

Chi Wang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1909079/publications.pdf>

Version: 2024-02-01

58
papers

1,658
citations

430442

18
h-index

301761

39
g-index

59
all docs

59
docs citations

59
times ranked

3403
citing authors

#	ARTICLE	IF	CITATIONS
1	Disrupting the Interaction of BRD4 with Diacetylated Twist Suppresses Tumorigenesis in Basal-like Breast Cancer. <i>Cancer Cell</i> , 2014, 25, 210-225.	7.7	401
2	A new shrinkage estimator for dispersion improves differential expression detection in RNA-seq data. <i>Biostatistics</i> , 2013, 14, 232-243.	0.9	210
3	Dub3 inhibition suppresses breast cancer invasion and metastasis by promoting Snail1 degradation. <i>Nature Communications</i> , 2017, 8, 14228.	5.8	101
4	NanoStringDiff: a novel statistical method for differential expression analysis based on NanoString nCounter data. <i>Nucleic Acids Research</i> , 2016, 44, gkw677.	6.5	100
5	Bayesian Effect Estimation Accounting for Adjustment Uncertainty. <i>Biometrics</i> , 2012, 68, 661-671.	0.8	84
6	Exosomal lipids for classifying early and late stage non-small cell lung cancer. <i>Analytica Chimica Acta</i> , 2018, 1037, 256-264.	2.6	72
7	Targeting the BRD4/FOXO3a/CDK6 axis sensitizes AKT inhibition in luminal breast cancer. <i>Nature Communications</i> , 2018, 9, 5200.	5.8	71
8	Autophagy Inhibition by Sustained Overproduction of IL6 Contributes to Arsenic Carcinogenesis. <i>Cancer Research</i> , 2014, 74, 3740-3752.	0.4	66
9	Spermine synthase and MYC cooperate to maintain colorectal cancer cell survival by repressing Bim expression. <i>Nature Communications</i> , 2020, 11, 3243.	5.8	55
10	A novel statistical method for quantitative comparison of multiple ChIP-seq datasets. <i>Bioinformatics</i> , 2015, 31, 1889-1896.	1.8	48
11	c-Abl and Arg induce cathepsin-mediated lysosomal degradation of the NM23-H1 metastasis suppressor in invasive cancer. <i>Oncogene</i> , 2014, 33, 4508-4520.	2.6	36
12	Accounting for uncertainty in confounder and effect modifier selection when estimating average causal effects in generalized linear models. <i>Biometrics</i> , 2015, 71, 654-665.	0.8	33
13	Novel Pharmacologic Targeting of Tight Junctions and Focal Adhesions in Prostate Cancer Cells. <i>PLoS ONE</i> , 2014, 9, e86238.	1.1	32
14	Snail determines the therapeutic response to mTOR kinase inhibitors by transcriptional repression of 4E-BP1. <i>Nature Communications</i> , 2017, 8, 2207.	5.8	27
15	Improved workflow for mass spectrometry-based metabolomics analysis of the heart. <i>Journal of Biological Chemistry</i> , 2020, 295, 2676-2686.	1.6	26
16	Test on existence of histology subtype-specific prognostic signatures among early stage lung adenocarcinoma and squamous cell carcinoma patients using a Cox-model based filter. <i>Biology Direct</i> , 2015, 10, 15.	1.9	25
17	Simultaneous quantitation of oxidized and reduced glutathione via LC-MS/MS: An insight into the redox state of hematopoietic stem cells. <i>Free Radical Biology and Medicine</i> , 2016, 97, 85-94.	1.3	24
18	Combating acquired resistance to MAPK inhibitors in melanoma by targeting Abl1/2-mediated reactivation of MEK/ERK/MYC signaling. <i>Nature Communications</i> , 2020, 11, 5463.	5.8	24

#	ARTICLE	IF	CITATIONS
19	Loss of Multidrug Resistance-associated Protein 1 Potentiates Chronic Doxorubicin-Induced Cardiac Dysfunction in Mice. <i>Journal of Pharmacology and Experimental Therapeutics</i> , 2015, 355, 280-287.	1.3	19
20	Elevated Glutathione Is Not Sufficient to Protect against Doxorubicin-Induced Nuclear Damage in Heart in Multidrug Resistance-associated Protein 1 (Mrp1/Abcc1) Null Mice. <i>Journal of Pharmacology and Experimental Therapeutics</i> , 2015, 355, 272-279.	1.3	18
21	EZH2 inhibition confers PIK3CA-driven lung tumors enhanced sensitivity to PI3K inhibition. <i>Cancer Letters</i> , 2022, 524, 151-160.	3.2	15
22	Weighted-SAMGSR: combining significance analysis of microarray-gene set reduction algorithm with pathway topology-based weights to select relevant genes. <i>Biology Direct</i> , 2016, 11, 50.	1.9	14
23	Cellular Origins of EGFR-driven Lung Cancer Cells Determine Sensitivity to Therapy. <i>Advanced Science</i> , 2021, 8, e2101999.	5.6	13
24	Incorporating Pathway Information into Feature Selection towards Better Performed Gene Signatures. <i>BioMed Research International</i> , 2019, 2019, 1-12.	0.9	12
25	Multi-TGDR, a multi-class regularization method, identifies the metabolic profiles of hepatocellular carcinoma and cirrhosis infected with hepatitis B or hepatitis C virus. <i>BMC Bioinformatics</i> , 2014, 15, 97.	1.2	10
26	DACH1 mutation frequency in endometrial cancer is associated with high tumor mutation burden. <i>PLoS ONE</i> , 2020, 15, e0244558.	1.1	10
27	Exponential tilt models for two-group comparison with censored data. <i>Journal of Statistical Planning and Inference</i> , 2011, 141, 1102-1117.	0.4	9
28	Identification of prognostic genes and gene sets for early-stage non-small cell lung cancer using bi-level selection methods. <i>Scientific Reports</i> , 2017, 7, 46164.	1.6	9
29	Predictive value of phenotypic signatures of bladder cancer response to cisplatin-based neoadjuvant chemotherapy. <i>Urologic Oncology: Seminars and Original Investigations</i> , 2019, 37, 572.e1-572.e11.	0.8	9
30	BRD4 modulates vulnerability of triple-negative breast cancer to targeting of integrin-dependent signaling pathways. <i>Cellular Oncology (Dordrecht)</i> , 2020, 43, 1049-1066.	2.1	9
31	Lapatinib and poziotinib overcome ABCB1-mediated paclitaxel resistance in ovarian cancer. <i>PLoS ONE</i> , 2021, 16, e0254205.	1.1	9
32	Genome-wide DNA methylation profiling in human breast tissue by Illumina TruSeq methyl capture EPIC sequencing and infinium methylation EPIC beadchip microarray. <i>Epigenetics</i> , 2021, 16, 754-769.	1.3	8
33	MEScan: a powerful statistical framework for genome-scale mutual exclusivity analysis of cancer mutations. <i>Bioinformatics</i> , 2021, 37, 1189-1197.	1.8	7
34	A longitudinal feature selection method identifies relevant genes to distinguish complicated injury and uncomplicated injury over time. <i>BMC Medical Informatics and Decision Making</i> , 2018, 18, 115.	1.5	5
35	Characterization of Squamous Cell Lung Cancers from Appalachian Kentucky. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019, 28, 348-356.	1.1	5
36	SDA: a semi-parametric differential abundance analysis method for metabolomics and proteomics data. <i>BMC Bioinformatics</i> , 2019, 20, 501.	1.2	4

#	ARTICLE	IF	CITATIONS
37	A Prognostic Model to Predict Recovery of COVID-19 Patients Based on Longitudinal Laboratory Findings. <i>Virologica Sinica</i> , 2020, 35, 811-819.	1.2	4
38	The cox-filter method identifies respective subtype-specific lncRNA prognostic signatures for two human cancers. <i>BMC Medical Genomics</i> , 2020, 13, 18.	0.7	4
39	Mitochondrial superoxide targets energy metabolism to modulate epigenetic regulation of NRF2-mediated transcription. <i>Free Radical Biology and Medicine</i> , 2022, 179, 181-189.	1.3	4
40	EBF1 promotes triple-negative breast cancer progression by surveillance of the HIF1 α pathway. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	4
41	Rejoinder: Bayesian Effect Estimation Accounting for Adjustment Uncertainty. <i>Biometrics</i> , 2012, 68, 680-686.	0.8	3
42	Feature Selection for Longitudinal Data by Using Sign Averages to Summarize Gene Expression Values over Time. <i>BioMed Research International</i> , 2019, 2019, 1-12.	0.9	3
43	To select relevant features for longitudinal gene expression data by extending a pathway analysis method. <i>F1000Research</i> , 2018, 7, 1166.	0.8	3
44	A Review on Differential Abundance Analysis Methods for Mass Spectrometry-Based Metabolomic Data. <i>Metabolites</i> , 2022, 12, 305.	1.3	3
45	Differential Abundance Analysis with Bayes Shrinkage Estimation of Variance (DASEV) for Zero-Inflated Proteomic and Metabolomic Data. <i>Scientific Reports</i> , 2020, 10, 876.	1.6	2
46	An ensemble of the iCluster method to analyze longitudinal lncRNA expression data for psoriasis patients. <i>Human Genomics</i> , 2021, 15, 23.	1.4	2
47	Causal effect estimation in sequencing studies: a Bayesian method to account for confounder adjustment uncertainty. <i>BMC Proceedings</i> , 2016, 10, 411-415.	1.8	1
48	Dose Reduction While Preserving Diagnostic Quality in Head CT: Advancing the Application of Iterative Reconstruction Using a Live Animal Model. <i>American Journal of Neuroradiology</i> , 2019, 40, 1864-1870.	1.2	1
49	Identification of Monotonically Differentially Expressed Genes across Pathologic Stages for Cancers. <i>Journal of Oncology</i> , 2020, 2020, 1-9.	0.6	1
50	Gene expression barcode values reveal a potential link between Parkinson's disease and gastric cancer. <i>Aging</i> , 2021, 13, 6171-6181.	1.4	1
51	GEE-TGDR: A Longitudinal Feature Selection Algorithm and Its Application to lncRNA Expression Profiles for Psoriasis Patients Treated with Immune Therapies. <i>BioMed Research International</i> , 2021, 2021, 1-9.	0.9	1
52	Identification of long non-coding RNA signatures for squamous cell carcinomas and adenocarcinomas. <i>Aging</i> , 2021, 13, 2459-2479.	1.4	1
53	A probabilistic method for leveraging functional annotations to enhance estimation of the temporal order of pathway mutations during carcinogenesis. <i>BMC Bioinformatics</i> , 2019, 20, 620.	1.2	0
54	An Exponential Tilt Mixture Model for Time-to-Event Data to Evaluate Treatment Effect Heterogeneity in Randomized Clinical Trials. <i>Biometrics & Biostatistics International Journal</i> , 2014, 1, .	0.2	0

#	ARTICLE	IF	CITATIONS
55	DACH1 mutation frequency in endometrial cancer is associated with high tumor mutation burden. , 2020, 15, e0244558.		0
56	DACH1 mutation frequency in endometrial cancer is associated with high tumor mutation burden. , 2020, 15, e0244558.		0
57	DACH1 mutation frequency in endometrial cancer is associated with high tumor mutation burden. , 2020, 15, e0244558.		0
58	DACH1 mutation frequency in endometrial cancer is associated with high tumor mutation burden. , 2020, 15, e0244558.		0