Youping Deng

List of Publications by Year
in descending order

124 papers	6,814 citations	94433 37 h-index	69250 77 g-index
130 all docs	130 docs citations	130 times ranked	12196 citing authors

#	Article	IF	Citations
1	Development of a tRNA-derived small RNA diagnostic and prognostic signature in liver cancer. Genes and Diseases, 2022, 9, 393-400.	3.4	12
2	T-cell activation decreases miRNA-15a/16 levels to promote MEK1â€"ERK1/2â€"Elk1 signaling and proliferative capacity. Journal of Biological Chemistry, 2022, 298, 101634.	3.4	3
3	Prognostic Factors for COVID-19 Hospitalized Patients with Preexisting Type 2 Diabetes. International Journal of Endocrinology, 2022, 2022, 1-13.	1.5	5
4	Analysis and Performance Assessment of the Whole Genome Bisulfite Sequencing Data Workflow: Currently Available Tools and a Practical Guide to Advance DNA Methylation Studies. Small Methods, 2022, 6, e2101251.	8.6	10
5	Editorial: Early Detection and Diagnosis of Cancer. Frontiers in Genetics, 2022, 13, 875421.	2.3	0
6	Sulfite preservatives effects on the mouth microbiome: Changes in viability, diversity and composition of microbiota. PLoS ONE, 2022, 17, e0265249.	2.5	5
7	Association of Septic Shock with Mortality in Hospitalized COVID-19 Patients in Wuhan, China. Advances in Virology, 2022, 2022, 1-9.	1.1	9
8	MRTF-A-mediated protection against amyloid-Î²-induced neuronal injury correlates with restoring autophagy via miR-1273g-3p/mTOR axis in Alzheimer models. Aging, 2022, 14, 4305-4325.	3.1	10
9	RNA-Sequencing based analysis of bovine endometrium during the maternal recognition of pregnancy. BMC Genomics, 2022, 23, .	2.8	7
10	Corrigendum to â€œPrognostic Factors for COVID-19 Hospitalized Patients with Preexisting Type 2 Diabetesâ€• International Journal of Endocrinology, 2022, 2022, 1-1.	1.5	0
11	Regulation of endoplasmic reticulum stress and trophectoderm lineage specification by the mevalonate pathway in the mouse preimplantation embryo. Molecular Human Reproduction, 2021, 27, .	2.8	4
12	COVID-19 drug practices risk antimicrobial resistance evolution. Lancet Microbe, The, 2021, 2, e135-e136.	7.3	47
13	The function of LncRNAs and their role in the prediction, diagnosis, and prognosis of lung cancer. Clinical and Translational Medicine, 2021, 11, e367.	4.0	61
14	Machine Learning and Metabolomics: Diagnosis of Malignant Breast Cancer. FASEB Journal, 2021, 35, .	0.5	0
15	RNA sequencing-based analysis of the magnum tissues revealed the novel genes and biological pathways involved in the egg-white formation in the laying hen. BMC Genomics, 2021, 22, 318.	2.8	9
16	Upregulated ethanolamine phospholipid synthesis via selenoprotein I is required for effective metabolic reprogramming during T cell activation. Molecular Metabolism, 2021, 47, 101170.	6.5	19
17	Comprehensive Analysis of a tRNA-Derived Small RNA in Colorectal Cancer. Frontiers in Oncology, 2021, 11, 701440.	2.8	9
18	Bacterial Diversity Correlates with Overall Survival in Cancers of the Head and Neck, Liver, and Stomach. Molecules, 2021, 26, 5659.	3.8	7

#	Article	IF	Citations
19	Dysregulated KRAS gene-signaling axis and abnormal chromatin remodeling drive therapeutic resistance in heterogeneous-sized circulating tumor cells in gastric cancer patients. Cancer Letters, 2021, 517, 78-87.	7.2	14
20	The miRNA Profile of Inflammatory Colorectal Tumors Identify TGF-β as a Companion Target for Checkpoint Blockade Immunotherapy. Frontiers in Cell and Developmental Biology, 2021, 9, 754507.	3.7	3
21	Focal Point of Fanconi Anemia Signaling. International Journal of Molecular Sciences, 2021, 22, 12976.	4.1	6
22	The SEQC2 epigenomics quality control (EpiQC) study. Genome Biology, 2021, 22, 332.	8.8	20
23	Identification of plasma lipid species as promising diagnostic markers for prostate cancer. BMC Medical Informatics and Decision Making, 2020, 20, 223.	3.0	14
24	Editorial: Cancer Informatics Toward Precision Medicine. Frontiers in Medicine, 2020, 7, 576611.	2.6	0
25	Development of predicitve models to distinguish metals from non-metal toxicants, and individual metal from one another. BMC Bioinformatics, 2020, 21, 239.	2.6	2
26	Tissue-associated microbial detection in cancer using human sequencing data. BMC Bioinformatics, 2020, 21, 523.	2.6	7
27	Current trend and development in bioinformatics research. BMC Bioinformatics, 2020, 21, 538.	2.6	20
28	miR-125 family regulates XIRP1 and FIH in response to myocardial infarction. Physiological Genomics, 2020, 52, 358-368.	2.3	1
29	The Function and Mechanism of Lipid Molecules and Their Roles in The Diagnosis and Prognosis of Breast Cancer. Molecules, 2020, 25, 4864.	3.8	31
30	Lack of Efficacy of Combined Carbohydrate Antigen Markers for Lung Cancer Diagnosis. Disease Markers, 2020, 2020, 1-10.	1.3	8
31	The values of AHCY and CBS promoter methylation on the diagnosis of cerebral infarction in Chinese Han population. BMC Medical Genomics, 2020, 13, 163.	1.5	3
32	Risk Factors Associated With Clinical Outcomes in 323 Coronavirus Disease 2019 (COVID-19) Hospitalized Patients in Wuhan, China. Clinical Infectious Diseases, 2020, 71, 2089-2098.	5.8	309
33	The landscape of bacterial presence in tumor and adjacent normal tissue across 9 major cancer types using TCGA exome sequencing. Computational and Structural Biotechnology Journal, 2020, 18, 631-641.	4.1	32
34	Disabled Homolog 2 (DAB2) Protein in Tumor Microenvironment Correlates with Aggressive Phenotype in Human Urothelial Carcinoma of the Bladder. Diagnostics, 2020, 10, 54.	2.6	13
35	Identification of lncRNA biomarkers for lung cancer through integrative cross-platform data analyses. Aging, 2020, 12, 14506-14527.	3.1	12
36	Protective effect of DLX6-AS1 silencing against cerebral ischemia/reperfusion induced impairments. Aging, 2020, 12, 23096-23113.	3.1	10

#	Article	IF	Citations
37	Multi-antigen Vaccination With Simultaneous Engagement of the OX40 Receptor Delays Malignant Mesothelioma Growth and Increases Survival in Animal Models. Frontiers in Oncology, 2019, 9, 720.	2.8	7
38	Combined Omics Reveals That Disruption of the Selenocysteine Lyase Gene Affects Amino Acid Pathways in Mice. Nutrients, 2019, 11, 2584.	4.1	6
39	Development of somatic mutation signatures for risk stratification and prognosis in lung and colorectal adenocarcinomas. BMC Medical Genomics, 2019, 12, 24.	1.5	9
40	Ratio-Based Method To Identify True Biomarkers by Normalizing Circulating ncRNA Sequencing and Quantitative PCR Data. Analytical Chemistry, 2019, 91, 6746-6753.	6.5	18
41	Development of a miRNA-seq based prognostic signature in lung adenocarcinoma. BMC Cancer, 2019, 19, 34.	2.6	22
42	Abstract 2828: Bacterial diversity correlates with tumor stage and survival in stomach and lung TCGA cancer cohorts. , 2019, , .		0
43	Strategy for an Association Study of the Intestinal Microbiome and Brain Metabolome Across the Lifespan of Rats. Analytical Chemistry, 2018, 90, 2475-2483.	6.5	32
44	RNA sequencing-based analysis of the laying hen uterus revealed the novel genes and biological pathways involved in the eggshell biomineralization. Scientific Reports, 2018, 8, 16853.	3.3	39
45	The emerging role of microRNA-4487/6845-3p in Alzheimerâ€™s disease pathologies is induced by AÎ²25â€"35 triggered in SH-SY5Y cell. BMC Systems Biology, 2018, 12, 119.	3.0	20
46	Increased AURKA promotes cell proliferation and predicts poor prognosis in bladder cancer. BMC Systems Biology, 2018, 12, 118.	3.0	38
47	The Evaluation of Serum Biomarkers for Non-small Cell Lung Cancer (NSCLC) Diagnosis. Frontiers in Physiology, 2018, 9, 1710.	2.8	22
48	Plasma small ncRNA pair panels as novel biomarkers for early-stage lung adenocarcinoma screening. BMC Genomics, 2018, 19, 545.	2.8	20
49	Global lipidomics reveals two plasma lipids as novel biomarkers for the detection of squamous cell lung cancer: A pilot study. Oncology Letters, 2018, 16, 761-768.	1.8	14
50	Plasma MicroRNA Pair Panels as Novel Biomarkers for Detection of Early Stage Breast Cancer. Frontiers in Physiology, 2018, 9, 1879.	2.8	44
51	Selenoprotein K deficiency inhibits melanoma by reducing calcium flux required for tumor growth and metastasis. Oncotarget, 2018, 9, 13407-13422.	1.8	25
52	Collagen type IV alpha 1 (COL4A1) and collagen type XIII alpha 1 (COL13A1) produced in cancer cells promote tumor budding at the invasion front in human urothelial carcinoma of the bladder. Oncotarget, 2017, 8, 36099-36114.	1.8	76
53	Global lipidomics identified plasma lipids as novel biomarkers for early detection of lung cancer. Oncotarget, 2017, 8, 107899-107906.	1.8	39
54	Evaluation of Plasma miR-21 and miR-152 as Diagnostic Biomarkers for Common Types of Human Cancers. Journal of Cancer, 2016, 7, 490-499.	2.5	68

#	Article	IF	Citations
55	Functional Genomics, Genetics, and Bioinformatics 2016. BioMed Research International, 2016, 2016, 1-3.	1.9	1
56	Lipoprotein(a) and Increased Cardiovascular Risk in Women. Clinical Cardiology, 2016, 39, 96-102.	1.8	10
57	Association of six CpG-SNPs in the inflammation-related genes with coronary heart disease. Human Genomics, 2016, 10, 21.	2.9	22
58	Gene silencing of USP1 by lentivirus effectively inhibits proliferation and invasion of human osteosarcoma cells. International Journal of Oncology, 2016, 49, 2549-2557.	3.3	29
59	The clinical significance of snail protein expression in gastric cancer: a meta-analysis. Human Genomics, 2016, 10, 22.	2.9	20
60	Integrative microRNA and gene profiling data analysis reveals novel biomarkers and mechanisms for lung cancer. Oncotarget, 2016, 7, 8441-8454.	1.8	53
61	Plasma lipidomics profiling identified lipid biomarkers in distinguishing early-stage breast cancer from benign lesions. Oncotarget, 2016, 7, 36622-36631.	1.8	91
62	Functional Genomics, Genetics, and Bioinformatics. BioMed Research International, 2015, 2015, 1-3.	1.9	1
63	Effect of Celastrol on Growth Inhibition of Prostate Cancer Cells through the Regulation of hERG Channel<i>In Vitro</i>. BioMed Research International, 2015, 2015, 1-7.	1.9	27
64	Epicardial adipose tissue has a unique transcriptome modified in severe coronary artery disease. Obesity, 2015, 23, 1267-1278.	3.0	86
65	Prevalent Polymorphism in Thyroid Hormone-Activating Enzyme Leaves a Genetic Fingerprint That Underlies Associated Clinical Syndromes. Journal of Clinical Endocrinology and Metabolism, 2015, 100, 920-933.	3.6	75
66	A lack of association between the IKZF2 rs12619285 polymorphism and coronary heart disease. Experimental and Therapeutic Medicine, 2015, 9, 1309-1313.	1.8	5
67	Comparison of RNA-seq and microarray-based models for clinical endpoint prediction. Genome Biology, 2015, 16, 133.	8.8	325
68	Characterization and Early Detection of Balance Deficits in Fragile X Premutation Carriers With and Without Fragile X-Associated Tremor/Ataxia Syndrome (FXTAS). Cerebellum, 2015, 14, 650-662.	2.5	31
69	A seven-gene CpG-island methylation panel predicts breast cancer progression. BMC Cancer, 2015, 15, 417.	2.6	30
70	PTHGRN: unraveling post-translational hierarchical gene regulatory networks using PPI, ChIP-seq and gene expression data. Nucleic Acids Research, 2014, 42, W130-W136.	14.5	34
71	CMGRN: a web server for constructing multilevel gene regulatory networks using ChIP-seq and gene expression data. Bioinformatics, 2014, 30, 1190-1192.	4.1	29
72	Identification and characterization of the novel Col10a1 regulatory mechanism during chondrocyte hypertrophic differentiation. Cell Death and Disease, 2014, 5, e1469-e1469.	6.3	75

#	ARTICLE	IF	CITATIONS
73	Hedgehog signaling induces osteosarcoma development through Yap1 and H19 overexpression. Oncogene, 2014, 33, 4857-4866.	5.9	136
74	Commonality and differences of methylation signatures in the plasma of patients with pancreatic cancer and colorectal cancer. International Journal of Cancer, 2014, 134, 2656-2662.	5.1	23
75	A comprehensive assessment of RNA-seq accuracy, reproducibility and information content by the Sequencing Quality Control Consortium. Nature Biotechnology, 2014, 32, 903-914.	17.5	883
76	The concordance between RNA-seq and microarray data depends on chemical treatment and transcript abundance. Nature Biotechnology, 2014, 32, 926-932.	17.5	420
77	Identification of biomarkers that distinguish chemical contaminants based on gene expression profiles. BMC Genomics, 2014, 15, 248.	2.8	24
78	Network and Pathway Analysis of Cancer Susceptibility (A). Cancer Informatics, 2014, 13s5, CIN.S24095.	1.9	9
79	RNA-Seq and Network Analysis Revealed Interacting Pathways in TGF-Î²-Treated Lung Cancer Cell Lines. Cancer Informatics, 2014, 13s5, CIN.S14073.	1.9	7
80	Pathway-based Biomarkers for Breast Cancer in Proteomics. Cancer Informatics, 2014, 13s5, CIN.S14069.	1.9	1
81	Identification of genes and pathways involved in kidney renal clear cell carcinoma. BMC Bioinformatics, 2014, 15, S2.	2.6	45
82	Circulating microRNA profiling for early detection of non-small cell lung cancer.. Journal of Clinical Oncology, 2014, 32, e22051-e22051.	1.6	2
83	Integrated lipidomics and transcriptomic analysis of peripheral blood reveals significantly enriched pathways in type 2 diabetes mellitus. BMC Medical Genomics, 2013, 6, S12.	1.5	51
84	HDAM: a resource of human disease associated mutations from next generation sequencing studies. BMC Medical Genomics, 2013, 6, S16.	1.5	3
85	Exploring the pathogenetic association between schizophrenia and type 2 diabetes mellitus diseases based on pathway analysis. BMC Medical Genomics, 2013, 6, S17.	1.5	63
86	Multiple Biomarker Panels for Early Detection of Breast Cancer in Peripheral Blood. BioMed Research International, 2013, 2013, 1-7.	1.9	9
87	Two lipids based on lipidomics as novel biomarkers for early detection of squamous cell lung cancer.. Journal of Clinical Oncology, 2013, 31, 11114-11114.	1.6	0
88	Identification of Plasma Lipid Biomarkers for Prostate Cancer by Lipidomics and Bioinformatics. PLoS ONE, 2012, 7, e48889.	2.5	169
89	State Space Model with hidden variables for reconstruction of gene regulatory networks. BMC Systems Biology, 2011, 5, S3.	3.0	24
90	Maximum predictive power of the microarray-based models for clinical outcomes is limited by correlation between endpoint and gene expression profile. BMC Genomics, 2011, 12, S3.	2.8	6

#	Article	IF	Citations
91	Maximizing biomarker discovery by minimizing gene signatures. BMC Genomics, 2011, 12, S6.	2.8	7
92	Analysis of Common and Specific Mechanisms of Liver Function Affected by Nitrotoluene Compounds. PLoS ONE, 2011, 6, e14662.	2.5	33
93	Primary Central Nervous System Lymphoma (PCNSL) in Immunocompetent Patients: An Analysis of Prognostic Factors and Treatment Strategies. Blood, 2011, 118, 4955-4955.	1.4	0
94	Chronic Lymphocytic Leukemia (CLL)/Small Lymphocytic Leukemia (SLL) Exhibit Altered Cytokine Protein Levels in Peripheral Blood Serum. Blood, 2011, 118, 2646-2646.	1.4	0
95	Recent advances in clustering methods for protein interaction networks. BMC Genomics, 2010, 11, S10.	2.8	104
96	A new approach to construct pathway connected networks and its application in dose responsive gene expression profiles of rat liver regulated by 2,4DNT. BMC Genomics, 2010, 11, S4.	2.8	5
97	In vitro gene regulatory networks predict in vivo function of liver. BMC Systems Biology, 2010, 4, 153.	3.0	25
98	The MicroArray Quality Control (MAQC)-II study of common practices for the development and validation of microarray-based predictive models. Nature Biotechnology, 2010, 28, 827-838.	17.5	795
99	A comparison of batch effect removal methods for enhancement of prediction performance using MAQC-II microarray gene expression data. Pharmacogenomics Journal, 2010, 10, 278-291.	2.0	249
100	Feature Selection and Classification of MAQC-II Breast Cancer and Multiple Myeloma Microarray Gene Expression Data. PLoS ONE, 2009, 4, e8250.	2.5	45
101	Essential role of PSM/SH2â€B variants in insulin receptor catalytic activation and the resulting cellular responses. Journal of Cellular Biochemistry, 2008, 103, 162-181.	2.6	14
102	PSM/SH2B1 splice variants: Critical role in src catalytic activation and the resulting STAT3sâ€mediated mitogenic response. Journal of Cellular Biochemistry, 2008, 104, 105-118.	2.6	11
103	Mitogenic roles of Gab1 and Grb10 as direct cellular partners in the regulation of MAP kinase signaling. Journal of Cellular Biochemistry, 2008, 105, 1172-1182.	2.6	19
104	Promoting synergistic research and education in genomics and bioinformatics. BMC Genomics, 2008, 9, I1.	2.8	19
105	A comparative study of different machine learning methods on microarray gene expression data. BMC Genomics, 2008, 9, S13.	2.8	199
106	Transcriptomic analysis of RDX and TNT interactive sublethal effects in the earthworm Eisenia fetida. BMC Genomics, 2008, 9, S15.	2.8	42
107	Genomics, molecular imaging, bioinformatics, and bio-nano-info integration are synergistic components of translational medicine and personalized healthcare research. BMC Genomics, 2008, 9, I1.	2.8	9
108	ILOOP â€" a web application for two-channel microarray interwoven loop design. BMC Genomics, 2008, 9, S11.	2.8	10

#	Article	IF	Citations
109	An Effective Interwoven Loop Design Application for Two-Channel Microarray Experiments. , 2007, , .		0
110	Toxicogenomic Analysis Provides New Insights into Molecular Mechanisms of the Sublethal Toxicity of 2,4,6-Trinitrotoluene in Eisenia fetida. Environmental Science & Technology, 2007, 41, 8195-8202.	10.0	58
111	PSM/SH2-B distributes selected mitogenic receptor signals to distinct components in the PI3-kinase and MAP kinase signaling pathways. Journal of Cellular Biochemistry, 2007, 100, 557-573.	2.6	9
112	Comparison of probabilistic Boolean network and dynamic Bayesian network approaches for inferring gene regulatory networks. BMC Bioinformatics, 2007, 8, S13.	2.6	78
113	Cloning, analysis and functional annotation of expressed sequence tags from the Earthworm Eisenia fetida. BMC Bioinformatics, 2007, 8, S7.	2.6	52
114	SVM Classifier â€" a comprehensive java interface for support vector machine classification of microarray data. BMC Bioinformatics, 2006, 7, S25.	2.6	40
115	Molecular Basis of Plant Gene Expression During Aphid Invasion: Wheat Pto- and Pti-Like Sequences Are Involved in Interactions Between Wheat and Russian Wheat Aphid (Homoptera: Aphididae). Journal of Economic Entomology, 2006, 99, 1430-1445.	1.8	77
116	Computational identification of novel chitinase-like proteins in the <i>Drosophila melanogaster</i> genome. Bioinformatics, 2004, 20, 161-169.	4.1	90
117	Incremental genetic K-means algorithm and its application in gene expression data analysis. BMC Bioinformatics, 2004, 5, 172.	2.6	87
118	Joint analysis of two microarray gene-expression data sets to select lung adenocarcinoma marker genes. BMC Bioinformatics, 2004, 5, 81.	2.6	228
119	FGKA. , 2004, , .		95
120	Growth Factor Receptor-binding Protein 10 (Grb10) as a Partner of Phosphatidylinositol 3-Kinase in Metabolic Insulin Action. Journal of Biological Chemistry, 2003, 278, 39311-39322.	3.4	53
121	Four PSM/SH2-B Alternative Splice Variants and Their Differential Roles in Mitogenesis. Journal of Biological Chemistry, 2001, 276, 40940-40948.	3.4	64
122	PSM, a mediator of PDGF-BB-, IGF-I-, and insulin-stimulated mitogenesis. Oncogene, 2000, 19, 39-50.	5.9	42
123	Arsenic trioxide induces apoptosis of HPV16 DNA-immortalized human cervical epithelial cells and selectively inhibits viral gene expression. , 1999, 82, 286-292.		77
124	Grb10, a Positive, Stimulatory Signaling Adapter in Platelet-Derived Growth Factor BB-, Insulin-Like Growth Factor I-, and Insulin-Mediated Mitogenesis. Molecular and Cellular Biology, 1999, 19, 6217-6228.	2.3	110