

An-Yuan Guo

List of Publications by Year in descending order

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Version: 2024-02-01

117
papers

12,276
citations

57719

44
h-index

29127

104
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120
all docs

120
docs citations

120
times ranked

17598
citing authors

#	ARTICLE	IF	CITATIONS
1	EVAtlas: a comprehensive database for ncRNA expression in human extracellular vesicles. <i>Nucleic Acids Research</i> , 2022, 50, D111-D117.	6.5	27
2	ImmuCellAI-mouse: a tool for comprehensive prediction of mouse immune cell abundance and immune microenvironment depiction. <i>Bioinformatics</i> , 2022, 38, 785-791.	1.8	53
3	A comprehensive platelet expression atlas (PEA) resource and platelet transcriptome landscape. <i>American Journal of Hematology</i> , 2022, 97, E18.	2.0	3
4	Genetic, Pharmacogenomic, and Immune Landscapes of Enhancer RNAs Across Human Cancers. <i>Cancer Research</i> , 2022, 82, 785-790.	0.4	11
5	CBX2 and EZH2 cooperatively promote the growth and metastasis of lung adenocarcinoma. <i>Molecular Therapy - Nucleic Acids</i> , 2022, 27, 670-684.	2.3	22
6	Tumor-derived extracellular vesicles induce invalid cytokine release and exhaustion of CD19 CAR-T Cells. <i>Cancer Letters</i> , 2022, 536, 215668.	3.2	11
7	Abstract LB168: Platelet RNA signature enables early and accurate detection of ovarian cancer: An intercontinental, biomarker identification study. <i>Cancer Research</i> , 2022, 82, LB168-LB168.	0.4	1
8	A miR-9-5p/FOXO1/CPEB3 Feed-Forward Loop Drives the Progression of Hepatocellular Carcinoma. <i>Cells</i> , 2022, 11, 2116.	1.8	4
9	An integrative multi-omics approach uncovers the regulatory role of CDK7 and CDK4 in autophagy activation induced by silica nanoparticles. <i>Autophagy</i> , 2021, 17, 1426-1447.	4.3	33
10	CCLA: an accurate method and web server for cancer cell line authentication using gene expression profiles. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	6
11	miRNASNP-v3: a comprehensive database for SNPs and disease-related variations in miRNAs and miRNA targets. <i>Nucleic Acids Research</i> , 2021, 49, D1276-D1281.	6.5	80
12	TCRdb: a comprehensive database for T-cell receptor sequences with powerful search function. <i>Nucleic Acids Research</i> , 2021, 49, D468-D474.	6.5	43
13	Germline Mutation of PLCD1 Contributes to Human Multiple Pilomatricomas through Protein Kinase D/Extracellular Signal-Regulated Kinase1/2 Cascade and TRPV6. <i>Journal of Investigative Dermatology</i> , 2021, 141, 533-544.	0.3	5
14	Expression profile of immune checkpoint genes and their roles in predicting immunotherapy response. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	147
15	A folate receptor 3 SNP promotes mitochondria-induced clonogenicity of CML leukemia cells: Implications for treatment free remission. <i>Clinical and Translational Medicine</i> , 2021, 11, e317.	1.7	6
16	A comprehensive survey for human transcription factors on expression, regulation, interaction, phenotype and cancer survival. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	8
17	Quercetin Ameliorates Gut Microbiota Dysbiosis That Drives Hypothalamic Damage and Hepatic Lipogenesis in Monosodium Glutamate-Induced Abdominal Obesity. <i>Frontiers in Nutrition</i> , 2021, 8, 671353.	1.6	19
18	Hypothalamic long noncoding RNA AK044061 is involved in the development of dietary obesity in mice. <i>International Journal of Obesity</i> , 2021, 45, 2638-2647.	1.6	4

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19	Case Report: Multi-Omics Analysis and CAR-T Treatment of a Chronic Myeloid Leukemia Blast Crisis Case 5 Years After the Discontinuation of TKI. <i>Frontiers in Oncology</i> , 2021, 11, 739871.	1.3	7
20	Extracellular vesicles deposit <i>PCNA</i> to rejuvenate aged bone marrow-derived mesenchymal stem cells and slow age-related degeneration. <i>Science Translational Medicine</i> , 2021, 13, .	5.8	65
21	Database Resources of the National Genomics Data Center in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D24-D33.	6.5	165
22	tRiC: a user-friendly data portal to explore the expression landscape of tRNAs in human cancers. <i>RNA Biology</i> , 2020, 17, 1674-1679.	1.5	18
23	A 6-Membrane Protein Gene score for prognostic prediction of cytogenetically normal acute myeloid leukemia in multiple cohorts. <i>Journal of Cancer</i> , 2020, 11, 251-259.	1.2	12
24	Landscape of cancer diagnostic biomarkers from specifically expressed genes. <i>Briefings in Bioinformatics</i> , 2020, 21, 2175-2184.	3.2	41
25	FFLtool: a web server for transcription factor and miRNA feed forward loop analysis in human. <i>Bioinformatics</i> , 2020, 36, 2605-2607.	1.8	19
26	Comparison of chronic myeloid leukemia stem cells and hematopoietic stem cells by global proteomic analysis. <i>Biochemical and Biophysical Research Communications</i> , 2020, 522, 362-367.	1.0	7
27	Systematic Transcriptome and Regulatory Network Analyses Reveal the Hypoglycemic Mechanism of <i>Dendrobium fimbriatum</i> . <i>Molecular Therapy - Nucleic Acids</i> , 2020, 19, 1-14.	2.3	11
28	hTFtarget: A Comprehensive Database for Regulations of Human Transcription Factors and Their Targets. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 120-128.	3.0	201
29	p.His16Arg of STXBP1 (MUNC18-1) Associated With Syntaxin 3B Causes Autosomal Dominant Congenital Nystagmus. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 591781.	1.8	6
30	Integrated omics in <i>Drosophila</i> uncover a circadian kinome. <i>Nature Communications</i> , 2020, 11, 2710.	5.8	23
31	An ultra-sensitive T-cell receptor detection method for TCR-Seq and RNA-Seq data. <i>Bioinformatics</i> , 2020, 36, 4255-4262.	1.8	13
32	The expression and regulation of HOX genes and membrane proteins among different cytogenetic groups of acute myeloid leukemia. <i>Molecular Genetics & Genomic Medicine</i> , 2020, 8, e1365.	0.6	9
33	SNP2APA: a database for evaluating effects of genetic variants on alternative polyadenylation in human cancers. <i>Nucleic Acids Research</i> , 2020, 48, D226-D232.	6.5	37
34	Genome-Wide DNA Methylation Enhances Stemness in the Mechanical Selection of Tumor-Repopulating Cells. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 88.	2.0	10
35	ImmuCellAI: A Unique Method for Comprehensive Cell Subsets Abundance Prediction and its Application in Cancer Immunotherapy. <i>Advanced Science</i> , 2020, 7, 1902880.	5.6	558
36	Time serial transcriptome reveals <i>Cyp2c29</i> as a key gene in hepatocellular carcinoma development. <i>Cancer Biology and Medicine</i> , 2020, 17, 401-417.	1.4	20

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37	Regulatory networks in mechanotransduction reveal key genes in promoting cancer cell stemness and proliferation. <i>Oncogene</i> , 2019, 38, 6818-6834.	2.6	34
38	GEDS: A Gene Expression Display Server for mRNAs, miRNAs and Proteins. <i>Cells</i> , 2019, 8, 675.	1.8	20
39	Identification of STAB1 in Multiple Datasets as a Prognostic Factor for Cytogenetically Normal AML: Mechanism and Drug Indications. <i>Molecular Therapy - Nucleic Acids</i> , 2019, 18, 476-484.	2.3	22
40	Tumor-derived extracellular vesicles inhibit osteogenesis and exacerbate myeloma bone disease. <i>Theranostics</i> , 2019, 9, 196-209.	4.6	50
41	Comprehensive characterization of circular RNAs in ~1000 human cancer cell lines. <i>Genome Medicine</i> , 2019, 11, 55.	3.6	116
42	Regulatory network analysis reveals the oncogenesis roles of feed-forward loops and therapeutic target in T-cell acute lymphoblastic leukemia. <i>BMC Medical Genomics</i> , 2019, 12, 8.	0.7	7
43	Transcriptome and Regulatory Network Analyses of CD19-CAR-T Immunotherapy for B-ALL. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 190-200.	3.0	33
44	High IL2RA mRNA expression is an independent adverse prognostic biomarker in core binding factor and intermediate-risk acute myeloid leukemia. <i>Journal of Translational Medicine</i> , 2019, 17, 191.	1.8	18
45	Tumor necrosis factor α knockout impaired tumorigenesis in chronic myeloid leukemia cells partly by metabolism modification and miRNA regulation. <i>OncoTargets and Therapy</i> , 2019, Volume 12, 2355-2364.	1.0	8
46	Transcriptome profiling reveals the anti-diabetic molecular mechanism of <i>Cyclocarya paliurus</i> polysaccharides. <i>Journal of Functional Foods</i> , 2019, 55, 1-8.	1.6	17
47	Pancan-meQTL: a database to systematically evaluate the effects of genetic variants on methylation in human cancer. <i>Nucleic Acids Research</i> , 2019, 47, D1066-D1072.	6.5	45
48	AnimalTFDB 3.0: a comprehensive resource for annotation and prediction of animal transcription factors. <i>Nucleic Acids Research</i> , 2019, 47, D33-D38.	6.5	592
49	EVmiRNA: a database of miRNA profiling in extracellular vesicles. <i>Nucleic Acids Research</i> , 2019, 47, D89-D93.	6.5	209
50	Database Resources of the BIG Data Center in 2019. <i>Nucleic Acids Research</i> , 2019, 47, D8-D14.	6.5	157
51	SAGD: a comprehensive sex-associated gene database from transcriptomes. <i>Nucleic Acids Research</i> , 2019, 47, D835-D840.	6.5	21
52	SEGreg: a database for human specifically expressed genes and their regulations in cancer and normal tissue. <i>Briefings in Bioinformatics</i> , 2019, 20, 1322-1328.	3.2	18
53	iUUCD 2.0: an update with rich annotations for ubiquitin and ubiquitin-like conjugations. <i>Nucleic Acids Research</i> , 2018, 46, D447-D453.	6.5	57
54	The Genomic Landscape and Pharmacogenomic Interactions of Clock Genes in Cancer Chronotherapy. <i>Cell Systems</i> , 2018, 6, 314-328.e2.	2.9	183

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55	Leukemia cell-derived microvesicles induce T cell exhaustion via miRNA delivery. <i>Oncolmmunology</i> , 2018, 7, e1448330.	2.1	24
56	SEGtool: a specifically expressed gene detection tool and applications in human tissue and single-cell sequencing data. <i>Briefings in Bioinformatics</i> , 2018, 19, 1325-1336.	3.2	20
57	PancanQTL: systematic identification of cis-eQTLs and trans-eQTLs in 33 cancer types. <i>Nucleic Acids Research</i> , 2018, 46, D971-D976.	6.5	191
58	lncRNASNP2: an updated database of functional SNPs and mutations in human and mouse lncRNAs. <i>Nucleic Acids Research</i> , 2018, 46, D276-D280.	6.5	199
59	dbCoRC: a database of core transcriptional regulatory circuitries modeled by H3K27ac ChIP-seq signals. <i>Nucleic Acids Research</i> , 2018, 46, D71-D77.	6.5	37
60	Global analysis of tRNA and translation factor expression reveals a dynamic landscape of translational regulation in human cancers. <i>Communications Biology</i> , 2018, 1, 234.	2.0	58
61	Integrating Transcriptome and Experiments Reveals the Anti-diabetic Mechanism of Cyclocarya paliurus Formula. <i>Molecular Therapy - Nucleic Acids</i> , 2018, 13, 419-430.	2.3	12
62	GSCALite: a web server for gene set cancer analysis. <i>Bioinformatics</i> , 2018, 34, 3771-3772.	1.8	671
63	Differential Co-expression and Regulatory Network Analysis Uncover the Relapse Factor and Mechanism of T Cell Acute Leukemia. <i>Molecular Therapy - Nucleic Acids</i> , 2018, 12, 184-194.	2.3	20
64	Investigating the Molecular Mechanism of Aqueous Extract of Cyclocarya paliurus on Ameliorating Diabetes by Transcriptome Profiling. <i>Frontiers in Pharmacology</i> , 2018, 9, 912.	1.6	9
65	Genomic landscape and mutational impacts of recurrently mutated genes in cancers. <i>Molecular Genetics & Genomic Medicine</i> , 2018, 6, 910-923.	0.6	15
66	The ASH1-miR-375-YWHAZ Signaling Axis Regulates Tumor Properties in Hepatocellular Carcinoma. <i>Molecular Therapy - Nucleic Acids</i> , 2018, 11, 538-553.	2.3	45
67	lncRInter: A database of experimentally validated long non-coding RNA interaction. <i>Journal of Genetics and Genomics</i> , 2017, 44, 265-268.	1.7	35
68	Interferon- β alters the immune-related miRNA expression of microvesicles derived from mesenchymal stem cells. <i>Journal of Huazhong University of Science and Technology [Medical Sciences]</i> , 2017, 37, 179-184.	1.0	14
69	Ablation of EYS in zebrafish causes mislocalisation of outer segment proteins, F-actin disruption and cone-rod dystrophy. <i>Scientific Reports</i> , 2017, 7, 46098.	1.6	52
70	A Pan-cancer Analysis of the Expression and Clinical Relevance of Small Nucleolar RNAs in Human Cancer. <i>Cell Reports</i> , 2017, 21, 1968-1981.	2.9	186
71	LNCEditing: a database for functional effects of RNA editing in lncRNAs. <i>Nucleic Acids Research</i> , 2017, 45, D79-D84.	6.5	111
72	Microvesicles as Potential Biomarkers for the Identification of Senescence in Human Mesenchymal Stem Cells. <i>Theranostics</i> , 2017, 7, 2673-2689.	4.6	82

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73	Tumor Cell-Derived Microvesicles Induced Not Epithelial-Mesenchymal Transition but Apoptosis in Human Proximal Tubular (HK-2) Cells: Implications for Renal Impairment in Multiple Myeloma. <i>International Journal of Molecular Sciences</i> , 2017, 18, 513.	1.8	6
74	Gene expression, regulation of DEN and HBx induced HCC mice models and comparisons of tumor, para-tumor and normal tissues. <i>BMC Cancer</i> , 2017, 17, 862.	1.1	19
75	MicroRNA regulatory pathway analysis identifies miR-142-5p as a negative regulator of TGF- β 2 pathway via targeting SMAD3. <i>Oncotarget</i> , 2016, 7, 71504-71513.	0.8	48
76	Mesenchymal Stem Cell-Derived Microvesicles Support Ex Vivo Expansion of Cord Blood-Derived CD34 ⁺ Cells. <i>Stem Cells International</i> , 2016, 2016, 1-13.	1.2	40
77	Loss-of-function Mutation in PMVK Causes Autosomal Dominant Disseminated Superficial Porokeratosis. <i>Scientific Reports</i> , 2016, 6, 24226.	1.6	21
78	miR-146b-5p within BCR-ABL1 ⁺ Positive Microvesicles Promotes Leukemic Transformation of Hematopoietic Cells. <i>Cancer Research</i> , 2016, 76, 2901-2911.	0.4	88
79	A clinical observation of Chinese chronic myelogenous leukemia patients after discontinuation of tyrosine kinase inhibitors. <i>Oncotarget</i> , 2016, 7, 58234-58243.	0.8	7
80	Transcription factor and miRNA co-regulatory network reveals shared and specific regulators in the development of B cell and T cell. <i>Scientific Reports</i> , 2015, 5, 15215.	1.6	60
81	Scoring the correlation of genes by their shared properties using OScal, an improved overlap quantification model. <i>Scientific Reports</i> , 2015, 5, 10583.	1.6	1
82	An update of miRNASNP database for better SNP selection by GWAS data, miRNA expression and online tools. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav029.	1.4	110
83	Impact of collection, isolation and storage methodology of circulating microvesicles on flow cytometric analysis. <i>Experimental and Therapeutic Medicine</i> , 2015, 10, 2093-2101.	0.8	12
84	GSDB 2.0: an upgraded gene feature visualization server. <i>Bioinformatics</i> , 2015, 31, 1296-1297.	1.8	3,092
85	lncRNASNP: a database of SNPs in lncRNAs and their potential functions in human and mouse. <i>Nucleic Acids Research</i> , 2015, 43, D181-D186.	6.5	204
86	MiRNA and TF co-regulatory network analysis for the pathology and recurrence of myocardial infarction. <i>Scientific Reports</i> , 2015, 5, 9653.	1.6	41
87	AnimalTFDB 2.0: a resource for expression, prediction and functional study of animal transcription factors. <i>Nucleic Acids Research</i> , 2015, 43, D76-D81.	6.5	287
88	The regulation of microRNA expression by DNA methylation in hepatocellular carcinoma. <i>Molecular BioSystems</i> , 2015, 11, 532-539.	2.9	64
89	Transcription factor and microRNA co-regulatory loops: important regulatory motifs in biological processes and diseases. <i>Briefings in Bioinformatics</i> , 2015, 16, 45-58.	3.2	175
90	Integrative Genomic Analysis Identifies That SERPINA6-rs1998056 Regulated by FOXA/ER α Is Associated with Female Hepatocellular Carcinoma. <i>PLoS ONE</i> , 2014, 9, e107246.	1.1	9

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91	Comprehensive analysis of human small RNA sequencing data provides insights into expression profiles and miRNA editing. <i>RNA Biology</i> , 2014, 11, 1375-1385.	1.5	78
92	The evolutionary analysis reveals domain fusion of proteins with Frizzled-like CRD domain. <i>Gene</i> , 2014, 533, 229-239.	1.0	23
93	Evolution, functional divergence and conserved exon-intron structure of bHLH/PAS gene family. <i>Molecular Genetics and Genomics</i> , 2014, 289, 25-36.	1.0	20
94	EKPD: a hierarchical database of eukaryotic protein kinases and protein phosphatases. <i>Nucleic Acids Research</i> , 2014, 42, D496-D502.	6.5	52
95	A genetic variant in microRNA target site of TGF- β 2 signaling pathway increases the risk of colorectal cancer in a Chinese population. <i>Tumor Biology</i> , 2014, 35, 4301-4306.	0.8	14
96	CPLM: a database of protein lysine modifications. <i>Nucleic Acids Research</i> , 2014, 42, D531-D536.	6.5	155
97	Bioinformatics analysis identifies miR-221 as a core regulator in hepatocellular carcinoma and its silencing suppresses tumor properties. <i>Oncology Reports</i> , 2014, 32, 1200-1210.	1.2	44
98	Exome Sequencing Identified NRG3 as a Novel Susceptible Gene of Hirschsprung's Disease in a Chinese Population. <i>Molecular Neurobiology</i> , 2013, 47, 957-966.	1.9	30
99	The sacred lotus genome provides insights into the evolution of flowering plants. <i>Plant Journal</i> , 2013, 76, 557-567.	2.8	75
100	Identification of Novel and Differentially Expressed MicroRNAs in the Ovaries of Laying and Non-Laying Ducks. <i>Journal of Integrative Agriculture</i> , 2013, 12, 136-146.	1.7	14
101	Phylogenetic analysis reveals the evolution and diversification of cyclins in eukaryotes. <i>Molecular Phylogenetics and Evolution</i> , 2013, 66, 1002-1010.	1.2	33
102	UUCD: a family-based database of ubiquitin and ubiquitin-like conjugation. <i>Nucleic Acids Research</i> , 2013, 41, D445-D451.	6.5	99
103	Integration of Transcriptome, Proteome and Metabolism Data Reveals the Alkaloids Biosynthesis in <i>Macleaya cordata</i> and <i>Macleaya microcarpa</i> . <i>PLoS ONE</i> , 2013, 8, e53409.	1.1	61
104	MLL1, a Histone H3K4 Methyltransferase, Regulates the Expression of TNF α -mediated NF- κ B Downstream Genes. <i>Journal of Cell Science</i> , 2012, 125, 4058-66.	1.2	63
105	AnimalTFDB: a comprehensive animal transcription factor database. <i>Nucleic Acids Research</i> , 2012, 40, D144-D149.	6.5	265
106	The Genome of <i>Ganderma lucidum</i> Provide Insights into Triterpense Biosynthesis and Wood Degradation. <i>PLoS ONE</i> , 2012, 7, e36146.	1.1	78
107	Comparative and Evolutionary Analysis of the HES/HEY Gene Family Reveal Exon/Intron Loss and Teleost Specific Duplication Events. <i>PLoS ONE</i> , 2012, 7, e40649.	1.1	26
108	Meta-analyses of genome-wide linkage scans of anxiety-related phenotypes. <i>European Journal of Human Genetics</i> , 2012, 20, 1078-1084.	1.4	28

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109	MicroRNA and transcription factor co-regulatory network analysis reveals miR-19 inhibits CYLD in T-cell acute lymphoblastic leukemia. <i>Nucleic Acids Research</i> , 2012, 40, 5201-5214.	6.5	119
110	Genome-wide identification of SNPs in microRNA genes and the SNP effects on microRNA target binding and biogenesis. <i>Human Mutation</i> , 2012, 33, 254-263.	1.1	343
111	Prioritization and Association Analysis of Murine-Derived Candidate Genes in Anxiety-Spectrum Disorders. <i>Biological Psychiatry</i> , 2011, 70, 888-896.	0.7	25
112	Network Analysis of EtOH-Related Candidate Genes. <i>Chemistry and Biodiversity</i> , 2010, 7, 1142-1152.	1.0	3
113	New Genomic Structure for Prostate Cancer Specific Gene PCA3 within BMCC1: Implications for Prostate Cancer Detection and Progression. <i>PLoS ONE</i> , 2009, 4, e4995.	1.1	74
114	Genome-wide identification and evolutionary analysis of the plant specific SBP-box transcription factor family. <i>Gene</i> , 2008, 418, 1-8.	1.0	227
115	PlantTFDB: a comprehensive plant transcription factor database. <i>Nucleic Acids Research</i> , 2007, 36, D966-D969.	6.5	210
116	Identification of a Naturally Occurring Recombinant Isolate of Sugarcane Mosaic Virus Causing Maize Dwarf Mosaic Disease. <i>Virus Genes</i> , 2005, 30, 75-83.	0.7	33
117	DATF: a database of Arabidopsis transcription factors. <i>Bioinformatics</i> , 2005, 21, 2568-2569.	1.8	296