Xinan Yang

List of Publications by Year
in descending order

14 **papers**	365 **citations**	1040056 9 **h-index**	1058476 14 **g-index**
15 **all docs**	15 **docs citations**	15 **times ranked**	965 **citing authors**

#	Article	IF	Citations
1	Foxf Genes Integrate Tbx5 and Hedgehog Pathways in the Second Heart Field for Cardiac Septation. PLoS Genetics, 2014, 10, e1004604.	3.5	79
2	The Cardiac TBX5 Interactome Reveals a Chromatin Remodeling Network Essential for Cardiac Septation. Developmental Cell, 2016, 36, 262-275.	7.0	71
3	Cilia gene mutations cause atrioventricular septal defects by multiple mechanisms. Human Molecular Genetics, 2016, 25, ddw155.	2.9	37
4	Bridging Cancer Biology with the Clinic: Relative Expression of a GRHL2-Mediated Gene-Set Pair Predicts Breast Cancer Metastasis. PLoS ONE, 2013, 8, e56195.	2.5	36
5	Transcription-factor-dependent enhancer transcription defines a gene regulatory network for cardiac rhythm. ELife, 2017, 6, .	6.0	36
6	A c-Myc-regulated stem cell-like signature in high-risk neuroblastoma: A systematic discovery (Target) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	3.3	30
7	Seq2pathway: an R/Bioconductor package for pathway analysis of next-generation sequencing data. Bioinformatics, 2015, 31, 3043-3045.	4.1	23
8	Systematic computation with functional gene-sets among leukemic and hematopoietic stem cells reveals a favorable prognostic signature for acute myeloid leukemia. BMC Bioinformatics, 2015, 16, 97.	2.6	11
9	Computational prognostic indicators for breast cancer. Cancer Management and Research, 2014, 6, 301.	1.9	10
10	Mechanism-anchored profiling derived from epigenetic networks predicts outcome in acute lymphoblastic leukemia. BMC Bioinformatics, 2009, 10, S6.	2.6	9
11	Detecting critical transition signals from single-cell transcriptomes to infer lineage-determining transcription factors. Nucleic Acids Research, 2022, 50, e91-e91.	14.5	8
12	Incorporating genomic, transcriptomic and clinical data: a prognostic and stem cell-like MYC and PRC imbalance in high-risk neuroblastoma. BMC Systems Biology, 2017, 11, 92.	3.0	7
13	Stromal microenvironment processes unveiled by biological component analysis of gene expression in xenograft tumor models. BMC Bioinformatics, 2010, 11, S11.	2.6	4
14	Chromatin-enriched RNAs mark active and repressive cis-regulation: An analysis of nuclear RNA-seq. PLoS Computational Biology, 2020, 16, e1007119.	3.2	4