Fengfeng Zhou

List of Publications by Year
in descending order

123 papers	3,666 citations	172457 29 h-index	155660 55 g-index
132 all docs	132 docs citations	132 times ranked	6342 citing authors

#	Article	IF	Citations
1	Cortical and Subcortical Brain Morphometry Differences Between Patients With Autism Spectrum Disorder and Healthy Individuals Across the Lifespan: Results From the ENIGMA ASD Working Group. American Journal of Psychiatry, 2018, 175, 359-369.	7.2	356
2	GPS: a comprehensive www server for phosphorylation sites prediction. Nucleic Acids Research, 2005, 33, W184-W187.	14.5	215
3	SUMOsp: a web server for sumoylation site prediction. Nucleic Acids Research, 2006, 34, W254-W257.	14.5	179
4	Altered structural brain asymmetry in autism spectrum disorder in a study of 54 datasets. Nature Communications, 2019, 10, 4958.	12.8	167
5	GPS: a novel group-based phosphorylation predicting and scoring method. Biochemical and Biophysical Research Communications, 2004, 325, 1443-1448.	2.1	149
6	CSS-Palm: palmitoylation site prediction with a clustering and scoring strategy (CSS). Bioinformatics, 2006, 22, 894-896.	4.1	130
7	Subcortical Brain Volume, Regional Cortical Thickness, and Cortical Surface Area Across Disorders: Findings From the ENIGMA ADHD, ASD, and OCD Working Groups. American Journal of Psychiatry, 2020, 177, 834-843.	7.2	120
8	cBar: a computer program to distinguish plasmid-derived from chromosome-derived sequence fragments in metagenomics data. Bioinformatics, 2010, 26, 2051-2052.	4.1	116
9	Machine learning based detection of age-related macular degeneration (AMD) and diabetic macular edema (DME) from optical coherence tomography (OCT) images. Biomedical Optics Express, 2016, 7, 4928.	2.9	115
10	Insights into plant biomass conversion from the genome of the anaerobic thermophilic bacterium Caldicellulosiruptor bescii DSM 6725. Nucleic Acids Research, 2011, 39, 3240-3254.	14.5	103
11	Gene expression profile based classification models of psoriasis. Genomics, 2014, 103, 48-55.	2.9	102
12	A novel electrocardiogram parameterization algorithm and its application in myocardial infarction detection. Computers in Biology and Medicine, 2015, 61, 178-184.	7.0	102
13	McTwo: a two-step feature selection algorithm based on maximal information coefficient. BMC Bioinformatics, 2016, 17, 142.	2.6	89
14	Severity Detection for the Coronavirus Disease 2019 (COVID-19) Patients Using a Machine Learning Model Based on the Blood and Urine Tests. Frontiers in Cell and Developmental Biology, 2020, 8, 683.	3.7	82
15	Barcodes for genomes and applications. BMC Bioinformatics, 2008, 9, 546.	2.6	80
16	Genome Sequence of the Anaerobic, Thermophilic, and Cellulolytic Bacterium â€œ <i>Anaerocellum thermophilum</i> â€•DSM 6725. Journal of Bacteriology, 2009, 191, 3760-3761.	2.2	78
17	MUST: A system for identification of miniature inverted-repeat transposable elements and applications to Anabaena variabilis and Haloquadratum walsbyi. Gene, 2009, 436, 1-7.	2.2	61
18	Feature selection may improve deep neural networks for the bioinformatics problems. Bioinformatics, 2020, 36, 1542-1552.	4.1	57

#	Article	IF	Citations
19	A genome-wide analysis of sumoylation-related biological processes and functions in human nucleus. FEBS Letters, 2005, 579, 3369-3375.	2.8	46
20	Combining High Speed ELM Learning with a Deep Convolutional Neural Network Feature Encoding for Predicting Protein-RNA Interactions. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 972-980.	3.0	43
21	XGraphBoost: Extracting Graph Neural Network-Based Features for a Better Prediction of Molecular Properties. Journal of Chemical Information and Modeling, 2021, 61, 2697-2705.	5.4	41
22	Integration of 24 Feature Types to Accurately Detect and Predict Seizures Using Scalp EEG Signals. Sensors, 2018, 18, 1372.	3.8	40
23	COVID19XrayNet: A Two-Step Transfer Learning Model for the COVID-19 Detecting Problem Based on a Limited Number of Chest X-Ray Images. Interdisciplinary Sciences, Computational Life Sciences, 2020, 12, 555-565.	3.6	40
24	Insertion Sequences show diverse recent activities in Cyanobacteria and Archaea. BMC Genomics, 2008, 9, 36.	2.8	38
25	<i>De novo</i> computational prediction of non-coding RNA genes in prokaryotic genomes. Bioinformatics, 2009, 25, 2897-2905.	4.1	37
26	Gly-PseAAC: Identifying protein lysine glycation through sequences. Gene, 2017, 602, 1-7.	2.2	37
27	Selection of features for patient-independent detection of seizure events using scalp EEG signals. Computers in Biology and Medicine, 2020, 119, 103671.	7.0	35
28	Dimension Reduction and Clustering Models for Single-Cell RNA Sequencing Data: A Comparative Study. International Journal of Molecular Sciences, 2020, 21, 2181.	4.1	33
29	Nezha, a novel active miniature inverted-repeat transposable element in cyanobacteria. Biochemical and Biophysical Research Communications, 2008, 365, 790-794.	2.1	32
30	RIFS: a randomly restarted incremental feature selection algorithm. Scientific Reports, 2017, 7, 13013.	3.3	31
31	RepPop: a database for repetitive elements in Populus trichocarpa. BMC Genomics, 2009, 10, 14.	2.8	30
32	Genomic and proteomic characterization of a thermophilic Geobacillus bacteriophage GBSV1. Research in Microbiology, 2009, 160, 166-171.	2.1	29
33	Large-Scale Analyses of Glycosylation in Cellulases. Genomics, Proteomics and Bioinformatics, 2009, 7, 194-199.	6.9	28
34	Accurate Prediction of Neoadjuvant Chemotherapy Pathological Complete Remission (pCR) for the Four Sub-Types of Breast Cancer. IEEE Access, 2019, 7, 134697-134706.	4.2	27
35	Using Machine Learning to Measure Relatedness Between Genes: A Multi-Features Model. Scientific Reports, 2019, 9, 4192.	3.3	27
36	Deep Residual Convolutional Neural Network for Protein-Protein Interaction Extraction. IEEE Access, 2019, 7, 89354-89365.	4.2	26

#	ARTICLE	IF	CITATIONS
37	A general user interface for prediction servers of proteins' post-translational modification sites. Nature Protocols, 2006, 1, 1318-1321.	12.0	25
38	Subtly altered topological asymmetry of brain structural covariance networks in autism spectrum disorder across 43 datasets from the ENIGMA consortium. Molecular Psychiatry, 2022, 27, 2114-2125.	7.9	25
39	Clinical Effects of Xinmailong Therapy in Patients with Chronic Heart Failure. International Journal of Medical Sciences, 2013, 10, 624-633.	2.5	24
40	A Recently Active Miniature Inverted-Repeat Transposable Element, *Chunjie*, Inserted Into an Operon Without Disturbing the Operon Structure in *Geobacter uraniireducens* Rf4. Genetics, 2008, 179, 2291-2297.	2.9	22
41	Spectral-Spatial Genetic Algorithm-Based Unsupervised Band Selection for Hyperspectral Image Classification. IEEE Transactions on Geoscience and Remote Sensing, 2021, 59, 9616-9632.	6.3	22
42	An OMIC biomarker detection algorithm TriVote and its application in methylomic biomarker detection. Epigenomics, 2018, 10, 335-347.	2.1	21
43	Accurate Fatigue Detection Based on Multiple Facial Morphological Features. Journal of Sensors, 2019, 2019, 1-10.	1.1	20
44	Prediction of pathogenicity islands in Enterohemorrhagic *Escherichia coli* O157:H7 using genomic barcodes. FEBS Letters, 2010, 584, 194-198.	2.8	19
45	CRISPRdigger: detecting CRISPRs with better direct repeat annotations. Scientific Reports, 2016, 6, 32942.	3.3	19
46	Improving Prediction of Self-interacting Proteins Using Stacked Sparse Auto-Encoder with PSSM profiles. International Journal of Biological Sciences, 2018, 14, 983-991.	6.4	19
47	Rectified-Linear-Unit-Based Deep Learning for Biomedical Multi-label Data. Interdisciplinary Sciences, Computational Life Sciences, 2017, 9, 419-422.	3.6	18
48	Multiple similarly effective solutions exist for biomedical feature selection and classification problems. Scientific Reports, 2017, 7, 12830.	3.3	17
49	A dynamic recursive feature elimination framework (dRFE) to further refine a set of OMIC biomarkers. Bioinformatics, 2021, 37, 2183-2189.	4.1	17
50	Reduced Serum Zinc Ion Concentration Is Associated with Coronary Heart Disease. Biological Trace Element Research, 2021, 199, 4109-4118.	3.5	17
51	HLAB: learning the BiLSTM features from the ProtBert-encoded proteins for the class I HLA-peptide binding prediction. Briefings in Bioinformatics, 2022, 23, .	6.5	17
52	Normalizing Electrocardiograms of Both Healthy Persons and Cardiovascular Disease Patients for Biometric Authentication. PLoS ONE, 2013, 8, e71523.	2.5	16
53	Multi-label Deep Learning for Gene Function Annotation in Cancer Pathways. Scientific Reports, 2018, 8, 267.	3.3	15
54	TriZ-a rotation-tolerant image feature and its application in endoscope-based disease diagnosis. Computers in Biology and Medicine, 2018, 99, 182-190.	7.0	15

#	Article	IF	Citations
55	A Machine Learning-Based Investigation of Gender-Specific Prognosis of Lung Cancers. Medicina (Lithuania), 2021, 57, 99.	2.0	15
56	MUSTv2: An Improved De Novo Detection Program for Recently Active Miniature Inverted Repeat Transposable Elements (MITEs). Journal of Integrative Bioinformatics, 2017, 14, .	1.5	14
57	pDAWG: An Integrated Database for Plant Cell Wall Genes. Bioenergy Research, 2009, 2, 209-216.	3.9	13
58	An accurate regression of developmental stages for breast cancer based on transcriptomic biomarkers. Biomarkers in Medicine, 2019, 13, 5-15.	1.4	13
59	Decreased Iron Ion Concentrations in the Peripheral Blood Correlate with Coronary Atherosclerosis. Nutrients, 2022, 14, 319.	4.1	13
60	QServer: A Biclustering Server for Prediction and Assessment of Co-Expressed Gene Clusters. PLoS ONE, 2012, 7, e32660.	2.5	12
61	RIFS2D: A two-dimensional version of a randomly restarted incremental feature selection algorithm with an application for detecting low-ranked biomarkers. Computers in Biology and Medicine, 2021, 133, 104405.	7.0	12
62	Computational prediction and experimental validation of novel markers for detection of STEC O157:H7. World Journal of Gastroenterology, 2011, 17, 1910.	3.3	12
63	Age Is Important for the Early-Stage Detection of Breast Cancer on Both Transcriptomic and Methylomic Biomarkers. Frontiers in Genetics, 2019, 10, 212.	2.3	11
64	GASdb: a large-scale and comparative exploration database of glycosyl hydrolysis systems. BMC Microbiology, 2010, 10, 69.	3.3	10
65	hMuLab: A Biomedical Hybrid MUlti-LABel Classifier Based on Multiple Linear Regression. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 1173-1180.	3.0	10
66	BioDog, biomarker detection for improving identification power of breast cancer histologic grade in methylomics. Epigenomics, 2019, 11, 1717-1732.	2.1	9
67	FeSTwo, a two-step feature selection algorithm based on feature engineering and sampling for the chronological age regression problem. Computers in Biology and Medicine, 2020, 125, 104008.	7.0	9
68	AgeGuess, a Methylomic Prediction Model for Human Ages. Frontiers in Bioengineering and Biotechnology, 2020, 8, 80.	4.1	9
69	Finding branched pathways in metabolic network via atom group tracking. PLoS Computational Biology, 2021, 17, e1008676.	3.2	9
70	A Novel Position-Specific Encoding Algorithm (SeqPose) of Nucleotide Sequences and Its Application for Detecting Enhancers. International Journal of Molecular Sciences, 2021, 22, 3079.	4.1	9
71	Describe Molecules by a Heterogeneous Graph Neural Network with Transformer-like Attention for Supervised Property Predictions. ACS Omega, 2022, 7, 3713-3721.	3.5	9
72	Screening features to improve the class prediction of acute myeloid leukemia and myelodysplastic syndrome. Gene, 2013, 512, 348-354.	2.2	8

#	Article	IF	Citations
73	AcneGrader: An ensemble pruning of the deep learning base models to grade acne. Skin Research and Technology, 2022, 28, 677-688.	1.6	8
74	Combinational effect of mutational bias and translational selection for translation efficiency in tomato (Solanum lycopersicum) cv. Micro-Tom. Genomics, 2013, 101, 290-295.	2.9	7
75	Proteomic biomarkers for lung cancer progression. Biomarkers in Medicine, 2018, 12, 205-215.	1.4	7
76	Diagnosis of Breast Hyperplasia and Evaluation of RuXian-I Based on Metabolomics Deep Belief Networks. International Journal of Molecular Sciences, 2019, 20, 2620.	4.1	7
77	WinHAP: An Efficient Haplotype Phasing Algorithm Based on Scalable Sliding Windows. PLoS ONE, 2012, 7, e43163.	2.5	6
78	Genome-wide screening of pathogenicity islands in Mycobacterium tuberculosis based on the genomic barcode visualization. Molecular Biology Reports, 2014, 41, 5883-5889.	2.3	6
79	WinHAP2: an extremely fast haplotype phasing program for long genotype sequences. BMC Bioinformatics, 2014, 15, 164.	2.6	6
80	Constraint Programming Based Biomarker Optimization. BioMed Research International, 2015, 2015, 1-5.	1.9	6
81	Epigenetic profiles capturing breast cancer stemness for triple negative breast cancer control. Epigenomics, 2019, 11, 1811-1825.	2.1	6
82	sefOri: selecting the best-engineered sequence features to predict DNA replication origins. Bioinformatics, 2020, 36, 49-55.	4.1	6
83	Detection and Independent Validation of Model-Based Quantitative Transcriptional Regulation Relationships Altered in Lung Cancers. Frontiers in Bioengineering and Biotechnology, 2020, 8, 582.	4.1	6
84	EnRank: An Ensemble Method to Detect Pulmonary Hypertension Biomarkers Based on Feature Selection and Machine Learning Models. Frontiers in Genetics, 2021, 12, 636429.	2.3	6
85	Computational pan-cancer characterization of model-based quantitative transcription regulations dysregulated in regional lymph node metastasis. Computers in Biology and Medicine, 2021, 135, 104571.	7.0	6
86	Comparative analyses of distributions and functions of Z-DNA in Arabidopsis and rice. Genomics, 2009, 93, 383-391.	2.9	5
87	A Comprehensive Curation Shows the Dynamic Evolutionary Patterns of Prokaryotic CRISPRs. BioMed Research International, 2016, 2016, 1-7.	1.9	5
88	Selecting Multiple Biomarker Subsets with Similarly Effective Binary Classification Performances. Journal of Visualized Experiments, 2018, , .	0.3	5
89	pyHIVE, a health-related image visualization and engineering system using Python. BMC Bioinformatics, 2018, 19, 452.	2.6	5
90	ELMO: An Efficient Logistic Regression-Based Multi-Omic Integrated Analysis Method for Breast Cancer Intrinsic Subtypes. IEEE Access, 2020, 8, 5121-5130.	4.2	5

#	Article	IF	Citations
91	MuscNet, a Weighted Voting Model of Multi-Source Connectivity Networks to Predict Mild Cognitive Impairment Using Resting-State Functional MRI. IEEE Access, 2020, 8, 174023-174031.	4.2	5
92	Evaluation of normalization methods for RNA-Seq gene expression estimation. , 2011, 2011, 50-57.		4
93	A novel molecular typing method of Mycobacteria based on DNA barcoding visualization. Journal of Clinical Bioinformatics, 2014, 4, 4.	1.2	4
94	CD3D and PRKCQ work together to discriminate between B-cell and T-cell acute lymphoblastic leukemia. Computers in Biology and Medicine, 2016, 77, 16-22.	7.0	4
95	Gender specificity improves the early-stage detection of clear cell renal cell carcinoma based on methylomic biomarkers. Biomarkers in Medicine, 2018, 12, 607-618.	1.4	4
96	The Transverse Ultrasonogram of Thyroid Papillary Carcinoma Has a Better Prediction Accuracy Than the Longitudinal One. IEEE Access, 2019, 7, 100763-100770.	4.2	4
97	Detection and Comparative Analysis of Methylomic Biomarkers of Rheumatoid Arthritis. Frontiers in Genetics, 2020, 11, 238.	2.3	4
98	Surgical resection of primary tumor is associated with prolonged survival in low-grade pancreatic neuroendocrine tumors. Clinics and Research in Hepatology and Gastroenterology, 2021, 45, 101432.	1.5	4
99	Survival Time Prediction of Breast Cancer Patients Using Feature Selection Algorithm Crystall. IEEE Access, 2021, 9, 24433-24445.	4.2	4
100	A polygenic stacking classifier revealed the complicated platelet transcriptomic landscape of adult immune thrombocytopenia. Molecular Therapy - Nucleic Acids, 2022, 28, 477-487.	5.1	4
101	Minimizing ADMs on WDM directed fiber trees. Journal of Computer Science and Technology, 2003, 18, 725-731.	1.5	3
102	Specific Biomarkers: Detection of Cancer Biomarkers Through High-Throughput Transcriptomics Data. Cognitive Computation, 2015, 7, 652-666.	5.2	3
103	jEcho: an Evolved weight vector to CHaracterize the protein's posttranslational modification mOtifs. Interdisciplinary Sciences, Computational Life Sciences, 2015, 7, 194-199.	3.6	3
104	Integrating Five Feature Types Extracted From Ultrasonograms to Improve the Prediction of Thyroid Papillary Carcinoma. IEEE Access, 2019, 7, 101820-101828.	4.2	3
105	A comprehensive comparison of residue-level methylation levels with the regression-based gene-level methylation estimations by ReGear. Briefings in Bioinformatics, 2021, 22, .	6.5	3
106	Evolutionary Optimization of Transcription Factor Binding Motif Detection. Advances in Experimental Medicine and Biology, 2015, 827, 261-274.	1.6	3
107	Superpixel-Level Global and Local Similarity Graph-Based Clustering for Large Hyperspectral Images. IEEE Transactions on Geoscience and Remote Sensing, 2022, 60, 1-16.	6.3	3
108	Construction of Network Biomarkers Using Inter-Feature Correlation Coefficients ($FeCO_3$) and their Application in Detecting High-Order Breast Cancer Biomarkers. Current Bioinformatics, 2022, 17, 310-326.	1.5	3

#	ARTICLE	IF	CITATIONS
109	DietLens-Eout. , 2019, , .		2
110	Application of Bayesian phylogenetic inference modelling for evolutionary genetic analysis and dynamic changes in 2019-nCoV. Briefings in Bioinformatics, 2021, 22, 896-904.	6.5	2
111	Zoo: Selecting Transcriptomic and Methylomic Biomarkers by Ensembling Animal-Inspired Swarm Intelligence Feature Selection Algorithms. Genes, 2021, 12, 1814.	2.4	2
112	Detecting Methylomic Biomarkers of Pediatric Autism in the Peripheral Blood Leukocytes. Interdisciplinary Sciences, Computational Life Sciences, 2019, 11, 237-246.	3.6	1
113	Females and Males Show Differences in Early-Stage Transcriptomic Biomarkers of Lung Adenocarcinoma and Lung Squamous Cell Carcinoma. Diagnostics, 2021, 11, 347.	2.6	1
114	Identification of Genomic Islands in Synechococcus sp. WH8102 Using Genomic Barcode and Whole-Genome Microarray Analysis. Current Bioinformatics, 2021, 16, 24-30.	1.5	1
115	Proactive Personality Measurement Using Item Response Theory and Social Media Text Mining. Frontiers in Psychology, 2021, 12, 705005.	2.1	1
116	Transforming OMIC features for classification using Siamese convolutional networks. Journal of Bioinformatics and Computational Biology, 0, , .	0.8	1
117	No-wait scheduling in single-hop multi-channel LANs. Information Processing Letters, 2005, 93, 19-24.	0.6	0
118	cLP: Linear programming with biological constraints and its application in classification problems. , 2014, , .		0
119	Personalized clinical data screening: Special issue on health informatics. Computers in Biology and Medicine, 2015, 61, 161-162.	7.0	0
120	Impacts of high-quality public data: Special issue on integrating public and in-house biomedical data. Journal of Bioinformatics and Computational Biology, 2021, 19, 2102002.	0.8	0
121	DiaMole: Mole Detection and Segmentation Software for Mobile Phone Skin Images. Journal of Healthcare Engineering, 2021, 2021, 1-10.	1.9	0
122	Algorithms for Loosely Constrained Multiple Sequence Alignment. Lecture Notes in Computer Science, 2004, , 213-218.	1.3	0
123	GPS: A computational protocol for kinase-specific phosphorylation site prediction. Protocol Exchange, 0, , .	0.3	0