

Xueqiu Lin

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11255146/publications.pdf>

Version: 2024-02-01

16
papers

1,535
citations

623734

14
h-index

940533

16
g-index

16
all docs

16
docs citations

16
times ranked

3181
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Multiplexed genome regulation in vivo with hyper-efficient Cas12a. <i>Nature Cell Biology</i> , 2022, 24, 590-600. | 10.3 | 39 |
| 2 | The disordered N-terminal domain of DNMT3A recognizes H2AK119ub and is required for postnatal development. <i>Nature Genetics</i> , 2022, 54, 625-636. | 21.4 | 31 |
| 3 | Broad-spectrum CRISPR-mediated inhibition of SARS-CoV-2 variants and endemic coronaviruses in vitro. <i>Nature Communications</i> , 2022, 13, 2766. | 12.8 | 20 |
| 4 | A comprehensive analysis and resource to use CRISPR-Cas13 for broad-spectrum targeting of RNA viruses. <i>Cell Reports Medicine</i> , 2021, 2, 100245. | 6.5 | 23 |
| 5 | Computational Methods for Analysis of Large-Scale CRISPR Screens. <i>Annual Review of Biomedical Data Science</i> , 2020, 3, 137-162. | 6.5 | 4 |
| 6 | A benchmark of algorithms for the analysis of pooled CRISPR screens. <i>Genome Biology</i> , 2020, 21, 62. | 8.8 | 45 |
| 7 | Development of CRISPR as an Antiviral Strategy to Combat SARS-CoV-2 and Influenza. <i>Cell</i> , 2020, 181, 865-876.e12. | 28.9 | 354 |
| 8 | CRISPhieRmix: a hierarchical mixture model for CRISPR pooled screens. <i>Genome Biology</i> , 2018, 19, 159. | 8.8 | 36 |
| 9 | CRISPR-Mediated Programmable 3D Genome Positioning and Nuclear Organization. <i>Cell</i> , 2018, 175, 1405-1417.e14. | 28.9 | 164 |
| 10 | CRISPR Activation Screens Systematically Identify Factors that Drive Neuronal Fate and Reprogramming. <i>Cell Stem Cell</i> , 2018, 23, 758-771.e8. | 11.1 | 161 |
| 11 | DNMT3A and TET1 cooperate to regulate promoter epigenetic landscapes in mouse embryonic stem cells. <i>Genome Biology</i> , 2018, 19, 88. | 8.8 | 120 |
| 12 | Homeobox oncogene activation by pan-cancer DNA hypermethylation. <i>Genome Biology</i> , 2018, 19, 108. | 8.8 | 94 |
| 13 | Sparse conserved under-methylated CpGs are associated with high-order chromatin structure. <i>Genome Biology</i> , 2017, 18, 163. | 8.8 | 16 |
| 14 | DNMT3A Loss Drives Enhancer Hypomethylation in FLT3-ITD-Associated Leukemias. <i>Cancer Cell</i> , 2016, 29, 922-934. | 16.8 | 107 |
| 15 | Broad H3K4me3 is associated with increased transcription elongation and enhancer activity at tumor-suppressor genes. <i>Nature Genetics</i> , 2015, 47, 1149-1157. | 21.4 | 276 |
| 16 | BSeQC: quality control of bisulfite sequencing experiments. <i>Bioinformatics</i> , 2013, 29, 3227-3229. | 4.1 | 45 |