

# Guo-Cheng Yuan

## List of Publications by Year in descending order

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Version: 2024-02-01

118  
papers

16,475  
citations

26610

56  
h-index

19726

117  
g-index

142  
all docs

142  
docs citations

142  
times ranked

25913  
citing authors

#	ARTICLE	IF	CITATIONS
1	The landscape of human tissue and cell type specific expression and co-regulation of senescence genes. <i>Molecular Neurodegeneration</i> , 2022, 17, 5.	4.4	34
2	Blocking PI3K p110 $\beta$ Attenuates Development of PTEN-Deficient Castration-Resistant Prostate Cancer. <i>Molecular Cancer Research</i> , 2022, 20, 673-685.	1.5	6
3	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.	4.5	21
4	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.	4.4	40
5	Analyzing Spatial Transcriptomics Data Using Giotto. <i>Current Protocols</i> , 2022, 2, e405.	1.3	10
6	A vaccine targeting resistant tumours by dual T cell plus NK cell attack. <i>Nature</i> , 2022, 606, 992-998.	13.7	65
7	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.	1.6	17
8	Integrated spatial genomics reveals global architecture of single nuclei. <i>Nature</i> , 2021, 590, 344-350.	13.7	228
9	Tracing cell-type evolution by cross-species comparison of cell atlases. <i>Cell Reports</i> , 2021, 34, 108803.	2.9	44
10	Transcription factor competition at the $\beta$ -globin promoters controls hemoglobin switching. <i>Nature Genetics</i> , 2021, 53, 511-520.	9.4	43
11	Giotto: a toolbox for integrative analysis and visualization of spatial expression data. <i>Genome Biology</i> , 2021, 22, 78.	3.8	367
12	SpatialDWLS: accurate deconvolution of spatial transcriptomic data. <i>Genome Biology</i> , 2021, 22, 145.	3.8	140
13	Inhibition of CDK4/6 Promotes CD8 T-cell Memory Formation. <i>Cancer Discovery</i> , 2021, 11, 2564-2581.	7.7	58
14	Single-nucleus transcriptome analysis of human brain immune response in patients with severe COVID-19. <i>Genome Medicine</i> , 2021, 13, 118.	3.6	81
15	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.	1.8	25
16	Massively parallel in vivo CRISPR screening identifies RNF20/40 as epigenetic regulators of cardiomyocyte maturation. <i>Nature Communications</i> , 2021, 12, 4442.	5.8	27
17	Community-wide hackathons to identify central themes in single-cell multi-omics. <i>Genome Biology</i> , 2021, 22, 220.	3.8	9
18	Single-cell nuclear architecture across cell types in the mouse brain. <i>Science</i> , 2021, 374, 586-594.	6.0	74

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19	Mapping the evolving landscape of super-enhancers during cell differentiation. <i>Genome Biology</i> , 2021, 22, 269.	3.8	19
20	Advances in spatial transcriptomic data analysis. <i>Genome Research</i> , 2021, 31, 1706-1718.	2.4	102
21	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, .	3.3	38
22	Inner nuclear protein Matrin-3 coordinates cell differentiation by stabilizing chromatin architecture. <i>Nature Communications</i> , 2021, 12, 6241.	5.8	25
23	CDK7 Inhibition Potentiates Genome Instability Triggering Anti-tumor Immunity in Small Cell Lung Cancer. <i>Cancer Cell</i> , 2020, 37, 37-54.e9.	7.7	138
24	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.	3.3	32
25	Molecular Pathways of Colon Inflammation Induced by Cancer Immunotherapy. <i>Cell</i> , 2020, 182, 655-671.e22.	13.5	259
26	Distinct Mesenchymal Cell Populations Generate the Essential Intestinal BMP Signaling Gradient. <i>Cell Stem Cell</i> , 2020, 26, 391-402.e5.	5.2	211
27	Two faces of bivalent domain regulate VEGFA responsiveness and angiogenesis. <i>Cell Death and Disease</i> , 2020, 11, 75.	2.7	9
28	GiniClust3: a fast and memory-efficient tool for rare cell type identification. <i>BMC Bioinformatics</i> , 2020, 21, 158.	1.2	28
29	BORIS promotes chromatin regulatory interactions in treatment-resistant cancer cells. <i>Nature</i> , 2019, 572, 676-680.	13.7	89
30	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.	2.6	48
31	RESCUE: imputing dropout events in single-cell RNA-sequencing data. <i>BMC Bioinformatics</i> , 2019, 20, 388.	1.2	30
32	Accurate estimation of cell-type composition from gene expression data. <i>Nature Communications</i> , 2019, 10, 2975.	5.8	125
33	A reference map of murine cardiac transcription factor chromatin occupancy identifies dynamic and conserved enhancers. <i>Nature Communications</i> , 2019, 10, 4907.	5.8	100
34	CUT&RUNTools: a flexible pipeline for CUT&RUN processing and footprint analysis. <i>Genome Biology</i> , 2019, 20, 192.	3.8	83
35	Single-cell trajectories reconstruction, exploration and mapping of omics data with STREAM. <i>Nature Communications</i> , 2019, 10, 1903.	5.8	198
36	CDK12 loss in cancer cells affects DNA damage response genes through premature cleavage and polyadenylation. <i>Nature Communications</i> , 2019, 10, 1757.	5.8	159

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37	Epithelial endoplasmic reticulum stress orchestrates a protective IgA response. <i>Science</i> , 2019, 363, 993-998.	6.0	51
38	Transcriptome-scale super-resolved imaging in tissues by RNA seqFISH+. <i>Nature</i> , 2019, 568, 235-239.	13.7	1,088
39	Estimating Sample-Specific Regulatory Networks. <i>IScience</i> , 2019, 14, 226-240.	1.9	120
40	Molecular Profiling Establishes Genetic Features Predictive of the Efficacy of the p110 $\beta$ Inhibitor KIN-193. <i>Cancer Research</i> , 2019, 79, 4524-4531.	0.4	7
41	TGF- $\beta$ 2 signaling underlies hematopoietic dysfunction and bone marrow failure in Shwachman-Diamond syndrome. <i>Journal of Clinical Investigation</i> , 2019, 129, 3821-3826.	3.9	25
42	Mapping the Mouse Cell Atlas by Microwell-Seq. <i>Cell</i> , 2018, 172, 1091-1107.e17.	13.5	1,068
43	Dissecting super-enhancer hierarchy based on chromatin interactions. <i>Nature Communications</i> , 2018, 9, 943.	5.8	179
44	Integrated design, execution, and analysis of arrayed and pooled CRISPR genome-editing experiments. <i>Nature Protocols</i> , 2018, 13, 946-986.	5.5	70
45	Haystack: systematic analysis of the variation of epigenetic states and cell-type specific regulatory elements. <i>Bioinformatics</i> , 2018, 34, 1930-1933.	1.8	16
46	A major chromatin regulator determines resistance of tumor cells to T cell-mediated killing. <i>Science</i> , 2018, 359, 770-775.	6.0	641
47	Antibody-mediated inhibition of MICA and MICB shedding promotes NK cell-driven tumor immunity. <i>Science</i> , 2018, 359, 1537-1542.	6.0	323
48	Assessing Inequality in Transcriptomic Data. <i>Cell Systems</i> , 2018, 6, 149-150.	2.9	4
49	Direct Promoter Repression by BCL11A Controls the Fetal to Adult Hemoglobin Switch. <i>Cell</i> , 2018, 173, 430-442.e17.	13.5	328
50	Revealing the Critical Regulators of Cell Identity in the Mouse Cell Atlas. <i>Cell Reports</i> , 2018, 25, 1436-1445.e3.	2.9	185
51	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.	2.9	70
52	Hierarchical and stage-specific regulation of murine cardiomyocyte maturation by serum response factor. <i>Nature Communications</i> , 2018, 9, 3837.	5.8	63
53	Identification of spatially associated subpopulations by combining scRNAseq and sequential fluorescence in situ hybridization data. <i>Nature Biotechnology</i> , 2018, 36, 1183-1190.	9.4	179
54	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.	3.1	17

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55	Mapping human pluripotent stem cell differentiation pathways using high throughput single-cell RNA-sequencing. <i>Genome Biology</i> , 2018, 19, 47.	3.8	96
56	GiniClust2: a cluster-aware, weighted ensemble clustering method for cell-type detection. <i>Genome Biology</i> , 2018, 19, 58.	3.8	59
57	Integrative epigenomic analysis in differentiated human primary bronchial epithelial cells exposed to cigarette smoke. <i>Scientific Reports</i> , 2018, 8, 12750.	1.6	11
58	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.	1.6	13
59	A molecular roadmap for induced multi-lineage trans-differentiation of fibroblasts by chemical combinations. <i>Cell Research</i> , 2017, 27, 386-401.	5.7	20
60	Recent progress in single-cell cancer genomics. <i>Current Opinion in Genetics and Development</i> , 2017, 42, 22-32.	1.5	54
61	Variant-aware saturating mutagenesis using multiple Cas9 nucleases identifies regulatory elements at trait-associated loci. <i>Nature Genetics</i> , 2017, 49, 625-634.	9.4	96
62	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.	5.2	190
63	Multi-scale chromatin state annotation using a hierarchical hidden Markov model. <i>Nature Communications</i> , 2017, 8, 15011.	5.8	40
64	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.	2.0	106
65	The histone demethylase UTX regulates the lineage-specific epigenetic program of invariant natural killer T cells. <i>Nature Immunology</i> , 2017, 18, 184-195.	7.0	56
66	Challenges and emerging directions in single-cell analysis. <i>Genome Biology</i> , 2017, 18, 84.	3.8	258
67	Identification of Transcribed Enhancers by Genome-Wide Chromatin Immunoprecipitation Sequencing. <i>Methods in Molecular Biology</i> , 2017, 1468, 91-109.	0.4	15
68	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.	1.6	58
69	Gene regulatory pattern analysis reveals essential role of core transcriptional factors' activation in triple-negative breast cancer. <i>Oncotarget</i> , 2017, 8, 21938-21953.	0.8	13
70	Analyzing CRISPR genome-editing experiments with CRISPResso. <i>Nature Biotechnology</i> , 2016, 34, 695-697.	9.4	410
71	GiniClust: detecting rare cell types from single-cell gene expression data with Gini index. <i>Genome Biology</i> , 2016, 17, 144.	3.8	238
72	Robust lineage reconstruction from high-dimensional single-cell data. <i>Nucleic Acids Research</i> , 2016, 44, e122-e122.	6.5	30

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73	Acquired Tissue-Specific Promoter Bivalency Is a Basis for PRC2 Necessity in Adult Cells. <i>Cell</i> , 2016, 165, 1389-1400.	13.5	101
74	Single-Cell Transcript Profiles Reveal Multilineage Priming in Early Progenitors Derived from Lgr5 + Intestinal Stem Cells. <i>Cell Reports</i> , 2016, 16, 2053-2060.	2.9	69
75	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.	15.2	105
76	The cohesin-associated protein Wapal is required for proper Polycomb-mediated gene silencing. <i>Epigenetics and Chromatin</i> , 2016, 9, 14.	1.8	10
77	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.	2.9	73
78	Mitochondrial iron chelation ameliorates cigarette smoke-induced bronchitis and emphysema in mice. <i>Nature Medicine</i> , 2016, 22, 163-174.	15.2	206
79	Dynamic Control of Enhancer Repertoires Drives Lineage and Stage-Specific Transcription during Hematopoiesis. <i>Developmental Cell</i> , 2016, 36, 9-23.	3.1	204
80	Multiparametric profiling of non-small-cell lung cancers reveals distinct immunophenotypes. <i>JCI Insight</i> , 2016, 1, e89014.	2.3	110
81	Functionally distinct patterns of nucleosome remodeling at enhancers in glucocorticoid-treated acute lymphoblastic leukemia. <i>Epigenetics and Chromatin</i> , 2015, 8, 53.	1.8	22
82	A network model for angiogenesis in ovarian cancer. <i>BMC Bioinformatics</i> , 2015, 16, 115.	1.2	60
83	Predicting chromatin organization using histone marks. <i>Genome Biology</i> , 2015, 16, 162.	3.8	98
84	Developmental Control of Polycomb Subunit Composition by GATA Factors Mediates a Switch to Non-Canonical Functions. <i>Molecular Cell</i> , 2015, 57, 304-316.	4.5	119
85	Impact of the N-Terminal Domain of STAT3 in STAT3-Dependent Transcriptional Activity. <i>Molecular and Cellular Biology</i> , 2015, 35, 3284-3300.	1.1	44
86	Haploinsufficiency of Hedgehog interacting protein causes increased emphysema induced by cigarette smoke through network rewiring. <i>Genome Medicine</i> , 2015, 7, 12.	3.6	61
87	Single-Cell Analysis in Cancer Genomics. <i>Trends in Genetics</i> , 2015, 31, 576-586.	2.9	164
88	BCL11A enhancer dissection by Cas9-mediated in situ saturating mutagenesis. <i>Nature</i> , 2015, 527, 192-197.	13.7	726
89	Sexually-dimorphic targeting of functionally-related genes in COPD. <i>BMC Systems Biology</i> , 2014, 8, 118.	3.0	47
90	Characterizing heterogeneity in leukemic cells using single-cell gene expression analysis. <i>Genome Biology</i> , 2014, 15, 525.	3.8	54

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91	Analysis of chromatin-state plasticity identifies cell-type-specific regulators of H3K27me3 patterns. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E344-53.	3.3	66
92	Bifurcation analysis of single-cell gene expression data reveals epigenetic landscape. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E5643-50.	3.3	263
93	Reprogramming Committed Murine Blood Cells to Induced Hematopoietic Stem Cells with Defined Factors. Cell, 2014, 157, 549-564.	13.5	290
94	Applications of alignment-free methods in epigenomics. Briefings in Bioinformatics, 2014, 15, 419-430.	3.2	40
95	Distinct and Combinatorial Functions of Jmjd2b/Kdm4b and Jmjd2c/Kdm4c in Mouse Embryonic Stem Cell Identity. Molecular Cell, 2014, 53, 32-48.	4.5	112
96	CDK7 Inhibition Suppresses Super-Enhancer-Linked Oncogenic Transcription in MYCN-Driven Cancer. Cell, 2014, 159, 1126-1139.	13.5	498
97	LincRNA-p21 Regulates Neointima Formation, Vascular Smooth Muscle Cell Proliferation, Apoptosis, and Atherosclerosis by Enhancing p53 Activity. Circulation, 2014, 130, 1452-1465.	1.6	425
98	Mapping Cellular Hierarchy by Single-Cell Analysis of the Cell Surface Repertoire. Cell Stem Cell, 2013, 13, 492-505.	5.2	214
99	Modeling the Dynamics of Bivalent Histone Modifications. PLoS ONE, 2013, 8, e77944.	1.1	15
100	Passing Messages between Biological Networks to Refine Predicted Interactions. PLoS ONE, 2013, 8, e64832.	1.1	183
101	Combinatorial Assembly of Developmental Stage-Specific Enhancers Controls Gene Expression Programs during Human Erythropoiesis. Developmental Cell, 2012, 23, 796-811.	3.1	183
102	Linking genome to epigenome. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2012, 4, 297-309.	6.6	26
103	MAnorm: a robust model for quantitative comparison of ChIP-Seq data sets. Genome Biology, 2012, 13, R16.	13.9	355
104	Chromatin States Accurately Classify Cell Differentiation Stages. PLoS ONE, 2012, 7, e31414.	1.1	13
105	Workshop: Targeting mechanism of epigenetic factors. , 2011, , .		0
106	A motif-independent metric for DNA sequence specificity. BMC Bioinformatics, 2011, 12, 408.	1.2	18
107	Prediction of Epigenetic Target Sites by Using Genomic DNA Sequence. , 2011, , 187-201.		2
108	Epigenetic domains found in mouse embryonic stem cells via a hidden Markov model. BMC Bioinformatics, 2010, 11, 557.	1.2	16

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109	Schizosaccharomyces pombe genome-wide nucleosome mapping reveals positioning mechanisms distinct from those of Saccharomyces cerevisiae. Nature Structural and Molecular Biology, 2010, 17, 251-257.	3.6	215
110	Prediction of Polycomb target genes in mouse embryonic stem cells. Genomics, 2010, 96, 17-26.	1.3	33
111	Targeted Recruitment of Histone Modifications in Humans Predicted by Genomic Sequences. Journal of Computational Biology, 2009, 16, 341-355.	0.8	16
112	Differential Cofactor Requirements for Histone Eviction from Two Nucleosomes at the Yeast <i>PHO84</i> Promoter Are Determined by Intrinsic Nucleosome Stability. Molecular and Cellular Biology, 2009, 29, 2960-2981.	1.1	34
113	Jumonji Modulates Polycomb Activity and Self-Renewal versus Differentiation of Stem Cells. Cell, 2009, 139, 1303-1314.	13.5	398
114	A multi-layer method to study genome-scale positions of nucleosomes. Genomics, 2009, 93, 140-145.	1.3	18
115	Genomic Sequence Is Highly Predictive of Local Nucleosome Depletion. PLoS Computational Biology, 2008, 4, e13.	1.5	156
116	Statistical assessment of the global regulatory role of histone acetylation in Saccharomyces cerevisiae. Genome Biology, 2006, 7, R70.	13.9	24
117	Genome-Scale Identification of Nucleosome Positions in S. cerevisiae. Science, 2005, 309, 626-630.	6.0	1,047
118	Prediction of Epigenetic Target Sites by Using Genomic DNA Sequence. , 0, , 498-512.		0