Chao Cheng

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

129 papers	5,402 citations	32 h-index	72 g-index
181 ext. papers	6,834 ext. citations	9.4 avg, IF	5.45 L-index

#	Paper	IF	Citations
129	Architecture of the human regulatory network derived from ENCODE data. *Nature*, **2012**, 489, 91-100	50.4	1104
128	Integrative analysis of the Caenorhabditis elegans genome by the modENCODE project. *Science*, **2010**, 330, 1775-87	33.3	744
127	Comparative analysis of the transcriptome across distant species. *Nature*, **2014**, 512, 445-8	50.4	207
126	Classification of human genomic regions based on experimentally determined binding sites of more than 100 transcription-related factors. *Genome Biology*, **2012**, 13, R48	18.3	194
125	Modeling gene expression using chromatin features in various cellular contexts. *Genome Biology*, **2012**, 13, R53	18.3	182
124	A deep learning framework for modeling structural features of RNA-binding protein targets. *Nucleic Acids Research*, **2016**, 44, e32	20.1	152
123	Comparative analysis of regulatory information and circuits across distant species. *Nature*, **2014**, 512, 453-6	50.4	135
122	Understanding transcriptional regulation by integrative analysis of transcription factor binding data. *Genome Research*, **2012**, 22, 1658-67	9.7	133
121	Reconstruction of enhancer-target networks in 935 samples of human primary cells, tissues and cell lines. *Nature Genetics*, **2017**, 49, 1428-1436	36.3	124
120	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, 553-68	20.1	118
119	Big data bioinformatics. *Journal of Cellular Physiology*, **2014**, 229, 1896-900	7	109
118	Immunoregulatory functions of VISTA. *Immunological Reviews*, **2017**, 276, 66-79	11.3	104
117	A statistical framework for modeling gene expression using chromatin features and application to modENCODE datasets. *Genome Biology*, **2011**, 12, R15	18.3	96
116	Analysis of clock-regulated genes in Neurospora reveals widespread posttranscriptional control of metabolic potential. *Proceedings of the National Academy of Sciences of the United States of America* , **2014**, 111, 16995-7002	11.5	94
115	The histone methyltransferase activity of MLL1 is dispensable for hematopoiesis and leukemogenesis. *Cell Reports*, **2014**, 7, 1239-47	10.6	91
114	mRNA expression profiles show differential regulatory effects of microRNAs between estrogen receptor-positive and estrogen receptor-negative breast cancer. *Genome Biology*, **2009**, 10, R90	18.3	85
113	Systematic Pan-Cancer Analysis Reveals Immune Cell Interactions in the Tumor Microenvironment. *Cancer Research*, **2017**, 77, 1271-1282	10.1	83

112	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	11.5	77
111	Association of gamma-aminobutyric acid A receptor ⍰ gene (GABRA2) with alcohol use disorder. *Neuropsychopharmacology*, **2014**, 39, 907-18	8.7	76
110	Hypoxia-Induced VISTA Promotes the Suppressive Function of Myeloid-Derived Suppressor Cells in the Tumor Microenvironment. *Cancer Immunology Research*, **2019**, 7, 1079-1090	12.5	75
109	Inferring microRNA activities by combining gene expression with microRNA target prediction. *PLoS ONE*, **2008**, 3, e1989	3.7	74
108	The relationship between the evolution of microRNA targets and the length of their UTRs. *BMC Genomics*, **2009**, 10, 431	4.5	72
107	Construction and analysis of an integrated regulatory network derived from high-throughput sequencing data. *PLoS Computational Biology*, **2011**, 7, e1002190	5	69
106	VISTA is a checkpoint regulator for na⍰e T cell quiescence and peripheral tolerance. *Science*, **2020**, 367,	33.3	63
105	Inferring activity changes of transcription factors by binding association with sorted expression profiles. *BMC Bioinformatics*, **2007**, 8, 452	3.6	60
104	Therapeutically targeting tumor microenvironment-mediated drug resistance in estrogen receptor-positive breast cancer. *Journal of Experimental Medicine*, **2018**, 215, 895-910	16.6	49
103	TIP: a probabilistic method for identifying transcription factor target genes from ChIP-seq binding profiles. *Bioinformatics*, **2011**, 27, 3221-7	7.2	45
102	VISTA expression on tumor-infiltrating inflammatory cells in primary cutaneous melanoma correlates with poor disease-specific survival. *Cancer Immunology, Immunotherapy*, **2018**, 67, 1113-1121	7.4	44
101	CD36-Mediated Metabolic Rewiring of Breast Cancer Cells Promotes Resistance to HER2-Targeted Therapies. *Cell Reports*, **2019**, 29, 3405-3420.e5	10.6	44
100	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	1.3	43
99	E2F4 regulatory program predicts patient survival prognosis in breast cancer. *Breast Cancer Research*, **2014**, 16, 486	8.3	39
98	Identification of Candidate Cyclin-dependent kinase 1 (Cdk1) Substrates in Mitosis by Quantitative Phosphoproteomics. *Molecular and Cellular Proteomics*, **2016**, 15, 2448-61	7.6	37
97	Integrative analysis of breast cancer reveals prognostic haematopoietic activity and patient-specific immune response profiles. *Nature Communications*, **2016**, 7, 10248	17.4	30
96	Adaptive immunity programmes in breast cancer. *Immunology*, **2017**, 150, 25-34	7.8	29
95	Inference of transcription modification in long-live yeast strains from their expression profiles. *BMC Genomics*, **2007**, 8, 219	4.5	29

94	UNSUPERVISED FEATURE CONSTRUCTION AND KNOWLEDGE EXTRACTION FROM GENOME-WIDE ASSAYS OF BREAST CANCER WITH DENOISING AUTOENCODERS **2014**,		27
93	Effect of estrogen receptor binding on functional DNA methylation in breast cancer. *Epigenetics*, **2014**, 9, 523-32	5.7	26
92	A P53-Deficiency Gene Signature Predicts Recurrence Risk of Patients with Early-Stage Lung Adenocarcinoma. *Cancer Epidemiology Biomarkers and Prevention*, **2018**, 27, 86-95	4	26
91	PDGF Engages an E2F-USP1 Signaling Pathway to Support ID2-Mediated Survival of Proneural Glioma Cells. *Cancer Research*, **2016**, 76, 2964-76	10.1	24
90	An approach for determining and measuring network hierarchy applied to comparing the phosphorylome and the regulome. *Genome Biology*, **2015**, 16, 63	18.3	21
89	Computational immune profiling in lung adenocarcinoma reveals reproducible prognostic associations with implications for immunotherapy. *OncoImmunology*, **2018**, 7, e1431084	7.2	20
88	A Leukocyte Infiltration Score Defined by a Gene Signature Predicts Melanoma Patient Prognosis. *Molecular Cancer Research*, **2019**, 17, 109-119	6.6	20
87	MYC Mediates mRNA Cap Methylation of Canonical Wnt/Catenin Signaling Transcripts By Recruiting CDK7 and RNA Methyltransferase. *Molecular Cancer Research*, **2017**, 15, 213-224	6.6	19
86	Systematic identification of cell cycle regulated transcription factors from microarray time series data. *BMC Genomics*, **2008**, 9, 116	4.5	19
85	Genomic Characterization of Six Virus-Associated Cancers Identifies Changes in the Tumor Immune Microenvironment and Altered Genetic Programs. *Cancer Research*, **2018**, 78, 6413-6423	10.1	19
84	Significant and systematic expression differentiation in long-lived yeast strains. *PLoS ONE*, **2007**, 2, e1095	3.7	18
83	REACTIN: regulatory activity inference of transcription factors underlying human diseases with application to breast cancer. *BMC Genomics*, **2013**, 14, 504	4.5	17
82	Resident and circulating memory T cells persist for years in melanoma patients with durable responses to immunotherapy. *Nature Cancer*, **2021**, 2, 300-311	15.4	17
81	Genome-wide analysis of chromatin features identifies histone modification sensitive and insensitive yeast transcription factors. *Genome Biology*, **2011**, 12, R111	18.3	16
80	An intestinal microRNA modulates the homeostatic adaptation to chronic oxidative stress in. *Aging*, **2016**, 8, 1979-2005	5.6	16
79	Integrative analysis of survival-associated gene sets in breast cancer. *BMC Medical Genomics*, **2015**, 8, 11	3.7	15
78	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	7.2	15
77	Single-cell RNA sequencing reveals the impact of chromosomal instability on glioblastoma cancer stem cells. *BMC Medical Genomics*, **2019**, 12, 79	3.7	13

76	The E2F4 prognostic signature predicts pathological response to neoadjuvant chemotherapy in breast cancer patients. *BMC Cancer*, **2017**, 17, 306	4.8	13
75	Sub-array normalization subject to differentiation. *Nucleic Acids Research*, **2005**, 33, 5565-73	20.1	12
74	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	6	12
73	Multifactorial Deep Learning Reveals Pan-Cancer Genomic Tumor Clusters with Distinct Immunogenomic Landscape and Response to Immunotherapy. *Clinical Cancer Research*, **2020**, 26, 2908-2920	12.9	12
72	Cross-Disciplinary Network Comparison: Matchmaking Between Hairballs. *Cell Systems*, **2016**, 2, 147-157	10.6	12
71	Statins associate with improved mortality among patients with certain histological subtypes of lung cancer. *Lung Cancer*, **2018**, 126, 89-96	5.9	12
70	Identification of gene expression levels in primary melanoma associated with clinically meaningful characteristics. *Melanoma Research*, **2018**, 28, 380-389	3.3	12
69	9p21 loss confers a cold tumor immune microenvironment and primary resistance to immune checkpoint therapy. *Nature Communications*, **2021**, 12, 5606	17.4	12
68	A gene expression-based immune signature for lung adenocarcinoma prognosis. *Cancer Immunology, Immunotherapy*, **2020**, 69, 1881-1890	7.4	11
67	VISTA Re-programs Macrophage Biology Through the Combined Regulation of Tolerance and Anti-inflammatory Pathways. *Frontiers in Immunology*, **2020**, 11, 580187	8.4	11
66	Systematic identification of transcription factors associated with patient survival in cancers. *BMC Genomics*, **2009**, 10, 225	4.5	10
65	Cytokine sensitivity screening highlights BMP4 pathway signaling as a therapeutic opportunity in ER breast cancer. *FASEB Journal*, **2019**, 33, 1644-1657	0.9	10
64	E2F4 Program Is Predictive of Progression and Intravesical Immunotherapy Efficacy in Bladder Cancer. *Molecular Cancer Research*, **2015**, 13, 1316-24	6.6	9
63	Relating gene expression evolution with CpG content changes. *BMC Genomics*, **2014**, 15, 693	4.5	9
62	Gene signature-based prediction of triple-negative breast cancer patient response to Neoadjuvant chemotherapy. *Cancer Medicine*, **2020**, 9, 6281-6295	4.8	9
61	Complex Patterns of Association between Pleiotropy and Transcription Factor Evolution. *Genome Biology and Evolution*, **2016**, 8, 3159-3170	3.9	9
60	Regulators associated with clinical outcomes revealed by DNA methylation data in breast cancer. *PLoS Computational Biology*, **2015**, 11, e1004269	5	8
59	MARD: a new method to detect differential gene expression in treatment-control time courses. *Bioinformatics*, **2006**, 22, 2650-7	7.2	8

58	Predictors of disease aggressiveness influence outcome from immunotherapy treatment in renal clear cell carcinoma. *OncoImmunology*, **2019**, 8, e1500106	7.2	8
57	Computational Investigation of Homologous Recombination DNA Repair Deficiency in Sporadic Breast Cancer. *Scientific Reports*, **2017**, 7, 15742	4.9	7
56	Gene signatures associated with genomic aberrations predict prognosis in neuroblastoma. *Cancer Communications*, **2020**, 40, 105-118	9.4	7
55	Performance and efficiency of machine learning algorithms for analyzing rectangular biomedical data. *Laboratory Investigation*, **2021**, 101, 430-441	5.9	7
54	Integrative analysis of cancer genes in a functional interactome. *Scientific Reports*, **2016**, 6, 29228	4.9	6
53	Transcription factor binding profiles reveal cyclic expression of human protein-coding genes and non-coding RNAs. *PLoS Computational Biology*, **2013**, 9, e1003132	5	6
52	Cancer cell line specific co-factors modulate the FOXM1 cistrome. *Oncotarget*, **2017**, 8, 76498-76515	3.3	6
51	Pan-cancer association of HLA gene expression with cancer prognosis and immunotherapy efficacy. *British Journal of Cancer*, **2021**, 125, 422-432	8.7	6
50	Computational STAT3 activity inference reveals its roles in the pancreatic tumor microenvironment. *Scientific Reports*, **2019**, 9, 18257	4.9	6
49	VISTA: A Target to Manage the Innate Cytokine Storm. *Frontiers in Immunology*, **2020**, 11, 595950	8.4	6
48	Identification of yeast cell cycle regulated genes based on genomic features. *BMC Systems Biology*, **2013**, 7, 70	3.5	5
47	Systematic analysis of hematopoietic gene expression profiles for prognostic prediction in acute myeloid leukemia. *Scientific Reports*, **2015**, 5, 16987	4.9	5
46	Contextual Refinement of Regulatory Targets Reveals Effects on Breast Cancer Prognosis of the Regulome. *PLoS Computational Biology*, **2017**, 13, e1005340	5	5
45	Impact of Oncotype DX testing on ER+ breast cancer treatment and survival in the first decade of use. *Breast Cancer Research*, **2021**, 23, 74	8.3	5
44	Resident memory CD8 T cells in regional lymph nodes mediate immunity to metastatic melanoma. *Immunity*, **2021**, 54, 2117-2132.e7	32.3	5
43	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	9.7	4
42	Integrative Genomic Analyses Yield Cell-Cycle Regulatory Programs with Prognostic Value. *Molecular Cancer Research*, **2016**, 14, 332-43	6.6	4
41	SARS-CoV-2 Impairs Dendritic Cells and Regulates DC-SIGN Gene Expression in Tissues. *International Journal of Molecular Sciences*, **2021**, 22,	6.3	4

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40	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	8.3	3
39	A TMPRSS2-ERG gene signature predicts prognosis of patients with prostate adenocarcinoma. *Clinical and Translational Medicine*, **2020**, 10, e216	5.7	3
38	An EGFR signature predicts cell line and patient sensitivity to multiple tyrosine kinase inhibitors. *International Journal of Cancer*, **2020**, 147, 2621-2633	7.5	3
37	Pan-cancer systematic identification of lncRNAs associated with cancer prognosis. *PeerJ*, **2020**, 8, e8797	3.1	3
36	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	4.7	3
35	Application of RNAi-induced gene expression profiles for prognostic prediction in breast cancer. *Genome Medicine*, **2016**, 8, 114	14.4	2
34	Application of Machine-Learning Methods to Understand Gene Expression Regulation. *Genetic and Evolutionary Computation*, **2015**, 1-15	0.8	2
33	MYC Activity Inference Captures Diverse Mechanisms of Aberrant MYC Pathway Activation in Human Cancers. *Molecular Cancer Research*, **2021**, 19, 414-428	6.6	2
32	iTAR: a web server for identifying target genes of transcription factors using ChIP-seq or ChIP-chip data. *BMC Genomics*, **2016**, 17, 632	4.5	2
31	In silico frameworks for systematic pre-clinical screening of potential anti-leukemia therapeutics. *Expert Opinion on Drug Discovery*, **2016**, 11, 1213-1222	6.2	2
30	Tumor immune infiltration estimated from gene expression profiles predicts colorectal cancer relapse. *OncoImmunology*, **2021**, 10, 1862529	7.2	2
29	Multimetric feature selection for analyzing multicategory outcomes of colorectal cancer: random forest and multinomial logistic regression models. *Laboratory Investigation*, **2021**,	5.9	2
28	Deep-Precognitive Diagnosis: Preventing Future Pandemics by Novel Disease Detection With Biologically-Inspired Conv-Fuzzy Network.. *IEEE Access*, **2022**, 10, 23167-23185	3.5	2
27	Abnormal global alternative RNA splicing in COVID-19 patients.. *PLoS Genetics*, **2022**, 18, e1010137	6	2
26	Whole transcriptome signature for prognostic prediction (WTSPP): application of whole transcriptome signature for prognostic prediction in cancer. *Laboratory Investigation*, **2020**, 100, 1356-1366	5.9	1
25	Inferring condition-specific targets of human TF-TF complexes using ChIP-seq data. *BMC Genomics*, **2017**, 18, 61	4.5	1
24	A B-Raf V600E gene signature for melanoma predicts prognosis and reveals sensitivity to targeted therapies.. *Cancer Medicine*, **2022**,	4.8	1
23	Genome-wide interaction analysis identified low-frequency variants with sex disparity in lung cancer risk.. *Human Molecular Genetics*, **2022**,	5.6	1

22	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	17.4	1
21	A unified framework for integrative study of heterogeneous gene regulatory mechanisms. *Nature Machine Intelligence*, **2020**, 2, 447-456	22.5	1
20	Systematic computational identification of prognostic cytogenetic markers in neuroblastoma. *BMC Medical Genomics*, **2019**, 12, 192	3.7	1
19	A Transcriptionally Definable Subgroup of Triple-Negative Breast and Ovarian Cancer Samples Shows Sensitivity to HSP90 Inhibition. *Clinical Cancer Research*, **2020**, 26, 159-170	12.9	1
18	B cell infiltration is highly associated with prognosis and an immune-infiltrated tumor microenvironment in neuroblastoma. *Journal of Cancer Metastasis and Treatment*, **2021**, 7,	3.8	1
17	Applications of ENCODE data to Systematic Analyses via Data Integration. *Current Opinion in Systems Biology*, **2018**, 11, 57-64	3.2	1
16	The histologic phenotype of lung cancers is associated with transcriptomic features rather than genomic characteristics. *Nature Communications*, **2021**, 12, 7081	17.4	1
15	The steroid hormone estriol (E) regulates epigenetic programming of fetal mouse brain and reproductive tract.. *BMC Biology*, **2022**, 20, 93	7.3	1
14	Predicting clinical outcomes of cancer patients with a p53 deficiency gene signature.. *Scientific Reports*, **2022**, 12, 1317	4.9	0
13	Influence of T Cell-Mediated Immune Surveillance on Somatic Mutation Occurrences in Melanoma.. *Frontiers in Immunology*, **2021**, 12, 703821	8.4	0
12	Rare Variant Genetic Association Study for Transplant-Associated Thrombotic Microangiopathy (TA-TMA) Via Whole Exome Sequencing. *Blood*, **2021**, 138, 745-745	2.2	0
11	Computational modeling of chromatin accessibility identified important epigenomic regulators.. *BMC Genomics*, **2022**, 23, 19	4.5	0
10	A lepidic gene signature predicts patient prognosis and sensitivity to immunotherapy in lung adenocarcinoma.. *Genome Medicine*, **2022**, 14, 5	14.4	0
9	Chr20q Amplification Defines a Distinct Molecular Subtype of Microsatellite Stable Colorectal Cancer. *Cancer Research*, **2021**, 81, 1977-1987	10.1	0
8	Rare deleterious germline variants and risk of lung cancer. *Npj Precision Oncology*, **2021**, 5, 12	9.8	0
7	Integrative Analysis Identifies Transcription FactorDNA Methylation Relationships and Introduces New Avenues for Translating Cancer Epigenetics into the Clinic **2015**, 211-228		
6	Genomics and Systems Biology **2018**, 725-733		
5	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	4.9	

LIST OF PUBLICATIONS

4	A network-based integration for understanding racial disparity in prostate cancer.. *Translational Oncology*, **2022**, 17, 101327	4.9
3	AutoEncoder-Based Computational Framework for Tumor Microenvironment Decomposition and Biomarker Identification in Metastatic Melanoma. *Frontiers in Genetics*, **2021**, 12, 665065	4.5
2	Genetic variants associated mRNA stability in lung.. *BMC Genomics*, **2022**, 23, 196	4.5
1	Tumor cell intrinsic and extrinsic features predict prognosis in estrogen receptor positive breast cancer.. *PLoS Computational Biology*, **2022**, 18, e1009495	5