Eunjee Lee

List of Publications by Year
in descending order

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	A functional genomics predictive network model identifies regulators of inflammatory bowel disease. Nature Genetics, 2017, 49, 1437-1449.	21.4	199
2	Genome-wide CRISPR-Cas9 Screens Reveal Loss of Redundancy between PKMYT1 and WEE1 in Glioblastoma Stem-like Cells. Cell Reports, 2015, 13, 2425-2439.	6.4	146
3	Comparison of glioblastoma (GBM) molecular classification methods. Seminars in Cancer Biology, 2018, 53, 201-211.	9.6	125
4	A pilot systematic genomic comparison of recurrence risks of hepatitis B virus-associated hepatocellular carcinoma with low- and high-degree liver fibrosis. BMC Medicine, 2017, 15, 214.	5.5	64
5	Sensitivity to *BUB1B* Inhibition Defines an Alternative Classification of Glioblastoma. Cancer Research, 2017, 77, 5518-5529.	0.9	38
6	Ion channel expression patterns in glioblastoma stem cells with functional and therapeutic implications for malignancy. PLoS ONE, 2017, 12, e0172884.	2.5	37
7	MODMatcher: Multi-Omics Data Matcher for Integrative Genomic Analysis. PLoS Computational Biology, 2014, 10, e1003790.	3.2	35
8	Inferred miRNA activity identifies miRNA-mediated regulatory networks underlying multiple cancers. Bioinformatics, 2016, 32, 96-105.	4.1	31
9	Targeting the SIN3A-PF1 interaction inhibits epithelial to mesenchymal transition and maintenance of a stem cell phenotype in triple negative breast cancer. Oncotarget, 2015, 6, 34087-34105.	1.8	26
10	A Network Analysis of Multiple Myeloma Related Gene Signatures. Cancers, 2019, 11, 1452.	3.7	23
11	Novel Predictors of Breast Cancer Survival Derived from miRNA Activity Analysis. Clinical Cancer Research, 2018, 24, 581-591.	7.0	21
12	Treatment-associated *TP53* DNA-binding domain missense mutations in the pathogenesis of secondary gliosarcoma. Oncotarget, 2018, 9, 2603-2621.	1.8	20
13	Identification of microR-106b as a prognostic biomarker of p53-like bladder cancers by ActMiR. Oncogene, 2018, 37, 5858-5872.	5.9	20
14	Integrative network analysis of early-stage lung adenocarcinoma identifies aurora kinase inhibition as interceptor of invasion and progression. Nature Communications, 2022, 13, 1592.	12.8	16
15	The polarity protein Scrib limits atherosclerosis development in mice. Cardiovascular Research, 2019, 115, 1963-1974.	3.8	11
16	A probabilistic multi-omics data matching method for detecting sample errors in integrative analysis. GigaScience, 2019, 8, .	6.4	9
17	Identifying regulatory mechanisms underlying tumorigenesis using locus expression signature analysis. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 5747-5752.	7.1	7
18	Network-based approaches that exploit inferred transcription factor activity to analyze the impact of genetic variation on gene expression. Current Opinion in Systems Biology, 2017, 2, 98-102.	2.6	4

#	Article	IF	Citations
19	Identification of Let-7 miRNA Activity as a Prognostic Biomarker of SHH Medulloblastoma. Cancers, 2022, 14, 139.	3.7	3
20	Function of microRNA activity by ActMiR in bladder cancer.. Journal of Clinical Oncology, 2016, 34, 4531-4531.	1.6	0
21	Inching towards precision medicine for multiple myeloma with causal network models.. Journal of Clinical Oncology, 2019, 37, e19526-e19526.	1.6	0