

Guo-Cheng Yuan

List of Publications by Year in descending order

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Version: 2024-02-01

118
papers

16,475
citations

26630

56
h-index

19749

117
g-index

142
all docs

142
docs citations

142
times ranked

25913
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcriptome-scale super-resolved imaging in tissues by RNA seqFISH+. <i>Nature</i> , 2019, 568, 235-239.	27.8	1,088
2	Mapping the Mouse Cell Atlas by Microwell-Seq. <i>Cell</i> , 2018, 172, 1091-1107.e17.	28.9	1,068
3	Genome-Scale Identification of Nucleosome Positions in <i>S. cerevisiae</i> . <i>Science</i> , 2005, 309, 626-630.	12.6	1,047
4	BCL11A enhancer dissection by Cas9-mediated in situ saturating mutagenesis. <i>Nature</i> , 2015, 527, 192-197.	27.8	726
5	A major chromatin regulator determines resistance of tumor cells to T cell-mediated killing. <i>Science</i> , 2018, 359, 770-775.	12.6	641
6	CDK7 Inhibition Suppresses Super-Enhancer-Linked Oncogenic Transcription in MYCN-Driven Cancer. <i>Cell</i> , 2014, 159, 1126-1139.	28.9	498
7	LincRNA-p21 Regulates Neointima Formation, Vascular Smooth Muscle Cell Proliferation, Apoptosis, and Atherosclerosis by Enhancing p53 Activity. <i>Circulation</i> , 2014, 130, 1452-1465.	1.6	425
8	Analyzing CRISPR genome-editing experiments with CRISPResso. <i>Nature Biotechnology</i> , 2016, 34, 695-697.	17.5	410
9	Jumonji Modulates Polycomb Activity and Self-Renewal versus Differentiation of Stem Cells. <i>Cell</i> , 2009, 139, 1303-1314.	28.9	398
10	Giotto: a toolbox for integrative analysis and visualization of spatial expression data. <i>Genome Biology</i> , 2021, 22, 78.	8.8	367
11	MANorm: a robust model for quantitative comparison of ChIP-Seq data sets. <i>Genome Biology</i> , 2012, 13, R16.	9.6	355
12	Direct Promoter Repression by BCL11A Controls the Fetal to Adult Hemoglobin Switch. <i>Cell</i> , 2018, 173, 430-442.e17.	28.9	328
13	Antibody-mediated inhibition of MICA and MICB shedding promotes NK cell-driven tumor immunity. <i>Science</i> , 2018, 359, 1537-1542.	12.6	323
14	Reprogramming Committed Murine Blood Cells to Induced Hematopoietic Stem Cells with Defined Factors. <i>Cell</i> , 2014, 157, 549-564.	28.9	290
15	Bifurcation analysis of single-cell gene expression data reveals epigenetic landscape. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E5643-50.	7.1	263
16	Molecular Pathways of Colon Inflammation Induced by Cancer Immunotherapy. <i>Cell</i> , 2020, 182, 655-671.e22.	28.9	259
17	Challenges and emerging directions in single-cell analysis. <i>Genome Biology</i> , 2017, 18, 84.	8.8	258
18	GiniClust: detecting rare cell types from single-cell gene expression data with Gini index. <i>Genome Biology</i> , 2016, 17, 144.	8.8	238

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19	Integrated spatial genomics reveals global architecture of single nuclei. <i>Nature</i> , 2021, 590, 344-350.	27.8	228
20	<i>Schizosaccharomyces pombe</i> genome-wide nucleosome mapping reveals positioning mechanisms distinct from those of <i>Saccharomyces cerevisiae</i> . <i>Nature Structural and Molecular Biology</i> , 2010, 17, 251-257.	8.2	215
21	Mapping Cellular Hierarchy by Single-Cell Analysis of the Cell Surface Repertoire. <i>Cell Stem Cell</i> , 2013, 13, 492-505.	11.1	214
22	Distinct Mesenchymal Cell Populations Generate the Essential Intestinal BMP Signaling Gradient. <i>Cell Stem Cell</i> , 2020, 26, 391-402.e5.	11.1	211
23	Mitochondrial iron chelation ameliorates cigarette smoke-induced bronchitis and emphysema in mice. <i>Nature Medicine</i> , 2016, 22, 163-174.	30.7	206
24	Dynamic Control of Enhancer Repertoires Drives Lineage and Stage-Specific Transcription during Hematopoiesis. <i>Developmental Cell</i> , 2016, 36, 9-23.	7.0	204
25	Single-cell trajectories reconstruction, exploration and mapping of omics data with STREAM. <i>Nature Communications</i> , 2019, 10, 1903.	12.8	198
26	Dynamic Reorganization of Chromatin Accessibility Signatures during Dedifferentiation of Secretory Precursors into Lgr5+ Intestinal Stem Cells. <i>Cell Stem Cell</i> , 2017, 21, 65-77.e5.	11.1	190
27	Revealing the Critical Regulators of Cell Identity in the Mouse Cell Atlas. <i>Cell Reports</i> , 2018, 25, 1436-1445.e3.	6.4	185
28	Combinatorial Assembly of Developmental Stage-Specific Enhancers Controls Gene Expression Programs during Human Erythropoiesis. <i>Developmental Cell</i> , 2012, 23, 796-811.	7.0	183
29	Passing Messages between Biological Networks to Refine Predicted Interactions. <i>PLoS ONE</i> , 2013, 8, e64832.	2.5	183
30	Dissecting super-enhancer hierarchy based on chromatin interactions. <i>Nature Communications</i> , 2018, 9, 943.	12.8	179
31	Identification of spatially associated subpopulations by combining scRNAseq and sequential fluorescence in situ hybridization data. <i>Nature Biotechnology</i> , 2018, 36, 1183-1190.	17.5	179
32	Single-Cell Analysis in Cancer Genomics. <i>Trends in Genetics</i> , 2015, 31, 576-586.	6.7	164
33	CDK12 loss in cancer cells affects DNA damage response genes through premature cleavage and polyadenylation. <i>Nature Communications</i> , 2019, 10, 1757.	12.8	159
34	Genomic Sequence Is Highly Predictive of Local Nucleosome Depletion. <i>PLoS Computational Biology</i> , 2008, 4, e13.	3.2	156
35	SpatialDWLS: accurate deconvolution of spatial transcriptomic data. <i>Genome Biology</i> , 2021, 22, 145.	8.8	140
36	CDK7 Inhibition Potentiates Genome Instability Triggering Anti-tumor Immunity in Small Cell Lung Cancer. <i>Cancer Cell</i> , 2020, 37, 37-54.e9.	16.8	138

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37	Accurate estimation of cell-type composition from gene expression data. <i>Nature Communications</i> , 2019, 10, 2975.	12.8	125
38	Estimating Sample-Specific Regulatory Networks. <i>IScience</i> , 2019, 14, 226-240.	4.1	120
39	Developmental Control of Polycomb Subunit Composition by GATA Factors Mediates a Switch to Non-Canonical Functions. <i>Molecular Cell</i> , 2015, 57, 304-316.	9.7	119
40	Distinct and Combinatorial Functions of Jmjd2b/Kdm4b and Jmjd2c/Kdm4c in Mouse Embryonic Stem Cell Identity. <i>Molecular Cell</i> , 2014, 53, 32-48.	9.7	112
41	Multiparametric profiling of non-small-cell lung cancers reveals distinct immunophenotypes. <i>JCI Insight</i> , 2016, 1, e89014.	5.0	110
42	Analysis of Cardiac Myocyte Maturation Using CASA AV, a Platform for Rapid Dissection of Cardiac Myocyte Gene Function In Vivo. <i>Circulation Research</i> , 2017, 120, 1874-1888.	4.5	106
43	Combination inhibition of PI3K and mTORC1 yields durable remissions in mice bearing orthotopic patient-derived xenografts of HER2-positive breast cancer brain metastases. <i>Nature Medicine</i> , 2016, 22, 723-726.	30.7	105
44	Advances in spatial transcriptomic data analysis. <i>Genome Research</i> , 2021, 31, 1706-1718.	5.5	102
45	Acquired Tissue-Specific Promoter Bivalency Is a Basis for PRC2 Necessity in Adult Cells. <i>Cell</i> , 2016, 165, 1389-1400.	28.9	101
46	A reference map of murine cardiac transcription factor chromatin occupancy identifies dynamic and conserved enhancers. <i>Nature Communications</i> , 2019, 10, 4907.	12.8	100
47	Predicting chromatin organization using histone marks. <i>Genome Biology</i> , 2015, 16, 162.	8.8	98
48	Variant-aware saturating mutagenesis using multiple Cas9 nucleases identifies regulatory elements at trait-associated loci. <i>Nature Genetics</i> , 2017, 49, 625-634.	21.4	96
49	Mapping human pluripotent stem cell differentiation pathways using high throughput single-cell RNA-sequencing. <i>Genome Biology</i> , 2018, 19, 47.	8.8	96
50	BORIS promotes chromatin regulatory interactions in treatment-resistant cancer cells. <i>Nature</i> , 2019, 572, 676-680.	27.8	89
51	CUT&RUNTools: a flexible pipeline for CUT&RUN processing and footprint analysis. <i>Genome Biology</i> , 2019, 20, 192.	8.8	83
52	Single-nucleus transcriptome analysis of human brain immune response in patients with severe COVID-19. <i>Genome Medicine</i> , 2021, 13, 118.	8.2	81
53	Single-cell nuclear architecture across cell types in the mouse brain. <i>Science</i> , 2021, 374, 586-594.	12.6	74
54	Serum-Based Culture Conditions Provoke Gene Expression Variability in Mouse Embryonic Stem Cells as Revealed by Single-Cell Analysis. <i>Cell Reports</i> , 2016, 14, 956-965.	6.4	73

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55	Integrated design, execution, and analysis of arrayed and pooled CRISPR genome-editing experiments. <i>Nature Protocols</i> , 2018, 13, 946-986.	12.0	70
56	Single-Cell Analysis Identifies LY6D as a Marker Linking Castration-Resistant Prostate Luminal Cells to Prostate Progenitors and Cancer. <i>Cell Reports</i> , 2018, 25, 3504-3518.e6.	6.4	70
57	Single-Cell Transcript Profiles Reveal Multilineage Priming in Early Progenitors Derived from Lgr5 + Intestinal Stem Cells. <i>Cell Reports</i> , 2016, 16, 2053-2060.	6.4	69
58	Analysis of chromatin-state plasticity identifies cell-type-specific regulators of H3K27me3 patterns. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E344-53.	7.1	66
59	A vaccine targeting resistant tumours by dual T cell plus NK cell attack. <i>Nature</i> , 2022, 606, 992-998.	27.8	65
60	Hierarchical and stage-specific regulation of murine cardiomyocyte maturation by serum response factor. <i>Nature Communications</i> , 2018, 9, 3837.	12.8	63
61	Haploinsufficiency of Hedgehog interacting protein causes increased emphysema induced by cigarette smoke through network rewiring. <i>Genome Medicine</i> , 2015, 7, 12.	8.2	61
62	A network model for angiogenesis in ovarian cancer. <i>BMC Bioinformatics</i> , 2015, 16, 115.	2.6	60
63	GiniClust2: a cluster-aware, weighted ensemble clustering method for cell-type detection. <i>Genome Biology</i> , 2018, 19, 58.	8.8	59
64	The role of Cdx2 as a lineage specific transcriptional repressor for pluripotent network during the first developmental cell lineage segregation. <i>Scientific Reports</i> , 2017, 7, 17156.	3.3	58
65	Inhibition of CDK4/6 Promotes CD8 T-cell Memory Formation. <i>Cancer Discovery</i> , 2021, 11, 2564-2581.	9.4	58
66	The histone demethylase UTX regulates the lineage-specific epigenetic program of invariant natural killer T cells. <i>Nature Immunology</i> , 2017, 18, 184-195.	14.5	56
67	Characterizing heterogeneity in leukemic cells using single-cell gene expression analysis. <i>Genome Biology</i> , 2014, 15, 525.	8.8	54
68	Recent progress in single-cell cancer genomics. <i>Current Opinion in Genetics and Development</i> , 2017, 42, 22-32.	3.3	54
69	Epithelial endoplasmic reticulum stress orchestrates a protective IgA response. <i>Science</i> , 2019, 363, 993-998.	12.6	51
70	LSD1 suppresses invasion, migration and metastasis of luminal breast cancer cells via activation of GATA3 and repression of TRIM37 expression. <i>Oncogene</i> , 2019, 38, 7017-7034.	5.9	48
71	Sexually-dimorphic targeting of functionally-related genes in COPD. <i>BMC Systems Biology</i> , 2014, 8, 118.	3.0	47
72	Impact of the N-Terminal Domain of STAT3 in STAT3-Dependent Transcriptional Activity. <i>Molecular and Cellular Biology</i> , 2015, 35, 3284-3300.	2.3	44

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73	Tracing cell-type evolution by cross-species comparison of cell atlases. <i>Cell Reports</i> , 2021, 34, 108803.	6.4	44
74	Transcription factor competition at the β -globin promoters controls hemoglobin switching. <i>Nature Genetics</i> , 2021, 53, 511-520.	21.4	43
75	Applications of alignment-free methods in epigenomics. <i>Briefings in Bioinformatics</i> , 2014, 15, 419-430.	6.5	40
76	Multi-scale chromatin state annotation using a hierarchical hidden Markov model. <i>Nature Communications</i> , 2017, 8, 15011.	12.8	40
77	Guidelines for bioinformatics of single-cell sequencing data analysis in Alzheimer's disease: review, recommendation, implementation and application. <i>Molecular Neurodegeneration</i> , 2022, 17, 17.	10.8	40
78	Sarcomeres regulate murine cardiomyocyte maturation through MRTF-SRF signaling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	38
79	Differential Cofactor Requirements for Histone Eviction from Two Nucleosomes at the Yeast <i>PHO84</i> Promoter Are Determined by Intrinsic Nucleosome Stability. <i>Molecular and Cellular Biology</i> , 2009, 29, 2960-2981.	2.3	34
80	The landscape of human tissue and cell type specific expression and co-regulation of senescence genes. <i>Molecular Neurodegeneration</i> , 2022, 17, 5.	10.8	34
81	Prediction of Polycomb target genes in mouse embryonic stem cells. <i>Genomics</i> , 2010, 96, 17-26.	2.9	33
82	Enhancer dependence of cell-type-specific gene expression increases with developmental age. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 21450-21458.	7.1	32
83	Robust lineage reconstruction from high-dimensional single-cell data. <i>Nucleic Acids Research</i> , 2016, 44, e122-e122.	14.5	30
84	RESCUE: imputing dropout events in single-cell RNA-sequencing data. <i>BMC Bioinformatics</i> , 2019, 20, 388.	2.6	30
85	GiniClust3: a fast and memory-efficient tool for rare cell type identification. <i>BMC Bioinformatics</i> , 2020, 21, 158.	2.6	28
86	Massively parallel in vivo CRISPR screening identifies RNF20/40 as epigenetic regulators of cardiomyocyte maturation. <i>Nature Communications</i> , 2021, 12, 4442.	12.8	27
87	Linking genome to epigenome. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2012, 4, 297-309.	6.6	26
88	CUT&RUNTools 2.0: a pipeline for single-cell and bulk-level CUT&RUN and CUT&Tag data analysis. <i>Bioinformatics</i> , 2021, 38, 252-254.	4.1	25
89	TGF- β signaling underlies hematopoietic dysfunction and bone marrow failure in Shwachman-Diamond syndrome. <i>Journal of Clinical Investigation</i> , 2019, 129, 3821-3826.	8.2	25
90	Inner nuclear protein Matrin-3 coordinates cell differentiation by stabilizing chromatin architecture. <i>Nature Communications</i> , 2021, 12, 6241.	12.8	25

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91	Statistical assessment of the global regulatory role of histone acetylation in <i>Saccharomyces cerevisiae</i> . <i>Genome Biology</i> , 2006, 7, R70.	9.6	24
92	Functionally distinct patterns of nucleosome remodeling at enhancers in glucocorticoid-treated acute lymphoblastic leukemia. <i>Epigenetics and Chromatin</i> , 2015, 8, 53.	3.9	22
93	MLL::AF9 degradation induces rapid changes in transcriptional elongation and subsequent loss of an active chromatin landscape. <i>Molecular Cell</i> , 2022, 82, 1140-1155.e11.	9.7	21
94	A molecular roadmap for induced multi-lineage trans-differentiation of fibroblasts by chemical combinations. <i>Cell Research</i> , 2017, 27, 386-401.	12.0	20
95	Mapping the evolving landscape of super-enhancers during cell differentiation. <i>Genome Biology</i> , 2021, 22, 269.	8.8	19
96	A multi-layer method to study genome-scale positions of nucleosomes. <i>Genomics</i> , 2009, 93, 140-145.	2.9	18
97	A motif-independent metric for DNA sequence specificity. <i>BMC Bioinformatics</i> , 2011, 12, 408.	2.6	18
98	Quantitative integration of epigenomic variation and transcription factor binding using MAMotif toolkit identifies an important role of IRF2 as transcription activator at gene promoters. <i>Cell Discovery</i> , 2018, 4, 38.	6.7	17
99	Immunosuppressive Myeloid Cells Induce Nitric Oxide-Dependent DNA Damage and p53 Pathway Activation in CD8+ T Cells. <i>Cancer Immunology Research</i> , 2021, 9, 470-485.	3.4	17
100	Targeted Recruitment of Histone Modifications in Humans Predicted by Genomic Sequences. <i>Journal of Computational Biology</i> , 2009, 16, 341-355.	1.6	16
101	Epigenetic domains found in mouse embryonic stem cells via a hidden Markov model. <i>BMC Bioinformatics</i> , 2010, 11, 557.	2.6	16
102	Haystack: systematic analysis of the variation of epigenetic states and cell-type specific regulatory elements. <i>Bioinformatics</i> , 2018, 34, 1930-1933.	4.1	16
103	Modeling the Dynamics of Bivalent Histone Modifications. <i>PLoS ONE</i> , 2013, 8, e77944.	2.5	15
104	Identification of Transcribed Enhancers by Genome-Wide Chromatin Immunoprecipitation Sequencing. <i>Methods in Molecular Biology</i> , 2017, 1468, 91-109.	0.9	15
105	The PRC2-binding long non-coding RNAs in human and mouse genomes are associated with predictive sequence features. <i>Scientific Reports</i> , 2017, 7, 41669.	3.3	13
106	Chromatin States Accurately Classify Cell Differentiation Stages. <i>PLoS ONE</i> , 2012, 7, e31414.	2.5	13
107	Gene regulatory pattern analysis reveals essential role of core transcriptional factors'™ activation in triple-negative breast cancer. <i>Oncotarget</i> , 2017, 8, 21938-21953.	1.8	13
108	Integrative epigenomic analysis in differentiated human primary bronchial epithelial cells exposed to cigarette smoke. <i>Scientific Reports</i> , 2018, 8, 12750.	3.3	11

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109	The cohesin-associated protein Wapal is required for proper Polycomb-mediated gene silencing. <i>Epigenetics and Chromatin</i> , 2016, 9, 14.	3.9	10
110	Analyzing Spatial Transcriptomics Data Using Giotto. <i>Current Protocols</i> , 2022, 2, e405.	2.9	10
111	Two faces of bivalent domain regulate VEGFA responsiveness and angiogenesis. <i>Cell Death and Disease</i> , 2020, 11, 75.	6.3	9
112	Community-wide hackathons to identify central themes in single-cell multi-omics. <i>Genome Biology</i> , 2021, 22, 220.	8.8	9
113	Molecular Profiling Establishes Genetic Features Predictive of the Efficacy of the p110 ^β Inhibitor KIN-193. <i>Cancer Research</i> , 2019, 79, 4524-4531.	0.9	7
114	Blocking PI3K p110 ^β Attenuates Development of PTEN-Deficient Castration-Resistant Prostate Cancer. <i>Molecular Cancer Research</i> , 2022, 20, 673-685.	3.4	6
115	Assessing Inequality in Transcriptomic Data. <i>Cell Systems</i> , 2018, 6, 149-150.	6.2	4
116	Prediction of Epigenetic Target Sites by Using Genomic DNA Sequence. , 2011, , 187-201.		2
117	Workshop: Targeting mechanism of epigenetic factors. , 2011, , .		0
118	Prediction of Epigenetic Target Sites by Using Genomic DNA Sequence. , 0, , 498-512.		0