Xizeng Mao

List of Publications by Year
in descending order

37 papers	10,787 citations	331670 21 h-index	345221 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. Laboratory Investigation, 2022, 102, 658-666.	3.7	7
2	Multi-omic molecular profiling reveals potentially targetable abnormalities shared across multiple histologies of brain metastasis. Acta Neuropathologica, 2021, 141, 303-321.	7.7	30
3	Enhancer reprogramming in PRC2-deficient malignant peripheral nerve sheath tumors induces a targetable de-differentiated state. Acta Neuropathologica, 2021, 142, 565-590.	7.7	12
4	Somatic Mutations in Circulating Cell-Free DNA and Risk for Hepatocellular Carcinoma in Hispanics. International Journal of Molecular Sciences, 2021, 22, 7411.	4.1	3
5	The histologic phenotype of lung cancers is associated with transcriptomic features rather than genomic characteristics. Nature Communications, 2021, 12, 7081.	12.8	16
6	Multiplex profiling of peritoneal metastases from gastric adenocarcinoma identified novel targets and molecular subtypes that predict treatment response. Gut, 2020, 69, 18-31.	12.1	94
7	Telomere dysfunction activates YAP1 to drive tissue inflammation. Nature Communications, 2020, 11, 4766.	12.8	42
8	Blocking immunosuppressive neutrophils deters pY696-EZH2â€"driven brain metastases. Science Translational Medicine, 2020, 12, .	12.4	64
9	Molecular Analysis of Clinically Defined Subsets of High-Grade Serous Ovarian Cancer. Cell Reports, 2020, 31, 107502.	6.4	69
10	Spatially resolved analyses link genomic and immune diversity and reveal unfavorable neutrophil activation in melanoma. Nature Communications, 2020, 11, 1839.	12.8	15
11	A Cryptic BCR-PDGFRB Fusion Resulting in a Chronic Myeloid Neoplasm With Monocytosis and Eosinophilia: A Novel Finding With Treatment Implications. Journal of the National Comprehensive Cancer Network: JNCCN, 2020, 18, 1300-1304.	4.9	4
12	Multi-region exome sequencing reveals genomic evolution from preneoplasia to lung adenocarcinoma. Nature Communications, 2019, 10, 2978.	12.8	91
13	PRDM16s transforms megakaryocyte-erythroid progenitors into myeloid leukemiaâ€"initiating cells. Blood, 2019, 134, 614-625.	1.4	16
14	Metabolic reprogramming toward oxidative phosphorylation identifies a therapeutic target for mantle cell lymphoma. Science Translational Medicine, 2019, 11, .	12.4	161
15	Variants with a low allele frequency detected in genomic DNA affect the accuracy of mutation detection in cellâ€free DNA by nextâ€generation sequencing. Cancer, 2018, 124, 1061-1069.	4.1	11
16	Combined Analysis of Antigen Presentation and T-cell Recognition Reveals Restricted Immune Responses in Melanoma. Cancer Discovery, 2018, 8, 1366-1375.	9.4	80
17	Genomic and immune heterogeneity are associated with differential responses to therapy in melanoma. Npj Genomic Medicine, 2017, 2, .	3.8	120
18	Genome-Scale Identification of Cell-Wall-Related Genes in Switchgrass through Comparative Genomics and Computational Analyses of Transcriptomic Data. Bioenergy Research, 2016, 9, 172-180.	3.9	10

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19	Revisiting operons: an analysis of the landscape of transcriptional units in E. coli. BMC Bioinformatics, 2015, 16, 356.	2.6	39
20	Comprehensive characterization of the genomic alterations in human gastric cancer. International Journal of Cancer, 2015, 137, 86-95.	5.1	67
21	Understanding the commonalities and differences in genomic organizations across closely related bacteria from an energy perspective. Science China Life Sciences, 2014, 57, 1121-1130.	4.9	4
22	DMINDA: an integrated web server for DNA motif identification and analyses. Nucleic Acids Research, 2014, 42, W12-W19.	14.5	30
23	DOOR 2.0: presenting operons and their functions through dynamic and integrated views. Nucleic Acids Research, 2014, 42, D654-D659.	14.5	171
24	New Insights into Clostridia Through Comparative Analyses of Their 40 Genomes. Bioenergy Research, 2014, 7, 1481-1492.	3.9	16
25	The percentage of bacterial genes on leading versus lagging strands is influenced by multiple balancing forces. Nucleic Acids Research, 2012, 40, 8210-8218.	14.5	41
26	Hypoxia and miscoupling between reduced energy efficiency and signaling to cell proliferation drive cancer to grow increasingly faster. Journal of Molecular Cell Biology, 2012, 4, 174-176.	3.3	23
27	dbCAN: a web resource for automated carbohydrate-active enzyme annotation. Nucleic Acids Research, 2012, 40, W445-W451.	14.5	1,554
28	CINPER: An Interactive Web System for Pathway Prediction for Prokaryotes. PLoS ONE, 2012, 7, e51252.	2.5	5
29	KOBAS 2.0: a web server for annotation and identification of enriched pathways and diseases. Nucleic Acids Research, 2011, 39, W316-W322.	14.5	3,897
30	Integration of sequence-similarity and functional association information can overcome intrinsic problems in orthology mapping across bacterial genomes. Nucleic Acids Research, 2011, 39, e150-e150.	14.5	11
31	SEAS: A System for SEED-Based Pathway Enrichment Analysis. PLoS ONE, 2011, 6, e22556.	2.5	8
32	Computational prediction of the osmoregulation network in Synechococcus sp. WH8102. BMC Genomics, 2010, 11, 291.	2.8	14
33	Genes and (Common) Pathways Underlying Drug Addiction. PLoS Computational Biology, 2008, 4, e2.	3.2	210
34	Isolation and analysis of differentially expressed genes in dominant genic male sterility (DGMS) Brassica napus L. using subtractive PCR and cDNA microarray. Plant Science, 2007, 172, 204-211.	3.6	15
35	Molecular analysis of early rice stamen development using organ-specific gene expression profiling. Plant Molecular Biology, 2006, 61, 845-861.	3.9	30
36	KOBAS server: a web-based platform for automated annotation and pathway identification. Nucleic Acids Research, 2006, 34, W720-W724.	14.5	682

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37	Automated genome annotation and pathway identification using the KEGG Orthology (KO) as a controlled vocabulary. Bioinformatics, 2005, 21, 3787-3793.	4.1	3,124