Xiangxiang Zeng

List of Publications by Year
in descending order

152 papers	7,900 citations	44069 48 h-index	54911 84 g-index
155 all docs	155 docs citations	155 times ranked	4288 citing authors

#	Article	IF	Citations
1	ADMETlab 2.0: an integrated online platform for accurate and comprehensive predictions of ADMET properties. Nucleic Acids Research, 2021, 49, W5-W14.	14.5	915
2	deepDR: a network-based deep learning approach to<i>in silico</i>drug repositioning. Bioinformatics, 2019, 35, 5191-5198.	4.1	343
3	A comprehensive overview and evaluation of circular RNA detection tools. PLoS Computational Biology, 2017, 13, e1005420.	3.2	313
4	Integrative approaches for predicting microRNA function and prioritizing disease-related microRNA using biological interaction networks. Briefings in Bioinformatics, 2016, 17, 193-203.	6.5	307
5	Inferring MicroRNA-Disease Associations by Random Walk on a Heterogeneous Network with Multiple Data Sources. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 905-915.	3.0	265
6	Prediction of potential disease-associated microRNAs using structural perturbation method. Bioinformatics, 2018, 34, 2425-2432.	4.1	229
7	Prediction and Validation of Disease Genes Using HeteSim Scores. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 687-695.	3.0	199
8	Target identification among known drugs by deep learning from heterogeneous networks. Chemical Science, 2020, 11, 1775-1797.	7.4	193
9	Repurpose Open Data to Discover Therapeutics for COVID-19 Using Deep Learning. Journal of Proteome Research, 2020, 19, 4624-4636.	3.7	183
10	Similarity computation strategies in the microRNA-disease network: a survey. Briefings in Functional Genomics, 2016, 15, elv024.	2.7	172
11	nDNA-prot: identification of DNA-binding proteins based on unbalanced classification. BMC Bioinformatics, 2014, 15, 298.	2.6	158
12	Pretata: predicting TATA binding proteins with novel features and dimensionality reduction strategy. BMC Systems Biology, 2016, 10, 114.	3.0	143
13	Identifying enhancerâ€"promoter interactions with neural network based on pre-trained DNA vectors and attention mechanism. Bioinformatics, 2020, 36, 1037-1043.	4.1	127
14	Meta-Path Methods for Prioritizing Candidate Disease miRNAs. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 283-291.	3.0	126
15	Spiking Neural P Systems With Colored Spikes. IEEE Transactions on Cognitive and Developmental Systems, 2018, 10, 1106-1115.	3.8	116
16	A Consensus Community-Based Particle Swarm Optimization for Dynamic Community Detection. IEEE Transactions on Cybernetics, 2020, 50, 2502-2513.	9.5	115
17	Spiking Neural P Systems with Thresholds. Neural Computation, 2014, 26, 1340-1361.	2.2	113
18	Deterministic solutions to QSAT and Q3SAT by spiking neural P systems with pre-computed resources. Theoretical Computer Science, 2010, 411, 2345-2358.	0.9	111

#	Article	IF	Citations
19	StackCPPred: a stacking and pairwise energy content-based prediction of cell-penetrating peptides and their uptake efficiency. Bioinformatics, 2020, 36, 3028-3034.	4.1	111
20	Application of deep learning methods in biological networks. Briefings in Bioinformatics, 2021, 22, 1902-1917.	6.5	111
21	MOEA/HD: A Multiobjective Evolutionary Algorithm Based on Hierarchical Decomposition. IEEE Transactions on Cybernetics, 2019, 49, 517-526.	9.5	109
22	Toward better drug discovery with knowledge graph. Current Opinion in Structural Biology, 2022, 72, 114-126.	5.7	108
23	Sequence clustering in bioinformatics: an empirical study. Briefings in Bioinformatics, 2018, , .	6.5	104
24	Network-based prediction of drug–target interactions using an arbitrary-order proximity embedded deep forest. Bioinformatics, 2020, 36, 2805-2812.	4.1	101
25	Predicting disease-associated circular RNAs using deep forests combined with positive-unlabeled learning methods. Briefings in Bioinformatics, 2020, 21, 1425-1436.	6.5	96
26	MUFFIN: multi-scale feature fusion for drug–drug interaction prediction. Bioinformatics, 2021, 37, 2651-2658.	4.1	91
27	An Evolutionary Algorithm Based on Minkowski Distance for Many-Objective Optimization. IEEE Transactions on Cybernetics, 2019, 49, 3968-3979.	9.5	85
28	A Network Reduction-Based Multiobjective Evolutionary Algorithm for Community Detection in Large-Scale Complex Networks. IEEE Transactions on Cybernetics, 2020, 50, 703-716.	9.5	83
29	Spiking Neural P Systems With Scheduled Synapses. IEEE Transactions on Nanobioscience, 2017, 16, 792-801.	3.3	82
30	Mobility Based Trust Evaluation for Heterogeneous Electric Vehicles Network in Smart Cities. IEEE Transactions on Intelligent Transportation Systems, 2021, 22, 1797-1806.	8.0	77
31	A decision-making framework for precision marketing. Expert Systems With Applications, 2015, 42, 3357-3367.	7.6	76
32	On languages generated by spiking neural P systems with weights. Information Sciences, 2014, 278, 423-433.	6.9	75
33	Probability-based collaborative filtering model for predicting gene–disease associations. BMC Medical Genomics, 2017, 10, 76.	1.5	73
34	Prediction of Potential Disease-Associated MicroRNAs by Using Neural Networks. Molecular Therapy - Nucleic Acids, 2019, 16, 566-575.	5.1	70
35	Time-Free Spiking Neural P Systems. Neural Computation, 2011, 23, 1320-1342.	2.2	69
36	Computational methods for identifying the critical nodes in biological networks. Briefings in Bioinformatics, 2020, 21, 486-497.	6.5	69

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37	A novel molecular representation with BiGRU neural networks for learning atom. Briefings in Bioinformatics, 2020, 21, 2099-2111.	6.5	69
38	Spiking Neural P Systems with Weighted Synapses. Neural Processing Letters, 2012, 35, 13-27.	3.2	68
39	Improving tRNAscan–SE Annotation Results via Ensemble Classifiers. Molecular Informatics, 2015, 34, 761-770.	2.5	66
40	Asynchronous spiking neural P systems with rules on synapses. Neurocomputing, 2015, 151, 1439-1445.	5.9	65
41	iEnhancer-XG: interpretable sequence-based enhancers and their strength predictor. Bioinformatics, 2021, 37, 1060-1067.	4.1	61
42	Performing Four Basic Arithmetic Operations With Spiking Neural P Systems. IEEE Transactions on Nanobioscience, 2012, 11, 366-374.	3.3	57
43	On Some Classes of Sequential Spiking Neural P Systems. Neural Computation, 2014, 26, 974-997.	2.2	57
44	Homogeneous Spiking Neural P Systems. Fundamenta Informaticae, 2009, 97, 275-294.	0.4	54
45	A Parallel Workflow Pattern Modeling Using Spiking Neural P Systems With Colored Spikes. IEEE Transactions on Nanobioscience, 2018, 17, 474-484.	3.3	54
46	Monodirectional Tissue *P* Systems With Promoters. IEEE Transactions on Cybernetics, 2021, 51, 438-450.	9.5	53
47	Implementation of Arithmetic Operations With Time-Free Spiking Neural P Systems. IEEE Transactions on Nanobioscience, 2015, 14, 617-624.	3.3	52
48	Deep learning methods for biomedical named entity recognition: a survey and qualitative comparison. Briefings in Bioinformatics, 2021, 22, .	6.5	52
49	On string languages generated by spiking neural P systems with exhaustive use of rules. Natural Computing, 2008, 7, 535-549.	3.0	51
50	Learning spatial structures of proteins improves protein–protein interaction prediction. Briefings in Bioinformatics, 2022, 23, .	6.5	51
51	Deep learning for drug repurposing: Methods, databases, and applications. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2022, 12, .	14.6	48
52	Approaches for Recognizing Disease Genes Based on Network. BioMed Research International, 2014, 2014, 1-10.	1.9	46
53	Small Universal Spiking Neural P Systems Working in Exhaustive Mode. IEEE Transactions on Nanobioscience, 2011, 10, 99-105.	3.3	45
54	Deep learning in retrosynthesis planning: datasets, models and tools. Briefings in Bioinformatics, 2022, 23, .	6.5	45

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55	Prediction and validation of association between microRNAs and diseases by multipath methods. Biochimica Et Biophysica Acta - General Subjects, 2016, 1860, 2735-2739.	2.4	43
56	Small Universal Spiking Neural P Systems with Anti-Spikes. Journal of Computational and Theoretical Nanoscience, 2013, 10, 999-1006.	0.4	38
57	A hybrid heuristic algorithm for the 2D variable-sized bin packing problem. European Journal of Operational Research, 2014, 238, 95-103.	5.7	38
58	On languages generated by asynchronous spiking neural P systems. Theoretical Computer Science, 2009, 410, 2478-2488.	0.9	37
59	Complex Network Clustering by a Multi-objective Evolutionary Algorithm Based on Decomposition and Membrane Structure. Scientific Reports, 2016, 6, 33870.	3.3	32
60	Predicting enhancer-promoter interactions by deep learning and matching heuristic. Briefings in Bioinformatics, 2021, 22, .	6.5	32
61	Review of Protein Subcellular Localization Prediction. Current Bioinformatics, 2014, 9, 331-342.	1.5	32
62	On solutions and representations of spiking neural P systems with rules on synapses. Information Sciences, 2019, 501, 30-49.	6.9	31
63	Monodirectional tissue P systems with channel states. Information Sciences, 2021, 546, 206-219.	6.9	31
64	Small universal simple spiking neural P systems with weights. Science China Information Sciences, 2014, 57, 1-11.	4.3	30
65	Prediction of Drug–Gene Interaction by Using Metapath2vec. Frontiers in Genetics, 2018, 9, 248.	2.3	29
66	Computing with viruses. Theoretical Computer Science, 2016, 623, 146-159.	0.9	28
67	Multiobjective Particle Swarm Optimization Based on Network Embedding for Complex Network Community Detection. IEEE Transactions on Computational Social Systems, 2020, 7, 437-449.	4.4	28
68	Homogeneous spiking neural P systems with structural plasticity. Journal of Membrane Computing, 2021, 3, 10-21.	1.8	28
69	Identification of cytokine via an improved genetic algorithm. Frontiers of Computer Science, 2015, 9, 643-651.	2.4	26
70	Asynchronous Spiking Neural P Systems with Anti-Spikes. Neural Processing Letters, 2015, 42, 633-647.	3.2	25
71	Deep collaborative filtering for prediction of disease genes. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 17, 1-1.	3.0	25
72	A network-based approach to uncover microRNA-mediated disease comorbidities and potential pathobiological implications. Npj Systems Biology and Applications, 2019, 5, 41.	3.0	24

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73	Matrix Representation of Spiking Neural P Systems. Lecture Notes in Computer Science, 2010, , 377-391.	1.3	24
74	The power of time-free tissue P systems: Attacking NP-complete problems. Neurocomputing, 2015, 159, 151-156.	5.9	23
75	On String Languages Generated by Spiking Neural P Systems With Structural Plasticity. IEEE Transactions on Nanobioscience, 2018, 17, 560-566.	3.3	22
76	Matrix representation and simulation algorithm of spiking neural P systems with structural plasticity. Journal of Membrane Computing, 2019, 1, 145-160.	1.8	21
77	A Polar-Metric-Based Evolutionary Algorithm. IEEE Transactions on Cybernetics, 2021, 51, 3429-3440.	9.5	21
78	RicyerDB: A Database For Collecting Rice Yield-related Genes with Biological Analysis. International Journal of Biological Sciences, 2018, 14, 965-970.	6.4	20
79	GraphCPI: Graph Neural Representation Learning for Compound-Protein Interaction. , 2019, , .		20
80	Review of unsupervised pretraining strategies for molecules representation. Briefings in Functional Genomics, 2021, 20, 323-332.	2.7	20
81	Monodirectional Evolutional Symport Tissue P Systems With Promoters and Cell Division. IEEE Transactions on Parallel and Distributed Systems, 2022, 33, 332-342.	5.6	20
82	Sc-ncDNAPred: A Sequence-Based Predictor for Identifying Non-coding DNA in Saccharomyces cerevisiae. Frontiers in Microbiology, 2018, 9, 2174.	3.5	19
83	Weighted Spiking Neural P Systems with Rules on Synapses. Fundamenta Informaticae, 2014, 134, 201-218.	0.4	16
84	A Note on Small Universal Spiking Neural P Systems. Lecture Notes in Computer Science, 2010, , 436-447.	1.3	16
85	Reconstructing evolutionary trees in parallel for massive sequences. BMC Systems Biology, 2017, 11, 100.	3.0	15
86	A spatial-temporal gated attention module for molecular property prediction based on molecular geometry. Briefings in Bioinformatics, 2021, 22, .	6.5	15
87	Investigation and development of maize fused network analysis with multi-omics. Plant Physiology and Biochemistry, 2019, 141, 380-387.	5.8	14
88	A component overlapping attribute clustering (COAC) algorithm for single-cell RNA sequencing data analysis and potential pathobiological implications. PLoS Computational Biology, 2019, 15, e1006772.	3.2	14
89	The computational power of cell-like P systems with one protein on membrane. Journal of Membrane Computing, 2020, 2, 332-340.	1.8	14
90	Minirmd: accurate and fast duplicate removal tool for short reads via multiple minimizers. Bioinformatics, 2021, 37, 1604-1606.	4.1	14

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91	preMLI: a pre-trained method to uncover microRNA–lncRNA potential interactions. Briefings in Bioinformatics, 2022, 23, .	6.5	14
92	Decision Tree Classification Model for Popularity Forecast of Chinese Colleges. Journal of Applied Mathematics, 2014, 2014, 1-7.	0.9	12
93	Neural-like P systems with plasmids. Information and Computation, 2021, 281, 104766.	0.7	12
94	HeTDR: Drug repositioning based on heterogeneous networks and text mining. Patterns, 2021, 2, 100307.	5.9	12
95	A decision support model for investment on P2P lending platform. PLoS ONE, 2017, 12, e0184242.	2.5	12
96	Prediction of MicroRNA-disease Associations by Matrix Completion. Current Proteomics, 2016, 13, 151-157.	0.3	12
97	scIMC: a platform for benchmarking comparison and visualization analysis of scRNA-seq data imputation methods. Nucleic Acids Research, 2022, 50, 4877-4899.	14.5	12
98	Investment behavior prediction in heterogeneous information network. Neurocomputing, 2016, 217, 125-132.	5.9	11
99	Artificial‐Intelligence‐Enabled Reagent‐Free Imaging Hematology Analyzer. Advanced Intelligent Systems, 2021, 3, 2000277.	6.1	11
100	Several Applications of Spiking Neural P Systems with Weights. Journal of Computational and Theoretical Nanoscience, 2012, 9, 769-777.	0.4	10
101	Normal forms for spiking neural P systems and some of its variants. Information Sciences, 2022, 595, 344-363.	6.9	9
102	A Multi-Population Multi-Objective Evolutionary Algorithm Based on the Contribution of Decision Variables to Objectives for Large-Scale Multi/Many-Objective Optimization. IEEE Transactions on Cybernetics, 2023, 53, 6998-7007.	9.5	9
103	HPTree: Reconstructing phylogenetic trees for ultra-large unaligned DNA sequences via NJ model and Hadoop. , 2016, , .		8
104	Iteratively collective prediction of disease-gene associations through the incomplete network. , 2017, , .		8
105	Details in the evaluation of circular RNA detection tools: Reply to Chen and Chuang. PLoS Computational Biology, 2019, 15, e1006916.	3.2	8
106	The computational power of monodirectional tissue P systems with symport rules. Information and Computation, 2021, 281, 104751.	0.7	8
107	A Stable Matching-Based Selection and Memory Enhanced MOEA/D for Evolutionary Dynamic Multiobjective Optimization. , 2015, , .		7
108	On the Computational Power of Asynchronous Axon Membrane Systems. IEEE Transactions on Emerging Topics in Computational Intelligence, 2020, 4, 696-704.	4.9	7

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109	*De novo* generation of dual-target ligands using adversarial training and reinforcement learning. Briefings in Bioinformatics, 2021, 22, .	6.5	7
110	A Classification Method for Microarrays Based on Diversity. Current Bioinformatics, 2016, 11, 590-597.	1.5	7
111	Solving a PSPACE-complete problem by symport/antiport P systems with promoters and membrane division. Journal of Membrane Computing, 2021, 3, 296-302.	1.8	6
112	A weakly universal spiking neural P system. Mathematical and Computer Modelling, 2010, 52, 1940-1946.	2.0	5
113	Small universal asynchronous spiking neural P systems. , 2010, , .		5
114	Predict the Relationship between Gene and Large Yellow Croaker's Economic Traits. Molecules, 2017, 22, 1978.	3.8	5
115	Using MOEA with Redistribution and Consensus Branches to Infer Phylogenies. International Journal of Molecular Sciences, 2018, 19, 62.	4.1	5
116	Learning to Predict Drug Target Interaction From Missing Not at Random Labels. IEEE Transactions on Nanobioscience, 2019, 18, 353-359.	3.3	5
117	Are dropout imputation methods for scRNA-seq effective for scATAC-seq data?. Briefings in Bioinformatics, 2022, 23, .	6.5	5
118	Solving Multidimensional 0-1 Knapsack Problem with Time-Free Tissue P Systems. Journal of Applied Mathematics, 2014, 2014, 1-6.	0.9	4
119	Identification and Analysis of Rice Yield-Related Candidate Genes by Walking on the Functional Network. Frontiers in Plant Science, 2018, 9, 1685.	3.6	4
120	CarSite-II: an integrated classification algorithm for identifying carbonylated sites based on K-means similarity-based undersampling and synthetic minority oversampling techniques. BMC Bioinformatics, 2021, 22, 216.	2.6	4
121	Active Semisupervised Model for Improving the Identification of Anticancer Peptides. ACS Omega, 2021, 6, 23998-24008.	3.5	4
122	A Bayesian Investment Model for Online P2P Lending. Communications in Computer and Information Science, 2013, , 21-30.	0.5	4
123	Editorial: Artificial Intelligence in Bioinformatics and Drug Repurposing: Methods and Applications. Frontiers in Genetics, 2022, 13, 870795.	2.3	4
124	Rule synchronization for monodirectional tissue-like P systems with channel states. Information and Computation, 2022, 285, 104895.	0.7	4
125	KG-MTL: Knowledge Graph Enhanced Multi-Task Learning for Molecular Interaction. IEEE Transactions on Knowledge and Data Engineering, 2022, , 1-12.	5.7	4
126	Spiking Neural P Systems for Arithmetic Operations. , 2011, , .		3

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127	Spiking neural P systems with anti-spikes and without annihilating priority working in a 'flip-flop' way. International Journal of Computing Science and Mathematics, 2013, 4, 152.	0.3	3
128	Simulating Spiking Neural P Systems with Circuits. Journal of Computational and Theoretical Nanoscience, 2015, 12, 2023-2026.	0.4	3
129	Latent factor model with heterogeneous similarity regularization for predicting gene-disease associations. , 2016, , .		3
130	LncRNA-disease association prediction based on neighborhood information aggregation in neural network. , 2018, , .		3
131	Structural Hole Spanner in HumanNet Identifies Disease Gene and Drug targets. IEEE Access, 2018, 6, 35392-35401.	4.2	3
132	Investigating Maize Yield-Related Genes in Multiple Omics Interaction Network Data. IEEE Transactions on Nanobioscience, 2020, 19, 142-151.	3.3	3
133	Integrative Approaches for Predicting microRNA Function and Prioritizing Disease-Related microRNA Using Biological Interaction Networks. , 2019, , 75-105.		3
134	WormStep: An Improved Compact Graphical Representation of DNA Sequences Based on Worm Curve. Journal of Computational and Theoretical Nanoscience, 2013, 10, 189-193.	0.4	2
135	Embedded Based Miniaturized Universal Electrochemical Sensing Platform. Journal of Sensors, 2016, 2016, 1-8.	1.1	2
136	Artificialâ€Intelligenceâ€Enabled Reagentâ€Free Imaging Hematology Analyzer. Advanced Intelligent Systems, 2021, 3, 2170060.	6.1	2
137	A weakly universal spiking neural P system. , 2009, , .		1
138	A uniform solution to the independent set problem through tissue P systems with cell separation. Frontiers of Computer Science, 2012, 6, 477.	2.4	1
139	MOEA/D for Energy-Aware Scheduling on Heterogeneous Computing Systems. Communications in Computer and Information Science, 2015, , 94-106.	0.5	1
140	Drug Target Interaction Prediction with Non-random Missing Labels. , 2018, , .		1
141	A Deep Neural Network for Antimicrobial Peptide Recognition. , 2019, , .		1
142	Time-Free Tissue P Systems for Solving the Hamilton Path Problem. Communications in Computer and Information Science, 2014, , 562-565.	0.5	1
143	LADstackING: Stacking Ensemble Learning-based Computational Model for Predicting Potential LncRNA-disease Associations. , 2021, , .		1
144	P Systems with 2D Picture Grammars. , 2011, , .		0

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145	A Modified Estimation of Distribution Algorithm for Numeric Optimization. , 2011, , .		0
146	Molecular Logic Computation with Debugging Method. Journal of Nanomaterials, 2015, 2015, 1-11.	2.7	0
147	A drug information embedding method based on graph convolution neural network. , 2021, , .		0
148	A New Graphical Representation of Protein Sequences Based on Dual-Vector Model. Communications in Computer and Information Science, 2014, , 629-632.	0.5	0
149	An Implementation of Elementary Arithmetic with Virus Machine. Lecture Notes in Computer Science, 2018, , 304-317.	1.3	0
150	Small Spiking Neural P Systems with Structural Plasticity. Lecture Notes in Computer Science, 2018, , 45-56.	1.3	0
151	A multi-task learning method for analyzing microbiota as cancer immunotherapy signal. , 2020, , .		0
152	Pm^6 A: an Integrated Classification Algorithm for 2021 IEEE International Conference on Bioinformatics and Biomedicine (BIBM) Identifying m^6 A Sites. , 2021, , .		0