Shengdar Q Tsai

List of Publications by Year
in descending order

72	17,057	94433 37	106344 65
papers	citations	h-index	g-index

81	81	81	19324
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Efficient genome editing in zebrafish using a CRISPR-Cas system. Nature Biotechnology, 2013, 31, 227-229.	17.5	2,638
2	High-fidelity CRISPRâ€“Cas9 nucleases with no detectable genome-wide off-target effects. Nature, 2016, 529, 490-495.	27.8	2,126
3	GUIDE-seq enables genome-wide profiling of off-target cleavage by CRISPR-Cas nucleases. Nature Biotechnology, 2015, 33, 187-197.	17.5	1,757
4	Engineered CRISPR-Cas9 nucleases with altered PAM specificities. Nature, 2015, 523, 481-485.	27.8	1,388
5	FLASH assembly of TALENs for high-throughput genome editing. Nature Biotechnology, 2012, 30, 460-465.	17.5	1,070
6	Dimeric CRISPR RNA-guided FokI nucleases for highly specific genome editing. Nature Biotechnology, 2014, 32, 569-576.	17.5	852
7	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
8	Genome-wide specificities of CRISPR-Cas Cpf1 nucleases in human cells. Nature Biotechnology, 2016, 34, 869-874.	17.5	566
9	Broadening the targeting range of Staphylococcus aureus CRISPR-Cas9 by modifying PAM recognition. Nature Biotechnology, 2015, 33, 1293-1298.	17.5	511
10	Toddler: An Embryonic Signal That Promotes Cell Movement via Apelin Receptors. Science, 2014, 343, 1248636.	12.6	498
11	Targeted DNA demethylation and activation of endogenous genes using programmable TALE-TET1 fusion proteins. Nature Biotechnology, 2013, 31, 1137-1142.	17.5	433
12	Targeted disruption of DNMT1, DNMT3A and DNMT3B in human embryonic stem cells. Nature Genetics, 2015, 47, 469-478.	21.4	409
13	Defining and improving the genome-wide specificities of CRISPRâ€“Cas9 nucleases. Nature Reviews Genetics, 2016, 17, 300-312.	16.3	380
14	Highly efficient therapeutic gene editing of human hematopoietic stem cells. Nature Medicine, 2019, 25, 776-783.	30.7	344
15	Genetic Inactivation of CD33 in Hematopoietic Stem Cells to Enable CAR T Cell Immunotherapy for Acute Myeloid Leukemia. Cell, 2018, 173, 1439-1453.e19.	28.9	323
16	In vivo CRISPR editing with no detectable genome-wide off-target mutations. Nature, 2018, 561, 416-419.	27.8	274
17	High levels of AAV vector integration into CRISPR-induced DNA breaks. Nature Communications, 2019, 10, 4439.	12.8	257
18	Highly efficient generation of heritable zebrafish gene mutations using homo- and heterodimeric TALENs. Nucleic Acids Research, 2012, 40, 8001-8010.	14.5	233

#	Article	IF	Citations
19	Broad specificity profiling of TALENs results in engineered nucleases with improved DNA-cleavage specificity. Nature Methods, 2014, 11, 429-435.	19.0	182
20	Base editing of haematopoietic stem cells rescues sickle cell disease in mice. Nature, 2021, 595, 295-302.	27.8	175
21	CHANGE-seq reveals genetic and epigenetic effects on CRISPRâ€“Cas9 genome-wide activity. Nature Biotechnology, 2020, 38, 1317-1327.	17.5	149
22	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
23	Deleting DNMT3A in CAR T cells prevents exhaustion and enhances antitumor activity. Science Translational Medicine, 2021, 13, eabh0272.	12.4	123
24	Genome editing of HBG1 and HBG2 to induce fetal hemoglobin. Blood Advances, 2019, 3, 3379-3392.	5.2	121
25	Transcriptional profiling of human placentas from pregnancies complicated by preeclampsia reveals disregulation of sialic acid acetylesterase and immune signalling pathways. Placenta, 2011, 32, 175-182.	1.5	117
26	Annotation of the Affymetrix1 porcine genome microarray. Animal Genetics, 2006, 37, 423-424.	1.7	110
27	Characterization of Conserved and Nonconserved Imprinted Genes in Swine1. Biology of Reproduction, 2009, 81, 906-920.	2.7	88
28	Continuous directed evolution of DNA-binding proteins to improve TALEN specificity. Nature Methods, 2015, 12, 939-942.	19.0	88
29	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
30	The NIH Somatic Cell Genome Editing program. Nature, 2021, 592, 195-204.	27.8	84
31	Defining CRISPRâ€“Cas9 genome-wide nuclease activities with CIRCLE-seq. Nature Protocols, 2018, 13, 2615-2642.	12.0	69
32	Differentially expressed microRNAs and affected biological pathways revealed byÂmodulated modularity clustering (MMC) analysis of human preeclamptic and IUGR placentas. Placenta, 2013, 34, 599-605.	1.5	65
33	Correction of theCrb1^{rd8}Allele and Retinal Phenotype in C57BL/6N Mice Via TALEN-Mediated Homology-Directed Repair. , 2014, 55, 387.		63
34	Prime editing in mice reveals the essentiality of a single base in driving tissue-specific gene expression. Genome Biology, 2021, 22, 83.	8.8	62
35	BCL11A enhancerâ€“edited hematopoietic stem cells persist in rhesus monkeys without toxicity. Journal of Clinical Investigation, 2020, 130, 6677-6687.	8.2	54
36	Nodal patterning without Lefty inhibitory feedback is functional but fragile. ELife, 2017, 6, .	6.0	52

#	Article	IF	Citations
37	Enhanced homology-directed repair for highly efficient gene editing in hematopoietic stem/progenitor cells. Blood, 2021, 137, 2598-2608.	1.4	51
38	Open-source guideseq software for analysis of GUIDE-seq data. Nature Biotechnology, 2016, 34, 483-483.	17.5	49
39	Differences in X-Chromosome Transcriptional Activity and Cholesterol Metabolism between Placentae from Swine Breeds from Asian and Western Origins. PLoS ONE, 2013, 8, e55345.	2.5	37
40	Easy-Prime: a machine learningâ€“based prime editor design tool. Genome Biology, 2021, 22, 235.	8.8	32
41	Safe and efficient peripheral blood stem cell collection in patients with sickle cell disease using plerixafor. Haematologica, 2020, 105, e497.	3.5	29
42	In vivo engineered B cells secrete high titers of broadly neutralizing anti-HIV antibodies in mice. Nature Biotechnology, 2022, 40, 1241-1249.	17.5	29
43	Detection of transcriptional difference of porcine imprinted genes using different microarray platforms. BMC Genomics, 2006, 7, 328.	2.8	28
44	Successful Cloning of the Yucatan Minipig Using Commercial/Occidental Breeds as Oocyte Donors and Embryo Recipients. Cloning and Stem Cells, 2008, 10, 287-296.	2.6	28
45	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
46	Illuminating the genome-wide activity of genome editors for safe and effective therapeutics. Genome Biology, 2018, 19, 226.	8.8	28
47	Defining genome-wide CRISPRâ€“Cas genome-editing nuclease activity with GUIDE-seq. Nature Protocols, 2021, 16, 5592-5615.	12.0	27
48	Disease severity impacts plerixafor-mobilized stem cell collection in patients with sickle cell disease. Blood Advances, 2021, 5, 2403-2411.	5.2	24
49	Whatâ€™s Changed with Genome Editing?. Cell Stem Cell, 2014, 15, 3-4.	11.1	23
50	731. High-Fidelity CRISPR-Cas9 Nucleases with No Detectable Genome-Wide Off-Target Effects. Molecular Therapy, 2016, 24, S288.	8.2	23
51	CRISPR-targetedMAGT1insertion restores XMEN patient hematopoietic stem cells and lymphocytes. Blood, 2021, 138, 2768-2780.	1.4	20
52	Prediction and validation of hematopoietic stem and progenitor cell off-target editing in transplanted rhesus macaques. Molecular Therapy, 2022, 30, 209-222.	8.2	17
53	Zebrafishdscaml1Deficiency Impairs Retinal Patterning and Oculomotor Function. Journal of Neuroscience, 2020, 40, 143-158.	3.6	15
54	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

#	Article	IF	Citations
55	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
56	Identification of SNPs and INDELS in swine transcribed sequences using short oligonucleotide microarrays. BMC Genomics, 2008, 9, 252.	2.8	10
57	Lack of genomic imprinting of DNA primase, polypeptide 2 (PRIM2) in human term placenta and white blood cells. Epigenetics, 2012, 7, 429-431.	2.7	8
58	Adenosine Base Editing of Î³-Globin Promoters Induces Fetal Hemoglobin and Inhibit Erythroid Sickling. Blood, 2020, 136, 21-22.	1.4	8
59	Discovering the Genome-Wide Activity of CRISPR-Cas Nucleases. ACS Chemical Biology, 2018, 13, 305-308.	3.4	6
60	Durable and Robust Fetal Globin Induction without Anemia in Rhesus Monkeys Following Autologous Hematopoietic Stem Cell Transplant with BCL11A Erythroid Enhancer Editing. Blood, 2019, 134, 4632-4632.	1.4	6
61	Base Editing Eliminates the Sickle Cell Mutation and Pathology in Hematopoietic Stem Cells Derived Erythroid Cells. Blood, 2020, 136, 13-14.	1.4	3
62	Highly Efficient Therapeutic Gene Editing of BCL11A enhancer in Human Hematopoietic Stem Cells from ÃŸ-Hemoglobinopathy Patients for Fetal Hemoglobin Induction. Blood, 2018, 132, 3482-3482.	1.4	2
63	Towards safe therapy for immunodeficiency. Nature Biomedical Engineering, 2017, 1, 937-938.	22.5	1
64	Circularization for In vitro Reporting of Cleavage Effects (CIRCLE-seq). Protocol Exchange, 0, , .	0.3	1
65	CRISPR-Cas9 Genome Editing of Î³-Globin Promoters in Human Hematopoietic Stem Cells to Induce Erythrocyte Fetal Hemoglobin for Treatment of Î²-Hemoglobinopathies. Blood, 2019, 134, 2066-2066.	1.4	1
66	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
67	The Epigenome and Its Relevance to Somatic Cell Nuclear Transfer and Nuclear Reprogramming. , 2010, , 291-316.		0
68	Challenges for Sensitive Quantification of Gene Editing â€œOffâ€Ÿtargetâ€•Activity. Small Methods, 2017, 1, 1600062.	8.6	0
69	CONSERVATION OF IMPRINTING IN SWINE AND COMPARATIVE ASPECTS OF IMPRINTING. Biology of Reproduction, 2007, 77, 70-71.	2.7	0
70	Differentially Expressed MicroRNAs Revealed by Molecular Signatures of Preeclampsia and IUGR in Human Placenta.. Biology of Reproduction, 2012, 87, 411-411.	2.7	0
71	Safe and Efficient Peripheral Blood Stem Cell Collection in Patients with Sickle Cell Disease Using Plerixafor. Blood, 2019, 134, 1964-1964.	1.4	0
72	Human Genetic Diversity Alters Therapeutic Gene Editing Off-Target Outcomes. Blood, 2021, 138, 3993-3993.	1.4	0