

Pei-Fen Kuan

List of Publications by Year in descending order

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Version: 2024-02-01

62
papers

3,580
citations

212478

28
h-index

169272

56
g-index

64
all docs

64
docs citations

64
times ranked

9338
citing authors

#	ARTICLE	IF	CITATIONS
1	Polygenic prediction of PTSD trajectories in 9/11 responders. <i>Psychological Medicine</i> , 2022, 52, 1981-1989.	2.7	18
2	Characterization of the CpG Island Hypermethylated Phenotype Subclass in Primary Melanomas. <i>Journal of Investigative Dermatology</i> , 2022, 142, 1869-1881.e10.	0.3	5
3	Efficient gradient boosting for prognostic biomarker discovery. <i>Bioinformatics</i> , 2022, 38, 1631-1638.	1.8	13
4	Early fish domestication affects methylation of key genes involved in the rapid onset of the farmed phenotype. <i>Epigenetics</i> , 2022, 17, 1281-1298.	1.3	10
5	Reduced cerebellar cortical thickness in World Trade Center responders with cognitive impairment. <i>Translational Psychiatry</i> , 2022, 12, 107.	2.4	8
6	Metabolomics analysis of post-traumatic stress disorder symptoms in World Trade Center responders. <i>Translational Psychiatry</i> , 2022, 12, 174.	2.4	3
7	Transformation based on likelihood ratio. <i>Statistical Methods in Medical Research</i> , 2021, 30, 354-356.	0.7	2
8	Mapping the transcriptomics landscape of post-traumatic stress disorder symptom dimensions in World Trade Center responders. <i>Translational Psychiatry</i> , 2021, 11, 310.	2.4	3
9	PTSD is associated with accelerated transcriptional aging in World Trade Center responders. <i>Translational Psychiatry</i> , 2021, 11, 311.	2.4	15
10	Fenchel duality of Cox partial likelihood with an application in survival kernel learning. <i>Artificial Intelligence in Medicine</i> , 2021, 116, 102077.	3.8	4
11	A deep learning approach for monitoring parietal-dominant Alzheimer's disease in World Trade Center responders at midlife. <i>Brain Communications</i> , 2021, 3, fcab145.	1.5	4
12	The Association of Posttraumatic Stress Disorder With Longitudinal Change in Glomerular Filtration Rate in World Trade Center Responders. <i>Psychosomatic Medicine</i> , 2021, 83, 978-986.	1.3	5
13	Non-monotone transformation of biomarkers to improve diagnostic and screening accuracy in a DNA methylation study with trichotomous phenotypes. <i>Statistical Methods in Medical Research</i> , 2020, 29, 2360-2389.	0.7	2
14	Epigenome-wide meta-analysis of PTSD across 10 military and civilian cohorts identifies methylation changes in AHRH. <i>Nature Communications</i> , 2020, 11, 5965.	5.8	84
15	Molecular linkage between post-traumatic stress disorder and cognitive impairment: a targeted proteomics study of World Trade Center responders. <i>Translational Psychiatry</i> , 2020, 10, 269.	2.4	19
16	RNAAgeCalc: A multi-tissue transcriptional age calculator. <i>PLoS ONE</i> , 2020, 15, e0237006.	1.1	40
17	Negative binomial additive model for RNA-Seq data analysis. <i>BMC Bioinformatics</i> , 2020, 21, 171.	1.2	18
18	Quantitative decision-making in randomized Phase II studies with a time-to-event endpoint. <i>Journal of Biopharmaceutical Statistics</i> , 2019, 29, 189-202.	0.4	1

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19	Cell type-specific gene expression patterns associated with posttraumatic stress disorder in World Trade Center responders. <i>Translational Psychiatry</i> , 2019, 9, 1.	2.4	383
20	Identification of a Robust Methylation Classifier for Cutaneous Melanoma Diagnosis. <i>Journal of Investigative Dermatology</i> , 2019, 139, 1349-1361.	0.3	23
21	Epigenetic Biomarkers Of PTSD: Updates From The EWAS Working Group of The PTSD PGC. <i>European Neuropsychopharmacology</i> , 2019, 29, S750.	0.3	2
22	Utility of TERT Promoter Mutations for Cutaneous Primary Melanoma Diagnosis. <i>American Journal of Dermatopathology</i> , 2019, 41, 264-272.	0.3	29
23	methylGSA: a Bioconductor package and Shiny app for DNA methylation data length bias adjustment in gene set testing. <i>Bioinformatics</i> , 2019, 35, 1958-1959.	1.8	120
24	Comparison of the restricted mean survival time with the hazard ratio in superiority trials with a time-to-event end point. <i>Pharmaceutical Statistics</i> , 2018, 17, 202-213.	0.7	58
25	A Guide to Illumina BeadChip Data Analysis. <i>Methods in Molecular Biology</i> , 2018, 1708, 303-330.	0.4	23
26	Epigenetic meta-analysis across three civilian cohorts identifies <i>NRG1</i> and <i>HGS</i> as blood-based biomarkers for post-traumatic stress disorder. <i>Epigenomics</i> , 2018, 10, 1585-1601.	1.0	39
27	A systematic evaluation of nucleotide properties for CRISPR sgRNA design. <i>BMC Bioinformatics</i> , 2017, 18, 297.	1.2	29
28	Breast tumor DNA methylation patterns associated with smoking in the Carolina Breast Cancer Study. <i>Breast Cancer Research and Treatment</i> , 2017, 163, 349-361.	1.1	15
29	methylDMV: SIMULTANEOUS DETECTION OF DIFFERENTIAL DNA METHYLATION AND VARIABILITY WITH CONFOUNDER ADJUSTMENT. , 2017, 22, 461-472.		2
30	An aberrant NOTCH2-BCR signaling axis in B cells from patients with chronic GVHD. <i>Blood</i> , 2017, 130, 2131-2145.	0.6	37
31	Epigenome-wide association of PTSD from heterogeneous cohorts with a common multi-site analysis pipeline. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2017, 174, 619-630.	1.1	69
32	904. DNA Methylation Associated with PTSD and Depression in World Trade Center Responders: An Epigenome-Wide Study. <i>Biological Psychiatry</i> , 2017, 81, S365.	0.7	2
33	Gene expression associated with PTSD in World Trade Center responders: An RNA sequencing study. <i>Translational Psychiatry</i> , 2017, 7, 1297.	2.4	61
34	IsoDOT Detects Differential RNA-Isoform Expression/Usage With Respect to a Categorical or Continuous Covariate With High Sensitivity and Specificity. <i>Journal of the American Statistical Association</i> , 2015, 110, 975-986.	1.8	10
35	IL2 Inducible T-cell Kinase, a Novel Therapeutic Target in Melanoma. <i>Clinical Cancer Research</i> , 2015, 21, 2167-2176.	3.2	16
36	Racial Variation in Breast Tumor Promoter Methylation in the Carolina Breast Cancer Study. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 921-930.	1.1	41

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37	A systematic assessment of normalization approaches for the Infinium 450K methylation platform. <i>Epigenetics</i> , 2014, 9, 318-329.	1.3	61
38	Covariate adjusted differential variability analysis of DNA methylation with propensity score method. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2014, 13, 645-58.	0.2	0
39	Variation in chromatin accessibility in human kidney cancer links H3K36 methyltransferase loss with widespread RNA processing defects. <i>Genome Research</i> , 2014, 24, 241-250.	2.4	160
40	The Cav ¹ 21a subunit regulates gene expression and suppresses myogenin in muscle progenitor cells. <i>Journal of Cell Biology</i> , 2014, 205, 829-846.	2.3	16
41	Multivariate Boosting for Integrative Analysis of High-Dimensional Cancer Genomic Data. <i>Cancer Informatics</i> , 2014, 13s7, CIN.S16353.	0.9	2
42	Propensity Score Method for Partially Matched Omics Studies. <i>Cancer Informatics</i> , 2014, 13s7, CIN.S16352.	0.9	24
43	Time-Event continual reassessment method incorporating treatment cycle information with application to an oncology phase I trial. <i>Biometrical Journal</i> , 2014, 56, 933-946.	0.6	20
44	The Role of Ect2 Nuclear RhoGEF Activity in Ovarian Cancer Cell Transformation. <i>Genes and Cancer</i> , 2013, 4, 460-475.	0.6	51
45	A simple and robust method for partially matched samples using the <i>p</i> -values pooling approach. <i>Statistics in Medicine</i> , 2013, 32, 3247-3259.	0.8	15
46	DiffSplice: the genome-wide detection of differential splicing events with RNA-seq. <i>Nucleic Acids Research</i> , 2013, 41, e39-e39.	6.5	138
47	MERTK receptor tyrosine kinase is a therapeutic target in melanoma. <i>Journal of Clinical Investigation</i> , 2013, 123, 2257-2267.	3.9	124
48	Application of Multiplexed Kinase Inhibitor Beads to Study Kinome Adaptations in Drug-Resistant Leukemia. <i>PLoS ONE</i> , 2013, 8, e66755.	1.1	60
49	HIF ¹ and HIF ² independently activate SRC to promote melanoma metastases. <i>Journal of Clinical Investigation</i> , 2013, 123, 2078-2093.	3.9	132
50	High-Throughput Immunoglobulin Heavy Chain Variable Region Repertoire Analysis Of CD27+ B Cell Subsets From Patients With Chronic Gvhd. <i>Blood</i> , 2013, 122, 2055-2055.	0.6	2
51	Dynamic Changes in Nucleosome Occupancy Are Not Predictive of Gene Expression Dynamics but Are Linked to Transcription and Chromatin Regulators. <i>Molecular and Cellular Biology</i> , 2012, 32, 1645-1653.	1.1	57
52	Dynamic Reprogramming of the Kinome in Response to Targeted MEK Inhibition in Triple-Negative Breast Cancer. <i>Cell</i> , 2012, 149, 307-321.	13.5	637
53	Metabolomic Profiling Reveals Mitochondrial-Derived Lipid Biomarkers That Drive Obesity-Associated Inflammation. <i>PLoS ONE</i> , 2012, 7, e38812.	1.1	111
54	Integrating Prior Knowledge in Multiple Testing under Dependence with Applications to Detecting Differential DNA Methylation. <i>Biometrics</i> , 2012, 68, 774-783.	0.8	35

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55	RhoGDI2 antagonizes ovarian carcinoma growth, invasion and metastasis. <i>Small GTPases</i> , 2011, 2, 202-210.	0.7	32
56	A Statistical Framework for the Analysis of ChIP-Seq Data. <i>Journal of the American Statistical Association</i> , 2011, 106, 891-903.	1.8	100
57	Discovering Transcription Factor Binding Sites in Highly Repetitive Regions of Genomes with Multi-Read Analysis of ChIP-Seq Data. <i>PLoS Computational Biology</i> , 2011, 7, e1002111.	1.5	73
58	A statistical framework for Illumina DNA methylation arrays. <i>Bioinformatics</i> , 2010, 26, 2849-2855.	1.8	86
59	Rho directs widespread termination of intragenic and stable RNA transcription. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 15406-15411.	3.3	192
60	Median Absolute Deviation to Improve Hit Selection for Genome-Scale RNAi Screens. <i>Journal of Biomolecular Screening</i> , 2008, 13, 149-158.	2.6	163
61	A study of the relationships between oligonucleotide properties and hybridization signal intensities from NimbleGen microarray datasets. <i>Nucleic Acids Research</i> , 2008, 36, 2926-2938.	6.5	38
62	Hit selection with false discovery rate control in genome-scale RNAi screens. <i>Nucleic Acids Research</i> , 2008, 36, 4667-4679.	6.5	32