

Da Yang

List of Publications by Year in descending order

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Version: 2024-02-01

69
papers

27,830
citations

136950

32
h-index

98798

67
g-index

70
all docs

70
docs citations

70
times ranked

45021
citing authors

#	ARTICLE	IF	CITATIONS
1	LincRNA-immunity landscape analysis identifies EPIC1 as a regulator of tumor immune evasion and immunotherapy resistance. <i>Science Advances</i> , 2021, 7, .	10.3	28
2	Interrogation of gender disparity uncovers androgen receptor as the transcriptional activator for oncogenic miR-125b in gastric cancer. <i>Cell Death and Disease</i> , 2021, 12, 441.	6.3	15
3	The regulation of RNA metabolism in hormone signaling and breast cancer. <i>Molecular and Cellular Endocrinology</i> , 2021, 529, 111221.	3.2	6
4	Intestinal Sulfation Is Essential to Protect Against Colitis and Colonic Carcinogenesis. <i>Gastroenterology</i> , 2021, 161, 271-286.e11.	1.3	28
5	The anti-fibrotic drug pirfenidone inhibits liver fibrosis by targeting the small oxidoreductase glutaredoxin-1. <i>Science Advances</i> , 2021, 7, eabg9241.	10.3	25
6	Targeting metabotropic glutamate receptor 4 for cancer immunotherapy. <i>Science Advances</i> , 2021, 7, eabj4226.	10.3	11
7	Long-noncoding RNAs (lncRNAs) in drug metabolism and disposition, implications in cancer chemo-resistance. <i>Acta Pharmaceutica Sinica B</i> , 2020, 10, 105-112.	12.0	49
8	<i>ERINA</i> Is an Estrogen-Responsive lncRNA That Drives Breast Cancer through the E2F1/RB1 Pathway. <i>Cancer Research</i> , 2020, 80, 4399-4413.	0.9	31
9	MYC-binding lncRNA EPIC1 promotes AKT-mTORC1 signaling and rapamycin resistance in breast and ovarian cancer. <i>Molecular Carcinogenesis</i> , 2020, 59, 1188-1198.	2.7	7
10	Copy Number Amplification of DNA Damage Repair Pathways Potentiates Therapeutic Resistance in Cancer. <i>Theranostics</i> , 2020, 10, 3939-3951.	10.0	35
11	Aryl Hydrocarbon Receptor Signaling Prevents Activation of Hepatic Stellate Cells and Liver Fibrogenesis in Mice. <i>Gastroenterology</i> , 2019, 157, 793-806.e14.	1.3	67
12	Discovery of HSPG2 (Perlecan) as a Therapeutic Target in Triple Negative Breast Cancer. <i>Scientific Reports</i> , 2019, 9, 12492.	3.3	30
13	Origin of mutations in genes associated with human glioblastoma multiform cancer: random polymerase errors versus deamination. <i>Heliyon</i> , 2019, 5, e01265.	3.2	11
14	Targeted codelivery of doxorubicin and IL-36 β expression plasmid for an optimal chemo-gene combination therapy against cancer lung metastasis. <i>Nanomedicine: Nanotechnology, Biology, and Medicine</i> , 2019, 15, 129-141.	3.3	28
15	Pregnane X receptor activation potentiates ritonavir hepatotoxicity. <i>Journal of Clinical Investigation</i> , 2019, 129, 2898-2903.	8.2	32
16	A landscape of synthetic viable interactions in cancer. <i>Briefings in Bioinformatics</i> , 2018, 19, bbw142.	6.5	9
17	The Adenomatous Polyposis Coli (APC) mutation spectra in different anatomical regions of the large intestine in colorectal cancer. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2018, 810, 1-5.	1.0	4
18	lncRNA Epigenetic Landscape Analysis Identifies EPIC1 as an Oncogenic lncRNA that Interacts with MYC and Promotes Cell-Cycle Progression in Cancer. <i>Cancer Cell</i> , 2018, 33, 706-720.e9.	16.8	400

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19	Novel glucosylceramide synthase inhibitor based prodrug copolymer micelles for delivery of anticancer agents. <i>Journal of Controlled Release</i> , 2018, 288, 212-226.	9.9	10
20	Cystathionine Î²-lyase regulates mitochondrial morphogenesis in ovarian cancer. <i>FASEB Journal</i> , 2018, 32, 4145-4157.	0.5	33
21	Systematic identification of non-coding pharmacogenomic landscape in cancer. <i>Nature Communications</i> , 2018, 9, 3192.	12.8	73
22	MICU1 drives glycolysis and chemoresistance in ovarian cancer. <i>Nature Communications</i> , 2017, 8, 14634.	12.8	118
23	MLIP haploinsufficiency induces chromosomal instability and promotes tumour progression in colorectal cancer. <i>Journal of Pathology</i> , 2017, 241, 67-79.	4.5	13
24	A rank-based transcriptional signature for predicting relapse risk of stage II colorectal cancer identified with proper data sources. <i>Oncotarget</i> , 2016, 7, 19060-19071.	1.8	27
25	A miR-192-EGR1-HOXB9 regulatory network controls the angiogenic switch in cancer. <i>Nature Communications</i> , 2016, 7, 11169.	12.8	100
26	MDR1 mediated chemoresistance: BMI1 and TIP60 in action. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2016, 1859, 983-993.	1.9	25
27	Copy number deletion of RAD50 as predictive marker of BRCAness and PARP inhibitor response in BRCA wild type ovarian cancer. <i>Gynecologic Oncology</i> , 2016, 141, 57-64.	1.4	33
28	Hypoxia-upregulated microRNA-630 targets Dicer, leading to increased tumor progression. <i>Oncogene</i> , 2016, 35, 4312-4320.	5.9	83
29	An individualized prognostic signature for gastric cancer patients treated with 5-Fluorouracil-based chemotherapy and distinct multi-omics characteristics of prognostic groups. <i>Oncotarget</i> , 2016, 7, 8743-8755.	1.8	36
30	Key nodes of a microRNA network associated with the integrated mesenchymal subtype of high-grade serous ovarian cancer. <i>Chinese Journal of Cancer</i> , 2015, 34, 28-40.	4.9	26
31	Augmentation of Response to Chemotherapy by microRNA-506 Through Regulation of RAD51 in Serous Ovarian Cancers. <i>Journal of the National Cancer Institute</i> , 2015, 107, .	6.3	102
32	Mutational landscape of gastric adenocarcinoma in Chinese: Implications for prognosis and therapy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 1107-1112.	7.1	137
33	Genomic Classification of Cutaneous Melanoma. <i>Cell</i> , 2015, 161, 1681-1696.	28.9	2,562
34	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , 2015, 372, 2481-2498.	27.0	2,582
35	miR-101 suppresses the epithelial-to-mesenchymal transition by targeting ZEB1 and ZEB2 in ovarian carcinoma. <i>Oncology Reports</i> , 2014, 31, 2021-2028.	2.6	75
36	miR-506 suppresses proliferation and induces senescence by directly targeting the CDK4/FOXO1 axis in ovarian cancer. <i>Journal of Pathology</i> , 2014, 233, 308-318.	4.5	112

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37	Integrated MicroRNA Network Analyses Identify a Poor-Prognosis Subtype of Gastric Cancer Characterized by the miR-200 Family. <i>Clinical Cancer Research</i> , 2014, 20, 878-889.	7.0	97
38	Comprehensive molecular characterization of gastric adenocarcinoma. <i>Nature</i> , 2014, 513, 202-209.	27.8	5,055
39	The genetic basis for inactivation of Wnt pathway in human osteosarcoma. <i>BMC Cancer</i> , 2014, 14, 450.	2.6	50
40	Post-transcriptional regulatory network of epithelial-to-mesenchymal and mesenchymal-to-epithelial transitions. <i>Journal of Hematology and Oncology</i> , 2014, 7, 19.	17.0	115
41	HINCUTs in cancer: hypoxia-induced noncoding ultraconserved transcripts. <i>Cell Death and Differentiation</i> , 2013, 20, 1675-1687.	11.2	99
42	The Cancer Genome Atlas Pan-Cancer analysis project. <i>Nature Genetics</i> , 2013, 45, 1113-1120.	21.4	6,265
43	Tumour angiogenesis regulation by the miR-200 family. <i>Nature Communications</i> , 2013, 4, 2427.	12.8	363
44	Integrated Analyses Identify a Master MicroRNA Regulatory Network for the Mesenchymal Subtype in Serous Ovarian Cancer. <i>Cancer Cell</i> , 2013, 23, 186-199.	16.8	340
45	Integrated Analyses Identify a Master MicroRNA Regulatory Network for the Mesenchymal Subtype in Serous Ovarian Cancer. <i>Cancer Cell</i> , 2013, 23, 705.	16.8	6
46	CA-125 Level as a Prognostic Indicator in Type I and Type II Epithelial Ovarian Cancer. <i>International Journal of Gynecological Cancer</i> , 2013, 23, 815-822.	2.5	32
47	Plasma miRNAs as Diagnostic and Prognostic Biomarkers for Ovarian Cancer. <i>PLoS ONE</i> , 2013, 8, e77853.	2.5	168
48	Translational genomics in cancer research: converting profiles into personalized cancer medicine. <i>Cancer Biology and Medicine</i> , 2013, 10, 214-20.	3.0	10
49	Pitfalls in Experimental Designs for Characterizing the Transcriptional, Methylation and Copy Number Changes of Oncogenes and Tumor Suppressor Genes. <i>PLoS ONE</i> , 2013, 8, e58163.	2.5	1
50	Differing clinical impact of <i>BRCA1</i> and <i>BRCA2</i> mutations in serous ovarian cancer. <i>Pharmacogenomics</i> , 2012, 13, 1523-1535.	1.3	63
51	Association of <i>BRCA1</i> and <i>BRCA2</i> Mutations With Survival, Chemotherapy Sensitivity, and Gene Mutator Phenotype in Patients With Ovarian Cancer. <i>Obstetrical and Gynecological Survey</i> , 2012, 67, 164-165.	0.4	2
52	Comprehensive molecular characterization of human colon and rectal cancer. <i>Nature</i> , 2012, 487, 330-337.	27.8	7,168
53	Association of <i>BRCA1</i> and <i>BRCA2</i> Mutations With Survival, Chemotherapy Sensitivity, and Gene Mutator Phenotype in Patients With Ovarian Cancer. <i>JAMA - Journal of the American Medical Association</i> , 2011, 306, 1557.	7.4	466
54	Genetic amplification of the vascular endothelial growth factor (VEGF) pathway genes, including <i>VEGFA</i> , in human osteosarcoma. <i>Cancer</i> , 2011, 117, 4925-4938.	4.1	104

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55	Genetic variants at the miR-124 binding site on the cytoskeleton-organizing IQGAP1 gene confer differential predisposition to breast cancer. <i>International Journal of Oncology</i> , 2011, 38, 1153-61.	3.3	24
56	Systematic Interpretation of Comutated Genes in Large-Scale Cancer Mutation Profiles. <i>Molecular Cancer Therapeutics</i> , 2010, 9, 2186-2195.	4.1	12
57	Viewing cancer genes from co-evolving gene modules. <i>Bioinformatics</i> , 2010, 26, 919-924.	4.1	3
58	Finding Finer Functions of Cancer Proteins and Rebuilding Cancer-Associated Functional Sub-Networks. <i>International Conference on Bioinformatics and Biomedical Engineering: [proceedings] International Conference on Bioinformatics and Biomedical Engineering</i> , 2010, , .	0.0	0
59	Deletion of the WWOX gene and frequent loss of its protein expression in human osteosarcoma. <i>Cancer Letters</i> , 2010, 291, 31-38.	7.2	49
60	Evaluation of cDNA Microarray Data by Multiple Clones Mapping to the Same Transcript. <i>OMICS A Journal of Integrative Biology</i> , 2009, 13, 493-499.	2.0	4
61	Finding disease-specific coordinated functions by multi-function genes: Insight into the coordination mechanisms in diseases. <i>Genomics</i> , 2009, 94, 94-100.	2.9	17
62	Gaining confidence in biological interpretation of the microarray data: the functional consistence of the significant GO categories. <i>Bioinformatics</i> , 2008, 24, 265-271.	4.1	49
63	Apparently low reproducibility of true differential expression discoveries in microarray studies. <i>Bioinformatics</i> , 2008, 24, 2057-2063.	4.1	110
64	Edge-based scoring and searching method for identifying condition-responsive protein protein interaction sub-network. <i>Bioinformatics</i> , 2007, 23, 2121-2128.	4.1	139
65	Characterizing Proteins with Finer Functions: A Case Study for Translational Functions of Yeast Proteins. , 2007, , .		1
66	GO-2D: identifying 2-dimensional cellular-localized functional modules in Gene Ontology. <i>BMC Genomics</i> , 2007, 8, 30.	2.8	15
67	Finding finer functions for partially characterized proteins by protein-protein interaction networks. <i>Science Bulletin</i> , 2007, 52, 3363-3370.	1.7	1
68	Identifying disease feature genes based on cellular localized gene functional modules and regulation networks. <i>Science Bulletin</i> , 2006, 51, 1848-1856.	1.7	3
69	Effects of replacing the unreliable cDNA microarray measurements on the disease classification based on gene expression profiles and functional modules. <i>Bioinformatics</i> , 2006, 22, 2883-2889.	4.1	36