Jun-Feng Xia

List of Publications by Year
in descending order

86 papers	2,823 citations	201385 27 h-index	189595 50 g-index
90 all docs	90 docs citations	90 times ranked	3749 citing authors

#	Article	IF	Citations
1	An Ensemble Framework for Improving the Prediction of Deleterious Synonymous Mutation. IEEE Transactions on Circuits and Systems for Video Technology, 2022, 32, 2603-2611.	5.6	6
2	Identifying multi-functional bioactive peptide functions using multi-label deep learning. Briefings in Bioinformatics, 2022, 23, .	3.2	30
3	PredAPP: Predicting Anti-Parasitic Peptides with Undersampling and Ensemble Approaches. Interdisciplinary Sciences, Computational Life Sciences, 2022, 14, 258-268.	2.2	10
4	scHFC: a hybrid fuzzy clustering method for single-cell RNA-seq data optimized by natural computation. Briefings in Bioinformatics, 2022, 23, .	3.2	6
5	dbBIP: a comprehensive bipolar disorder database for genetic research. Database: the Journal of Biological Databases and Curation, 2022, 2022, .	1.4	3
6	Prediction of circRNA-Disease Associations Based on the Combination of Multi-Head Graph Attention Network and Graph Convolutional Network. Biomolecules, 2022, 12, 932.	1.8	8
7	A Deep Learning-Based Method for Identification of Bacteriophage-Host Interaction. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1801-1810.	1.9	31
8	PredCID: prediction of driver frameshift indels in human cancer. Briefings in Bioinformatics, 2021, 22, .	3.2	29
9	Extra Trees Method for Predicting LncRNA-Disease Association Based on Multi-layer Graph Embedding Aggregation. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, PP, 1-1.	1.9	19
10	GAERF: predicting lncRNA-disease associations by graph auto-encoder and random forest. Briefings in Bioinformatics, 2021, 22, .	3.2	51
11	usDSM: a novel method for deleterious synonymous mutation prediction using undersampling scheme. Briefings in Bioinformatics, 2021, 22, .	3.2	12
12	An improved DNA-binding hot spot residues prediction method by exploring interfacial neighbor properties. BMC Bioinformatics, 2021, 22, 253.	1.2	4
13	Identification of driver genes based on gene mutational effects and network centrality. BMC Bioinformatics, 2021, 22, 457.	1.2	3
14	Sequence-Based Prediction of Transmembrane Protein Crystallization Propensity. Interdisciplinary Sciences, Computational Life Sciences, 2021, 13, 693-702.	2.2	0
15	Double matrix completion for circRNA-disease association prediction. BMC Bioinformatics, 2021, 22, 307.	1.2	10
16	BBPpred: Sequence-Based Prediction of Blood-Brain Barrier Peptides with Feature Representation Learning and Logistic Regression. Journal of Chemical Information and Modeling, 2021, 61, 525-534.	2.5	49
17	Comparison and integration of computational methods for deleterious synonymous mutation prediction. Briefings in Bioinformatics, 2020, 21, 970-981.	3.2	56
18	A feature-based approach to predict hot spots in proteinâ€“DNA binding interfaces. Briefings in Bioinformatics, 2020, 21, 1038-1046.	3.2	31

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19	Prediction of Radiosensitivity in Head and Neck Squamous Cell Carcinoma Based on Multiple Omics Data. Frontiers in Genetics, 2020, 11, 960.	1.1	8
20	Prediction of Neuropeptides from Sequence Information Using Ensemble Classifier and Hybrid Features. Journal of Proteome Research, 2020, 19, 3732-3740.	1.8	31
21	Prediction of hot spots in proteinâ€“DNA binding interfaces based on supervised isometric feature mapping and extreme gradient boosting. BMC Bioinformatics, 2020, 21, 381.	1.2	18
22	Prioritizing Cancer Genes Based on an Improved Random Walk Method. Frontiers in Genetics, 2020, 11, 377.	1.1	22
23	Prediction of circRNA-disease associations based on inductive matrix completion. BMC Medical Genomics, 2020, 13, 42.	0.7	42
24	Somatic synonymous mutations in regulatory elements contribute to the genetic aetiology of melanoma. BMC Medical Genomics, 2020, 13, 43.	0.7	20
25	Pan-Cancer Analysis of Radiotherapy Benefits and Immune Infiltration in Multiple Human Cancers. Cancers, 2020, 12, 957.	1.7	10
26	dbCID: a manually curated resource for exploring the driver indels in human cancer. Briefings in Bioinformatics, 2019, 20, 1925-1933.	3.2	11
27	Comprehensive Analysis of Alzheimerâ€™s Disease Biologically Candidate Causal Genes Revealed by Function Association Study With GWAS. IEEE Access, 2019, 7, 114236-114245.	2.6	2
28	SPHot: Prediction of Hot Spots in Protein-RNA Complexes by Protein Sequence Information and Ensemble Classifier. IEEE Access, 2019, 7, 104941-104946.	2.6	7
29	MECoRank: cancer driver genes discovery simultaneously evaluating the impact of SNVs and differential expression on transcriptional networks. BMC Medical Genomics, 2019, 12, 140.	0.7	3
30	An analysis of mutational signatures of synonymous mutations across 15 cancer types. BMC Medical Genetics, 2019, 20, 190.	2.1	15
31	Computational identification of deleterious synonymous variants in human genomes using a feature-based approach. BMC Medical Genomics, 2019, 12, 12.	0.7	47
32	dbCPM: a manually curated database for exploring the cancer passenger mutations. Briefings in Bioinformatics, 2018, , .	3.2	10
33	dbCRSR: a manually curated database for regulation of cancer radiosensitivity. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	8
34	Complete Genome Sequence of Clostridium kluyveri JZZ Applied in Chinese Strong-Flavor Liquor Production. Current Microbiology, 2018, 75, 1429-1433.	1.0	11
35	Computational Prediction of Driver Missense Mutations in Melanoma. Lecture Notes in Computer Science, 2018, , 438-447.	1.0	0
36	Cancer Subtype Discovery Based on Integrative Model of Multigenomic Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 1115-1121.	1.9	32

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37	DriverFinder: A Gene Length-Based Network Method to Identify Cancer Driver Genes. Complexity, 2017, 2017, 1-10.	0.9	12
38	Identification of driver pathways in cancer based on combinatorial patterns of somatic gene mutations. Neoplasma, 2016, 63, 57-63.	0.7	5
39	Cancer genes discovery based on integtating transcriptomic data and the impact of gene length. , 2016, , .		0
40	LNDriver: identifying driver genes by integrating mutation and expression data based on gene-gene interaction network. BMC Bioinformatics, 2016, 17, 467.	1.2	28
41	Concordance between somatic copy number loss and down-regulated expression: A pan-cancer study of cancer predisposition genes. Scientific Reports, 2016, 6, 37358.	1.6	13
42	Prediction of proteinâ€“protein interaction sites by means of ensemble learning and weighted feature descriptor. Journal of Biological Research, 2016, 23, 10.	2.2	7
43	MET Exon 14 Skipping in Non-Small Cell Lung Cancer. Oncologist, 2016, 21, 481-486.	1.9	94
44	CINOEDV: a co-information based method for detecting and visualizing n-order epistatic interactions. BMC Bioinformatics, 2016, 17, 214.	1.2	27
45	Identification of mutated driver pathways in cancer using a multi-objective optimization model. Computers in Biology and Medicine, 2016, 72, 22-29.	3.9	18
46	A Sequence-Based Dynamic Ensemble Learning System for Protein Ligand-Binding Site Prediction. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2016, 13, 901-912.	1.9	32
47	dbDSM: a manually curated database for deleterious synonymous mutations. Bioinformatics, 2016, 32, 1914-1916.	1.8	33
48	Identification of ovarian cancer subtype-specific network modules and candidate drivers through an integrative genomics approach. Oncotarget, 2016, 7, 4298-4309.	0.8	20
49	Predicting hot spots in protein interfaces based on protrusion index, pseudo hydrophobicity and electron-ion interaction pseudopotential features. Oncotarget, 2016, 7, 18065-18075.	0.8	21
50	Identification of breast cancer candidate genes using gene co-expression and protein-protein interaction information. Oncotarget, 2016, 7, 36092-36100.	0.8	19
51	dbCPG: A web resource for cancer predisposition genes. Oncotarget, 2016, 7, 37803-37811.	0.8	15
52	MGDB: a comprehensive database of genes involved in melanoma. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav097.	1.4	11
53	Module Based Differential Coexpression Analysis Method for Type 2 Diabetes. BioMed Research International, 2015, 2015, 1-8.	0.9	12
54	OCGene: a database of experimentally verified ovarian cancer-related genes with precomputed regulation information. Cell Death and Disease, 2015, 6, e2036-e2036.	2.7	13

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55	Inconsistency and features of single nucleotide variants detected in whole exome sequencing versus transcriptome sequencing: A case study in lung cancer. Methods, 2015, 83, 118-127.	1.9	33
56	Automatic classification for field crop insects via multiple-task sparse representation and multiple-kernel learning. Computers and Electronics in Agriculture, 2015, 119, 123-132.	3.7	120
57	Prediction of cancer cell sensitivity to natural products based on genomic and chemical properties. PeerJ, 2015, 3, e1425.	0.9	11
58	Biomedical Data Integration, Modeling, and Simulation in the Era of Big Data and Translational Medicine. BioMed Research International, 2014, 2014, 1-1.	0.9	6
59	A Meta-analysis of Somatic Mutations from Next Generation Sequencing of 241 Melanomas: A Road Map for the Study of Genes with Potential Clinical Relevance. Molecular Cancer Therapeutics, 2014, 13, 1918-1928.	1.9	84
60	Potential Driver Genes Regulated by OncomiRNA Are Associated with Druggability in Pan-Negative Melanoma. Lecture Notes in Computer Science, 2014, , 315-321.	1.0	0
61	Comparative Assessment of Data Sets of Protein Interaction Hot Spots Used in the Computational Method. Lecture Notes in Computer Science, 2014, , 478-486.	1.0	0
62	Prediction of protein-protein interactions from amino acid sequences with ensemble extreme learning machines and principal component analysis. BMC Bioinformatics, 2013, 14, S10.	1.2	232
63	Network analysis of gene fusions in human cancer. BMC Bioinformatics, 2013, 14, A13.	1.2	2
64	Prediction of cytochrome P450 inhibition using ensemble of extreme learning machine. , 2013, , .		0
65	Differential coexpression analysis in gene modules level and its application to type 2 diabetes. , 2013, , .		1
66	Application of next generation sequencing to human gene fusion detection: computational tools, features and perspectives. Briefings in Bioinformatics, 2013, 14, 506-519.	3.2	102
67	Next-generation sequencing of paired tyrosine kinase inhibitor-sensitive and -resistant EGFR mutant lung cancer cell lines identifies spectrum of DNA changes associated with drug resistance. Genome Research, 2013, 23, 1434-1445.	2.4	48
68	BRAF L597 Mutations in Melanoma Are Associated with Sensitivity to MEK Inhibitors. Cancer Discovery, 2012, 2, 791-797.	7.7	194
69	Investigating the relationship of DNA methylation with mutation rate and allele frequency in the human genome. BMC Genomics, 2012, 13, S7.	1.2	92
70	NGS catalog: A database of next generation sequencing studies in humans. Human Mutation, 2012, 33, E2341-E2355.	1.1	32
71	Exploiting a Reduced Set of Weighted Average Features to Improve Prediction of DNA-Binding Residues from 3D Structures. PLoS ONE, 2011, 6, e28440.	1.1	30
72	Virus interactions with human signal transduction pathways. International Journal of Computational Biology and Drug Design, 2011, 4, 83.	0.3	19

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73	Functional complementation between transcriptional methylation regulation and post-transcriptional microRNA regulation in the human genome. BMC Genomics, 2011, 12, S15.	1.2	52
74	Do cancer proteins really interact strongly in the human proteinâ€“protein interaction network?. Computational Biology and Chemistry, 2011, 35, 121-125.	1.1	38
75	Sequence-Based Prediction of Protein-Protein Interactions by Means of Rotation Forest and Autocorrelation Descriptor. Protein and Peptide Letters, 2010, 17, 137-145.	0.4	144
76	Prediction of β-Hairpins in Proteins Using Physicochemical Properties and Structure Information. Protein and Peptide Letters, 2010, 17, 1123-1128.	0.4	11
77	Prediction of Protein-Protein Interactions from Protein Sequence Using Local Descriptors. Protein and Peptide Letters, 2010, 17, 1085-1090.	0.4	144
78	Improved Method for Predicting π-Turns in Proteins Using a Two-Stage Classifier. Protein and Peptide Letters, 2010, 17, 1117-1122.	0.4	11
79	Predicting proteinâ€“protein interactions from sequence using correlation coefficient and high-quality interaction dataset. Amino Acids, 2010, 38, 891-899.	1.2	82
80	Predicting proteinâ€“protein interactions from protein sequences using meta predictor. Amino Acids, 2010, 39, 1595-1599.	1.2	78
81	APIS: accurate prediction of hot spots in protein interfaces by combining protrusion index with solvent accessibility. BMC Bioinformatics, 2010, 11, 174.	1.2	178
82	WEIGHTED NEIGHBORHOOD CLASSIFIER FOR THE CLASSIFICATION OF IMBALANCED TUMOR DATASET. Journal of Circuits, Systems and Computers, 2010, 19, 259-273.	1.0	9
83	Computational Methods for the Prediction of Protein-Protein Interactions. Protein and Peptide Letters, 2010, 17, 1069-1078.	0.4	23
84	Prediction of Protein-Protein Interaction Sites by Using Autocorrelation Descriptor and Support Vector Machine. Lecture Notes in Computer Science, 2010, , 76-82.	1.0	0
85	Efficient Ensemble Schemes for Protein Secondary Structure Prediction. Protein and Peptide Letters, 2008, 15, 488-493.	0.4	7
86	Inferring Strengths of Protein-Protein Interaction Using Artificial Neural Network. Neural Networks (IJCNN), International Joint Conference on, 2007, , .	0.0	1