

Shaoliang Peng

List of Publications by Year in descending order

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107
papers

7,062
citations

279487
23
h-index

62479
80
g-index

117
all docs

117
docs citations

117
times ranked

13441
citing authors

#	ARTICLE	IF	CITATIONS
1	A review of artificial intelligence methods combined with Raman spectroscopy to identify the composition of substances. Journal of Raman Spectroscopy, 2022, 53, 6-19.	1.2	31
2	Machine Learning Applications in Drug Repurposing. Interdisciplinary Sciences, Computational Life Sciences, 2022, 14, 15-21.	2.2	27
3	OUP accepted manuscript. Briefings in Bioinformatics, 2022, 23, .	3.2	5
4	Channel pruning guided by global channel relation. Applied Intelligence, 2022, 52, 16202-16213.	3.3	2
5	D3AI-CoV: a deep learning platform for predicting drug targets and for virtual screening against COVID-19. Briefings in Bioinformatics, 2022, 23, .	3.2	13
6	Discriminant Projection Shared Dictionary Learning for Classification of Tumors Using Gene Expression Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1464-1473.	1.9	3
7	CRISP-view: a database of functional genetic screens spanning multiple phenotypes. Nucleic Acids Research, 2021, 49, D848-D854.	6.5	15
8	A-CaMP: a tool for anti-cancer and antimicrobial peptide generation. Journal of Biomolecular Structure and Dynamics, 2021, 39, 285-293.	2.0	10
9	<i>In silico</i> and <i>in vitro</i> evaluation of kaempferol as a potential inhibitor of the SARS-CoV-2 main protease (3CLpro). Phytotherapy Research, 2021, 35, 2841-2845.	2.8	80
10	MDA-GCNFTG: identifying miRNA-disease associations based on graph convolutional networks via graph sampling through the feature and topology graph. Briefings in Bioinformatics, 2021, 22, .	3.2	43
11	Cotton D genome assemblies built with long-read data unveil mechanisms of centromere evolution and stress tolerance divergence. BMC Biology, 2021, 19, 115.	1.7	14
12	MultiDTI: drug-target interaction prediction based on multi-modal representation learning to bridge the gap between new chemical entities and known heterogeneous network. Bioinformatics, 2021, 37, 4485-4492.	1.8	39
13	DeepR2cov: deep representation learning on heterogeneous drug networks to discover anti-inflammatory agents for COVID-19. Briefings in Bioinformatics, 2021, 22, .	3.2	26
14	Performance Improvement of Atmospheric Continuous-Variable Quantum Key Distribution with Untrusted Source. Entropy, 2021, 23, 760.	1.1	1
15	VISPR-online: a web-based interactive tool to visualize CRISPR screening experiments. BMC Bioinformatics, 2021, 22, 344.	1.2	2
16	LUNAR :Drug Screening for Novel Coronavirus Based on Representation Learning Graph Convolutional Network. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1290-1298.	1.9	8
17	BioERP: biomedical heterogeneous network-based self-supervised representation learning approach for entity relationship predictions. Bioinformatics, 2021, 37, 4793-4800.	1.8	12
18	Heterogeneous graph attention networks for drug virus association prediction. Methods, 2021, 198, 11-11.	1.9	8

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19	D2D-Enabled Mobile-Edge Computation Offloading for Multiuser IoT Network. IEEE Internet of Things Journal, 2021, 8, 12490-12504.	5.5	37
20	Discovery of Genetic Biomarkers for Alzheimer's Disease Using Adaptive Convolutional Neural Networks Ensemble and Genome-Wide Association Studies. Interdisciplinary Sciences, Computational Life Sciences, 2021, 13, 787-800.	2.2	5
21	A Radiomics Signature to Quantitatively Analyze COVID-19-Infected Pulmonary Lesions. Interdisciplinary Sciences, Computational Life Sciences, 2021, 13, 61-72.	2.2	18
22	Emerging Mutations in Nsp1 of SARS-CoV-2 and Their Effect on the Structural Stability. Pathogens, 2021, 10, 1285.	1.2	18
23	Guest Editorial for the 17th Asia Pacific Bioinformatics Conference. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2123-2124.	1.9	0
24	DFL-PiDA: Prediction of Piwi-interacting RNA-Disease Associations based on Deep Feature Learning. , 2021, , .		5
25	H-VAE: A Hybrid Variational AutoEncoder with Data Augmentation in Predicting CRISPR/Cas9 Off-target. , 2021, , .		0
26	A Knowledge-aware Machine Reading Comprehension Framework for Dialogue Symptom Diagnosis. , 2021, , .		1
27	LADstackING: Stacking Ensemble Learning-based Computational Model for Predicting Potential LncRNA-disease Associations. , 2021, , .		1
28	FEDI: Few-shot learning based on Earth Mover's Distance algorithm combined with deep residual network to identify diabetic retinopathy. , 2021, , .		2
29	High-Scalable Collaborated Parallel Framework for Large-Scale Molecular Dynamic Simulation on Tianhe-2 Supercomputer. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 804-816.	1.9	2
30	COPCOP: A Novel Algorithm and Parallel Optimization Framework for Co-Evolutionary Domain Detection. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, , 1-1.	1.9	1
31	Joint consensus and diversity for multi-view semi-supervised classification. Machine Learning, 2020, 109, 445-465.	3.4	20
32	An efficient framework for generating robust adversarial examples. International Journal of Intelligent Systems, 2020, 35, 1433-1449.	3.3	8
33	Clustering-Evolutionary Random Support Vector Machine Ensemble for fMRI-Based Asperger Syndrome Diagnosis. Computer Journal, 2020, , .	1.5	1
34	An Efficient Double-Layer Blockchain Method for Vaccine Production Supervision. IEEE Transactions on Nanobioscience, 2020, 19, 579-587.	2.2	35
35	OffScan: a universal and fast CRISPR off-target sites detection tool. BMC Genomics, 2020, 21, 872.	1.2	14
36	A hybrid two-stage financial stock forecasting algorithm based on clustering and ensemble learning. Applied Intelligence, 2020, 50, 3852-3867.	3.3	42

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37	A Scheme to Optimize Roadside Parking Management by Using Blockchain Technology. , 2020, , .		3
38	Predicting Drugs for COVID-19/SARS-CoV-2 via Heterogeneous Graph Attention Networks. , 2020, , .		2
39	Predicting CRISPR-Cas9 Off-target with Self-supervised Neural Networks. , 2020, , .		6
40	A Review on Scalability of Blockchain. , 2020, , .		38
41	Blockchain for Data Science. , 2020, , .		10
42	DMCM: a Data-adaptive Mutation Clustering Method to identify cancer-related mutation clusters. Bioinformatics, 2019, 35, 389-397.	1.8	28
43	Voluntary Vaccination through Perceiving Epidemic Severity in Social Networks. Complexity, 2019, 2019, 1-13.	0.9	1
44	Guide Positioning Sequencing identifies aberrant DNA methylation patterns that alter cell identity and tumor-immune surveillance networks. Genome Research, 2019, 29, 270-280.	2.4	25
45	A Latency-Aware Multiple Data Replicas Placement Strategy for Fog Computing. Journal of Signal Processing Systems, 2019, 91, 1191-1204.	1.4	24
46	LIVE: a manually curated encyclopedia of experimentally validated interactions of lncRNAs. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	8
47	Academic research trend analysis based on big data technology. International Journal of Computational Science and Engineering, 2019, 20, 31.	0.4	1
48	vGuard: A Spatiotemporal Efficiency Supervision Method For Vaccine Production Based On Double-level Blockchain. , 2019, , .		2
49	A General Fine-tuned Transfer Learning Model for Predicting Clinical Task Acrossing Diverse EHRs Datasets. , 2019, , .		4
50	Deep learning in omics: a survey and guideline. Briefings in Functional Genomics, 2019, 18, 41-57.	1.3	119
51	A CPU/MIC Collaborated Parallel Framework for GROMACS on Tianhe-2 Supercomputer. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 425-433.	1.9	9
52	Review of CRISPR/Cas9 sgRNA Design Tools. Interdisciplinary Sciences, Computational Life Sciences, 2018, 10, 455-465.	2.2	180
53	Complete Genomes of Two Novel Active Prophages Discovered by Bioinformatics Methods from High-Throughput Sequencing Data. IOP Conference Series: Materials Science and Engineering, 2018, 466, 012032.	0.3	1
54	ConfVD: System Reactions Analysis and Evaluation Through Misconfiguration Injection. IEEE Transactions on Reliability, 2018, 67, 1393-1405.	3.5	10

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55	A Dictionary Learning Algorithm for Gene Expression Profile Classification Based on Feature Selection. , 2018, , .		0
56	mSNP: A Massively Parallel Algorithm for Large-Scale SNP Detection. IEEE Transactions on Parallel and Distributed Systems, 2018, 29, 2557-2567.	4.0	4
57	VCSRA: A fast and accurate multiple sequence alignment algorithm with a high degree of parallelism. Journal of Genetics and Genomics, 2018, 45, 407-410.	1.7	5
58	Special issue on Computational Resources and Methods in Biological Sciences. International Journal of Biological Sciences, 2018, 14, 807-810.	2.6	3
59	Comparative analysis on precise distribution-patterns of microsatellites in HIV-1 with differential statistical method. Gene Reports, 2018, 12, 141-148.	0.4	3
60	The Integrative Method Based on the Module-Network for Identifying Driver Genes in Cancer Subtypes. Molecules, 2018, 23, 183.	1.7	23
61	cmFSM: a scalable CPU-MIC coordinated drug-finding tool by frequent subgraph mining. BMC Bioinformatics, 2018, 19, 98.	1.2	7
62	Efficient computation of motif discovery on Intel Many Integrated Core (MIC) Architecture. BMC Bioinformatics, 2018, 19, 282.	1.2	9
63	Bioinformatics applications on Apache Spark. GigaScience, 2018, 7, .	3.3	55
64	Parallelization of Molecular Docking: A Review. Current Topics in Medicinal Chemistry, 2018, 18, 1015-1028.	1.0	53
65	MyPhi: Efficient Levenshtein Distance Computation on Xeon Phi Based Architectures. Current Bioinformatics, 2018, 13, 479-486.	0.7	4
66	MicroRNAs activate gene transcription epigenetically as an enhancer trigger. RNA Biology, 2017, 14, 1326-1334.	1.5	262
67	Exploring Voluntary Vaccinating Behaviors using Evolutionary N-person Threshold Games. Scientific Reports, 2017, 7, 16355.	1.6	6
68	Multiple Sequence Alignment Based on a Suffix Tree and Center-Star Strategy: A Linear Method for Multiple Nucleotide Sequence Alignment on Spark Parallel Framework. Journal of Computational Biology, 2017, 24, 1230-1242.	0.8	17
69	mD3DOCKxb: An Ultra-Scalable CPU-MIC Coordinated Virtual Screening Framework. , 2017, , .		5
70	P-Hint-Hunt: a deep parallelized whole genome DNA methylation detection tool. BMC Genomics, 2017, 18, 134.	1.2	2
71	paraGSEA: a scalable approach for large-scale gene expression profiling. Nucleic Acids Research, 2017, 45, e155-e155.	6.5	9
72	A novel algorithm for detecting co-evolutionary domains in protein and nucleotide sequences. , 2017, , .		0

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73	mAMBER: A CPU/MIC collaborated parallel framework for AMBER on Tianhe-2 supercomputer. , 2016, , .		3
74	Parallel algorithms for large-scale biological sequence alignment on Xeon-Phi based clusters. BMC Bioinformatics, 2016, 17, 267.	1.2	9
75	Distinct Subtypes of Gastric Cancer Defined by Molecular Characterization Include Novel Mutational Signatures with Prognostic Capability. Cancer Research, 2016, 76, 1724-1732.	0.4	120
76	Whole-Genome Sequencing Reveals Diverse Models of Structural Variations in Esophageal Squamous Cell Carcinoma. American Journal of Human Genetics, 2016, 98, 256-274.	2.6	109
77	A Hybrid Parallel Strategy Based on String Graph Theory to Improve De Novo DNA Assembly on the TianHe-2 Supercomputer. Interdisciplinary Sciences, Computational Life Sciences, 2016, 8, 169-176.	2.2	0
78	B-MIC: An Ultrafast Three-Level Parallel Sequence Aligner Using MIC. Interdisciplinary Sciences, Computational Life Sciences, 2016, 8, 28-34.	2.2	2
79	MICA: A fast short-read aligner that takes full advantage of Many Integrated Core Architecture (MIC). BMC Bioinformatics, 2015, 16, S10.	1.2	14
80	Large-Scale Neo-Heterogeneous Programming and Optimization of SNP Detection on Tianhe-2. Lecture Notes in Computer Science, 2015, , 74-86.	1.0	1
81	HeMatch: A redundancy layout placement scheme for erasure-coded storages in practical heterogeneous failure patterns. Science China Information Sciences, 2015, 58, 1-11.	2.7	4
82	mD3DOCKxb: A Deep Parallel Optimized Software for Molecular Docking with Intel Xeon Phi Coprocessors. , 2015, , .		6
83	The Challenge of Scaling Genome Big Data Analysis Software on TH-2 Supercomputer. , 2015, , .		0
84	A Massively Parallel Computational Method of Reading Index Files for SOAPsnv. Interdisciplinary Sciences, Computational Life Sciences, 2015, 7, 397-404.	2.2	1
85	BWTCp: A Parallel Method for Constructing BWT in Large Collection of Genomic Reads. Lecture Notes in Computer Science, 2015, , 171-178.	1.0	3
86	Know by a handful the whole sack: efficient sampling for top-k influential user identification in large graphs. World Wide Web, 2014, 17, 627-647.	2.7	6
87	IMGPU: GPU-Accelerated Influence Maximization in Large-Scale Social Networks. IEEE Transactions on Parallel and Distributed Systems, 2014, 25, 136-145.	4.0	49
88	Mapping Central α -Helix Linker Mediated Conformational Transition Pathway of Calmodulin via Simple Computational Approach. Journal of Physical Chemistry B, 2014, 118, 9677-9685.	1.2	16
89	Genome-wide adaptive complexes to underground stresses in blind mole rats Spalax. Nature Communications, 2014, 5, 3966.	5.8	124
90	mBWA: A Massively Parallel Sequence Reads Aligner. Advances in Intelligent Systems and Computing, 2014, , 113-120.	0.5	9

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91	SOAPfuse: an algorithm for identifying fusion transcripts from paired-end RNA-Seq data. Genome Biology, 2013, 14, R12.	13.9	197
92	INCOME: Practical land monitoring in precision agriculture with sensor networks. Computer Communications, 2013, 36, 459-467.	3.1	20
93	The architecture and traffic management of wireless collaborated hybrid data center network. Computer Communication Review, 2013, 43, 511-512.	1.5	2
94	Interface structure and work function of W-Cu interfaces. Applied Physics Letters, 2013, 103, .	1.5	43
95	SOAP3-dp: Fast, Accurate and Sensitive GPU-Based Short Read Aligner. PLoS ONE, 2013, 8, e65632.	1.1	104
96	HLA-Based Parallel Simulation: A Case Study. , 2012, , .		3
97	Fast Release/Capture Sampling in Large-Scale Sensor Networks. IEEE Transactions on Mobile Computing, 2012, 11, 1274-1286.	3.9	4
98	SOAPdenovo2: an empirically improved memory-efficient short-read de novo assembler. GigaScience, 2012, 1, 18.	3.3	4,510
99	A scalable code dissemination protocol in heterogeneous wireless sensor networks. Science China Information Sciences, 2012, 55, 1323-1336.	2.7	7
100	Empirical Study on Entity Interaction Graph of Large-Scale Parallel Simulations. , 2011, , .		1
101	MPIActor: A thread-based MPI program accelerator. , 2010, , .		0
102	Exploring the practicability of mobile sensors in complex environment surveillance. , 2010, , .		0
103	Fish a lake: Fast release/capture sampling in large-scale sensor networks. , 2010, , .		0
104	Experimental Analysis of Optimistic Synchronization Algorithms for Parallel Simulation of Reaction-Diffusion Systems. , 2009, , .		9
105	EDEVs : A Scalable DEVs Formalism for Event-Scheduling Based Parallel and Distributed Simulations. , 2009, , .		6
106	SenCast: Scalable multicast in wireless sensor networks. Parallel and Distributed Processing Symposium (IPDPS), Proceedings of the International Conference on, 2008, , .	1.0	2
107	A Framework for Congestion Control for Reliable Data Delivery in Wireless Sensor Networks. , 2007, , .		2