Neville E Sanjana

List of Publications by Year in Descending Order

66 papers	12,579 citations	30 h-index	78 g-index
78 ext. papers	16,335 ext. citations	21.4 avg, IF	6.7 L-index

#	Paper	IF	Citations
66	CRISPR in cancer biology and therapy.. *Nature Reviews Cancer*, **2022**,	31.3	11
65	The BTB transcription factors ZBTB11 and ZFP131 maintain pluripotency by repressing pro-differentiation genes.. *Cell Reports*, **2022**, 38, 110524	10.6	0
64	A genome-scale screen for synthetic drivers of T cell proliferation.. *Nature*, **2022**, 603, 728-735	50.4	3
63	Development of Novel CAR Therapies for Diffuse Large B-Cell Lymphoma Using Genome-Wide Overexpression Screens. *Blood*, **2021**, 138, 1726-1726	2.2	
62	Automated design of CRISPR prime editors for 56,000 human pathogenic variants. *IScience*, **2021**, 103380	6.1	1
61	Profiling the genetic determinants of chromatin accessibility with scalable single-cell CRISPR screens. *Nature Biotechnology*, **2021**, 39, 1270-1277	44.5	4
60	Integrative approach identifies and as putative causal genes for the COVID-19 GWAS signal in the 3p21.31 locus **2021**,		3
59	Tracking cell lineages to improve research reproducibility. *Nature Biotechnology*, **2021**, 39, 666-670	44.5	1
58	Identification of Required Host Factors for SARS-CoV-2 Infection in Human Cells. *Cell*, **2021**, 184, 92-105.e16	50.5	240
57	Author response: The Spike D614G mutation increases SARS-CoV-2 infection of multiple human cell types **2021**,		3
56	The Spike D614G mutation increases SARS-CoV-2 infection of multiple human cell types. *ELife*, **2021** , 10,	8.9	86
55	Integrative approach identifies SLC6A20 and CXCR6 as putative causal genes for the COVID-19 GWAS signal in the 3p21.31 locus. *Genome Biology*, **2021**, 22, 242	18.3	11
54	Chemically modified guide RNAs enhance CRISPR-Cas13 knockdown in human cells. *Cell Chemical Biology*, **2021**,	8.2	3
53	Voices of the new generation: open science is good for science (and for you). *Nature Reviews Molecular Cell Biology*, **2021**, 22, 709	48.7	
52	Transcriptome-wide Cas13 guide RNA design for model organisms and viral RNA pathogens. *Cell Genomics*, **2021**, 1, 100001		3
51	Massively parallel Cas13 screens reveal principles for guide RNA design. *Nature Biotechnology*, **2020** , 38, 722-727	44.5	92
50	Applying genome-wide CRISPR-Cas9 screens for therapeutic discovery in facioscapulohumeral muscular dystrophy. *Science Translational Medicine*, **2020**, 12,	17.5	24

49	High-Throughput Screens of PAM-Flexible Cas9 Variants for Gene Knockout and Transcriptional Modulation. *Cell Reports*, **2020**, 30, 2859-2868.e5	10.6	27
48	The Spike D614G mutation increases SARS-CoV-2 infection of multiple human cell types **2020**,		62
47	Immunomagnetic cell sorting. *Nature Biomedical Engineering*, **2019**, 3, 759-760	19	1
46	Overexpression of NEUROG2 and NEUROG1 in human embryonic stem cells produces a network of excitatory and inhibitory neurons. *FASEB Journal*, **2019**, 33, 5287-5299	0.9	12
45	Identification of Cancer Drivers at CTCF Insulators in 1,962 Whole Genomes. *Cell Systems*, **2019**, 8, 446-455.e8	10.6	29
44	Multiplexed detection of proteins, transcriptomes, clonotypes and CRISPR perturbations in single cells. *Nature Methods*, **2019**, 16, 409-412	21.6	175
43	Generation of a knock-in MAP2-tdTomato reporter human embryonic stem cell line with inducible expression of NEUROG2/1 (NYGCe001-A). *Stem Cell Research*, **2019**, 41, 101643	1.6	4
42	Effects of 3D culturing conditions on the transcriptomic profile of stem-cell-derived neurons. *Nature Biomedical Engineering*, **2018**, 2, 540-554	19	52
41	Integrated design, execution, and analysis of arrayed and pooled CRISPR genome-editing experiments. *Nature Protocols*, **2018**, 13, 946-986	18.8	42
40	GFAP Mutations in Astrocytes Impair Oligodendrocyte Progenitor Proliferation and Myelination in an hiPSC Model of Alexander Disease. *Cell Stem Cell*, **2018**, 23, 239-251.e6	18	65
39	Two Angelman families with unusually advanced neurodevelopment carry a start codon variant in the most highly expressed UBE3A isoform. *American Journal of Medical Genetics, Part A*, **2018**, 176, 1641-1647	2.5	12
38	Genome-scale CRISPR pooled screens. *Analytical Biochemistry*, **2017**, 532, 95-99	3.1	35
37	Genome-Scale Networks Link Neurodegenerative Disease Genes to Synuclein through Specific Molecular Pathways. *Cell Systems*, **2017**, 4, 157-170.e14	10.6	76
36	Transcription control by the ENL YEATS domain in acute leukaemia. *Nature*, **2017**, 543, 270-274	50.4	159
35	Genome-scale CRISPR-Cas9 knockout and transcriptional activation screening. *Nature Protocols*, **2017**, 12, 828-863	18.8	459
34	High-Throughput Approaches to Pinpoint Function within the Noncoding Genome. *Molecular Cell*, **2017**, 68, 44-59	17.6	37
33	GUIDES: sgRNA design for loss-of-function screens. *Nature Methods*, **2017**, 14, 831-832	21.6	42
32	Identification of essential genes for cancer immunotherapy. *Nature*, **2017**, 548, 537-542	50.4	460

31	Genome-scale activation screen identifies a lncRNA locus regulating a gene neighbourhood. *Nature*, **2017**, 548, 343-346	50.4	243
30	Target Discovery for Precision Medicine Using High-Throughput Genome Engineering. *Advances in Experimental Medicine and Biology*, **2017**, 1016, 123-145	3.6	5
29	Multiscale Genome Engineering: Genome-Wide Screens and Targeted Approaches. *Research and Perspectives in Neurosciences*, **2017**, 83-86		
28	CRISPR Screens to Discover Functional Noncoding Elements. *Trends in Genetics*, **2016**, 32, 526-529	8.5	24
27	GENOME ENGINEERING. The Genome Project-Write. *Science*, **2016**, 353, 126-7	33.3	138
26	Mice with Shank3 Mutations Associated with ASD and Schizophrenia Display Both Shared and Distinct Defects. *Neuron*, **2016**, 89, 147-62	13.9	180
25	Hypoxia as a therapy for mitochondrial disease. *Science*, **2016**, 352, 54-61	33.3	251
24	High-resolution interrogation of functional elements in the noncoding genome. *Science*, **2016**, 353, 1545-1549	33.3	197
23	Genome-wide CRISPR screen in a mouse model of tumor growth and metastasis. *Cell*, **2015**, 160, 1246-60	56.2	544
22	A Genome-wide CRISPR Screen in Primary Immune Cells to Dissect Regulatory Networks. *Cell*, **2015**, 162, 675-86	56.2	288
21	High-throughput functional genomics using CRISPR-Cas9. *Nature Reviews Genetics*, **2015**, 16, 299-311	30.1	748
20	BCL11A enhancer dissection by Cas9-mediated in situ saturating mutagenesis. *Nature*, **2015**, 527, 192-7	50.4	528
19	Crispr-Cas9 Saturating Mutagenesis Reveals an Achilles Heel in the BCL11A Erythroid Enhancer for Fetal Hemoglobin Induction (by Genome Editing). *Blood*, **2015**, 126, 638-638	2.2	3
18	Genome-scale CRISPR-Cas9 knockout screening in human cells. *Science*, **2014**, 343, 84-87	33.3	3080
17	Perturbation of m6A writers reveals two distinct classes of mRNA methylation at internal and 5V sites. *Cell Reports*, **2014**, 8, 284-96	10.6	700
16	Improved vectors and genome-wide libraries for CRISPR screening. *Nature Methods*, **2014**, 11, 783-784	21.6	2552
15	Rapid neurogenesis through transcriptional activation in human stem cells. *Molecular Systems Biology*, **2014**, 10, 760	12.2	130
14	Genome-Scale Crispr-Cas9 Knockout Studies Reveal Mutifactorial and Functionally Overlapping Mechanisms of Myeloma Cell Resistance to Proteasome Inhibition. *Blood*, **2014**, 124, 273-273	2.2	2

List of Publications

13	A transcription activator-like effector toolbox for genome engineering. *Nature Protocols*, **2012**, 7, 171-92	18.8	480
12	Activity-dependent A-to-I RNA editing in rat cortical neurons. *Genetics*, **2012**, 192, 281-7	4	30
11	The wanderlust of newborn neocortical interneurons. *Journal of Neuroscience*, **2009**, 29, 7114-5	6.6	
10	A fast flexible ink-jet printing method for patterning dissociated neurons in culture. *Journal of Neuroscience Methods*, **2004**, 136, 151-63	3	189
9	High-throughput screens of PAM-flexible Cas9 variants for gene knock-out and transcriptional modulation		2
8	High-resolution interrogation of functional elements in the noncoding genome		2
7	Principles for rational Cas13d guide design		3
6	Automated design of CRISPR prime editors for thousands of human pathogenic variants		5
5	Transcriptome-wide Cas13 guide RNA design for model organisms and viral RNA pathogens		3
4	Scalable pooled CRISPR screens with single-cell chromatin accessibility profiling		4
3	Expanding the CITE-seq tool-kit: Detection of proteins, transcriptomes, clonotypes and CRISPR perturbations with multiplexing, in a single assay		1
2	Protocol: Genome-scale CRISPR-Cas9 Knockout and Transcriptional Activation Screening		2
1	Discovery of target genes and pathways of blood trait loci using pooled CRISPR screens and single cell RNA sequencing		5