

Ka-Chun Wong

List of Publications by Year in descending order

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141
papers

2,609
citations

236612

25
h-index

243296

44
g-index

144
all docs

144
docs citations

144
times ranked

2676
citing authors

#	ARTICLE	IF	CITATIONS
1	Particle Swarm Optimization With a Balanceable Fitness Estimation for Many-Objective Optimization Problems. IEEE Transactions on Evolutionary Computation, 2018, 22, 32-46.	7.5	202
2	Collective Human Mobility Pattern from Taxi Trips in Urban Area. PLoS ONE, 2012, 7, e34487.	1.1	150
3	Off-target predictions in CRISPR-Cas9 gene editing using deep learning. Bioinformatics, 2018, 34, i656-i663.	1.8	121
4	An External Archive-Guided Multiobjective Particle Swarm Optimization Algorithm. IEEE Transactions on Cybernetics, 2017, 47, 2794-2808.	6.2	96
5	A Clustering-Based Evolutionary Algorithm for Many-Objective Optimization Problems. IEEE Transactions on Evolutionary Computation, 2019, 23, 391-405.	7.5	91
6	Adaptive multiple-elites-guided composite differential evolution algorithm with a shift mechanism. Information Sciences, 2018, 422, 122-143.	4.0	87
7	Mirsynergy: detecting synergistic miRNA regulatory modules by overlapping neighbourhood expansion. Bioinformatics, 2014, 30, 2627-2635.	1.8	79
8	A novel artificial bee colony algorithm with an adaptive population size for numerical function optimization. Information Sciences, 2017, 414, 53-67.	4.0	70
9	Evolutionary multimodal optimization using the principle of locality. Information Sciences, 2012, 194, 138-170.	4.0	57
10	SNPdryad: predicting deleterious non-synonymous human SNPs using only orthologous protein sequences. Bioinformatics, 2014, 30, 1112-1119.	1.8	57
11	Inferring probabilistic miRNA-mRNA interaction signatures in cancers: a role-switch approach. Nucleic Acids Research, 2014, 42, e76-e76.	6.5	55
12	DNA motif elucidation using belief propagation. Nucleic Acids Research, 2013, 41, e153-e153.	6.5	53
13	An adaptive immune-inspired multi-objective algorithm with multiple differential evolution strategies. Information Sciences, 2018, 430-431, 46-64.	4.0	53
14	Discovering protein-DNA binding sequence patterns using association rule mining. Nucleic Acids Research, 2010, 38, 6324-6337.	6.5	49
15	Evolutionary Multiobjective Clustering and Its Applications to Patient Stratification. IEEE Transactions on Cybernetics, 2019, 49, 1680-1693.	6.2	49
16	iCircRBP-DHN: identification of circRNA-RBP interaction sites using deep hierarchical network. Briefings in Bioinformatics, 2021, 22, .	3.2	45
17	CRISPRNet: A Recurrent Convolutional Network Quantifies CRISPR Off-Target Activities with Mismatches and Indels. Advanced Science, 2020, 7, 1903562.	5.6	43
18	Verbal aggression detection on Twitter comments: convolutional neural network for short-text sentiment analysis. Neural Computing and Applications, 2020, 32, 10809-10818.	3.2	40

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19	SignalSpider: probabilistic pattern discovery on multiple normalized ChIP-Seq signal profiles. <i>Bioinformatics</i> , 2015, 31, 17-24.	1.8	39
20	Protein structure prediction on a lattice model via multimodal optimization techniques. , 2010, , .		38
21	A self-adaptive weighted differential evolution approach for large-scale feature selection. <i>Knowledge-Based Systems</i> , 2022, 235, 107633.	4.0	38
22	A probabilistic approach to explore human miRNA targetome by integrating miRNA-overexpression data and sequence information. <i>Bioinformatics</i> , 2014, 30, 621-628.	1.8	37
23	Intrusion detection using multi-objective evolutionary convolutional neural network for Internet of Things in Fog computing. <i>Knowledge-Based Systems</i> , 2022, 244, 108505.	4.0	37
24	Zinc-finger protein 471 suppresses gastric cancer through transcriptionally repressing downstream oncogenic PLS3 and TFAP2A. <i>Oncogene</i> , 2018, 37, 3601-3616.	2.6	35
25	A Diversity-Enhanced Resource Allocation Strategy for Decomposition-Based Multiobjective Evolutionary Algorithm. <i>IEEE Transactions on Cybernetics</i> , 2018, 48, 2388-2401.	6.2	35
26	Herd Clustering: A synergistic data clustering approach using collective intelligence. <i>Applied Soft Computing Journal</i> , 2014, 23, 61-75.	4.1	29
27	Machine Learning Protocols in Early Cancer Detection Based on Liquid Biopsy: A Survey. <i>Life</i> , 2021, 11, 638.	1.1	28
28	A Short Survey on Data Clustering Algorithms. , 2015, , .		27
29	A novel multi-objective evolutionary algorithm with dynamic decomposition strategy. <i>Swarm and Evolutionary Computation</i> , 2019, 48, 182-200.	4.5	26
30	An Effective Ensemble Framework for Multiobjective Optimization. <i>IEEE Transactions on Evolutionary Computation</i> , 2019, 23, 645-659.	7.5	26
31	Generalizing and learning protein-DNA binding sequence representations by an evolutionary algorithm. <i>Soft Computing</i> , 2011, 15, 1631-1642.	2.1	25
32	Synergizing CRISPR/Cas9 off-target predictions for ensemble insights and practical applications. <i>Bioinformatics</i> , 2019, 35, 1108-1115.	1.8	25
33	A Self-Guided Reference Vector Strategy for Many-Objective Optimization. <i>IEEE Transactions on Cybernetics</i> , 2022, 52, 1164-1178.	6.2	25
34	Computational learning on specificity-determining residue-nucleotide interactions. <i>Nucleic Acids Research</i> , 2015, 43, gkv1134.	6.5	20
35	MotifHyades: expectation maximization for <i>de novo</i> DNA motif pair discovery on paired sequences. <i>Bioinformatics</i> , 2017, 33, 3028-3035.	1.8	20
36	Early Cancer Detection from Multianalyte Blood Test Results. <i>IScience</i> , 2019, 15, 332-341.	1.9	20

#	ARTICLE	IF	CITATIONS
37	A novel surrogate-assisted evolutionary algorithm with an uncertainty grouping based infill criterion. <i>Swarm and Evolutionary Computation</i> , 2021, 60, 100787.	4.5	20
38	Single-cell RNA-seq interpretations using evolutionary multiobjective ensemble pruning. <i>Bioinformatics</i> , 2019, 35, 2809-2817.	1.8	19
39	An evolutionary algorithm with species-specific explosion for multimodal optimization. , 2009, , .		17
40	Nature-Inspired Multiobjective Epistasis Elucidation from Genome-Wide Association Studies. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 17, 1-1.	1.9	17
41	Context awareness and embedding for biomedical event extraction. <i>Bioinformatics</i> , 2020, 36, 637-643.	1.8	17
42	Discovering approximate-associated sequence patterns for protein-DNA interactions. <i>Bioinformatics</i> , 2011, 27, 471-478.	1.8	16
43	A Comparison Study for DNA Motif Modeling on Protein Binding Microarray. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2016, 13, 261-271.	1.9	16
44	Increased expression of GATA zinc finger domain containing 1 through gene amplification promotes liver cancer by directly inducing phosphatase of regenerating liver 3. <i>Hepatology</i> , 2018, 67, 2302-2319.	3.6	16
45	Evolutionary Large-Scale Multiobjective Optimization: Benchmarks and Algorithms. <i>IEEE Transactions on Evolutionary Computation</i> , 2023, 27, 401-415.	7.5	16
46	Effect of Spatial Locality on an Evolutionary Algorithm for Multimodal Optimization. <i>Lecture Notes in Computer Science</i> , 2010, , 481-490.	1.0	16
47	Leveraging Multi-source knowledge for Chinese clinical named entity recognition via relational graph convolutional network. <i>Journal of Biomedical Informatics</i> , 2022, 128, 104035.	2.5	16
48	Nature-Inspired Multiobjective Cancer Subtype Diagnosis. <i>IEEE Journal of Translational Engineering in Health and Medicine</i> , 2019, 7, 1-12.	2.2	15
49	SECOM: A Novel Hash Seed and Community Detection Based-Approach for Genome-Scale Protein Domain Identification. <i>PLoS ONE</i> , 2012, 7, e39475.	1.1	15
50	Multiple source transfer learning for dynamic multiobjective optimization. <i>Information Sciences</i> , 2022, 607, 739-757.	4.0	15
51	New Tricks for "Old" Domains: How Novel Architectures and Promiscuous Hubs Contributed to the Organization and Evolution of the ECM. <i>Genome Biology and Evolution</i> , 2014, 6, 2897-2917.	1.1	14
52	Noninvasive early diagnosis of intestinal diseases based on artificial intelligence in genomics and microbiome. <i>Journal of Gastroenterology and Hepatology (Australia)</i> , 2021, 36, 823-831.	1.4	13
53	HCRNet: high-throughput circRNA-binding event identification from CLIP-seq data using deep temporal convolutional network. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	13
54	Mini-review: Recent advances in post-translational modification site prediction based on deep learning. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 3522-3532.	1.9	13

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55	A novel semi-supervised model for miRNA-disease association prediction based on ℓ_1 -norm graph. <i>Journal of Translational Medicine</i> , 2018, 16, 357.	1.8	12
56	Big data challenges in genome informatics. <i>Biophysical Reviews</i> , 2019, 11, 51-54.	1.5	12
57	Transmission trend of the COVID-19 pandemic predicted by dendritic neural regression. <i>Applied Soft Computing Journal</i> , 2021, 111, 107683.	4.1	12
58	Decomposition-based multiobjective optimization with bicriteria assisted adaptive operator selection. <i>Swarm and Evolutionary Computation</i> , 2021, 60, 100790.	4.5	11
59	Human host status inference from temporal microbiome changes via recurrent neural networks. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	11
60	Evolutionary Multitasking for Large-Scale Multiobjective Optimization. <i>IEEE Transactions on Evolutionary Computation</i> , 2023, 27, 863-877.	7.5	11
61	scEFSC: Accurate single-cell RNA-seq data analysis via ensemble consensus clustering based on multiple feature selections. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 2181-2197.	1.9	11
62	Identification of coupling DNA motif pairs on long-range chromatin interactions in human K562 cells. <i>Bioinformatics</i> , 2016, 32, 321-324.	1.8	10
63	Multiobjective Patient Stratification Using Evolutionary Multiobjective Optimization. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2018, 22, 1619-1629.	3.9	10
64	Identification of pan-cancer Ras pathway activation with deep learning. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	10
65	Early cancer detection from genome-wide cell-free DNA fragmentation via shuffled frog leaping algorithm and support vector machine. <i>Bioinformatics</i> , 2021, 37, 3099-3105.	1.8	10
66	Evolutionary Multiobjective Clustering Algorithms With Ensemble for Patient Stratification. <i>IEEE Transactions on Cybernetics</i> , 2022, 52, 11027-11040.	6.2	10
67	Implication of Light Absorption Enhancement and Mixing State of Black Carbon (BC) by Coatings in Hong Kong. <i>Aerosol and Air Quality Research</i> , 2018, 18, 2753-2763.	0.9	10
68	Human disease prediction from microbiome data by multiple feature fusion and deep learning. <i>IScience</i> , 2022, 25, 104081.	1.9	10
69	Uncovering the key dimensions of high-throughput biomolecular data using deep learning. <i>Nucleic Acids Research</i> , 2020, 48, e56-e56.	6.5	9
70	A novel web-based system for tropical cyclone analysis and prediction. <i>International Journal of Geographical Information Science</i> , 2012, 26, 75-97.	2.2	8
71	An Improved Neural Network Cascade for Face Detection in Large Scene Surveillance. <i>Applied Sciences (Switzerland)</i> , 2018, 8, 2222.	1.3	8
72	DNA Sequencing Technologies. <i>ACM Computing Surveys</i> , 2020, 52, 1-30.	16.1	8

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73	Single-Cell RNA Sequencing Data Interpretation by Evolutionary Multiobjective Clustering. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 17, 1-1.	1.9	8
74	Nature-inspired multiobjective patient stratification from cancer gene expression data. Information Sciences, 2020, 526, 245-262.	4.0	8
75	iDeepSubMito: identification of protein submitochondrial localization with deep learning. Briefings in Bioinformatics, 2021, 22, .	3.2	8
76	EDCNN: identification of genome-wide RNA-binding proteins using evolutionary deep convolutional neural network. Bioinformatics, 2022, 38, 678-686.	1.8	8
77	Evolving Spatial Clusters of Genomic Regions From High-Throughput Chromatin Conformation Capture Data. IEEE Transactions on Nanobioscience, 2017, 16, 400-407.	2.2	7
78	DNA Motif Recognition Modeling from Protein Sequences. IScience, 2018, 7, 198-211.	1.9	7
79	Elucidating Genome-Wide Protein-RNA Interactions Using Differential Evolution. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 272-282.	1.9	7
80	Deep embedded clustering with multiple objectives on scRNA-seq data. Briefings in Bioinformatics, 2021, 22, .	3.2	7
81	High-throughput single-cell RNA-seq data imputation and characterization with surrogate-assisted automated deep learning. Briefings in Bioinformatics, 2022, 23, .	3.2	7
82	EGFI: drug-drug interaction extraction and generation with fusion of enriched entity and sentence information. Briefings in Bioinformatics, 2022, 23, .	3.2	7
83	Evolving Transcription Factor Binding Site Models From Protein Binding Microarray Data. IEEE Transactions on Cybernetics, 2017, 47, 415-424.	6.2	6
84	NSSRF: global network similarity search with subgraph signatures and its applications. Bioinformatics, 2017, 33, 1696-1702.	1.8	6
85	Deep Learning Resolves Representative Movement Patterns in a Marine Predator Species. Applied Sciences (Switzerland), 2019, 9, 2935.	1.3	6
86	Future DNA computing device and accompanied tool stack: Towards high-throughput computation. Future Generation Computer Systems, 2021, 117, 111-124.	4.9	6
87	A self-organizing weighted optimization based framework for large-scale multi-objective optimization. Swarm and Evolutionary Computation, 2022, 72, 101084.	4.5	6
88	A scalable community detection algorithm for large graphs using stochastic block models. Intelligent Data Analysis, 2017, 21, 1463-1485.	0.4	5
89	PathEmb: Random Walk Based Document Embedding for Global Pathway Similarity Search. IEEE Journal of Biomedical and Health Informatics, 2019, 23, 1329-1335.	3.9	5
90	Heterodimeric DNA motif synthesis and validations. Nucleic Acids Research, 2019, 47, 1628-1636.	6.5	5

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91	Multiobjective Genome-Wide RNA-Binding Event Identification From CLIP-Seq Data. IEEE Transactions on Cybernetics, 2021, 51, 5811-5824.	6.2	5
92	Elucidating transcriptomic profiles from single-cell RNA sequencing data using nature-inspired compressed sensing. Briefings in Bioinformatics, 2021, 22, .	3.2	5
93	The comprehensive and systematic identification of BLCA-specific SF-regulated, survival-related AS events. Gene, 2022, 835, 146657.	1.0	5
94	Probabilistic Inference on Multiple Normalized Signal Profiles from Next Generation Sequencing: Transcription Factor Binding Sites. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 1416-1428.	1.9	4
95	Unsupervised Learning in Genome Informatics. , 2016, , 405-448.		4
96	Elucidating high-dimensional cancer hallmark annotation via enriched ontology. Journal of Biomedical Informatics, 2017, 73, 84-94.	2.5	4
97	A Comparative Study for Identifying the Chromosome-Wide Spatial Clusters from High-Throughput Chromatin Conformation Capture Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 774-787.	1.9	4
98	ToBio: Global Pathway Similarity Search Based on Topological and Biological Features. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 336-349.	1.9	4
99	Deleterious Non-Synonymous Single Nucleotide Polymorphism Predictions on Human Transcription Factors. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 327-333.	1.9	4
100	GESgnExt: Gene Expression Signature Extraction and Meta-Analysis on Gene Expression Omnibus. IEEE Journal of Biomedical and Health Informatics, 2020, 24, 311-318.	3.9	4
101	Nature-Inspired Compressed Sensing for Transcriptomic Profiling From Random Composite Measurements. IEEE Transactions on Cybernetics, 2021, 51, 4476-4487.	6.2	4
102	Evolving Multiobjective Cancer Subtype Diagnosis From Cancer Gene Expression Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2431-2444.	1.9	4
103	Multiplicative Algorithms for Constrained Non-negative Matrix Factorization. , 2012, , .		3
104	A cone order sequence based multi-objective evolutionary algorithm. , 2016, , .		3
105	Categorical Matrix Completion With Active Learning for High-Throughput Screening. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2261-2270.	1.9	3
106	Protocol for Epistasis Detection with Machine Learning Using GenEpi Package. Methods in Molecular Biology, 2021, 2212, 291-305.	0.4	3
107	Reducing healthcare disparities using multiple multiethnic data distributions with fine-tuning of transfer learning. Briefings in Bioinformatics, 2022, 23, .	3.2	3
108	A dynamic multi-objective evolutionary algorithm based on polynomial regression and adaptive clustering. Swarm and Evolutionary Computation, 2022, 71, 101075.	4.5	3

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109	Active Learning Based on Single-Hidden Layer Feed-Forward Neural Network. , 2015, , .		2
110	A Novel Approach to Predict Core Residues on Cancer-Related DNA-Binding Domains. Cancer Informatics, 2016, 15s2, CIN.S39366.	0.9	2
111	Multiobjective Deep Clustering and its Applications in Single-cell RNA-seq Data. IEEE Transactions on Systems, Man, and Cybernetics: Systems, 2022, 52, 5016-5027.	5.9	2
112	CancerEMC: frontline non-invasive cancer screening from circulating protein biomarkers and mutations in cell-free DNA. Bioinformatics, 2021, 37, 3319-3327.	1.8	2
113	Evolutionary Algorithms. , 0, , 111-137.		2
114	Exploring high-throughput biomolecular data with multiobjective robust continuous clustering. Information Sciences, 2022, 583, 239-265.	4.0	2
115	GMHCC: high-throughput analysis of biomolecular data using graph-based multiple hierarchical consensus clustering. Bioinformatics, 2022, 38, 3020-3028.	1.8	2
116	Colorectal cancer subtype identification from differential gene expression levels using minimalist deep learning. BioData Mining, 2022, 15, 12.	2.2	2
117	Aggressivity Detection on Social Network Comments. , 2017, , .		1
118	Evolving Transcriptomic Profiles from Single-cell RNA-seq Data using Nature-Inspired Multiobjective Optimization. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 18, 1-1.	1.9	1
119	RNCE: network integration with reciprocal neighbors contextual encoding for multi-modal drug community study on cancer targets. Briefings in Bioinformatics, 2021, 22, .	3.2	1
120	Particle Swarm Optimized Gaussian Process Classifier for Treatment Discontinuation Prediction in Multicohort Metastatic Castration-Resistant Prostate Cancer Patients. IEEE Journal of Biomedical and Health Informatics, 2022, 26, 1309-1317.	3.9	1
121	Epistasis Analysis: Classification Through Machine Learning Methods. Methods in Molecular Biology, 2021, 2212, 337-345.	0.4	1
122	Feature Selection and Feature Extraction: Highlights. , 2021, , .		1
123	Accurate Sequence-Based Prediction of Deleterious nsSNPs with Multiple Sequence Profiles and Putative Binding Residues. Biomolecules, 2021, 11, 1337.	1.8	1
124	Evolutionary Algorithms. Advances in Computational Intelligence and Robotics Book Series, 2016, , 190-215.	0.4	1
125	An Artificial Intelligence Approach for Gene Editing Off-Target Quantification: Convolutional Self-attention Neural Network Designs and Considerations. Statistics in Biosciences, 0, , .	0.6	1
126	Exploring Mixed Membership Stochastic Block Models via Non-negative Matrix Factorization. , 2014, , .		0

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127	Data Analytics for Protein-DNA Binding Interactions. , 2015, , .		0
128	Probabilistic Inference on Multiple Normalized Genome-Wide Signal Profiles With Model Regularization. IEEE Transactions on Nanobioscience, 2017, 16, 43-50.	2.2	0
129	Zinc-Finger Protein 471 Functions as a Tumor Suppressor in Gastric Cancer through Transcriptionally Repressing TFAP2A and PLS3. Gastroenterology, 2017, 152, S801-S802.	0.6	0
130	GATAD1 Promotes Hepatocellular Carcinogenesis through Directly Inducing PTP4A3 and Activating Akt Pathway. Gastroenterology, 2017, 152, S1182.	0.6	0
131	A scalable community detection algorithm for large graphs using stochastic block models. Intelligent Data Analysis, 2018, 22, 239.	0.4	0
132	EDITORIAL: Special Issue of 2018 India International Congress on Computational Intelligence. Neural Computing and Applications, 2020, 32, 15427-15428.	3.2	0
133	Special issue of 2017 India International Congress on Computational Intelligence. Neural Computing and Applications, 2020, 32, 10797-10798.	3.2	0
134	Identification of haploinsufficient genes from epigenomic data using deep forest. Briefings in Bioinformatics, 2021, 22, .	3.2	0
135	Analyzing High-Order Epistasis from Genotype-Phenotype Maps Using "Epistasis"™ Package. Methods in Molecular Biology, 2021, 2212, 265-275.	0.4	0
136	Epistasis Detection Based on Epi-GTBN. Methods in Molecular Biology, 2021, 2212, 325-335.	0.4	0
137	DeepMotifSyn: a deep learning approach to synthesize heterodimeric DNA motifs. Briefings in Bioinformatics, 2022, 23, .	3.2	0
138	Finding core"periphery structures in large networks. Physica A: Statistical Mechanics and Its Applications, 2021, 581, 126224.	1.2	0
139	A Belief Degree"Associated Fuzzy Multifactor Dimensionality Reduction Framework for Epistasis Detection. Methods in Molecular Biology, 2021, 2212, 307-323.	0.4	0
140	Reactions"™ Descriptors Selection and Yield Estimation Using Metaheuristic Algorithms and Voting Ensemble. Computers, Materials and Continua, 2022, 70, 4745-4762.	1.5	0
141	Metric Learning Based Vision Transformer for"Product Matching. Lecture Notes in Computer Science, 2021, , 3-13.	1.0	0