

# Ming Yi

## List of Publications by Year in descending order

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Version: 2024-02-01

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	ssGSEA score-based Ras dependency indexes derived from gene expression data reveal potential Ras addiction mechanisms with possible clinical implications. <i>Scientific Reports</i> , 2020, 10, 10258.	3.3	105
2	Undermining Glutaminolysis Bolsters Chemotherapy While NRF2 Promotes Chemoresistance in KRAS-Driven Pancreatic Cancers. <i>Cancer Research</i> , 2020, 80, 1630-1643.	0.9	157
3	Differential Effector Engagement by Oncogenic KRAS. <i>Cell Reports</i> , 2018, 22, 1889-1902.	6.4	101
4	GradientScanSurvâ€”An exhaustive association test method for gene expression data with censored survival outcome. <i>PLoS ONE</i> , 2018, 13, e0207590.	2.5	2
5	Tumor RAS Gene Expression Levels Are Influenced by the Mutational Status of RAS Genes and Both Upstream and Downstream RAS Pathway Genes. <i>Cancer Informatics</i> , 2017, 16, 117693511771194.	1.9	21
6	An Immune-Inflammation Gene Expression Signature in Prostate Tumors of Smokers. <i>Cancer Research</i> , 2016, 76, 1055-1065.	0.9	31
7	The Cancer Genome Atlas Analysis Predicts MicroRNA for Targeting Cancer Growth and Vascularization in Glioblastoma. <i>Molecular Therapy</i> , 2015, 23, 1234-1247.	8.2	62
8	MicroRNA-10b inhibition reduces E2F1-mediated transcription and miR-15/16 activity in glioblastoma. <i>Oncotarget</i> , 2015, 6, 3770-3783.	1.8	42
9	Abstract 1092: Interpreting and navigating the TCGA in the context of the RAS pathway. , 2015, , .		0
10	MYC-driven accumulation of 2-hydroxyglutarate is associated with breast cancer prognosis. <i>Journal of Clinical Investigation</i> , 2014, 124, 398-412.	8.2	348
11	Performance comparison of SNP detection tools with illumina exome sequencing dataâ€”an assessment using both family pedigree information and sample-matched SNP array data. <i>Nucleic Acids Research</i> , 2014, 42, e101-e101.	14.5	50
12	miR-126 contributes to Parkinson's disease by dysregulating the insulin-like growth factor/phosphoinositide 3-kinase signaling. <i>Neurobiology of Aging</i> , 2014, 35, 1712-1721.	3.1	120
13	Pathway-Specific Engineered Mouse Allograft Models Functionally Recapitulate Human Serous Epithelial Ovarian Cancer. <i>PLoS ONE</i> , 2014, 9, e95649.	2.5	16
14	Transcription signatures encoded by ultraconserved genomic regions in human prostate cancer. <i>Molecular Cancer</i> , 2013, 12, 13.	19.2	63
15	Aneuploidy, oncogene amplification and epithelial to mesenchymal transition define spontaneous transformation of murine epithelial cells. <i>Carcinogenesis</i> , 2013, 34, 1929-1939.	2.8	11
16	Guanine Holes Are Prominent Targets for Mutation in Cancer and Inherited Disease. <i>PLoS Genetics</i> , 2013, 9, e1003816.	3.5	34
17	An integrated understanding of the physiological response to elevated extracellular phosphate. <i>Journal of Cellular Physiology</i> , 2013, 228, 1536-1550.	4.1	94
18	MicroRNA-1 is a candidate tumor suppressor and prognostic marker in human prostate cancer. <i>Nucleic Acids Research</i> , 2012, 40, 3689-3703.	14.5	165

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19	Non-B DB v2.0: a database of predicted non-B DNA-forming motifs and its associated tools. <i>Nucleic Acids Research</i> , 2012, 41, D94-D100.	14.5	133
20	IL-1R $\alpha$ MyD88 signaling in keratinocyte transformation and carcinogenesis. <i>Journal of Experimental Medicine</i> , 2012, 209, 1689-1702.	8.5	99
21	Non-B DB: a database of predicted non-B DNA-forming motifs in mammalian genomes. <i>Nucleic Acids Research</i> , 2011, 39, D383-D391.	14.5	73
22	Integrated miRNA and mRNA expression profiling of mouse mammary tumor models identifies miRNA signatures associated with mammary tumor lineage. <i>Genome Biology</i> , 2011, 12, R77.	9.6	76
23	High recombination rates and hotspots in a <i>Plasmodium falciparum</i> genetic cross. <i>Genome Biology</i> , 2011, 12, R33.	8.8	80
24	miRNA-7 Attenuation in Schwannoma Tumors Stimulates Growth by Upregulating Three Oncogenic Signaling Pathways. <i>Cancer Research</i> , 2011, 71, 852-861.	0.9	142
25	Human Glioma Growth Is Controlled by MicroRNA-10b. <i>Cancer Research</i> , 2011, 71, 3563-3572.	0.9	267
26	Bioinformatics of High-Throughput Insertional Mutagenesis. , 2011, , 167-188.		0
27	Evidence for Gender-Specific Transcriptional Profiles of Nigral Dopamine Neurons in Parkinson Disease. <i>PLoS ONE</i> , 2010, 5, e8856.	2.5	113
28	The role of miR-31 and its target gene SATB2 in cancer-associated fibroblasts. <i>Cell Cycle</i> , 2010, 9, 4387-4398.	2.6	152
29	Increased NOS2 predicts poor survival in estrogen receptor $\alpha$ negative breast cancer patients. <i>Journal of Clinical Investigation</i> , 2010, 120, 3843-3854.	8.2	202
30	Murine Leukemias with Retroviral Insertions at Lmo2 Are Predictive of the Leukemias Induced in SCID-X1 Patients Following Retroviral Gene Therapy. <i>PLoS Genetics</i> , 2009, 5, e1000491.	3.5	66
31	Differences in the Tumor Microenvironment between African-American and European-American Breast Cancer Patients. <i>PLoS ONE</i> , 2009, 4, e4531.	2.5	179
32	bioDBnet: the biological database network. <i>Bioinformatics</i> , 2009, 25, 555-556.	4.1	328
33	Seeking unique and common biological themes in multiple gene lists or datasets: pathway pattern extraction pipeline for pathway-level comparative analysis. <i>BMC Bioinformatics</i> , 2009, 10, 200.	2.6	16
34	Gene expression profiling of substantia nigra dopamine neurons: further insights into Parkinson's disease pathology. <i>Brain</i> , 2009, 132, 1795-1809.	7.6	332
35	Downregulated MicroRNA-200a in Meningiomas Promotes Tumor Growth by Reducing E-Cadherin and Activating the Wnt/ $\beta$ -Catenin Signaling Pathway. <i>Molecular and Cellular Biology</i> , 2009, 29, 5923-5940.	2.3	240
36	Large-scale Genotyping and Genetic Mapping in <i>Plasmodium</i> Parasites. <i>Korean Journal of Parasitology</i> , 2009, 47, 83.	1.3	10

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37	Pathway analysis: Pathway signatures and classification. , 2009, , 132-159.		0
38	Expression of microRNAs and protein-coding genes associated with perineural invasion in prostate cancer. Prostate, 2008, 68, 1152-1164.	2.3	134
39	A stromal gene signature associated with inflammatory breast cancer. International Journal of Cancer, 2008, 122, 1324-1332.	5.1	154
40	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
41	Genomic Profiling of MicroRNA and Messenger RNA Reveals Deregulated MicroRNA Expression in Prostate Cancer. Cancer Research, 2008, 68, 6162-6170.	0.9	661
42	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
43	Tumor Immunobiological Differences in Prostate Cancer between African-American and European-American Men. Cancer Research, 2008, 68, 927-936.	0.9	438
44	Chromatin-Associated Genes Protect the Yeast Genome From Ty1 Insertional Mutagenesis. Genetics, 2008, 178, 197-214.	2.9	81
45	Genome-Wide Compensatory Changes Accompany Drug- Selected Mutations in the Plasmodium falciparum crt Gene. PLoS ONE, 2008, 3, e2484.	2.5	70
46	SLEPR: A Sample-Level Enrichment-Based Pathway Ranking Method " Seeking Biological Themes through Pathway-Level Consistency. PLoS ONE, 2008, 3, e3288.	2.5	18
47	Parallel Analysis of Transcript and Translation Profiles: 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	Unique microRNA molecular profiles in lung cancer diagnosis and prognosis. Cancer Cell, 2006, 9, 189-198.	16.8	2,870
49	WholePathwayScope: a comprehensive pathway-based analysis tool for high-throughput data. BMC Bioinformatics, 2006, 7, 30.	2.6	188
50	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
51	A Combined Proteome and Microarray Investigation of Inorganic Phosphate-induced Pre-osteoblast Cells. Molecular and Cellular Proteomics, 2005, 4, 1284-1296.	3.8	113