

# Xinan Yang

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/12201672/publications.pdf>

Version: 2024-02-01

22  
papers

1,295  
citations

623574

14  
h-index

677027

22  
g-index

22  
all docs

22  
docs citations

22  
times ranked

2962  
citing authors

#	ARTICLE	IF	CITATIONS
1	A c-Myc-regulated stem cell-like signature in high-risk neuroblastoma: A systematic discovery (Target) Tj ETQq1 1 0,784314 rgBT /Ove	1.6	90
2	<i>Pitx2</i> modulates a <i>Tbx5</i> -dependent gene regulatory network to maintain atrial rhythm. Science Translational Medicine, 2016, 8, 354ra115.	5.8	123
3	Integrative genomics analyses unveil downstream biological effectors of disease-specific polymorphisms buried in intergenic regions. Npj Genomic Medicine, 2016, 1, .	1.7	19
4	Seq2pathway: an R/Bioconductor package for pathway analysis of next-generation sequencing data. Bioinformatics, 2015, 31, 3043-3045.	1.8	23
5	Computational prognostic indicators for breast cancer. Cancer Management and Research, 2014, 6, 301.	0.9	10
6	Curation-free biomodules mechanisms in prostate cancer predict recurrent disease. BMC Medical Genomics, 2013, 6, S4.	0.7	9
7	Identification of a 24-Gene Prognostic Signature That Improves the European LeukemiaNet Risk Classification of Acute Myeloid Leukemia: An International Collaborative Study. Journal of Clinical Oncology, 2013, 31, 1172-1181.	0.8	164
8	Bridging Cancer Biology with the Clinic: Relative Expression of a GRHL2-Mediated Gene-Set Pair Predicts Breast Cancer Metastasis. PLoS ONE, 2013, 8, e56195.	1.1	36
9	Up-regulation of a HOXA-PBX3 homeobox-gene signature following down-regulation of miR-181 is associated with adverse prognosis in patients with cytogenetically abnormal AML. Blood, 2012, 119, 2314-2324.	0.6	145
10	Single Sample Expression-Anchored Mechanisms Predict Survival in Head and Neck Cancer. PLoS Computational Biology, 2012, 8, e1002350.	1.5	75
11	Towards mechanism classifiers: expression-anchored Gene Ontology signature predicts clinical outcome in lung adenocarcinoma patients. AMIA ... Annual Symposium proceedings, 2012, 2012, 1040-9.	0.2	7
12	MicroRNA Expression Characterizes Oligometastasis(es). PLoS ONE, 2011, 6, e28650.	1.1	242
13	<i>GO-Module</i> : functional synthesis and improved interpretation of Gene Ontology patterns. Bioinformatics, 2011, 27, 1444-1446.	1.8	97
14	Identification of common microRNA-mRNA regulatory biomodules in human epithelial cancer. Science Bulletin, 2010, 55, 3576-3589.	1.7	8
15	Stromal microenvironment processes unveiled by biological component analysis of gene expression in xenograft tumor models. BMC Bioinformatics, 2010, 11, S11.	1.2	4
16	Network Modeling Identifies Molecular Functions Targeted by miR-204 to Suppress Head and Neck Tumor Metastasis. PLoS Computational Biology, 2010, 6, e1000730.	1.5	140
17	Meta-analysis of Cancer Gene-Profiling Data. Methods in Molecular Biology, 2009, 576, 409-426.	0.4	3
18	Mechanism-anchored profiling derived from epigenetic networks predicts outcome in acute lymphoblastic leukemia. BMC Bioinformatics, 2009, 10, S6.	1.2	9

#	ARTICLE	IF	CITATIONS
19	Meta-analysis of several gene lists for distinct types of cancer: A simple way to reveal common prognostic markers. <i>BMC Bioinformatics</i> , 2007, 8, 118.	1.2	26
20	OrderedList--a bioconductor package for detecting similarity in ordered gene lists. <i>Bioinformatics</i> , 2006, 22, 2315-2316.	1.8	65
21	SIMILARITIES OF ORDERED GENE LISTS. <i>Journal of Bioinformatics and Computational Biology</i> , 2006, 04, 693-708.	0.3	48
22	Detecting Common Gene Expression Patterns in Multiple Cancer Outcome Entities. <i>Biomedical Microdevices</i> , 2005, 7, 247-251.	1.4	12