

Cheng-Hong Yang

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.

189
papers

3,032
citations

27
h-index

47
g-index

224
ext. papers

3,666
ext. citations

3.6
avg, IF

5.45
L-index

#	Paper	IF	Citations
189	AIS-Based Intelligent Vessel Trajectory Prediction Using Bi-LSTM. <i>IEEE Access</i> , 2022 , 10, 24302-24315	3.5	0
188	Identifying the Association of Time-Averaged Serum Albumin Levels with Clinical Factors among Patients on Hemodialysis Using Whale Optimization Algorithm. <i>Mathematics</i> , 2022 , 10, 1030	2.3	0
187	Analyzing the Performance of Machine Learning Techniques in Disease Prediction. <i>Journal of Food Quality</i> , 2022 , 2022, 1-9	2.7	4
186	Effect of Money Supply, Population, and Rent on Real Estate: A Clustering Analysis in Taiwan. <i>Mathematics</i> , 2022 , 10, 1155	2.3	2
185	Deep Hybrid Convolutional Neural Network for Segmentation of Melanoma Skin Lesion. <i>Computational Intelligence and Neuroscience</i> , 2021 , 2021, 9409508	3	1
184	Effect of clinical factors on trajectory of functional performance in patients undergoing hemodialysis. <i>Renal Failure</i> , 2021 , 43, 90-96	2.9	
183	Associations between Circulating Markers of Cholesterol Homeostasis and Macrovascular Events among Patients Undergoing Hemodialysis. <i>Nutrients</i> , 2021 , 13,	6.7	1
182	An Effective Hybrid Approach for Forecasting Currency Exchange Rates. <i>Sustainability</i> , 2021 , 13, 2761	3.6	3
181	Application of the Interaction between Tissue Immunohistochemistry Staining and Clinicopathological Factors for Evaluating the Risk of Oral Cancer Progression by Hierarchical Clustering Analysis: A Case-Control Study in a Taiwanese Population. <i>Diagnostics</i> , 2021 , 11,	3.8	1
180	Applications of Deep Learning and Fuzzy Systems to Detect Cancer Mortality in Next-Generation Genomic Data. <i>IEEE Transactions on Fuzzy Systems</i> , 2021 , 1-1	8.3	7
179	Association of proportion of the HDL-cholesterol subclasses HDL-2b and HDL-3 and macrovascular events among patients undergoing hemodialysis. <i>Scientific Reports</i> , 2021 , 11, 1871	4.9	0
178	Deep Learning for Imputation and Forecasting Tidal Level. <i>IEEE Journal of Oceanic Engineering</i> , 2021 , 1-11	3.3	0
177	Identification of mortality-risk-related missense variant for renal clear cell carcinoma using deep learning. <i>Therapeutic Advances in Chronic Disease</i> , 2021 , 12, 2040622321992624	4.9	2
176	Machine Learning Data Imputation and Prediction of Foraging Group Size in a Kleptoparasitic Spider. <i>Mathematics</i> , 2021 , 9, 415	2.3	1
175	Forecasting of the Prevalence of Dementia Using the LSTM Neural Network in Taiwan. <i>Mathematics</i> , 2021 , 9, 488	2.3	2
174	Effective multinational trade forecasting using LSTM recurrent neural network. <i>Expert Systems With Applications</i> , 2021 , 182, 115199	7.8	5
173	Forecasting the Demand for Container Throughput Using a Mixed-Precision Neural Architecture Based on CNN-LSTM. <i>Mathematics</i> , 2020 , 8, 1784	2.3	6

172	. <i>IEEE Access</i> , 2020 , 8, 82382-82390	3.5	3
171	Fuzzy Logic System Application for Detecting SNP-SNP Interaction. <i>IEEE Access</i> , 2020 , 8, 49951-49960	3.5	2
170	Identification of High-Order Single-Nucleotide Polymorphism Barcodes in Breast Cancer Using a Hybrid Taguchi-Genetic Algorithm: Case-Control Study. <i>JMIR Medical Informatics</i> , 2020 , 8, e16886	3.6	2
169	An improved fuzzy set-based multifactor dimensionality reduction for detecting epistasis. <i>Artificial Intelligence in Medicine</i> , 2020 , 102, 101768	7.4	4
168	Mutual Interaction of Clinical Factors and Specific microRNAs to Predict Mild Cognitive Impairment in Patients Receiving Hemodialysis. <i>Cells</i> , 2020 , 9,	7.9	2
167	Student Enrollment and Teacher Statistics Forecasting Based on Time-Series Analysis. <i>Computational Intelligence and Neuroscience</i> , 2020 , 2020, 1246920	3	1
166	Higher-order clinical risk factor interaction analysis for overall mortality in maintenance hemodialysis patients. <i>Therapeutic Advances in Chronic Disease</i> , 2020 , 11, 2040622320949060	4.9	2
165	Immersive Virtual Reality-Based Cardiopulmonary Resuscitation Interactive Learning Support System. <i>IEEE Access</i> , 2020 , 8, 120870-120880	3.5	3
164	Importance of non-medical reasons for dropout in patients on peritoneal dialysis. <i>Clinical and Experimental Nephrology</i> , 2020 , 24, 1050-1057	2.5	0
163	Forecasting outbound student mobility: A machine learning approach. <i>PLoS ONE</i> , 2020 , 15, e0238129	3.7	2
162	. <i>IEEE Access</i> , 2020 , 8, 159389-159401	3.5	8
161	Epistasis Analysis Using an Improved Fuzzy C-Means-Based Entropy Approach. <i>IEEE Transactions on Fuzzy Systems</i> , 2020 , 28, 718-730	8.3	10
160	Class Balanced Multifactor Dimensionality Reduction to Detect Gene-Gene Interactions. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020 , 17, 71-81	3	6
159	Effective hybrid approach for protein structure prediction in a two-dimensional Hydrophobic-Polar model. <i>Computers in Biology and Medicine</i> , 2019 , 113, 103397	7	0
158	Application of simulation-based CYP26 SNP-environment barcodes for evaluating the occurrence of oral malignant disorders by odds ratio-based binary particle swarm optimization: A case-control study in the Taiwanese population. <i>PLoS ONE</i> , 2019 , 14, e0220719	3.7	1
157	Biofilm Formation in : Genotype-Phenotype Correlation. <i>Molecules</i> , 2019 , 24,	4.8	48
156	Relationship between Clinicopathologic Variables in Breast Cancer Overall Survival Using Biogeography-Based Optimization Algorithm. <i>BioMed Research International</i> , 2019 , 2019, 2304128	3	1
155	Decision Theory-Based COI-SNP Tagging Approach for 126 Scombriformes Species Tagging. <i>Frontiers in Genetics</i> , 2019 , 10, 259	4.5	1

154	Comparison of Solute Clearance, Hospitalization Rate, and Aortic Arch Calcification between Online Hemodiafiltration and High-Flux Hemodialysis: A 6-Year Observational Study. <i>Kidney and Blood Pressure Research</i> , 2019 , 44, 264-276	3.1	0
153	Time-varying serum albumin levels and all-cause mortality in prevalent peritoneal dialysis patients: a 5-year observational study. <i>BMC Nephrology</i> , 2019 , 20, 254	2.7	9
152	Identifying Risk Stratification Associated With a Cancer for Overall Survival by Deep Learning-Based CoxPH. <i>IEEE Access</i> , 2019 , 7, 67708-67717	3.5	13
151	An Interactive Digital Somatosensory Game System That Implements a Decision Tree Algorithm. <i>IEEE Access</i> , 2019 , 7, 140190-140196	3.5	3
150	. <i>IEEE Access</i> , 2019 , 7, 143036-143045	3.5	1
149	Improved Classification Method for Detecting Potential Interactions Between Genes. <i>Advances in Intelligent Systems and Computing</i> , 2019 , 394-403	0.4	1
148	PBMDR: A particle swarm optimization-based multifactor dimensionality reduction for the detection of multilocus interactions. <i>Journal of Theoretical Biology</i> , 2019 , 461, 68-75	2.3	9
147	Comparison of tunneled central venous catheters and native arteriovenous fistulae by evaluating the mortality and morbidity of patients with prevalent hemodialysis. <i>Journal of the Formosan Medical Association</i> , 2019 , 118, 807-814	3.2	3
146	Multiple-Criteria Decision Analysis-Based Multifactor Dimensionality Reduction for Detecting Gene-Gene Interactions. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2019 , 23, 416-426	7.2	8
145	Factors Associated with Functional Performance among Patients on Hemodialysis in Taiwan. <i>Blood Purification</i> , 2018 , 46, 12-18	3.1	6
144	Decision Tree Algorithm-Generated Single-Nucleotide Polymorphism Barcodes of Genes for 38 Brassicaceae Species Tagging. <i>Evolutionary Bioinformatics</i> , 2018 , 14, 1176934318760856	1.9	4
143	Multiobjective multifactor dimensionality reduction to detect SNP-SNP interactions. <i>Bioinformatics</i> , 2018 , 34, 2228-2236	7.2	14
142	A CpGCluster-Teaching-Learning-Based Optimization for Prediction of CpG Islands in the Human Genome. <i>Journal of Computational Biology</i> , 2018 , 25, 158-169	1.7	2
141	Cumulative receiver operating characteristics for analyzing interaction between tissue visfatin and clinicopathologic factors in breast cancer progression. <i>Cancer Cell International</i> , 2018 , 18, 19	6.4	9
140	Longitudinal analysis of cardiac structure and function in incident-automated peritoneal dialysis: comparison between icodextrin solution and glucose-based solution. <i>BMC Nephrology</i> , 2018 , 19, 109	2.7	4
139	Protein folding prediction in the HP model using ions motion optimization with a greedy algorithm. <i>BioData Mining</i> , 2018 , 11, 17	4.3	10
138	Catfish Taguchi-Based Binary Differential Evolution Algorithm for Analyzing Single Nucleotide Polymorphism Interactions in Chronic Dialysis. <i>IEEE Transactions on Nanobioscience</i> , 2018 , 17, 291-299	3.4	7
137	Hybrid High Exploration Particle Swarm Optimization Algorithm Improves the Prediction of the 2-Dimensional Hydrophobic-Polar Model for Protein Folding. <i>Current Bioinformatics</i> , 2018 , 13, 182-192	4.7	

136	Particle Swarm Optimization-Based Support Vector Regression for Tourist Arrivals Forecasting. <i>Computational Intelligence and Neuroscience</i> , 2018 , 2018, 6076475	3	16
135	Association between clinical variables and mortality after parathyroidectomy in maintenance hemodialysis patients. <i>American Journal of Surgery</i> , 2017 , 213, 140-145	2.7	9
134	Identification of SNP-SNP interaction for chronic dialysis patients. <i>Computers in Biology and Medicine</i> , 2017 , 83, 94-101	7	6
133	CMDR based differential evolution identifies the epistatic interaction in genome-wide association studies. <i>Bioinformatics</i> , 2017 , 33, 2354-2362	7.2	28
132	A Particle Swarm Optimization-Based Approach with Local Search for Predicting Protein Folding. <i>Journal of Computational Biology</i> , 2017 , 24, 981-994	1.7	6
131	Multiobjective differential evolution-based multifactor dimensionality reduction for detecting gene-gene interactions. <i>Scientific Reports</i> , 2017 , 7, 12869	4.9	6
130	Use of Genetic Algorithm Combinational Single-nucleotide Polymorphisms Could Modify the Association of Blood Lead Levels and Bone Matrix Density. <i>Epidemiology</i> , 2017 , 28 Suppl 1, S121-S125	3.1	
129	Interaction of MRE11 and Clinicopathologic Characteristics in Recurrence of Breast Cancer: Individual and Cumulated Receiver Operating Characteristic Analyses. <i>BioMed Research International</i> , 2017 , 2017, 2563910	3	3
128	Joint Analysis of SNP-SNP-Environment Interactions for Chronic Dialysis by an Improved Branch and Bound Algorithm. <i>Journal of Computational Biology</i> , 2017 , 24, 1212-1225	1.7	5
127	Single nucleotide polymorphism barcoding of cytochrome c oxidase I sequences for discriminating 17 species of Columbidae by decision tree algorithm. <i>Ecology and Evolution</i> , 2017 , 7, 4717-4725	2.8	6
126	The expression of transglutaminase 2 (TG-2) in oral squamous cell carcinoma and its clinical significance. <i>Journal of the Chinese Medical Association</i> , 2017 , 80, 515-520	2.8	3
125	Impact of risk factors on functional status in maintenance hemodialysis patients. <i>European Journal of Medical Research</i> , 2017 , 22, 54	4.8	11
124	Prevalence and molecular characterization of plasmidmediated beta-lactamase genes among nosocomial Staphylococcus aureus isolated in Taiwan. <i>Tropical Journal of Pharmaceutical Research</i> , 2017 , 16, 155	0.8	
123	Analysis of high-order SNP barcodes in mitochondrial D-loop for chronic dialysis susceptibility. <i>Journal of Biomedical Informatics</i> , 2016 , 63, 112-119	10.2	8
122	MicroRNA-122 as a predictor of HBsAg seroclearance in hepatitis B and C dual infected patients treated with interferon and ribavirin. <i>Scientific Reports</i> , 2016 , 6, 33816	4.9	5
121	An association between time-varying serum albumin level and the mortality rate in maintenance haemodialysis patients: a five-year clinical cohort study. <i>BMC Nephrology</i> , 2016 , 17, 117	2.7	14
120	tRNAfeature: An algorithm for tRNA features to identify tRNA genes in DNA sequences. <i>Journal of Theoretical Biology</i> , 2016 , 404, 251-261	2.3	2
119	Chemical Composition, Antioxidant, and Antibacterial Activity of Wood Vinegar from Litchi chinensis. <i>Molecules</i> , 2016 , 21,	4.8	74

118	Changes in Serum Concentrations of Fibroblast Growth Factor 23 and Soluble Klotho in Hemodialysis Patients after Total Parathyroidectomy. <i>BioMed Research International</i> , 2016 , 2016, 6453803	3.3	16
117	A Hybrid Approach for CpG Island Detection in the Human Genome. <i>PLoS ONE</i> , 2016 , 11, e0144748	3.7	6
116	Genetic Algorithm Combined with a Local Search Method for Identifying Susceptibility Genes. <i>Journal of Artificial Intelligence and Soft Computing Research</i> , 2016 , 6, 203-212	5.1	12
115	A comparative analysis of chaotic particle swarm optimizations for detecting single nucleotide polymorphism barcodes. <i>Artificial Intelligence in Medicine</i> , 2016 , 73, 23-33	7.4	14
114	Breast cancer-associated high-order SNP-SNP interaction of CXCL12/CXCR4-related genes by an improved multifactor dimensionality reduction (MDR-ER). <i>Oncology Reports</i> , 2016 , 36, 1739-47	3.5	22
113	A systematic gene-gene and gene-environment interaction analysis of DNA repair genes XRCC1, XRCC2, XRCC3, XRCC4, and oral cancer risk. <i>OMICS A Journal of Integrative Biology</i> , 2015 , 19, 238-47	3.8	31
112	An efficiency analysis of high-order combinations of gene-gene interactions using multifactor-dimensionality reduction. <i>BMC Genomics</i> , 2015 , 16, 489	4.5	17
111	PCR-CTPP design for enzyme-free SNP genotyping using memetic algorithm. <i>IEEE Transactions on Nanobioscience</i> , 2015 , 14, 13-23	3.4	2
110	Antibacterial Activities and Antibacterial Mechanism of Polygonum cuspidatum Extracts against Nosocomial Drug-Resistant Pathogens. <i>Molecules</i> , 2015 , 20, 11119-30	4.8	49
109	High order gene-gene interactions in eight single nucleotide polymorphisms of renin-angiotensin system genes for hypertension association study. <i>BioMed Research International</i> , 2015 , 2015, 454091	3	13
108	The Combinational Polymorphisms of ORAI1 Gene Are Associated with Preventive Models of Breast Cancer in the Taiwanese. <i>BioMed Research International</i> , 2015 , 2015, 281263	3	11
107	The expert system application for diagnosing human vitamin deficiency through forward chaining method 2015 ,		2
106	2014 ,		2
105	Identifying association model for single-nucleotide polymorphisms of ORAI1 gene for breast cancer. <i>Cancer Cell International</i> , 2014 , 14, 29	6.4	17
104	Identification of SNP barcode biomarkers for genes associated with facial emotion perception using particle swarm optimization algorithm. <i>Annals of General Psychiatry</i> , 2014 , 13, 15	3.4	11
103	Genetic algorithm-generated SNP barcodes of the mitochondrial D-loop for chronic dialysis susceptibility. <i>Mitochondrial DNA</i> , 2014 , 25, 231-7		14
102	0138 The association of blood lead levels and bone density in different combinational SNP polymorphisms among Taiwan lead workers. <i>Occupational and Environmental Medicine</i> , 2014 , 71, A77.3-A78	2.1	18
101	Improved candidate drug mining for Alzheimer's disease. <i>BioMed Research International</i> , 2014 , 2014, 897653	3	2

100	Double-bottom chaotic map particle swarm optimization based on chi-square test to determine gene-gene interactions. <i>BioMed Research International</i> , 2014 , 2014, 172049	3	13
99	Improved branch and bound algorithm for detecting SNP-SNP interactions in breast cancer. <i>Journal of Clinical Bioinformatics</i> , 2013 , 3, 4		13
98	Particle swarm optimization algorithm for analyzing SNP-SNP interaction of renin-angiotensin system genes against hypertension. <i>Molecular Biology Reports</i> , 2013 , 40, 4227-33	2.8	23
97	Specific primer design for the polymerase chain reaction. <i>Biotechnology Letters</i> , 2013 , 35, 1541-9	3	32
96	Associate PCR-RFLP assay design with SNPs based on genetic algorithm in appropriate parameters estimation. <i>IEEE Transactions on Nanobioscience</i> , 2013 , 12, 119-27	3.4	7
95	Operon prediction using chaos embedded particle swarm optimization. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013 , 10, 1299-309	3	14
94	Evaluation of breast cancer susceptibility using improved genetic algorithms to generate genotype SNP barcodes. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013 , 10, 361-71	3	38
93	Preventive SNP-SNP interactions in the mitochondrial displacement loop (D-loop) from chronic dialysis patients. <i>Mitochondrion</i> , 2013 , 13, 698-704	4.9	18
92	Comparison of classification algorithms with wrapper-based feature selection for predicting osteoporosis outcome based on genetic factors in a taiwanese women population. <i>International Journal of Endocrinology</i> , 2013 , 2013, 850735	2.7	15
91	Drug-SNPing: an integrated drug-based, protein interaction-based tagSNP-based pharmacogenomics platform for SNP genotyping. <i>Bioinformatics</i> , 2013 , 29, 758-64	7.2	12
90	Identifying the association rules between clinicopathologic factors and higher survival performance in operation-centric oral cancer patients using the Apriori algorithm. <i>BioMed Research International</i> , 2013 , 2013, 359634	3	13
89	MDR-ER: balancing functions for adjusting the ratio in risk classes and classification errors for imbalanced cases and controls using multifactor-dimensionality reduction. <i>PLoS ONE</i> , 2013 , 8, e79387	3.7	25
88	SNP barcodes generated using particle swarm optimization to detect susceptibility to breast cancer. <i>Natural Science</i> , 2013 , 05, 359-367	0.5	2
87	CpGPAP: CpG island predictor analysis platform. <i>BMC Genetics</i> , 2012 , 13, 13	2.6	7
86	Complementary distribution BPSO for feature selection. <i>Intelligent Data Analysis</i> , 2012 , 16, 183-198	1.1	
85	An improved particle swarm optimization with double-bottom chaotic maps for numerical optimization. <i>Applied Mathematics and Computation</i> , 2012 , 219, 260-279	2.7	26
84	Mutagenic primer design for mismatch PCR-RFLP SNP genotyping using a genetic algorithm. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012 , 9, 837-45	3	7
83	URPD: a specific product primer design tool. <i>BMC Research Notes</i> , 2012 , 5, 306	2.3	12

82	Single nucleotide polymorphism barcoding to evaluate oral cancer risk using odds ratio-based genetic algorithms. <i>Kaohsiung Journal of Medical Sciences</i> , 2012 , 28, 362-8	2.4	29
81	An improved PSO algorithm for generating protective SNP barcodes in breast cancer. <i>PLoS ONE</i> , 2012 , 7, e37018	3.7	38
80	ANTIMICROBIAL ACTIVITY OF VARIOUS PARTS OF CINNAMOMUM CASSIA EXTRACTED WITH DIFFERENT EXTRACTION METHODS. <i>Journal of Food Biochemistry</i> , 2012 , 36, 690-698	3.3	11
79	Features for computational operon prediction in prokaryotes. <i>Briefings in Functional Genomics</i> , 2012 , 11, 291-9	4.9	14
78	Chaotic particle swarm optimization for detecting SNP-SNP interactions for CXCL12-related genes in breast cancer prevention. <i>European Journal of Cancer Prevention</i> , 2012 , 21, 336-42	2	25
77	Antioxidant activity of various parts of Cinnamomum cassia extracted with different extraction methods. <i>Molecules</i> , 2012 , 17, 7294-304	4.8	62
76	A Quantum Genetic Algorithm for Operon Prediction 2012 ,		1
75	A hybrid BPSO-CGA approach for gene selection and classification of microarray data. <i>Journal of Computational Biology</i> , 2012 , 19, 68-82	1.7	41
74	The importance of integrating SNP and cheminformatics resources to pharmacogenomics. <i>Current Drug Metabolism</i> , 2012 , 13, 991-9	3.5	16
73	Sequence-based polymorphisms in the mitochondrial D-loop and potential SNP predictors for chronic dialysis. <i>PLoS ONE</i> , 2012 , 7, e41125	3.7	27
72	2011 ,		5
71	Conserved PCR primer set designing for closely-related species to complete mitochondrial genome sequencing using a sliding window-based PSO algorithm. <i>PLoS ONE</i> , 2011 , 6, e17729	3.7	28
70	Chaotic particle swarm optimization for data clustering. <i>Expert Systems With Applications</i> , 2011 , 38, 1455-1463	3.8	91
69	Chaotic catfish particle swarm optimization for solving global numerical optimization problems. <i>Applied Mathematics and Computation</i> , 2011 , 217, 6900-6916	2.7	41
68	Computational analysis of simulated SNP interactions between 26 growth factor-related genes in a breast cancer association study. <i>OMICS A Journal of Integrative Biology</i> , 2011 , 15, 399-407	3.8	30
67	A hybrid feature selection method for DNA microarray data. <i>Computers in Biology and Medicine</i> , 2011 , 41, 228-37	7	72
66	Improved binary particle swarm optimization using catfish effect for feature selection. <i>Expert Systems With Applications</i> , 2011 , 38, 12699-12707	7.8	162
65	Gene selection and classification using Taguchi chaotic binary particle swarm optimization. <i>Expert Systems With Applications</i> , 2011 , 38, 13367-13377	7.8	54

64	Chaotic maps based on binary particle swarm optimization for feature selection. <i>Applied Soft Computing Journal</i> , 2011 , 11, 239-248	7.5	159
63	Particle swarm optimization with reinforcement learning for the prediction of CpG islands in the human genome. <i>PLoS ONE</i> , 2011 , 6, e21036	3.7	14
62	A combined bisulfite restriction analysis bioinformatics tool: methyl-typing. <i>Methods in Molecular Biology</i> , 2011 , 791, 73-88	1.4	
61	hSAGEing: an improved SAGE-based software for identification of human tissue-specific or common tumor markers and suppressors. <i>PLoS ONE</i> , 2010 , 5, e14369	3.7	
60	Binary particle swarm optimization for operon prediction. <i>Nucleic Acids Research</i> , 2010 , 38, e128	20.1	21
59	PPO: predictor for prokaryotic operons. <i>Bioinformatics</i> , 2010 , 26, 3127-8	7.2	4
58	Chemical composition and antibacterial activities of <i>Illicium verum</i> against antibiotic-resistant pathogens. <i>Journal of Medicinal Food</i> , 2010 , 13, 1254-62	2.8	50
57	A Novel Chaotic Inertia Weight Particle Swarm Optimization for PCR Primer Design 2010 ,		4
56	Operon Prediction Using Particle Swarm Optimization and Reinforcement Learning 2010 ,		4
55	Tag SNP selection using particle swarm optimization. <i>Biotechnology Progress</i> , 2010 , 26, 580-8	2.8	3
54	SNP-RFLPing 2: an updated and integrated PCR-RFLP tool for SNP genotyping. <i>BMC Bioinformatics</i> , 2010 , 11, 173	3.6	28
53	Confronting two-pair primer design for enzyme-free SNP genotyping based on a genetic algorithm. <i>BMC Bioinformatics</i> , 2010 , 11, 509	3.6	14
52	Methyl-Typing: an improved and visualized COBRA software for epigenomic studies. <i>FEBS Letters</i> , 2010 , 584, 739-44	3.8	7
51	An introduction to mitochondrial informatics. <i>Methods in Molecular Biology</i> , 2010 , 628, 259-74	1.4	1
50	Confronting Two-Pair Primer Design Using Particle Swarm Optimization. <i>Lecture Notes in Computer Science</i> , 2010 , 448-456	0.9	2
49	Prim-SNPing: a primer designer for cost-effective SNP genotyping. <i>BioTechniques</i> , 2009 , 46, 421-31	2.5	19
48	Tabu search and binary particle swarm optimization for feature selection using microarray data. <i>Journal of Computational Biology</i> , 2009 , 16, 1689-703	1.7	46
47	Seq-SNPing: multiple-alignment tool for SNP discovery, SNP ID identification, and RFLP genotyping. <i>OMICS A Journal of Integrative Biology</i> , 2009 , 13, 253-60	3.8	8

46	Specific PCR product primer design using memetic algorithm. <i>Biotechnology Progress</i> , 2009 , 25, 745-53	2.8	18
45	Novel generating protective single nucleotide polymorphism barcode for breast cancer using particle swarm optimization. <i>Cancer Epidemiology</i> , 2009 , 33, 147-54	2.8	21
44	LD2SNPping: linkage disequilibrium plotter and RFLP enzyme mining for tag SNPs. <i>BMC Genetics</i> , 2009 , 10, 26	2.6	3
43	A wireless internet interface for person with physical disability. <i>Mathematical and Computer Modelling</i> , 2009 , 50, 72-80		2
42	Generating SNP barcode to evaluate SNP-SNP interaction of disease by particle swarm optimization. <i>Computational Biology and Chemistry</i> , 2009 , 33, 114-9	3.6	17
41	Combinational polymorphisms of seven CXCL12-related genes are protective against breast cancer in Taiwan. <i>OMICS A Journal of Integrative Biology</i> , 2009 , 13, 165-72	3.8	67
40	A two-stage feature selection method for gene expression data. <i>OMICS A Journal of Integrative Biology</i> , 2009 , 13, 127-37	3.8	22
39	Chaotic genetic algorithm for gene selection and classification problems. <i>OMICS A Journal of Integrative Biology</i> , 2009 , 13, 407-20	3.8	7
38	Genetic Algorithm for the Design of Confronting Two-Pair Primers 2009 ,		2
37	A Hybrid Feature Selection Method Using Gene Expression Data 2009 ,		4
36	Fuzzy adaptive particle swarm optimization for a specific primer design problem 2009 ,		1
35	Dynamic programming for single nucleotide polymorphism ID identification in systematic association studies. <i>Kaohsiung Journal of Medical Sciences</i> , 2009 , 25, 165-76	2.4	1
34	Extract-SAGE: an integrated platform for cross-analysis and GA-based selection of SAGE data. <i>Bioinformatics</i> , 2009 , 3, 291-2	1.1	1
33	An Interactive Wireless Morse Code Learning System 2009 , 3361-3367		
32	Chaotic maps in binary particle swarm optimization for feature selection 2008 ,		31
31	Odds ratio-based genetic algorithms for generating SNP barcodes of genotypes to predict disease susceptibility. <i>OMICS A Journal of Integrative Biology</i> , 2008 , 12, 71-81	3.8	21
30	A hybrid approach for selecting gene subsets using gene expression data 2008 ,		1
29	Boolean binary particle swarm optimization for feature selection 2008 ,		18

28	Hybrid feature selection method using gene expression data 2008 ,		1
27	Comparative Particle Swarm Optimization (CPSO) for solving optimization problems 2008 ,		1
26	Catfish particle swarm optimization 2008 ,		7
25	Improved tag SNP selection using binary particle swarm optimization 2008 ,		1
24	Feature Selection Using Memetic Algorithms 2008 ,		14
23	Genotype and antibiotic susceptibility patterns of drug-resistant <i>Pseudomonas aeruginosa</i> and <i>Acinetobacter baumannii</i> isolates in Taiwan. <i>Microbial Drug Resistance</i> , 2008 , 14, 281-8	2.9	14
22	Information gain with chaotic genetic algorithm for gene selection and classification problem. <i>Conference Proceedings IEEE International Conference on Systems, Man, and Cybernetics</i> , 2008 ,	2	1
21	A hybrid filter/wrapper approach of feature selection for gene expression data. <i>Conference Proceedings IEEE International Conference on Systems, Man, and Cybernetics</i> , 2008 ,	2	2
20	SNP ID-info: SNP ID searching and visualization platform. <i>OMICS A Journal of Integrative Biology</i> , 2008 , 12, 217-26	3.8	5
19	COMBAT GA-BASED GENE SELECTION FOR CLASSIFICATION OF MICROARRAY DATA. <i>Biomedical Engineering - Applications, Basis and Communications</i> , 2008 , 20, 345-352	0.6	
18	Combinational polymorphisms of four DNA repair genes XRCC1, XRCC2, XRCC3, and XRCC4 and their association with oral cancer in Taiwan. <i>Journal of Oral Pathology and Medicine</i> , 2008 , 37, 271-7	3.3	93
17	Antibacterial and antioxidant properties of <i>Ramulus Cinnamomi</i> using supercritical CO ₂ extraction. <i>European Food Research and Technology</i> , 2008 , 227, 1387-1396	3.4	20
16	A mobile communication aid system for persons with physical disabilities. <i>Mathematical and Computer Modelling</i> , 2008 , 47, 318-327		11
15	Improved binary PSO for feature selection using gene expression data. <i>Computational Biology and Chemistry</i> , 2008 , 32, 29-37	3.6	365
14	SNP-Flankplus: SNP ID-centric retrieval for SNP flanking sequences. <i>Bioinformatics</i> , 2008 , 3, 147-9	1.1	11
13	SNP combinations in chromosome-wide genes are associated with bone mineral density in Taiwanese women. <i>Chinese Journal of Physiology</i> , 2008 , 51, 32-41	1.6	18
12	Restriction enzyme mining for SNPs in genomes. <i>Anticancer Research</i> , 2008 , 28, 2001-7	2.3	21
11	Antibacterial properties of Chinese herbal medicines against nosocomial antibiotic resistant strains of <i>Pseudomonas aeruginosa</i> in Taiwan. <i>The American Journal of Chinese Medicine</i> , 2007 , 35, 1047-60	6	24

10	V-MitoSNP: visualization of human mitochondrial SNPs. <i>BMC Bioinformatics</i> , 2006 , 7, 379	3.6	13
9	SNP-RFLPing: restriction enzyme mining for SNPs in genomes. <i>BMC Genomics</i> , 2006 , 7, 30	4.5	35
8	AN INTELLIGENT CHINESE PHONETIC ON-SCREEN VIRTUAL KEYBOARD SYSTEM. <i>Biomedical Engineering - Applications, Basis and Communications</i> , 2006 , 18, 178-184	0.6	0
7	Fuzzy support vector machines for adaptive Morse code recognition. <i>Medical Engineering and Physics</i> , 2006 , 28, 925-31	2.4	15
6	A NOVEL APPROACH TO MANDARIN MORSE CODE RECOGNITION. <i>Biomedical Engineering - Applications, Basis and Communications</i> , 2005 , 17, 267-274	0.6	3
5	CLASSIFICATION OF MULTIPLE CANCER TYPES USING FUZZY SUPPORT VECTOR MACHINES AND OUTLIER DETECTION METHODS. <i>Biomedical Engineering - Applications, Basis and Communications</i> , 2005 , 17, 300-308	0.6	5
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