J Keith Joung

List of Publications by Year
in descending order

90 papers	32,843 citations	26630 56 h-index	42399 92 g-index
102 all docs	102 docs citations	102 times ranked	30541 citing authors

#	Article	IF	Citations
1	High-frequency off-target mutagenesis induced by CRISPR-Cas nucleases in human cells. Nature Biotechnology, 2013, 31, 822-826.	17.5	2,754
2	CRISPR-Cas systems for editing, regulating and targeting genomes. Nature Biotechnology, 2014, 32, 347-355.	17.5	2,648
3	Efficient genome editing in zebrafish using a CRISPR-Cas system. Nature Biotechnology, 2013, 31, 227-229.	17.5	2,638
4	High-fidelity CRISPRâ€“Cas9 nucleases with no detectable genome-wide off-target effects. Nature, 2016, 529, 490-495.	27.8	2,126
5	GUIDE-seq enables genome-wide profiling of off-target cleavage by CRISPR-Cas nucleases. Nature Biotechnology, 2015, 33, 187-197.	17.5	1,757
6	Improving CRISPR-Cas nuclease specificity using truncated guide RNAs. Nature Biotechnology, 2014, 32, 279-284.	17.5	1,706
7	Engineered CRISPR-Cas9 nucleases with altered PAM specificities. Nature, 2015, 523, 481-485.	27.8	1,388
8	TALENs: a widely applicable technology for targeted genome editing. Nature Reviews Molecular Cell Biology, 2013, 14, 49-55.	37.0	1,326
9	Cationic lipid-mediated delivery of proteins enables efficient protein-based genome editing in vitro and in vivo. Nature Biotechnology, 2015, 33, 73-80.	17.5	1,180
10	FLASH assembly of TALENs for high-throughput genome editing. Nature Biotechnology, 2012, 30, 460-465.	17.5	1,070
11	CRISPR RNAâ€“guided activation of endogenous human genes. Nature Methods, 2013, 10, 977-979.	19.0	996
12	Gene therapy comes of age. Science, 2018, 359, .	12.6	936
13	Enhanced proofreading governs CRISPRâ€“Cas9 targeting accuracy. Nature, 2017, 550, 407-410.	27.8	901
14	CRISPResso2 provides accurate and rapid genome editing sequence analysis. Nature Biotechnology, 2019, 37, 224-226.	17.5	891
15	Dimeric CRISPR RNA-guided FokI nucleases for highly specific genome editing. Nature Biotechnology, 2014, 32, 569-576.	17.5	852
16	CIRCLE-seq: a highly sensitive in vitro screen for genome-wide CRISPRâ€“Cas9 nuclease off-targets. Nature Methods, 2017, 14, 607-614.	19.0	601
17	Genome-wide specificities of CRISPR-Cas Cpf1 nucleases in human cells. Nature Biotechnology, 2016, 34, 869-874.	17.5	566
18	Broadening the targeting range of Staphylococcus aureus CRISPR-Cas9 by modifying PAM recognition. Nature Biotechnology, 2015, 33, 1293-1298.	17.5	511

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19	Engineered CRISPRâ€“Cas12a variants with increased activities and improved targeting ranges for gene, epigenetic and base editing. Nature Biotechnology, 2019, 37, 276-282.	17.5	439
20	Transcriptome-wide off-target RNA editing induced by CRISPR-guided DNA base editors. Nature, 2019, 569, 433-437.	27.8	434
21	Targeted disruption of DNMT1, DNMT3A and DNMT3B in human embryonic stem cells. Nature Genetics, 2015, 47, 469-478.	21.4	409
22	Pathways Disrupted in Human ALS Motor Neurons Identified through Genetic Correction of Mutant SOD1. Cell Stem Cell, 2014, 14, 781-795.	11.1	392
23	Defining and improving the genome-wide specificities of CRISPRâ€“Cas9 nucleases. Nature Reviews Genetics, 2016, 17, 300-312.	16.3	380
24	An APOBEC3A-Cas9 base editor with minimized bystander and off-target activities. Nature Biotechnology, 2018, 36, 977-982.	17.5	328
25	CRISPR C-to-G base editors for inducing targeted DNA transversions in human cells. Nature Biotechnology, 2021, 39, 41-46.	17.5	328
26	Interactome Maps of Mouse Gene Regulatory Domains Reveal Basic Principles of Transcriptional Regulation. Cell, 2013, 155, 1507-1520.	28.9	299
27	Activation of prokaryotic transcription through arbitrary proteinâ€“protein contacts. Nature, 1997, 386, 627-630.	27.8	282
28	In vivo CRISPR editing with no detectable genome-wide off-target mutations. Nature, 2018, 561, 416-419.	27.8	274
29	High levels of AAV vector integration into CRISPR-induced DNA breaks. Nature Communications, 2019, 10, 4439.	12.8	257
30	CRISPR DNA base editors with reduced RNA off-target and self-editing activities. Nature Biotechnology, 2019, 37, 1041-1048.	17.5	236
31	Prediction of off-target activities for the end-to-end design of CRISPR guide RNAs. Nature Biomedical Engineering, 2018, 2, 38-47.	22.5	230
32	Discovery of widespread type I and type V CRISPR-Cas inhibitors. Science, 2018, 362, 240-242.	12.6	214
33	Therapeutic base editing of human hematopoietic stem cells. Nature Medicine, 2020, 26, 535-541.	30.7	196
34	Activities and specificities of <scp>CRISPR</scp>/Cas9 and Cas12a nucleases for targeted mutagenesis in maize. Plant Biotechnology Journal, 2019, 17, 362-372.	8.3	192
35	Broad specificity profiling of TALENs results in engineered nucleases with improved DNA-cleavage specificity. Nature Methods, 2014, 11, 429-435.	19.0	182
36	Inducible and multiplex gene regulation using CRISPRâ€“Cpf1-based transcription factors. Nature Methods, 2017, 14, 1163-1166.	19.0	170

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37	A dual-deaminase CRISPR base editor enables concurrent adenine and cytosine editing. Nature Biotechnology, 2020, 38, 861-864.	17.5	168
38	Allele-specific gene editing prevents deafness in a model of dominant progressive hearing loss. Nature Medicine, 2019, 25, 1123-1130.	30.7	149
39	Dimeric CRISPR RNA-Guided FokI-dCas9 Nucleases Directed by Truncated gRNAs for Highly Specific Genome Editing. Human Gene Therapy, 2015, 26, 425-431.	2.7	127
40	Isocitrate Dehydrogenase Mutations Confer Dasatinib Hypersensitivity and SRC Dependence in Intrahepatic Cholangiocarcinoma. Cancer Discovery, 2016, 6, 727-739.	9.4	126
41	CRISPR prime editing with ribonucleoprotein complexes in zebrafish and primary human cells. Nature Biotechnology, 2022, 40, 189-193.	17.5	118
42	CRISPR/Cas9 Mediated Disruption of the Swedish APP Allele as a Therapeutic Approach for Early-Onset Alzheimerâ€™s Disease. Molecular Therapy - Nucleic Acids, 2018, 11, 429-440.	5.1	116
43	PrimeDesign software for rapid and simplified design of prime editing guide RNAs. Nature Communications, 2021, 12, 1034.	12.8	105
44	Allele-Specific CRISPR-Cas9 Genome Editing of the Single-Base P23H Mutation for Rhodopsin-Associated Dominant Retinitis Pigmentosa. CRISPR Journal, 2018, 1, 55-64.	2.9	96
45	Optimization of AsCas12a for combinatorial genetic screens in human cells. Nature Biotechnology, 2021, 39, 94-104.	17.5	96
46	CAUSEL: an epigenome- and genome-editing pipeline for establishing function of noncoding GWAS variants. Nature Medicine, 2015, 21, 1357-1363.	30.7	90
47	Chromatin regulation at the frontier of synthetic biology. Nature Reviews Genetics, 2015, 16, 159-171.	16.3	89
48	Continuous directed evolution of DNA-binding proteins to improve TALEN specificity. Nature Methods, 2015, 12, 939-942.	19.0	88
49	Systematic screening reveals a role for BRCA1 in the response to transcription-associated DNA damage. Genes and Development, 2014, 28, 1957-1975.	5.9	86
50	Efficient CRISPR/Cas9-mediated editing of trinucleotide repeat expansion in myotonic dystrophy patient-derived iPS and myogenic cells. Nucleic Acids Research, 2018, 46, 8275-8298.	14.5	78
51	Hypoxia drives transient site-specific copy gain and drug-resistant gene expression. Genes and Development, 2015, 29, 1018-1031.	5.9	72
52	Reply to â€œGenome editing with modularly assembled zinc-finger nucleasesâ€• Nature Methods, 2010, 7, 91-92.	19.0	71
53	Defining CRISPRâ€“Cas9 genome-wide nuclease activities with CIRCLE-seq. Nature Protocols, 2018, 13, 2615-2642.	12.0	69
54	Engineering Designer Transcription Activatorâ€â€Like Effector Nucleases (TALENs) by REAL or REALâ€Fast Assembly. Current Protocols in Molecular Biology, 2012, 100, Unit 12.15.	2.9	68

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55	A Zebrafish Model of Myelodysplastic Syndrome Produced through tet2 Genomic Editing. Molecular and Cellular Biology, 2015, 35, 789-804.	2.3	58
56	Targeted mutagenesis of zebrafish antithrombin III triggers disseminated intravascular coagulation and thrombosis, revealing insight into function. Blood, 2014, 124, 142-150.	1.4	52
57	Nodal patterning without Lefty inhibitory feedback is functional but fragile. ELife, 2017, 6, .	6.0	52
58	Open-source guideseq software for analysis of GUIDE-seq data. Nature Biotechnology, 2016, 34, 483-483.	17.5	49
59	Targeted Genome Editing in Human Cells Using CRISPR/Cas Nucleases and Truncated Guide RNAs. Methods in Enzymology, 2014, 546, 21-45.	1.0	43
60	CRISPR-SURF: discovering regulatory elements by deconvolution of CRISPR tiling screen data. Nature Methods, 2018, 15, 992-993.	19.0	33
61	Context influences on TALEâ€“DNA binding revealed by quantitative profiling. Nature Communications, 2015, 6, 7440.	12.8	30
62	Engineering Customized TALE Nucleases (TALENs) and TALE Transcription Factors by Fast Ligationâ€Based Automatable Solidâ€Phase Highâ€Throughput (FLASH) Assembly. Current Protocols in Molecular Biology, 2013, 103, Unit 12.16.	2.9	28
63	Technologies and Computational Analysis Strategies for CRISPR Applications. Molecular Cell, 2020, 79, 11-29.	9.7	28
64	Analysis of off-target effects in CRISPR-based gene drives in the human malaria mosquito. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	27
65	Defining genome-wide CRISPRâ€“Cas genome-editing nuclease activity with GUIDE-seq. Nature Protocols, 2021, 16, 5592-5615.	12.0	27
66	Response to â€œUnexpected mutations after CRISPRâ€“Cas9 editing in vivoâ€• Nature Methods, 2018, 15, 238-239.	19.0	25
67	Impact of Genetic Variation on CRISPR-Cas Targeting. CRISPR Journal, 2018, 1, 159-170.	2.9	24
68	A Code of Ethics for Gene Drive Research. CRISPR Journal, 2021, 4, 19-24.	2.9	24
69	Whatâ€™s Changed with Genome Editing?. Cell Stem Cell, 2014, 15, 3-4.	11.1	23
70	Scalable characterization of the PAM requirements of CRISPRâ€“Cas enzymes using HT-PAMDA. Nature Protocols, 2021, 16, 1511-1547.	12.0	23
71	IÎºB Kinase Î² (IKBKB) Mutations in Lymphomas That Constitutively Activate Canonical Nuclear Factor ÎºB (NFÎºB) Signaling. Journal of Biological Chemistry, 2014, 289, 26960-26972.	3.4	20
72	Camptothecin resistance is determined by the regulation of topoisomerase I degradation mediated by ubiquitin proteasome pathway. Oncotarget, 2017, 8, 43733-43751.	1.8	20

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73	Standards needed for gene-editing errors. Nature, 2015, 523, 158-158.	27.8	19
74	Temporal and Spatial Post-Transcriptional Regulation of Zebrafishtie1mRNA by Long Noncoding RNA During Brain Vascular Assembly. Arteriosclerosis, Thrombosis, and Vascular Biology, 2018, 38, 1562-1575.	2.4	19
75	Rescue of DNA-PK Signaling and T-Cell Differentiation by Targeted Genome Editing in a prkdc Deficient iPSC Disease Model. PLoS Genetics, 2015, 11, e1005239.	3.5	17
76	Augmenting and directing long-range CRISPR-mediated activation in human cells. Nature Methods, 2021, 18, 1075-1081.	19.0	17
77	Engineering Designer Nucleases with Customized Cleavage Specificities. Current Protocols in Molecular Biology, 2011, 96, Unit12.13.	2.9	16
78	Zebrafishdscaml1Deficiency Impairs Retinal Patterning and Oculomotor Function. Journal of Neuroscience, 2020, 40, 143-158.	3.6	15
79	Genome Editing: A Tool For Research and Therapy: Towards a functional understanding of variants for molecular diagnostics using genome editing. Nature Medicine, 2014, 20, 1103-1104.	30.7	14
80	Identifying and modifying protein-DNA and protein-protein interactions using a bacterial two-hybrid selection system. Journal of Cellular Biochemistry, 2001, 84, 53-57.	2.6	13
81	Cell-based artificial APC resistant to lentiviral transduction for efficient generation of CAR-T cells from various cell sources. , 2020, 8, e000990.		13
82	CRISPR-Cas9 treatment partially restores amyloid-Î² 42/40 in human fibroblasts with the Alzheimerâ€™s disease PSEN1 M146L mutation. Molecular Therapy - Nucleic Acids, 2022, 28, 450-461.	5.1	13
83	Genome Editing in Human Cells Using CRISPR/Cas Nucleases. Current Protocols in Molecular Biology, 2015, 112, 31.3.1-31.3.18.	2.9	12
84	Disruption of the kringle 1 domain of prothrombin leads to late onset mortality in zebrafish. Scientific Reports, 2020, 10, 4049.	3.3	10
85	Mutant Allele-Specific CRISPR Disruption in DYT1 Dystonia Fibroblasts Restores Cell Function. Molecular Therapy - Nucleic Acids, 2020, 21, 1-12.	5.1	8
86	Genome-wide functional perturbation of human microsatellite repeats using engineered zinc finger transcription factors. Cell Genomics, 2022, 2, 100119.	6.5	3
87	Factor X Mutant Zebrafish Tolerate a Severe Hemostatic Defect in Early Development Yet Develop Lethal Hemorrhage in Adulthood. Blood, 2015, 126, 426-426.	1.4	1
88	A Zebrafish Model Of Antithrombin III Deficiency Displays Bleeding and Thrombosis Secondary To Disseminated Intravascular Coagulation. Blood, 2013, 122, 200-200.	1.4	1
89	Combined +58 and +55 BCL11A enhancer Editing Yields Exceptional Efficiency, Specificity and HbF Induction in Human and NHP Preclinical Models. Blood, 2021, 138, 1852-1852.	1.4	1
90	Genome and Epigenome Editing: A Revolution in Science and Medicine. Blood, 2014, 124, SCI-10-SCI-10.	1.4	0