

# Chao Cheng

## List of Publications by Year in Descending Order

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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	Predicting clinical outcomes of cancer patients with a p53 deficiency gene signature.. <i>Scientific Reports</i> , <b>2022</b> , 12, 1317	4.9	0
128	A B-Raf V600E gene signature for melanoma predicts prognosis and reveals sensitivity to targeted therapies.. <i>Cancer Medicine</i> , <b>2022</b> ,	4.8	1
127	Genome-wide interaction analysis identified low-frequency variants with sex disparity in lung cancer risk.. <i>Human Molecular Genetics</i> , <b>2022</b> ,	5.6	1
126	A framework to predict the applicability of Oncotype DX, MammaPrint, and E2F4 gene signatures for improving breast cancer prognostic prediction.. <i>Scientific Reports</i> , <b>2022</b> , 12, 2211	4.9	
125	Computational modeling of chromatin accessibility identified important epigenomic regulators.. <i>BMC Genomics</i> , <b>2022</b> , 23, 19	4.5	0
124	A lepidic gene signature predicts patient prognosis and sensitivity to immunotherapy in lung adenocarcinoma.. <i>Genome Medicine</i> , <b>2022</b> , 14, 5	14.4	0
123	A network-based integration for understanding racial disparity in prostate cancer.. <i>Translational Oncology</i> , <b>2022</b> , 17, 101327	4.9	
122	Deep-Precognitive Diagnosis: Preventing Future Pandemics by Novel Disease Detection With Biologically-Inspired Conv-Fuzzy Network.. <i>IEEE Access</i> , <b>2022</b> , 10, 23167-23185	3.5	2
121	Genetic variants associated mRNA stability in lung.. <i>BMC Genomics</i> , <b>2022</b> , 23, 196	4.5	
120	Tumor cell intrinsic and extrinsic features predict prognosis in estrogen receptor positive breast cancer.. <i>PLoS Computational Biology</i> , <b>2022</b> , 18, e1009495	5	
119	Abnormal global alternative RNA splicing in COVID-19 patients.. <i>PLoS Genetics</i> , <b>2022</b> , 18, e1010137	6	2
118	The steroid hormone estriol (E) regulates epigenetic programming of fetal mouse brain and reproductive tract.. <i>BMC Biology</i> , <b>2022</b> , 20, 93	7.3	1
117	Influence of T Cell-Mediated Immune Surveillance on Somatic Mutation Occurrences in Melanoma.. <i>Frontiers in Immunology</i> , <b>2021</b> , 12, 703821	8.4	0
116	MYC Activity Inference Captures Diverse Mechanisms of Aberrant MYC Pathway Activation in Human Cancers. <i>Molecular Cancer Research</i> , <b>2021</b> , 19, 414-428	6.6	2
115	Rare Variant Genetic Association Study for Transplant-Associated Thrombotic Microangiopathy (TA-TMA) Via Whole Exome Sequencing. <i>Blood</i> , <b>2021</b> , 138, 745-745	2.2	0
114	Cold and heterogeneous T cell repertoire is associated with copy number aberrations and loss of immune genes in small-cell lung cancer. <i>Nature Communications</i> , <b>2021</b> , 12, 6655	17.4	1
113	Resident and circulating memory T cells persist for years in melanoma patients with durable responses to immunotherapy. <i>Nature Cancer</i> , <b>2021</b> , 2, 300-311	15.4	17

112	AutoEncoder-Based Computational Framework for Tumor Microenvironment Decomposition and Biomarker Identification in Metastatic Melanoma. <i>Frontiers in Genetics</i> , <b>2021</b> , 12, 665065	4.5	
111	Pan-cancer association of HLA gene expression with cancer prognosis and immunotherapy efficacy. <i>British Journal of Cancer</i> , <b>2021</b> , 125, 422-432	8.7	6
110	B cell infiltration is highly associated with prognosis and an immune-infiltrated tumor microenvironment in neuroblastoma. <i>Journal of Cancer Metastasis and Treatment</i> , <b>2021</b> , 7,	3.8	1
109	Tumor immune infiltration estimated from gene expression profiles predicts colorectal cancer relapse. <i>Oncotmunology</i> , <b>2021</b> , 10, 1862529	7.2	2
108	Chr20q Amplification Defines a Distinct Molecular Subtype of Microsatellite Stable Colorectal Cancer. <i>Cancer Research</i> , <b>2021</b> , 81, 1977-1987	10.1	0
107	Performance and efficiency of machine learning algorithms for analyzing rectangular biomedical data. <i>Laboratory Investigation</i> , <b>2021</b> , 101, 430-441	5.9	7
106	Rare deleterious germline variants and risk of lung cancer. <i>Npj Precision Oncology</i> , <b>2021</b> , 5, 12	9.8	0
105	Impact of Oncotype DX testing on ER+ breast cancer treatment and survival in the first decade of use. <i>Breast Cancer Research</i> , <b>2021</b> , 23, 74	8.3	5
104	SARS-CoV-2 Impairs Dendritic Cells and Regulates DC-SIGN Gene Expression in Tissues. <i>International Journal of Molecular Sciences</i> , <b>2021</b> , 22,	6.3	4
103	Multimetric feature selection for analyzing multicategory outcomes of colorectal cancer: random forest and multinomial logistic regression models. <i>Laboratory Investigation</i> , <b>2021</b> ,	5.9	2
102	Resident memory CD8 T cells in regional lymph nodes mediate immunity to metastatic melanoma. <i>Immunity</i> , <b>2021</b> , 54, 2117-2132.e7	32.3	5
101	9p21 loss confers a cold tumor immune microenvironment and primary resistance to immune checkpoint therapy. <i>Nature Communications</i> , <b>2021</b> , 12, 5606	17.4	12
100	The histologic phenotype of lung cancers is associated with transcriptomic features rather than genomic characteristics. <i>Nature Communications</i> , <b>2021</b> , 12, 7081	17.4	1
99	A TMPRSS2-ERG gene signature predicts prognosis of patients with prostate adenocarcinoma. <i>Clinical and Translational Medicine</i> , <b>2020</b> , 10, e216	5.7	3
98	A gene expression-based immune signature for lung adenocarcinoma prognosis. <i>Cancer Immunology, Immunotherapy</i> , <b>2020</b> , 69, 1881-1890	7.4	11
97	An EGFR signature predicts cell line and patient sensitivity to multiple tyrosine kinase inhibitors. <i>International Journal of Cancer</i> , <b>2020</b> , 147, 2621-2633	7.5	3
96	Coexpression enrichment analysis at the single-cell level reveals convergent defects in neural progenitor cells and their cell-type transitions in neurodevelopmental disorders. <i>Genome Research</i> , <b>2020</b> , 30, 835-848	9.7	4
95	Whole transcriptome signature for prognostic prediction (WTSP): application of whole transcriptome signature for prognostic prediction in cancer. <i>Laboratory Investigation</i> , <b>2020</b> , 100, 1356-1366	5.9	1

94	VISTA is a checkpoint regulator for naïve T cell quiescence and peripheral tolerance. <i>Science</i> , <b>2020</b> , 367,	33.3	63
93	Pan-cancer systematic identification of lncRNAs associated with cancer prognosis. <i>PeerJ</i> , <b>2020</b> , 8, e8797	3.1	3
92	Multifactorial Deep Learning Reveals Pan-Cancer Genomic Tumor Clusters with Distinct Immunogenomic Landscape and Response to Immunotherapy. <i>Clinical Cancer Research</i> , <b>2020</b> , 26, 2908-2920	12.8	12
91	Transcriptional and proteomic insights into the host response in fatal COVID-19 cases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2020</b> , 117, 28336-28343	11.5	77
90	Gene signature-based prediction of triple-negative breast cancer patient response to Neoadjuvant chemotherapy. <i>Cancer Medicine</i> , <b>2020</b> , 9, 6281-6295	4.8	9
89	A unified framework for integrative study of heterogeneous gene regulatory mechanisms. <i>Nature Machine Intelligence</i> , <b>2020</b> , 2, 447-456	22.5	1
88	VISTA Re-programs Macrophage Biology Through the Combined Regulation of Tolerance and Anti-inflammatory Pathways. <i>Frontiers in Immunology</i> , <b>2020</b> , 11, 580187	8.4	11
87	Gene signatures associated with genomic aberrations predict prognosis in neuroblastoma. <i>Cancer Communications</i> , <b>2020</b> , 40, 105-118	9.4	7
86	A Transcriptionally Definable Subgroup of Triple-Negative Breast and Ovarian Cancer Samples Shows Sensitivity to HSP90 Inhibition. <i>Clinical Cancer Research</i> , <b>2020</b> , 26, 159-170	12.9	1
85	VISTA: A Target to Manage the Innate Cytokine Storm. <i>Frontiers in Immunology</i> , <b>2020</b> , 11, 595950	8.4	6
84	Molecular and epigenetic profiles of BRCA1-like hormone-receptor-positive breast tumors identified with development and application of a copy-number-based classifier. <i>Breast Cancer Research</i> , <b>2019</b> , 21, 14	8.3	3
83	Single-cell RNA sequencing reveals the impact of chromosomal instability on glioblastoma cancer stem cells. <i>BMC Medical Genomics</i> , <b>2019</b> , 12, 79	3.7	13
82	Hypoxia-Induced VISTA Promotes the Suppressive Function of Myeloid-Derived Suppressor Cells in the Tumor Microenvironment. <i>Cancer Immunology Research</i> , <b>2019</b> , 7, 1079-1090	12.5	75
81	Computational STAT3 activity inference reveals its roles in the pancreatic tumor microenvironment. <i>Scientific Reports</i> , <b>2019</b> , 9, 18257	4.9	6
80	Systematic computational identification of prognostic cytogenetic markers in neuroblastoma. <i>BMC Medical Genomics</i> , <b>2019</b> , 12, 192	3.7	1
79	CD36-Mediated Metabolic Rewiring of Breast Cancer Cells Promotes Resistance to HER2-Targeted Therapies. <i>Cell Reports</i> , <b>2019</b> , 29, 3405-3420.e5	10.6	44
78	Cytokine sensitivity screening highlights BMP4 pathway signaling as a therapeutic opportunity in ER breast cancer. <i>FASEB Journal</i> , <b>2019</b> , 33, 1644-1657	0.9	10
77	A Leukocyte Infiltration Score Defined by a Gene Signature Predicts Melanoma Patient Prognosis. <i>Molecular Cancer Research</i> , <b>2019</b> , 17, 109-119	6.6	20

76	Predictors of disease aggressiveness influence outcome from immunotherapy treatment in renal clear cell carcinoma. <i>OncolImmunology</i> , <b>2019</b> , 8, e1500106	7.2	8
75	Novel putative drugs and key initiating genes for neurodegenerative disease determined using network-based genetic integrative analysis. <i>Journal of Cellular Biochemistry</i> , <b>2019</b> , 120, 5459-5471	4.7	3
74	A B cell-derived gene expression signature associates with an immunologically active tumor microenvironment and response to immune checkpoint blockade therapy. <i>OncolImmunology</i> , <b>2019</b> , 8, e1513440	7.2	15
73	Therapeutically targeting tumor microenvironment-mediated drug resistance in estrogen receptor-positive breast cancer. <i>Journal of Experimental Medicine</i> , <b>2018</b> , 215, 895-910	16.6	49
72	Computational immune profiling in lung adenocarcinoma reveals reproducible prognostic associations with implications for immunotherapy. <i>OncolImmunology</i> , <b>2018</b> , 7, e1431084	7.2	20
71	Genomics and Systems Biology <b>2018</b> , 725-733		
70	VISTA expression on tumor-infiltrating inflammatory cells in primary cutaneous melanoma correlates with poor disease-specific survival. <i>Cancer Immunology, Immunotherapy</i> , <b>2018</b> , 67, 1113-1121	7.4	44
69	A P53-Deficiency Gene Signature Predicts Recurrence Risk of Patients with Early-Stage Lung Adenocarcinoma. <i>Cancer Epidemiology Biomarkers and Prevention</i> , <b>2018</b> , 27, 86-95	4	26
68	Statins associate with improved mortality among patients with certain histological subtypes of lung cancer. <i>Lung Cancer</i> , <b>2018</b> , 126, 89-96	5.9	12
67	Genomic Characterization of Six Virus-Associated Cancers Identifies Changes in the Tumor Immune Microenvironment and Altered Genetic Programs. <i>Cancer Research</i> , <b>2018</b> , 78, 6413-6423	10.1	19
66	Identification of gene expression levels in primary melanoma associated with clinically meaningful characteristics. <i>Melanoma Research</i> , <b>2018</b> , 28, 380-389	3.3	12
65	Applications of ENCODE data to Systematic Analyses via Data Integration. <i>Current Opinion in Systems Biology</i> , <b>2018</b> , 11, 57-64	3.2	1
64	Systematic Pan-Cancer Analysis Reveals Immune Cell Interactions in the Tumor Microenvironment. <i>Cancer Research</i> , <b>2017</b> , 77, 1271-1282	10.1	83
63	Immunoregulatory functions of VISTA. <i>Immunological Reviews</i> , <b>2017</b> , 276, 66-79	11.3	104
62	MYC Mediates mRNA Cap Methylation of Canonical Wnt/ $\beta$ Catenin Signaling Transcripts By Recruiting CDK7 and RNA Methyltransferase. <i>Molecular Cancer Research</i> , <b>2017</b> , 15, 213-224	6.6	19
61	Computational Investigation of Homologous Recombination DNA Repair Deficiency in Sporadic Breast Cancer. <i>Scientific Reports</i> , <b>2017</b> , 7, 15742	4.9	7
60	Inferring condition-specific targets of human TF-TF complexes using ChIP-seq data. <i>BMC Genomics</i> , <b>2017</b> , 18, 61	4.5	1
59	The E2F4 prognostic signature predicts pathological response to neoadjuvant chemotherapy in breast cancer patients. <i>BMC Cancer</i> , <b>2017</b> , 17, 306	4.8	13

58	Adaptive immunity programmes in breast cancer. <i>Immunology</i> , <b>2017</b> , 150, 25-34	7.8	29
57	Contextual Refinement of Regulatory Targets Reveals Effects on Breast Cancer Prognosis of the Regulome. <i>PLoS Computational Biology</i> , <b>2017</b> , 13, e1005340	5	5
56	Intestinal stem cell overproliferation resulting from inactivation of the APC tumor suppressor requires the transcription cofactors Earthbound and Erect wing. <i>PLoS Genetics</i> , <b>2017</b> , 13, e1006870	6	12
55	Cancer cell line specific co-factors modulate the FOXM1 cistrome. <i>Oncotarget</i> , <b>2017</b> , 8, 76498-76515	3.3	6
54	Reconstruction of enhancer-target networks in 935 samples of human primary cells, tissues and cell lines. <i>Nature Genetics</i> , <b>2017</b> , 49, 1428-1436	36.3	124
53	A deep learning framework for modeling structural features of RNA-binding protein targets. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, e32	20.1	152
52	Application of RNAi-induced gene expression profiles for prognostic prediction in breast cancer. <i>Genome Medicine</i> , <b>2016</b> , 8, 114	14.4	2
51	Integrative analysis of cancer genes in a functional interactome. <i>Scientific Reports</i> , <b>2016</b> , 6, 29228	4.9	6
50	Identification of Candidate Cyclin-dependent kinase 1 (Cdk1) Substrates in Mitosis by Quantitative Phosphoproteomics. <i>Molecular and Cellular Proteomics</i> , <b>2016</b> , 15, 2448-61	7.6	37
49	Integrative Genomic Analyses Yield Cell-Cycle Regulatory Programs with Prognostic Value. <i>Molecular Cancer Research</i> , <b>2016</b> , 14, 332-43	6.6	4
48	PDGF Engages an E2F-USP1 Signaling Pathway to Support ID2-Mediated Survival of Proneural Glioma Cells. <i>Cancer Research</i> , <b>2016</b> , 76, 2964-76	10.1	24
47	Integrative analysis of breast cancer reveals prognostic haematopoietic activity and patient-specific immune response profiles. <i>Nature Communications</i> , <b>2016</b> , 7, 10248	17.4	30
46	An intestinal microRNA modulates the homeostatic adaptation to chronic oxidative stress in. <i>Aging</i> , <b>2016</b> , 8, 1979-2005	5.6	16
45	iTAR: a web server for identifying target genes of transcription factors using CHIP-seq or CHIP-chip data. <i>BMC Genomics</i> , <b>2016</b> , 17, 632	4.5	2
44	Cross-Disciplinary Network Comparison: Matchmaking Between Hairballs. <i>Cell Systems</i> , <b>2016</b> , 2, 147-157	10.6	12
43	In silico frameworks for systematic pre-clinical screening of potential anti-leukemia therapeutics. <i>Expert Opinion on Drug Discovery</i> , <b>2016</b> , 11, 1213-1222	6.2	2
42	Complex Patterns of Association between Pleiotropy and Transcription Factor Evolution. <i>Genome Biology and Evolution</i> , <b>2016</b> , 8, 3159-3170	3.9	9
41	Integrative Analysis Identifies Transcription Factor-DNA Methylation Relationships and Introduces New Avenues for Translating Cancer Epigenetics into the Clinic <b>2015</b> , 211-228		

40	Regulators associated with clinical outcomes revealed by DNA methylation data in breast cancer. <i>PLoS Computational Biology</i> , <b>2015</b> , 11, e1004269	5	8
39	Integrative analysis of survival-associated gene sets in breast cancer. <i>BMC Medical Genomics</i> , <b>2015</b> , 8, 11	3.7	15
38	An approach for determining and measuring network hierarchy applied to comparing the phosphorylome and the regulome. <i>Genome Biology</i> , <b>2015</b> , 16, 63	18.3	21
37	E2F4 Program Is Predictive of Progression and Intravesical Immunotherapy Efficacy in Bladder Cancer. <i>Molecular Cancer Research</i> , <b>2015</b> , 13, 1316-24	6.6	9
36	Systematic analysis of hematopoietic gene expression profiles for prognostic prediction in acute myeloid leukemia. <i>Scientific Reports</i> , <b>2015</b> , 5, 16987	4.9	5
35	Application of Machine-Learning Methods to Understand Gene Expression Regulation. <i>Genetic and Evolutionary Computation</i> , <b>2015</b> , 1-15	0.8	2
34	Unsupervised feature construction and knowledge extraction from genome-wide assays of breast cancer with denoising autoencoders. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , <b>2015</b> , 132-43	1.3	43
33	The histone methyltransferase activity of MLL1 is dispensable for hematopoiesis and leukemogenesis. <i>Cell Reports</i> , <b>2014</b> , 7, 1239-47	10.6	91
32	Analysis of clock-regulated genes in <i>Neurospora</i> reveals widespread posttranscriptional control of metabolic potential. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, 16995-7002	11.5	94
31	Comparative analysis of the transcriptome across distant species. <i>Nature</i> , <b>2014</b> , 512, 445-8	50.4	207
30	Comparative analysis of regulatory information and circuits across distant species. <i>Nature</i> , <b>2014</b> , 512, 453-6	50.4	135
29	Relating gene expression evolution with CpG content changes. <i>BMC Genomics</i> , <b>2014</b> , 15, 693	4.5	9
28	Association of gamma-aminobutyric acid A receptor $\alpha$ gene (GABRA2) with alcohol use disorder. <i>Neuropsychopharmacology</i> , <b>2014</b> , 39, 907-18	8.7	76
27	Big data bioinformatics. <i>Journal of Cellular Physiology</i> , <b>2014</b> , 229, 1896-900	7	109
26	UNSUPERVISED FEATURE CONSTRUCTION AND KNOWLEDGE EXTRACTION FROM GENOME-WIDE ASSAYS OF BREAST CANCER WITH DENOISING AUTOENCODERS <b>2014</b> ,		27
25	Effect of estrogen receptor binding on functional DNA methylation in breast cancer. <i>Epigenetics</i> , <b>2014</b> , 9, 523-32	5.7	26
24	E2F4 regulatory program predicts patient survival prognosis in breast cancer. <i>Breast Cancer Research</i> , <b>2014</b> , 16, 486	8.3	39
23	Identification of yeast cell cycle regulated genes based on genomic features. <i>BMC Systems Biology</i> , <b>2013</b> , 7, 70	3.5	5



22	REACTIN: regulatory activity inference of transcription factors underlying human diseases with application to breast cancer. <i>BMC Genomics</i> , <b>2013</b> , 14, 504	4.5	17
21	Transcription factor binding profiles reveal cyclic expression of human protein-coding genes and non-coding RNAs. <i>PLoS Computational Biology</i> , <b>2013</b> , 9, e1003132	5	6
20	Classification of human genomic regions based on experimentally determined binding sites of more than 100 transcription-related factors. <i>Genome Biology</i> , <b>2012</b> , 13, R48	18.3	194
19	Modeling gene expression using chromatin features in various cellular contexts. <i>Genome Biology</i> , <b>2012</b> , 13, R53	18.3	182
18	Architecture of the human regulatory network derived from ENCODE data. <i>Nature</i> , <b>2012</b> , 489, 91-100	50.4	1104
17	Understanding transcriptional regulation by integrative analysis of transcription factor binding data. <i>Genome Research</i> , <b>2012</b> , 22, 1658-67	9.7	133
16	Modeling the relative relationship of transcription factor binding and histone modifications to gene expression levels in mouse embryonic stem cells. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, 553-68	20.1	118
15	A statistical framework for modeling gene expression using chromatin features and application to modENCODE datasets. <i>Genome Biology</i> , <b>2011</b> , 12, R15	18.3	96
14	TIP: a probabilistic method for identifying transcription factor target genes from ChIP-seq binding profiles. <i>Bioinformatics</i> , <b>2011</b> , 27, 3221-7	7.2	45
13	Genome-wide analysis of chromatin features identifies histone modification sensitive and insensitive yeast transcription factors. <i>Genome Biology</i> , <b>2011</b> , 12, R111	18.3	16
12	Construction and analysis of an integrated regulatory network derived from high-throughput sequencing data. <i>PLoS Computational Biology</i> , <b>2011</b> , 7, e1002190	5	69
11	Integrative analysis of the <i>Caenorhabditis elegans</i> genome by the modENCODE project. <i>Science</i> , <b>2010</b> , 330, 1775-87	33.3	744
10	Systematic identification of transcription factors associated with patient survival in cancers. <i>BMC Genomics</i> , <b>2009</b> , 10, 225	4.5	10
9	The relationship between the evolution of microRNA targets and the length of their UTRs. <i>BMC Genomics</i> , <b>2009</b> , 10, 431	4.5	72
8	mRNA expression profiles show differential regulatory effects of microRNAs between estrogen receptor-positive and estrogen receptor-negative breast cancer. <i>Genome Biology</i> , <b>2009</b> , 10, R90	18.3	85
7	Systematic identification of cell cycle regulated transcription factors from microarray time series data. <i>BMC Genomics</i> , <b>2008</b> , 9, 116	4.5	19
6	Inferring microRNA activities by combining gene expression with microRNA target prediction. <i>PLoS ONE</i> , <b>2008</b> , 3, e1989	3.7	74
5	Significant and systematic expression differentiation in long-lived yeast strains. <i>PLoS ONE</i> , <b>2007</b> , 2, e1095.7		18



4	Inferring activity changes of transcription factors by binding association with sorted expression profiles. <i>BMC Bioinformatics</i> , <b>2007</b> , 8, 452	3.6	60
3	Inference of transcription modification in long-live yeast strains from their expression profiles. <i>BMC Genomics</i> , <b>2007</b> , 8, 219	4.5	29
2	MARD: a new method to detect differential gene expression in treatment-control time courses. <i>Bioinformatics</i> , <b>2006</b> , 22, 2650-7	7.2	8
1	Sub-array normalization subject to differentiation. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, 5565-73	20.1	12