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	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
2	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
3	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
4	Decreased Iron Ion Concentrations in the Peripheral Blood Correlate with Coronary Atherosclerosis. Nutrients, 2022, 14, 319.	4.1	13
5	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
6	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
7	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
8	AcneGrader: An ensemble pruning of the deep learning base models to grade acne. Skin Research and Technology, 2022, 28, 677-688.	1.6	8
9	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
10	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
11	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
12	A dynamic recursive feature elimination framework (dRFE) to further refine a set of OMIC biomarkers. Bioinformatics, 2021, 37, 2183-2189.	4.1	17
13	Reduced Serum Zinc Ion Concentration Is Associated with Coronary Heart Disease. Biological Trace Element Research, 2021, 199, 4109-4118.	3.5	17
14	Survival Time Prediction of Breast Cancer Patients Using Feature Selection Algorithm Crystall. IEEE Access, 2021, 9, 24433-24445.	4.2	4
15	A Machine Learning-Based Investigation of Gender-Specific Prognosis of Lung Cancers. Medicina (Lithuania), 2021, 57, 99.	2.0	15
16	Finding branched pathways in metabolic network via atom group tracking. PLoS Computational Biology, 2021, 17, e1008676.	3.2	9
17	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
18	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

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19	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
20	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
21	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
22	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
23	DiaMole: Mole Detection and Segmentation Software for Mobile Phone Skin Images. Journal of Healthcare Engineering, 2021, 2021, 1-10.	1.9	0
24	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
25	Proactive Personality Measurement Using Item Response Theory and Social Media Text Mining. Frontiers in Psychology, 2021, 12, 705005.	2.1	1
26	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
27	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
28	Zoo: Selecting Transcriptomic and Methylomic Biomarkers by Ensembling Animal-Inspired Swarm Intelligence Feature Selection Algorithms. Genes, 2021, 12, 1814.	2.4	2
29	Feature selection may improve deep neural networks for the bioinformatics problems. Bioinformatics, 2020, 36, 1542-1552.	4.1	57
30	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
31	sefOri: selecting the best-engineered sequence features to predict DNA replication origins. Bioinformatics, 2020, 36, 49-55.	4.1	6
32	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
33	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
34	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
35	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
36	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

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37	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
38	AgeGuess, a Methylomic Prediction Model for Human Ages. Frontiers in Bioengineering and Biotechnology, 2020, 8, 80.	4.1	9
39	Detection and Comparative Analysis of Methylomic Biomarkers of Rheumatoid Arthritis. Frontiers in Genetics, 2020, 11, 238.	2.3	4
40	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
41	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
42	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
43	DietLens-Eout. , 2019, , .		2
44	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
45	Deep Residual Convolutional Neural Network for Protein-Protein Interaction Extraction. IEEE Access, 2019, 7, 89354-89365.	4.2	26
46	BioDog, biomarker detection for improving identification power of breast cancer histologic grade in methylomics. Epigenomics, 2019, 11, 1717-1732.	2.1	9
47	Altered structural brain asymmetry in autism spectrum disorder in a study of 54 datasets. Nature Communications, 2019, 10, 4958.	12.8	167
48	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
49	Integrating Five Feature Types Extracted From Ultrasonograms to Improve the Prediction of Thyroid Papillary Carcinoma. IEEE Access, 2019, 7, 101820-101828.	4.2	3
50	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
51	Detecting Methylomic Biomarkers of Pediatric Autism in the Peripheral Blood Leukocytes. Interdisciplinary Sciences, Computational Life Sciences, 2019, 11, 237-246.	3.6	1
52	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
53	Using Machine Learning to Measure Relatedness Between Genes: A Multi-Features Model. Scientific Reports, 2019, 9, 4192.	3.3	27
54	Accurate Fatigue Detection Based on Multiple Facial Morphological Features. Journal of Sensors, 2019, 2019, 1-10.	1.1	20

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55	Epigenetic profiles capturing breast cancer stemness for triple negative breast cancer control. Epigenomics, 2019, 11, 1811-1825.	2.1	6
56	An accurate regression of developmental stages for breast cancer based on transcriptomic biomarkers. Biomarkers in Medicine, 2019, 13, 5-15.	1.4	13
57	Proteomic biomarkers for lung cancer progression. Biomarkers in Medicine, 2018, 12, 205-215.	1.4	7
58	An OMIC biomarker detection algorithm TriVote and its application in methylomic biomarker detection. Epigenomics, 2018, 10, 335-347.	2.1	21
59	Multi-label Deep Learning for Gene Function Annotation in Cancer Pathways. Scientific Reports, 2018, 8, 267.	3.3	15
60	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
61	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
62	Selecting Multiple Biomarker Subsets with Similarly Effective Binary Classification Performances. Journal of Visualized Experiments, 2018, , .	0.3	5
63	pyHIVE, a health-related image visualization and engineering system using Python. BMC Bioinformatics, 2018, 19, 452.	2.6	5
64	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
65	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
66	Integration of 24 Feature Types to Accurately Detect and Predict Seizures Using Scalp EEG Signals. Sensors, 2018, 18, 1372.	3.8	40
67	Multiple similarly effective solutions exist for biomedical feature selection and classification problems. Scientific Reports, 2017, 7, 12830.	3.3	17
68	RIFS: a randomly restarted incremental feature selection algorithm. Scientific Reports, 2017, 7, 13013.	3.3	31
69	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
70	Rectified-Linear-Unit-Based Deep Learning for Biomedical Multi-label Data. Interdisciplinary Sciences, Computational Life Sciences, 2017, 9, 419-422.	3.6	18
71	Gly-PseAAC: Identifying protein lysine glycation through sequences. Gene, 2017, 602, 1-7.	2.2	37
72	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

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73	A Comprehensive Curation Shows the Dynamic Evolutionary Patterns of Prokaryotic CRISPRs. BioMed Research International, 2016, 2016, 1-7.	1.9	5
74	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
75	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
76	CRISPRdigger: detecting CRISPRs with better direct repeat annotations. Scientific Reports, 2016, 6, 32942.	3.3	19
77	McTwo: a two-step feature selection algorithm based on maximal information coefficient. BMC Bioinformatics, 2016, 17, 142.	2.6	89
78	Constraint Programming Based Biomarker Optimization. BioMed Research International, 2015, 2015, 1-5.	1.9	6
79	Specific Biomarkers: Detection of Cancer Biomarkers Through High-Throughput Transcriptomics Data. Cognitive Computation, 2015, 7, 652-666.	5.2	3
80	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
81	Personalized clinical data screening: Special issue on health informatics. Computers in Biology and Medicine, 2015, 61, 161-162.	7.0	0
82	A novel electrocardiogram parameterization algorithm and its application in myocardial infarction detection. Computers in Biology and Medicine, 2015, 61, 178-184.	7.0	102
83	Evolutionary Optimization of Transcription Factor Binding Motif Detection. Advances in Experimental Medicine and Biology, 2015, 827, 261-274.	1.6	3
84	cLP: Linear programming with biological constraints and its application in classification problems. , 2014, , .		0
85	A novel molecular typing method of Mycobacteria based on DNA barcoding visualization. Journal of Clinical Bioinformatics, 2014, 4, 4.	1.2	4
86	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
87	WinHAP2: an extremely fast haplotype phasing program for long genotype sequences. BMC Bioinformatics, 2014, 15, 164.	2.6	6
88	Gene expression profile based classification models of psoriasis. Genomics, 2014, 103, 48-55.	2.9	102
89	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
90	Screening features to improve the class prediction of acute myeloid leukemia and myelodysplastic syndrome. Gene, 2013, 512, 348-354.	2.2	8

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91	Clinical Effects of Xinmailong Therapy in Patients with Chronic Heart Failure. International Journal of Medical Sciences, 2013, 10, 624-633.	2.5	24
92	Normalizing Electrocardiograms of Both Healthy Persons and Cardiovascular Disease Patients for Biometric Authentication. PLoS ONE, 2013, 8, e71523.	2.5	16
93	QServer: A Biclustering Server for Prediction and Assessment of Co-Expressed Gene Clusters. PLoS ONE, 2012, 7, e32660.	2.5	12
94	WinHAP: An Efficient Haplotype Phasing Algorithm Based on Scalable Sliding Windows. PLoS ONE, 2012, 7, e43163.	2.5	6
95	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
96	Evaluation of normalization methods for RNA-Seq gene expression estimation. , 2011, 2011, 50-57.		4
97	Computational prediction and experimental validation of novel markers for detection of STEC O157:H7. World Journal of Gastroenterology, 2011, 17, 1910.	3.3	12
98	GASdb: a large-scale and comparative exploration database of glycosyl hydrolysis systems. BMC Microbiology, 2010, 10, 69.	3.3	10
99	Prediction of pathogenicity islands in Enterohemorrhagic <i>Escherichia coli</i> O157:H7 using genomic barcodes. FEBS Letters, 2010, 584, 194-198.	2.8	19
100	cBar: a computer program to distinguish plasmid-derived from chromosome-derived sequence fragments in metagenomics data. Bioinformatics, 2010, 26, 2051-2052.	4.1	116
101	<i>De novo</i> computational prediction of non-coding RNA genes in prokaryotic genomes. Bioinformatics, 2009, 25, 2897-2905.	4.1	37
102	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
103	RepPop: a database for repetitive elements in Populus trichocarpa. BMC Genomics, 2009, 10, 14.	2.8	30
104	pDAWG: An Integrated Database for Plant Cell Wall Genes. Bioenergy Research, 2009, 2, 209-216.	3.9	13
105	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
106	Genomic and proteomic characterization of a thermophilic Geobacillus bacteriophage GBSV1. Research in Microbiology, 2009, 160, 166-171.	2.1	29
107	Comparative analyses of distributions and functions of Z-DNA in Arabidopsis and rice. Genomics, 2009, 93, 383-391.	2.9	5
108	Large-Scale Analyses of Glycosylation in Cellulases. Genomics, Proteomics and Bioinformatics, 2009, 7, 194-199.	6.9	28

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109	Barcodes for genomes and applications. BMC Bioinformatics, 2008, 9, 546.	2.6	80
110	Insertion Sequences show diverse recent activities in Cyanobacteria and Archaea. BMC Genomics, 2008, 9, 36.	2.8	38
111	Nezha, a novel active miniature inverted-repeat transposable element in cyanobacteria. Biochemical and Biophysical Research Communications, 2008, 365, 790-794.	2.1	32
112	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
113	A general user interface for prediction servers of proteins' post-translational modification sites. Nature Protocols, 2006, 1, 1318-1321.	12.0	25
114	SUMOsp: a web server for sumoylation site prediction. Nucleic Acids Research, 2006, 34, W254-W257.	14.5	179
115	CSS-Palm: palmitoylation site prediction with a clustering and scoring strategy (CSS). Bioinformatics, 2006, 22, 894-896.	4.1	130
116	No-wait scheduling in single-hop multi-channel LANs. Information Processing Letters, 2005, 93, 19-24.	0.6	0
117	GPS: a comprehensive www server for phosphorylation sites prediction. Nucleic Acids Research, 2005, 33, W184-W187.	14.5	215
118	A genome-wide analysis of sumoylation-related biological processes and functions in human nucleus. FEBS Letters, 2005, 579, 3369-3375.	2.8	46
119	GPS: a novel group-based phosphorylation predicting and scoring method. Biochemical and Biophysical Research Communications, 2004, 325, 1443-1448.	2.1	149
120	Algorithms for Loosely Constrained Multiple Sequence Alignment. Lecture Notes in Computer Science, 2004, , 213-218.	1.3	0
121	Minimizing ADMs on WDM directed fiber trees. Journal of Computer Science and Technology, 2003, 18, 725-731.	1.5	3
122	GPS: A computational protocol for kinase-specific phosphorylation site prediction. Protocol Exchange, 0, , .	0.3	0
123	Transforming OMIC features for classification using Siamese convolutional networks. Journal of Bioinformatics and Computational Biology, 0, , .	0.8	1