumanMethylationEPIC BeadArray. <i>Genome Biology</i> , 2018, 19, 64.	8.8	245
46	Pan-Cancer Analysis Reveals Differential Susceptibility of Bidirectional Gene Promoters to DNA Methylation, Somatic Mutations, and Copy Number Alterations. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2296.	4.1	15
47	A New Dimension of Breast Cancer Epigenetics - Applications of Variational Autoencoders with DNA Methylation. , 2018, , .		12
48	Immunomethylomic approach to explore the blood neutrophil lymphocyte ratio (NLR) in glioma survival. <i>Clinical Epigenetics</i> , 2017, 9, 10.	4.1	60
49	Integrative epigenetic and genetic pan-cancer somatic alteration portraits. <i>Epigenetics</i> , 2017, 12, 561-574.	2.7	18
50	DNA Methylation-Derived Neutrophil-to-Lymphocyte Ratio: An Epigenetic Tool to Explore Cancer Inflammation and Outcomes. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017, 26, 328-338.	2.5	62
51	Deconvolution of DNA methylation identifies differentially methylated gene regions on 1p36 across breast cancer subtypes. <i>Scientific Reports</i> , 2017, 7, 11594.	3.3	20
52	Cell-type deconvolution from DNA methylation: a review of recent applications. <i>Human Molecular Genetics</i> , 2017, 26, R216-R224.	2.9	153
53	Concordance of DNA methylation profiles between breast core biopsy and surgical excision specimens containing ductal carcinoma in situ (DCIS). <i>Experimental and Molecular Pathology</i> , 2017, 103, 78-83.	2.1	5
54	Normal breast tissue DNA methylation differences at regulatory elements are associated with the cancer risk factor age. <i>Breast Cancer Research</i> , 2017, 19, 81.	5.0	66

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55	Refractory testicular germ cell tumors are highly sensitive to the second generation DNA methylation inhibitor guadecitabine. <i>Oncotarget</i> , 2017, 8, 2949-2959.	1.8	57
56	Epigenetic and genetic burden measures are associated with tumor characteristics in invasive breast carcinoma. <i>Epigenetics</i> , 2016, 11, 344-353.	2.7	14
57	OxyBS: estimation of 5-methylcytosine and 5-hydroxymethylcytosine from tandem-treated oxidative bisulfite and bisulfite DNA. <i>Bioinformatics</i> , 2016, 32, 2505-2507.	4.1	33
58	Hydroxymethylation is uniquely distributed within term placenta, and is associated with gene expression. <i>FASEB Journal</i> , 2016, 30, 2874-2884.	0.5	38
59	5-Hydroxymethylcytosine localizes to enhancer elements and is associated with survival in glioblastoma patients. <i>Nature Communications</i> , 2016, 7, 13177.	12.8	102
60	A new timepiece: an epigenetic mitotic clock. <i>Genome Biology</i> , 2016, 17, 216.	8.8	8
61	Improving cell mixture deconvolution by identifying optimal DNA methylation libraries (IDOL). <i>BMC Bioinformatics</i> , 2016, 17, 120.	2.6	142
62	Deficiency of mitochondrial modulator MCJ promotes chemoresistance in breast cancer. <i>JCI Insight</i> , 2016, 1, .	5.0	16
63	DNA methylation in ductal carcinoma in situ related with future development of invasive breast cancer. <i>Clinical Epigenetics</i> , 2015, 7, 75.	4.1	49
64	A Coding Variant in TMC8 (EVER2) Is Associated with High Risk HPV Infection and Head and Neck Cancer Risk. <i>PLoS ONE</i> , 2015, 10, e0123716.	2.5	9
65	RNASL and MIR146A SNP-SNP Interaction as a Susceptibility Factor for Non-Melanoma Skin Cancer. <i>PLoS ONE</i> , 2014, 9, e93602.	2.5	18
66	Leukocyte-adjusted epigenome-wide association studies of blood from solid tumor patients. <i>Epigenetics</i> , 2014, 9, 884-895.	2.7	35
67	Genome-wide DNA methylation profiles in progression to in situ and invasive carcinoma of the breast with impact on gene transcription and prognosis. <i>Genome Biology</i> , 2014, 15, 435.	8.8	147
68	Age-related DNA methylation in normal breast tissue and its relationship with invasive breast tumor methylation. <i>Epigenetics</i> , 2014, 9, 268-275.	2.7	67
69	Genome-wide DNA methylation profiles in progression to. <i>Genome Biology</i> , 2014, 15, 435.	9.6	105
70	A recursively partitioned mixture model for clustering time-course gene expression data. <i>Translational Cancer Research</i> , 2014, 3, 217-232.	1.0	4
71	Recursively partitioned mixture model clustering of DNA methylation data using biologically informed correlation structures. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2013, 12, 225-40.	0.6	13
72	Blood-based profiles of DNA methylation predict the underlying distribution of cell types. <i>Epigenetics</i> , 2013, 8, 816-826.	2.7	213

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73	DNA methylation arrays as surrogate measures of cell mixture distribution. BMC Bioinformatics, 2012, 13, 86.	2.6	2,563
74	Peripheral blood DNA methylation profiles are indicative of head and neck squamous cell carcinoma: An epigenome-wide association study. Epigenetics, 2012, 7, 291-299.	2.7	84
75	Acute Hypersensitivity of Pluripotent Testicular Cancer-Derived Embryonal Carcinoma to Low-Dose 5-Aza Deoxycytidine Is Associated with Global DNA Damage-Associated p53 Activation, Anti-Pluripotency and DNA Demethylation. PLoS ONE, 2012, 7, e53003.	2.5	49
76	Analgesic and nonsteroidal anti-inflammatory use in relation to nonmelanoma skin cancer: A population-based case-control study. Journal of the American Academy of Dermatology, 2011, 65, 304-312.	1.2	30
77	DNA Methylation, Isocitrate Dehydrogenase Mutation, and Survival in Glioma. Journal of the National Cancer Institute, 2011, 103, 143-153.	6.3	224
78	Mature MicroRNA Sequence Polymorphism in <i>MIR196A2</i> Is Associated with Risk and Prognosis of Head and Neck Cancer. Clinical Cancer Research, 2010, 16, 3713-3720.	7.0	122
79	Integrated Profiling Reveals a Global Correlation between Epigenetic and Genetic Alterations in Mesothelioma. Cancer Research, 2010, 70, 5686-5694.	0.9	50
80	Breast Cancer DNA Methylation Profiles Are Associated with Tumor Size and Alcohol and Folate Intake. PLoS Genetics, 2010, 6, e1001043.	3.5	149
81	A let-7 microRNA-binding site polymorphism in the KRAS 3' UTR is associated with reduced survival in oral cancers. Carcinogenesis, 2009, 30, 1003-1007.	2.8	185
82	Copy number variation has little impact on bead-array-based measures of DNA methylation. Bioinformatics, 2009, 25, 1999-2005.	4.1	34
83	Ageing and Environmental Exposures Alter Tissue-Specific DNA Methylation Dependent upon CpG Island Context. PLoS Genetics, 2009, 5, e1000602.	3.5	931
84	Smoking modifies the relationship between <i>XRCC1</i> haplotypes and HPV16-negative head and neck squamous cell carcinoma. International Journal of Cancer, 2009, 124, 2690-2696.	5.1	31
85	Model-based clustering of DNA methylation array data: a recursive-partitioning algorithm for high-dimensional data arising as a mixture of beta distributions. BMC Bioinformatics, 2008, 9, 365.	2.6	171