

# Jeongbin Park

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6733054/publications.pdf>

Version: 2024-02-01

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	Cas-OFFinder: a fast and versatile algorithm that searches for potential off-target sites of Cas9 RNA-guided endonucleases. <i>Bioinformatics</i> , 2014, 30, 1473-1475.	4.1	1,651
2	Digenome-seq: genome-wide profiling of CRISPR-Cas9 off-target effects in human cells. <i>Nature Methods</i> , 2015, 12, 237-243.	19.0	850
3	Cas-analyzer: an online tool for assessing genome editing results using NGS data. <i>Bioinformatics</i> , 2017, 33, 286-288.	4.1	313
4	Cas-Designer: a web-based tool for choice of CRISPR-Cas9 target sites. <i>Bioinformatics</i> , 2015, 31, 4014-4016.	4.1	306
5	Genome-wide target specificities of CRISPR-Cas9 nucleases revealed by multiplex Digenome-seq. <i>Genome Research</i> , 2016, 26, 406-415.	5.5	184
6	Screening drug effects in patient-derived cancer cells links organoid responses to genome alterations. <i>Molecular Systems Biology</i> , 2017, 13, 955.	7.2	163
7	Web-based design and analysis tools for CRISPR base editing. <i>BMC Bioinformatics</i> , 2018, 19, 542.	2.6	127
8	Protein conformational dynamics dictate the binding affinity for a ligand. <i>Nature Communications</i> , 2014, 5, 3724.	12.8	113
9	RAS-pathway mutation patterns define epigenetic subclasses in juvenile myelomonocytic leukemia. <i>Nature Communications</i> , 2017, 8, 2126.	12.8	91
10	Modeling glioblastoma invasion using human brain organoids and single-cell transcriptomics. <i>Neuro-Oncology</i> , 2020, 22, 1138-1149.	1.2	75
11	Methylation profiling identifies two subclasses of squamous cell carcinoma related to distinct cells of origin. <i>Nature Communications</i> , 2018, 9, 577.	12.8	64
12	Cell segmentation-free inference of cell types from in situ transcriptomics data. <i>Nature Communications</i> , 2021, 12, 3545.	12.8	52
13	IG-MYC+ neoplasms with precursor B-cell phenotype are molecularly distinct from Burkitt lymphomas. <i>Blood</i> , 2018, 132, 2280-2285.	1.4	50
14	Cas-Database: web-based genome-wide guide RNA library design for gene knockout screens using CRISPR-Cas9. <i>Bioinformatics</i> , 2016, 32, 2017-2023.	4.1	46
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.	3.4	33
16	Digenome-seq web tool for profiling CRISPR specificity. <i>Nature Methods</i> , 2017, 14, 548-549.	19.0	31
17	Cpf1-Database: web-based genome-wide guide RNA library design for gene knockout screens using CRISPR-Cpf1. <i>Bioinformatics</i> , 2018, 34, 1077-1079.	4.1	22
18	Response to unexpected mutations after CRISPR-Cas9 editing in vivo. <i>Nature Methods</i> , 2018, 15, 239-240.	19.0	22

#	ARTICLE	IF	CITATIONS
19	Pheno-seq “ linking visual features and gene expression in 3D cell culture systems. Scientific Reports, 2019, 9, 12367.	3.3	16
20	Functional States in Tumor-Initiating Cell Differentiation in Human Colorectal Cancer. Cancers, 2021, 13, 1097.	3.7	11
21	Abstract 1491: Transcriptional heterogeneity identifies functional states of tumor-initiating cell differentiation in human colorectal cancer. , 2020, , .		0