Ka-Chun Wong

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Exploring high-throughput biomolecular data with multiobjective robust continuous clustering. *Information Sciences*, **2022**, 583, 239-265	7.7	
116	Leveraging Multi-source knowledge for Chinese clinical named entity recognition via relational graph convolutional network.. *Journal of Biomedical Informatics*, **2022**, 128, 104035	10.2	2
115	A Dynamic Multi-objective Evolutionary Algorithm based on Polynomial Regression and Adaptive Clustering. *Swarm and Evolutionary Computation*, **2022**, 101075	9.8	1
114	Human disease prediction from microbiome data by multiple feature fusion and deep learning.. *IScience*, **2022**, 25, 104081	6.1	1
113	Intrusion detection using multi-objective evolutionary convolutional neural network for Internet of Things in Fog computing. *Knowledge-Based Systems*, **2022**, 244, 108505	7.3	3
112	Evolutionary Multitasking for Large-Scale Multiobjective Optimization. *IEEE Transactions on Evolutionary Computation*, **2022**, 1-1	15.6	1
111	Colorectal cancer subtype identification from differential gene expression levels using minimalist deep learning.. *BioData Mining*, **2022**, 15, 12	4.3	0
110	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	6.8	2
109	A Self-organizing Weighted Optimization based Framework for Large-scale Multi-objective Optimization. *Swarm and Evolutionary Computation*, **2022**, 101084	9.8	0
108	Categorical Matrix Completion With Active Learning for High-Throughput Screening. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2021**, 18, 2261-2270	3	2
107	Evolving Multiobjective Cancer Subtype Diagnosis From Cancer Gene Expression Data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2021**, 18, 2431-2444	3	1
106	Evolving Transcriptomic Profiles From Single-Cell RNA-Seq Data Using Nature-Inspired Multiobjective Optimization. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2021**, 18, 2445-2458	3	
105	Metric Learning Based Vision Transformer for Product Matching. *Lecture Notes in Computer Science*, **2021**, 3-13	0.9	
104	EDCNN: Identification of Genome-Wide RNA-binding Proteins Using Evolutionary Deep Convolutional Neural Network. *Bioinformatics*, **2021**,	7.2	1
103	A self-adaptive weighted differential evolution approach for large-scale feature selection. *Knowledge-Based Systems*, **2021**, 235, 107633	7.3	4
102	Nature-Inspired Compressed Sensing for Transcriptomic Profiling From Random Composite Measurements. *IEEE Transactions on Cybernetics*, **2021**, 51, 4476-4487	10.2	2
101	iCircRBP-DHN: identification of circRNA-RBP interaction sites using deep hierarchical network. *Briefings in Bioinformatics*, **2021**, 22,	13.4	9

100	Identification of pan-cancer Ras pathway activation with deep learning. *Briefings in Bioinformatics*, **2021**, 22,	13.4	2
99	Noninvasive early diagnosis of intestinal diseases based on artificial intelligence in genomics and microbiome. *Journal of Gastroenterology and Hepatology (Australia)*, **2021**, 36, 823-831	4	4
98	Deep embedded clustering with multiple objectives on scRNA-seq data. *Briefings in Bioinformatics*, **2021**, 22,	13.4	2
97	Elucidating transcriptomic profiles from single-cell RNA sequencing data using nature-inspired compressed sensing. *Briefings in Bioinformatics*, **2021**, 22,	13.4	4
96	Early Cancer Detection from Genome-wide Cell-free DNA Fragmentation via Shuffled Frog Leaping Algorithm and Support Vector Machine. *Bioinformatics*, **2021**,	7.2	4
95	Machine Learning Protocols in Early Cancer Detection Based on Liquid Biopsy: A Survey. *Life*, **2021**, 11,	3	6
94	Decomposition-based multiobjective optimization with bicriteria assisted adaptive operator selection. *Swarm and Evolutionary Computation*, **2021**, 60, 100790	9.8	5
93	A novel surrogate-assisted evolutionary algorithm with an uncertainty grouping based infill criterion. *Swarm and Evolutionary Computation*, **2021**, 60, 100787	9.8	2
92	Future DNA computing device and accompanied tool stack: Towards high-throughput computation. *Future Generation Computer Systems*, **2021**, 117, 111-124	7.5	3
91	Protocol for Epistasis Detection with Machine Learning Using GenEpi Package. *Methods in Molecular Biology*, **2021**, 2212, 291-305	1.4	2
90	Evolutionary Large-Scale Multiobjective Optimization: Benchmarks and Algorithms. *IEEE Transactions on Evolutionary Computation*, **2021**, 1-1	15.6	6
89	Epistasis Analysis: Classification Through Machine Learning Methods. *Methods in Molecular Biology*, **2021**, 2212, 337-345	1.4	1
88	Analyzing High-Order Epistasis from Genotype-Phenotype Maps Using "EpistasisT"Package. *Methods in Molecular Biology*, **2021**, 2212, 265-275	1.4	
87	Epistasis Detection Based on Epi-GTBN. *Methods in Molecular Biology*, **2021**, 2212, 325-335	1.4	
86	iDeepSubMito: identification of protein submitochondrial localization with deep learning. *Briefings in Bioinformatics*, **2021**, 22,	13.4	2
85	High-throughput single-cell RNA-seq data imputation and characterization with surrogate-assisted automated deep learning. *Briefings in Bioinformatics*, **2021**,	13.4	1
84	Transmission trend of the COVID-19 pandemic predicted by dendritic neural regression. *Applied Soft Computing Journal*, **2021**, 111, 107683	7.5	3
83	Finding core–periphery structures in large networks. *Physica A: Statistical Mechanics and Its Applications*, **2021**, 581, 126224	3.3	

82	A Belief Degree-Associated Fuzzy Multifactor Dimensionality Reduction Framework for Epistasis Detection. *Methods in Molecular Biology*, **2021**, 2212, 307-323	1.4	
81	Evolutionary Multiobjective Clustering Algorithms With Ensemble for Patient Stratification. *IEEE Transactions on Cybernetics*, **2021**, PP,	10.2	3
80	Multiobjective Deep Clustering and Its Applications in Single-cell RNA-seq Data. *IEEE Transactions on Systems, Man, and Cybernetics: Systems*, **2021**, 1-12	7.3	0
79	CancerEMC: frontline non-invasive cancer screening from circulating protein biomarkers and mutations in cell-free DNA. *Bioinformatics*, **2021**,	7.2	1
78	Single-Cell RNA Sequencing Data Interpretation by Evolutionary Multiobjective Clustering. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2020**, 17, 1773-1784	3	3
77	CRISPR-Net: A Recurrent Convolutional Network Quantifies CRISPR Off-Target Activities with Mismatches and Indels. *Advanced Science*, **2020**, 7, 1903562	13.6	7
76	Multiobjective Genome-Wide RNA-Binding Event Identification From CLIP-Seq Data. *IEEE Transactions on Cybernetics*, **2020**,	10.2	1
75	Uncovering the key dimensions of high-throughput biomolecular data using deep learning. *Nucleic Acids Research*, **2020**, 48, e56	20.1	4
74	Nature-Inspired Multiobjective Epistasis Elucidation from Genome-Wide Association Studies. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2020**, 17, 226-237	3	12
73	Context awareness and embedding for biomedical event extraction. *Bioinformatics*, **2020**, 36, 637-643	7.2	5
72	A Self-Guided Reference Vector Strategy for Many-Objective Optimization. *IEEE Transactions on Cybernetics*, **2020**,	10.2	4
71	Verbal aggression detection on Twitter comments: convolutional neural network for short-text sentiment analysis. *Neural Computing and Applications*, **2020**, 32, 10809-10818	4.8	20
70	Deleterious Non-Synonymous Single Nucleotide Polymorphism Predictions on Human Transcription Factors. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2020**, 17, 327-333	3	1
69	GESgnExt: Gene Expression Signature Extraction and Meta-Analysis on Gene Expression Omnibus. *IEEE Journal of Biomedical and Health Informatics*, **2020**, 24, 311-318	7.2	1
68	Nature-inspired multiobjective patient stratification from cancer gene expression data. *Information Sciences*, **2020**, 526, 245-262	7.7	4
67	DNA Sequencing Technologies. *ACM Computing Surveys*, **2019**, 52, 1-30	13.4	4
66	Big data challenges in genome informatics. *Biophysical Reviews*, **2019**, 11, 51-54	3.7	6
65	Early Cancer Detection from Multianalyte Blood Test Results. *IScience*, **2019**, 15, 332-341	6.1	13

64	A novel multi-objective evolutionary algorithm with dynamic decomposition strategy. *Swarm and Evolutionary Computation*, **2019**, 48, 182-200	9.8	14
63	Nature-Inspired Multiobjective Cancer Subtype Diagnosis. *IEEE Journal of Translational Engineering in Health and Medicine*, **2019**, 7, 4300112	3	9
62	A Clustering-Based Evolutionary Algorithm for Many-Objective Optimization Problems. *IEEE Transactions on Evolutionary Computation*, **2019**, 23, 391-405	15.6	45
61	ToBio: Global Pathway Similarity Search Based on Topological and Biological Features. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2019**, 16, 336-349	3	4
60	PathEmb: Random Walk Based Document Embedding for Global Pathway Similarity Search. *IEEE Journal of Biomedical and Health Informatics*, **2019**, 23, 1329-1335	7.2	5
59	Elucidating Genome-Wide Protein-RNA Interactions Using Differential Evolution. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2019**, 16, 272-282	3	5
58	Deep Learning Resolves Representative Movement Patterns in a Marine Predator Species. *Applied Sciences (Switzerland)*, **2019**, 9, 2935	2.6	1
57	Synergizing CRISPR/Cas9 off-target predictions for ensemble insights and practical applications. *Bioinformatics*, **2019**, 35, 1108-1115	7.2	13
56	Single-cell RNA-seq interpretations using evolutionary multiobjective ensemble pruning. *Bioinformatics*, **2019**, 35, 2809-2817	7.2	9
55	An Effective Ensemble Framework for Multiobjective Optimization. *IEEE Transactions on Evolutionary Computation*, **2019**, 23, 645-659	15.6	15
54	Heterodimeric DNA motif synthesis and validations. *Nucleic Acids Research*, **2019**, 47, 1628-1636	20.1	1
53	Evolutionary Multiobjective Clustering and Its Applications to Patient Stratification. *IEEE Transactions on Cybernetics*, **2019**, 49, 1680-1693	10.2	31
52	Zinc-finger protein 471 suppresses gastric cancer through transcriptionally repressing downstream oncogenic PLS3 and TFAP2A. *Oncogene*, **2018**, 37, 3601-3616	9.2	21
51	Increased expression of GATA zinc finger domain containing 1 through gene amplification promotes liver cancer by directly inducing phosphatase of regenerating liver 3. *Hepatology*, **2018**, 67, 2302-2319	11.2	8
50	Particle Swarm Optimization With a Balanceable Fitness Estimation for Many-Objective Optimization Problems. *IEEE Transactions on Evolutionary Computation*, **2018**, 22, 32-46	15.6	116
49	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	3	4
48	A Diversity-Enhanced Resource Allocation Strategy for Decomposition-Based Multiobjective Evolutionary Algorithm. *IEEE Transactions on Cybernetics*, **2018**, 48, 2388-2401	10.2	25
47	Adaptive multiple-elites-guided composite differential evolution algorithm with a shift mechanism. *Information Sciences*, **2018**, 422, 122-143	7.7	56

46	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	4.6	7
45	An adaptive immune-inspired multi-objective algorithm with multiple differential evolution strategies. *Information Sciences*, **2018**, 430-431, 46-64	7.7	40
44	Multiobjective Patient Stratification Using Evolutionary Multiobjective Optimization. *IEEE Journal of Biomedical and Health Informatics*, **2018**, 22, 1619-1629	7.2	8
43	An Improved Neural Network Cascade for Face Detection in Large Scene Surveillance. *Applied Sciences (Switzerland)*, **2018**, 8, 2222	2.6	6
42	A novel semi-supervised model for miRNA-disease association prediction based on [Formula: see text]-norm graph. *Journal of Translational Medicine*, **2018**, 16, 357	8.5	7
41	DNA Motif Recognition Modeling from Protein Sequences. *IScience*, **2018**, 7, 198-211	6.1	5
40	Off-target predictions in CRISPR-Cas9 gene editing using deep learning. *Bioinformatics*, **2018**, 34, i656-i663	7.2	65
39	Evolving Transcription Factor Binding Site Models From Protein Binding Microarray Data. *IEEE Transactions on Cybernetics*, **2017**, 47, 415-424	10.2	4
38	Probabilistic Inference on Multiple Normalized Genome-Wide Signal Profiles With Model Regularization. *IEEE Transactions on Nanobioscience*, **2017**, 16, 43-50	3.4	
37	NSSRF: global network similarity search with subgraph signatures and its applications. *Bioinformatics*, **2017**, 33, 1696-1702	7.2	6
36	Aggressivity Detection on Social Network Comments **2017**,		1
35	A novel artificial bee colony algorithm with an adaptive population size for numerical function optimization. *Information Sciences*, **2017**, 414, 53-67	7.7	50
34	An External Archive-Guided Multiobjective Particle Swarm Optimization Algorithm. *IEEE Transactions on Cybernetics*, **2017**, 47, 2794-2808	10.2	58
33	MotifHyades: expectation maximization for de novo DNA motif pair discovery on paired sequences. *Bioinformatics*, **2017**, 33, 3028-3035	7.2	14
32	Evolving Spatial Clusters of Genomic Regions From High-Throughput Chromatin Conformation Capture Data. *IEEE Transactions on Nanobioscience*, **2017**, 16, 400-407	3.4	7
31	Elucidating high-dimensional cancer hallmark annotation via enriched ontology. *Journal of Biomedical Informatics*, **2017**, 73, 84-94	10.2	2
30	A scalable community detection algorithm for large graphs using stochastic block models. *Intelligent Data Analysis*, **2017**, 21, 1463-1485	1.1	3
29	A Comparison Study for DNA Motif Modeling on Protein Binding Microarray. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2016**, 13, 261-71	3	9

28	A cone order sequence based multi-objective evolutionary algorithm **2016**,		2
27	Identification of coupling DNA motif pairs on long-range chromatin interactions in human K562 cells. *Bioinformatics*, **2016**, 32, 321-4	7.2	6
26	Evolutionary Algorithms. *Advances in Computational Intelligence and Robotics Book Series*, **2016**, 190-215	0.4	1
25	A Novel Approach to Predict Core Residues on Cancer-Related DNA-Binding Domains. *Cancer Informatics*, **2016**, 15, 1-7	2.4	1
24	Unsupervised Learning in Genome Informatics **2016**, 405-448		2
23	Computational learning on specificity-determining residue-nucleotide interactions. *Nucleic Acids Research*, **2015**, 43, 10180-9	20.1	20
22	A Short Survey on Data Clustering Algorithms **2015**,		16
21	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, 1416-28	3	3
20	SignalSpider: probabilistic pattern discovery on multiple normalized ChIP-Seq signal profiles. *Bioinformatics*, **2015**, 31, 17-24	7.2	26
19	SNPdryad: predicting deleterious non-synonymous human SNPs using only orthologous protein sequences. *Bioinformatics*, **2014**, 30, 1112-1119	7.2	49
18	Mirsynergy: detecting synergistic miRNA regulatory modules by overlapping neighbourhood expansion. *Bioinformatics*, **2014**, 30, 2627-35	7.2	65
17	New tricks for "old" domains: how novel architectures and promiscuous hubs contributed to the organization and evolution of the ECM. *Genome Biology and Evolution*, **2014**, 6, 2897-917	3.9	11
16	A probabilistic approach to explore human miRNA targetome by integrating miRNA-overexpression data and sequence information. *Bioinformatics*, **2014**, 30, 621-8	7.2	31
15	Inferring probabilistic miRNA-mRNA interaction signatures in cancers: a role-switch approach. *Nucleic Acids Research*, **2014**, 42, e76	20.1	33
14	Herd Clustering: A synergistic data clustering approach using collective intelligence. *Applied Soft Computing Journal*, **2014**, 23, 61-75	7.5	23
13	DNA motif elucidation using belief propagation. *Nucleic Acids Research*, **2013**, 41, e153	20.1	38
12	Evolutionary multimodal optimization using the principle of locality. *Information Sciences*, **2012**, 194, 138-170	7.7	43
11	A novel web-based system for tropical cyclone analysis and prediction. *International Journal of Geographical Information Science*, **2012**, 26, 75-97	4.1	6

10	Multiplicative Algorithms for Constrained Non-negative Matrix Factorization **2012**,		2
9	Collective human mobility pattern from taxi trips in urban area. *PLoS ONE*, **2012**, 7, e34487	3.7	128
8	SECOM: a novel hash seed and community detection based-approach for genome-scale protein domain identification. *PLoS ONE*, **2012**, 7, e39475	3.7	14
7	Generalizing and learning protein-DNA binding sequence representations by an evolutionary algorithm. *Soft Computing*, **2011**, 15, 1631-1642	3.5	19
6	Discovering approximate-associated sequence patterns for protein-DNA interactions. *Bioinformatics*, **2011**, 27, 471-8	7.2	13
5	Discovering protein-DNA binding sequence patterns using association rule mining. *Nucleic Acids Research*, **2010**, 38, 6324-37	20.1	39
4	Protein structure prediction on a lattice model via multimodal optimization techniques **2010**,		31
3	Effect of Spatial Locality on an Evolutionary Algorithm for Multimodal Optimization. *Lecture Notes in Computer Science*, **2010**, 481-490	0.9	12
2	An evolutionary algorithm with species-specific explosion for multimodal optimization **2009**,		14
1	Evolutionary Algorithms111-137		2