

Da Yang

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

67
papers

20,105
citations

31
h-index

70
g-index

70
ext. papers

24,872
ext. citations

12.2
avg, IF

7.99
L-index

#	Paper	IF	Citations
67	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	9.8	3
66	The regulation of RNA metabolism in hormone signaling and breast cancer. <i>Molecular and Cellular Endocrinology</i> , 2021 , 529, 111221	4.4	1
65	LincRNA-immunity landscape analysis identifies EPIC1 as a regulator of tumor immune evasion and immunotherapy resistance. <i>Science Advances</i> , 2021 , 7,	14.3	9
64	Intestinal Sulfation Is Essential to Protect Against Colitis and Colonic Carcinogenesis. <i>Gastroenterology</i> , 2021 , 161, 271-286.e11	13.3	8
63	The anti-fibrotic drug pirfenidone inhibits liver fibrosis by targeting the small oxidoreductase glutaredoxin-1. <i>Science Advances</i> , 2021 , 7, eabg9241	14.3	3
62	Targeting metabotropic glutamate receptor 4 for cancer immunotherapy. <i>Science Advances</i> , 2021 , 7, eabj4226	14.3	0
61	Copy Number Amplification of DNA Damage Repair Pathways Potentiates Therapeutic Resistance in Cancer. <i>Theranostics</i> , 2020 , 10, 3939-3951	12.1	16
60	Long-noncoding RNAs (lncRNAs) in drug metabolism and disposition, implications in cancer chemo-resistance. <i>Acta Pharmaceutica Sinica B</i> , 2020 , 10, 105-112	15.5	31
59	Is an Estrogen-Responsive LncRNA That Drives Breast Cancer through the E2F1/RB1 Pathway. <i>Cancer Research</i> , 2020 , 80, 4399-4413	10.1	11
58	MYC-binding lncRNA EPIC1 promotes AKT-mTORC1 signaling and rapamycin resistance in breast and ovarian cancer. <i>Molecular Carcinogenesis</i> , 2020 , 59, 1188-1198	5	1
57	Discovery of HSPG2 (Perlecan) as a Therapeutic Target in Triple Negative Breast Cancer. <i>Scientific Reports</i> , 2019 , 9, 12492	4.9	14
56	Origin of mutations in genes associated with human glioblastoma multiform cancer: random polymerase errors versus deamination. <i>Heliyon</i> , 2019 , 5, e01265	3.6	7
55	Aryl Hydrocarbon Receptor Signaling Prevents Activation of Hepatic Stellate Cells and Liver Fibrogenesis in Mice. <i>Gastroenterology</i> , 2019 , 157, 793-806.e14	13.3	37
54	Pregnane X receptor activation potentiates ritonavir hepatotoxicity. <i>Journal of Clinical Investigation</i> , 2019 , 129, 2898-2903	15.9	15
53	Targeted codelivery of doxorubicin and IL-36 expression plasmid for an optimal chemo-gene combination therapy against cancer lung metastasis. <i>Nanomedicine: Nanotechnology, Biology, and Medicine</i> , 2019 , 15, 129-141	6	20
52	A landscape of synthetic viable interactions in cancer. <i>Briefings in Bioinformatics</i> , 2018 , 19, 644-655	13.4	6
51	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	3.3	3

50	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	24.3	275
49	Cystathionine Synthase regulates mitochondrial morphogenesis in ovarian cancer. <i>FASEB Journal</i> , 2018 , 32, 4145-4157	0.9	23
48	Systematic identification of non-coding pharmacogenomic landscape in cancer. <i>Nature Communications</i> , 2018 , 9, 3192	17.4	44
47	Novel glucosylceramide synthase inhibitor based prodrug copolymer micelles for delivery of anticancer agents. <i>Journal of Controlled Release</i> , 2018 , 288, 212-226	11.7	6
46	MICU1 drives glycolysis and chemoresistance in ovarian cancer. <i>Nature Communications</i> , 2017 , 8, 14634	17.4	81
45	MIIP haploinsufficiency induces chromosomal instability and promotes tumour progression in colorectal cancer. <i>Journal of Pathology</i> , 2017 , 241, 67-79	9.4	8
44	A miR-192-EGR1-HOXB9 regulatory network controls the angiogenic switch in cancer. <i>Nature Communications</i> , 2016 , 7, 11169	17.4	83
43	MDR1 mediated chemoresistance: BMI1 and TIP60 in action. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2016 , 1859, 983-93	6	20
42	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	4.9	24
41	Hypoxia-upregulated microRNA-630 targets Dicer, leading to increased tumor progression. <i>Oncogene</i> , 2016 , 35, 4312-20	9.2	70
40	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, 8743-55	3.3	23
39	A rank-based transcriptional signature for predicting relapse risk of stage II colorectal cancer identified with proper data sources. <i>Oncotarget</i> , 2016 , 7, 19060-71	3.3	18
38	Genomic Classification of Cutaneous Melanoma. <i>Cell</i> , 2015 , 161, 1681-96	56.2	1807
37	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , 2015 , 372, 2481-98	59.2	1828
36	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		23
35	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,	9.7	80
34	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, 1107-12	11.5	112
33	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, 878-89	12.9	84

32	Comprehensive molecular characterization of gastric adenocarcinoma. <i>Nature</i> , 2014 , 513, 202-9	50.4	3659
31	The genetic basis for inactivation of Wnt pathway in human osteosarcoma. <i>BMC Cancer</i> , 2014 , 14, 450	4.8	36
30	Post-transcriptional regulatory network of epithelial-to-mesenchymal and mesenchymal-to-epithelial transitions. <i>Journal of Hematology and Oncology</i> , 2014 , 7, 19	22.4	96
29	MiR-101 suppresses the epithelial-to-mesenchymal transition by targeting ZEB1 and ZEB2 in ovarian carcinoma. <i>Oncology Reports</i> , 2014 , 31, 2021-8	3.5	65
28	MiR-506 suppresses proliferation and induces senescence by directly targeting the CDK4/6-FOXM1 axis in ovarian cancer. <i>Journal of Pathology</i> , 2014 , 233, 308-18	9.4	96
27	HINCUTs in cancer: hypoxia-induced noncoding ultraconserved transcripts. <i>Cell Death and Differentiation</i> , 2013 , 20, 1675-87	12.7	85
26	The Cancer Genome Atlas Pan-Cancer analysis project. <i>Nature Genetics</i> , 2013 , 45, 1113-20	36.3	3933
25	Tumour angiogenesis regulation by the miR-200 family. <i>Nature Communications</i> , 2013 , 4, 2427	17.4	295
24	Integrated analyses identify a master microRNA regulatory network for the mesenchymal subtype in serous ovarian cancer. <i>Cancer Cell</i> , 2013 , 23, 186-99	24.3	305
23	Integrated Analyses Identify a Master MicroRNA Regulatory Network for the Mesenchymal Subtype in Serous Ovarian Cancer. <i>Cancer Cell</i> , 2013 , 23, 705	24.3	6
22	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, 815-22	3.5	30
21	Plasma miRNAs as diagnostic and prognostic biomarkers for ovarian cancer. <i>PLoS ONE</i> , 2013 , 8, e77853	3.7	147
20	Translational genomics in cancer research: converting profiles into personalized cancer medicine. <i>Cancer Biology and Medicine</i> , 2013 , 10, 214-20	5.2	8
19	Pitfalls in experimental designs for characterizing the transcriptional, methylational and copy number changes of oncogenes and tumor suppressor genes. <i>PLoS ONE</i> , 2013 , 8, e58163	3.7	1
18	Comprehensive molecular characterization of human colon and rectal cancer. <i>Nature</i> , 2012 , 487, 330-7	50.4	5640
17	Differing clinical impact of BRCA1 and BRCA2 mutations in serous ovarian cancer. <i>Pharmacogenomics</i> , 2012 , 13, 1523-35	2.6	50
16	Association of BRCA1 and BRCA2 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, 1557-65	27.4	379
15	Genetic amplification of the vascular endothelial growth factor (VEGF) pathway genes, including VEGFA, in human osteosarcoma. <i>Cancer</i> , 2011 , 117, 4925-38	6.4	81

14	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	4.4	23
13	Systematic interpretation of comutated genes in large-scale cancer mutation profiles. <i>Molecular Cancer Therapeutics</i> , 2010 , 9, 2186-95	6.1	11
12	Viewing cancer genes from co-evolving gene modules. <i>Bioinformatics</i> , 2010 , 26, 919-24	7.2	2
11	Deletion of the WWOX gene and frequent loss of its protein expression in human osteosarcoma. <i>Cancer Letters</i> , 2010 , 291, 31-8	9.9	45
10	Evaluation of cDNA microarray data by multiple clones mapping to the same transcript. <i>OMICS A Journal of Integrative Biology</i> , 2009 , 13, 493-9	3.8	4
9	Finding disease-specific coordinated functions by multi-function genes: insight into the coordination mechanisms in diseases. <i>Genomics</i> , 2009 , 94, 94-100	4.3	15
8	Gaining confidence in biological interpretation of the microarray data: the functional consistence of the significant GO categories. <i>Bioinformatics</i> , 2008 , 24, 265-71	7.2	40
7	Apparently low reproducibility of true differential expression discoveries in microarray studies. <i>Bioinformatics</i> , 2008 , 24, 2057-63	7.2	95
6	Characterizing Proteins with Finer Functions: A Case Study for Translational Functions of Yeast Proteins 2007 ,		1
5	GO-2D: identifying 2-dimensional cellular-localized functional modules in Gene Ontology. <i>BMC Genomics</i> , 2007 , 8, 30	4.5	13
4	Finding finer functions for partially characterized proteins by protein-protein interaction networks. <i>Science Bulletin</i> , 2007 , 52, 3363-3370		1
3	Edge-based scoring and searching method for identifying condition-responsive protein-protein interaction sub-network. <i>Bioinformatics</i> , 2007 , 23, 2121-8	7.2	115
2	Identifying disease feature genes based on cellular localized gene functional modules and regulation networks. <i>Science Bulletin</i> , 2006 , 51, 1848-1856		2
1	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, 2883-9	7.2	31