

Jeongbin Park

List of Publications by Citations

Source: <https://exaly.com/author-pdf/6733054/jeongbin-park-publications-by-citations.pdf>

Version: 2024-04-25

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	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
23	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
22	Cas-analyzer: an online tool for assessing genome editing results using NGS data. <i>Bioinformatics</i> , 2017 , 33, 286-288	7.2	198
21	Cas-Designer: a web-based tool for choice of CRISPR-Cas9 target sites. <i>Bioinformatics</i> , 2015 , 31, 4014-6	7.2	149
20	Genome-wide target specificities of CRISPR-Cas9 nucleases revealed by multiplex Digenome-seq. <i>Genome Research</i> , 2016 , 26, 406-15	9.7	141
19	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
18	Protein conformational dynamics dictate the binding affinity for a ligand. <i>Nature Communications</i> , 2014 , 5, 3724	17.4	88
17	Web-based design and analysis tools for CRISPR base editing. <i>BMC Bioinformatics</i> , 2018 , 19, 542	3.6	70
16	RAS-pathway mutation patterns define epigenetic subclasses in juvenile myelomonocytic leukemia. <i>Nature Communications</i> , 2017 , 8, 2126	17.4	52
15	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
14	Modeling glioblastoma invasion using human brain organoids and single-cell transcriptomics. <i>Neuro-Oncology</i> , 2020 , 22, 1138-1149	1	37
13	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
12	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
11	Response to "Unexpected mutations after CRISPR-Cas9 editing in vivo". <i>Nature Methods</i> , 2018 , 15, 239-240	21.6	22
10	IG- neoplasms with precursor B-cell phenotype are molecularly distinct from Burkitt lymphomas. <i>Blood</i> , 2018 , 132, 2280-2285	2.2	19
9	Digenome-seq web tool for profiling CRISPR specificity. <i>Nature Methods</i> , 2017 , 14, 548-549	21.6	18
8	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

7	Cell segmentation-free inference of cell types from in situ transcriptomics data. <i>Nature Communications</i> , 2021 , 12, 3545	17.4	14
6	Pheno-seq - linking visual features and gene expression in 3D cell culture systems. <i>Scientific Reports</i> , 2019 , 9, 12367	4.9	10
5	Cell segmentation-free inference of cell types from in situ transcriptomics data		9
4	Deciphering programs of transcriptional regulation by combined deconvolution of multiple omics layers		6
3	Questioning unexpected CRISPR off-target mutations in vivo		5
2	Functional States in Tumor-Initiating Cell Differentiation in Human Colorectal Cancer. <i>Cancers</i> , 2021 , 13,	6.6	2
1	Modeling glioblastoma invasion using human brain organoids and single-cell transcriptomics		1