Benjamin P Kleinstiver

List of Publications by Citations

Source: https://exaly.com/author-pdf/5014177/benjamin-p-kleinstiver-publications-by-citations.pdf
Version: 2024-04-23

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.

52 papers	5,999 citations	22 h-index	63 g-index
63 ext. papers	7,810 ext. citations	20.3 avg, IF	6.04 L-index

#	Paper	IF	Citations
52	High-fidelity CRISPR-Cas9 nucleases with no detectable genome-wide off-target effects. *Nature*, **2016**, 529, 490-5	50.4	1600
51	Engineered CRISPR-Cas9 nucleases with altered PAM specificities. *Nature*, **2015**, 523, 481-5	50.4	1061
50	Enhanced proofreading governs CRISPR-Cas9 targeting accuracy. *Nature*, **2017**, 550, 407-410	50.4	619
49	Genome-wide specificities of CRISPR-Cas Cpf1 nucleases in human cells. *Nature Biotechnology*, **2016**, 34, 869-74	44.5	415
48	Broadening the targeting range of Staphylococcus aureus CRISPR-Cas9 by modifying PAM recognition. *Nature Biotechnology*, **2015**, 33, 1293-1298	44.5	381
47	Unconstrained genome targeting with near-PAMless engineered CRISPR-Cas9 variants. *Science*, **2020**, 368, 290-296	33.3	325
46	Engineered CRISPR-Cas12a variants with increased activities and improved targeting ranges for gene, epigenetic and base editing. *Nature Biotechnology*, **2019**, 37, 276-282	44.5	235
45	Inducible and multiplex gene regulation using CRISPR-Cpf1-based transcription factors. *Nature Methods*, **2017**, 14, 1163-1166	21.6	132
44	Discovery of widespread type I and type V CRISPR-Cas inhibitors. *Science*, **2018**, 362, 240-242	33.3	129
43	Prediction of off-target activities for the end-to-end design of CRISPR guide RNAs. *Nature Biomedical Engineering*, **2018**, 2, 38-47	19	127
42	Activities and specificities of CRISPR/Cas9 and Cas12a nucleases for targeted mutagenesis in maize. *Plant Biotechnology Journal*, **2019**, 17, 362-372	11.6	125
41	High levels of AAV vector integration into CRISPR-induced DNA breaks. *Nature Communications*, **2019**, 10, 4439	17.4	119
40	Isocitrate Dehydrogenase Mutations Confer Dasatinib Hypersensitivity and SRC Dependence in Intrahepatic Cholangiocarcinoma. *Cancer Discovery*, **2016**, 6, 727-39	24.4	94
39	Allele-specific gene editing prevents deafness in a model of dominant progressive hearing loss. *Nature Medicine*, **2019**, 25, 1123-1130	50.5	84
38	CRISPR/Cas9 Mediated Disruption of the Swedish APP Allele as a Therapeutic Approach for Early-Onset Alzheimer's Disease. *Molecular Therapy - Nucleic Acids*, **2018**, 11, 429-440	10.7	71
37	Allele-Specific CRISPR-Cas9 Genome Editing of the Single-Base P23H Mutation for Rhodopsin-Associated Dominant Retinitis Pigmentosa. *CRISPR Journal*, **2018**, 1, 55-64	2.5	60
36	Hypoxia drives transient site-specific copy gain and drug-resistant gene expression. *Genes and Development*, **2015**, 29, 1018-31	12.6	55

35	Monomeric site-specific nucleases for genome editing. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 8061-6	11.5	47
34	Astrocytic interleukin-3 programs microglia and limits Alzheimer's disease. *Nature*, **2021**, 595, 701-706	50.4	41
33	Optimization of AsCas12a for combinatorial genetic screens in human cells. *Nature Biotechnology*, **2021**, 39, 94-104	44.5	34
32	Listeria Phages Induce Cas9 Degradation to Protect Lysogenic Genomes. *Cell Host and Microbe*, **2020**, 28, 31-40.e9	23.4	30
31	Broad-spectrum anti-CRISPR proteins facilitate horizontal gene transfer. *Nature Microbiology*, **2020**, 5, 620-629	26.6	29
30	The I-TevI nuclease and linker domains contribute to the specificity of monomeric TALENs. *G3: Genes, Genomes, Genetics*, **2014**, 4, 1155-65	3.2	17
29	Strand-specific contacts and divalent metal ion regulate double-strand break formation by the GIY-YIG homing endonuclease I-BmoI. *Journal of Molecular Biology*, **2007**, 374, 306-21	6.5	15
28	Camptothecin resistance is determined by the regulation of topoisomerase I degradation mediated by ubiquitin proteasome pathway. *Oncotarget*, **2017**, 8, 43733-43751	3.3	15
27	A unified genetic, computational and experimental framework identifies functionally relevant residues of the homing endonuclease I-BmoI. *Nucleic Acids Research*, **2010**, 38, 2411-27	20.1	13
26	Enhanced homology-directed repair for highly efficient gene editing in hematopoietic stem/progenitor cells. *Blood*, **2021**, 137, 2598-2608	2.2	13
25	Temporal and Spatial Post-Transcriptional Regulation of Zebrafish mRNA by Long Noncoding RNA During Brain Vascular Assembly. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2018**, 38, 1562-1575	9.4	12
24	The monomeric GIY-YIG homing endonuclease I-BmoI uses a molecular anchor and a flexible tether to sequentially nick DNA. *Nucleic Acids Research*, **2013**, 41, 5413-27	20.1	11
23	Optimization of AsCas12a for combinatorial genetic screens in human cells		11
22	Listeriaphages induce Cas9 degradation to protect lysogenic genomes		11
21	In vivo engineering of lymphocytes after systemic exosome-associated AAV delivery. *Scientific Reports*, **2020**, 10, 4544	4.9	10
20	Divalent metal ion differentially regulates the sequential nicking reactions of the GIY-YIG homing endonuclease I-BmoI. *PLoS ONE*, **2011**, 6, e23804	3.7	6
19	Enhanced proofreading governs CRISPR-Cas9 targeting accuracy		5
18	Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. *American Journal of Human Genetics*, **2021**, 108, 874-893	11	5

17	NNT mediates redox-dependent pigmentation via a UVB- and MITF-independent mechanism. *Cell*, **2021**, 184, 4268-4283.e20	56.2	5
16	Cell-based artificial APC resistant to lentiviral transduction for efficient generation of CAR-T cells from various cell sources **2020**, 8,		4
15	Scalable characterization of the PAM requirements of CRISPR-Cas enzymes using HT-PAMDA. *Nature Protocols*, **2021**, 16, 1511-1547	18.8	4
14	enAsCas12a Enables CRISPR-Directed Evolution to Screen for Functional Drug Resistance Mutations in Sequences Inaccessible to SpCas9. *Molecular Therapy*, **2021**, 29, 208-224	11.7	4
13	Mutant Allele-Specific CRISPR Disruption in DYT1 Dystonia Fibroblasts Restores Cell Function. *Molecular Therapy - Nucleic Acids*, **2020**, 21, 1-12	10.7	3
12	Plant genome editing branches out. *Nature Plants*, **2021**, 7, 4-5	11.5	3
11	Genome-wide specificity profiles of CRISPR-Cas Cpf1 nucleases in human cells		2
10	Allele-specific CRISPR/Cas9 genome editing of the single-base P23H mutation for rhodopsin associated dominant retinitis pigmentosa		2
9	Rapid screening of endonuclease target site preference using a modified bacterial two-plasmid selection. *Methods in Molecular Biology*, **2014**, 1123, 97-104	1.4	1
8	Estimating the evidence of selection and the reliability of inference in unigenic evolution. *Algorithms for Molecular Biology*, **2010**, 5, 35	1.8	1
7	Whole genome sequencing association analysis of quantitative red blood cell phenotypes: the NHLBI TOPMed program		1
6	Inducible, tunable and multiplex human gene regulation using CRISPR-Cpf1-based transcription factors		1
5	CRISPR-targeted MAGT1 insertion restores XMEN patient hematopoietic stem cells and lymphocytes. *Blood*, **2021**,	2.2	1
4	Genome editing in animals with minimal PAM CRISPR-Cas9 enzymes.. *Nature Communications*, **2022**, 13, 2601	17.4	1
3	Making the cut with PAMless CRISPR-Cas enzymes. *Trends in Genetics*, **2021**, 37, 1053-1055	8.5	0
2	CRISPR-Cas knockout of miR21 reduces glioma growth.. *Molecular Therapy - Oncolytics*, **2022**, 25, 121-136	6.4	0
1	Lack of Cas13a inhibition by anti-CRISPR proteins from Leptotrichia prophages. *Molecular Cell*, **2022**, 82, 2161-2166.e3	17.6	0