

Shengdar Q Tsai

List of Publications by Year in descending order

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Version: 2024-02-01

72
papers

17,057
citations

94269

37
h-index

106150

65
g-index

81
all docs

81
docs citations

81
times ranked

19324
citing authors

#	ARTICLE	IF	CITATIONS
1	Prediction and validation of hematopoietic stem and progenitor cell off-target editing in transplanted rhesus macaques. <i>Molecular Therapy</i> , 2022, 30, 209-222.	3.7	17
2	In vivo engineered B cells secrete high titers of broadly neutralizing anti-HIV antibodies in mice. <i>Nature Biotechnology</i> , 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. <i>Genome Biology</i> , 2021, 22, 83.	3.8	62
4	The NIH Somatic Cell Genome Editing program. <i>Nature</i> , 2021, 592, 195-204.	13.7	84
5	Disease severity impacts plerixafor-mobilized stem cell collection in patients with sickle cell disease. <i>Blood Advances</i> , 2021, 5, 2403-2411.	2.5	24
6	Enhanced homology-directed repair for highly efficient gene editing in hematopoietic stem/progenitor cells. <i>Blood</i> , 2021, 137, 2598-2608.	0.6	51
7	CRISPR-targeted <i>MAGT1</i> insertion restores XMEN patient hematopoietic stem cells and lymphocytes. <i>Blood</i> , 2021, 138, 2768-2780.	0.6	20
8	Base editing of haematopoietic stem cells rescues sickle cell disease in mice. <i>Nature</i> , 2021, 595, 295-302.	13.7	175
9	Easy-Prime: a machine learning-based prime editor design tool. <i>Genome Biology</i> , 2021, 22, 235.	3.8	32
10	Defining genome-wide CRISPR-Cas genome-editing nuclease activity with GUIDE-seq. <i>Nature Protocols</i> , 2021, 16, 5592-5615.	5.5	27
11	Combined +58 and +55 <i>BCL11A</i> enhancer Editing Yields Exceptional Efficiency, Specificity and HbF Induction in Human and NHP Preclinical Models. <i>Blood</i> , 2021, 138, 1852-1852.	0.6	1
12	Human Genetic Diversity Alters Therapeutic Gene Editing Off-Target Outcomes. <i>Blood</i> , 2021, 138, 3993-3993.	0.6	0
13	Deleting DNMT3A in CAR T cells prevents exhaustion and enhances antitumor activity. <i>Science Translational Medicine</i> , 2021, 13, eabh0272.	5.8	123
14	Zebrafish <i>dscaml1</i> Deficiency Impairs Retinal Patterning and Oculomotor Function. <i>Journal of Neuroscience</i> , 2020, 40, 143-158.	1.7	15
15	CHANGE-seq reveals genetic and epigenetic effects on CRISPR-Cas9 genome-wide activity. <i>Nature Biotechnology</i> , 2020, 38, 1317-1327.	9.4	149
16	Safe and efficient peripheral blood stem cell collection in patients with sickle cell disease using plerixafor. <i>Haematologica</i> , 2020, 105, e497.	1.7	29
17	<i>BCL11A</i> enhancer-edited hematopoietic stem cells persist in rhesus monkeys without toxicity. <i>Journal of Clinical Investigation</i> , 2020, 130, 6677-6687.	3.9	54
18	Base Editing Eliminates the Sickle Cell Mutation and Pathology in Hematopoietic Stem Cells Derived Erythroid Cells. <i>Blood</i> , 2020, 136, 13-14.	0.6	3

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19	Adenosine Base Editing of $\hat{\Gamma}^3$ -Globin Promoters Induces Fetal Hemoglobin and Inhibit Erythroid Sickling. <i>Blood</i> , 2020, 136, 21-22.	0.6	8
20	High levels of AAV vector integration into CRISPR-induced DNA breaks. <i>Nature Communications</i> , 2019, 10, 4439.	5.8	257
21	Highly efficient therapeutic gene editing of human hematopoietic stem cells. <i>Nature Medicine</i> , 2019, 25, 776-783.	15.2	344
22	Genome editing of HBG1 and HBG2 to induce fetal hemoglobin. <i>Blood Advances</i> , 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. <i>Blood</i> , 2019, 134, 4632-4632.	0.6	6
24	CRISPR-Cas9 Genome Editing of $\hat{\Gamma}^3$ -Globin Promoters in Human Hematopoietic Stem Cells to Induce Erythrocyte Fetal Hemoglobin for Treatment of $\hat{\Gamma}^2$ -Hemoglobinopathies. <i>Blood</i> , 2019, 134, 2066-2066.	0.6	1
25	Safe and Efficient Peripheral Blood Stem Cell Collection in Patients with Sickle Cell Disease Using Plerixafor. <i>Blood</i> , 2019, 134, 1964-1964.	0.6	0
26	Discovering the Genome-Wide Activity of CRISPR-Cas Nucleases. <i>ACS Chemical Biology</i> , 2018, 13, 305-308.	1.6	6
27	Illuminating the genome-wide activity of genome editors for safe and effective therapeutics. <i>Genome Biology</i> , 2018, 19, 226.	3.8	28
28	Defining CRISPR-Cas9 genome-wide nuclease activities with CIRCLE-seq. <i>Nature Protocols</i> , 2018, 13, 2615-2642.	5.5	69
29	In vivo CRISPR editing with no detectable genome-wide off-target mutations. <i>Nature</i> , 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. <i>Cell</i> , 2018, 173, 1439-1453.e19.	13.5	323
31	Highly Efficient Therapeutic Gene Editing of BCL11A enhancer in Human Hematopoietic Stem Cells from $\hat{\Delta}^Y$ -Hemoglobinopathy Patients for Fetal Hemoglobin Induction. <i>Blood</i> , 2018, 132, 3482-3482.	0.6	2
32	Challenges for Sensitive Quantification of Gene Editing $\hat{\alpha}$ Off-Target $\hat{\alpha}$ Activity. <i>Small Methods</i> , 2017, 1, 1600062.	4.6	0
33	CIRCLE-seq: a highly sensitive in vitro screen for genome-wide CRISPR-Cas9 nuclease off-targets. <i>Nature Methods</i> , 2017, 14, 607-614.	9.0	601
34	Towards safe therapy for immunodeficiency. <i>Nature Biomedical Engineering</i> , 2017, 1, 937-938.	11.6	1
35	Nodal patterning without Lefty inhibitory feedback is functional but fragile. <i>ELife</i> , 2017, 6, .	2.8	52
36	731. High-Fidelity CRISPR-Cas9 Nucleases with No Detectable Genome-Wide Off-Target Effects. <i>Molecular Therapy</i> , 2016, 24, S288.	3.7	23

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37	Defining and improving the genome-wide specificities of CRISPR-Cas9 nucleases. <i>Nature Reviews Genetics</i> , 2016, 17, 300-312.	7.7	380
38	Open-source guideseq software for analysis of GUIDE-seq data. <i>Nature Biotechnology</i> , 2016, 34, 483-483.	9.4	49
39	Genome-wide specificities of CRISPR-Cas Cpf1 nucleases in human cells. <i>Nature Biotechnology</i> , 2016, 34, 869-874.	9.4	566
40	High-fidelity CRISPR-Cas9 nucleases with no detectable genome-wide off-target effects. <i>Nature</i> , 2016, 529, 490-495.	13.7	2,126
41	Genome Editing in Human Cells Using CRISPR/Cas Nucleases. <i>Current Protocols in Molecular Biology</i> , 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. <i>Human Gene Therapy</i> , 2015, 26, 425-431.	1.4	127
43	Engineered CRISPR-Cas9 nucleases with altered PAM specificities. <i>Nature</i> , 2015, 523, 481-485.	13.7	1,388
44	Targeted disruption of DNMT1, DNMT3A and DNMT3B in human embryonic stem cells. <i>Nature Genetics</i> , 2015, 47, 469-478.	9.4	409
45	Broadening the targeting range of <i>Staphylococcus aureus</i> CRISPR-Cas9 by modifying PAM recognition. <i>Nature Biotechnology</i> , 2015, 33, 1293-1298.	9.4	511
46	Continuous directed evolution of DNA-binding proteins to improve TALEN specificity. <i>Nature Methods</i> , 2015, 12, 939-942.	9.0	88
47	GUIDE-seq enables genome-wide profiling of off-target cleavage by CRISPR-Cas nucleases. <i>Nature Biotechnology</i> , 2015, 33, 187-197.	9.4	1,757
48	Correction of the <i>Crb1</i> 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. <i>Genes and Development</i> , 2014, 28, 1957-1975.	2.7	86
50	Broad specificity profiling of TALENs results in engineered nucleases with improved DNA-cleavage specificity. <i>Nature Methods</i> , 2014, 11, 429-435.	9.0	182
51	Dimeric CRISPR RNA-guided FokI nucleases for highly specific genome editing. <i>Nature Biotechnology</i> , 2014, 32, 569-576.	9.4	852
52	Toddler: An Embryonic Signal That Promotes Cell Movement via Apelin Receptors. <i>Science</i> , 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. <i>Nature Medicine</i> , 2014, 20, 1103-1104.	15.2	14
54	What's Changed with Genome Editing?. <i>Cell Stem Cell</i> , 2014, 15, 3-4.	5.2	23

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55	Differentially expressed microRNAs and affected biological pathways revealed by a modulated modularity clustering (MMC) analysis of human preeclamptic and IUGR placentas. <i>Placenta</i> , 2013, 34, 599-605.	0.7	65
56	Targeted DNA demethylation and activation of endogenous genes using programmable TALE-TET1 fusion proteins. <i>Nature Biotechnology</i> , 2013, 31, 1137-1142.	9.4	433
57	Engineering Customized TALE Nucleases (TALENs) and TALE Transcription Factors by Fast Ligation-Based Automatable Solid-Phase High-Throughput (FLASH) Assembly. <i>Current Protocols in Molecular Biology</i> , 2013, 103, Unit 12.16.	2.9	28
58	Efficient genome editing in zebrafish using a CRISPR-Cas system. <i>Nature Biotechnology</i> , 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. <i>PLoS ONE</i> , 2013, 8, e55345.	1.1	37
60	Lack of genomic imprinting of DNA primase, polypeptide 2 (<i>PRIM2</i>) in human term placenta and white blood cells. <i>Epigenetics</i> , 2012, 7, 429-431.	1.3	8
61	Highly efficient generation of heritable zebrafish gene mutations using homo- and heterodimeric TALENs. <i>Nucleic Acids Research</i> , 2012, 40, 8001-8010.	6.5	233
62	FLASH assembly of TALENs for high-throughput genome editing. <i>Nature Biotechnology</i> , 2012, 30, 460-465.	9.4	1,070
63	Differentially Expressed MicroRNAs Revealed by Molecular Signatures of Preeclampsia and IUGR in Human Placenta. <i>Biology of Reproduction</i> , 2012, 87, 411-411.	1.2	0
64	Transcriptional profiling of human placentas from pregnancies complicated by preeclampsia reveals dysregulation of sialic acid acetyltransferase and immune signaling pathways. <i>Placenta</i> , 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 Swine. <i>Biology of Reproduction</i> , 2009, 81, 906-920.	1.2	88
67	Identification of SNPs and INDELS in swine transcribed sequences using short oligonucleotide microarrays. <i>BMC Genomics</i> , 2008, 9, 252.	1.2	10
68	Successful Cloning of the Yucatan Minipig Using Commercial/Occidental Breeds as Oocyte Donors and Embryo Recipients. <i>Cloning and Stem Cells</i> , 2008, 10, 287-296.	2.6	28
69	CONSERVATION OF IMPRINTING IN SWINE AND COMPARATIVE ASPECTS OF IMPRINTING. <i>Biology of Reproduction</i> , 2007, 77, 70-71.	1.2	0
70	Annotation of the Affymetrix1 porcine genome microarray. <i>Animal Genetics</i> , 2006, 37, 423-424.	0.6	110
71	Detection of transcriptional difference of porcine imprinted genes using different microarray platforms. <i>BMC Genomics</i> , 2006, 7, 328.	1.2	28
72	Circularization for In vitro Reporting of Cleavage Effects (CIRCLE-seq). <i>Protocol Exchange</i> , 0, , .	0.3	1