

# 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	Improved prediction of protein-protein interactions using novel negative samples, features, and an ensemble classifier. <i>Artificial Intelligence in Medicine</i> , 2017, 83, 67-74.	3.8	220
2	Identification of drug-side effect association via multiple information integration with centered kernel alignment. <i>Neurocomputing</i> , 2019, 325, 211-224.	3.5	182
3	Identification of drug-target interactions via multiple information integration. <i>Information Sciences</i> , 2017, 418-419, 546-560.	4.0	168
4	Identification of protein subcellular localization via integrating evolutionary and physicochemical information into Chou's general PseAAC. <i>Journal of Theoretical Biology</i> , 2019, 462, 230-239.	0.8	135
5	Predicting protein-protein interactions via multivariate mutual information of protein sequences. <i>BMC Bioinformatics</i> , 2016, 17, 398.	1.2	130
6	Application of Machine Learning in Microbiology. <i>Frontiers in Microbiology</i> , 2019, 10, 827.	1.5	130
7	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
8	Identification of membrane protein types via multivariate information fusion with Hilbert-Schmidt Independence Criterion. <i>Neurocomputing</i> , 2020, 383, 257-269.	3.5	105
9	Identification of Protein-Protein Interactions via a Novel Matrix-Based Sequence Representation Model with Amino Acid Contact Information. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1623.	1.8	83
10	Identification of drug-target interactions via fuzzy bipartite local model. <i>Neural Computing and Applications</i> , 2020, 32, 10303-10319.	3.2	83
11	Identifying N6-methyladenosine sites using multi-interval nucleotide pair position specificity and support vector machine. <i>Scientific Reports</i> , 2017, 7, 46757.	1.6	77
12	MDA-SKF: Similarity Kernel Fusion for Accurately Discovering miRNA-Disease Association. <i>Frontiers in Genetics</i> , 2018, 9, 618.	1.1	74
13	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
14	Identification of Drug-Side Effect Association via Semisupervised Model and Multiple Kernel Learning. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2019, 23, 2619-2632.	3.9	70
15	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
16	Identification of Protein-Ligand Binding Sites by Sequence Information and Ensemble Classifier. <i>Journal of Chemical Information and Modeling</i> , 2017, 57, 3149-3161.	2.5	67
17	Improved detection of DNA-binding proteins via compression technology on PSSM information. <i>PLoS ONE</i> , 2017, 12, e0185587.	1.1	63
18	Protein-protein binding site identification by enumerating the configurations. <i>BMC Bioinformatics</i> , 2012, 13, 158.	1.2	57

#	ARTICLE	IF	CITATIONS
19	Human protein subcellular localization identification via fuzzy model on Kernelized Neighborhood Representation. <i>Applied Soft Computing Journal</i> , 2020, 96, 106596.	4.1	54
20	A comprehensive overview and critical evaluation of gene regulatory network inference technologies. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	54
21	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
22	Discovering Cancer Subtypes via an Accurate Fusion Strategy on Multiple Profile Data. <i>Frontiers in Genetics</i> , 2019, 10, 20.	1.1	49
23	An Ameliorated Prediction of Drug-Target Interactions Based on Multi-Scale Discrete Wavelet Transform and Network Features. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1781.	1.8	46
24	FKL-Spa-LapRLS: an accurate method for identifying human microRNA-disease association. <i>BMC Genomics</i> , 2018, 19, 911.	1.2	46
25	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
26	DeepATT: a hybrid category attention neural network for identifying functional effects of DNA sequences. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	46
27	Critical evaluation of web-based prediction tools for human protein subcellular localization. <i>Briefings in Bioinformatics</i> , 2020, 21, 1628-1640.	3.2	45
28	Multi-scale encoding of amino acid sequences for predicting protein interactions using gradient boosting decision tree. <i>PLoS ONE</i> , 2017, 12, e0181426.	1.1	41
29	Protein Crystallization Identification via Fuzzy Model on Linear Neighborhood Representation. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 1986-1995.	1.9	41
30	A Novel Computational Method for Detecting DNA Methylation Sites with DNA Sequence Information and Physicochemical Properties. <i>International Journal of Molecular Sciences</i> , 2018, 19, 511.	1.8	38
31	Identification of drug-target interactions via multiple kernel-based triple collaborative matrix factorization. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	38
32	Identification of DNA-protein Binding Sites through Multi-Scale Local Average Blocks on Sequence Information. <i>Molecules</i> , 2017, 22, 2079.	1.7	32
33	AIEdpred: 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
34	Identification of drug-target interactions via multi-view graph regularized link propagation model. <i>Neurocomputing</i> , 2021, 461, 618-631.	3.5	30
35	Multivariate Information Fusion With Fast Kernel Learning to Kernel Ridge Regression in Predicting LncRNA-Protein Interactions. <i>Frontiers in Genetics</i> , 2018, 9, 716.	1.1	28
36	Identification of Protein-Protein Interactions by Detecting Correlated Mutation at the Interface. <i>Journal of Chemical Information and Modeling</i> , 2015, 55, 2042-2049.	2.5	27

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37	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
38	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
39	EP3: an ensemble predictor that accurately identifies type III secreted effectors. <i>Briefings in Bioinformatics</i> , 2021, 22, 1918-1928.	3.2	26
40	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
41	Progressive approach for SNP calling and haplotype assembly using single molecular sequencing data. <i>Bioinformatics</i> , 2018, 34, 2012-2018.	1.8	24
42	Drug-disease associations prediction via Multiple Kernel-based Dual Graph Regularized Least Squares. <i>Applied Soft Computing Journal</i> , 2021, 112, 107811.	4.1	24
43	Taxonomy dimension reduction for colorectal cancer prediction. <i>Computational Biology and Chemistry</i> , 2019, 83, 107160.	1.1	23
44	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
45	C-Loss Based Higher Order Fuzzy Inference Systems for Identifying DNA N4-Methylcytosine Sites. <i>IEEE Transactions on Fuzzy Systems</i> , 2022, 30, 4754-4765.	6.5	22
46	Identification of human microRNA-disease association via hypergraph embedded bipartite local model. <i>Computational Biology and Chemistry</i> , 2020, 89, 107369.	1.1	21
47	Inferring human microbe-drug associations via multiple kernel fusion on graph neural network. <i>Knowledge-Based Systems</i> , 2022, 238, 107888.	4.0	21
48	LightCpG: a multi-view CpG sites detection on single-cell whole genome sequence data. <i>BMC Genomics</i> , 2019, 20, 306.	1.2	20
49	A hybrid deep learning framework for gene regulatory network inference from single-cell transcriptomic data. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	20
50	Machine learning aided construction of the quorum sensing communication network for human gut microbiota. <i>Nature Communications</i> , 2022, 13, .	5.8	20
51	Prediction of tumor metastasis from sequencing data in the era of genome sequencing. <i>Briefings in Functional Genomics</i> , 2019, 18, 412-418.	1.3	19
52	HSM6AP: a high-precision predictor for the Homo sapiens N6-methyladenosine (m <sup>6</sup> A) based on multiple weights and feature stitching. <i>RNA Biology</i> , 2021, 18, 1882-1892.	1.5	19
53	Identification of 14-3-3 Proteins Phosphopeptide-Binding Specificity Using an Affinity-Based Computational Approach. <i>PLoS ONE</i> , 2016, 11, e0147467.	1.1	19
54	Detecting complexes from edge-weighted PPI networks via genes expression analysis. <i>BMC Systems Biology</i> , 2018, 12, 40.	3.0	18

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55	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
56	SubLocEP: a novel ensemble predictor of subcellular localization of eukaryotic mRNA based on machine learning. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	18
57	CrystalM: a multi-view fusion approach for protein crystallization prediction. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 18, 1-1.	1.9	17
58	Kernel Fusion Method for Detecting Cancer Subtypes via Selecting Relevant Expression Data. <i>Frontiers in Genetics</i> , 2020, 11, 979.	1.1	17
59	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
60	Identify RNA-associated subcellular localizations based on multi-label learning using Chou's 5-steps rule. <i>BMC Genomics</i> , 2021, 22, 56.	1.2	17
61	Identification of Inhibitors of MMPS Enzymes via a Novel Computational Approach. <i>International Journal of Biological Sciences</i> , 2018, 14, 863-871.	2.6	16
62	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
63	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
64	Analysis of Co-Associated Transcription Factors via Ordered Adjacency Differences on Motif Distribution. <i>Scientific Reports</i> , 2017, 7, 43597.	1.6	15
65	Probabilistic Models for Capturing More Physicochemical Properties on Protein-Protein Interface. <i>Journal of Chemical Information and Modeling</i> , 2014, 54, 1798-1809.	2.5	13
66	Protein-protein interface prediction based on hexagon structure similarity. <i>Computational Biology and Chemistry</i> , 2016, 63, 83-88.	1.1	13
67	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
68	Laplacian Regularized Sparse Representation based Classifier for Identifying DNA N4-methylcytosine Sites via L2,1/2-matrix Norm. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, PP, 1-1.	1.9	13
69	Two-Stage Deep Neural Network via Ensemble Learning for Melanoma Classification. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 758495.	2.0	12
70	Core-genome scaffold comparison reveals the prevalence that inversion events are associated with pairs of inverted repeats. <i>BMC Genomics</i> , 2017, 18, 268.	1.2	11
71	TsHD1 and TsNAC1 cooperatively play roles in plant growth and abiotic stress resistance of <i>Thellungiella halophila</i> . <i>Plant Journal</i> , 2019, 99, 81-97.	2.8	11
72	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

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73	6mA-Pred: identifying DNA N6-methyladenine sites based on deep learning. PeerJ, 2021, 9, e10813.	0.9	11
74	Res2Unet: A multi-scale channel attention network for retinal vessel segmentation. Neural Computing and Applications, 2022, 34, 12001-12015.	3.2	11
75	Identifying protein-protein interface via a novel multi-scale local sequence and structural representation. BMC Bioinformatics, 2019, 20, 483.	1.2	9
76	iEnhancer-KL: A Novel Two-Layer Predictor for Identifying Enhancers by Position Specific of Nucleotide Composition. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2809-2815.	1.9	9
77	A Multichannel Deep Neural Network for Retina Vessel Segmentation via a Fusion Mechanism. Frontiers in Bioengineering and Biotechnology, 2021, 9, 697915.	2.0	9
78	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
79	The Computational Models of Drug-target Interaction Prediction. Protein and Peptide Letters, 2020, 27, 348-358.	0.4	9
80	A multi-layer multi-kernel neural network for determining associations between non-coding RNAs and diseases. Neurocomputing, 2022, 493, 91-105.	3.5	9
81	SMDB: pivotal somatic sequence alterations reprogramming regulatory cascades. NAR Cancer, 2020, 2, zcaa030.	1.6	8
82	SBSA: an online service for somatic binding sequence annotation. Nucleic Acids Research, 2022, 50, e4-e4.	6.5	8
83	Comprehensive Analysis of Co-Mutations Identifies Cooperating Mechanisms of Tumorigenesis. Cancers, 2022, 14, 415.	1.7	8
84	Detecting Protein Conformational Changes in Interactions via Scaling Known Structures. Journal of Computational Biology, 2013, 20, 765-779.	0.8	7
85	An approximation algorithm for maximum internal spanning tree. Journal of Combinatorial Optimization, 2018, 35, 955-979.	0.8	7
86	A sequence-based multiple kernel model for identifying DNA-binding proteins. BMC Bioinformatics, 2021, 22, 291.	1.2	7
87	Multi-Task Deep Supervision on Attention R2U-Net for Brain Tumor Segmentation. Frontiers in Oncology, 2021, 11, 704850.	1.3	7
88	Computing the protein binding sites. BMC Bioinformatics, 2012, 13, S2.	1.2	6
89	QSldb: quorum sensing interference molecules. Briefings in Bioinformatics, 2021, 22, .	3.2	6
90	iPro2L-PSTKNC: A Two-Layer Predictor for Discovering Various Types of Promoters by Position Specific of Nucleotide Composition. IEEE Journal of Biomedical and Health Informatics, 2021, 25, 2329-2337.	3.9	6

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91	Predicting MHC class I binder: existing approaches and a novel recurrent neural network solution. Briefings in Bioinformatics, 2021, 22, .	3.2	6
92	Identification of Residue-Residue Contacts Using a Novel Coevolution- Based Method. Current Proteomics, 2016, 13, 122-129.	0.1	6
93	Structural neighboring property for identifying protein-protein binding sites. BMC Systems Biology, 2015, 9, S3.	3.0	5
94	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
95	Diagnosis of Brain Diseases via Multi-Scale Time-Series Model. Frontiers in Neuroscience, 2019, 13, 197.	1.4	5
96	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
97	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
98	Inferring gene regulatory network via fusing gene expression image and RNA-seq data. Bioinformatics, 2022, 38, 1716-1723.	1.8	5
99	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
100	A systematic view of computational methods for identifying driver genes based on somatic mutation data. Briefings in Functional Genomics, 2021, 20, 333-343.	1.3	4
101	A Zero-Shot Method for 3D Medical Image Segmentation. , 2021, , .		4
102	Identification of DNA N4-methylcytosine Sites via Multiview Kernel Sparse Representation Model. IEEE Transactions on Artificial Intelligence, 2023, 4, 1236-1245.	3.4	4
103	CEPZ: A Novel Predictor for Identification of DNase I Hypersensitive Sites. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2768-2774.	1.9	3
104	Exploring effectiveness of <i>ab-initio</i> protein-protein docking methods on a novel antibacterial protein complex dataset. Briefings in Bioinformatics, 2021, 22, .	3.2	3
105	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
106	Identifying potential association on gene-disease network via dual hypergraph regularized least squares. BMC Genomics, 2021, 22, 605.	1.2	3
107	Identification of DNA-Binding Proteins via Fuzzy Multiple Kernel Model and Sequence Information. Lecture Notes in Computer Science, 2019, , 468-479.	1.0	2
108	Identifying Protein-Protein Binding Sites with a Combined Energy Function. Current Protein and Peptide Science, 2014, 15, 540-552.	0.7	2

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109	Complex Detection in PPI Network Using Genes Expression Information. Current Proteomics, 2018, 15, 119-127.	0.1	2
110	An two-layer predictive model of ensemble classifier chain for detecting antimicrobial peptides. , 2020, , .		2
111	MIASNet: A medical image segmentation method predicting future based on past and current cases. , 2021, , .		2
112	Identification of DNA N4-methylcytosine sites via fuzzy model on self representation. Applied Soft Computing Journal, 2022, 122, 108840.	4.1	2
113	Improvement of phylogenetic method to analyze compositional heterogeneity. BMC Systems Biology, 2017, 11, 79.	3.0	1
114	Global Autozygosity Is Associated with Cancer Risk, Mutational Signature and Prognosis. Cancers, 2020, 12, 3646.	1.7	1
115	GEU-Net: Rethinking the information transmission in the skip connection of U-Net architecture. , 2021, , .		1
116	Multi-AMP: detecting the antimicrobial peptides and their activities using the multi-task learning. , 2021, , .		1
117	Prediction of Major Histocompatibility Complex Binding with Bilateral and Variable Long Short Term Memory Networks. Biology, 2022, 11, 848.	1.3	1