

Xinan Yang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1466910/publications.pdf>

Version: 2024-02-01

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	Detecting critical transition signals from single-cell transcriptomes to infer lineage-determining transcription factors. <i>Nucleic Acids Research</i> , 2022, 50, e91-e91.	14.5	8
2	Chromatin-enriched RNAs mark active and repressive cis-regulation: An analysis of nuclear RNA-seq. <i>PLoS Computational Biology</i> , 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 /Ove	3.3	80
4	Transcription-factor-dependent enhancer transcription defines a gene regulatory network for cardiac rhythm. <i>ELife</i> , 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. <i>BMC Systems Biology</i> , 2017, 11, 92.	3.0	7
6	Cilia gene mutations cause atrioventricular septal defects by multiple mechanisms. <i>Human Molecular Genetics</i> , 2016, 25, ddw155.	2.9	37
7	The Cardiac TBX5 Interactome Reveals a Chromatin Remodeling Network Essential for Cardiac Septation. <i>Developmental Cell</i> , 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. <i>BMC Bioinformatics</i> , 2015, 16, 97.	2.6	11
9	Seq2pathway: an R/Bioconductor package for pathway analysis of next-generation sequencing data. <i>Bioinformatics</i> , 2015, 31, 3043-3045.	4.1	23
10	Computational prognostic indicators for breast cancer. <i>Cancer Management and Research</i> , 2014, 6, 301.	1.9	10
11	Foxf Genes Integrate Tbx5 and Hedgehog Pathways in the Second Heart Field for Cardiac Septation. <i>PLoS Genetics</i> , 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. <i>PLoS ONE</i> , 2013, 8, e56195.	2.5	36
13	Stromal microenvironment processes unveiled by biological component analysis of gene expression in xenograft tumor models. <i>BMC Bioinformatics</i> , 2010, 11, S11.	2.6	4
14	Mechanism-anchored profiling derived from epigenetic networks predicts outcome in acute lymphoblastic leukemia. <i>BMC Bioinformatics</i> , 2009, 10, S6.	2.6	9