

Research Publications Featuring the SH800 Cell Sorter in CRISPR/Cas 9 Studies

2023

Wessels HH, Méndez-Mancilla A, Hao Y, et al. Efficient combinatorial targeting of RNA transcripts in single cells with Cas13 RNA Perturb-seq. *Nat Methods*. 2023;20:86-94. [PubMed](#)

Najm FJ, DeWeirdt P, Moore MM, et al. Chromatin complex dependencies reveal targeting opportunities in leukemia. *Nat Commun*. 2023;14:448. [PubMed](#)

Choudhary MNK, Quaid K, Xing X, Schmidt H, Wang T. Widespread contribution of transposable elements to the rewiring of mammalian 3D genomes. *Nat Commun*. 2023;14:634. [PubMed](#)

Rahme GJ, Javed NM, Puorro KL, et al. Modeling epigenetic lesions that cause gliomas. *Cell*. 2023;186:3674-3685.e14. [PubMed](#)

Dawes P, Murray LF, Olson MN, et al. oFlowSeq: a quantitative approach to identify protein coding mutations affecting cell type enrichment using mosaic CRISPR-Cas9 edited cerebral organoids. *Hum Genet*. 2023;142:1281-1291. [PubMed](#)

2022

Xu Y, Kuppe C, Perales-Patón J, et al. Adult human kidney organoids originate from CD24+ cells and represent an advanced model for adult polycystic kidney disease. *Nat Genet*. 2022;54:1690-1701. [PubMed](#)

de Rooij MFM, Thus YJ, Swier N, Beijersbergen RL, Pals ST, Spaargaren M. A loss-of-adhesion CRISPR-Cas9 screening platform to identify cell adhesion-regulatory proteins and signaling pathways. *Nat Commun*. 2022;13:2136. [Nature](#)

Niekamp P, Scharte F, Sokoya T, et al. Ca2+-activated sphingomyelin scrambling and turnover mediate ESCRT-independent lysosomal repair. *Nat Commun*. 2022;13:1875. [PubMed](#)

Wu Q, Shichino Y, Abe T, et al. Selective translation of epigenetic modifiers affects the temporal pattern and differentiation of neural stem cells. *Nat Commun*. 2022;13:470. [PubMed](#)

Antoniou P, Hardouin G, Martinucci P, et al. Base-editing-mediated dissection of a γ-globin cis-regulatory element for the therapeutic reactivation of fetal hemoglobin expression. *Nat Commun*. 2022;13:6618. [PubMed](#)

2021

Gemberling MP, Siklenka K, Rodriguez E, et al. Transgenic mice for in vivo epigenome editing with CRISPR-based systems. *Nat Methods*. 2021;18:965-974. [PubMed](#)

Xu X, Chemparathy A, Zeng L, et al. Engineered miniature CRISPR-Cas system for mammalian genome regulation and editing. *Mol Cell*. 2021;81:4333-4345.e4. [PubMed](#)

Dubrot J, Lane-Reticker SK, Kessler EA, et al. In vivo screens using a selective CRISPR antigen removal lentiviral vector system reveal immune dependencies in renal cell carcinoma. *Immunity*. 2021;54:571-585.e6. [PubMed](#)

Papalexi E, Mimitou EP, Butler AW, et al. Characterizing the molecular regulation of inhibitory immune checkpoints with multimodal single-cell screens. *Nat Genet*. 2021;53:322-331. [PubMed](#)

Wang R, Simoneau CR, Kulsuputrakul J, et al. Genetic screens identify host factors for SARS-CoV-2 and common cold coronaviruses. *Cell*. 2021;184:106-119.e14. [PubMed](#)

2020

Angenent-Mari, Garruss AS, Soenksen LR, Church G, Collins JJ. A deep learning approach to programmable RNA switches. *Nat Commun*. 2020;11 5057. [PubMed](#)

Porter CE, Shaw AR, Jung Y, et al. Oncolytic adenovirus armed with BiTE, cytokine, and checkpoint inhibitor enables CART T cells to control the growth of heterogeneous tumors. *Mol Ther*. 2020;28:1251-1262. [PubMed](#)

Kwon JB, Vankara A, Ettyreddy AR, Bohning JD, Gersbach CA. Myogenic progenitor cell lineage specification by CRISPR/Cas9-based transcriptional activators. *Stem Cell Reports*. 2020;14:755-769. [PubMed](#)

Kempton HR, Goudy LE, Love KS, Qi LS. Multiple input sensing and signal integration using a split Cas12a system. *Mol Cell*. 2020;78:184-191.e3. [PubMed](#)

2019

Oakes BL, et al. "CRISPR-Cas9 Circular Permutants as Programmable Scaffolds for Genome Modification." *Cell*. 2019;176:254-267.e16. [PubMed](#)

Dolan AE, Hou Z, Xiao Y, et al. CRISPR Cas9 circular permutants as programmable scaffolds for genome modification. *Mol Cell*. 2019;74:936-950.e5. [PubMed](#)

Goto T, Hara H, Sanbo M, et al. Generation of pluripotent stem cell-derived mouse kidneys in Sall1-targeted anephric rats. *Nat Commun*. 2019;10:451. [PubMed](#)

Zou Y, Palte MJ, Deik AA, et al. A GPX4-dependent cancer cell state underlies the clear-cell morphology and confers sensitivity to ferroptosis. *Nat Commun*. 2019;10:1617. [PubMed](#)

Egbert RG, Rishi RS, Adler BA, et al. A versatile platform strain for high-fidelity multiplex genome editing. *Nucleic Acids Res.* 2019;47:3244-3256. [PubMed](#)

Hojo MA, Masuda K, Hojo H, et al. Identification of a genomic enhancer that enforces proper apoptosis induction in thymic negative selection. *Nat Commun.* 2019;10:2603. [PubMed](#)

Ludwig LS, Lareau CA, Bao EL, et al. Transcriptional states and chromatin accessibility underlying human erythropoiesis. *Cell Rep.* 2019;27:3228-3240.e7. [PubMed](#)

Narimatsu Y, Joshi H, Nason R, et al. An atlas of human glycosylation pathways enables display of the human glycome by gene engineered cells. *Mol Cell.* 2019;75:394-407.e5. [PubMed](#)

Tagaya H, Ishikawa K, Hosokawa Y, et al. A method of producing genetically manipulated mouse mammary gland. *Breast Cancer Res.* 2019;21:1. [PubMed](#)

2018

Klann TS, Crawford GE, Reddy TE, Gersbach CA. Screening regulatory element function with CRISPR/Cas9-based epigenome editing. *Methods Mol Biol.* 2018;1767:447-480. [PubMed](#)

2017

Klann TS, Black JB, Chellappan M, et al. CRISPR-Cas9 epigenome editing enables high-throughput screening for functional regulatory elements in the human genome. *Nat Biotechnol.* 2017;35:561-568. [PubMed](#)

Li H, Horns F, Wu B, et al. Classifying drosophila olfactory projection neuron subtypes by single-cell RNA sequencing. *Cell.* 2017;171:1206-1220.e22. [PubMed](#)

2016

Oakes BL, Nadler DC, Flamholz A, et al. Profiling of engineering hotspots identifies an allosteric CRISPR-Cas9 switch. *Nat Biotechnol.* 2016;34:646-651. [PubMed](#)

2014

Oakes BL, Nadler DC, Savage DF, et al. Protein engineering of Cas9 for enhanced function. *Methods Enzymol.* 2014;546:491-511. [PubMed](#)

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sonybiotechnology.com/us/instruments/sh800s-cell-sorter