# Neville E Sanjana

List of Publications by Year
in descending order



| 57 | 18,850 | 117453 | 161609 |
|---|---|---|---|
| papers | citations | 34 h-index | 54 g-index |

| 78 | 78 | 78 | 32993 |
|---|---|---|---|
| all docs | docs citations | times ranked | citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Genome-Scale CRISPR-Cas9 Knockout Screening in Human Cells. Science, 2014, 343, 84-87. | 6.0 | 4,210 |
| 2 | Improved vectors and genome-wide libraries for CRISPR screening. Nature Methods, 2014, 11, 783-784. | 9.0 | 4,032 |
| 3 | High-throughput functional genomics using CRISPRâ€“Cas9. Nature Reviews Genetics, 2015, 16, 299-311. | 7.7 | 998 |
| 4 | Perturbation of m6A Writers Reveals Two Distinct Classes of mRNA Methylation at Internal and 5â€² Sites. Cell Reports, 2014, 8, 284-296. | 2.9 | 972 |
| 5 | Genome-scale CRISPR-Cas9 knockout and transcriptional activation screening. Nature Protocols, 2017, 12, 828-863. | 5.5 | 858 |
| 6 | Genome-wide CRISPR Screen in a Mouse Model of Tumor Growth and Metastasis. Cell, 2015, 160, 1246-1260. | 13.5 | 746 |
| 7 | BCL11A enhancer dissection by Cas9-mediated in situ saturating mutagenesis. Nature, 2015, 527, 192-197. | 13.7 | 726 |
| 8 | Identification of essential genes for cancer immunotherapy. Nature, 2017, 548, 537-542. | 13.7 | 668 |
| 9 | A transcription activator-like effector toolbox for genome engineering. Nature Protocols, 2012, 7, 171-192. | 5.5 | 568 |
| 10 | Identification of Required Host Factors for SARS-CoV-2 Infection in Human Cells. Cell, 2021, 184, 92-105.e16. | 13.5 | 480 |
| 11 | A Genome-wide CRISPR Screen in Primary Immune Cells to Dissect Regulatory Networks. Cell, 2015, 162, 675-686. | 13.5 | 383 |
| 12 | Multiplexed detection of proteins, transcriptomes, clonotypes and CRISPR perturbations in single cells. Nature Methods, 2019, 16, 409-412. | 9.0 | 364 |
| 13 | Hypoxia as a therapy for mitochondrial disease. Science, 2016, 352, 54-61. | 6.0 | 339 |
| 14 | Genome-scale activation screen identifies a lncRNA locus regulating a gene neighbourhood. Nature, 2017, 548, 343-346. | 13.7 | 336 |
| 15 | Mice with Shank3 Mutations Associated with ASD and Schizophrenia Display Both Shared and Distinct Defects. Neuron, 2016, 89, 147-162. | 3.8 | 279 |
| 16 | High-resolution interrogation of functional elements in the noncoding genome. Science, 2016, 353, 1545-1549. | 6.0 | 251 |
| 17 | Transcription control by the ENL YEATS domain in acute leukaemia. Nature, 2017, 543, 270-274. | 13.7 | 248 |
| 18 | Massively parallel Cas13 screens reveal principles for guide RNA design. Nature Biotechnology, 2020, 38, 722-727. | 9.4 | 233 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | A fast flexible ink-jet printing method for patterning dissociated neurons in culture. Journal of Neuroscience Methods, 2004, 136, 151-163. | 1.3 | 205 |
| 20 | The Genome Project-Write. Science, 2016, 353, 126-127. | 6.0 | 194 |
| 21 | Rapid neurogenesis through transcriptional activation in human stem cells. Molecular Systems Biology, 2014, 10, 760. | 3.2 | 187 |
| 22 | The Spike D614G mutation increases SARS-CoV-2 infection of multiple human cell types. ELife, 2021, 10, . | 2.8 | 173 |
| 23 | CRISPR in cancer biology and therapy. Nature Reviews Cancer, 2022, 22, 259-279. | 12.8 | 157 |
| 24 | Genome-Scale Networks Link Neurodegenerative Disease Genes to Î±-Synuclein through Specific Molecular Pathways. Cell Systems, 2017, 4, 157-170.e14. | 2.9 | 102 |
| 25 | 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. | 5.2 | 91 |
| 26 | A genome-scale screen for synthetic drivers of T cell proliferation. Nature, 2022, 603, 728-735. | 13.7 | 84 |
| 27 | Effects of 3D culturing conditions on the transcriptomic profile of stem-cell-derived neurons. Nature Biomedical Engineering, 2018, 2, 540-554. | 11.6 | 78 |
| 28 | GUIDES: sgRNA design for loss-of-function screens. Nature Methods, 2017, 14, 831-832. | 9.0 | 71 |
| 29 | Integrated design, execution, and analysis of arrayed and pooled CRISPR genome-editing experiments. Nature Protocols, 2018, 13, 946-986. | 5.5 | 70 |
| 30 | Identification of Cancer Drivers at CTCF Insulators in 1,962 Whole Genomes. Cell Systems, 2019, 8, 446-455.e8. | 2.9 | 65 |
| 31 | High-Throughput Approaches to Pinpoint Function within the Noncoding Genome. Molecular Cell, 2017, 68, 44-59. | 4.5 | 54 |
| 32 | Genome-scale CRISPR pooled screens. Analytical Biochemistry, 2017, 532, 95-99. | 1.1 | 52 |
| 33 | High-Throughput Screens of PAM-Flexible Cas9 Variants for Gene Knockout and Transcriptional Modulation. Cell Reports, 2020, 30, 2859-2868.e5. | 2.9 | 46 |
| 34 | Applying genome-wide CRISPR-Cas9 screens for therapeutic discovery in facioscapulohumeral muscular dystrophy. Science Translational Medicine, 2020, 12, . | 5.8 | 44 |
| 35 | Profiling the genetic determinants of chromatin accessibility with scalable single-cell CRISPR screens. Nature Biotechnology, 2021, 39, 1270-1277. | 9.4 | 43 |
| 36 | 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. | 3.8 | 40 |

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|---|---|---|---|
| 37 | CRISPR Screens to Discover Functional Noncoding Elements. Trends in Genetics, 2016, 32, 526-529. | 2.9 | 38 |
| 38 | Activity-Dependent A-to-I RNA Editing in Rat Cortical Neurons. Genetics, 2012, 192, 281-287. | 1.2 | 36 |
| 39 | Overexpression of NEUROG2 and NEUROG1 in human embryonic stem cells produces a network of excitatory and inhibitory neurons. FASEB Journal, 2019, 33, 5287-5299. | 0.2 | 30 |
| 40 | Transcriptome-wide Cas13 guide RNA design for model organisms and viral RNA pathogens. Cell Genomics, 2021, 1, 100001. | 3.0 | 30 |
| 41 | Chemically modified guide RNAs enhance CRISPR-Cas13 knockdown in human cells. Cell Chemical Biology, 2022, 29, 321-327.e4. | 2.5 | 25 |
| 42 | 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. | 0.7 | 17 |
| 43 | Genome-Scale Crispr-Cas9 Knockout Studies Reveal Mutifactorial and Functionally Overlapping Mechanisms of Myeloma Cell Resistance to Proteasome Inhibition. Blood, 2014, 124, 273-273. | 0.6 | 16 |
| 44 | Recurrent somatic mutations as predictors of immunotherapy response. Nature Communications, 2022, 13, . | 5.8 | 12 |
| 45 | Automated design of CRISPR prime editors for 56,000 human pathogenic variants. IScience, 2021, 24, 103380. | 1.9 | 11 |
| 46 | The BTB transcription factors ZBTB11 and ZFP131 maintain pluripotency by repressing pro-differentiation genes. Cell Reports, 2022, 38, 110524. | 2.9 | 7 |
| 47 | Target Discovery for Precision Medicine Using High-Throughput Genome Engineering. Advances in Experimental Medicine and Biology, 2017, 1016, 123-145. | 0.8 | 6 |
| 48 | 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. | 0.3 | 6 |
| 49 | Immunomagnetic cell sorting. Nature Biomedical Engineering, 2019, 3, 759-760. | 11.6 | 5 |
| 50 | 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. | 0.6 | 5 |
| 51 | Tracking cell lineages to improve research reproducibility. Nature Biotechnology, 2021, 39, 666-670. | 9.4 | 3 |
| 52 | A genome-wide net to catch and understand cancer. Science Translational Medicine, 2018, 10, . | 5.8 | 2 |
| 53 | Voices of the new generation: open science is good for science (and for you). Nature Reviews Molecular Cell Biology, 2021, 22, 709-709. | 16.1 | 2 |
| 54 | The Wanderlust of Newborn Neocortical Interneurons. Journal of Neuroscience, 2009, 29, 7114-7115. | 1.7 | 0 |

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|---|---|---|---|
| 55 | Multiscale Genome Engineering: Genome-Wide Screens and Targeted Approaches. Research and Perspectives in Neurosciences, 2017, , 83-86. | 0.4 | 0 |
| 56 | Development of Novel CAR Therapies for Diffuse Large B-Cell Lymphoma Using Genome-Wide Overexpression Screens. Blood, 2021, 138, 1726-1726. | 0.6 | 0 |
| 57 | Voices on technology: The molecular biologistsâ€™ ever-expanding toy box. Molecular Cell, 2022, 82, 221-226. | 4.5 | 0 |