

# Ka-Chun Wong

## List of Publications by Year in descending order

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141  
papers

2,609  
citations

236925

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144  
all docs

144  
docs citations

144  
times ranked

2676  
citing authors

#	ARTICLE	IF	CITATIONS
1	Evolutionary Large-Scale Multiobjective Optimization: Benchmarks and Algorithms. IEEE Transactions on Evolutionary Computation, 2023, 27, 401-415.	10.0	16
2	Evolutionary Multitasking for Large-Scale Multiobjective Optimization. IEEE Transactions on Evolutionary Computation, 2023, 27, 863-877.	10.0	11
3	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.	6.3	1
4	DeepMotifSyn: a deep learning approach to synthesize heterodimeric DNA motifs. Briefings in Bioinformatics, 2022, 23, .	6.5	0
5	High-throughput single-cell RNA-seq data imputation and characterization with surrogate-assisted automated deep learning. Briefings in Bioinformatics, 2022, 23, .	6.5	7
6	Evolutionary Multiobjective Clustering Algorithms With Ensemble for Patient Stratification. IEEE Transactions on Cybernetics, 2022, 52, 11027-11040.	9.5	10
7	Multiobjective Deep Clustering and its Applications in Single-cell RNA-seq Data. IEEE Transactions on Systems, Man, and Cybernetics: Systems, 2022, 52, 5016-5027.	9.3	2
8	EDCNN: identification of genome-wide RNA-binding proteins using evolutionary deep convolutional neural network. Bioinformatics, 2022, 38, 678-686.	4.1	8
9	A self-adaptive weighted differential evolution approach for large-scale feature selection. Knowledge-Based Systems, 2022, 235, 107633.	7.1	38
10	EGFI: drug-drug interaction extraction and generation with fusion of enriched entity and sentence information. Briefings in Bioinformatics, 2022, 23, .	6.5	7
11	Reactions™ Descriptors Selection and Yield Estimation Using Metaheuristic Algorithms and Voting Ensemble. Computers, Materials and Continua, 2022, 70, 4745-4762.	1.9	0
12	A Self-Guided Reference Vector Strategy for Many-Objective Optimization. IEEE Transactions on Cybernetics, 2022, 52, 1164-1178.	9.5	25
13	Exploring high-throughput biomolecular data with multiobjective robust continuous clustering. Information Sciences, 2022, 583, 239-265.	6.9	2
14	HCRNet: high-throughput circRNA-binding event identification from CLIP-seq data using deep temporal convolutional network. Briefings in Bioinformatics, 2022, 23, .	6.5	13
15	Reducing healthcare disparities using multiple multiethnic data distributions with fine-tuning of transfer learning. Briefings in Bioinformatics, 2022, 23, .	6.5	3
16	Leveraging Multi-source knowledge for Chinese clinical named entity recognition via relational graph convolutional network. Journal of Biomedical Informatics, 2022, 128, 104035.	4.3	16
17	A dynamic multi-objective evolutionary algorithm based on polynomial regression and adaptive clustering. Swarm and Evolutionary Computation, 2022, 71, 101075.	8.1	3
18	Human disease prediction from microbiome data by multiple feature fusion and deep learning. IScience, 2022, 25, 104081.	4.1	10

#	ARTICLE	IF	CITATIONS
19	Intrusion detection using multi-objective evolutionary convolutional neural network for Internet of Things in Fog computing. Knowledge-Based Systems, 2022, 244, 108505.	7.1	37
20	GMHCC: high-throughput analysis of biomolecular data using graph-based multiple hierarchical consensus clustering. Bioinformatics, 2022, 38, 3020-3028.	4.1	2
21	Colorectal cancer subtype identification from differential gene expression levels using minimalist deep learning. BioData Mining, 2022, 15, 12.	4.0	2
22	scEFSC: Accurate single-cell RNA-seq data analysis via ensemble consensus clustering based on multiple feature selections. Computational and Structural Biotechnology Journal, 2022, 20, 2181-2197.	4.1	11
23	A self-organizing weighted optimization based framework for large-scale multi-objective optimization. Swarm and Evolutionary Computation, 2022, 72, 101084.	8.1	6
24	Multiple source transfer learning for dynamic multiobjective optimization. Information Sciences, 2022, 607, 739-757.	6.9	15
25	The comprehensive and systematic identification of BLCA-specific SF-regulated, survival-related AS events. Gene, 2022, 835, 146657.	2.2	5
26	Mini-review: Recent advances in post-translational modification site prediction based on deep learning. Computational and Structural Biotechnology Journal, 2022, 20, 3522-3532.	4.1	13
27	Nature-Inspired Compressed Sensing for Transcriptomic Profiling From Random Composite Measurements. IEEE Transactions on Cybernetics, 2021, 51, 4476-4487.	9.5	4
28	iCircRBP-DHN: identification of circRNA-RBP interaction sites using deep hierarchical network. Briefings in Bioinformatics, 2021, 22, .	6.5	45
29	Identification of pan-cancer Ras pathway activation with deep learning. Briefings in Bioinformatics, 2021, 22, .	6.5	10
30	Categorical Matrix Completion With Active Learning for High-Throughput Screening. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2261-2270.	3.0	3
31	Evolving Multiobjective Cancer Subtype Diagnosis From Cancer Gene Expression Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2431-2444.	3.0	4
32	Multiobjective Genome-Wide RNA-Binding Event Identification From CLIP-Seq Data. IEEE Transactions on Cybernetics, 2021, 51, 5811-5824.	9.5	5
33	RNCE: network integration with reciprocal neighbors contextual encoding for multi-modal drug community study on cancer targets. Briefings in Bioinformatics, 2021, 22, .	6.5	1
34	Decomposition-based multiobjective optimization with bicriteria assisted adaptive operator selection. Swarm and Evolutionary Computation, 2021, 60, 100790.	8.1	11
35	A novel surrogate-assisted evolutionary algorithm with an uncertainty grouping based infill criterion. Swarm and Evolutionary Computation, 2021, 60, 100787.	8.1	20
36	Future DNA computing device and accompanied tool stack: Towards high-throughput computation. Future Generation Computer Systems, 2021, 117, 111-124.	7.5	6

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37	Protocol for Epistasis Detection with Machine Learning Using GenEpi Package. <i>Methods in Molecular Biology</i> , 2021, 2212, 291-305.	0.9	3
38	Identification of haploinsufficient genes from epigenomic data using deep forest. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	0
39	Epistasis Analysis: Classification Through Machine Learning Methods. <i>Methods in Molecular Biology</i> , 2021, 2212, 337-345.	0.9	1
40	Analyzing High-Order Epistasis from Genotype-Phenotype Maps Using “Epistasis” Package. <i>Methods in Molecular Biology</i> , 2021, 2212, 265-275.	0.9	0
41	Epistasis Detection Based on Epi-GTBN. <i>Methods in Molecular Biology</i> , 2021, 2212, 325-335.	0.9	0
42	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.	2.8	13
43	Feature Selection and Feature Extraction: Highlights. , 2021, , .		1
44	Deep embedded clustering with multiple objectives on scRNA-seq data. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	7
45	Elucidating transcriptomic profiles from single-cell RNA sequencing data using nature-inspired compressed sensing. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	5
46	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.	4.1	10
47	Machine Learning Protocols in Early Cancer Detection Based on Liquid Biopsy: A Survey. <i>Life</i> , 2021, 11, 638.	2.4	28
48	Human host status inference from temporal microbiome changes via recurrent neural networks. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	11
49	iDeepSubMito: identification of protein submitochondrial localization with deep learning. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	8
50	Accurate Sequence-Based Prediction of Deleterious nsSNPs with Multiple Sequence Profiles and Putative Binding Residues. <i>Biomolecules</i> , 2021, 11, 1337.	4.0	1
51	Transmission trend of the COVID-19 pandemic predicted by dendritic neural regression. <i>Applied Soft Computing Journal</i> , 2021, 111, 107683.	7.2	12
52	Finding core“periphery structures in large networks. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2021, 581, 126224.	2.6	0
53	A Belief Degree“Associated Fuzzy Multifactor Dimensionality Reduction Framework for Epistasis Detection. <i>Methods in Molecular Biology</i> , 2021, 2212, 307-323.	0.9	0
54	CancerEMC: frontline non-invasive cancer screening from circulating protein biomarkers and mutations in cell-free DNA. <i>Bioinformatics</i> , 2021, 37, 3319-3327.	4.1	2

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55	Metric Learning Based Vision Transformer for Product Matching. Lecture Notes in Computer Science, 2021, , 3-13.	1.3	0
56	Context awareness and embedding for biomedical event extraction. Bioinformatics, 2020, 36, 637-643.	4.1	17
57	DNA Sequencing Technologies. ACM Computing Surveys, 2020, 52, 1-30.	23.0	8
58	Verbal aggression detection on Twitter comments: convolutional neural network for short-text sentiment analysis. Neural Computing and Applications, 2020, 32, 10809-10818.	5.6	40
59	Deleterious Non-Synonymous Single Nucleotide Polymorphism Predictions on Human Transcription Factors. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 327-333.	3.0	4
60	GESgnExt: Gene Expression Signature Extraction and Meta-Analysis on Gene Expression Omnibus. IEEE Journal of Biomedical and Health Informatics, 2020, 24, 311-318.	6.3	4
61	EDITORIAL: Special Issue of 2018 India International Congress on Computational Intelligence. Neural Computing and Applications, 2020, 32, 15427-15428.	5.6	0
62	CRISPRNet: A Recurrent Convolutional Network Quantifies CRISPR Off-Target Activities with Mismatches and Indels. Advanced Science, 2020, 7, 1903562.	11.2	43
63	Special issue of 2017 India International Congress on Computational Intelligence. Neural Computing and Applications, 2020, 32, 10797-10798.	5.6	0
64	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.	3.0	1
65	Uncovering the key dimensions of high-throughput biomolecular data using deep learning. Nucleic Acids Research, 2020, 48, e56-e56.	14.5	9
66	Nature-inspired multiobjective patient stratification from cancer gene expression data. Information Sciences, 2020, 526, 245-262.	6.9	8
67	A Clustering-Based Evolutionary Algorithm for Many-Objective Optimization Problems. IEEE Transactions on Evolutionary Computation, 2019, 23, 391-405.	10.0	91
68	ToBio: Global Pathway Similarity Search Based on Topological and Biological Features. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 336-349.	3.0	4
69	PathEmb: Random Walk Based Document Embedding for Global Pathway Similarity Search. IEEE Journal of Biomedical and Health Informatics, 2019, 23, 1329-1335.	6.3	5
70	Elucidating Genome-Wide Protein-RNA Interactions Using Differential Evolution. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 272-282.	3.0	7
71	Deep Learning Resolves Representative Movement Patterns in a Marine Predator Species. Applied Sciences (Switzerland), 2019, 9, 2935.	2.5	6
72	Big data challenges in genome informatics. Biophysical Reviews, 2019, 11, 51-54.	3.2	12

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73	Early Cancer Detection from Multianalyte Blood Test Results. <i>IScience</i> , 2019, 15, 332-341.	4.1	20
74	A novel multi-objective evolutionary algorithm with dynamic decomposition strategy. <i>Swarm and Evolutionary Computation</i> , 2019, 48, 182-200.	8.1	26
75	Nature-Inspired Multiobjective Cancer Subtype Diagnosis. <i>IEEE Journal of Translational Engineering in Health and Medicine</i> , 2019, 7, 1-12.	3.7	15
76	Single-Cell RNA Sequencing Data Interpretation by Evolutionary Multiobjective Clustering. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 17, 1-1.	3.0	8
77	Synergizing CRISPR/Cas9 off-target predictions for ensemble insights and practical applications. <i>Bioinformatics</i> , 2019, 35, 1108-1115.	4.1	25
78	Single-cell RNA-seq interpretations using evolutionary multiobjective ensemble pruning. <i>Bioinformatics</i> , 2019, 35, 2809-2817.	4.1	19
79	An Effective Ensemble Framework for Multiobjective Optimization. <i>IEEE Transactions on Evolutionary Computation</i> , 2019, 23, 645-659.	10.0	26
80	Heterodimeric DNA motif synthesis and validations. <i>Nucleic Acids Research</i> , 2019, 47, 1628-1636.	14.5	5
81	Evolutionary Multiobjective Clustering and Its Applications to Patient Stratification. <i>IEEE Transactions on Cybernetics</i> , 2019, 49, 1680-1693.	9.5	49
82	Zinc-finger protein 471 suppresses gastric cancer through transcriptionally repressing downstream oncogenic PLS3 and TFAP2A. <i>Oncogene</i> , 2018, 37, 3601-3616.	5.9	35
83	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.	7.3	16
84	A scalable community detection algorithm for large graphs using stochastic block models. <i>Intelligent Data Analysis</i> , 2018, 22, 239.	0.9	0
85	Particle Swarm Optimization With a Balanceable Fitness Estimation for Many-Objective Optimization Problems. <i>IEEE Transactions on Evolutionary Computation</i> , 2018, 22, 32-46.	10.0	202
86	A Comparative Study for Identifying the Chromosome-Wide Spatial Clusters from High-Throughput Chromatin Conformation Capture Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 774-787.	3.0	4
87	A Diversity-Enhanced Resource Allocation Strategy for Decomposition-Based Multiobjective Evolutionary Algorithm. <i>IEEE Transactions on Cybernetics</i> , 2018, 48, 2388-2401.	9.5	35
88	Adaptive multiple-elites-guided composite differential evolution algorithm with a shift mechanism. <i>Information Sciences</i> , 2018, 422, 122-143.	6.9	87
89	An adaptive immune-inspired multi-objective algorithm with multiple differential evolution strategies. <i>Information Sciences</i> , 2018, 430-431, 46-64.	6.9	53
90	Multiobjective Patient Stratification Using Evolutionary Multiobjective Optimization. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2018, 22, 1619-1629.	6.3	10

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91	An Improved Neural Network Cascade for Face Detection in Large Scene Surveillance. Applied Sciences (Switzerland), 2018, 8, 2222.	2.5	8
92	A novel semi-supervised model for miRNA-disease association prediction based on $\ell_1$ -norm graph. Journal of Translational Medicine, 2018, 16, 357.	4.4	12
93	DNA Motif Recognition Modeling from Protein Sequences. IScience, 2018, 7, 198-211.	4.1	7
94	Off-target predictions in CRISPR-Cas9 gene editing using deep learning. Bioinformatics, 2018, 34, i656-i663.	4.1	121
95	Nature-Inspired Multiobjective Epistasis Elucidation from Genome-Wide Association Studies. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 17, 1-1.	3.0	17
96	Implication of Light Absorption Enhancement and Mixing State of Black Carbon (BC) by Coatings in Hong Kong. Aerosol and Air Quality Research, 2018, 18, 2753-2763.	2.1	10
97	Evolving Transcription Factor Binding Site Models From Protein Binding Microarray Data. IEEE Transactions on Cybernetics, 2017, 47, 415-424.	9.5	6
98	Probabilistic Inference on Multiple Normalized Genome-Wide Signal Profiles With Model Regularization. IEEE Transactions on Nanobioscience, 2017, 16, 43-50.	3.3	0
99	NSSRF: global network similarity search with subgraph signatures and its applications. Bioinformatics, 2017, 33, 1696-1702.	4.1	6
100	Aggressivity Detection on Social Network Comments. , 2017, , .		1
101	A novel artificial bee colony algorithm with an adaptive population size for numerical function optimization. Information Sciences, 2017, 414, 53-67.	6.9	70
102	An External Archive-Guided Multiobjective Particle Swarm Optimization Algorithm. IEEE Transactions on Cybernetics, 2017, 47, 2794-2808.	9.5	96
103	MotifHyades: expectation maximization for <i>de novo</i> DNA motif pair discovery on paired sequences. Bioinformatics, 2017, 33, 3028-3035.	4.1	20
104	Evolving Spatial Clusters of Genomic Regions From High-Throughput Chromatin Conformation Capture Data. IEEE Transactions on Nanobioscience, 2017, 16, 400-407.	3.3	7
105	Zinc-Finger Protein 471 Functions as a Tumor Suppressor in Gastric Cancer through Transcriptionally Repressing TFAP2A and PLS3. Gastroenterology, 2017, 152, S801-S802.	1.3	0
106	GATAD1 Promotes Hepatocellular Carcinogenesis through Directly Inducing PTP4A3 and Activating Akt Pathway. Gastroenterology, 2017, 152, S1182.	1.3	0
107	Elucidating high-dimensional cancer hallmark annotation via enriched ontology. Journal of Biomedical Informatics, 2017, 73, 84-94.	4.3	4
108	A scalable community detection algorithm for large graphs using stochastic block models. Intelligent Data Analysis, 2017, 21, 1463-1485.	0.9	5

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109	A Novel Approach to Predict Core Residues on Cancer-Related DNA-Binding Domains. <i>Cancer Informatics</i> , 2016, 15s2, CIN.S39366.	1.9	2
110	Unsupervised Learning in Genome Informatics. , 2016, , 405-448.		4
111	A cone order sequence based multi-objective evolutionary algorithm. , 2016, , .		3
112	Identification of coupling DNA motif pairs on long-range chromatin interactions in human K562 cells. <i>Bioinformatics</i> , 2016, 32, 321-324.	4.1	10
113	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.	3.0	16
114	Evolutionary Algorithms. <i>Advances in Computational Intelligence and Robotics Book Series</i> , 2016, , 190-215.	0.4	1
115	Data Analytics for Protein-DNA Binding Interactions. , 2015, , .		0
116	Active Learning Based on Single-Hidden Layer Feed-Forward Neural Network. , 2015, , .		2
117	Computational learning on specificity-determining residue-nucleotide interactions. <i>Nucleic Acids Research</i> , 2015, 43, gkv1134.	14.5	20
118	A Short Survey on Data Clustering Algorithms. , 2015, , .		27
119	Probabilistic Inference on Multiple Normalized Signal Profiles from Next Generation Sequencing: Transcription Factor Binding Sites. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015, 12, 1416-1428.	3.0	4
120	SignalSpider: probabilistic pattern discovery on multiple normalized ChIP-Seq signal profiles. <i>Bioinformatics</i> , 2015, 31, 17-24.	4.1	39
121	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.	2.5	14
122	A probabilistic approach to explore human miRNA targetome by integrating miRNA-overexpression data and sequence information. <i>Bioinformatics</i> , 2014, 30, 621-628.	4.1	37
123	Inferring probabilistic miRNA-mRNA interaction signatures in cancers: a role-switch approach. <i>Nucleic Acids Research</i> , 2014, 42, e76-e76.	14.5	55
124	Herd Clustering: A synergistic data clustering approach using collective intelligence. <i>Applied Soft Computing Journal</i> , 2014, 23, 61-75.	7.2	29
125	SNPdryad: predicting deleterious non-synonymous human SNPs using only orthologous protein sequences. <i>Bioinformatics</i> , 2014, 30, 1112-1119.	4.1	57
126	Mirsynergy: detecting synergistic miRNA regulatory modules by overlapping neighbourhood expansion. <i>Bioinformatics</i> , 2014, 30, 2627-2635.	4.1	79



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127	Exploring Mixed Membership Stochastic Block Models via Non-negative Matrix Factorization. , 2014, , .		0
128	DNA motif elucidation using belief propagation. Nucleic Acids Research, 2013, 41, e153-e153.	14.5	53
129	A novel web-based system for tropical cyclone analysis and prediction. International Journal of Geographical Information Science, 2012, 26, 75-97.	4.8	8
130	Multiplicative Algorithms for Constrained Non-negative Matrix Factorization. , 2012, , .		3
131	Evolutionary multimodal optimization using the principle of locality. Information Sciences, 2012, 194, 138-170.	6.9	57
132	Collective Human Mobility Pattern from Taxi Trips in Urban Area. PLoS ONE, 2012, 7, e34487.	2.5	150
133	SECOM: A Novel Hash Seed and Community Detection Based-Approach for Genome-Scale Protein Domain Identification. PLoS ONE, 2012, 7, e39475.	2.5	15
134	Generalizing and learning protein-DNA binding sequence representations by an evolutionary algorithm. Soft Computing, 2011, 15, 1631-1642.	3.6	25
135	Discovering approximate-associated sequence patterns for proteinâ€“DNA interactions. Bioinformatics, 2011, 27, 471-478.	4.1	16
136	Discovering proteinâ€“DNA binding sequence patterns using association rule mining. Nucleic Acids Research, 2010, 38, 6324-6337.	14.5	49
137	Protein structure prediction on a lattice model via multimodal optimization techniques. , 2010, , .		38
138	Effect of Spatial Locality on an Evolutionary Algorithm for Multimodal Optimization. Lecture Notes in Computer Science, 2010, , 481-490.	1.3	16
139	An evolutionary algorithm with species-specific explosion for multimodal optimization. , 2009, , .		17
140	Evolutionary Algorithms. , 0, , 111-137.		2
141	An Artificial Intelligence Approach for Gene Editing Off-Target Quantification: Convolutional Self-attention Neural Network Designs and Considerations. Statistics in Biosciences, 0, , .	1.2	1