

# Ka-Chun Wong

## List of Publications by Citations

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**Version:** 2024-04-23

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117  
papers

1,491  
citations

21  
h-index

34  
g-index

144  
ext. papers

2,049  
ext. citations

7.2  
avg, IF

5.42  
L-index

#	Paper	IF	Citations
117	Collective human mobility pattern from taxi trips in urban area. <i>PLoS ONE</i> , <b>2012</b> , 7, e34487	3.7	128
116	Particle Swarm Optimization With a Balanceable Fitness Estimation for Many-Objective Optimization Problems. <i>IEEE Transactions on Evolutionary Computation</i> , <b>2018</b> , 22, 32-46	15.6	116
115	Mirsynergy: detecting synergistic miRNA regulatory modules by overlapping neighbourhood expansion. <i>Bioinformatics</i> , <b>2014</b> , 30, 2627-35	7.2	65
114	Off-target predictions in CRISPR-Cas9 gene editing using deep learning. <i>Bioinformatics</i> , <b>2018</b> , 34, i656-i663	6.3	65
113	An External Archive-Guided Multiobjective Particle Swarm Optimization Algorithm. <i>IEEE Transactions on Cybernetics</i> , <b>2017</b> , 47, 2794-2808	10.2	58
112	Adaptive multiple-elites-guided composite differential evolution algorithm with a shift mechanism. <i>Information Sciences</i> , <b>2018</b> , 422, 122-143	7.7	56
111	A novel artificial bee colony algorithm with an adaptive population size for numerical function optimization. <i>Information Sciences</i> , <b>2017</b> , 414, 53-67	7.7	50
110	SNPdryad: predicting deleterious non-synonymous human SNPs using only orthologous protein sequences. <i>Bioinformatics</i> , <b>2014</b> , 30, 1112-1119	7.2	49
109	A Clustering-Based Evolutionary Algorithm for Many-Objective Optimization Problems. <i>IEEE Transactions on Evolutionary Computation</i> , <b>2019</b> , 23, 391-405	15.6	45
108	Evolutionary multimodal optimization using the principle of locality. <i>Information Sciences</i> , <b>2012</b> , 194, 138-170	7.7	43
107	An adaptive immune-inspired multi-objective algorithm with multiple differential evolution strategies. <i>Information Sciences</i> , <b>2018</b> , 430-431, 46-64	7.7	40
106	Discovering protein-DNA binding sequence patterns using association rule mining. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, 6324-37	20.1	39
105	DNA motif elucidation using belief propagation. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, e153	20.1	38
104	Inferring probabilistic miRNA-mRNA interaction signatures in cancers: a role-switch approach. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, e76	20.1	33
103	A probabilistic approach to explore human miRNA targetome by integrating miRNA-overexpression data and sequence information. <i>Bioinformatics</i> , <b>2014</b> , 30, 621-8	7.2	31
102	Protein structure prediction on a lattice model via multimodal optimization techniques <b>2010</b> ,		31
101	Evolutionary Multiobjective Clustering and Its Applications to Patient Stratification. <i>IEEE Transactions on Cybernetics</i> , <b>2019</b> , 49, 1680-1693	10.2	31

100	SignalSpider: probabilistic pattern discovery on multiple normalized ChIP-Seq signal profiles. <i>Bioinformatics</i> , <b>2015</b> , 31, 17-24	7.2	26
99	A Diversity-Enhanced Resource Allocation Strategy for Decomposition-Based Multiobjective Evolutionary Algorithm. <i>IEEE Transactions on Cybernetics</i> , <b>2018</b> , 48, 2388-2401	10.2	25
98	Herd Clustering: A synergistic data clustering approach using collective intelligence. <i>Applied Soft Computing Journal</i> , <b>2014</b> , 23, 61-75	7.5	23
97	Zinc-finger protein 471 suppresses gastric cancer through transcriptionally repressing downstream oncogenic PLS3 and TFAP2A. <i>Oncogene</i> , <b>2018</b> , 37, 3601-3616	9.2	21
96	Computational learning on specificity-determining residue-nucleotide interactions. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, 10180-9	20.1	20
95	Verbal aggression detection on Twitter comments: convolutional neural network for short-text sentiment analysis. <i>Neural Computing and Applications</i> , <b>2020</b> , 32, 10809-10818	4.8	20
94	Generalizing and learning protein-DNA binding sequence representations by an evolutionary algorithm. <i>Soft Computing</i> , <b>2011</b> , 15, 1631-1642	3.5	19
93	A Short Survey on Data Clustering Algorithms <b>2015</b> ,		16
92	An Effective Ensemble Framework for Multiobjective Optimization. <i>IEEE Transactions on Evolutionary Computation</i> , <b>2019</b> , 23, 645-659	15.6	15
91	MotifHyades: expectation maximization for de novo DNA motif pair discovery on paired sequences. <i>Bioinformatics</i> , <b>2017</b> , 33, 3028-3035	7.2	14
90	A novel multi-objective evolutionary algorithm with dynamic decomposition strategy. <i>Swarm and Evolutionary Computation</i> , <b>2019</b> , 48, 182-200	9.8	14
89	An evolutionary algorithm with species-specific explosion for multimodal optimization <b>2009</b> ,		14
88	SECOM: a novel hash seed and community detection based-approach for genome-scale protein domain identification. <i>PLoS ONE</i> , <b>2012</b> , 7, e39475	3.7	14
87	Early Cancer Detection from Multianalyte Blood Test Results. <i>IScience</i> , <b>2019</b> , 15, 332-341	6.1	13
86	Discovering approximate-associated sequence patterns for protein-DNA interactions. <i>Bioinformatics</i> , <b>2011</b> , 27, 471-8	7.2	13
85	Synergizing CRISPR/Cas9 off-target predictions for ensemble insights and practical applications. <i>Bioinformatics</i> , <b>2019</b> , 35, 1108-1115	7.2	13
84	Nature-Inspired Multiobjective Epistasis Elucidation from Genome-Wide Association Studies. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2020</b> , 17, 226-237	3	12
83	Effect of Spatial Locality on an Evolutionary Algorithm for Multimodal Optimization. <i>Lecture Notes in Computer Science</i> , <b>2010</b> , 481-490	0.9	12

82	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> , <b>2014</b> , 6, 2897-917	3.9	11
81	A Comparison Study for DNA Motif Modeling on Protein Binding Microarray. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2016</b> , 13, 261-71	3	9
80	Nature-Inspired Multiobjective Cancer Subtype Diagnosis. <i>IEEE Journal of Translational Engineering in Health and Medicine</i> , <b>2019</b> , 7, 4300112	3	9
79	iCircRBP-DHN: identification of circRNA-RBP interaction sites using deep hierarchical network. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22,	13.4	9
78	Single-cell RNA-seq interpretations using evolutionary multiobjective ensemble pruning. <i>Bioinformatics</i> , <b>2019</b> , 35, 2809-2817	7.2	9
77	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> , <b>2018</b> , 67, 2302-2319	11.2	8
76	Multiobjective Patient Stratification Using Evolutionary Multiobjective Optimization. <i>IEEE Journal of Biomedical and Health Informatics</i> , <b>2018</b> , 22, 1619-1629	7.2	8
75	CRISPR-Net: A Recurrent Convolutional Network Quantifies CRISPR Off-Target Activities with Mismatches and Indels. <i>Advanced Science</i> , <b>2020</b> , 7, 1903562	13.6	7
74	Evolving Spatial Clusters of Genomic Regions From High-Throughput Chromatin Conformation Capture Data. <i>IEEE Transactions on Nanobioscience</i> , <b>2017</b> , 16, 400-407	3.4	7
73	Implication of Light Absorption Enhancement and Mixing State of Black Carbon (BC) by Coatings in Hong Kong. <i>Aerosol and Air Quality Research</i> , <b>2018</b> , 18, 2753-2763	4.6	7
72	A novel semi-supervised model for miRNA-disease association prediction based on [Formula: see text]-norm graph. <i>Journal of Translational Medicine</i> , <b>2018</b> , 16, 357	8.5	7
71	NSSRF: global network similarity search with subgraph signatures and its applications. <i>Bioinformatics</i> , <b>2017</b> , 33, 1696-1702	7.2	6
70	Big data challenges in genome informatics. <i>Biophysical Reviews</i> , <b>2019</b> , 11, 51-54	3.7	6
69	Identification of coupling DNA motif pairs on long-range chromatin interactions in human K562 cells. <i>Bioinformatics</i> , <b>2016</b> , 32, 321-4	7.2	6
68	A novel web-based system for tropical cyclone analysis and prediction. <i>International Journal of Geographical Information Science</i> , <b>2012</b> , 26, 75-97	4.1	6
67	Machine Learning Protocols in Early Cancer Detection Based on Liquid Biopsy: A Survey. <i>Life</i> , <b>2021</b> , 11,	3	6
66	Evolutionary Large-Scale Multiobjective Optimization: Benchmarks and Algorithms. <i>IEEE Transactions on Evolutionary Computation</i> , <b>2021</b> , 1-1	15.6	6
65	An Improved Neural Network Cascade for Face Detection in Large Scene Surveillance. <i>Applied Sciences (Switzerland)</i> , <b>2018</b> , 8, 2222	2.6	6

64	PathEmb: Random Walk Based Document Embedding for Global Pathway Similarity Search. <i>IEEE Journal of Biomedical and Health Informatics</i> , <b>2019</b> , 23, 1329-1335	7.2	5
63	Elucidating Genome-Wide Protein-RNA Interactions Using Differential Evolution. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2019</b> , 16, 272-282	3	5
62	Context awareness and embedding for biomedical event extraction. <i>Bioinformatics</i> , <b>2020</b> , 36, 637-643	7.2	5
61	Decomposition-based multiobjective optimization with bicriteria assisted adaptive operator selection. <i>Swarm and Evolutionary Computation</i> , <b>2021</b> , 60, 100790	9.8	5
60	DNA Motif Recognition Modeling from Protein Sequences. <i>IScience</i> , <b>2018</b> , 7, 198-211	6.1	5
59	Evolving Transcription Factor Binding Site Models From Protein Binding Microarray Data. <i>IEEE Transactions on Cybernetics</i> , <b>2017</b> , 47, 415-424	10.2	4
58	DNA Sequencing Technologies. <i>ACM Computing Surveys</i> , <b>2019</b> , 52, 1-30	13.4	4
57	Uncovering the key dimensions of high-throughput biomolecular data using deep learning. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, e56	20.1	4
56	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> , <b>2018</b> , 15, 774-787	3	4
55	ToBio: Global Pathway Similarity Search Based on Topological and Biological Features. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2019</b> , 16, 336-349	3	4
54	A Self-Guided Reference Vector Strategy for Many-Objective Optimization. <i>IEEE Transactions on Cybernetics</i> , <b>2020</b> ,	10.2	4
53	A self-adaptive weighted differential evolution approach for large-scale feature selection. <i>Knowledge-Based Systems</i> , <b>2021</b> , 235, 107633	7.3	4
52	Noninvasive early diagnosis of intestinal diseases based on artificial intelligence in genomics and microbiome. <i>Journal of Gastroenterology and Hepatology (Australia)</i> , <b>2021</b> , 36, 823-831	4	4
51	Elucidating transcriptomic profiles from single-cell RNA sequencing data using nature-inspired compressed sensing. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22,	13.4	4
50	Early Cancer Detection from Genome-wide Cell-free DNA Fragmentation via Shuffled Frog Leaping Algorithm and Support Vector Machine. <i>Bioinformatics</i> , <b>2021</b> ,	7.2	4
49	Nature-inspired multiobjective patient stratification from cancer gene expression data. <i>Information Sciences</i> , <b>2020</b> , 526, 245-262	7.7	4
48	Single-Cell RNA Sequencing Data Interpretation by Evolutionary Multiobjective Clustering. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2020</b> , 17, 1773-1784	3	3
47	A scalable community detection algorithm for large graphs using stochastic block models. <i>Intelligent Data Analysis</i> , <b>2017</b> , 21, 1463-1485	1.1	3

46	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> , <b>2015</b> , 12, 1416-28	3	3
45	Future DNA computing device and accompanied tool stack: Towards high-throughput computation. <i>Future Generation Computer Systems</i> , <b>2021</b> , 117, 111-124	7.5	3
44	Transmission trend of the COVID-19 pandemic predicted by dendritic neural regression. <i>Applied Soft Computing Journal</i> , <b>2021</b> , 111, 107683	7.5	3
43	Evolutionary Multiobjective Clustering Algorithms With Ensemble for Patient Stratification. <i>IEEE Transactions on Cybernetics</i> , <b>2021</b> , PP,	10.2	3
42	Intrusion detection using multi-objective evolutionary convolutional neural network for Internet of Things in Fog computing. <i>Knowledge-Based Systems</i> , <b>2022</b> , 244, 108505	7.3	3
41	Categorical Matrix Completion With Active Learning for High-Throughput Screening. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2021</b> , 18, 2261-2270	3	2
40	A cone order sequence based multi-objective evolutionary algorithm <b>2016</b> ,		2
39	Elucidating high-dimensional cancer hallmark annotation via enriched ontology. <i>Journal of Biomedical Informatics</i> , <b>2017</b> , 73, 84-94	10.2	2
38	Multiplicative Algorithms for Constrained Non-negative Matrix Factorization <b>2012</b> ,		2
37	Evolutionary Algorithms 111-137		2
36	Nature-Inspired Compressed Sensing for Transcriptomic Profiling From Random Composite Measurements. <i>IEEE Transactions on Cybernetics</i> , <b>2021</b> , 51, 4476-4487	10.2	2
35	Identification of pan-cancer Ras pathway activation with deep learning. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22,	13.4	2
34	Deep embedded clustering with multiple objectives on scRNA-seq data. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22,	13.4	2
33	Unsupervised Learning in Genome Informatics <b>2016</b> , 405-448		2
32	A novel surrogate-assisted evolutionary algorithm with an uncertainty grouping based infill criterion. <i>Swarm and Evolutionary Computation</i> , <b>2021</b> , 60, 100787	9.8	2
31	Protocol for Epistasis Detection with Machine Learning Using GenEpi Package. <i>Methods in Molecular Biology</i> , <b>2021</b> , 2212, 291-305	1.4	2
30	iDeepSubMito: identification of protein submitochondrial localization with deep learning. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22,	13.4	2
29	Leveraging Multi-source knowledge for Chinese clinical named entity recognition via relational graph convolutional network.. <i>Journal of Biomedical Informatics</i> , <b>2022</b> , 128, 104035	10.2	2

28	scEFSC: Accurate single-cell RNA-seq data analysis via ensemble consensus clustering based on multiple feature selections. <i>Computational and Structural Biotechnology Journal</i> , <b>2022</b> , 20, 2181-2197	6.8	2
27	Aggressivity Detection on Social Network Comments <b>2017</b> ,		1
26	Evolving Multiobjective Cancer Subtype Diagnosis From Cancer Gene Expression Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2021</b> , 18, 2431-2444	3	1
25	Multiobjective Genome-Wide RNA-Binding Event Identification From CLIP-Seq Data. <i>IEEE Transactions on Cybernetics</i> , <b>2020</b> ,	10.2	1
24	Deep Learning Resolves Representative Movement Patterns in a Marine Predator Species. <i>Applied Sciences (Switzerland)</i> , <b>2019</b> , 9, 2935	2.6	1
23	Evolutionary Algorithms. <i>Advances in Computational Intelligence and Robotics Book Series</i> , <b>2016</b> , 190-215	0.4	1
22	EDCNN: Identification of Genome-Wide RNA-binding Proteins Using Evolutionary Deep Convolutional Neural Network. <i>Bioinformatics</i> , <b>2021</b> ,	7.2	1
21	A Novel Approach to Predict Core Residues on Cancer-Related DNA-Binding Domains. <i>Cancer Informatics</i> , <b>2016</b> , 15, 1-7	2.4	1
20	Heterodimeric DNA motif synthesis and validations. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, 1628-1636	20.1	1
19	Deleterious Non-Synonymous Single Nucleotide Polymorphism Predictions on Human Transcription Factors. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2020</b> , 17, 327-333	3	1
18	GESgnExt: Gene Expression Signature Extraction and Meta-Analysis on Gene Expression Omnibus. <i>IEEE Journal of Biomedical and Health Informatics</i> , <b>2020</b> , 24, 311-318	7.2	1
17	Epistasis Analysis: Classification Through Machine Learning Methods. <i>Methods in Molecular Biology</i> , <b>2021</b> , 2212, 337-345	1.4	1
16	High-throughput single-cell RNA-seq data imputation and characterization with surrogate-assisted automated deep learning. <i>Briefings in Bioinformatics</i> , <b>2021</b> ,	13.4	1
15	CancerEMC: frontline non-invasive cancer screening from circulating protein biomarkers and mutations in cell-free DNA. <i>Bioinformatics</i> , <b>2021</b> ,	7.2	1
14	A Dynamic Multi-objective Evolutionary Algorithm based on Polynomial Regression and Adaptive Clustering. <i>Swarm and Evolutionary Computation</i> , <b>2022</b> , 101075	9.8	1
13	Human disease prediction from microbiome data by multiple feature fusion and deep learning.. <i>IScience</i> , <b>2022</b> , 25, 104081	6.1	1
12	Evolutionary Multitasking for Large-Scale Multiobjective Optimization. <i>IEEE Transactions on Evolutionary Computation</i> , <b>2022</b> , 1-1	15.6	1
11	Multiobjective Deep Clustering and Its Applications in Single-cell RNA-seq Data. <i>IEEE Transactions on Systems, Man, and Cybernetics: Systems</i> , <b>2021</b> , 1-12	7.3	0

10	Colorectal cancer subtype identification from differential gene expression levels using minimalist deep learning.. <i>BioData Mining</i> , <b>2022</b> , 15, 12	4.3	o
9	A Self-organizing Weighted Optimization based Framework for Large-scale Multi-objective Optimization. <i>Swarm and Evolutionary Computation</i> , <b>2022</b> , 101084	9.8	o
8	Probabilistic Inference on Multiple Normalized Genome-Wide Signal Profiles With Model Regularization. <i>IEEE Transactions on Nanobioscience</i> , <b>2017</b> , 16, 43-50	3.4	
7	Evolving Transcriptomic Profiles From Single-Cell RNA-Seq Data Using Nature-Inspired Multiobjective Optimization. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2021</b> , 18, 2445-2458	3	
6	Exploring high-throughput biomolecular data with multiobjective robust continuous clustering. <i>Information Sciences</i> , <b>2022</b> , 583, 239-265	7.7	
5	Metric Learning Based Vision Transformer for Product Matching. <i>Lecture Notes in Computer Science</i> , <b>2021</b> , 3-13	0.9	
4	Analyzing High-Order Epistasis from Genotype-Phenotype Maps Using EpistasisTPackage. <i>Methods in Molecular Biology</i> , <b>2021</b> , 2212, 265-275	1.4	
3	Epistasis Detection Based on Epi-GTBN. <i>Methods in Molecular Biology</i> , <b>2021</b> , 2212, 325-335	1.4	
2	Finding core-periphery structures in large networks. <i>Physica A: Statistical Mechanics and Its Applications</i> , <b>2021</b> , 581, 126224	3.3	
1	A Belief Degree-Associated Fuzzy Multifactor Dimensionality Reduction Framework for Epistasis Detection. <i>Methods in Molecular Biology</i> , <b>2021</b> , 2212, 307-323	1.4	