Jeongbin Park

List of Publications by Year
in descending order

21 papers	4,250 citations	430874 18 h-index	752698 20 g-index
27 all docs	27 docs citations	27 times ranked	6951 citing authors

#	Article	IF	Citations
1	Functional States in Tumor-Initiating Cell Differentiation in Human Colorectal Cancer. Cancers, 2021, 13, 1097.	3.7	11
2	Cell segmentation-free inference of cell types from in situ transcriptomics data. Nature Communications, 2021, 12, 3545.	12.8	52
3	Modeling glioblastoma invasion using human brain organoids and single-cell transcriptomics. Neuro-Oncology, 2020, 22, 1138-1149.	1.2	75
4	Abstract 1491: Transcriptional heterogeneity identifies functional states of tumor-initiating cell differentiation in human colorectal cancer. , 2020, , .		0
5	Pheno-seq â€" linking visual features and gene expression in 3D cell culture systems. Scientific Reports, 2019, 9, 12367.	3.3	16
6	Methylation profiling identifies two subclasses of squamous cell carcinoma related to distinct cells of origin. Nature Communications, 2018, 9, 577.	12.8	64
7	Cpf1-Database: web-based genome-wide guide RNA library design for gene knockout screens using CRISPR-Cpf1. Bioinformatics, 2018, 34, 1077-1079.	4.1	22
8	Response to â€œUnexpected mutations after CRISPRâ€"Cas9 editing in vivoâ€. Nature Methods, 2018, 15, 239-240.	19.0	22
9	Web-based design and analysis tools for CRISPR base editing. BMC Bioinformatics, 2018, 19, 542.	2.6	127
10	IG-MYC+ neoplasms with precursor B-cell phenotype are molecularly distinct from Burkitt lymphomas. Blood, 2018, 132, 2280-2285.	1.4	50
11	CRISPR/Cas9-mediated gene knockout screens and target identification via whole-genome sequencing uncover host genes required for picornavirus infection. Journal of Biological Chemistry, 2017, 292, 10664-10671.	3.4	33
12	Digenome-seq web tool for profiling CRISPR specificity. Nature Methods, 2017, 14, 548-549.	19.0	31
13	Screening drug effects in patientâ€derived cancer cells links organoid responses to genome alterations. Molecular Systems Biology, 2017, 13, 955.	7.2	163
14	Cas-analyzer: an online tool for assessing genome editing results using NGS data. Bioinformatics, 2017, 33, 286-288.	4.1	313
15	RAS-pathway mutation patterns define epigenetic subclasses in juvenile myelomonocytic leukemia. Nature Communications, 2017, 8, 2126.	12.8	91
16	Genome-wide target specificities of CRISPR-Cas9 nucleases revealed by multiplex Digenome-seq. Genome Research, 2016, 26, 406-415.	5.5	184
17	Cas-Database: web-based genome-wide guide RNA library design for gene knockout screens using CRISPR-Cas9. Bioinformatics, 2016, 32, 2017-2023.	4.1	46
18	Digenome-seq: genome-wide profiling of CRISPR-Cas9 off-target effects in human cells. Nature Methods, 2015, 12, 237-243.	19.0	850

#	Article	IF	Citations
19	Cas-Designer: a web-based tool for choice of CRISPR-Cas9 target sites. Bioinformatics, 2015, 31, 4014-4016.	4.1	306
20	Protein conformational dynamics dictate the binding affinity for a ligand. Nature Communications, 2014, 5, 3724.	12.8	113
21	Cas-OFFinder: a fast and versatile algorithm that searches for potential off-target sites of Cas9 RNA-guided endonucleases. Bioinformatics, 2014, 30, 1473-1475.	4.1	1,651