Shengdar Q Tsai

List of Publications by Year
in descending order

72	17,057	108046	120465
papers	citations	37 h-index	65 g-index

81	81	81	21195
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Prediction and validation of hematopoietic stem and progenitor cell off-target editing in transplanted rhesus macaques. Molecular Therapy, 2022, 30, 209-222.	3.7	17
2	In vivo engineered B cells secrete high titers of broadly neutralizing anti-HIV antibodies in mice. Nature Biotechnology, 2022, 40, 1241-1249.	9.4	29
3	Prime editing in mice reveals the essentiality of a single base in driving tissue-specific gene expression. Genome Biology, 2021, 22, 83.	3.8	62
4	The NIH Somatic Cell Genome Editing program. Nature, 2021, 592, 195-204.	13.7	84
5	Disease severity impacts plerixafor-mobilized stem cell collection in patients with sickle cell disease. Blood Advances, 2021, 5, 2403-2411.	2.5	24
6	Enhanced homology-directed repair for highly efficient gene editing in hematopoietic stem/progenitor cells. Blood, 2021, 137, 2598-2608.	0.6	51
7	CRISPR-targetedMAGT1insertion restores XMEN patient hematopoietic stem cells and lymphocytes. Blood, 2021, 138, 2768-2780.	0.6	20
8	Base editing of haematopoietic stem cells rescues sickle cell disease in mice. Nature, 2021, 595, 295-302.	13.7	175
9	Easy-Prime: a machine learningâ€“based prime editor design tool. Genome Biology, 2021, 22, 235.	3.8	32
10	Defining genome-wide CRISPRâ€“Cas genome-editing nuclease activity with GUIDE-seq. Nature Protocols, 2021, 16, 5592-5615.	5.5	27
11	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.	0.6	1
12	Human Genetic Diversity Alters Therapeutic Gene Editing Off-Target Outcomes. Blood, 2021, 138, 3993-3993.	0.6	0
13	Deleting DNMT3A in CAR T cells prevents exhaustion and enhances antitumor activity. Science Translational Medicine, 2021, 13, eabh0272.	5.8	123
14	Zebrafishdscaml1Deficiency Impairs Retinal Patterning and Oculomotor Function. Journal of Neuroscience, 2020, 40, 143-158.	1.7	15
15	CHANGE-seq reveals genetic and epigenetic effects on CRISPRâ€“Cas9 genome-wide activity. Nature Biotechnology, 2020, 38, 1317-1327.	9.4	149
16	Safe and efficient peripheral blood stem cell collection in patients with sickle cell disease using plerixafor. Haematologica, 2020, 105, e497.	1.7	29
17	BCL11A enhancerâ€“edited hematopoietic stem cells persist in rhesus monkeys without toxicity. Journal of Clinical Investigation, 2020, 130, 6677-6687.	3.9	54
18	Base Editing Eliminates the Sickle Cell Mutation and Pathology in Hematopoietic Stem Cells Derived Erythroid Cells. Blood, 2020, 136, 13-14.	0.6	3

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19	Adenosine Base Editing of Î³-Globin Promoters Induces Fetal Hemoglobin and Inhibit Erythroid Sickling. Blood, 2020, 136, 21-22.	0.6	8
20	High levels of AAV vector integration into CRISPR-induced DNA breaks. Nature Communications, 2019, 10, 4439.	5.8	257
21	Highly efficient therapeutic gene editing of human hematopoietic stem cells. Nature Medicine, 2019, 25, 776-783.	15.2	344
22	Genome editing of HBG1 and HBG2 to induce fetal hemoglobin. Blood Advances, 2019, 3, 3379-3392.	2.5	121
23	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.	0.6	6
24	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.	0.6	1
25	Safe and Efficient Peripheral Blood Stem Cell Collection in Patients with Sickle Cell Disease Using Plerixafor. Blood, 2019, 134, 1964-1964.	0.6	0
26	Discovering the Genome-Wide Activity of CRISPR-Cas Nucleases. ACS Chemical Biology, 2018, 13, 305-308.	1.6	6
27	Illuminating the genome-wide activity of genome editors for safe and effective therapeutics. Genome Biology, 2018, 19, 226.	3.8	28
28	Defining CRISPRâ€“Cas9 genome-wide nuclease activities with CIRCLE-seq. Nature Protocols, 2018, 13, 2615-2642.	5.5	69
29	In vivo CRISPR editing with no detectable genome-wide off-target mutations. Nature, 2018, 561, 416-419.	13.7	274
30	Genetic Inactivation of CD33 in Hematopoietic Stem Cells to Enable CAR T Cell Immunotherapy for Acute Myeloid Leukemia. Cell, 2018, 173, 1439-1453.e19.	13.5	323
31	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.	0.6	2
32	Challenges for Sensitive Quantification of Gene Editing â€œOffâ€Targetâ€•Activity. Small Methods, 2017, 1, 1600062.	4.6	0
33	CIRCLE-seq: a highly sensitive in vitro screen for genome-wide CRISPRâ€“Cas9 nuclease off-targets. Nature Methods, 2017, 14, 607-614.	9.0	601
34	Towards safe therapy for immunodeficiency. Nature Biomedical Engineering, 2017, 1, 937-938.	11.6	1
35	Nodal patterning without Lefty inhibitory feedback is functional but fragile. ELife, 2017, 6, .	2.8	52
36	731. High-Fidelity CRISPR-Cas9 Nucleases with No Detectable Genome-Wide Off-Target Effects. Molecular Therapy, 2016, 24, S288.	3.7	23

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37	Defining and improving the genome-wide specificities of CRISPRâ€“Cas9 nucleases. Nature Reviews Genetics, 2016, 17, 300-312.	7.7	380
38	Open-source guideseq software for analysis of GUIDE-seq data. Nature Biotechnology, 2016, 34, 483-483.	9.4	49
39	Genome-wide specificities of CRISPR-Cas Cpf1 nucleases in human cells. Nature Biotechnology, 2016, 34, 869-874.	9.4	566
40	High-fidelity CRISPRâ€“Cas9 nucleases with no detectable genome-wide off-target effects. Nature, 2016, 529, 490-495.	13.7	2,126
41	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
42	Dimeric CRISPR RNA-Guided FokI-dCas9 Nucleases Directed by Truncated gRNAs for Highly Specific Genome Editing. Human Gene Therapy, 2015, 26, 425-431.	1.4	127
43	Engineered CRISPR-Cas9 nucleases with altered PAM specificities. Nature, 2015, 523, 481-485.	13.7	1,388
44	Targeted disruption of DNMT1, DNMT3A and DNMT3B in human embryonic stem cells. Nature Genetics, 2015, 47, 469-478.	9.4	409
45	Broadening the targeting range of Staphylococcus aureus CRISPR-Cas9 by modifying PAM recognition. Nature Biotechnology, 2015, 33, 1293-1298.	9.4	511
46	Continuous directed evolution of DNA-binding proteins to improve TALEN specificity. Nature Methods, 2015, 12, 939-942.	9.0	88
47	GUIDE-seq enables genome-wide profiling of off-target cleavage by CRISPR-Cas nucleases. Nature Biotechnology, 2015, 33, 187-197.	9.4	1,757
48	Correction of theCrb1^{rd8}Allele and Retinal Phenotype in C57BL/6N Mice Via TALEN-Mediated Homology-Directed Repair. , 2014, 55, 387.		63
49	Systematic screening reveals a role for BRCA1 in the response to transcription-associated DNA damage. Genes and Development, 2014, 28, 1957-1975.	2.7	86
50	Broad specificity profiling of TALENs results in engineered nucleases with improved DNA-cleavage specificity. Nature Methods, 2014, 11, 429-435.	9.0	182
51	Dimeric CRISPR RNA-guided FokI nucleases for highly specific genome editing. Nature Biotechnology, 2014, 32, 569-576.	9.4	852
52	Toddler: An Embryonic Signal That Promotes Cell Movement via Apelin Receptors. Science, 2014, 343, 1248636.	6.0	498
53	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.	15.2	14
54	Whatâ€™s Changed with Genome Editing?. Cell Stem Cell, 2014, 15, 3-4.	5.2	23

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55	Differentially expressed microRNAs and affected biological pathways revealed byÂmodulated modularity clustering (MMC) analysis of human preeclamptic and IUGR placentas. Placenta, 2013, 34, 599-605.	0.7	65
56	Targeted DNA demethylation and activation of endogenous genes using programmable TALE-TET1 fusion proteins. Nature Biotechnology, 2013, 31, 1137-1142.	9.4	433
57	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
58	Efficient genome editing in zebrafish using a CRISPR-Cas system. Nature Biotechnology, 2013, 31, 227-229.	9.4	2,638
59	Differences in X-Chromosome Transcriptional Activity and Cholesterol Metabolism between Placentae from Swine Breeds from Asian and Western Origins. PLoS ONE, 2013, 8, e55345.	1.1	37
60	Lack of genomic imprinting of DNA primase, polypeptide 2 (PRIM2) in human term placenta and white blood cells. Epigenetics, 2012, 7, 429-431.	1.3	8
61	Highly efficient generation of heritable zebrafish gene mutations using homo- and heterodimeric TALENs. Nucleic Acids Research, 2012, 40, 8001-8010.	6.5	233
62	FLASH assembly of TALENs for high-throughput genome editing. Nature Biotechnology, 2012, 30, 460-465.	9.4	1,070
63	Differentially Expressed MicroRNAs Revealed by Molecular Signatures of Preeclampsia and IUGR in Human Placenta.. Biology of Reproduction, 2012, 87, 411-411.	1.2	0
64	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.	0.7	117
65	The Epigenome and Its Relevance to Somatic Cell Nuclear Transfer and Nuclear Reprogramming. , 2010, , 291-316.		0
66	Characterization of Conserved and Nonconserved Imprinted Genes in Swine1. Biology of Reproduction, 2009, 81, 906-920.	1.2	88
67	Identification of SNPs and INDELS in swine transcribed sequences using short oligonucleotide microarrays. BMC Genomics, 2008, 9, 252.	1.2	10
68	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
69	CONSERVATION OF IMPRINTING IN SWINE AND COMPARATIVE ASPECTS OF IMPRINTING. Biology of Reproduction, 2007, 77, 70-71.	1.2	0
70	Annotation of the Affymetrix1 porcine genome microarray. Animal Genetics, 2006, 37, 423-424.	0.6	110
71	Detection of transcriptional difference of porcine imprinted genes using different microarray platforms. BMC Genomics, 2006, 7, 328.	1.2	28
72	Circularization for In vitro Reporting of Cleavage Effects (CIRCLE-seq). Protocol Exchange, 0, , .	0.3	1