Pei-Fen Kuan

List of Publications by Year
in descending order

62 papers	3,580 citations	186265 28 h-index	149698 56 g-index
64 all docs	64 docs citations	64 times ranked	8394 citing authors

#	Article	IF	Citations
1	Polygenic prediction of PTSD trajectories in 9/11 responders. Psychological Medicine, 2022, 52, 1981-1989.	4.5	18
2	Characterization of the CpG Island Hypermethylated Phenotype Subclass in Primary Melanomas. Journal of Investigative Dermatology, 2022, 142, 1869-1881.e10.	0.7	5
3	Efficient gradient boosting for prognostic biomarker discovery. Bioinformatics, 2022, 38, 1631-1638.	4.1	13
4	Early fish domestication affects methylation of key genes involved in the rapid onset of the farmed phenotype. Epigenetics, 2022, 17, 1281-1298.	2.7	10
5	Reduced cerebellar cortical thickness in World Trade Center responders with cognitive impairment. Translational Psychiatry, 2022, 12, 107.	4.8	8
6	Metabolomics analysis of post-traumatic stress disorder symptoms in World Trade Center responders. Translational Psychiatry, 2022, 12, 174.	4.8	3
7	Transformation based on likelihood ratio. Statistical Methods in Medical Research, 2021, 30, 354-356.	1.5	2
8	Mapping the transcriptomics landscape of post-traumatic stress disorder symptom dimensions in World Trade Center responders. Translational Psychiatry, 2021, 11, 310.	4.8	3
9	PTSD is associated with accelerated transcriptional aging in World Trade Center responders. Translational Psychiatry, 2021, 11, 311.	4.8	15
10	Fenchel duality of Cox partial likelihood with an application in survival kernel learning. Artificial Intelligence in Medicine, 2021, 116, 102077.	6.5	4
11	A deep learning approach for monitoring parietal-dominant Alzheimer's disease in World Trade Center responders at midlife. Brain Communications, 2021, 3, fcab145.	3.3	4
12	The Association of Posttraumatic Stress Disorder With Longitudinal Change in Glomerular Filtration Rate in World Trade Center Responders. Psychosomatic Medicine, 2021, 83, 978-986.	2.0	5
13	Non-monotone transformation of biomarkers to improve diagnostic and screening accuracy in a DNA methylation study with trichotomous phenotypes. Statistical Methods in Medical Research, 2020, 29, 2360-2389.	1.5	2
14	Epigenome-wide meta-analysis of PTSD across 10 military and civilian cohorts identifies methylation changes in AHRR. Nature Communications, 2020, 11, 5965.	12.8	84
15	Molecular linkage between post-traumatic stress disorder and cognitive impairment: a targeted proteomics study of World Trade Center responders. Translational Psychiatry, 2020, 10, 269.	4.8	19
16	RNAAgeCalc: A multi-tissue transcriptional age calculator. PLoS ONE, 2020, 15, e0237006.	2.5	40
17	Negative binomial additive model for RNA-Seq data analysis. BMC Bioinformatics, 2020, 21, 171.	2.6	18
18	Quantitative decision-making in randomized Phase II studies with a time-to-event endpoint. Journal of Biopharmaceutical Statistics, 2019, 29, 189-202.	0.8	1

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19	Cell type-specific gene expression patterns associated with posttraumatic stress disorder in World Trade Center responders. Translational Psychiatry, 2019, 9, 1.	4.8	383
20	Identification of a Robust Methylation Classifier for Cutaneous Melanoma Diagnosis. Journal of Investigative Dermatology, 2019, 139, 1349-1361.	0.7	23
21	Epigenetic Biomarkers Of PTSD: Updates From The EWAS Working Group of The PTSD PGC. European Neuropsychopharmacology, 2019, 29, S750.	0.7	2
22	Utility of TERT Promoter Mutations for Cutaneous Primary Melanoma Diagnosis. American Journal of Dermatopathology, 2019, 41, 264-272.	0.6	29
23	methylGSA: a Bioconductor package and Shiny app for DNA methylation data length bias adjustment in gene set testing. Bioinformatics, 2019, 35, 1958-1959.	4.1	120
24	Comparison of the restricted mean survival time with the hazard ratio in superiority trials with a timeâ€toâ€event end point. Pharmaceutical Statistics, 2018, 17, 202-213.	1.3	58
25	A Guide to Illumina BeadChip Data Analysis. Methods in Molecular Biology, 2018, 1708, 303-330.	0.9	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. Epigenomics, 2018, 10, 1585-1601.	2.1	39
27	A systematic evaluation of nucleotide properties for CRISPR sgRNA design. BMC Bioinformatics, 2017, 18, 297.	2.6	29
28	Breast tumor DNA methylation patterns associated with smoking in the Carolina Breast Cancer Study. Breast Cancer Research and Treatment, 2017, 163, 349-361.	2.5	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. Blood, 2017, 130, 2131-2145.	1.4	37
31	Epigenomeâ€wide association of PTSD from heterogeneous cohorts with a common multiâ€site analysis pipeline. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2017, 174, 619-630.	1.7	69
32	904. DNA Methylation Associated with PTSD and Depression in World Trade Center Responders: An Epigenome-Wide Study. Biological Psychiatry, 2017, 81, S365.	1.3	2
33	Gene expression associated with PTSD in World Trade Center responders: An RNA sequencing study. Translational Psychiatry, 2017, 7, 1297.	4.8	61
34	IsoDOT Detects Differential RNA-Isoform Expression/Usage With Respect to a Categorical or Continuous Covariate With High Sensitivity and Specificity. Journal of the American Statistical Association, 2015, 110, 975-986.	3.1	10
35	IL2 Inducible T-cell Kinase, a Novel Therapeutic Target in Melanoma. Clinical Cancer Research, 2015, 21, 2167-2176.	7.0	16
36	Racial Variation in Breast Tumor Promoter Methylation in the Carolina Breast Cancer Study. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 921-930.	2.5	41

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37	A systematic assessment of normalization approaches for the Infinium 450K methylation platform. Epigenetics, 2014, 9, 318-329.	2.7	61
38	Covariate adjusted differential variability analysis of DNA methylation with propensity score method. Statistical Applications in Genetics and Molecular Biology, 2014, 13, 645-58.	0.6	0
39	Variation in chromatin accessibility in human kidney cancer links H3K36 methyltransferase loss with widespread RNA processing defects. Genome Research, 2014, 24, 241-250.	5.5	160
40	The CavÎ²1a subunit regulates gene expression and suppresses myogenin in muscle progenitor cells. Journal of Cell Biology, 2014, 205, 829-846.	5.2	16
41	Multivariate Boosting for Integrative Analysis of High-Dimensional Cancer Genomic Data. Cancer Informatics, 2014, 13s7, CIN.S16353.	1.9	2
42	Propensity Score Method for Partially Matched Omics Studies. Cancer Informatics, 2014, 13s7, CIN.S16352.	1.9	24
43	Timeâ€toâ€event continual reassessment method incorporating treatment cycle information with application to an oncology phase I trial. Biometrical Journal, 2014, 56, 933-946.	1.0	20
44	The Role of Ect2 Nuclear RhoGEF Activity in Ovarian Cancer Cell Transformation. Genes and Cancer, 2013, 4, 460-475.	1.9	51
45	A simple and robust method for partially matched samples using the pâ€values pooling approach. Statistics in Medicine, 2013, 32, 3247-3259.	1.6	15
46	DiffSplice: the genome-wide detection of differential splicing events with RNA-seq. Nucleic Acids Research, 2013, 41, e39-e39.	14.5	138
47	MERTK receptor tyrosine kinase is a therapeutic target in melanoma. Journal of Clinical Investigation, 2013, 123, 2257-2267.	8.2	124
48	Application of Multiplexed Kinase Inhibitor Beads to Study Kinome Adaptations in Drug-Resistant Leukemia. PLoS ONE, 2013, 8, e66755.	2.5	60
49	HIF1Î± and HIF2Î± independently activate SRC to promote melanoma metastases. Journal of Clinical Investigation, 2013, 123, 2078-2093.	8.2	132
50	High-Throughput Immunoglobulin Heavy Chain Variable Region Repertoire Analysis Of CD27+ B Cell Subsets From Patients With Chronic Gvhd. Blood, 2013, 122, 2055-2055.	1.4	2
51	Dynamic Changes in Nucleosome Occupancy Are Not Predictive of Gene Expression Dynamics but Are Linked to Transcription and Chromatin Regulators. Molecular and Cellular Biology, 2012, 32, 1645-1653.	2.3	57
52	Dynamic Reprogramming of the Kinome in Response to Targeted MEK Inhibition in Triple-Negative Breast Cancer. Cell, 2012, 149, 307-321.	28.9	637
53	Metabolomic Profiling Reveals Mitochondrial-Derived Lipid Biomarkers That Drive Obesity-Associated Inflammation. PLoS ONE, 2012, 7, e38812.	2.5	111
54	Integrating Prior Knowledge in Multiple Testing under Dependence with Applications to Detecting Differential DNA Methylation. Biometrics, 2012, 68, 774-783.	1.4	35

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55	RhoGDI2 antagonizes ovarian carcinoma growth, invasion and metastasis. Small GTPases, 2011, 2, 202-210.	1.6	32
56	A Statistical Framework for the Analysis of ChIP-Seq Data. Journal of the American Statistical Association, 2011, 106, 891-903.	3.1	100
57	Discovering Transcription Factor Binding Sites in Highly Repetitive Regions of Genomes with Multi-Read Analysis of ChIP-Seq Data. PLoS Computational Biology, 2011, 7, e1002111.	3.2	73
58	A statistical framework for Illumina DNA methylation arrays. Bioinformatics, 2010, 26, 2849-2855.	4.1	86
59	Rho directs widespread termination of intragenic and stable RNA transcription. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 15406-15411.	7.1	192
60	Median Absolute Deviation to Improve Hit Selection for Genome-Scale RNAi Screens. Journal of Biomolecular Screening, 2008, 13, 149-158.	2.6	163
61	A study of the relationships between oligonucleotide properties and hybridization signal intensities from NimbleGen microarray datasets. Nucleic Acids Research, 2008, 36, 2926-2938.	14.5	38
62	Hit selection with false discovery rate control in genome-scale RNAi screens. Nucleic Acids Research, 2008, 36, 4667-4679.	14.5	32