Chao Cheng

List of Publications by Year
in descending order

134 papers	7,844 citations	94269 37 h-index	60497 81 g-index
181 all docs	181 docs citations	181 times ranked	14251 citing authors

#	Article	IF	Citations
1	Architecture of the human regulatory network derived from ENCODE data. Nature, 2012, 489, 91-100.	13.7	1,384
2	Integrative Analysis of the <i>Caenorhabditis elegans</i> Genome by the modENCODE Project. Science, 2010, 330, 1775-1787.	6.0	912
3	Comparative analysis of the transcriptome across distant species. Nature, 2014, 512, 445-448.	13.7	289
4	Classification of human genomic regions based on experimentally determined binding sites of more than 100 transcription-related factors. Genome Biology, 2012, 13, R48.	13.9	233
5	Modeling gene expression using chromatin features in various cellular contexts. Genome Biology, 2012, 13, R53.	13.9	231
6	A deep learning framework for modeling structural features of RNA-binding protein targets. Nucleic Acids Research, 2016, 44, e32-e32.	6.5	213
7	Reconstruction of enhancer–target networks in 935 samples of human primary cells, tissues and cell lines. Nature Genetics, 2017, 49, 1428-1436.	9.4	194
8	Comparative analysis of regulatory information and circuits across distant species. Nature, 2014, 512, 453-456.	13.7	184
9	Understanding transcriptional regulation by integrative analysis of transcription factor binding data. Genome Research, 2012, 22, 1658-1667.	2.4	166
10	Big Data Bioinformatics. Journal of Cellular Physiology, 2014, 229, 1896-1900.	2.0	161
11	VISTA is a checkpoint regulator for naÃ¯ve T cell quiescence and peripheral tolerance. Science, 2020, 367, .	6.0	156
12	Immunoregulatory functions of <scp>VISTA</scp>. Immunological Reviews, 2017, 276, 66-79.	2.8	154
13	Transcriptional and proteomic insights into the host response in fatal COVID-19 cases. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 28336-28343.	3.3	149
14	Modeling the relative relationship of transcription factor binding and histone modifications to gene expression levels in mouse embryonic stem cells. Nucleic Acids Research, 2012, 40, 553-568.	6.5	145
15	Systematic Pan-Cancer Analysis Reveals Immune Cell Interactions in the Tumor Microenvironment. Cancer Research, 2017, 77, 1271-1282.	0.4	134
16	Analysis of clock-regulated genes in <i>Neurospora</i> reveals widespread posttranscriptional control of metabolic potential. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 16995-17002.	3.3	131
17	Hypoxia-Induced VISTA Promotes the Suppressive Function of Myeloid-Derived Suppressor Cells in the Tumor Microenvironment. Cancer Immunology Research, 2019, 7, 1079-1090.	1.6	129
18	A statistical framework for modeling gene expression using chromatin features and application to modENCODE datasets. Genome Biology, 2011, 12, R15.	13.9	118

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19	The Histone Methyltransferase Activity of MLL1 Is Dispensable for Hematopoiesis and Leukemogenesis. Cell Reports, 2014, 7, 1239-1247.	2.9	110
20	CD36-Mediated Metabolic Rewiring of Breast Cancer Cells Promotes Resistance to HER2-Targeted Therapies. Cell Reports, 2019, 29, 3405-3420.e5.	2.9	104
21	Association of Gamma-Aminobutyric Acid A Receptor Î±2 Gene (GABRA2) with Alcohol Use Disorder. Neuropsychopharmacology, 2014, 39, 907-918.	2.8	93
22	Construction and Analysis of an Integrated Regulatory Network Derived from High-Throughput Sequencing Data. PLoS Computational Biology, 2011, 7, e1002190.	1.5	92
23	mRNA expression profiles show differential regulatory effects of microRNAs between estrogen receptor-positive and estrogen receptor-negative breast cancer. Genome Biology, 2009, 10, R90.	13.9	90
24	UNSUPERVISED FEATURE CONSTRUCTION AND KNOWLEDGE EXTRACTION FROM GENOME-WIDE ASSAYS OF BREAST CANCER WITH DENOISING AUTOENCODERS. , 2014, , .		79
25	VISTA expression on tumor-infiltrating inflammatory cells in primary cutaneous melanoma correlates with poor disease-specific survival. Cancer Immunology, Immunotherapy, 2018, 67, 1113-1121.	2.0	79
26	Inferring MicroRNA Activities by Combining Gene Expression with MicroRNA Target Prediction. PLoS ONE, 2008, 3, e1989.	1.1	79
27	9p21 loss confers a cold tumor immune microenvironment and primary resistance to immune checkpoint therapy. Nature Communications, 2021, 12, 5606.	5.8	76
28	The relationship between the evolution of microRNA targets and the length of their UTRs. BMC Genomics, 2009, 10, 431.	1.2	75
29	Inferring activity changes of transcription factors by binding association with sorted expression profiles. BMC Bioinformatics, 2007, 8, 452.	1.2	72
30	Resident and circulating memory T cells persist for years in melanoma patients with durable responses to immunotherapy. Nature Cancer, 2021, 2, 300-311.	5.7	70
31	Therapeutically targeting tumor microenvironmentâ€"mediated drug resistance in estrogen receptorâ€"positive breast cancer. Journal of Experimental Medicine, 2018, 215, 895-910.	4.2	63
32	Pan-cancer association of HLA gene expression with cancer prognosis and immunotherapy efficacy. British Journal of Cancer, 2021, 125, 422-432.	2.9	59
33	Identification of Candidate Cyclin-dependent kinase 1 (Cdk1) Substrates in Mitosis by Quantitative Phosphoproteomics. Molecular and Cellular Proteomics, 2016, 15, 2448-2461.	2.5	54
34	TIP: A probabilistic method for identifying transcription factor target genes from ChIP-seq binding profiles. Bioinformatics, 2011, 27, 3221-3227.	1.8	52
35	Resident memory CD8+ TÂcells in regional lymph nodes mediate immunity to metastatic melanoma. Immunity, 2021, 54, 2117-2132.e7.	6.6	50
36	E2F4 regulatory program predicts patient survival prognosis in breast cancer. Breast Cancer Research, 2014, 16, 486.	2.2	46

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37	Unsupervised feature construction and knowledge extraction from genome-wide assays of breast cancer with denoising autoencoders. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2015, , 132-43.	0.7	45
38	Adaptive immunity programmes in breast cancer. Immunology, 2017, 150, 25-34.	2.0	43
39	Computational immune profiling in lung adenocarcinoma reveals reproducible prognostic associations with implications for immunotherapy. OncoImmunology, 2018, 7, e1431084.	2.1	43
40	A P53-Deficiency Gene Signature Predicts Recurrence Risk of Patients with Early-Stage Lung Adenocarcinoma. Cancer Epidemiology Biomarkers and Prevention, 2018, 27, 86-95.	1.1	42
41	Regulators Associated with Clinical Outcomes Revealed by DNA Methylation Data in Breast Cancer. PLoS Computational Biology, 2015, 11, e1004269.	1.5	34
42	Integrative analysis of breast cancer reveals prognostic haematopoietic activity and patient-specific immune response profiles. Nature Communications, 2016, 7, 10248.	5.8	34
43	Genomic Characterization of Six Virus-Associated Cancers Identifies Changes in the Tumor Immune Microenvironment and Altered Genetic Programs. Cancer Research, 2018, 78, 6413-6423.	0.4	33
44	Inference of transcription modification in long-live yeast strains from their expression profiles. BMC Genomics, 2007, 8, 219.	1.2	32
45	MYC Mediates mRNA Cap Methylation of Canonical Wnt/Î²-Catenin Signaling Transcripts By Recruiting CDK7 and RNA Methyltransferase. Molecular Cancer Research, 2017, 15, 213-224.	1.5	32
46	Effect of estrogen receptor Î± binding on functional DNA methylation in breast cancer. Epigenetics, 2014, 9, 523-532.	1.3	31
47	Single-cell RNA sequencing reveals the impact of chromosomal instability on glioblastoma cancer stem cells. BMC Medical Genomics, 2019, 12, 79.	0.7	30
48	Multifactorial Deep Learning Reveals Pan-Cancer Genomic Tumor Clusters with Distinct Immunogenomic Landscape and Response to Immunotherapy. Clinical Cancer Research, 2020, 26, 2908-2920.	3.2	30
49	An intestinal microRNA modulates the homeostatic adaptation to chronic oxidative stress in C. elegans. Aging, 2016, 8, 1979-2005.	1.4	29
50	PDGF Engages an E2F-USP1 Signaling Pathway to Support ID2-Mediated Survival of Proneural Glioma Cells. Cancer Research, 2016, 76, 2964-2976.	0.4	28
51	A Leukocyte Infiltration Score Defined by a Gene Signature Predicts Melanoma Patient Prognosis. Molecular Cancer Research, 2019, 17, 109-119.	1.5	28
52	An approach for determining and measuring network hierarchy applied to comparing the phosphorylome and the regulome. Genome Biology, 2015, 16, 63.	3.8	27
53	Impact of Oncotype DX testing on ER+ breast cancer treatment and survival in the first decade of use. Breast Cancer Research, 2021, 23, 74.	2.2	27
54	Systematic identification of cell cycle regulated transcription factors from microarray time series data. BMC Genomics, 2008, 9, 116.	1.2	26

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55	Artificial intelligence, machine learning, and deep learning for clinical outcome prediction. Emerging Topics in Life Sciences, 2021, 5, 729-745.	1.1	26
56	Coexpression enrichment analysis at the single-cell level reveals convergent defects in neural progenitor cells and their cell-type transitions in neurodevelopmental disorders. Genome Research, 2020, 30, 835-848.	2.4	25
57	A lepidic gene signature predicts patient prognosis and sensitivity to immunotherapy in lung adenocarcinoma. Genome Medicine, 2022, 14, 5.	3.6	25
58	VISTA Re-programs Macrophage Biology Through the Combined Regulation of Tolerance and Anti-inflammatory Pathways. Frontiers in Immunology, 2020, 11, 580187.	2.2	24
59	VISTA: A Target to Manage the Innate Cytokine Storm. Frontiers in Immunology, 2020, 11, 595950.	2.2	24
60	Cold and heterogeneous T cell repertoire is associated with copy number aberrations and loss of immune genes in small-cell lung cancer. Nature Communications, 2021, 12, 6655.	5.8	24
61	Statins associate with improved mortality among patients with certain histological subtypes of lung cancer. Lung Cancer, 2018, 126, 89-96.	0.9	22
62	Significant and Systematic Expression Differentiation in Long-Lived Yeast Strains. PLoS ONE, 2007, 2, e1095.	1.1	21
63	Gene signature–based prediction of triple–negative breast cancer patient response to Neoadjuvant chemotherapy. Cancer Medicine, 2020, 9, 6281-6295.	1.3	21
64	Performance and efficiency of machine learning algorithms for analyzing rectangular biomedical data. Laboratory Investigation, 2021, 101, 430-441.	1.7	21
65	Abnormal global alternative RNA splicing in COVID-19 patients. PLoS Genetics, 2022, 18, e1010137.	1.5	21
66	REACTIN: Regulatory activity inference of transcription factors underlying human diseases with application to breast cancer. BMC Genomics, 2013, 14, 504.	1.2	20
67	A B cell-derived gene expression signature associates with an immunologically active tumor microenvironment and response to immune checkpoint blockade therapy. OncoImmunology, 2019, 8, e1513440.	2.1	20
68	Intestinal stem cell overproliferation resulting from inactivation of the APC tumor suppressor requires the transcription cofactors Earthbound and Erect wing. PLoS Genetics, 2017, 13, e1006870.	1.5	20
69	Rare deleterious germline variants and risk of lung cancer. Npj Precision Oncology, 2021, 5, 12.	2.3	19
70	Predictors of disease aggressiveness influence outcome from immunotherapy treatment in renal clear cell carcinoma. OncoImmunology, 2019, 8, e1500106.	2.1	18
71	A gene expression-based immune signature for lung adenocarcinoma prognosis. Cancer Immunology, Immunotherapy, 2020, 69, 1881-1890.	2.0	18
72	Relating gene expression evolution with CpG content changes. BMC Genomics, 2014, 15, 693.	1.2	17

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73	Integrative analysis of survival-associated gene sets in breast cancer. BMC Medical Genomics, 2015, 8, 11.	0.7	17
74	Complex Patterns of Association between Pleiotropy and Transcription Factor Evolution. Genome Biology and Evolution, 2016, 8, 3159-3170.	1.1	17
75	Identification of gene expression levels in primary melanoma associated with clinically meaningful characteristics. Melanoma Research, 2018, 28, 380-389.	0.6	17
76	Genome-wide analysis of chromatin features identifies histone modification sensitive and insensitive yeast transcription factors. Genome Biology, 2011, 12, R111.	13.9	16
77	The histologic phenotype of lung cancers is associated with transcriptomic features rather than genomic characteristics. Nature Communications, 2021, 12, 7081.	5.8	16
78	The E2F4 prognostic signature predicts pathological response to neoadjuvant chemotherapy in breast cancer patients. BMC Cancer, 2017, 17, 306.	1.1	15
79	Chr20q Amplification Defines a Distinct Molecular Subtype of Microsatellite Stable Colorectal Cancer. Cancer Research, 2021, 81, 1977-1987.	0.4	15
80	SARS-CoV-2 Impairs Dendritic Cells and Regulates DC-SIGN Gene Expression in Tissues. International Journal of Molecular Sciences, 2021, 22, 9228.	1.8	15
81	Sub-array normalization subject to differentiation. Nucleic Acids Research, 2005, 33, 5565-5573.	6.5	13
82	Cross-Disciplinary Network Comparison: Matchmaking between Hairballs. Cell Systems, 2016, 2, 147-157.	2.9	13
83	Cytokine sensitivity screening highlights BMP4 pathway signaling as a therapeutic opportunity in ER + breast cancer. FASEB Journal, 2019, 33, 1644-1657.	0.2	13
84	An <scp>EGFR</scp> signature predicts cell line and patient sensitivity to multiple tyrosine kinase inhibitors. International Journal of Cancer, 2020, 147, 2621-2633.	2.3	13
85	Gene signatures associated with genomic aberrations predict prognosis in neuroblastoma. Cancer Communications, 2020, 40, 105-118.	3.7	13
86	E2F4 Program Is Predictive of Progression and Intravesical Immunotherapy Efficacy in Bladder Cancer. Molecular Cancer Research, 2015, 13, 1316-1324.	1.5	12
87	Systematic identification of transcription factors associated with patient survival in cancers. BMC Genomics, 2009, 10, 225.	1.2	11
88	A TMPRSS2â€ERG gene signature predicts prognosis of patients with prostate adenocarcinoma. Clinical and Translational Medicine, 2020, 10, e216.	1.7	11
89	Clonal Hematopoiesis Mutations in Patients with Lung Cancer Are Associated with Lung Cancer Risk Factors. Cancer Research, 2022, 82, 199-209.	0.4	11
90	B cell infiltration is highly associated with prognosis and an immune-infiltrated tumor microenvironment in neuroblastoma. , 2021, 7, .		10

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91	MARD: a new method to detect differential gene expression in treatment-control time courses. Bioinformatics, 2006, 22, 2650-2657.	1.8	9
92	Computational Investigation of Homologous Recombination DNA Repair Deficiency in Sporadic Breast Cancer. Scientific Reports, 2017, 7, 15742.	1.6	9
93	Tumor immune infiltration estimated from gene expression profiles predicts colorectal cancer relapse. OncoImmunology, 2021, 10, 1862529.	2.1	9
94	Multimetric feature selection for analyzing multicategory outcomes of colorectal cancer: random forest and multinomial logistic regression models. Laboratory Investigation, 2022, 102, 236-244.	1.7	9
95	Predicting clinical outcomes of cancer patients with a p53 deficiency gene signature. Scientific Reports, 2022, 12, 1317.	1.6	9
96	Identification of yeast cell cycle regulated genes based on genomic features. BMC Systems Biology, 2013, 7, 70.	3.0	8
97	Cancer cell line specific co-factors modulate the FOXM1 cistrome. Oncotarget, 2017, 8, 76498-76515.	0.8	8
98	Transcription Factor Binding Profiles Reveal Cyclic Expression of Human Protein-coding Genes and Non-coding RNAs. PLoS Computational Biology, 2013, 9, e1003132.	1.5	7
99	Computational STAT3 activity inference reveals its roles in the pancreatic tumor microenvironment. Scientific Reports, 2019, 9, 18257.	1.6	7
100	The steroid hormone estriol (E3) regulates epigenetic programming of fetal mouse brain and reproductive tract. BMC Biology, 2022, 20, 93.	1.7	7
101	Integrative analysis of cancer genes in a functional interactome. Scientific Reports, 2016, 6, 29228.	1.6	6
102	A unified framework for integrative study of heterogeneous gene regulatory mechanisms. Nature Machine Intelligence, 2020, 2, 447-456.	8.3	6
103	MYC Activity Inference Captures Diverse Mechanisms of Aberrant MYC Pathway Activation in Human Cancers. Molecular Cancer Research, 2021, 19, 414-428.	1.5	6
104	Contextual Refinement of Regulatory Targets Reveals Effects on Breast Cancer Prognosis of the Regulome. PLoS Computational Biology, 2017, 13, e1005340.	1.5	6
105	Deep Learning Predicts EBV Status in Gastric Cancer Based on Spatial Patterns of Lymphocyte Infiltration. Cancers, 2021, 13, 6002.	1.7	6
106	Systematic analysis of hematopoietic gene expression profiles for prognostic prediction in acute myeloid leukemia. Scientific Reports, 2015, 5, 16987.	1.6	5
107	Molecular and epigenetic profiles of BRCA1-like hormone-receptor-positive breast tumors identified with development and application of a copy-number-based classifier. Breast Cancer Research, 2019, 21, 14.	2.2	5
108	Deep-Precognitive Diagnosis: Preventing Future Pandemics by Novel Disease Detection With Biologically-Inspired Conv-Fuzzy Network. IEEE Access, 2022, 10, 23167-23185.	2.6	5

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109	APPLICATIONS OF BIOINFORMATICS TO NON-CODING RNAS IN THE ERA OF NEXT-GENERATION SEQUENCING. , 2013, , .		4
110	Integrative Genomic Analyses Yield Cell-Cycle Regulatory Programs with Prognostic Value. Molecular Cancer Research, 2016, 14, 332-343.	1.5	4
111	Inferring condition-specific targets of human TF-TF complexes using ChIP-seq data. BMC Genomics, 2017, 18, 61.	1.2	4
112	Novel putative drugs and key initiating genes for neurodegenerative disease determined using network‐based genetic integrative analysis. Journal of Cellular Biochemistry, 2019, 120, 5459-5471.	1.2	4
113	A B‐Raf V600E gene signature for melanoma predicts prognosis and reveals sensitivity to targeted therapies. Cancer Medicine, 2022, , .	1.3	4
114	Genome-wide interaction analysis identified low-frequency variants with sex disparity in lung cancer risk. Human Molecular Genetics, 2022, 31, 2831-2843.	1.4	4
115	A framework to predict the applicability of Oncotype DX, MammaPrint, and E2F4 gene signatures for improving breast cancer prognostic prediction. Scientific Reports, 2022, 12, 2211.	1.6	4
116	iTAR: a web server for identifying target genes of transcription factors using ChIP-seq or ChIP-chip data. BMC Genomics, 2016, 17, 632.	1.2	3
117	*In silico* frameworks for systematic pre-clinical screening of potential anti-leukemia therapeutics. Expert Opinion on Drug Discovery, 2016, 11, 1213-1222.	2.5	3
118	Application of RNAi-induced gene expression profiles for prognostic prediction in breast cancer. Genome Medicine, 2016, 8, 114.	3.6	3
119	Pan-cancer systematic identification of lncRNAs associated with cancer prognosis. PeerJ, 2020, 8, e8797.	0.9	3
120	Immune infiltration difference between tumour and adjacent normal regions is prognostic for gastric cancer patients. Clinical and Translational Discovery, 2022, 2, .	0.2	3
121	Application of Machine-Learning Methods to Understand Gene Expression Regulation. Genetic and Evolutionary Computation, 2015, , 1-15.	1.0	2
122	Systematic computational identification of prognostic cytogenetic markers in neuroblastoma. BMC Medical Genomics, 2019, 12, 192.	0.7	2
123	A Transcriptionally Definable Subgroup of Triple-Negative Breast and Ovarian Cancer Samples Shows Sensitivity to HSP90 Inhibition. Clinical Cancer Research, 2020, 26, 159-170.	3.2	2
124	A network-based integration for understanding racial disparity in prostate cancer. Translational Oncology, 2022, 17, 101327.	1.7	2
125	Influence of T Cell-Mediated Immune Surveillance on Somatic Mutation Occurrences in Melanoma. Frontiers in Immunology, 2021, 12, 703821.	2.2	2
126	Genetic variants associated mRNA stability in lung. BMC Genomics, 2022, 23, 196.	1.2	2

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127	Applications of ENCODE data to systematic analyses via data integration. Current Opinion in Systems Biology, 2018, 11, 57-64.	1.3	1
128	Whole transcriptome signature for prognostic prediction (WTSPP): application of whole transcriptome signature for prognostic prediction in cancer. Laboratory Investigation, 2020, 100, 1356-1366.	1.7	1
129	Rare Variant Genetic Association Study for Transplant-Associated Thrombotic Microangiopathy (TA-TMA) Via Whole Exome Sequencing. Blood, 2021, 138, 745-745.	0.6	1
130	Computational modeling of chromatin accessibility identified important epigenomic regulators. BMC Genomics, 2022, 23, 19.	1.2	1
131	Genomics and Systems Biology. , 2018, , 725-733.		0
132	AutoEncoder-Based Computational Framework for Tumor Microenvironment Decomposition and Biomarker Identification in Metastatic Melanoma. Frontiers in Genetics, 2021, 12, 665065.	1.1	0
133	447â€¦VISTA targeting remodels the tumor microenvironment to overcome adaptive resistance. , 2020, , .		0
134	Tumor cell intrinsic and extrinsic features predictÂprognosis in estrogen receptor positive breast cancer. PLoS Computational Biology, 2022, 18, e1009495.	1.5	0