

Chao Cheng

List of Publications by Year in descending order

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Version: 2024-02-01

134
papers

7,844
citations

94433

37
h-index

60623

81
g-index

181
all docs

181
docs citations

181
times ranked

14251
citing authors

#	ARTICLE	IF	CITATIONS
1	Multimetric feature selection for analyzing multicategory outcomes of colorectal cancer: random forest and multinomial logistic regression models. <i>Laboratory Investigation</i> , 2022, 102, 236-244.	3.7	9
2	Clonal Hematopoiesis Mutations in Patients with Lung Cancer Are Associated with Lung Cancer Risk Factors. <i>Cancer Research</i> , 2022, 82, 199-209.	0.9	11
3	Computational modeling of chromatin accessibility identified important epigenomic regulators. <i>BMC Genomics</i> , 2022, 23, 19.	2.8	1
4	A lepidic gene signature predicts patient prognosis and sensitivity to immunotherapy in lung adenocarcinoma. <i>Genome Medicine</i> , 2022, 14, 5.	8.2	25
5	A network-based integration for understanding racial disparity in prostate cancer. <i>Translational Oncology</i> , 2022, 17, 101327.	3.7	2
6	Predicting clinical outcomes of cancer patients with a p53 deficiency gene signature. <i>Scientific Reports</i> , 2022, 12, 1317.	3.3	9
7	A Bâ€Raf V600E gene signature for melanoma predicts prognosis and reveals sensitivity to targeted therapies. <i>Cancer Medicine</i> , 2022, , .	2.8	4
8	Genome-wide interaction analysis identified low-frequency variants with sex disparity in lung cancer risk. <i>Human Molecular Genetics</i> , 2022, 31, 2831-2843.	2.9	4
9	A framework to predict the applicability of Oncotype DX, MammaPrint, and E2F4 gene signatures for improving breast cancer prognostic prediction. <i>Scientific Reports</i> , 2022, 12, 2211.	3.3	4
10	Deep-Precognitive Diagnosis: Preventing Future Pandemics by Novel Disease Detection With Biologically-Inspired Conv-Fuzzy Network. <i>IEEE Access</i> , 2022, 10, 23167-23185.	4.2	5
11	Immune infiltration difference between tumour and adjacent normal regions is prognostic for gastric cancer patients. <i>Clinical and Translational Discovery</i> , 2022, 2, .	0.5	3
12	Genetic variants associated mRNA stability in lung. <i>BMC Genomics</i> , 2022, 23, 196.	2.8	2
13	Tumor cell intrinsic and extrinsic features predictÂprognosis in estrogen receptor positive breast cancer. <i>PLoS Computational Biology</i> , 2022, 18, e1009495.	3.2	0
14	Abnormal global alternative RNA splicing in COVID-19 patients. <i>PLoS Genetics</i> , 2022, 18, e1010137.	3.5	21
15	The steroid hormone estriol (E3) regulates epigenetic programming of fetal mouse brain and reproductive tract. <i>BMC Biology</i> , 2022, 20, 93.	3.8	7
16	B cell infiltration is highly associated with prognosis and an immune-infiltrated tumor microenvironment in neuroblastoma. , 2021, 7, .		10
17	Tumor immune infiltration estimated from gene expression profiles predicts colorectal cancer relapse. <i>Oncolmmunology</i> , 2021, 10, 1862529.	4.6	9
18	Chr20q Amplification Defines a Distinct Molecular Subtype of Microsatellite Stable Colorectal Cancer. <i>Cancer Research</i> , 2021, 81, 1977-1987.	0.9	15

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19	Performance and efficiency of machine learning algorithms for analyzing rectangular biomedical data. <i>Laboratory Investigation</i> , 2021, 101, 430-441.	3.7	21
20	Rare deleterious germline variants and risk of lung cancer. <i>Npj Precision Oncology</i> , 2021, 5, 12.	5.4	19
21	Resident and circulating memory T cells persist for years in melanoma patients with durable responses to immunotherapy. <i>Nature Cancer</i> , 2021, 2, 300-311.	13.2	70
22	AutoEncoder-Based Computational Framework for Tumor Microenvironment Decomposition and Biomarker Identification in Metastatic Melanoma. <i>Frontiers in Genetics</i> , 2021, 12, 665065.	2.3	0
23	Pan-cancer association of HLA gene expression with cancer prognosis and immunotherapy efficacy. <i>British Journal of Cancer</i> , 2021, 125, 422-432.	6.4	59
24	Impact of Oncotype DX testing on ER+ breast cancer treatment and survival in the first decade of use. <i>Breast Cancer Research</i> , 2021, 23, 74.	5.0	27
25	SARS-CoV-2 Impairs Dendritic Cells and Regulates DC-SIGN Gene Expression in Tissues. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9228.	4.1	15
26	Resident memory CD8+ T cells in regional lymph nodes mediate immunity to metastatic melanoma. <i>Immunity</i> , 2021, 54, 2117-2132.e7.	14.3	50
27	9p21 loss confers a cold tumor immune microenvironment and primary resistance to immune checkpoint therapy. <i>Nature Communications</i> , 2021, 12, 5606.	12.8	76
28	MYC Activity Inference Captures Diverse Mechanisms of Aberrant MYC Pathway Activation in Human Cancers. <i>Molecular Cancer Research</i> , 2021, 19, 414-428.	3.4	6
29	Deep Learning Predicts EBV Status in Gastric Cancer Based on Spatial Patterns of Lymphocyte Infiltration. <i>Cancers</i> , 2021, 13, 6002.	3.7	6
30	Rare Variant Genetic Association Study for Transplant-Associated Thrombotic Microangiopathy (TA-TMA) Via Whole Exome Sequencing. <i>Blood</i> , 2021, 138, 745-745.	1.4	1
31	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> , 2021, 12, 6655.	12.8	24
32	Influence of T Cell-Mediated Immune Surveillance on Somatic Mutation Occurrences in Melanoma. <i>Frontiers in Immunology</i> , 2021, 12, 703821.	4.8	2
33	Artificial intelligence, machine learning, and deep learning for clinical outcome prediction. <i>Emerging Topics in Life Sciences</i> , 2021, 5, 729-745.	2.6	26
34	The histologic phenotype of lung cancers is associated with transcriptomic features rather than genomic characteristics. <i>Nature Communications</i> , 2021, 12, 7081.	12.8	16
35	Multifactorial Deep Learning Reveals Pan-Cancer Genomic Tumor Clusters with Distinct Immunogenomic Landscape and Response to Immunotherapy. <i>Clinical Cancer Research</i> , 2020, 26, 2908-2920.	7.0	30
36	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> , 2020, 117, 28336-28343.	7.1	149

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37	Gene signature-based prediction of triple-negative breast cancer patient response to Neoadjuvant chemotherapy. <i>Cancer Medicine</i> , 2020, 9, 6281-6295.	2.8	21
38	A unified framework for integrative study of heterogeneous gene regulatory mechanisms. <i>Nature Machine Intelligence</i> , 2020, 2, 447-456.	16.0	6
39	VISTA Re-programs Macrophage Biology Through the Combined Regulation of Tolerance and Anti-inflammatory Pathways. <i>Frontiers in Immunology</i> , 2020, 11, 580187.	4.8	24
40	A TMPRSS2-ERG gene signature predicts prognosis of patients with prostate adenocarcinoma. <i>Clinical and Translational Medicine</i> , 2020, 10, e216.	4.0	11
41	A gene expression-based immune signature for lung adenocarcinoma prognosis. <i>Cancer Immunology, Immunotherapy</i> , 2020, 69, 1881-1890.	4.2	18
42	An EGFR signature predicts cell line and patient sensitivity to multiple tyrosine kinase inhibitors. <i>International Journal of Cancer</i> , 2020, 147, 2621-2633.	5.1	13
43	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> , 2020, 30, 835-848.	5.5	25
44	Whole transcriptome signature for prognostic prediction (WTSP): application of whole transcriptome signature for prognostic prediction in cancer. <i>Laboratory Investigation</i> , 2020, 100, 1356-1366.	3.7	1
45	VISTA is a checkpoint regulator for naive T cell quiescence and peripheral tolerance. <i>Science</i> , 2020, 367, .	12.6	156
46	Gene signatures associated with genomic aberrations predict prognosis in neuroblastoma. <i>Cancer Communications</i> , 2020, 40, 105-118.	9.2	13
47	A Transcriptionally Definable Subgroup of Triple-Negative Breast and Ovarian Cancer Samples Shows Sensitivity to HSP90 Inhibition. <i>Clinical Cancer Research</i> , 2020, 26, 159-170.	7.0	2
48	VISTA: A Target to Manage the Innate Cytokine Storm. <i>Frontiers in Immunology</i> , 2020, 11, 595950.	4.8	24
49	Pan-cancer systematic identification of lncRNAs associated with cancer prognosis. <i>PeerJ</i> , 2020, 8, e8797.	2.0	3
50	447-...VISTA targeting remodels the tumor microenvironment to overcome adaptive resistance. , 2020, , .		0
51	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> , 2019, 21, 14.	5.0	5
52	Single-cell RNA sequencing reveals the impact of chromosomal instability on glioblastoma cancer stem cells. <i>BMC Medical Genomics</i> , 2019, 12, 79.	1.5	30
53	Hypoxia-Induced VISTA Promotes the Suppressive Function of Myeloid-Derived Suppressor Cells in the Tumor Microenvironment. <i>Cancer Immunology Research</i> , 2019, 7, 1079-1090.	3.4	129
54	Computational STAT3 activity inference reveals its roles in the pancreatic tumor microenvironment. <i>Scientific Reports</i> , 2019, 9, 18257.	3.3	7

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55	Systematic computational identification of prognostic cytogenetic markers in neuroblastoma. <i>BMC Medical Genomics</i> , 2019, 12, 192.	1.5	2
56	CD36-Mediated Metabolic Rewiring of Breast Cancer Cells Promotes Resistance to HER2-Targeted Therapies. <i>Cell Reports</i> , 2019, 29, 3405-3420.e5.	6.4	104
57	Cytokine sensitivity screening highlights BMP4 pathway signaling as a therapeutic opportunity in ER + breast cancer. <i>FASEB Journal</i> , 2019, 33, 1644-1657.	0.5	13
58	A Leukocyte Infiltration Score Defined by a Gene Signature Predicts Melanoma Patient Prognosis. <i>Molecular Cancer Research</i> , 2019, 17, 109-119.	3.4	28
59	Predictors of disease aggressiveness influence outcome from immunotherapy treatment in renal clear cell carcinoma. <i>Oncolmmunology</i> , 2019, 8, e1500106.	4.6	18
60	Novel putative drugs and key initiating genes for neurodegenerative disease determined using network-based genetic integrative analysis. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 5459-5471.	2.6	4
61	A B cell-derived gene expression signature associates with an immunologically active tumor microenvironment and response to immune checkpoint blockade therapy. <i>Oncolmmunology</i> , 2019, 8, e1513440.	4.6	20
62	Therapeutically targeting tumor microenvironment-mediated drug resistance in estrogen receptor-positive breast cancer. <i>Journal of Experimental Medicine</i> , 2018, 215, 895-910.	8.5	63
63	Computational immune profiling in lung adenocarcinoma reveals reproducible prognostic associations with implications for immunotherapy. <i>Oncolmmunology</i> , 2018, 7, e1431084.	4.6	43
64	A P53-Deficiency Gene Signature Predicts Recurrence Risk of Patients with Early-Stage Lung Adenocarcinoma. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2018, 27, 86-95.	2.5	42
65	Statins associate with improved mortality among patients with certain histological subtypes of lung cancer. <i>Lung Cancer</i> , 2018, 126, 89-96.	2.0	22
66	Genomic Characterization of Six Virus-Associated Cancers Identifies Changes in the Tumor Immune Microenvironment and Altered Genetic Programs. <i>Cancer Research</i> , 2018, 78, 6413-6423.	0.9	33
67	Identification of gene expression levels in primary melanoma associated with clinically meaningful characteristics. <i>Melanoma Research</i> , 2018, 28, 380-389.	1.2	17
68	Applications of ENCODE data to systematic analyses via data integration. <i>Current Opinion in Systems Biology</i> , 2018, 11, 57-64.	2.6	1
69	<i>Genomics and Systems Biology</i> , 2018, , 725-733.		0
70	VISTA expression on tumor-infiltrating inflammatory cells in primary cutaneous melanoma correlates with poor disease-specific survival. <i>Cancer Immunology, Immunotherapy</i> , 2018, 67, 1113-1121.	4.2	79
71	Systematic Pan-Cancer Analysis Reveals Immune Cell Interactions in the Tumor Microenvironment. <i>Cancer Research</i> , 2017, 77, 1271-1282.	0.9	134
72	Immunoregulatory functions of VISTA. <i>Immunological Reviews</i> , 2017, 276, 66-79.	6.0	154

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73	MYC Mediates mRNA Cap Methylation of Canonical Wnt/ β 2-Catenin Signaling Transcripts By Recruiting CDK7 and RNA Methyltransferase. <i>Molecular Cancer Research</i> , 2017, 15, 213-224.	3.4	32
74	Inferring condition-specific targets of human TF-TF complexes using ChIP-seq data. <i>BMC Genomics</i> , 2017, 18, 61.	2.8	4
75	The E2F4 prognostic signature predicts pathological response to neoadjuvant chemotherapy in breast cancer patients. <i>BMC Cancer</i> , 2017, 17, 306.	2.6	15
76	Adaptive immunity programmes in breast cancer. <i>Immunology</i> , 2017, 150, 25-34.	4.4	43
77	Computational Investigation of Homologous Recombination DNA Repair Deficiency in Sporadic Breast Cancer. <i>Scientific Reports</i> , 2017, 7, 15742.	3.3	9
78	Reconstruction of enhancer target networks in 935 samples of human primary cells, tissues and cell lines. <i>Nature Genetics</i> , 2017, 49, 1428-1436.	21.4	194
79	Contextual Refinement of Regulatory Targets Reveals Effects on Breast Cancer Prognosis of the Regulome. <i>PLoS Computational Biology</i> , 2017, 13, e1005340.	3.2	6
80	Intestinal stem cell overproliferation resulting from inactivation of the APC tumor suppressor requires the transcription cofactors Earthbound and Erect wing. <i>PLoS Genetics</i> , 2017, 13, e1006870.	3.5	20
81	Cancer cell line specific co-factors modulate the FOXM1 cistrome. <i>Oncotarget</i> , 2017, 8, 76498-76515.	1.8	8
82	iTAR: a web server for identifying target genes of transcription factors using ChIP-seq or ChIP-chip data. <i>BMC Genomics</i> , 2016, 17, 632.	2.8	3
83	Cross-Disciplinary Network Comparison: Matchmaking between Hairballs. <i>Cell Systems</i> , 2016, 2, 147-157.	6.2	13
84	<i>In silico</i> frameworks for systematic pre-clinical screening of potential anti-leukemia therapeutics. <i>Expert Opinion on Drug Discovery</i> , 2016, 11, 1213-1222.	5.0	3
85	Complex Patterns of Association between Pleiotropy and Transcription Factor Evolution. <i>Genome Biology and Evolution</i> , 2016, 8, 3159-3170.	2.5	17
86	Application of RNAi-induced gene expression profiles for prognostic prediction in breast cancer. <i>Genome Medicine</i> , 2016, 8, 114.	8.2	3
87	Integrative analysis of cancer genes in a functional interactome. <i>Scientific Reports</i> , 2016, 6, 29228.	3.3	6
88	Identification of Candidate Cyclin-dependent kinase 1 (Cdk1) Substrates in Mitosis by Quantitative Phosphoproteomics. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2448-2461.	3.8	54
89	Integrative Genomic Analyses Yield Cell-Cycle Regulatory Programs with Prognostic Value. <i>Molecular Cancer Research</i> , 2016, 14, 332-343.	3.4	4
90	PDGF Engages an E2F-USP1 Signaling Pathway to Support ID2-Mediated Survival of Proneural Glioma Cells. <i>Cancer Research</i> , 2016, 76, 2964-2976.	0.9	28

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91	Integrative analysis of breast cancer reveals prognostic haematopoietic activity and patient-specific immune response profiles. <i>Nature Communications</i> , 2016, 7, 10248.	12.8	34
92	A deep learning framework for modeling structural features of RNA-binding protein targets. <i>Nucleic Acids Research</i> , 2016, 44, e32-e32.	14.5	213
93	An intestinal microRNA modulates the homeostatic adaptation to chronic oxidative stress in <i>C. elegans</i> . <i>Aging</i> , 2016, 8, 1979-2005.	3.1	29
94	Systematic analysis of hematopoietic gene expression profiles for prognostic prediction in acute myeloid leukemia. <i>Scientific Reports</i> , 2015, 5, 16987.	3.3	5
95	Application of Machine-Learning Methods to Understand Gene Expression Regulation. <i>Genetic and Evolutionary Computation</i> , 2015, , 1-15.	1.0	2
96	Regulators Associated with Clinical Outcomes Revealed by DNA Methylation Data in Breast Cancer. <i>PLoS Computational Biology</i> , 2015, 11, e1004269.	3.2	34
97	Integrative analysis of survival-associated gene sets in breast cancer. <i>BMC Medical Genomics</i> , 2015, 8, 11.	1.5	17
98	An approach for determining and measuring network hierarchy applied to comparing the phosphorylome and the regulome. <i>Genome Biology</i> , 2015, 16, 63.	8.8	27
99	E2F4 Program Is Predictive of Progression and Intravesical Immunotherapy Efficacy in Bladder Cancer. <i>Molecular Cancer Research</i> , 2015, 13, 1316-1324.	3.4	12
100	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> , 2015, , 132-43.	0.7	45
101	Effect of estrogen receptor $\hat{\pm}$ binding on functional DNA methylation in breast cancer. <i>Epigenetics</i> , 2014, 9, 523-532.	2.7	31
102	E2F4 regulatory program predicts patient survival prognosis in breast cancer. <i>Breast Cancer Research</i> , 2014, 16, 486.	5.0	46
103	The Histone Methyltransferase Activity of MLL1 Is Dispensable for Hematopoiesis and Leukemogenesis. <i>Cell Reports</i> , 2014, 7, 1239-1247.	6.4	110
104	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> , 2014, 111, 16995-17002.	7.1	131
105	Comparative analysis of the transcriptome across distant species. <i>Nature</i> , 2014, 512, 445-448.	27.8	289
106	Comparative analysis of regulatory information and circuits across distant species. <i>Nature</i> , 2014, 512, 453-456.	27.8	184
107	Relating gene expression evolution with CpG content changes. <i>BMC Genomics</i> , 2014, 15, 693.	2.8	17
108	Association of Gamma-Aminobutyric Acid A Receptor $\hat{\pm}2$ Gene (GABRA2) with Alcohol Use Disorder. <i>Neuropsychopharmacology</i> , 2014, 39, 907-918.	5.4	93

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109	Big Data Bioinformatics. <i>Journal of Cellular Physiology</i> , 2014, 229, 1896-1900.	4.1	161
110	UNSUPERVISED FEATURE CONSTRUCTION AND KNOWLEDGE EXTRACTION FROM GENOME-WIDE ASSAYS OF BREAST CANCER WITH DENOISING AUTOENCODERS. , 2014, , .		79
111	Identification of yeast cell cycle regulated genes based on genomic features. <i>BMC Systems Biology</i> , 2013, 7, 70.	3.0	8
112	REACTIN: Regulatory activity inference of transcription factors underlying human diseases with application to breast cancer. <i>BMC Genomics</i> , 2013, 14, 504.	2.8	20
113	Transcription Factor Binding Profiles Reveal Cyclic Expression of Human Protein-coding Genes and Non-coding RNAs. <i>PLoS Computational Biology</i> , 2013, 9, e1003132.	3.2	7
114	APPLICATIONS OF BIOINFORMATICS TO NON-CODING RNAS IN THE ERA OF NEXT-GENERATION SEQUENCING. , 2013, , .		4
115	Classification of human genomic regions based on experimentally determined binding sites of more than 100 transcription-related factors. <i>Genome Biology</i> , 2012, 13, R48.	9.6	233
116	Modeling gene expression using chromatin features in various cellular contexts. <i>Genome Biology</i> , 2012, 13, R53.	9.6	231
117	Architecture of the human regulatory network derived from ENCODE data. <i>Nature</i> , 2012, 489, 91-100.	27.8	1,384
118	Understanding transcriptional regulation by integrative analysis of transcription factor binding data. <i>Genome Research</i> , 2012, 22, 1658-1667.	5.5	166
119	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> , 2012, 40, 553-568.	14.5	145
120	A statistical framework for modeling gene expression using chromatin features and application to modENCODE datasets. <i>Genome Biology</i> , 2011, 12, R15.	9.6	118
121	TIP: A probabilistic method for identifying transcription factor target genes from ChIP-seq binding profiles. <i>Bioinformatics</i> , 2011, 27, 3221-3227.	4.1	52
122	Genome-wide analysis of chromatin features identifies histone modification sensitive and insensitive yeast transcription factors. <i>Genome Biology</i> , 2011, 12, R111.	9.6	16
123	Construction and Analysis of an Integrated Regulatory Network Derived from High-Throughput Sequencing Data. <i>PLoS Computational Biology</i> , 2011, 7, e1002190.	3.2	92
124	Integrative Analysis of the <i>Caenorhabditis elegans</i> Genome by the modENCODE Project. <i>Science</i> , 2010, 330, 1775-1787.	12.6	912
125	Systematic identification of transcription factors associated with patient survival in cancers. <i>BMC Genomics</i> , 2009, 10, 225.	2.8	11
126	The relationship between the evolution of microRNA targets and the length of their UTRs. <i>BMC Genomics</i> , 2009, 10, 431.	2.8	75

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127	mRNA expression profiles show differential regulatory effects of microRNAs between estrogen receptor-positive and estrogen receptor-negative breast cancer. <i>Genome Biology</i> , 2009, 10, R90.	9.6	90
128	Systematic identification of cell cycle regulated transcription factors from microarray time series data. <i>BMC Genomics</i> , 2008, 9, 116.	2.8	26
129	Inferring MicroRNA Activities by Combining Gene Expression with MicroRNA Target Prediction. <i>PLoS ONE</i> , 2008, 3, e1989.	2.5	79
130	Significant and Systematic Expression Differentiation in Long-Lived Yeast Strains. <i>PLoS ONE</i> , 2007, 2, e1095.	2.5	21
131	Inferring activity changes of transcription factors by binding association with sorted expression profiles. <i>BMC Bioinformatics</i> , 2007, 8, 452.	2.6	72
132	Inference of transcription modification in long-live yeast strains from their expression profiles. <i>BMC Genomics</i> , 2007, 8, 219.	2.8	32
133	MARD: a new method to detect differential gene expression in treatment-control time courses. <i>Bioinformatics</i> , 2006, 22, 2650-2657.	4.1	9
134	Sub-array normalization subject to differentiation. <i>Nucleic Acids Research</i> , 2005, 33, 5565-5573.	14.5	13