

Xizeng Mao

List of Publications by Year in descending order

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Version: 2024-02-01

37
papers

10,787
citations

331259

21
h-index

344852

36
g-index

39
all docs

39
docs citations

39
times ranked

16160
citing authors

#	ARTICLE	IF	CITATIONS
1	Experimental models of undifferentiated pleomorphic sarcoma and malignant peripheral nerve sheath tumor. <i>Laboratory Investigation</i> , 2022, 102, 658-666.	1.7	7
2	Multi-omic molecular profiling reveals potentially targetable abnormalities shared across multiple histologies of brain metastasis. <i>Acta Neuropathologica</i> , 2021, 141, 303-321.	3.9	30
3	Enhancer reprogramming in PRC2-deficient malignant peripheral nerve sheath tumors induces a targetable de-differentiated state. <i>Acta Neuropathologica</i> , 2021, 142, 565-590.	3.9	12
4	Somatic Mutations in Circulating Cell-Free DNA and Risk for Hepatocellular Carcinoma in Hispanics. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7411.	1.8	3
5	The histologic phenotype of lung cancers is associated with transcriptomic features rather than genomic characteristics. <i>Nature Communications</i> , 2021, 12, 7081.	5.8	16
6	Multiplex profiling of peritoneal metastases from gastric adenocarcinoma identified novel targets and molecular subtypes that predict treatment response. <i>Gut</i> , 2020, 69, 18-31.	6.1	94
7	Telomere dysfunction activates YAP1 to drive tissue inflammation. <i>Nature Communications</i> , 2020, 11, 4766.	5.8	42
8	Blocking immunosuppressive neutrophils deters pY696-EZH2-driven brain metastases. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	64
9	Molecular Analysis of Clinically Defined Subsets of High-Grade Serous Ovarian Cancer. <i>Cell Reports</i> , 2020, 31, 107502.	2.9	69
10	Spatially resolved analyses link genomic and immune diversity and reveal unfavorable neutrophil activation in melanoma. <i>Nature Communications</i> , 2020, 11, 1839.	5.8	15
11	A Cryptic BCR-PDGFRB Fusion Resulting in a Chronic Myeloid Neoplasm With Monocytosis and Eosinophilia: A Novel Finding With Treatment Implications. <i>Journal of the National Comprehensive Cancer Network: JNCCN</i> , 2020, 18, 1300-1304.	2.3	4
12	Multi-region exome sequencing reveals genomic evolution from preneoplasia to lung adenocarcinoma. <i>Nature Communications</i> , 2019, 10, 2978.	5.8	91
13	PRDM16s transforms megakaryocyte-erythroid progenitors into myeloid leukemia-initiating cells. <i>Blood</i> , 2019, 134, 614-625.	0.6	16
14	Metabolic reprogramming toward oxidative phosphorylation identifies a therapeutic target for mantle cell lymphoma. <i>Science Translational Medicine</i> , 2019, 11, .	5.8	161
15	Variants with a low allele frequency detected in genomic DNA affect the accuracy of mutation detection in cell-free DNA by next-generation sequencing. <i>Cancer</i> , 2018, 124, 1061-1069.	2.0	11
16	Combined Analysis of Antigen Presentation and T-cell Recognition Reveals Restricted Immune Responses in Melanoma. <i>Cancer Discovery</i> , 2018, 8, 1366-1375.	7.7	80
17	Genomic and immune heterogeneity are associated with differential responses to therapy in melanoma. <i>Npj Genomic Medicine</i> , 2017, 2, .	1.7	120
18	Genome-Scale Identification of Cell-Wall-Related Genes in Switchgrass through Comparative Genomics and Computational Analyses of Transcriptomic Data. <i>Bioenergy Research</i> , 2016, 9, 172-180.	2.2	10

#	ARTICLE	IF	CITATIONS
19	Revisiting operons: an analysis of the landscape of transcriptional units in <i>E. coli</i> . <i>BMC Bioinformatics</i> , 2015, 16, 356.	1.2	39
20	Comprehensive characterization of the genomic alterations in human gastric cancer. <i>International Journal of Cancer</i> , 2015, 137, 86-95.	2.3	67
21	Understanding the commonalities and differences in genomic organizations across closely related bacteria from an energy perspective. <i>Science China Life Sciences</i> , 2014, 57, 1121-1130.	2.3	4
22	DMINDA: an integrated web server for DNA motif identification and analyses. <i>Nucleic Acids Research</i> , 2014, 42, W12-W19.	6.5	30
23	DOOR 2.0: presenting operons and their functions through dynamic and integrated views. <i>Nucleic Acids Research</i> , 2014, 42, D654-D659.	6.5	171
24	New Insights into Clostridia Through Comparative Analyses of Their 40 Genomes. <i>Bioenergy Research</i> , 2014, 7, 1481-1492.	2.2	16
25	The percentage of bacterial genes on leading versus lagging strands is influenced by multiple balancing forces. <i>Nucleic Acids Research</i> , 2012, 40, 8210-8218.	6.5	41
26	Hypoxia and miscoupling between reduced energy efficiency and signaling to cell proliferation drive cancer to grow increasingly faster. <i>Journal of Molecular Cell Biology</i> , 2012, 4, 174-176.	1.5	23
27	dbCAN: a web resource for automated carbohydrate-active enzyme annotation. <i>Nucleic Acids Research</i> , 2012, 40, W445-W451.	6.5	1,554
28	CINPER: An Interactive Web System for Pathway Prediction for Prokaryotes. <i>PLoS ONE</i> , 2012, 7, e51252.	1.1	5
29	KOBAS 2.0: a web server for annotation and identification of enriched pathways and diseases. <i>Nucleic Acids Research</i> , 2011, 39, W316-W322.	6.5	3,897
30	Integration of sequence-similarity and functional association information can overcome intrinsic problems in orthology mapping across bacterial genomes. <i>Nucleic Acids Research</i> , 2011, 39, e150-e150.	6.5	11
31	SEAS: A System for SEED-Based Pathway Enrichment Analysis. <i>PLoS ONE</i> , 2011, 6, e22556.	1.1	8
32	Computational prediction of the osmoregulation network in <i>Synechococcus</i> sp. WH8102. <i>BMC Genomics</i> , 2010, 11, 291.	1.2	14
33	Genes and (Common) Pathways Underlying Drug Addiction. <i>PLoS Computational Biology</i> , 2008, 4, e2.	1.5	210
34	Isolation and analysis of differentially expressed genes in dominant genic male sterility (DGMS) <i>Brassica napus</i> L. using subtractive PCR and cDNA microarray. <i>Plant Science</i> , 2007, 172, 204-211.	1.7	15
35	Molecular analysis of early rice stamen development using organ-specific gene expression profiling. <i>Plant Molecular Biology</i> , 2006, 61, 845-861.	2.0	30
36	KOBAS server: a web-based platform for automated annotation and pathway identification. <i>Nucleic Acids Research</i> , 2006, 34, W720-W724.	6.5	682

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37	Automated genome annotation and pathway identification using the KEGG Orthology (KO) as a controlled vocabulary. <i>Bioinformatics</i> , 2005, 21, 3787-3793.	1.8	3,124