

Jeongbin Park

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

24
papers

2,735
citations

17
h-index

27
g-index

27
ext. papers

3,618
ext. citations

10.4
avg, IF

5.47
L-index

#	Paper	IF	Citations
24	Functional States in Tumor-Initiating Cell Differentiation in Human Colorectal Cancer. <i>Cancers</i> , 2021 , 13,	6.6	2
23	Cell segmentation-free inference of cell types from in situ transcriptomics data. <i>Nature Communications</i> , 2021 , 12, 3545	17.4	14
22	Modeling glioblastoma invasion using human brain organoids and single-cell transcriptomics. <i>Neuro-Oncology</i> , 2020 , 22, 1138-1149	1	37
21	Pheno-seq - linking visual features and gene expression in 3D cell culture systems. <i>Scientific Reports</i> , 2019 , 9, 12367	4.9	10
20	Methylation profiling identifies two subclasses of squamous cell carcinoma related to distinct cells of origin. <i>Nature Communications</i> , 2018 , 9, 577	17.4	42
19	Cpf1-Database: web-based genome-wide guide RNA library design for gene knockout screens using CRISPR-Cpf1. <i>Bioinformatics</i> , 2018 , 34, 1077-1079	7.2	17
18	Response to "Unexpected mutations after CRISPR-Cas9 editing in vivo". <i>Nature Methods</i> , 2018 , 15, 239-240	10	22
17	Web-based design and analysis tools for CRISPR base editing. <i>BMC Bioinformatics</i> , 2018 , 19, 542	3.6	70
16	IG- neoplasms with precursor B-cell phenotype are molecularly distinct from Burkitt lymphomas. <i>Blood</i> , 2018 , 132, 2280-2285	2.2	19
15	CRISPR/Cas9-mediated gene knockout screens and target identification via whole-genome sequencing uncover host genes required for picornavirus infection. <i>Journal of Biological Chemistry</i> , 2017 , 292, 10664-10671	5.4	27
14	Digenome-seq web tool for profiling CRISPR specificity. <i>Nature Methods</i> , 2017 , 14, 548-549	21.6	18
13	Screening drug effects in patient-derived cancer cells links organoid responses to genome alterations. <i>Molecular Systems Biology</i> , 2017 , 13, 955	12.2	113
12	Cas-analyzer: an online tool for assessing genome editing results using NGS data. <i>Bioinformatics</i> , 2017 , 33, 286-288	7.2	198
11	RAS-pathway mutation patterns define epigenetic subclasses in juvenile myelomonocytic leukemia. <i>Nature Communications</i> , 2017 , 8, 2126	17.4	52
10	Genome-wide target specificities of CRISPR-Cas9 nucleases revealed by multiplex Digenome-seq. <i>Genome Research</i> , 2016 , 26, 406-15	9.7	141
9	Cas-Database: web-based genome-wide guide RNA library design for gene knockout screens using CRISPR-Cas9. <i>Bioinformatics</i> , 2016 , 32, 2017-23	7.2	28
8	Cas-Designer: a web-based tool for choice of CRISPR-Cas9 target sites. <i>Bioinformatics</i> , 2015 , 31, 4014-6	7.2	149

7	Digenome-seq: genome-wide profiling of CRISPR-Cas9 off-target effects in human cells. <i>Nature Methods</i> , 2015 , 12, 237-43, 1 p following 243	21.6	652
6	Protein conformational dynamics dictate the binding affinity for a ligand. <i>Nature Communications</i> , 2014 , 5, 3724	17.4	88
5	Cas-OFFinder: a fast and versatile algorithm that searches for potential off-target sites of Cas9 RNA-guided endonucleases. <i>Bioinformatics</i> , 2014 , 30, 1473-5	7.2	1015
4	Questioning unexpected CRISPR off-target mutations in vivo		5
3	Deciphering programs of transcriptional regulation by combined deconvolution of multiple omics layers		6
2	Modeling glioblastoma invasion using human brain organoids and single-cell transcriptomics		1
1	Cell segmentation-free inference of cell types from in situ transcriptomics data		9