Ming Yi

List of Publications by Year
in descending order

51 papers	8,792 citations	94433 37 h-index	206112 48 g-index
52 all docs	52 docs citations	52 times ranked	15009 citing authors

#	Article	IF	Citations
1	Unique microRNA molecular profiles in lung cancer diagnosis and prognosis. Cancer Cell, 2006, 9, 189-198.	16.8	2,870
2	Genomic Profiling of MicroRNA and Messenger RNA Reveals Deregulated MicroRNA Expression in Prostate Cancer. Cancer Research, 2008, 68, 6162-6170.	0.9	661
3	Tumor Immunobiological Differences in Prostate Cancer between African-American and European-American Men. Cancer Research, 2008, 68, 927-936.	0.9	438
4	MYC-driven accumulation of 2-hydroxyglutarate is associated with breast cancer prognosis. Journal of Clinical Investigation, 2014, 124, 398-412.	8.2	348
5	Gene expression profiling of substantia nigra dopamine neurons: further insights into Parkinson's disease pathology. Brain, 2009, 132, 1795-1809.	7.6	332
6	bioDBnet: the biological database network. Bioinformatics, 2009, 25, 555-556.	4.1	328
7	Human Glioma Growth Is Controlled by MicroRNA-10b. Cancer Research, 2011, 71, 3563-3572.	0.9	267
8	Downregulated MicroRNA-200a in Meningiomas Promotes Tumor Growth by Reducing E-Cadherin and Activating the Wnt/β-Catenin Signaling Pathway. Molecular and Cellular Biology, 2009, 29, 5923-5940.	2.3	240
9	Increased NOS2 predicts poor survival in estrogen receptor–negative breast cancer patients. Journal of Clinical Investigation, 2010, 120, 3843-3854.	8.2	202
10	WholePathwayScope: a comprehensive pathway-based analysis tool for high-throughput data. BMC Bioinformatics, 2006, 7, 30.	2.6	188
11	Differences in the Tumor Microenvironment between African-American and European-American Breast Cancer Patients. PLoS ONE, 2009, 4, e4531.	2.5	179
12	MicroRNA-1 is a candidate tumor suppressor and prognostic marker in human prostate cancer. Nucleic Acids Research, 2012, 40, 3689-3703.	14.5	165
13	Undermining Glutaminolysis Bolsters Chemotherapy While NRF2 Promotes Chemoresistance in KRAS-Driven Pancreatic Cancers. Cancer Research, 2020, 80, 1630-1643.	0.9	157
14	A stromal gene signature associated with inflammatory breast cancer. International Journal of Cancer, 2008, 122, 1324-1332.	5.1	154
15	The role of miR-31 and its target gene SATB2 in cancer-associated fibroblasts. Cell Cycle, 2010, 9, 4387-4398.	2.6	152
16	miRNA-7 Attenuation in Schwannoma Tumors Stimulates Growth by Upregulating Three Oncogenic Signaling Pathways. Cancer Research, 2011, 71, 852-861.	0.9	142
17	Expression of microRNAs and protein–coding genes associated with perineural invasion in prostate cancer. Prostate, 2008, 68, 1152-1164.	2.3	134
18	Non-B DB v2.0: a database of predicted non-B DNA-forming motifs and its associated tools. Nucleic Acids Research, 2012, 41, D94-D100.	14.5	133

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19	miR-126 contributes to Parkinson's disease by dysregulating the insulin-like growth factor/phosphoinositide 3-kinase signaling. Neurobiology of Aging, 2014, 35, 1712-1721.	3.1	120
20	A Combined Proteome and Microarray Investigation of Inorganic Phosphate-induced Pre-osteoblast Cells. Molecular and Cellular Proteomics, 2005, 4, 1284-1296.	3.8	113
21	Evidence for Gender-Specific Transcriptional Profiles of Nigral Dopamine Neurons in Parkinson Disease. PLoS ONE, 2010, 5, e8856.	2.5	113
22	ssGSEA score-based Ras dependency indexes derived from gene expression data reveal potential Ras addiction mechanisms with possible clinical implications. Scientific Reports, 2020, 10, 10258.	3.3	105
23	Differential Effector Engagement by Oncogenic KRAS. Cell Reports, 2018, 22, 1889-1902.	6.4	101
24	IL-1Râ€"MyD88 signaling in keratinocyte transformation and carcinogenesis. Journal of Experimental Medicine, 2012, 209, 1689-1702.	8.5	99
25	An integrated understanding of the physiological response to elevated extracellular phosphate. Journal of Cellular Physiology, 2013, 228, 1536-1550.	4.1	94
26	Chromatin-Associated Genes Protect the Yeast Genome From Ty1 Insertional Mutagenesis. Genetics, 2008, 178, 197-214.	2.9	81
27	High recombination rates and hotspots in a Plasmodium falciparum genetic cross. Genome Biology, 2011, 12, R33.	8.8	80
28	Integrated miRNA and mRNA expression profiling of mouse mammary tumor models identifies miRNA signatures associated with mammary tumor lineage. Genome Biology, 2011, 12, R77.	9.6	76
29	Non-B DB: a database of predicted non-B DNA-forming motifs in mammalian genomes. Nucleic Acids Research, 2011, 39, D383-D391.	14.5	73
30	Genome-Wide Compensatory Changes Accompany Drug- Selected Mutations in the Plasmodium falciparum crt Gene. PLoS ONE, 2008, 3, e2484.	2.5	70
31	Murine Leukemias with Retroviral Insertions at Lmo2 Are Predictive of the Leukemias Induced in SCID-X1 Patients Following Retroviral Gene Therapy. PLoS Genetics, 2009, 5, e1000491.	3.5	66
32	Transcription signatures encoded by ultraconserved genomic regions in human prostate cancer. Molecular Cancer, 2013, 12, 13.	19.2	63
33	The Cancer Genome Atlas Analysis Predicts MicroRNA for Targeting Cancer Growth and Vascularization in Glioblastoma. Molecular Therapy, 2015, 23, 1234-1247.	8.2	62
34	Long homopurine*homopyrimidine sequences are characteristic of genes expressed in brain and the pseudoautosomal region. Nucleic Acids Research, 2006, 34, 2663-2675.	14.5	60
35	Detection of genome-wide polymorphisms in the AT-rich Plasmodium falciparum genome using a high-density microarray. BMC Genomics, 2008, 9, 398.	2.8	54
36	Performance comparison of SNP detection tools with illumina exome sequencing dataâ€"an assessment using both family pedigree information and sample-matched SNP array data. Nucleic Acids Research, 2014, 42, e101-e101.	14.5	50

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37	MicroRNA-10b inhibition reduces E2F1-mediated transcription and miR-15/16 activity in glioblastoma. Oncotarget, 2015, 6, 3770-3783.	1.8	42
38	Guanine Holes Are Prominent Targets for Mutation in Cancer and Inherited Disease. PLoS Genetics, 2013, 9, e1003816.	3.5	34
39	An Immune-Inflammation Gene Expression Signature in Prostate Tumors of Smokers. Cancer Research, 2016, 76, 1055-1065.	0.9	31
40	Tumor RAS Gene Expression Levels Are Influenced by the Mutational Status of RAS Genes and Both Upstream and Downstream RAS Pathway Genes. Cancer Informatics, 2017, 16, 117693511771194.	1.9	21
41	SLEPR: A Sample-Level Enrichment-Based Pathway Ranking Method â€" Seeking Biological Themes through Pathway-Level Consistency. PLoS ONE, 2008, 3, e3288.	2.5	18
42	Seeking unique and common biological themes in multiple gene lists or datasets: pathway pattern extraction pipeline for pathway-level comparative analysis. BMC Bioinformatics, 2009, 10, 200.	2.6	16
43	Pathway-Specific Engineered Mouse Allograft Models Functionally Recapitulate Human Serous Epithelial Ovarian Cancer. PLoS ONE, 2014, 9, e95649.	2.5	16
44	Altered Gene Expression Profiles Define Pathways in Colorectal Cancer Cell Lines Affected by Celecoxib. Cancer Epidemiology Biomarkers and Prevention, 2008, 17, 3051-3061.	2.5	12
45	Aneuploidy, oncogene amplification and epithelial to mesenchymal transition define spontaneous transformation of murine epithelial cells. Carcinogenesis, 2013, 34, 1929-1939.	2.8	11
46	Large-scale Genotyping and Genetic Mapping in Plasmodium Parasites. Korean Journal of Parasitology, 2009, 47, 83.	1.3	10
47	Parallel Analysis of Transcript and Translation Profiles:Â Identification of Metastasis-Related Signal Pathways Differentially Regulated by Drug and Genetic Modifications. Journal of Proteome Research, 2006, 5, 1555-1567.	3.7	9
48	GradientScanSurvâ€"An exhaustive association test method for gene expression data with censored survival outcome. PLoS ONE, 2018, 13, e0207590.	2.5	2
49	Pathway analysis: Pathway signatures and classification. , 2009, , 132-159.		0
50	Bioinformatics of High-Throughput Insertional Mutagenesis. , 2011, , 167-188.		0
51	Abstract 1092: Interpreting and navigating the TCGA in the context of the RAS pathway. , 2015, , .		0