

A Multiplexed Single-Cell CRISPR Screening Platform E Unfolded Protein Response

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Perturb-Seq: Dissecting Molecular Circuits with Scalable Single-Cell RNA Profiling of Pooled Genetic Screens. <i>Cell</i> , 2016, 167, 1853-1866.e17.	13.5	1,144
2	Pooled CRISPR screening with single-cell transcriptome readout. <i>Nature Methods</i> , 2017, 14, 297-301.	9.0	749
3	Combining CRISPR perturbations and RNA-seq. <i>Nature Reviews Genetics</i> , 2017, 18, 67-67.	7.7	1
4	Genetic screening enters the single-cell era. <i>Nature Methods</i> , 2017, 14, 237-238.	9.0	8
6	Single-minded CRISPR screening. <i>Nature Biotechnology</i> , 2017, 35, 339-340.	9.4	4
7	Multiplexed Engineering and Analysis of Combinatorial Enhancer Activity in Single Cells. <i>Molecular Cell</i> , 2017, 66, 285-299.e5.	4.5	245
8	Functional Enhancer Screening in Single Cells. <i>Molecular Cell</i> , 2017, 66, 167-168.	4.5	1
9	A CRISPR toolbox to study virus-host interactions. <i>Nature Reviews Microbiology</i> , 2017, 15, 351-364.	13.6	147
10	Single-cell CRISPR screening in drug resistance. <i>Cell Biology and Toxicology</i> , 2017, 33, 207-210.	2.4	35
11	Human organomics: a fresh approach to understanding human development using single-cell transcriptomics. <i>Development (Cambridge)</i> , 2017, 144, 1584-1587.	1.2	26
12	Applications of CRISPR-Cas for synthetic biology and genetic recording. <i>Current Opinion in Systems Biology</i> , 2017, 5, 9-15.	1.3	18
13	Microfluidics as a Strategic Player to Decipher Single-Cell Omics?. <i>Trends in Biotechnology</i> , 2017, 35, 713-727.	4.9	27
14	The Dimensions, Dynamics, and Relevance of the Mammalian Noncoding Transcriptome. <i>Trends in Genetics</i> , 2017, 33, 464-478.	2.9	181
15	Dynamic chromatin technologies: from individual molecules to epigenomic regulation in cells. <i>Nature Reviews Genetics</i> , 2017, 18, 457-472.	7.7	60
16	Generic membrane-spanning features endow IRE1 \pm with responsiveness to membrane aberrancy. <i>Molecular Biology of the Cell</i> , 2017, 28, 2318-2332.	0.9	38
17	Mammalian synthetic biology in the age of genome editing and personalized medicine. <i>Current Opinion in Chemical Biology</i> , 2017, 40, 57-64.	2.8	16
18	System-level perturbations of cell metabolism using CRISPR/Cas9. <i>Current Opinion in Biotechnology</i> , 2017, 46, 134-140.	3.3	25
19	Scaling by shrinking: empowering single-cell 'omics' with microfluidic devices. <i>Nature Reviews Genetics</i> , 2017, 18, 345-361.	7.7	274

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20	Progress towards precision functional genomics in cancer. <i>Current Opinion in Systems Biology</i> , 2017, 2, 74-83.	1.3	7
21	Functional interrogation of non-coding DNA through CRISPR genome editing. <i>Methods</i> , 2017, 121-122, 118-129.	1.9	28
23	High-throughput, image-based screening of pooled genetic-variant libraries. <i>Nature Methods</i> , 2017, 14, 1159-1162.	9.0	53
24	High-Throughput Approaches to Pinpoint Function within the Noncoding Genome. <i>Molecular Cell</i> , 2017, 68, 44-59.	4.5	54
25	CRISPR/Cas9-Based Engineering of the Epigenome. <i>Cell Stem Cell</i> , 2017, 21, 431-447.	5.2	215
26	CRISPR/Cas9 screening using unique molecular identifiers. <i>Molecular Systems Biology</i> , 2017, 13, 945.	3.2	51
27	Combined CRISPRi/a-Based Chemical Genetic Screens Reveal that Rigosertib Is a Microtubule-Destabilizing Agent. <i>Molecular Cell</i> , 2017, 68, 210-223.e6.	4.5	197
28	Enhancer connectome in primary human cells identifies target genes of disease-associated DNA elements. <i>Nature Genetics</i> , 2017, 49, 1602-1612.	9.4	419
29	CRISPR-UMI: single-cell lineage tracing of pooled CRISPR-Cas9 screens. <i>Nature Methods</i> , 2017, 14, 1191-1197.	9.0	95
30	Unravelling biology and shifting paradigms in cancer with single-cell sequencing. <i>Nature Reviews Cancer</i> , 2017, 17, 557-569.	12.8	280
31	Single-cell insights into transcriptomic diversity in immunity. <i>Current Opinion in Systems Biology</i> , 2017, 5, 63-71.	1.3	5
32	Edited course of biomedical research: leaping forward with CRISPR. <i>Pharmacological Research</i> , 2017, 125, 258-265.	3.1	5
33	Adapting Secretory Proteostasis and Function Through the Unfolded Protein Response. <i>Current Topics in Microbiology and Immunology</i> , 2017, 414, 1-25.	0.7	19
34	By CyTOF. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2017, 37, 1423-1424.	1.1	4
35	Systematic single-cell analysis provides new insights into heterogeneity and plasticity of the pancreas. <i>Molecular Metabolism</i> , 2017, 6, 974-990.	3.0	95
36	Trap Seq : An RNA Sequencing-Based Pipeline for the Identification of Gene-Trap Insertions in Mammalian Cells. <i>Journal of Molecular Biology</i> , 2017, 429, 2780-2789.	2.0	10
37	AJ-Protein Co-chaperone Recruits BiP to Monomerize IRE1 and Repress the Unfolded Protein Response. <i>Cell</i> , 2017, 171, 1625-1637.e13.	13.5	176
38	Efficient Generation of Transcriptomic Profiles by Random Composite Measurements. <i>Cell</i> , 2017, 171, 1424-1436.e18.	13.5	95

#	ARTICLE	IF	CITATIONS
39	Coupling shRNA screens with single-cell RNA-seq identifies a dual role for mTOR in reprogramming-induced senescence. <i>Genes and Development</i> , 2017, 31, 2085-2098.	2.7	53
40	Precision Medicine, CRISPR, and Genome Engineering. <i>Advances in Experimental Medicine and Biology</i> , 2017, , .	0.8	2
41	Target Discovery for Precision Medicine Using High-Throughput Genome Engineering. <i>Advances in Experimental Medicine and Biology</i> , 2017, 1016, 123-145.	0.8	6
42	Synthetic lethality and cancer. <i>Nature Reviews Genetics</i> , 2017, 18, 613-623.	7.7	444
43	Transcriptional determination and functional specificity of myeloid cells: making sense of diversity. <i>Nature Reviews Immunology</i> , 2017, 17, 595-607.	10.6	75
44	Challenges and emerging directions in single-cell analysis. <i>Genome Biology</i> , 2017, 18, 84.	3.8	258
45	Single cell transcriptomics of pluripotent stem cells: reprogramming and differentiation. <i>Current Opinion in Genetics and Development</i> , 2017, 46, 66-76.	1.5	17
46	Massively parallel single-nucleus RNA-seq with DroNc-seq. <i>Nature Methods</i> , 2017, 14, 955-958.	9.0	859
47	Elucidating the Role of Host Long Non-Coding RNA during Viral Infection: Challenges and Paths Forward. <i>Vaccines</i> , 2017, 5, 37.	2.1	12
48	The Sec61 translocon limits IRE1 β signaling during the unfolded protein response. <i>ELife</i> , 2017, 6, .	2.8	52
49	The Human Cell Atlas. <i>ELife</i> , 2017, 6, .	2.8	1,547
50	Poxviruses Utilize Multiple Strategies to Inhibit Apoptosis. <i>Viruses</i> , 2017, 9, 215.	1.5	49
51	A practical guide to single-cell RNA-sequencing for biomedical research and clinical applications. <i>Genome Medicine</i> , 2017, 9, 75.	3.6	712
52	Cell ontology in an age of data-driven cell classification. <i>BMC Bioinformatics</i> , 2017, 18, 558.	1.2	12
53	Big knowledge from big data in functional genomics. <i>Emerging Topics in Life Sciences</i> , 2017, 1, 245-248.	1.1	4
54	THE CELL SEEKER. <i>Nature</i> , 2017, 547, 24-26.	13.7	4
55	Recent insights into PERK-dependent signaling from the stressed endoplasmic reticulum. <i>F1000Research</i> , 2017, 6, 1897.	0.8	75
56	The protein kinase PERK/EIF2AK3 regulates proinsulin processing not via protein synthesis but by controlling endoplasmic reticulum chaperones. <i>Journal of Biological Chemistry</i> , 2018, 293, 5134-5149.	1.6	33

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57	Assessing sufficiency and necessity of enhancer activities for gene expression and the mechanisms of transcription activation. <i>Genes and Development</i> , 2018, 32, 202-223.	2.7	171
58	CRISPR-based methods for high-throughput annotation of regulatory DNA. <i>Current Opinion in Biotechnology</i> , 2018, 52, 32-41.	3.3	13
59	Systems Immunology: Learning the Rules of the Immune System. <i>Annual Review of Immunology</i> , 2018, 36, 813-842.	9.5	70
60	High Intracellular Seed Train BiP Levels Correlate With Poor Production Culture Performance in CHO Cells. <i>Biotechnology Journal</i> , 2018, 13, e1700746.	1.8	3
61	Using single-cell genomics to understand developmental processes and cell fate decisions. <i>Molecular Systems Biology</i> , 2018, 14, e8046.	3.2	190
62	Development and application of CRISPR/Cas9 technologies in genomic editing. <i>Human Molecular Genetics</i> , 2018, 27, R79-R88.	1.4	47
63	Mapping gene regulatory networks from single-cell omics data. <i>Briefings in Functional Genomics</i> , 2018, 17, 246-254.	1.3	194
64	Chemical stresses fail to mimic the unfolded protein response resulting from luminal load with unfolded polypeptides. <i>Journal of Biological Chemistry</i> , 2018, 293, 5600-5612.	1.6	53
65	On the design of CRISPR-based single-cell molecular screens. <i>Nature Methods</i> , 2018, 15, 271-274.	9.0	170
66	CRISPR interference-based specific and efficient gene inactivation in the brain. <i>Nature Neuroscience</i> , 2018, 21, 447-454.	7.1	133
67	Large-scale image-based profiling of single-cell phenotypes in arrayed CRISPR-Cas9 gene perturbation screens. <i>Molecular Systems Biology</i> , 2018, 14, e8064.	3.2	56
68	Single-Cell Genomics: A Stepping Stone for Future Immunology Discoveries. <i>Cell</i> , 2018, 172, 14-21.	13.5	214
69	Orthologous CRISPR-Cas9 enzymes for combinatorial genetic screens. <i>Nature Biotechnology</i> , 2018, 36, 179-189.	9.4	216
70	CRISPR Approaches to Small Molecule Target Identification. <i>ACS Chemical Biology</i> , 2018, 13, 366-375.	1.6	68
71	Implementing CRISPR-Cas technologies in conventional and non-conventional yeasts: Current state and future prospects. <i>Biotechnology Advances</i> , 2018, 36, 641-665.	6.0	120
72	CCPG1 Is a Non-canonical Autophagy Cargo Receptor Essential for ER-Phagy and Pancreatic ER Proteostasis. <i>Developmental Cell</i> , 2018, 44, 217-232.e11.	3.1	315
73	MicroRNA-focused CRISPR-Cas9 library screen reveals fitness-associated miRNAs. <i>Rna</i> , 2018, 24, 966-981.	1.6	58
74	Promoter of lncRNA Gene PVT1 Is a Tumor-Suppressor DNA Boundary Element. <i>Cell</i> , 2018, 173, 1398-1412.e22.	13.5	362

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75	The Ftx Noncoding Locus Controls X Chromosome Inactivation Independently of Its RNA Products. <i>Molecular Cell</i> , 2018, 70, 462-472.e8.	4.5	75
76	The unknown face of IRE1 β – Beyond ER stress. <i>European Journal of Cell Biology</i> , 2018, 97, 359-368.	1.6	39
77	Advances in Transcriptomics. <i>Circulation Research</i> , 2018, 122, 1200-1220.	2.0	38
78	CRISPR-based genomic tools for the manipulation of genetically intractable microorganisms. <i>Nature Reviews Microbiology</i> , 2018, 16, 333-339.	13.6	88
79	Inhibition of Sec61-dependent translocation by mycolactone uncouples the integrated stress response from ER stress, driving cytotoxicity via translational activation of ATF4. <i>Cell Death and Disease</i> , 2018, 9, 397.	2.7	59
80	Molecular mechanisms driving transcriptional stress responses. <i>Nature Reviews Genetics</i> , 2018, 19, 385-397.	7.7	206
81	Single-Cell Sequencing in Normal and Malignant Hematopoiesis. <i>HemaSphere</i> , 2018, 2, e34.	1.2	13
82	CHO-omics Review: The Impact of Current and Emerging Technologies on Chinese Hamster Ovary Based Bioproduction. <i>Biotechnology Journal</i> , 2018, 13, e1700227.	1.8	71
83	Precision medicine – A promising, yet challenging road lies ahead. <i>Current Opinion in Systems Biology</i> , 2018, 7, 1-7.	1.3	13
84	CRISPRi and CRISPRa Screens in Mammalian Cells for Precision Biology and Medicine. <i>ACS Chemical Biology</i> , 2018, 13, 406-416.	1.6	248
85	The emerging role of systems biology for engineering protein production in CHO cells. <i>Current Opinion in Biotechnology</i> , 2018, 51, 64-69.	3.3	67
86	Multiplexed droplet single-cell RNA-sequencing using natural genetic variation. <i>Nature Biotechnology</i> , 2018, 36, 89-94.	9.4	745
87	The Future of Multiplexed Eukaryotic Genome Engineering. <i>ACS Chemical Biology</i> , 2018, 13, 313-325.	1.6	30
88	DnaJ Homolog Subfamily B Member 9 Is a Putative Autoantigen in Fibrillary GN. <i>Journal of the American Society of Nephrology: JASN</i> , 2018, 29, 231-239.	3.0	75
89	Modeling Cancer in the CRISPR Era. <i>Annual Review of Cancer Biology</i> , 2018, 2, 111-131.	2.3	15
90	Single-cell RNA sequencing: Technical advancements and biological applications. <i>Molecular Aspects of Medicine</i> , 2018, 59, 36-46.	2.7	258
91	Single-cell analysis of tumors: Creating new value for molecular biomarker discovery of cancer stem cells and tumor-infiltrating immune cells. <i>World Journal of Stem Cells</i> , 2018, 10, 160-171.	1.3	12
92	Recent advances in functional genome analysis. <i>F1000Research</i> , 2018, 7, 1968.	0.8	16

#	ARTICLE	IF	CITATIONS
93	Mapping Cellular Reprogramming via Pooled Overexpression Screens with Paired Fitness and Single-Cell RNA-Sequencing Readout. <i>Cell Systems</i> , 2018, 7, 548-555.e8.	2.9	35
94	Paring down to the essentials. <i>Science</i> , 2018, 362, 904-904.	6.0	0
95	Genome-wide CRISPR Screens in Primary Human T Cells Reveal Key Regulators of Immune Function. <i>Cell</i> , 2018, 175, 1958-1971.e15.	13.5	378
96	Identification of phagocytosis regulators using magnetic genome-wide CRISPR screens. <i>Nature Genetics</i> , 2018, 50, 1716-1727.	9.4	135
97	An integrative approach for building personalized gene regulatory networks for precision medicine. <i>Genome Medicine</i> , 2018, 10, 96.	3.6	49
98	Understanding the Biology and Pathogenesis of the Kidney by Single-Cell Transcriptomic Analysis. <i>Kidney Diseases (Basel, Switzerland)</i> , 2018, 4, 214-225.	1.2	5
99	SEC24A identified as an essential mediator of thapsigargin-induced cell death in a genome-wide CRISPR/Cas9 screen. <i>Cell Death Discovery</i> , 2018, 4, 115.	2.0	13
100	Pathway sensor-based functional genomics screening identifies modulators of neuronal activity. <i>Scientific Reports</i> , 2018, 8, 17597.	1.6	7
101	Guide Swap enables genome-scale pooled CRISPR-Cas9 screening in human primary cells. <i>Nature Methods</i> , 2018, 15, 941-946.	9.0	63
102	Microfluidic and Paper-Based Devices for Disease Detection and Diagnostic Research. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2731.	1.8	49
103	Blank spots on the map: some current questions on nuclear organization and genome architecture. <i>Histochemistry and Cell Biology</i> , 2018, 150, 579-592.	0.8	24
104	Towards quantitative and multiplexed in vivo functional cancer genomics. <i>Nature Reviews Genetics</i> , 2018, 19, 741-755.	7.7	45
105	CRISPR Activation Screens Systematically Identify Factors that Drive Neuronal Fate and Reprogramming. <i>Cell Stem Cell</i> , 2018, 23, 758-771.e8.	5.2	161
106	A New Era in Functional Genomics Using CRISPR/Cas9 Knockout Screening. <i>Journal of Molecular and Genetic Medicine: an International Journal of Biomedical Research</i> , 2018, 12, .	0.1	0
107	Activity-Regulated Transcription: Bridging the Gap between Neural Activity and Behavior. <i>Neuron</i> , 2018, 100, 330-348.	3.8	408
108	The chromatin accessibility landscape of primary human cancers. <i>Science</i> , 2018, 362, .	6.0	781
109	Stem Cells, Genome Editing, and the Path to Translational Medicine. <i>Cell</i> , 2018, 175, 615-632.	13.5	105
110	Protein Barcodes Enable High-Dimensional Single-Cell CRISPR Screens. <i>Cell</i> , 2018, 175, 1141-1155.e16.	13.5	107

#	ARTICLE	IF	CITATIONS
111	Cellular barcoding: lineage tracing, screening and beyond. <i>Nature Methods</i> , 2018, 15, 871-879.	9.0	136
112	Emerging Roles for Mesencephalic Astrocyte-Derived Neurotrophic Factor (MANF) in Pancreatic Beta Cells and Diabetes. <i>Frontiers in Physiology</i> , 2018, 9, 1457.	1.3	17
113	Capturing functional long non-coding RNAs through integrating large-scale causal relations from gene perturbation experiments. <i>EBioMedicine</i> , 2018, 35, 369-380.	2.7	19
114	A case of mistaken identity. <i>Nature Biotechnology</i> , 2018, 36, 802-804.	9.4	17
115	Quantitative single-cell transcriptomics. <i>Briefings in Functional Genomics</i> , 2018, 17, 220-232.	1.3	50
116	Power in Numbers: Single-Cell RNA-Seq Strategies to Dissect Complex Tissues. <i>Annual Review of Genetics</i> , 2018, 52, 203-221.	3.2	94
117	Single-cell genomics to guide human stem cell and tissue engineering. <i>Nature Methods</i> , 2018, 15, 661-667.	9.0	52
118	Synthetic transcription factors for cell fate reprogramming. <i>Current Opinion in Genetics and Development</i> , 2018, 52, 13-21.	1.5	29
119	From Tissues to Cell Types and Back: Single-Cell Gene Expression Analysis of Tissue Architecture. <i>Annual Review of Biomedical Data Science</i> , 2018, 1, 29-51.	2.8	91
120	Antigen presentation unfolded: identifying convergence points between the UPR and antigen presentation pathways. <i>Current Opinion in Immunology</i> , 2018, 52, 100-107.	2.4	31
121	Is Pooled CRISPR-Screening the Dawn of a New Era for Functional Genomics. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1068, 171-176.	0.8	3
123	Uncovering pseudotemporal trajectories with covariates from single cell and bulk expression data. <i>Nature Communications</i> , 2018, 9, 2442.	5.8	80
124	Neuro-Immuno-Gene- and Genome-Editing-Therapy for Alzheimer's Disease: Are We There Yet?. <i>Journal of Alzheimer's Disease</i> , 2018, 65, 321-344.	1.2	17
125	Uncoupling of sgRNAs from their associated barcodes during PCR amplification of combinatorial CRISPR screens. <i>PLoS ONE</i> , 2018, 13, e0197547.	1.1	37
126	Three branches to rule them all? UPR signalling in response to chemically versus misfolded proteins-induced ER stress. <i>Biology of the Cell</i> , 2018, 110, 197-204.	0.7	29
127	Application of CRISPR-Cas9 Based Genome-Wide Screening Approaches to Study Cellular Signalling Mechanisms. <i>International Journal of Molecular Sciences</i> , 2018, 19, 933.	1.8	42
128	Single-Cell Multi-omics: An Engine for New Quantitative Models of Gene Regulation. <i>Trends in Genetics</i> , 2018, 34, 653-665.	2.9	86
129	Mapping the Genetic Landscape of Human Cells. <i>Cell</i> , 2018, 174, 953-967.e22.	13.5	226

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130	Dynamic changes in complexes of IRE1 $\hat{\pm}$, PERK, and ATF6 $\hat{\pm}$ during endoplasmic reticulum stress. <i>Molecular Biology of the Cell</i> , 2018, 29, 1376-1388.	0.9	48
131	A high-throughput screen of real-time ATP levels in individual cells reveals mechanisms of energy failure. <i>PLoS Biology</i> , 2018, 16, e2004624.	2.6	47
132	Genome-wide identification of directed gene networks using large-scale population genomics data. <i>Nature Communications</i> , 2018, 9, 3097.	5.8	18
133	Molecular Diversity and Specializations among the Cells of the Adult Mouse Brain. <i>Cell</i> , 2018, 174, 1015-1030.e16.	13.5	1,231
134	Human Genetics of Obesity and Type 2 Diabetes Mellitus. <i>Circulation Genomic and Precision Medicine</i> , 2018, 11, e002090.	1.6	58
135	Decoding the noncoding genome via large-scale CRISPR screens. <i>Current Opinion in Genetics and Development</i> , 2018, 52, 70-76.	1.5	20
136	From Identification to Function: Current Strategies to Prioritise and Follow-Up GWAS Results. <i>Methods in Molecular Biology</i> , 2018, 1793, 259-275.	0.4	2
137	Functional Genomics via CRISPR-Cas. <i>Journal of Molecular Biology</i> , 2019, 431, 48-65.	2.0	62
138	Progenitor and Stem Cell Heterogeneity. , 2019, , 93-111.		0
139	Exploring genetic interaction manifolds constructed from rich single-cell phenotypes. <i>Science</i> , 2019, 365, 786-793.	6.0	155
140	Identification of hyper-rewired genomic stress non-oncogene addiction genes across 15 cancer types. <i>Npj Systems Biology and Applications</i> , 2019, 5, 27.	1.4	11
141	CRISPR Interference-Based Platform for Multimodal Genetic Screens in Human iPSC-Derived Neurons. <i>Neuron</i> , 2019, 104, 239-255.e12.	3.8	288
142	Decoding pluripotency: Genetic screens to interrogate the acquisition, maintenance, and exit of pluripotency. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2020, 12, e1464.	6.6	11
143	scGen predicts single-cell perturbation responses. <i>Nature Methods</i> , 2019, 16, 715-721.	9.0	290
144	CRISPR Tools for Systematic Studies of RNA Regulation. <i>Cold Spring Harbor Perspectives in Biology</i> , 2019, 11, a035386.	2.3	22
145	The ability of transcription factors to differentially regulate gene expression is a crucial component of the mechanism underlying inversion, a frequently observed genetic interaction pattern. <i>PLoS Computational Biology</i> , 2019, 15, e1007061.	1.5	4
146	Small Molecule Targets TMED9 and Promotes Lysosomal Degradation to Reverse Proteinopathy. <i>Cell</i> , 2019, 178, 521-535.e23.	13.5	124
147	Importance of genetic screens in precision oncology. <i>ESMO Open</i> , 2019, 4, e000505.	2.0	10

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148	An LKB1-SIK Axis Suppresses Lung Tumor Growth and Controls Differentiation. <i>Cancer Discovery</i> , 2019, 9, 1590-1605.	7.7	71
149	The evolving concept of cell identity in the single cell era. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	115
150	Concepts and limitations for learning developmental trajectories from single cell genomics. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	177
151	Optical Pooled Screens in Human Cells. <i>Cell</i> , 2019, 179, 787-799.e17.	13.5	170
152	Compromised function of the ESCRT pathway promotes endolysosomal escape of tau seeds and propagation of tau aggregation. <i>Journal of Biological Chemistry</i> , 2019, 294, 18952-18966.	1.6	103
153	CRISPR-Cas9-mediated loss-of-function screens. <i>Frontiers in Life Science: Frontiers of Interdisciplinary Research in the Life Sciences</i> , 2019, 12, 1-13.	1.1	3
154	New insights into transcriptional reprogramming during cellular stress. <i>Journal of Cell Science</i> , 2019, 132, .	1.2	36
155	A Toolkit for Rapid Modular Construction of Biological Circuits in Mammalian Cells. <i>ACS Synthetic Biology</i> , 2019, 8, 2593-2606.	1.9	49
156	Recent insights into the genotype-phenotype relationship from massively parallel genetic assays. <i>Evolutionary Applications</i> , 2019, 12, 1721-1742.	1.5	52
157	CRISPR Screens: The Right Tool for the Job. <i>Genetic Engineering and Biotechnology News</i> , 2019, 39, S24-S25.	0.1	0
158	A pooled single-cell genetic screen identifies regulatory checkpoints in the continuum of the epithelial-to-mesenchymal transition. <i>Nature Genetics</i> , 2019, 51, 1389-1398.	9.4	150
159	A fresh approach to synthesizing ammonia from air and water. <i>Nature</i> , 2019, 568, 464-466.	13.7	22
160	Lethal clues to cancer-cell vulnerability. <i>Nature</i> , 2019, 568, 463-464.	13.7	5
161	Systematic Identification of Host Cell Regulators of <i>Legionella pneumophila</i> Pathogenesis Using a Genome-wide CRISPR Screen. <i>Cell Host and Microbe</i> , 2019, 26, 551-563.e6.	5.1	62
162	Mapping human cell phenotypes to genotypes with single-cell genomics. <i>Science</i> , 2019, 365, 1401-1405.	6.0	71
163	Validation of a Miniaturized Permeability Assay Compatible with CRISPR-Mediated Genome-Wide Screen. <i>Scientific Reports</i> , 2019, 9, 14238.	1.6	1
164	Simultaneous repression of multiple bacterial genes using nonrepetitive extra-long sgRNA arrays. <i>Nature Biotechnology</i> , 2019, 37, 1294-1301.	9.4	107
165	The Unfolded Protein Response: Detecting and Responding to Fluctuations in the Protein-Folding Capacity of the Endoplasmic Reticulum. <i>Cold Spring Harbor Perspectives in Biology</i> , 2019, 11, a033886.	2.3	202

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166	Integrative single-cell analysis. <i>Nature Reviews Genetics</i> , 2019, 20, 257-272.	7.7	932
167	CRISPR-Based Tools in Immunity. <i>Annual Review of Immunology</i> , 2019, 37, 571-597.	9.5	38
168	Exploiting Molecular Barcodes in High-Throughput Cellular Assays. <i>SLAS Technology</i> , 2019, 24, 298-307.	1.0	6
169	Identification of rheumatoid arthritis causal genes using functional genomics. <i>Scandinavian Journal of Immunology</i> , 2019, 89, e12753.	1.3	14
170	Multiplexed CRISPR/Cas9 gene knockout with simple crRNA:tracrRNA co-transfection. <i>Cell and Bioscience</i> , 2019, 9, 41.	2.1	11
171	CRISPR/Cas-based devices for mammalian synthetic biology. <i>Current Opinion in Chemical Biology</i> , 2019, 52, 23-30.	2.8	10
172	MULTI-seq: sample multiplexing for single-cell RNA sequencing using lipid-tagged indices. <i>Nature Methods</i> , 2019, 16, 619-626.	9.0	421
173	Genome-wide CRISPR screen identifies suppressors of endoplasmic reticulum stress-induced apoptosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 13384-13393.	3.3	45
174	<sc>ER</sc> p18 regulates activation of <sc>ATF</sc> 6± during unfolded protein response. <i>EMBO Journal</i> , 2019, 38, e100990.	3.5	44
175	CRISPR/Cas9 guided genome and epigenome engineering and its therapeutic applications in immune mediated diseases. <i>Seminars in Cell and Developmental Biology</i> , 2019, 96, 32-43.	2.3	9
176	Development of CRISPR-Cas systems for genome editing and beyond. <i>Quarterly Reviews of Biophysics</i> , 2019, 52, .	2.4	108
177	Large scale control and programming of gene expression using CRISPR. <i>Seminars in Cell and Developmental Biology</i> , 2019, 96, 124-132.	2.3	5
178	Model-based understanding of single-cell CRISPR screening. <i>Nature Communications</i> , 2019, 10, 2233.	5.8	61
179	Investigating Cell Fate Decisions with ICGS Analysis of Single Cells. <i>Methods in Molecular Biology</i> , 2019, 1975, 251-275.	0.4	3
180	CellTag Indexing: genetic barcode-based sample multiplexing for single-cell genomics. <i>Genome Biology</i> , 2019, 20, 90.	3.8	61
181	Imaging-based pooled CRISPR screening reveals regulators of lncRNA localization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 10842-10851.	3.3	79
182	Molecular recording of mammalian embryogenesis. <i>Nature</i> , 2019, 570, 77-82.	13.7	257
183	Multiplexed detection of proteins, transcriptomes, clonotypes and CRISPR perturbations in single cells. <i>Nature Methods</i> , 2019, 16, 409-412.	9.0	364

#	ARTICLE	IF	CITATIONS
184	Single-Cell RNA-Sequencing-Based CRISPRi Screening Resolves Molecular Drivers of Early Human Endoderm Development. <i>Cell Reports</i> , 2019, 27, 708-718.e10.	2.9	81
186	CRISPR Screening in Single Cells. <i>Methods in Molecular Biology</i> , 2019, 1979, 395-406.	0.4	2
187	Single-Cell Genomics. <i>Clinical Chemistry</i> , 2019, 65, 972-985.	1.5	47
188	Cellular response to small molecules that selectively stall protein synthesis by the ribosome. <i>PLoS Genetics</i> , 2019, 15, e1008057.	1.5	31
189	Targeting chromatin complexes in fusion protein-driven malignancies. <i>Nature Reviews Cancer</i> , 2019, 19, 255-269.	12.8	55
190	Genetic interaction networks in cancer cells. <i>Current Opinion in Genetics and Development</i> , 2019, 54, 64-72.	1.5	28
191	From cell lines to living biosensors: new opportunities to prioritize cancer dependencies using ex vivo tumor cultures. <i>Current Opinion in Genetics and Development</i> , 2019, 54, 33-40.	1.5	20
192	Scrublet: Computational Identification of Cell Doublets in Single-Cell Transcriptomic Data. <i>Cell Systems</i> , 2019, 8, 281-291.e9.	2.9	1,274
193	CRISPR Screens: The Right Tool for the Job. <i>CRISPR Journal</i> , 2019, 2, 9-11.	1.4	0
194	Deubiquitinases Maintain Protein Homeostasis and Survival of Cancer Cells upon Glutathione Depletion. <i>Cell Metabolism</i> , 2019, 29, 1166-1181.e6.	7.2	121
195	New insights into hematopoietic differentiation landscapes from single-cell RNA sequencing. <i>Blood</i> , 2019, 133, 1415-1426.	0.6	60
196	Comprehensive, integrated, and phased whole-genome analysis of the primary ENCODE cell line K562. <i>Genome Research</i> , 2019, 29, 472-484.	2.4	78
197	Unconventional secretion factor GRASP55 is increased by pharmacological unfolded protein response inducers in neurons. <i>Scientific Reports</i> , 2019, 9, 1567.	1.6	17
198	The Hyaluronidase, TMEM2, Promotes ER Homeostasis and Longevity Independent of the UPRER. <i>Cell</i> , 2019, 179, 1306-1318.e18.	13.5	87
199	Advancing CRISPR-Based Programmable Platforms beyond Genome Editing in Mammalian Cells. <i>ACS Synthetic Biology</i> , 2019, 8, 2607-2619.	1.9	5
200	High-throughput Droplet Array Generated by Roller Nanoimprint Lithography with Biomimetic Surfaces. , 2019, 2019, 1074-1077.		3
201	Leaky endosomes push tau over the seed limit. <i>Journal of Biological Chemistry</i> , 2019, 294, 18967-18968.	1.6	5
202	Recent developments of microfluidics as a tool for biotechnology and microbiology. <i>Current Opinion in Biotechnology</i> , 2019, 55, 60-67.	3.3	63

#	ARTICLE	IF	CITATIONS
203	RNAi/CRISPR Screens: from a Pool to a Valid Hit. Trends in Biotechnology, 2019, 37, 38-55.	4.9	90
204	A Genome-wide Framework for Mapping Gene Regulation via Cellular Genetic Screens. Cell, 2019, 176, 377-390.e19.	13.5	379
205	Coupled Single-Cell CRISPR Screening and Epigenomic Profiling Reveals Causal Gene Regulatory Networks. Cell, 2019, 176, 361-376.e17.	13.5	215
206	Early Events in the Endoplasmic Reticulum Unfolded Protein Response. Cold Spring Harbor Perspectives in Biology, 2019, 11, a033894.	2.3	132
207	Recent Advances in Microfluidic Techniques for Systems Biology. Analytical Chemistry, 2019, 91, 315-329.	3.2	5
208	Dynamic genome and transcriptional network-based biomarkers and drugs: precision in breast cancer therapy. Medicinal Research Reviews, 2019, 39, 1205-1227.	5.0	21
209	One-step bonding and hydrophobic surface modification method for rapid fabrication of polycarbonate-based droplet microfluidic chips. Sensors and Actuators B: Chemical, 2019, 282, 60-68.	4.0	40
210	Transcription of the NKG2D ligand MICA is suppressed by the IRE1/XBP1 pathway of the unfolded protein response through the regulation of E2F1. FASEB Journal, 2019, 33, 3481-3495.	0.2	23
211	Single-Cell Applications of Next-Generation Sequencing. Cold Spring Harbor Perspectives in Medicine, 2019, 9, a026898.	2.9	23
212	Ribosomal protein RPL26 is the principal target of UFMylation. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 1299-1308.	3.3	126
213	Gene Regulatory Networks. Methods in Molecular Biology, 2019, , .	0.4	41
214	Network Inference from Single-Cell Transcriptomic Data. Methods in Molecular Biology, 2019, 1883, 235-249.	0.4	23
215	Functional Genomics for Cancer Research: Applications In Vivo and In Vitro. Annual Review of Cancer Biology, 2019, 3, 345-363.	2.3	9
216	CRISPR/Cas9 for cancer research and therapy. Seminars in Cancer Biology, 2019, 55, 106-119.	4.3	206
217	100 Years of evolving geneâ€“disease complexities and scientific debutants. Briefings in Bioinformatics, 2020, 21, 885-905.	3.2	36
218	No evidence for cellâ€“toâ€“cell transmission of the unfolded protein response in cell culture. Journal of Neurochemistry, 2020, 152, 208-220.	2.1	10
219	CRISPR: A Screenerâ€™s Guide. SLAS Discovery, 2020, 25, 233-240.	1.4	11
220	Synthetic lethality as an engine for cancer drug target discovery. Nature Reviews Drug Discovery, 2020, 19, 23-38.	21.5	295

#	ARTICLE	IF	CITATIONS
221	Tracking the immune response with single-cell genomics. <i>Vaccine</i> , 2020, 38, 4487-4490.	1.7	7
222	Time-resolved imaging-based CRISPRi screening. <i>Nature Methods</i> , 2020, 17, 86-92.	9.0	57
223	Single-cell multimodal omics: the power of many. <i>Nature Methods</i> , 2020, 17, 11-14.	9.0	277
224	Prostate cancer research: The next generation; report from the 2019 Coffeyâ€Holden Prostate Cancer Academy Meeting. <i>Prostate</i> , 2020, 80, 113-132.	1.2	25
225	Data generation and network reconstruction strategies for single cell transcriptomic profiles of CRISPR-mediated gene perturbations. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020, 1863, 194441.	0.9	4
226	Wnt-regulated lncRNA discovery enhanced by in vivo identification and CRISPRi functional validation. <i>Genome Medicine</i> , 2020, 12, 89.	3.6	12
227	Targeted Single-Cell RNA and DNA Sequencing With Fluorescence-Activated Droplet Merger. <i>Analytical Chemistry</i> , 2020, 92, 14616-14623.	3.2	9
228	Profiling the Non-genetic Origins of Cancer Drug Resistance with a Single-Cell Functional Genomics Approach Using Predictive Cell Dynamics. <i>Cell Systems</i> , 2020, 11, 367-374.e5.	2.9	21
229	Computational Methods for Analysis of Large-Scale CRISPR Screens. <i>Annual Review of Biomedical Data Science</i> , 2020, 3, 137-162.	2.8	4
230	High-performance CRISPR-Cas12a genome editing for combinatorial genetic screening. <i>Nature Communications</i> , 2020, 11, 3455.	5.8	63
231	Single-cell lineage analysis reveals genetic and epigenetic interplay in glioblastoma drug resistance. <i>Genome Biology</i> , 2020, 21, 174.	3.8	59
232	Comprehensive Mapping of Key Regulatory Networks that Drive Oncogene Expression. <i>Cell Reports</i> , 2020, 33, 108426.	2.9	14
233	Mapping replication timing domains genome wide in single mammalian cells with single-cell DNA replication sequencing. <i>Nature Protocols</i> , 2020, 15, 4058-4100.	5.5	19
234	In vivo Perturb-Seq reveals neuronal and glial abnormalities associated with autism risk genes. <i>Science</i> , 2020, 370, .	6.0	155
235	Master Regulators and Cofactors of Human Neuronal Cell Fate Specification Identified by CRISPR Gene Activation Screens. <i>Cell Reports</i> , 2020, 33, 108460.	2.9	38
236	CIGARâ€seq, a CRISPR/Casâ€based method for unbiased screening of novel mRNA modification regulators. <i>Molecular Systems Biology</i> , 2020, 16, e10025.	3.2	17
237	SITC cancer immunotherapy resource document: a compass in the land of biomarker discovery. , 2020, 8, e000705.		20
238	Cell Reprogramming With CRISPR/Cas9 Based Transcriptional Regulation Systems. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 882.	2.0	29

#	ARTICLE	IF	CITATIONS
239	Integration of CRISPR-engineering and hiPSC-based models of psychiatric genomics. <i>Molecular and Cellular Neurosciences</i> , 2020, 107, 103532.	1.0	8
240	A Three-Way Combinatorial CRISPR Screen for Analyzing Interactions among Druggable Targets. <i>Cell Reports</i> , 2020, 32, 108020.	2.9	27
241	Antibody-secreting cell destiny emerges during the initial stages of B-cell activation. <i>Nature Communications</i> , 2020, 11, 3989.	5.8	41
242	Time for remodeling: SNF2-family DNA translocases in replication fork metabolism and human disease. <i>DNA Repair</i> , 2020, 95, 102943.	1.3	25
243	Interactions between lineage-associated transcription factors govern haematopoietic progenitor states. <i>EMBO Journal</i> , 2020, 39, e104983.	3.5	20
244	High-throughput single-cell functional elucidation of neurodevelopmental disease-associated genes reveals convergent mechanisms altering neuronal differentiation. <i>Genome Research</i> , 2020, 30, 1317-1331.	2.4	50
245	Multiplatform genomic profiling and magnetic resonance imaging identify mechanisms underlying intratumor heterogeneity in meningioma. <i>Nature Communications</i> , 2020, 11, 4803.	5.8	56
246	Designing custom CRISPR libraries for hypothesis-driven drug target discovery. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 2237-2246.	1.9	10
247	Interrogating genome function using CRISPR tools: a narrative review. <i>Journal of Bio-X Research</i> , 2020, 3, 83-91.	0.3	0
248	Resolving Neurodevelopmental and Vision Disorders Using Organoid Single-Cell Multi-omics. <i>Neuron</i> , 2020, 107, 1000-1013.	3.8	24
249	Mapping cancer genetics at single-cell resolution. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	3
250	Multiplexed single-cell transcriptional response profiling to define cancer vulnerabilities and therapeutic mechanism of action. <i>Nature Communications</i> , 2020, 11, 4296.	5.8	98
251	CiBER-seq dissects genetic networks by quantitative CRISPRi profiling of expression phenotypes. <i>Science</i> , 2020, 370, .	6.0	19
252	Defining the Teratoma as a Model for Multi-lineage Human Development. <i>Cell</i> , 2020, 183, 1402-1419.e18.	13.5	32
253	Multimodal Screeningâ€”The Future of Drug Discovery and Development. <i>Genetic Engineering and Biotechnology News</i> , 2020, 40, 32-33.	0.1	0
254	Gene regulatory network reconstruction using single-cell RNA sequencing of barcoded genotypes in diverse environments. <i>ELife</i> , 2020, 9, .	2.8	116
255	Pooled CRISPR screens with imaging on microwell arrays reveals stress granule-regulatory factors. <i>Nature Methods</i> , 2020, 17, 636-642.	9.0	60
256	Targeted Perturb-seq enables genome-scale genetic screens in single cells. <i>Nature Methods</i> , 2020, 17, 629-635.	9.0	139

#	ARTICLE	IF	CITATIONS
257	A Multiplexed Barcodelet Single-Cell RNA-Seq Approach Elucidates Combinatorial Signaling Pathways that Drive ESC Differentiation. <i>Cell Stem Cell</i> , 2020, 26, 938-950.e6.	5.2	12
258	Genomics-guided pre-clinical development of cancer therapies. <i>Nature Cancer</i> , 2020, 1, 482-492.	5.7	23
259	Towards systems tissue engineering: Elucidating the dynamics, spatial coordination, and individual cells driving emergent behaviors. <i>Biomaterials</i> , 2020, 255, 120189.	5.7	8
260	Keap1 mutation renders lung adenocarcinomas dependent on Slc33a1. <i>Nature Cancer</i> , 2020, 1, 589-602.	5.7	44
261	Direct-seq: A programmed gRNA scaffold for streamlined scRNA-seq in CRISPR screen. <i>Genome Biology</i> , 2020, 21, 136.	3.8	10
262	Pitfalls in Single Clone CRISPR-Cas9 Mutagenesis to Fine-Map Regulatory Intervals. <i>Genes</i> , 2020, 11, 504.	1.0	6
263	Genetic interaction mapping and exon-resolution functional genomics with a hybrid Cas9-Cas12a platform. <i>Nature Biotechnology</i> , 2020, 38, 638-648.	9.4	85
264	Multiplexed CRISPR technologies for gene editing and transcriptional regulation. <i>Nature Communications</i> , 2020, 11, 1281.	5.8	279
265	Regulation of B cell receptor-dependent NF- κ B signaling by the tumor suppressor KLHL14. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 6092-6102.	3.3	28
266	Pervasive functional translation of noncanonical human open reading frames. <i>Science</i> , 2020, 367, 1140-1146.	6.0	400
267	A gene signal amplifier platform for monitoring the unfolded protein response. <i>Nature Chemical Biology</i> , 2020, 16, 520-528.	3.9	8
268	Mini™ U6 Pol III promoter exhibits nucleosome redundancy and supports multiplexed coupling of CRISPR/Cas9 effects. <i>Gene Therapy</i> , 2020, 27, 451-458.	2.3	8
269	Modeling the complex genetic architectures of brain disease. <i>Nature Genetics</i> , 2020, 52, 363-369.	9.4	35
270	Integrative Methods and Practical Challenges for Single-Cell Multi-omics. <i>Trends in Biotechnology</i> , 2020, 38, 1007-1022.	4.9	149
271	Multiparametric Assays for Accelerating Early Drug Discovery. <i>Trends in Pharmacological Sciences</i> , 2020, 41, 318-335.	4.0	14
272	Combinatorial single-cell CRISPR screens by direct guide RNA capture and targeted sequencing. <i>Nature Biotechnology</i> , 2020, 38, 954-961.	9.4	232
273	Mitochondrial stress is relayed to the cytosol by an OMA1-DELE1-HRI pathway. <i>Nature</i> , 2020, 579, 427-432.	13.7	343
274	Technologies and Computational Analysis Strategies for CRISPR Applications. <i>Molecular Cell</i> , 2020, 79, 11-29.	4.5	28

#	ARTICLE	IF	CITATIONS
275	3D Brain Organoids: Studying Brain Development and Disease Outside the Embryo. <i>Annual Review of Neuroscience</i> , 2020, 43, 375-389.	5.0	59
276	A Single-Cell Transcriptomics CRISPR-Activation Screen Identifies Epigenetic Regulators of the Zygotic Genome Activation Program. <i>Cell Systems</i> , 2020, 11, 25-41.e9.	2.9	59
277	CRISPR-based functional genomics for neurological disease. <i>Nature Reviews Neurology</i> , 2020, 16, 465-480.	4.9	89
278	Dual threshold optimization and network inference reveal convergent evidence from TF binding locations and TF perturbation responses. <i>Genome Research</i> , 2020, 30, 459-471.	2.4	24
279	Impact of CRISPR interference on strain development in biotechnology. <i>Biotechnology and Applied Biochemistry</i> , 2020, 67, 7-21.	1.4	31
280	CRISPRpic: fast and precise analysis for CRISPR-induced mutations via CRISPRpic counting. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa012.	1.5	15
281	Titrating gene expression using libraries of systematically attenuated CRISPR guide RNAs. <i>Nature Biotechnology</i> , 2020, 38, 355-364.	9.4	108
282	Identification and transfer of spatial transcriptomics signatures for cancer diagnosis. <i>Breast Cancer Research</i> , 2020, 22, 6.	2.2	54
283	scMAGeCK links genotypes with multiple phenotypes in single-cell CRISPR screens. <i>Genome Biology</i> , 2020, 21, 19.	3.8	46
284	Single-cell analysis of a mutant library generated using CRISPR-guided deaminase in human melanoma cells. <i>Communications Biology</i> , 2020, 3, 154.	2.0	25
285	Multiplex T Cell Stimulation Assay Utilizing a T Cell Activation Reporter-Based Detection System. <i>Frontiers in Immunology</i> , 2020, 11, 633.	2.2	25
286	Pooled Knockin Targeting for Genome Engineering of Cellular Immunotherapies. <i>Cell</i> , 2020, 181, 728-744.e21.	13.5	131
287	Inference of single-cell phylogenies from lineage tracing data using Cassiopeia. <i>Genome Biology</i> , 2020, 21, 92.	3.8	61
288	Deconstructing cerebellar development cell by cell. <i>PLoS Genetics</i> , 2020, 16, e1008630.	1.5	32
289	Single Cell Sequencing and Kidney Organoids Generated from Pluripotent Stem Cells. <i>Clinical Journal of the American Society of Nephrology: CJASN</i> , 2020, 15, 550-556.	2.2	19
290	Optimization of AsCas12a for combinatorial genetic screens in human cells. <i>Nature Biotechnology</i> , 2021, 39, 94-104.	9.4	96
291	Leveraging large genomic datasets to illuminate the pathobiology of autism spectrum disorders. <i>Neuropsychopharmacology</i> , 2021, 46, 55-69.	2.8	31
292	Macrophage imaging and subset analysis using single-cell RNA sequencing. <i>Nanotheranostics</i> , 2021, 5, 36-56.	2.7	5

#	ARTICLE	IF	CITATIONS
293	Alterations in inter-organelle crosstalk and Ca ²⁺ signaling through mitochondria during proteotoxic stresses. <i>Mitochondrion</i> , 2021, 57, 37-46.	1.6	10
294	Oligodendrocyte-specific deletion of <i>Xbp1</i> exacerbates the endoplasmic reticulum stress response and restricts locomotor recovery after thoracic spinal cord injury. <i>Glia</i> , 2021, 69, 424-435.	2.5	14
295	Single-cell genomics to understand disease pathogenesis. <i>Journal of Human Genetics</i> , 2021, 66, 75-84.	1.1	26
297	QRICH1 dictates the outcome of ER stress through transcriptional control of proteostasis. <i>Science</i> , 2021, 371, .	6.0	73
299	Functional genomics of psychiatric disease risk using genome engineering. , 2021, , 711-734.		0
300	Multiplex T-cell Stimulation Assay Utilizing a T-cell Activation Reporter-based Detection System. <i>Bio-protocol</i> , 2021, 11, e3883.	0.2	4
301	CRISPR technologies for precise epigenome editing. <i>Nature Cell Biology</i> , 2021, 23, 11-22.	4.6	248
302	Genome editing of immune cells using CRISPR/Cas9. <i>BMB Reports</i> , 2021, 54, 59-69.	1.1	8
303	A microfluidic device enabling deterministic single cell trapping and release. <i>Lab on A Chip</i> , 2021, 21, 2486-2494.	3.1	23
305	CellBox: Interpretable Machine Learning for Perturbation Biology with Application to the Design of Cancer Combination Therapy. <i>Cell Systems</i> , 2021, 12, 128-140.e4.	2.9	67
306	Profiling Chromatin Accessibility at Single-cell Resolution. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 172-190.	3.0	18
307	Evaluating Capture Sequence Performance for Single-Cell CRISPR Activation Experiments. <i>ACS Synthetic Biology</i> , 2021, 10, 640-645.	1.9	3
308	Identification of cardiovascular high-risk groups from dynamic retinal vessel signals using untargeted machine learning. <i>Cardiovascular Research</i> , 2022, 118, 612-621.	1.8	8
310	Imaging-based screens of pool-synthesized cell libraries. <i>Nature Methods</i> , 2021, 18, 358-365.	9.0	15
311	Advanced single-cell pooled CRISPR screening identifies C19orf53 required for cell proliferation based on mTORC1 regulators. <i>Cell Biology and Toxicology</i> , 2022, 38, 43-68.	2.4	6
312	Single-cell lineages reveal the rates, routes, and drivers of metastasis in cancer xenografts. <i>Science</i> , 2021, 371, .	6.0	166
313	Inferring perturbation profiles of cancer samples. <i>Bioinformatics</i> , 2021, 37, 2441-2449.	1.8	1
314	Detection of gene cis-regulatory element perturbations in single-cell transcriptomes. <i>PLoS Computational Biology</i> , 2021, 17, e1008789.	1.5	0

#	ARTICLE	IF	CITATIONS
315	Multimodal pooled Perturb-CITE-seq screens in patient models define mechanisms of cancer immune evasion. <i>Nature Genetics</i> , 2021, 53, 332-341.	9.4	112
316	Cellular Models and High-Throughput Screening for Genetic Causality of Intellectual Disability. <i>Trends in Molecular Medicine</i> , 2021, 27, 220-230.	3.5	8
317	A Detailed Catalogue of Multi-Omics Methodologies for Identification of Putative Biomarkers and Causal Molecular Networks in Translational Cancer Research. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2822.	1.8	8
318	Single-Cell Toolkits Opening a New Era for Cell Engineering. <i>Molecules and Cells</i> , 2021, 44, 127-135.	1.0	11
321	Extensible combinatorial CRISPR screening in mammalian cells. <i>STAR Protocols</i> , 2021, 2, 100255.	0.5	4
322	Smoothed-activating lipids drive resistance to CDK4/6 inhibition in Hedgehog-associated medulloblastoma cells and preclinical models. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	17
323	Functional annotation of lncRNA in high-throughput screening. <i>Essays in Biochemistry</i> , 2021, 65, 761-773.	2.1	14
324	Hypoxia-inducible factor prolyl hydroxylase domain (PHD) inhibition after contusive spinal cord injury does not improve locomotor recovery. <i>PLoS ONE</i> , 2021, 16, e0249591.	1.1	3
325	ER-phagy responses in yeast, plants, and mammalian cells and their crosstalk with UPR and ERAD. <i>Developmental Cell</i> , 2021, 56, 949-966.	3.1	72
327	Profiling the genetic determinants of chromatin accessibility with scalable single-cell CRISPR screens. <i>Nature Biotechnology</i> , 2021, 39, 1270-1277.	9.4	43
328	Using CRISPR to understand and manipulate gene regulation. <i>Development (Cambridge)</i> , 2021, 148, .	1.2	9
329	Bayesian inference of gene expression states from single-cell RNA-seq data. <i>Nature Biotechnology</i> , 2021, 39, 1008-1016.	9.4	50
330	Decoding Neuronal Diversification by Multiplexed Single-cell RNA-Seq. <i>Stem Cell Reports</i> , 2021, 16, 810-824.	2.3	8
331	Genome-wide programmable transcriptional memory by CRISPR-based epigenome editing. <i>Cell</i> , 2021, 184, 2503-2519.e17.	13.5	312
333	CRISPR screens in plants: approaches, guidelines, and future prospects. <i>Plant Cell</i> , 2021, 33, 794-813.	3.1	54
334	Rational engineering of a modular bacterial CRISPR-Cas activation platform with expanded target range. <i>Nucleic Acids Research</i> , 2021, 49, 4793-4802.	6.5	22
336	Ultra-high-throughput single-cell RNA sequencing and perturbation screening with combinatorial fluidic indexing. <i>Nature Methods</i> , 2021, 18, 635-642.	9.0	129
338	Pharmacological or TRIB3-Mediated Suppression of ATF4 Transcriptional Activity Promotes Hepatoma Cell Resistance to Proteasome Inhibitor Bortezomib. <i>Cancers</i> , 2021, 13, 2341.	1.7	9

#	ARTICLE	IF	CITATIONS
340	Genome-wide CRISPRi/a screens in human neurons link lysosomal failure to ferroptosis. <i>Nature Neuroscience</i> , 2021, 24, 1020-1034.	7.1	170
341	Modular barcode beads for microfluidic single cell genomics. <i>Scientific Reports</i> , 2021, 11, 10857.	1.6	14
342	Big data analytics in single-cell transcriptomics: Five grand opportunities. <i>Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery</i> , 2021, 11, e1414.	4.6	1
343	Discovering antiviral restriction factors and pathways using genetic screens. <i>Journal of General Virology</i> , 2021, 102, .	1.3	5
344	Single-cell advances in stromal-leukocyte interactions in cancer. <i>Immunological Reviews</i> , 2021, 302, 286-298.	2.8	10
345	Interrogating immune cells and cancer with CRISPR-Cas9. <i>Trends in Immunology</i> , 2021, 42, 432-446.	2.9	13
346	The Known Unknowns of the Immune Response to <i>Coccidioides</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 377.	1.5	6
350	Applying CRISPR Screen in Diabetes Research. <i>Diabetes</i> , 2021, 70, 1962-1969.	0.3	2
351	Undisclosed, unmet and neglected challenges in multi-omics studies. <i>Nature Computational Science</i> , 2021, 1, 395-402.	3.8	59
353	Tumor immunology in the age of single-cell genomics. <i>Journal of Leukocyte Biology</i> , 2021, 110, 1069-1079.	1.5	0
354	Potent programmable antiviral against dengue virus in primary human cells by Cas13b RNP with short spacer and delivery by VLP. <i>Molecular Therapy - Methods and Clinical Development</i> , 2021, 21, 729-740.	1.8	11
355	Machine learning for perturbational single-cell omics. <i>Cell Systems</i> , 2021, 12, 522-537.	2.9	52
356	How Machine Learning and Statistical Models Advance Molecular Diagnostics of Rare Disorders Via Analysis of RNA Sequencing Data. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 647277.	1.6	12
357	Localization of Organelle Proteins by Isotope Tagging: Current status and potential applications in drug discovery research. <i>Drug Discovery Today: Technologies</i> , 2021, 39, 57-67.	4.0	5
358	dCas9 techniques for transcriptional repression in mammalian cells: Progress, applications and challenges. <i>BioEssays</i> , 2021, 43, 2100086.	1.2	3
359	A first perturbome of <i>Pseudomonas aeruginosa</i> : Identification of core genes related to multiple perturbations by a machine learning approach. <i>BioSystems</i> , 2021, 205, 104411.	0.9	6
360	Exploiting Single-Cell Tools in Gene and Cell Therapy. <i>Frontiers in Immunology</i> , 2021, 12, 702636.	2.2	21
362	High-resolution characterization of gene function using single-cell CRISPR tiling screen. <i>Nature Communications</i> , 2021, 12, 4063.	5.8	23

#	ARTICLE	IF	CITATIONS
363	3-Ketodihydrosphingosine reductase maintains ER homeostasis and unfolded protein response in leukemia. <i>Leukemia</i> , 2022, 36, 100-110.	3.3	13
364	In vivo Pooled Screening: A Scalable Tool to Study the Complexity of Aging and Age-Related Disease. <i>Frontiers in Aging</i> , 2021, 2, .	1.2	1
365	Transcriptional enhancers and their communication with gene promoters. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 6453-6485.	2.4	25
366	An optimized genome-wide, virus-free CRISPR screen for mammalian cells. <i>Cell Reports Methods</i> , 2021, 1, 100062.	1.4	14
367	Mapping the dynamic transfer functions of eukaryotic gene regulation. <i>Cell Systems</i> , 2021, 12, 1079-1093.e6.	2.9	12
368	LKB1 inactivation modulates chromatin accessibility to drive metastatic progression. <i>Nature Cell Biology</i> , 2021, 23, 915-924.	4.6	26
371	Genome-wide association studies. <i>Nature Reviews Methods Primers</i> , 2021, 1, .	11.8	529
372	From variant to function in human disease genetics. <i>Science</i> , 2021, 373, 1464-1468.	6.0	75
373	CRISPR-Cas Gene Perturbation and Editing in Human Induced Pluripotent Stem Cells. <i>CRISPR Journal</i> , 2021, 4, 634-655.	1.4	5
374	A new era in functional genomics screens. <i>Nature Reviews Genetics</i> , 2022, 23, 89-103.	7.7	104
375	Targeting the IRE1 α /XBP1 Endoplasmic Reticulum Stress Response Pathway in <i>ARID1A</i> -Mutant Ovarian Cancers. <i>Cancer Research</i> , 2021, 81, 5325-5335.	0.4	12
376	Comprehensive deletion landscape of CRISPR-Cas9 identifies minimal RNA-guided DNA-binding modules. <i>Nature Communications</i> , 2021, 12, 5664.	5.8	25
377	Modeling glioblastoma heterogeneity as a dynamic network of cell states. <i>Molecular Systems Biology</i> , 2021, 17, e10105.	3.2	19
378	Neurodevelopmental Disorders (NDD) Caused by Genomic Alterations of the Ubiquitin-Proteasome System (UPS): the Possible Contribution of Immune Dysregulation to Disease Pathogenesis. <i>Frontiers in Molecular Neuroscience</i> , 2021, 14, 733012.	1.4	15
379	Crel2 function during unfolded protein response is essential for liver metabolism homeostasis. <i>FASEB Journal</i> , 2021, 35, e21939.	0.2	15
380	Combinatorial CRISPR/Cas9 Screening Reveals Epistatic Networks of Interacting Tumor Suppressor Genes and Therapeutic Targets in Human Breast Cancer. <i>Cancer Research</i> , 2021, 81, 6090-6105.	0.4	12
381	Application of CHyMErA Cas9-Cas12a combinatorial genome-editing platform for genetic interaction mapping and gene fragment deletion screening. <i>Nature Protocols</i> , 2021, 16, 4722-4765.	5.5	8
382	Parallel characterization of cis-regulatory elements for multiple genes using CRISPRpath. <i>Science Advances</i> , 2021, 7, eabi4360.	4.7	16

#	ARTICLE	IF	CITATIONS
383	SLC5A3-Dependent Myo-inositol Auxotrophy in Acute Myeloid Leukemia. <i>Cancer Discovery</i> , 2022, 12, 450-467.	7.7	14
385	Droplet microfluidics on analysis of pathogenic microbes for wastewater-based epidemiology. <i>TrAC - Trends in Analytical Chemistry</i> , 2021, 143, 116333.	5.8	14
386	Moving from in vitro to in vivo CRISPR screens. <i>Gene and Genome Editing</i> , 2021, 2, 100008.	1.3	25
387	Towards a CRISPeR understanding of homologous recombination with high-throughput functional genomics. <i>Current Opinion in Genetics and Development</i> , 2021, 71, 171-181.	1.5	6
388	Minimal genome-wide human CRISPR-Cas9 library. <i>Genome Biology</i> , 2021, 22, 40.	3.8	40
389	Image-based pooled whole-genome CRISPRi screening for subcellular phenotypes. <i>Journal of Cell Biology</i> , 2021, 220, .	2.3	48
390	Functions and Mechanisms of the Human Ribosome-Translocon Complex. <i>Sub-Cellular Biochemistry</i> , 2019, 93, 83-141.	1.0	15
391	A Molecular Mechanism for Turning Off IRE1 $\hat{\pm}$ Signaling during Endoplasmic Reticulum Stress. <i>Cell Reports</i> , 2020, 33, 108563.	2.9	31
392	Am I ready for CRISPR? A user's guide to genetic screens. <i>Nature Reviews Genetics</i> , 2018, 19, 67-80.	7.7	325
393	Distribution and storage of inflammatory memory in barrier tissues. <i>Nature Reviews Immunology</i> , 2020, 20, 308-320.	10.6	47
394	HyPR-seq: Single-cell quantification of chosen RNAs via hybridization and sequencing of DNA probes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 33404-33413.	3.3	21
395	UFMylation inhibits the proinflammatory capacity of interferon- $\hat{\pm}$ activated macrophages. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	24
448	Recent advances in signal integration mechanisms in the unfolded protein response. <i>F1000Research</i> , 2019, 8, 1840.	0.8	20
449	Inferring modulators of genetic interactions with epistatic nested effects models. <i>PLoS Computational Biology</i> , 2017, 13, e1005496.	1.5	13
450	The new technologies of high-throughput single-cell RNA sequencing. <i>Vavilovskii Zhurnal Genetiki i Seleksii</i> , 2019, 23, 508-518.	0.4	1
451	eIF2B activator prevents neurological defects caused by a chronic integrated stress response. <i>ELife</i> , 2019, 8, .	2.8	124
452	The unfolded protein response and endoplasmic reticulum protein targeting machineries converge on the stress sensor IRE1. <i>ELife</i> , 2018, 7, .	2.8	71
453	Ceapins block the unfolded protein response sensor ATF6 $\hat{\pm}$ by inducing a neomorphic inter-organelle tether. <i>ELife</i> , 2019, 8, .	2.8	46

#	ARTICLE	IF	CITATIONS
454	A new protocol for single-cell RNA-seq reveals stochastic gene expression during lag phase in budding yeast. <i>ELife</i> , 2020, 9, .	2.8	43
455	Interaction mapping of endoplasmic reticulum ubiquitin ligases identifies modulators of innate immune signalling. <i>ELife</i> , 2020, 9, .	2.8	61
456	Single-Cell Genomics: Catalyst for Cell Fate Engineering. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 748942.	2.0	1
457	A global cancer data integrator reveals principles of synthetic lethality, sex disparity and immunotherapy. <i>Genome Medicine</i> , 2021, 13, 167.	3.6	0
458	Functional single-cell genomics of human cytomegalovirus infection. <i>Nature Biotechnology</i> , 2022, 40, 391-401.	9.4	60
459	A Combinatorial CRISPR-Cas9 Screen Identifies Iifenprodil as an Adjunct to Sorafenib for Liver Cancer Treatment. <i>Cancer Research</i> , 2021, 81, 6219-6232.	0.4	13
461	DNA barcode to trace the development and differentiation of cord blood stem cells (Review). <i>Molecular Medicine Reports</i> , 2021, 24, .	1.1	4
483	Single-Cell Convert-Seq Decodes Regulatory Factors Driving Neuronal Diversity. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1
486	CRISPR Screens: The Right Tool for the Job. <i>Genetic Engineering and Biotechnology News</i> , 2019, 39, S24-S25.	0.1	0
498	CRISPR/Cas-based Functional Genomic Approaches to Phenotypic Screening. <i>RSC Drug Discovery Series</i> , 2020, , 58-82.	0.2	0
505	Single-cell normalization and association testing unifying CRISPR screen and gene co-expression analyses with Normalizr. <i>Nature Communications</i> , 2021, 12, 6395.	5.8	13
508	Gene surgery: Potential applications for human diseases. <i>EXCLI Journal</i> , 2019, 18, 908-930.	0.5	4
509	Droplet-based microfluidics in biomedical applications. <i>Biofabrication</i> , 2022, 14, 022001.	3.7	50
510	Mammalian chemical genomics towards identifying targets and elucidating modes of action of bioactive compounds. <i>ChemBioChem</i> , 2021, , .	1.3	2
511	Genome-wide screening in human kidney organoids identifies developmental and disease-related aspects of nephrogenesis. <i>Cell Stem Cell</i> , 2022, 29, 160-175.e7.	5.2	35
512	Protein Aggregation in the ER: Calm behind the Storm. <i>Cells</i> , 2021, 10, 3337.	1.8	18
513	Integrated genome and tissue engineering enables screening of cancer vulnerabilities in physiologically relevant perfusable ex vivo cultures. <i>Biomaterials</i> , 2022, 280, 121276.	5.7	5
514	Multi-omic insights into Parkinson's Disease: From genetic associations to functional mechanisms. <i>Neurobiology of Disease</i> , 2022, 163, 105580.	2.1	20

#	ARTICLE	IF	CITATIONS
515	Phiclust: a clusterability measure for single-cell transcriptomics reveals phenotypic subpopulations. <i>Genome Biology</i> , 2022, 23, 18.	3.8	4
516	THEM6-mediated reprogramming of lipid metabolism supports treatment resistance in prostate cancer. <i>EMBO Molecular Medicine</i> , 2022, 14, e14764.	3.3	12
518	Editing the Epigenome in Neurodegenerative Diseases. <i>Neurochemical Journal</i> , 2021, 15, 359-366.	0.2	0
519	BRD2 inhibition blocks SARS-CoV-2 infection by reducing transcription of the host cell receptor ACE2. <i>Nature Cell Biology</i> , 2022, 24, 24-34.	4.6	47
520	New horizons in the stormy sea of multimodal single-cell data integration. <i>Molecular Cell</i> , 2022, 82, 248-259.	4.5	9
521	Advances and application of CRISPR-Cas systems. , 2022, , 331-348.		0
522	Massively parallel phenotyping of coding variants in cancer with Perturb-seq. <i>Nature Biotechnology</i> , 2022, 40, 896-905.	9.4	44
523	Pooled genetic perturbation screens with image-based phenotypes. <i>Nature Protocols</i> , 2022, 17, 476-512.	5.5	21
524	Mapping transcriptomic vector fields of single cells. <i>Cell</i> , 2022, 185, 690-711.e45.	13.5	167
525	Single-Cell Technologies to Decipher the Immune Microenvironment in Myeloid Neoplasms: Perspectives and Opportunities. <i>Frontiers in Oncology</i> , 2021, 11, 796477.	1.3	0
527	High-content CRISPR screening. <i>Nature Reviews Methods Primers</i> , 2022, 2, .	11.8	155
528	Control of Gene Expression via the Yeast CWI Pathway. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1791.	1.8	17
529	High-content CRISPR screening. <i>Nature Reviews Methods Primers</i> , 2022, 2, .	11.8	24
530	The use of new CRISPR tools in cardiovascular research and medicine. <i>Nature Reviews Cardiology</i> , 2022, 19, 505-521.	6.1	21
532	BACH2 inhibition reverses β 2 cell failure in type 2 diabetes models. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	43
534	Base editing sensor libraries for high-throughput engineering and functional analysis of cancer-associated single nucleotide variants. <i>Nature Biotechnology</i> , 2022, 40, 862-873.	9.4	44
535	CoSpar identifies early cell fate biases from single-cell transcriptomic and lineage information. <i>Nature Biotechnology</i> , 2022, 40, 1066-1074.	9.4	43
536	Computational identification of clonal cells in single-cell CRISPR screens. <i>BMC Genomics</i> , 2022, 23, 135.	1.2	4

#	ARTICLE	IF	CITATIONS
537	CRISPR in cancer biology and therapy. <i>Nature Reviews Cancer</i> , 2022, 22, 259-279.	12.8	157
538	Rebuilding limbs, one cell at a time. <i>Developmental Dynamics</i> , 2022, 251, 1389-1403.	0.8	5
539	Single-cell immunology: Past, present, and future. <i>Immunity</i> , 2022, 55, 393-404.	6.6	47
540	Spatial CRISPR genomics identifies regulators of the tumor microenvironment. <i>Cell</i> , 2022, 185, 1223-1239.e20.	13.5	79
547	High-resolution Slide-seqV2 spatial transcriptomics enables discovery of disease-specific cell neighborhoods and pathways. <i>iScience</i> , 2022, 25, 104097.	1.9	32
548	Antigen identification and high-throughput interaction mapping by reprogramming viral entry. <i>Nature Methods</i> , 2022, 19, 449-460.	9.0	32
549	IRE1 β drives lung epithelial progenitor dysfunction to establish a niche for pulmonary fibrosis. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2022, 322, L564-L580.	1.3	12
550	Secretory defects in pediatric osteosarcoma result from downregulation of selective COPII coatomer proteins. <i>iScience</i> , 2022, 25, 104100.	1.9	2
552	Gene network modeling via TopNet reveals functional dependencies between diverse tumor-critical mediator genes. <i>Cell Reports</i> , 2021, 37, 110136.	2.9	1
554	Identifying cancer pathway dysregulations using differential causal effects. <i>Bioinformatics</i> , 2022, 38, 1550-1559.	1.8	4
556	Tools for Decoding Ubiquitin Signaling in DNA Repair. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 760226.	1.8	4
557	geneBasis: an iterative approach for unsupervised selection of targeted gene panels from scRNA-seq. <i>Genome Biology</i> , 2021, 22, 333.	3.8	15
558	CRISPR Screens to Identify Regulators of Tumor Immunity. <i>Annual Review of Cancer Biology</i> , 2022, 6, 103-122.	2.3	5
559	SCEPTRE improves calibration and sensitivity in single-cell CRISPR screen analysis. <i>Genome Biology</i> , 2021, 22, 344.	3.8	19
560	Single-cell characterization of CRISPR-modified transcript isoforms with nanopore sequencing. <i>Genome Biology</i> , 2021, 22, 331.	3.8	12
561	Gene editing and its applications in biomedicine. <i>Science China Life Sciences</i> , 2022, 65, 660-700.	2.3	20
562	The use of base editing technology to characterize single nucleotide variants. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 1670-1680.	1.9	4
563	Genomics, convergent neuroscience and progress in understanding autism spectrum disorder. <i>Nature Reviews Neuroscience</i> , 2022, 23, 323-341.	4.9	81

#	ARTICLE	IF	CITATIONS
565	Reshaping endoplasmic reticulum quality control through the unfolded protein response. <i>Molecular Cell</i> , 2022, 82, 1477-1491.	4.5	105
567	Single-Cell RNA Sequencing in Yeast Using the 10X Genomics Chromium Device. <i>Methods in Molecular Biology</i> , 2022, 2477, 3-20.	0.4	2
568	The myogenesis program drives clonal selection and drug resistance in rhabdomyosarcoma. <i>Developmental Cell</i> , 2022, 57, 1226-1240.e8.	3.1	24
569	Meningioma DNA methylation groups identify biological drivers and therapeutic vulnerabilities. <i>Nature Genetics</i> , 2022, 54, 649-659.	9.4	93
570	Endoplasmic reticulum stress in nonalcoholic (metabolic associated) fatty liver disease (NAFLD/MAFLD). <i>Journal of Cellular Biochemistry</i> , 2022, 123, 1585-1606.	1.2	23
571	Comparative optimization of combinatorial CRISPR screens. <i>Nature Communications</i> , 2022, 13, 2469.	5.8	13
572	Lineage tracing reveals the phylodynamics, plasticity, and paths of tumor evolution. <i>Cell</i> , 2022, 185, 1905-1923.e25.	13.5	108
573	Regulatory events controlling ER-phagy. <i>Current Opinion in Cell Biology</i> , 2022, 76, 102084.	2.6	4
574	A CRISPR view on autophagy. <i>Trends in Cell Biology</i> , 2022, , .	3.6	2
575	Single-Cell Analysis of the Transcriptome and Epigenome. <i>Methods in Molecular Biology</i> , 2022, , 21-60.	0.4	5
577	Pediatric Sarcomas: The Next Generation of Molecular Studies. <i>Cancers</i> , 2022, 14, 2515.	1.7	0
580	Epigenetic regulation of T cell exhaustion. <i>Nature Immunology</i> , 2022, 23, 848-860.	7.0	82
581	Machine-learning-optimized Cas12a barcoding enables the recovery of single-cell lineages and transcriptional profiles. <i>Molecular Cell</i> , 2022, 82, 3103-3118.e8.	4.5	14
582	Genome-wide CRISPR screens of T cell exhaustion identify chromatin remodeling factors that limit T cell persistence. <i>Cancer Cell</i> , 2022, 40, 768-786.e7.	7.7	104
583	CRISPR screening in cancer stem cells. <i>Essays in Biochemistry</i> , 0, , .	2.1	1
584	Endogenous spacing enables co-processing of microRNAs and efficient combinatorial RNAi. <i>Cell Reports Methods</i> , 2022, , 100239.	1.4	3
585	Mapping information-rich genotype-phenotype landscapes with genome-scale Perturb-seq. <i>Cell</i> , 2022, 185, 2559-2575.e28.	13.5	169
586	FoxA1 and FoxA2 control growth and cellular identity in NKX2-1-positive lung adenocarcinoma. <i>Developmental Cell</i> , 2022, 57, 1866-1882.e10.	3.1	15

#	ARTICLE	IF	CITATIONS
587	Transcriptional Regulation of the Hippo Pathway: Current Understanding and Insights from Single-Cell Technologies. <i>Cells</i> , 2022, 11, 2225.	1.8	5
588	Tutorial: design and execution of CRISPR in vivo screens. <i>Nature Protocols</i> , 2022, 17, 1903-1925.	5.5	12
590	Systematic identification of cell-fate regulatory programs using a single-cell atlas of mouse development. <i>Nature Genetics</i> , 2022, 54, 1051-1061.	9.4	29
591	Identification of Runs of Homozygosity Islands and Genomic Estimated Inbreeding Values in Caqueteño Creole Cattle (Colombia). <i>Genes</i> , 2022, 13, 1232.	1.0	3
592	Systematic discovery and perturbation of regulatory genes in human T cells reveals the architecture of immune networks. <i>Nature Genetics</i> , 2022, 54, 1133-1144.	9.4	31
597	The role of single-cell genomics in human genetics. <i>Journal of Medical Genetics</i> , 2022, 59, 827-839.	1.5	11
598	What is a cell type and how to define it?. <i>Cell</i> , 2022, 185, 2739-2755.	13.5	144
600	High throughput CRISPRi and CRISPRa technologies in 3D genome regulation for neuropsychiatric diseases. <i>Human Molecular Genetics</i> , 0, , .	1.4	1
602	Functional genomic assays to annotate enhancer-promoter interactions genome wide. <i>Human Molecular Genetics</i> , 2022, 31, R97-R104.	1.4	3
604	Inferring gene regulation from stochastic transcriptional variation across single cells at steady state. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	14
605	Multi-omics data integration and modeling unravels new mechanisms for pancreatic cancer and improves prognostic prediction. <i>Npj Precision Oncology</i> , 2022, 6, .	2.3	7
606	Metabolic adaption of cancer cells toward autophagy: Is there a role for ER-phagy?. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	1.6	3
607	Genome-wide screening identified SEC61A1 as an essential factor for mycolactone-dependent apoptosis in human premonocytic THP-1 cells. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010672.	1.3	1
609	Sample-multiplexing approaches for single-cell sequencing. <i>Cellular and Molecular Life Sciences</i> , 2022, 79, .	2.4	12
610	Large-scale multiplexed mosaic CRISPR perturbation in the whole organism. <i>Cell</i> , 2022, 185, 3008-3024.e16.	13.5	15
612	Scalable Functional Assays for the Interpretation of Human Genetic Variation. <i>Annual Review of Genetics</i> , 2022, 56, 441-465.	3.2	18
613	FGFR redundancy limits the efficacy of FGFR4-selective inhibitors in hepatocellular carcinoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	12
614	Smart software untangles gene regulation in cells. <i>Nature</i> , 2022, 609, 428-431.	13.7	3

#	ARTICLE	IF	CITATIONS
615	Dual genome-wide coding and lncRNA screens in neural induction of induced pluripotent stem cells. <i>Cell Genomics</i> , 2022, 2, 100177.	3.0	10
616	Chronic activation of pDCs in autoimmunity is linked to dysregulated ER stress and metabolic responses. <i>Journal of Experimental Medicine</i> , 2022, 219, .	4.2	12
617	Recent advances in the use of CRISPR/Cas for understanding the early development of molecular gaps in glial cells. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	1.8	0
618	Cold shock domain-containing protein E1 is a posttranscriptional regulator of the LDL receptor. <i>Science Translational Medicine</i> , 2022, 14, .	5.8	8
619	Mostly natural sequencing-by-synthesis for scRNA-seq using Ultima sequencing. <i>Nature Biotechnology</i> , 2023, 41, 204-211.	9.4	17
621	From multitude to singularity: An up-to-date overview of scRNA-seq data generation and analysis. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	9
622	Characterizing the biology of primary brain tumors and their microenvironment via single-cell profiling methods. <i>Neuro-Oncology</i> , 2023, 25, 234-247.	0.6	9
623	The expanding vistas of spatial transcriptomics. <i>Nature Biotechnology</i> , 2023, 41, 773-782.	9.4	84
625	Quantitative Framework for Bench-to-Bedside Cancer Research. <i>Cancers</i> , 2022, 14, 5254.	1.7	0
626	Adding a Chemical Biology Twist to CRISPR Screening. <i>Israel Journal of Chemistry</i> , 0, , .	1.0	0
627	The Proteostasis Network: A Global Therapeutic Target for Neuroprotection after Spinal Cord Injury. <i>Cells</i> , 2022, 11, 3339.	1.8	2
628	Multiplexed Single-Nucleus RNA Sequencing Using Lipid-Oligo Barcodes. <i>Current Protocols</i> , 2022, 2, .	1.3	1
630	The industrial genomic revolution: A new era in neuroimmunology. <i>Neuron</i> , 2022, 110, 3429-3443.	3.8	2
633	Genome-wide base editor screen identifies regulators of protein abundance in yeast. <i>ELife</i> , 0, 11, .	2.8	7
634	Antibody-mediated delivery of CRISPR-Cas9 ribonucleoproteins in human cells. <i>Protein Engineering, Design and Selection</i> , 2022, 35, .	1.0	3
636	Pooled genetic screens with image-based profiling. <i>Molecular Systems Biology</i> , 2022, 18, .	3.2	8
638	Towards elucidating disease-relevant states of neurons and glia by CRISPR-based functional genomics. <i>Genome Medicine</i> , 2022, 14, .	3.6	1
639	Generation of single-cell and single-nuclei suspensions from embryonic and adult mouse brains. <i>STAR Protocols</i> , 2023, 4, 101944.	0.5	1

#	ARTICLE	IF	CITATIONS
640	Single-cell CRISPR immune screens reveal immunological roles of tumor intrinsic factors. <i>NAR Cancer</i> , 2022, 4, .	1.6	3
642	High-content CRISPR screening in tumor immunology. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	3
644	Long noncoding RNA study: Genome-wide approaches. <i>Genes and Diseases</i> , 2023, 10, 2491-2510.	1.5	2
645	Single-cell RNA-seq methods to interrogate virus-host interactions. <i>Seminars in Immunopathology</i> , 2023, 45, 71-89.	2.8	17
646	Single-cell sequencing: promises and challenges for human genetics. <i>Medizinische Genetik</i> , 2022, 34, 261-273.	0.1	1
647	CRISPR screens for functional interrogation of immunity. <i>Nature Reviews Immunology</i> , 2023, 23, 363-380.	10.6	11
648	Genomic characterization and therapeutic utilization of IL-13-responsive sequences in asthma. <i>Cell Genomics</i> , 2023, 3, 100229.	3.0	5
649	The Emerging Role of uORF-Encoded uPeptides and HLA uLigands in Cellular and Tumor Biology. <i>Cancers</i> , 2022, 14, 6031.	1.7	1
650	Massively Parallel CRISPR-Based Genetic Perturbation Screening at Single-Cell Resolution. <i>Advanced Science</i> , 2023, 10, .	5.6	6
651	Efficient combinatorial targeting of RNA transcripts in single cells with Cas13 RNA Perturb-seq. <i>Nature Methods</i> , 2023, 20, 86-94.	9.0	20
652	IFITM proteins assist cellular uptake of diverse linked chemotypes. <i>Science</i> , 2022, 378, 1097-1104.	6.0	12
653	Human iPSC-hepatocyte modeling of alpha-1 antitrypsin heterozygosity reveals metabolic dysregulation and cellular heterogeneity. <i>Cell Reports</i> , 2022, 41, 111775.	2.9	4
655	Impact of the Human Cell Atlas on medicine. <i>Nature Medicine</i> , 2022, 28, 2486-2496.	15.2	59
657	Gene regulatory network reconfiguration in direct lineage reprogramming. <i>Stem Cell Reports</i> , 2023, 18, 97-112.	2.3	6
659	New Tools for Lineage Tracing in Cancer In Vivo. <i>Annual Review of Cancer Biology</i> , 2023, 7, 111-129.	2.3	1
660	Single-cell omics: A new direction for functional genetic research in human diseases and animal models. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	9
661	Correlated gene modules uncovered by high-precision single-cell transcriptomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	8
662	Maximizing CRISPRi efficacy and accessibility with dual-sgRNA libraries and optimal effectors. <i>ELife</i> , 0, 11, .	2.8	27

#	ARTICLE	IF	CITATIONS
665	Gene Modulation with CRISPR-based Tools in Human iPSC-Cardiomyocytes. <i>Stem Cell Reviews and Reports</i> , 0, , .	1.7	3
671	CCPG1 recognizes endoplasmic reticulum luminal proteins for selective ER-phagy. <i>Molecular Biology of the Cell</i> , 2023, 34, .	0.9	8
672	Human-specific genetics: new tools to explore the molecular and cellular basis of human evolution. <i>Nature Reviews Genetics</i> , 2023, 24, 687-711.	7.7	21
674	Single-cell RNA sequencing to identify cellular heterogeneity and targets in cardiovascular diseases: from bench to bedside. <i>Basic Research in Cardiology</i> , 2023, 118, .	2.5	8
675	Dissecting cell identity via network inference and in silico gene perturbation. <i>Nature</i> , 2023, 614, 742-751.	13.7	124
676	Transition from Animal-Based to Human Induced Pluripotent Stem Cells (iPSCs)-Based Models of Neurodevelopmental Disorders: Opportunities and Challenges. <i>Cells</i> , 2023, 12, 538.	1.8	1
677	Application of perturbation gene expression profiles in drug discoveryâ€”From mechanism of action to quantitative modelling. <i>Frontiers in Systems Biology</i> , 0, 3, .	0.5	0
678	Mechanisms of Protein Trafficking and Quality Control in the Kidney and Beyond. <i>Annual Review of Physiology</i> , 2023, 85, 407-423.	5.6	1
680	Revolutionizing DNA repair research and cancer therapy with CRISPRâ€”Cas screens. <i>Nature Reviews Molecular Cell Biology</i> , 2023, 24, 477-494.	16.1	17
681	Optimization of Genomewide CRISPR Screens Using AsCas12a and Multi-Guide Arrays. <i>CRISPR Journal</i> , 2023, 6, 75-82.	1.4	2
682	Hacking hematopoiesis â€” emerging tools for examining variant effects. <i>DMM Disease Models and Mechanisms</i> , 2023, 16, .	1.2	0
684	VMP1 affects endoplasmic reticulum stress sensitivity via differential modulation of the three unfolded protein response arms. <i>Cell Reports</i> , 2023, 42, 112209.	2.9	6
685	CRISPR-Cas9 genetic screen leads to the discovery of L-Moses, a KAT2B inhibitor that attenuates Tunicamycin-mediated neuronal cell death. <i>Scientific Reports</i> , 2023, 13, .	1.6	4
687	SCREE: a comprehensive pipeline for single-cell multi-modal CRISPR screen data processing and analysis. <i>Briefings in Bioinformatics</i> , 2023, 24, .	3.2	2
689	Bioinformatics approaches to analyzing CRISPR screen data: from dropout screens to singleâ€”cell CRISPR screens. <i>Quantitative Biology</i> , 2022, 10, 307-320.	0.3	3
690	Functional characterization of human genomic variation linked to polygenic diseases. <i>Trends in Genetics</i> , 2023, 39, 462-490.	2.9	5
691	Single-cell protein-DNA interactomics and multiomics tools for deciphering genome regulation. , 2023, , 20220057.		0
692	Multiomic Analysis and CRISPR Perturbation Screens Identify Endothelial Cell Programs and Novel Therapeutic Targets for Coronary Artery Disease. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 0, , .	1.1	3

#	ARTICLE	IF	CITATIONS
693	Multi-omic single cell sequencing: Overview and opportunities for kidney disease therapeutic development. <i>Frontiers in Molecular Biosciences</i> , 0, 10, .	1.6	1
694	Structural and functional properties of mSWI/SNF chromatin remodeling complexes revealed through single-cell perturbation screens. <i>Molecular Cell</i> , 2023, 83, 1350-1367.e7.	4.5	8
695	Spatial Transcriptomics: Technical Aspects of Recent Developments and Their Applications in Neuroscience and Cancer Research. <i>Advanced Science</i> , 2023, 10, .	5.6	7
696	Understanding neural development and diseases using CRISPR screens in human pluripotent stem cell-derived cultures. <i>Frontiers in Cell and Developmental Biology</i> , 0, 11, .	1.8	1
697	Accelerating the understanding of cancer biology through the lens of genomics. <i>Cell</i> , 2023, 186, 1755-1771.	13.5	9
700	Insulin secretion deficits in a Prader-Willi syndrome β -cell model are associated with a concerted downregulation of multiple endoplasmic reticulum chaperones. <i>PLoS Genetics</i> , 2023, 19, e1010710.	1.5	1
701	CRISPR/Cas9 genetic screens in hepatocellular carcinoma gene discovery. <i>Current Research in Biotechnology</i> , 2023, 5, 100127.	1.9	1
702	Protein quality control and aggregation in the endoplasmic reticulum: From basic to bedside. <i>Frontiers in Cell and Developmental Biology</i> , 0, 11, .	1.8	2
717	Applications of single-cell RNA sequencing in drug discovery and development. <i>Nature Reviews Drug Discovery</i> , 2023, 22, 496-520.	21.5	31
737	Mechanisms of substrate processing during ER-associated protein degradation. <i>Nature Reviews Molecular Cell Biology</i> , 2023, 24, 777-796.	16.1	17
742	Dissecting key regulators of transcriptome kinetics through scalable single-cell RNA profiling of pooled CRISPR screens. <i>Nature Biotechnology</i> , 0, , .	9.4	3
762	Factoring single-cell perturbations. <i>Nature Methods</i> , 0, , .	9.0	0
768	A Graph Neural Network with Multiple Auxiliary Tasks for Accurate Single Cell Classification. , 2023, , .		0
797	Disentanglement of single-cell data with biolord. <i>Nature Biotechnology</i> , 0, , .	9.4	0
813	Unbiased genome-wide approaches to identify vulnerability factors in Huntington's disease. , 2024, , 397-410.		0