Kosuke Yusa

List of Publications by Year
in descending order

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54	7,387	117625	168389
papers	citations	34 h-index	53 g-index

56	56	56	11826
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	TheCADM1tumor suppressor gene is a major candidate gene in MDS with deletion of the long arm of chromosome 11. Blood Advances, 2022, 6, 386-398.	5.2	3
2	Selective targeting of multiple myeloma cells with a monoclonal antibody recognizing the ubiquitous protein CD98 heavy chain. Science Translational Medicine, 2022, 14, eaax7706.	12.4	10
3	Genome-wide screening identifies Polycomb repressive complex 1.3 as an essential regulator of human naÃ¯ve pluripotent cell reprogramming. Science Advances, 2022, 8, eabk0013.	10.3	7
4	KAT7 is a genetic vulnerability of acute myeloid leukemias driven by MLL rearrangements. Leukemia, 2021, 35, 1012-1022.	7.2	26
5	Measurement of the nuclear concentration of Î±-ketoglutarate during adipocyte differentiation by using a fluorescence resonance energy transfer-based biosensor with nuclear localization signals. Endocrine Journal, 2021, 68, 1429-1438.	1.6	2
6	Minimal genome-wide human CRISPR-Cas9 library. Genome Biology, 2021, 22, 40.	8.8	40
7	ARID1A influences HDAC1/BRD4 activity, intrinsic proliferative capacity and breast cancer treatment response. Nature Genetics, 2020, 52, 187-197.	21.4	108
8	Low rates of mutation in clinical grade human pluripotent stem cells under different culture conditions. Nature Communications, 2020, 11, 1528.	12.8	67
9	JACKS: joint analysis of CRISPR/Cas9 knockout screens. Genome Research, 2019, 29, 464-471.	5.5	64
10	Functional linkage of gene fusions to cancer cell fitness assessed by pharmacological and CRISPR-Cas9 screening. Nature Communications, 2019, 10, 2198.	12.8	92
11	Genome-wide CRISPR-Cas9 screening in mammalian cells. Methods, 2019, 164-165, 29-35.	3.8	49
12	Prioritization of cancer therapeutic targets using CRISPRâ€“Cas9 screens. Nature, 2019, 568, 511-516.	27.8	886
13	CRISPR-Knockout Screen Identifies Dmap1 as a Regulator of Chemically Induced Reprogramming and Differentiation of Cardiac Progenitors. Stem Cells, 2019, 37, 958-972.	3.2	11
14	Agreement between two large pan-cancer CRISPR-Cas9 gene dependency data sets. Nature Communications, 2019, 10, 5817.	12.8	160
15	Genetic Vulnerabilities of DNMT3AR882H in Myeloid Malignancies. Blood, 2019, 134, 111-111.	1.4	8
16	A CRISPR knockout screen identifies SETDB1-target retroelement silencing factors in embryonic stem cells. Genome Research, 2018, 28, 846-858.	5.5	54
17	Pooled extracellular receptor-ligand interaction screening using CRISPR activation. Genome Biology, 2018, 19, 205.	8.8	44
18	SRPK1 maintains acute myeloid leukemia through effects on isoform usage of epigenetic regulators including BRD4. Nature Communications, 2018, 9, 5378.	12.8	60

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19	Unsupervised correction of gene-independent cell responses to CRISPR-Cas9 targeting. BMC Genomics, 2018, 19, 604.	2.8	75
20	Genome-scale identification of cellular pathways required for cell surface recognition. Genome Research, 2018, 28, 1372-1382.	5.5	29
21	Applications of CRISPR genome editing technology in drug target identification and validation. Expert Opinion on Drug Discovery, 2017, 12, 541-552.	5.0	15
22	Molecular synergy underlies the co-occurrence patterns and phenotype of NPM1-mutant acute myeloid leukemia. Blood, 2017, 130, 1911-1922.	1.4	63
23	Optimised metrics for CRISPR-KO screens with second-generation gRNA libraries. Scientific Reports, 2017, 7, 7384.	3.3	37
24	SRPK1 Is a Therapeutic Vulnerability in Acute Myeloid Leukemia through Its Effects on Alternative Isoforms of Epigenetic Regulators Including BRD4. Blood, 2017, 130, 781-781.	1.4	0
25	A CRISPR Dropout Screen Identifies Genetic Vulnerabilities and Therapeutic Targets in Acute Myeloid Leukemia. Cell Reports, 2016, 17, 1193-1205.	6.4	556
26	Mutational History of a Human Cell Lineage from Somatic to Induced Pluripotent Stem Cells. PLoS Genetics, 2016, 12, e1005932.	3.5	96
27	A Crispr/Cas9 Drop-out Screen Identifies Genome-Wide Genetic Valnerubilities in Acute Myeloid Leukaemia. Blood, 2015, 126, 554-554.	1.4	1
28	Removal of Reprogramming Transgenes Improves the Tissue Reconstitution Potential of Keratinocytes Generated From Human Induced Pluripotent Stem Cells. Stem Cells Translational Medicine, 2014, 3, 992-1001.	3.3	14
29	Genome-wide recessive genetic screening in mammalian cells with a lentiviral CRISPR-guide RNA library. Nature Biotechnology, 2014, 32, 267-273.	17.5	943
30	Nuclear Wave1 Is Required for Reprogramming Transcription in Oocytes and for Normal Development. Science, 2013, 341, 1002-1005.	12.6	82
31	Seamless genome editing in human pluripotent stem cells using custom endonucleaseâ€“based gene targeting and the piggyBac transposon. Nature Protocols, 2013, 8, 2061-2078.	12.0	80
32	A Genetic Progression Model of BrafV600E-Induced Intestinal Tumorigenesis Reveals Targets for Therapeutic Intervention. Cancer Cell, 2013, 24, 15-29.	16.8	183
33	The piggyBac Transposon Displays Local and Distant Reintegration Preferences and Can Cause Mutations at Noncanonical Integration Sites. Molecular and Cellular Biology, 2013, 33, 1317-1330.	2.3	77
34	Enhancement of microhomology-mediated genomic rearrangements by transient loss of mouse Bloom syndrome helicase. Genome Research, 2013, 23, 1462-1473.	5.5	13
35	Hyperactive piggyBac Gene Transfer in Human Cells and In Vivo. Human Gene Therapy, 2012, 23, 311-320.	2.7	94
36	The critical role of histone H2A-deubiquitinase Mysm1 in hematopoiesis and lymphocyte differentiation. Blood, 2012, 119, 1370-1379.	1.4	87

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37	Targeted gene correction of Î±1-antitrypsin deficiency in induced pluripotent stem cells. Nature, 2011, 478, 391-394.	27.8	635
38	Mobilization of giant piggyBac transposons in the mouse genome. Nucleic Acids Research, 2011, 39, e148-e148.	14.5	141
39	A hyperactive piggyBac transposase for mammalian applications. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 1531-1536.	7.1	603
40	Interhomolog recombination and loss of heterozygosity in wild-type and Bloom syndrome helicase (BLM)-deficient mammalian cells. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 11971-11976.	7.1	72
41	A homozygous mutant embryonic stem cell bank applicable for phenotype-driven genetic screening. Nature Methods, 2011, 8, 1071-1077.	19.0	36
42	Butyrate Greatly Enhances Derivation of Human Induced Pluripotent Stem Cells by Promoting Epigenetic Remodeling and the Expression of Pluripotency-Associated Genes. Stem Cells, 2010, 28, 713-720.	3.2	385
43	PiggyBac Transposon Mutagenesis: A Tool for Cancer Gene Discovery in Mice. Science, 2010, 330, 1104-1107.	12.6	217
44	Genome-Wide Forward Genetic Screens in Mouse ES Cells. Methods in Enzymology, 2010, 477, 217-242.	1.0	22
45	Fezf1 is required for penetration of the basal lamina by olfactory axons to promote olfactory development. Journal of Comparative Neurology, 2009, 515, 565-584.	1.6	39
46	Generation of transgene-free induced pluripotent mouse stem cells by the piggyBac transposon. Nature Methods, 2009, 6, 363-369.	19.0	575
47	Sleeping Beauty Transposase Has an Affinity for Heterochromatin Conformation. Molecular and Cellular Biology, 2007, 27, 1665-1676.	2.3	46
48	Bloom's syndrome gene-deficient phenotype in mouse primary cells induced by a modified tetracycline-controlled trans-silencer. Gene, 2006, 369, 80-89.	2.2	7
49	Rad54 is dispensable for the ALT pathway. Genes To Cells, 2006, 11, 1305-1315.	1.2	7
50	Sleeping Beauty Transposon-Based Phenotypic Analysis of Mice: Lack of Arpc3 Results in Defective Trophoblast Outgrowth. Molecular and Cellular Biology, 2006, 26, 6185-6196.	2.3	49
51	Region-specific saturation germline mutagenesis in mice using the Sleeping Beauty transposon system. Nature Methods, 2005, 2, 763-769.	19.0	112
52	Enhancement of Sleeping Beauty Transposition by CpG Methylation: Possible Role of Heterochromatin Formation. Molecular and Cellular Biology, 2004, 24, 4004-4018.	2.3	74
53	Genome-wide phenotype analysis in ES cells by regulated disruption of Bloom's syndrome gene. Nature, 2004, 429, 896-899.	27.8	76
54	Characterization of Sleeping Beauty Transposition and Its Application to Genetic Screening in Mice. Molecular and Cellular Biology, 2003, 23, 9189-9207.	2.3	146