

# 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  | 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        |
| 2  | Blocking PI3K p110 $\beta$ Attenuates Development of PTEN-Deficient Castration-Resistant Prostate Cancer. <i>Molecular Cancer Research</i> , 2022, 20, 673-685.  | 3.4  | 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.                          | 9.7  | 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. | 10.8 | 40        |
| 5  | Analyzing Spatial Transcriptomics Data Using Giotto. <i>Current Protocols</i> , 2022, 2, e405.   | 2.9  | 10        |
| 6  | A vaccine targeting resistant tumours by dual T cell plus NK cell attack. <i>Nature</i> , 2022, 606, 992-998.  | 27.8 | 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.                               | 3.4  | 17        |
| 8  | Integrated spatial genomics reveals global architecture of single nuclei. <i>Nature</i> , 2021, 590, 344-350.  | 27.8 | 228       |
| 9  | Tracing cell-type evolution by cross-species comparison of cell atlases. <i>Cell Reports</i> , 2021, 34, 108803.   | 6.4  | 44        |
| 10 | Transcription factor competition at the $\beta$ -globin promoters controls hemoglobin switching. <i>Nature Genetics</i> , 2021, 53, 511-520.   | 21.4 | 43        |
| 11 | Giotto: a toolbox for integrative analysis and visualization of spatial expression data. <i>Genome Biology</i> , 2021, 22, 78.   | 8.8  | 367       |
| 12 | SpatialDWLS: accurate deconvolution of spatial transcriptomic data. <i>Genome Biology</i> , 2021, 22, 145.   | 8.8  | 140       |
| 13 | Inhibition of CDK4/6 Promotes CD8 T-cell Memory Formation. <i>Cancer Discovery</i> , 2021, 11, 2564-2581.  | 9.4  | 58        |
| 14 | 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        |
| 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.  | 4.1  | 25        |
| 16 | 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        |
| 17 | Community-wide hackathons to identify central themes in single-cell multi-omics. <i>Genome Biology</i> , 2021, 22, 220.  | 8.8  | 9         |
| 18 | Single-cell nuclear architecture across cell types in the mouse brain. <i>Science</i> , 2021, 374, 586-594.  | 12.6 | 74        |

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|----|--|------|-----------|
| 19 | Mapping the evolving landscape of super-enhancers during cell differentiation. <i>Genome Biology</i> , 2021, 22, 269.  | 8.8  | 19        |
| 20 | Advances in spatial transcriptomic data analysis. <i>Genome Research</i> , 2021, 31, 1706-1718.  | 5.5  | 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, .                        | 7.1  | 38        |
| 22 | Inner nuclear protein Matrin-3 coordinates cell differentiation by stabilizing chromatin architecture. <i>Nature Communications</i> , 2021, 12, 6241.  | 12.8 | 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.  | 16.8 | 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. | 7.1  | 32        |
| 25 | Molecular Pathways of Colon Inflammation Induced by Cancer Immunotherapy. <i>Cell</i> , 2020, 182, 655-671.e22.  | 28.9 | 259       |
| 26 | Distinct Mesenchymal Cell Populations Generate the Essential Intestinal BMP Signaling Gradient. <i>Cell Stem Cell</i> , 2020, 26, 391-402.e5.  | 11.1 | 211       |
| 27 | Two faces of bivalent domain regulate VEGFA responsiveness and angiogenesis. <i>Cell Death and Disease</i> , 2020, 11, 75.   | 6.3  | 9         |
| 28 | GiniClust3: a fast and memory-efficient tool for rare cell type identification. <i>BMC Bioinformatics</i> , 2020, 21, 158.   | 2.6  | 28        |
| 29 | BORIS promotes chromatin regulatory interactions in treatment-resistant cancer cells. <i>Nature</i> , 2019, 572, 676-680.  | 27.8 | 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.                        | 5.9  | 48        |
| 31 | RESCUE: imputing dropout events in single-cell RNA-sequencing data. <i>BMC Bioinformatics</i> , 2019, 20, 388.   | 2.6  | 30        |
| 32 | Accurate estimation of cell-type composition from gene expression data. <i>Nature Communications</i> , 2019, 10, 2975.   | 12.8 | 125       |
| 33 | A reference map of murine cardiac transcription factor chromatin occupancy identifies dynamic and conserved enhancers. <i>Nature Communications</i> , 2019, 10, 4907.  | 12.8 | 100       |
| 34 | CUT&RUNTools: a flexible pipeline for CUT&RUN processing and footprint analysis. <i>Genome Biology</i> , 2019, 20, 192.  | 8.8  | 83        |
| 35 | Single-cell trajectories reconstruction, exploration and mapping of omics data with STREAM. <i>Nature Communications</i> , 2019, 10, 1903.   | 12.8 | 198       |
| 36 | CDK12 loss in cancer cells affects DNA damage response genes through premature cleavage and polyadenylation. <i>Nature Communications</i> , 2019, 10, 1757.  | 12.8 | 159       |

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|----|---|------|-----------|
| 37 | Epithelial endoplasmic reticulum stress orchestrates a protective IgA response. <i>Science</i> , 2019, 363, 993-998.  | 12.6 | 51        |
| 38 | Transcriptome-scale super-resolved imaging in tissues by RNA seqFISH+. <i>Nature</i> , 2019, 568, 235-239.  | 27.8 | 1,088     |
| 39 | Estimating Sample-Specific Regulatory Networks. <i>IScience</i> , 2019, 14, 226-240.  | 4.1  | 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.  | 0.9  | 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.  | 8.2  | 25        |
| 42 | Mapping the Mouse Cell Atlas by Microwell-Seq. <i>Cell</i> , 2018, 172, 1091-1107.e17.  | 28.9 | 1,068     |
| 43 | Dissecting super-enhancer hierarchy based on chromatin interactions. <i>Nature Communications</i> , 2018, 9, 943.   | 12.8 | 179       |
| 44 | Integrated design, execution, and analysis of arrayed and pooled CRISPR genome-editing experiments. <i>Nature Protocols</i> , 2018, 13, 946-986.  | 12.0 | 70        |
| 45 | 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        |
| 46 | A major chromatin regulator determines resistance of tumor cells to T cell-mediated killing. <i>Science</i> , 2018, 359, 770-775.   | 12.6 | 641       |
| 47 | Antibody-mediated inhibition of MICA and MICB shedding promotes NK cell-driven tumor immunity. <i>Science</i> , 2018, 359, 1537-1542.   | 12.6 | 323       |
| 48 | Assessing Inequality in Transcriptomic Data. <i>Cell Systems</i> , 2018, 6, 149-150.  | 6.2  | 4         |
| 49 | Direct Promoter Repression by BCL11A Controls the Fetal to Adult Hemoglobin Switch. <i>Cell</i> , 2018, 173, 430-442.e17.   | 28.9 | 328       |
| 50 | Revealing the Critical Regulators of Cell Identity in the Mouse Cell Atlas. <i>Cell Reports</i> , 2018, 25, 1436-1445.e3.   | 6.4  | 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.  | 6.4  | 70        |
| 52 | Hierarchical and stage-specific regulation of murine cardiomyocyte maturation by serum response factor. <i>Nature Communications</i> , 2018, 9, 3837.   | 12.8 | 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.  | 17.5 | 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. | 6.7  | 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.  | 8.8  | 96        |
| 56 | GiniClust2: a cluster-aware, weighted ensemble clustering method for cell-type detection. <i>Genome Biology</i> , 2018, 19, 58.   | 8.8  | 59        |
| 57 | Integrative epigenomic analysis in differentiated human primary bronchial epithelial cells exposed to cigarette smoke. <i>Scientific Reports</i> , 2018, 8, 12750.                            | 3.3  | 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.                                | 3.3  | 13        |
| 59 | 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        |
| 60 | Recent progress in single-cell cancer genomics. <i>Current Opinion in Genetics and Development</i> , 2017, 42, 22-32.   | 3.3  | 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.                       | 21.4 | 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.   | 11.1 | 190       |
| 63 | Multi-scale chromatin state annotation using a hierarchical hidden Markov model. <i>Nature Communications</i> , 2017, 8, 15011.   | 12.8 | 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.           | 4.5  | 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.                              | 14.5 | 56        |
| 66 | Challenges and emerging directions in single-cell analysis. <i>Genome Biology</i> , 2017, 18, 84.   | 8.8  | 258       |
| 67 | Identification of Transcribed Enhancers by Genome-Wide Chromatin Immunoprecipitation Sequencing. <i>Methods in Molecular Biology</i> , 2017, 1468, 91-109.                                    | 0.9  | 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. | 3.3  | 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.               | 1.8  | 13        |
| 70 | Analyzing CRISPR genome-editing experiments with CRISPResso. <i>Nature Biotechnology</i> , 2016, 34, 695-697.   | 17.5 | 410       |
| 71 | GiniClust: detecting rare cell types from single-cell gene expression data with Gini index. <i>Genome Biology</i> , 2016, 17, 144.  | 8.8  | 238       |
| 72 | Robust lineage reconstruction from high-dimensional single-cell data. <i>Nucleic Acids Research</i> , 2016, 44, e122-e122.  | 14.5 | 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.  | 28.9 | 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.   | 6.4  | 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. | 30.7 | 105       |
| 76 | The cohesin-associated protein Wapal is required for proper Polycomb-mediated gene silencing. <i>Epigenetics and Chromatin</i> , 2016, 9, 14.  | 3.9  | 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.   | 6.4  | 73        |
| 78 | Mitochondrial iron chelation ameliorates cigarette smoke-induced bronchitis and emphysema in mice. <i>Nature Medicine</i> , 2016, 22, 163-174.   | 30.7 | 206       |
| 79 | Dynamic Control of Enhancer Repertoires Drives Lineage and Stage-Specific Transcription during Hematopoiesis. <i>Developmental Cell</i> , 2016, 36, 9-23.  | 7.0  | 204       |
| 80 | Multiparametric profiling of non-small-cell lung cancers reveals distinct immunophenotypes. <i>JCI Insight</i> , 2016, 1, e89014.  | 5.0  | 110       |
| 81 | 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        |
| 82 | A network model for angiogenesis in ovarian cancer. <i>BMC Bioinformatics</i> , 2015, 16, 115.   | 2.6  | 60        |
| 83 | Predicting chromatin organization using histone marks. <i>Genome Biology</i> , 2015, 16, 162.  | 8.8  | 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.   | 9.7  | 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.   | 2.3  | 44        |
| 86 | 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        |
| 87 | Single-Cell Analysis in Cancer Genomics. <i>Trends in Genetics</i> , 2015, 31, 576-586.  | 6.7  | 164       |
| 88 | BCL11A enhancer dissection by Cas9-mediated in situ saturating mutagenesis. <i>Nature</i> , 2015, 527, 192-197.  | 27.8 | 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.  | 8.8  | 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. | 7.1  | 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.               | 7.1  | 263       |
| 93  | Reprogramming Committed Murine Blood Cells to Induced Hematopoietic Stem Cells with Defined Factors. Cell, 2014, 157, 549-564.   | 28.9 | 290       |
| 94  | Applications of alignment-free methods in epigenomics. Briefings in Bioinformatics, 2014, 15, 419-430.   | 6.5  | 40        |
| 95  | Distinct and Combinatorial Functions of Jmjd2b/Kdm4b and Jmjd2c/Kdm4c in Mouse Embryonic Stem Cell Identity. Molecular Cell, 2014, 53, 32-48.  | 9.7  | 112       |
| 96  | CDK7 Inhibition Suppresses Super-Enhancer-Linked Oncogenic Transcription in MYCN-Driven Cancer. Cell, 2014, 159, 1126-1139.  | 28.9 | 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.  | 11.1 | 214       |
| 99  | Modeling the Dynamics of Bivalent Histone Modifications. PLoS ONE, 2013, 8, e77944.  | 2.5  | 15        |
| 100 | Passing Messages between Biological Networks to Refine Predicted Interactions. PLoS ONE, 2013, 8, e64832.  | 2.5  | 183       |
| 101 | Combinatorial Assembly of Developmental Stage-Specific Enhancers Controls Gene Expression Programs during Human Erythropoiesis. Developmental Cell, 2012, 23, 796-811.                                     | 7.0  | 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.   | 9.6  | 355       |
| 104 | Chromatin States Accurately Classify Cell Differentiation Stages. PLoS ONE, 2012, 7, e31414.   | 2.5  | 13        |
| 105 | Workshop: Targeting mechanism of epigenetic factors. , 2011, , .   |      | 0         |
| 106 | A motif-independent metric for DNA sequence specificity. BMC Bioinformatics, 2011, 12, 408.  | 2.6  | 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.   | 2.6  | 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.                   | 8.2  | 215       |
| 110 | Prediction of Polycomb target genes in mouse embryonic stem cells. Genomics, 2010, 96, 17-26.  | 2.9  | 33        |
| 111 | Targeted Recruitment of Histone Modifications in Humans Predicted by Genomic Sequences. Journal of Computational Biology, 2009, 16, 341-355.   | 1.6  | 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. | 2.3  | 34        |
| 113 | Jumonji Modulates Polycomb Activity and Self-Renewal versus Differentiation of Stem Cells. Cell, 2009, 139, 1303-1314.   | 28.9 | 398       |
| 114 | A multi-layer method to study genome-scale positions of nucleosomes. Genomics, 2009, 93, 140-145.  | 2.9  | 18        |
| 115 | Genomic Sequence Is Highly Predictive of Local Nucleosome Depletion. PLoS Computational Biology, 2008, 4, e13.   | 3.2  | 156       |
| 116 | Statistical assessment of the global regulatory role of histone acetylation in Saccharomyces cerevisiae. Genome Biology, 2006, 7, R70.   | 9.6  | 24        |
| 117 | Genome-Scale Identification of Nucleosome Positions in <i>S. cerevisiae</i> . Science, 2005, 309, 626-630.   | 12.6 | 1,047     |
| 118 | Prediction of Epigenetic Target Sites by Using Genomic DNA Sequence. , 0, , 498-512.   |      | 0         |