

Fei Guo

List of Publications by Year in descending order

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117
papers

3,526
citations

147566

31
h-index

161609

54
g-index

119
all docs

119
docs citations

119
times ranked

1797
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification of DNA N4-methylcytosine Sites via Multiview Kernel Sparse Representation Model. IEEE Transactions on Artificial Intelligence, 2023, 4, 1236-1245.	3.4	4
2	Two-stage-vote ensemble framework based on integration of mutation data and gene interaction network for uncovering driver genes. Briefings in Bioinformatics, 2022, 23, .	3.2	5
3	Identification of protein-nucleotide binding residues via graph regularized k-local hyperplane distance nearest neighbor model. Applied Intelligence, 2022, 52, 6598-6612.	3.3	9
4	SBSA: an online service for somatic binding sequence annotation. Nucleic Acids Research, 2022, 50, e4-e4.	6.5	8
5	Inferring human microbe-drug associations via multiple kernel fusion on graph neural network. Knowledge-Based Systems, 2022, 238, 107888.	4.0	21
6	Identification of drug-target interactions via multiple kernel-based triple collaborative matrix factorization. Briefings in Bioinformatics, 2022, 23, .	3.2	38
7	Comprehensive Analysis of Co-Mutations Identifies Cooperating Mechanisms of Tumorigenesis. Cancers, 2022, 14, 415.	1.7	8
8	A hybrid deep learning framework for gene regulatory network inference from single-cell transcriptomic data. Briefings in Bioinformatics, 2022, 23, .	3.2	20
9	Inferring gene regulatory network via fusing gene expression image and RNA-seq data. Bioinformatics, 2022, 38, 1716-1723.	1.8	5
10	C-Loss Based Higher Order Fuzzy Inference Systems for Identifying DNA N4-Methylcytosine Sites. IEEE Transactions on Fuzzy Systems, 2022, 30, 4754-4765.	6.5	22
11	Res2Unet: A multi-scale channel attention network for retinal vessel segmentation. Neural Computing and Applications, 2022, 34, 12001-12015.	3.2	11
12	HDContact: a novel predictor of residue-residue contacts on hetero-dimer interfaces via sequential information and transfer learning strategy. Briefings in Bioinformatics, 2022, 23, .	3.2	5
13	Identification of DNA N4-methylcytosine sites via fuzzy model on self representation. Applied Soft Computing Journal, 2022, 122, 108840.	4.1	2
14	A multi-layer multi-kernel neural network for determining associations between non-coding RNAs and diseases. Neurocomputing, 2022, 493, 91-105.	3.5	9
15	Machine learning aided construction of the quorum sensing communication network for human gut microbiota. Nature Communications, 2022, 13, .	5.8	20
16	Prediction of Major Histocompatibility Complex Binding with Bilateral and Variable Long Short Term Memory Networks. Biology, 2022, 11, 848.	1.3	1
17	Protein Crystallization Identification via Fuzzy Model on Linear Neighborhood Representation. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1986-1995.	1.9	41
18	QSIdb: quorum sensing interference molecules. Briefings in Bioinformatics, 2021, 22, .	3.2	6

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19	AEpred: An Ensemble Predictive Model of Classifier Chain to Identify Anti-Inflammatory Peptides. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 1831-1840.	1.9	31
20	Multi-Scale Time-Series Kernel-Based Learning Method for Brain Disease Diagnosis. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2021, 25, 209-217.	3.9	16
21	EP3: an ensemble predictor that accurately identifies type III secreted effectors. <i>Briefings in Bioinformatics</i> , 2021, 22, 1918-1928.	3.2	26
22	iPro2L-PSTKNC: A Two-Layer Predictor for Discovering Various Types of Promoters by Position Specific of Nucleotide Composition. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2021, 25, 2329-2337.	3.9	6
23	DeepATT: a hybrid category attention neural network for identifying functional effects of DNA sequences. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	46
24	Granular multiple kernel learning for identifying RNA-binding protein residues via integrating sequence and structure information. <i>Neural Computing and Applications</i> , 2021, 33, 11387.	3.2	16
25	Exploring associations of non-coding RNAs in human diseases via three-matrix factorization with hypergraph-regular terms on center kernel alignment. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	51
26	CEPZ: A Novel Predictor for Identification of DNase I Hypersensitive Sites. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 2768-2774.	1.9	3
27	iEnhancer-KL: A Novel Two-Layer Predictor for Identifying Enhancers by Position Specific of Nucleotide Composition. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 2809-2815.	1.9	9
28	A comprehensive overview and critical evaluation of gene regulatory network inference technologies. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	54
29	6mA-Pred: identifying DNA N6-methyladenine sites based on deep learning. <i>PeerJ</i> , 2021, 9, e10813.	0.9	11
30	HSM6AP: a high-precision predictor for the Homo <i>sapiens</i> N6-methyladenosine (m ⁶ A) based on multiple weights and feature stitching. <i>RNA Biology</i> , 2021, 18, 1882-1892.	1.5	19
31	An Efficient Multiple Kernel Support Vector Regression Model for Assessing Dry Weight of Hemodialysis Patients. <i>Current Bioinformatics</i> , 2021, 16, 284-293.	0.7	13
32	MK-FSVM-SVDD: A Multiple Kernel-based Fuzzy SVM Model for Predicting DNA-binding Proteins via Support Vector Data Description. <i>Current Bioinformatics</i> , 2021, 16, 274-283.	0.7	71
33	Exploring effectiveness of <i>ab-initio</i> protein-protein docking methods on a novel antibacterial protein complex dataset. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	3
34	A sequence-based multiple kernel model for identifying DNA-binding proteins. <i>BMC Bioinformatics</i> , 2021, 22, 291.	1.2	7
35	Predicting MHC class I binder: existing approaches and a novel recurrent neural network solution. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	6
36	A systematic view of computational methods for identifying driver genes based on somatic mutation data. <i>Briefings in Functional Genomics</i> , 2021, 20, 333-343.	1.3	4

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37	A Zero-Shot Method for 3D Medical Image Segmentation. , 2021, , .		4
38	Weighted RSA: An Improved Framework on the Perception of Audio-visual Affective Speech in Left Insula and Superior Temporal Gyrus. Neuroscience, 2021, 469, 46-58.	1.1	3
39	Identifying potential association on gene-disease network via dual hypergraph regularized least squares. BMC Genomics, 2021, 22, 605.	1.2	3
40	A Multichannel Deep Neural Network for Retina Vessel Segmentation via a Fusion Mechanism. Frontiers in Bioengineering and Biotechnology, 2021, 9, 697915.	2.0	9
41	Multi-Task Deep Supervision on Attention R2U-Net for Brain Tumor Segmentation. Frontiers in Oncology, 2021, 11, 704850.	1.3	7
42	Identification of drug-target interactions via multi-view graph regularized link propagation model. Neurocomputing, 2021, 461, 618-631.	3.5	30
43	Drug-disease associations prediction via Multiple Kernel-based Dual Graph Regularized Least Squares. Applied Soft Computing Journal, 2021, 112, 107811.	4.1	24
44	Identify ncRNA subcellular localization via graph regularized k-local hyperplane distance nearest neighbor model on multi-kernel learning. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, PP, 1-1.	1.9	5
45	Identify RNA-associated subcellular localizations based on multi-label learning using Chou's 5-steps rule. BMC Genomics, 2021, 22, 56.	1.2	17
46	SubLocEP: a novel ensemble predictor of subcellular localization of eukaryotic mRNA based on machine learning. Briefings in Bioinformatics, 2021, 22, .	3.2	18
47	Laplacian Regularized Sparse Representation based Classifier for Identifying DNA N4-methylcytosine Sites via L2,1/2-matrix Norm. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, PP, 1-1.	1.9	13
48	Two-Stage Deep Neural Network via Ensemble Learning for Melanoma Classification. Frontiers in Bioengineering and Biotechnology, 2021, 9, 758495.	2.0	12
49	MIASNet: A medical image segmentation method predicting future based on past and current cases. , 2021, , .		2
50	GEU-Net: Rethinking the information transmission in the skip connection of U-Net architecture. , 2021, , .		1
51	Multi-AMP: detecting the antimicrobial peptides and their activities using the multi-task learning. , 2021, , .		1
52	Critical evaluation of web-based prediction tools for human protein subcellular localization. Briefings in Bioinformatics, 2020, 21, 1628-1640.	3.2	45
53	Identification of drug-target interactions via fuzzy bipartite local model. Neural Computing and Applications, 2020, 32, 10303-10319.	3.2	83
54	Identification of membrane protein types via multivariate information fusion with Hilbert-Schmidt Independence Criterion. Neurocomputing, 2020, 383, 257-269.	3.5	105

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55	Kernel Fusion Method for Detecting Cancer Subtypes via Selecting Relevant Expression Data. <i>Frontiers in Genetics</i> , 2020, 11, 979.	1.1	17
56	CWLy-pred: A novel cell wall lytic enzyme identifier based on an improved MRMD feature selection method. <i>Genomics</i> , 2020, 112, 4715-4721.	1.3	11
57	Identification of human microRNA-disease association via hypergraph embedded bipartite local model. <i>Computational Biology and Chemistry</i> , 2020, 89, 107369.	1.1	21
58	Identification of Drug-Target Interactions via Dual Laplacian Regularized Least Squares with Multiple Kernel Fusion. <i>Knowledge-Based Systems</i> , 2020, 204, 106254.	4.0	106
59	Human protein subcellular localization identification via fuzzy model on Kernelized Neighborhood Representation. <i>Applied Soft Computing Journal</i> , 2020, 96, 106596.	4.1	54
60	SMDB: pivotal somatic sequence alterations reprogramming regulatory cascades. <i>NAR Cancer</i> , 2020, 2, zcaa030.	1.6	8
61	Global Autozygosity Is Associated with Cancer Risk, Mutational Signature and Prognosis. <i>Cancers</i> , 2020, 12, 3646.	1.7	1
62	CWLy-SVM: A support vector machine-based tool for identifying cell wall lytic enzymes. <i>Computational Biology and Chemistry</i> , 2020, 87, 107304.	1.1	18
63	DeepAVP: A Dual-Channel Deep Neural Network for Identifying Variable-Length Antiviral Peptides. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2020, 24, 3012-3019.	3.9	69
64	Review and comparative analysis of machine learning-based phage virion protein identification methods. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2020, 1868, 140406.	1.1	25
65	A Novel Triple Matrix Factorization Method for Detecting Drug-Side Effect Association Based on Kernel Target Alignment. <i>BioMed Research International</i> , 2020, 2020, 1-11.	0.9	17
66	Identification of Highest-Affinity Binding Sites of Yeast Transcription Factor Families. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 1876-1883.	2.5	26
67	PSBP-SVM: A Machine Learning-Based Computational Identifier for Predicting Polystyrene Binding Peptides. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 245.	2.0	22
68	The Computational Models of Drug-target Interaction Prediction. <i>Protein and Peptide Letters</i> , 2020, 27, 348-358.	0.4	9
69	An two-layer predictive model of ensemble classifier chain for detecting antimicrobial peptides. , 2020, , .		2
70	Identification of DNA-Binding Proteins via Fuzzy Multiple Kernel Model and Sequence Information. <i>Lecture Notes in Computer Science</i> , 2019, , 468-479.	1.0	2
71	FKRR-MVSF: A Fuzzy Kernel Ridge Regression Model for Identifying DNA-Binding Proteins by Multi-View Sequence Features via Chou's Five-Step Rule. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4175.	1.8	26
72	LPI-KTASLP: Prediction of LncRNA-Protein Interaction by Semi-Supervised Link Learning With Multivariate Information. <i>IEEE Access</i> , 2019, 7, 13486-13496.	2.6	46

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73	LightCpG: a multi-view CpG sites detection on single-cell whole genome sequence data. BMC Genomics, 2019, 20, 306.	1.2	20
74	CrystalM: a multi-view fusion approach for protein crystallization prediction. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 18, 1-1.	1.9	17
75	Diagnosis of Brain Diseases via Multi-Scale Time-Series Model. Frontiers in Neuroscience, 2019, 13, 197.	1.4	5
76	TsHD1 and TsNAC1 cooperatively play roles in plant growth and abiotic stress resistance of <i>Thellungiella halophila</i> . Plant Journal, 2019, 99, 81-97.	2.8	11
77	Application of Machine Learning in Microbiology. Frontiers in Microbiology, 2019, 10, 827.	1.5	130
78	Discovering Cancer Subtypes via an Accurate Fusion Strategy on Multiple Profile Data. Frontiers in Genetics, 2019, 10, 20.	1.1	49
79	Taxonomy dimension reduction for colorectal cancer prediction. Computational Biology and Chemistry, 2019, 83, 107160.	1.1	23
80	Prediction of tumor metastasis from sequencing data in the era of genome sequencing. Briefings in Functional Genomics, 2019, 18, 412-418.	1.3	19
81	Identifying protein-protein interface via a novel multi-scale local sequence and structural representation. BMC Bioinformatics, 2019, 20, 483.	1.2	9
82	Identification of protein subcellular localization via integrating evolutionary and physicochemical information into Chou's general PseAAC. Journal of Theoretical Biology, 2019, 462, 230-239.	0.8	135
83	Identification of drug-side effect association via multiple information integration with centered kernel alignment. Neurocomputing, 2019, 325, 211-224.	3.5	182
84	Identification of Drug-Side Effect Association via Semisupervised Model and Multiple Kernel Learning. IEEE Journal of Biomedical and Health Informatics, 2019, 23, 2619-2632.	3.9	70
85	Progressive approach for SNP calling and haplotype assembly using single molecular sequencing data. Bioinformatics, 2018, 34, 2012-2018.	1.8	24
86	An approximation algorithm for maximum internal spanning tree. Journal of Combinatorial Optimization, 2018, 35, 955-979.	0.8	7
87	FKL-Spa-LapRLS: an accurate method for identifying human microRNA-disease association. BMC Genomics, 2018, 19, 911.	1.2	46
88	MDA-SKF: Similarity Kernel Fusion for Accurately Discovering miRNA-Disease Association. Frontiers in Genetics, 2018, 9, 618.	1.1	74
89	A Novel Computational Method for Detecting DNA Methylation Sites with DNA Sequence Information and Physicochemical Properties. International Journal of Molecular Sciences, 2018, 19, 511.	1.8	38
90	Identification of Inhibitors of MMPS Enzymes via a Novel Computational Approach. International Journal of Biological Sciences, 2018, 14, 863-871.	2.6	16

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91	Detecting complexes from edge-weighted PPI networks via genes expression analysis. BMC Systems Biology, 2018, 12, 40.	3.0	18
92	Multivariate Information Fusion With Fast Kernel Learning to Kernel Ridge Regression in Predicting LncRNA-Protein Interactions. Frontiers in Genetics, 2018, 9, 716.	1.1	28
93	Complex Detection in PPI Network Using Genes Expression Information. Current Proteomics, 2018, 15, 119-127.	0.1	2
94	Improved prediction of protein-protein interactions using novel negative samples, features, and an ensemble classifier. Artificial Intelligence in Medicine, 2017, 83, 67-74.	3.8	220
95	Analysis of Co-Associated Transcription Factors via Ordered Adjacency Differences on Motif Distribution. Scientific Reports, 2017, 7, 43597.	1.6	15
96	Identifying N6-methyladenosine sites using multi-interval nucleotide pair position specificity and support vector machine. Scientific Reports, 2017, 7, 46757.	1.6	77
97	Identification of drug-target interactions via multiple information integration. Information Sciences, 2017, 418-419, 546-560.	4.0	168
98	Identification of Protein-Ligand Binding Sites by Sequence Information and Ensemble Classifier. Journal of Chemical Information and Modeling, 2017, 57, 3149-3161.	2.5	67
99	Core-genome scaffold comparison reveals the prevalence that inversion events are associated with pairs of inverted repeats. BMC Genomics, 2017, 18, 268.	1.2	11
100	Identification of DNA-protein Binding Sites through Multi-Scale Local Average Blocks on Sequence Information. Molecules, 2017, 22, 2079.	1.7	32
101	An Ameliorated Prediction of Drug-Target Interactions Based on Multi-Scale Discrete Wavelet Transform and Network Features. International Journal of Molecular Sciences, 2017, 18, 1781.	1.8	46
102	Multi-scale encoding of amino acid sequences for predicting protein interactions using gradient boosting decision tree. PLoS ONE, 2017, 12, e0181426.	1.1	41
103	Improvement of phylogenetic method to analyze compositional heterogeneity. BMC Systems Biology, 2017, 11, 79.	3.0	1
104	Improved detection of DNA-binding proteins via compression technology on PSSM information. PLoS ONE, 2017, 12, e0185587.	1.1	63
105	A Novel Peptide Binding Prediction Approach for HLA-DR Molecule Based on Sequence and Structural Information. BioMed Research International, 2016, 2016, 1-10.	0.9	5
106	Identification of Protein-Protein Interactions via a Novel Matrix-Based Sequence Representation Model with Amino Acid Contact Information. International Journal of Molecular Sciences, 2016, 17, 1623.	1.8	83
107	Predicting protein-protein interactions via multivariate mutual information of protein sequences. BMC Bioinformatics, 2016, 17, 398.	1.2	130
108	Protein-protein interface prediction based on hexagon structure similarity. Computational Biology and Chemistry, 2016, 63, 83-88.	1.1	13

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109	Identification of 14-3-3 Proteins Phosphopeptide-Binding Specificity Using an Affinity-Based Computational Approach. PLoS ONE, 2016, 11, e0147467.	1.1	19
110	Identification of Residue-Residue Contacts Using a Novel Coevolution- Based Method. Current Proteomics, 2016, 13, 122-129.	0.1	6
111	Structural neighboring property for identifying protein-protein binding sites. BMC Systems Biology, 2015, 9, S3.	3.0	5
112	Identification of Protein-Protein Interactions by Detecting Correlated Mutation at the Interface. Journal of Chemical Information and Modeling, 2015, 55, 2042-2049.	2.5	27
113	Probabilistic Models for Capturing More Physicochemical Properties on Protein-Protein Interface. Journal of Chemical Information and Modeling, 2014, 54, 1798-1809.	2.5	13
114	Identifying Protein-Protein Binding Sites with a Combined Energy Function. Current Protein and Peptide Science, 2014, 15, 540-552.	0.7	2
115	Detecting Protein Conformational Changes in Interactions via Scaling Known Structures. Journal of Computational Biology, 2013, 20, 765-779.	0.8	7
116	Protein-protein binding site identification by enumerating the configurations. BMC Bioinformatics, 2012, 13, 158.	1.2	57
117	Computing the protein binding sites. BMC Bioinformatics, 2012, 13, S2.	1.2	6