

Euna Jeong

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6607735/publications.pdf>

Version: 2024-02-01

13
papers

161
citations

1307594

7
h-index

1125743

13
g-index

13
all docs

13
docs citations

13
times ranked

265
citing authors

#	ARTICLE	IF	CITATIONS
1	Q-omics: Smart Software for Assisting Oncology and Cancer Research. <i>Molecules and Cells</i> , 2021, 44, 843-850.	2.6	18
2	Analysis of Cross-Association between mRNA Expression and RNAi Efficacy for Predictive Target Discovery in Colon Cancers. <i>Cancers</i> , 2020, 12, 3091.	3.7	12
3	Overexpression and Selective Anticancer Efficacy of in Mutant Lung Cancers. <i>Molecules and Cells</i> , 2019, 42, 804-809.	2.6	23
4	QSurface: fast identification of surface expression markers in cancers. <i>BMC Systems Biology</i> , 2018, 12, 17.	3.0	6
5	β -catenin/TCF activity regulates IGF-1R tyrosine kinase inhibitor sensitivity in colon cancer. <i>Oncogene</i> , 2018, 37, 5466-5475.	5.9	12
6	Patient sample-oriented analysis of gene expression highlights extracellular signatures in breast cancer progression. <i>Biochemical and Biophysical Research Communications</i> , 2017, 487, 307-312.	2.1	6
7	Transcriptome modeling and phenotypic assays for cancer precision medicine. <i>Archives of Pharmacal Research</i> , 2017, 40, 906-914.	6.3	7
8	Loss of function screens of druggable targetome against cancer stem-like cells. <i>FASEB Journal</i> , 2017, 31, 625-635.	0.5	32
9	Cardiac glycosides display selective efficacy for STK11 mutant lung cancer. <i>Scientific Reports</i> , 2016, 6, 29721.	3.3	27
10	Glucose starvation induces mutation and lineage-dependent adaptive responses in a large collection of cancer cell lines. <i>International Journal of Oncology</i> , 2016, 48, 67-72.	3.3	7
11	MACE: mutation-oriented profiling of chemical response and gene expression in cancers. <i>Bioinformatics</i> , 2015, 31, 1508-1514.	4.1	5
12	Analysis of image-based phenotypic parameters for high throughput gene perturbation assays. <i>Computational Biology and Chemistry</i> , 2015, 58, 192-198.	2.3	5
13	Dissecting the global variation of gene expression for the functional interpretation of transcriptome data. <i>Genomics</i> , 2014, 104, 279-286.	2.9	1