

Kosuke Yusa

List of Publications by Year in descending order

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Version: 2024-02-01

54
papers

7,387
citations

117625

34
h-index

168389

53
g-index

56
all docs

56
docs citations

56
times ranked

11826
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide recessive genetic screening in mammalian cells with a lentiviral CRISPR-guide RNA library. <i>Nature Biotechnology</i> , 2014, 32, 267-273.	17.5	943
2	Prioritization of cancer therapeutic targets using CRISPR-Cas9 screens. <i>Nature</i> , 2019, 568, 511-516.	27.8	886
3	Targeted gene correction of α 1-antitrypsin deficiency in induced pluripotent stem cells. <i>Nature</i> , 2011, 478, 391-394.	27.8	635
4	A hyperactive <i>piggyBac</i> transposase for mammalian applications. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 1531-1536.	7.1	603
5	Generation of transgene-free induced pluripotent mouse stem cells by the <i>piggyBac</i> transposon. <i>Nature Methods</i> , 2009, 6, 363-369.	19.0	575
6	A CRISPR Dropout Screen Identifies Genetic Vulnerabilities and Therapeutic Targets in Acute Myeloid Leukemia. <i>Cell Reports</i> , 2016, 17, 1193-1205.	6.4	556
7	Butyrate Greatly Enhances Derivation of Human Induced Pluripotent Stem Cells by Promoting Epigenetic Remodeling and the Expression of Pluripotency-Associated Genes. <i>Stem Cells</i> , 2010, 28, 713-720.	3.2	385
8	<i>PiggyBac</i> Transposon Mutagenesis: A Tool for Cancer Gene Discovery in Mice. <i>Science</i> , 2010, 330, 1104-1107.	12.6	217
9	A Genetic Progression Model of BrafV600E-Induced Intestinal Tumorigenesis Reveals Targets for Therapeutic Intervention. <i>Cancer Cell</i> , 2013, 24, 15-29.	16.8	183
10	Agreement between two large pan-cancer CRISPR-Cas9 gene dependency data sets. <i>Nature Communications</i> , 2019, 10, 5817.	12.8	160
11	Characterization of Sleeping Beauty Transposition and Its Application to Genetic Screening in Mice. <i>Molecular and Cellular Biology</i> , 2003, 23, 9189-9207.	2.3	146
12	Mobilization of giant <i>piggyBac</i> transposons in the mouse genome. <i>Nucleic Acids Research</i> , 2011, 39, e148-e148.	14.5	141
13	Region-specific saturation germline mutagenesis in mice using the Sleeping Beauty transposon system. <i>Nature Methods</i> , 2005, 2, 763-769.	19.0	112
14	ARID1A influences HDAC1/BRD4 activity, intrinsic proliferative capacity and breast cancer treatment response. <i>Nature Genetics</i> , 2020, 52, 187-197.	21.4	108
15	Mutational History of a Human Cell Lineage from Somatic to Induced Pluripotent Stem Cells. <i>PLoS Genetics</i> , 2016, 12, e1005932.	3.5	96
16	Hyperactive <i>piggyBac</i> Gene Transfer in Human Cells and <i>In Vivo</i> . <i>Human Gene Therapy</i> , 2012, 23, 311-320.	2.7	94
17	Functional linkage of gene fusions to cancer cell fitness assessed by pharmacological and CRISPR-Cas9 screening. <i>Nature Communications</i> , 2019, 10, 2198.	12.8	92
18	The critical role of histone H2A-deubiquitinase Mym1 in hematopoiesis and lymphocyte differentiation. <i>Blood</i> , 2012, 119, 1370-1379.	1.4	87

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19	Nuclear Wave1 Is Required for Reprogramming Transcription in Oocytes and for Normal Development. <i>Science</i> , 2013, 341, 1002-1005.	12.6	82
20	Seamless genome editing in human pluripotent stem cells using custom endonuclease-based gene targeting and the piggyBac transposon. <i>Nature Protocols</i> , 2013, 8, 2061-2078.	12.0	80
21	The piggyBac Transposon Displays Local and Distant Reintegration Preferences and Can Cause Mutations at Noncanonical Integration Sites. <i>Molecular and Cellular Biology</i> , 2013, 33, 1317-1330.	2.3	77
22	Genome-wide phenotype analysis in ES cells by regulated disruption of Bloom's syndrome gene. <i>Nature</i> , 2004, 429, 896-899.	27.8	76
23	Unsupervised correction of gene-independent cell responses to CRISPR-Cas9 targeting. <i>BMC Genomics</i> , 2018, 19, 604.	2.8	75
24	Enhancement of Sleeping Beauty Transposition by CpG Methylation: Possible Role of Heterochromatin Formation. <i>Molecular and Cellular Biology</i> , 2004, 24, 4004-4018.	2.3	74
25	Interhomolog recombination and loss of heterozygosity in wild-type and Bloom syndrome helicase (BLM)-deficient mammalian cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 11971-11976.	7.1	72
26	Low rates of mutation in clinical grade human pluripotent stem cells under different culture conditions. <i>Nature Communications</i> , 2020, 11, 1528.	12.8	67
27	JACKS: joint analysis of CRISPR/Cas9 knockout screens. <i>Genome Research</i> , 2019, 29, 464-471.	5.5	64
28	Molecular synergy underlies the co-occurrence patterns and phenotype of NPM1-mutant acute myeloid leukemia. <i>Blood</i> , 2017, 130, 1911-1922.	1.4	63
29	SRPK1 maintains acute myeloid leukemia through effects on isoform usage of epigenetic regulators including BRD4. <i>Nature Communications</i> , 2018, 9, 5378.	12.8	60
30	A CRISPR knockout screen identifies SETDB1-target retroelement silencing factors in embryonic stem cells. <i>Genome Research</i> , 2018, 28, 846-858.	5.5	54
31	Sleeping Beauty Transposon-Based Phenotypic Analysis of Mice: Lack of Arpc3 Results in Defective Trophoblast Outgrowth. <i>Molecular and Cellular Biology</i> , 2006, 26, 6185-6196.	2.3	49
32	Genome-wide CRISPR-Cas9 screening in mammalian cells. <i>Methods</i> , 2019, 164-165, 29-35.	3.8	49
33	Sleeping Beauty Transposase Has an Affinity for Heterochromatin Conformation. <i>Molecular and Cellular Biology</i> , 2007, 27, 1665-1676.	2.3	46
34	Pooled extracellular receptor-ligand interaction screening using CRISPR activation. <i>Genome Biology</i> , 2018, 19, 205.	8.8	44
35	Minimal genome-wide human CRISPR-Cas9 library. <i>Genome Biology</i> , 2021, 22, 40.	8.8	40
36	Fezf1 is required for penetration of the basal lamina by olfactory axons to promote olfactory development. <i>Journal of Comparative Neurology</i> , 2009, 515, 565-584.	1.6	39

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37	Optimised metrics for CRISPR-KO screens with second-generation gRNA libraries. <i>Scientific Reports</i> , 2017, 7, 7384.	3.3	37
38	A homozygous mutant embryonic stem cell bank applicable for phenotype-driven genetic screening. <i>Nature Methods</i> , 2011, 8, 1071-1077.	19.0	36
39	Genome-scale identification of cellular pathways required for cell surface recognition. <i>Genome Research</i> , 2018, 28, 1372-1382.	5.5	29
40	KAT7 is a genetic vulnerability of acute myeloid leukemias driven by MLL rearrangements. <i>Leukemia</i> , 2021, 35, 1012-1022.	7.2	26
41	Genome-Wide Forward Genetic Screens in Mouse ES Cells. <i>Methods in Enzymology</i> , 2010, 477, 217-242.	1.0	22
42	Applications of CRISPR genome editing technology in drug target identification and validation. <i>Expert Opinion on Drug Discovery</i> , 2017, 12, 541-552.	5.0	15
43	Removal of Reprogramming Transgenes Improves the Tissue Reconstitution Potential of Keratinocytes Generated From Human Induced Pluripotent Stem Cells. <i>Stem Cells Translational Medicine</i> , 2014, 3, 992-1001.	3.3	14
44	Enhancement of microhomology-mediated genomic rearrangements by transient loss of mouse Bloom syndrome helicase. <i>Genome Research</i> , 2013, 23, 1462-1473.	5.5	13
45	CRISPR-Knockout Screen Identifies Dmap1 as a Regulator of Chemically Induced Reprogramming and Differentiation of Cardiac Progenitors. <i>Stem Cells</i> , 2019, 37, 958-972.	3.2	11
46	Selective targeting of multiple myeloma cells with a monoclonal antibody recognizing the ubiquitous protein CD98 heavy chain. <i>Science Translational Medicine</i> , 2022, 14, eaax7706.	12.4	10
47	Genetic Vulnerabilities of DNMT3AR882H in Myeloid Malignancies. <i>Blood</i> , 2019, 134, 111-111.	1.4	8
48	Bloom's syndrome gene-deficient phenotype in mouse primary cells induced by a modified tetracycline-controlled trans-silencer. <i>Gene</i> , 2006, 369, 80-89.	2.2	7
49	Rad54 is dispensable for the ALT pathway. <i>Genes To Cells</i> , 2006, 11, 1305-1315.	1.2	7
50	Genome-wide screening identifies Polycomb repressive complex 1.3 as an essential regulator of human naïve pluripotent cell reprogramming. <i>Science Advances</i> , 2022, 8, eabk0013.	10.3	7
51	The <i>CADM1</i> tumor suppressor gene is a major candidate gene in MDS with deletion of the long arm of chromosome 11. <i>Blood Advances</i> , 2022, 6, 386-398.	5.2	3
52	Measurement of the nuclear concentration of α -ketoglutarate during adipocyte differentiation by using a fluorescence resonance energy transfer-based biosensor with nuclear localization signals. <i>Endocrine Journal</i> , 2021, 68, 1429-1438.	1.6	2
53	A Crispr/Cas9 Drop-out Screen Identifies Genome-Wide Genetic Vulnerabilities in Acute Myeloid Leukaemia. <i>Blood</i> , 2015, 126, 554-554.	1.4	1
54	SRPK1 Is a Therapeutic Vulnerability in Acute Myeloid Leukemia through Its Effects on Alternative Isoforms of Epigenetic Regulators Including BRD4. <i>Blood</i> , 2017, 130, 781-781.	1.4	0