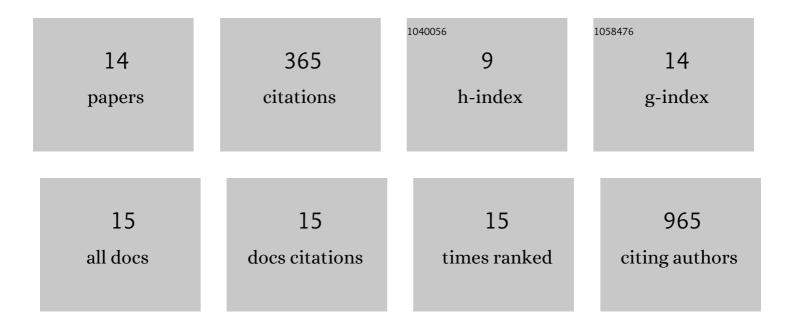
Xinan Yang

List of Publications by Year in descending order

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XINAN YANG

#	Article	IF	CITATIONS
1	Detecting critical transition signals from single-cell transcriptomes to infer lineage-determining transcription factors. Nucleic Acids Research, 2022, 50, e91-e91.	14.5	8
2	Chromatin-enriched RNAs mark active and repressive cis-regulation: An analysis of nuclear RNA-seq. PLoS Computational Biology, 2020, 16, e1007119.	3.2	4
3	A c-Myc-regulated stem cell-like signature in high-risk neuroblastoma: A systematic discovery (Target) Tj ETQq1 1	0.784314	rgBT /Over
4	Transcription-factor-dependent enhancer transcription defines a gene regulatory network for cardiac rhythm. ELife, 2017, 6, .	6.0	36
5	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
6	Cilia gene mutations cause atrioventricular septal defects by multiple mechanisms. Human Molecular Genetics, 2016, 25, ddw155.	2.9	37
7	The Cardiac TBX5 Interactome Reveals a Chromatin Remodeling Network Essential for Cardiac Septation. Developmental Cell, 2016, 36, 262-275.	7.0	71
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	Seq2pathway: an R/Bioconductor package for pathway analysis of next-generation sequencing data. Bioinformatics, 2015, 31, 3043-3045.	4.1	23
10	Computational prognostic indicators for breast cancer. Cancer Management and Research, 2014, 6, 301.	1.9	10
11	Foxf Genes Integrate Tbx5 and Hedgehog Pathways in the Second Heart Field for Cardiac Septation. PLoS Genetics, 2014, 10, e1004604.	3.5	79
12	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
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	Mechanism-anchored profiling derived from epigenetic networks predicts outcome in acute lymphoblastic leukemia. BMC Bioinformatics, 2009, 10, S6.	2.6	9