

Eunjee Lee

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/791456/publications.pdf>

Version: 2024-02-01

21
papers

835
citations

687363

13
h-index

794594

19
g-index

22
all docs

22
docs citations

22
times ranked

2168
citing authors

#	ARTICLE	IF	CITATIONS
1	Integrative network analysis of early-stage lung adenocarcinoma identifies aurora kinase inhibition as interceptor of invasion and progression. <i>Nature Communications</i> , 2022, 13, 1592.	12.8	16
2	Identification of Let-7 miRNA Activity as a Prognostic Biomarker of SHH Medulloblastoma. <i>Cancers</i> , 2022, 14, 139.	3.7	3
3	A probabilistic multi-omics data matching method for detecting sample errors in integrative analysis. <i>GigaScience</i> , 2019, 8, .	6.4	9
4	A Network Analysis of Multiple Myeloma Related Gene Signatures. <i>Cancers</i> , 2019, 11, 1452.	3.7	23
5	The polarity protein Scrib limits atherosclerosis development in mice. <i>Cardiovascular Research</i> , 2019, 115, 1963-1974.	3.8	11
6	Inching towards precision medicine for multiple myeloma with causal network models.. <i>Journal of Clinical Oncology</i> , 2019, 37, e19526-e19526.	1.6	0
7	Novel Predictors of Breast Cancer Survival Derived from miRNA Activity Analysis. <i>Clinical Cancer Research</i> , 2018, 24, 581-591.	7.0	21
8	Treatment-associated <i>TP53</i> DNA-binding domain missense mutations in the pathogenesis of secondary gliosarcoma. <i>Oncotarget</i> , 2018, 9, 2603-2621.	1.8	20
9	Identification of microR-106b as a prognostic biomarker of p53-like bladder cancers by ActMiR. <i>Oncogene</i> , 2018, 37, 5858-5872.	5.9	20
10	Comparison of glioblastoma (GBM) molecular classification methods. <i>Seminars in Cancer Biology</i> , 2018, 53, 201-211.	9.6	125
11	Network-based approaches that exploit inferred transcription factor activity to analyze the impact of genetic variation on gene expression. <i>Current Opinion in Systems Biology</i> , 2017, 2, 98-102.	2.6	4
12	Sensitivity to <i>BUB1B</i> Inhibition Defines an Alternative Classification of Glioblastoma. <i>Cancer Research</i> , 2017, 77, 5518-5529.	0.9	38
13	A functional genomics predictive network model identifies regulators of inflammatory bowel disease. <i>Nature Genetics</i> , 2017, 49, 1437-1449.	21.4	199
14	Ion channel expression patterns in glioblastoma stem cells with functional and therapeutic implications for malignancy. <i>PLoS ONE</i> , 2017, 12, e0172884.	2.5	37
15	A pilot systematic genomic comparison of recurrence risks of hepatitis B virus-associated hepatocellular carcinoma with low- and high-degree liver fibrosis. <i>BMC Medicine</i> , 2017, 15, 214.	5.5	64
16	Inferred miRNA activity identifies miRNA-mediated regulatory networks underlying multiple cancers. <i>Bioinformatics</i> , 2016, 32, 96-105.	4.1	31
17	Function of microRNA activity by ActMiR in bladder cancer.. <i>Journal of Clinical Oncology</i> , 2016, 34, 4531-4531.	1.6	0
18	Genome-wide CRISPR-Cas9 Screens Reveal Loss of Redundancy between PKMYT1 and WEE1 in Glioblastoma Stem-like Cells. <i>Cell Reports</i> , 2015, 13, 2425-2439.	6.4	146

#	ARTICLE	IF	CITATIONS
19	Targeting the SIN3A-PF1 interaction inhibits epithelial to mesenchymal transition and maintenance of a stem cell phenotype in triple negative breast cancer. <i>Oncotarget</i> , 2015, 6, 34087-34105.	1.8	26
20	MODMatcher: Multi-Omics Data Matcher for Integrative Genomic Analysis. <i>PLoS Computational Biology</i> , 2014, 10, e1003790.	3.2	35
21	Identifying regulatory mechanisms underlying tumorigenesis using locus expression signature analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 5747-5752.	7.1	7