

Cheng-Hong Yang

List of Publications by Citations

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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 | Improved binary PSO for feature selection using gene expression data. <i>Computational Biology and Chemistry</i> , 2008 , 32, 29-37 | 3.6 | 365 |
| 188 | Improved binary particle swarm optimization using catfish effect for feature selection. <i>Expert Systems With Applications</i> , 2011 , 38, 12699-12707 | 7.8 | 162 |
| 187 | Chaotic maps based on binary particle swarm optimization for feature selection. <i>Applied Soft Computing Journal</i> , 2011 , 11, 239-248 | 7.5 | 159 |
| 186 | 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 |
| 185 | Chaotic particle swarm optimization for data clustering. <i>Expert Systems With Applications</i> , 2011 , 38, 14555-14563 | 7.8 | 14563 |
| 184 | Chemical Composition, Antioxidant, and Antibacterial Activity of Wood Vinegar from Litchi chinensis. <i>Molecules</i> , 2016 , 21, | 4.8 | 74 |
| 183 | A hybrid feature selection method for DNA microarray data. <i>Computers in Biology and Medicine</i> , 2011 , 41, 228-37 | 7 | 72 |
| 182 | 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 |
| 181 | Antioxidant activity of various parts of Cinnamomum cassia extracted with different extraction methods. <i>Molecules</i> , 2012 , 17, 7294-304 | 4.8 | 62 |
| 180 | Gene selection and classification using Taguchi chaotic binary particle swarm optimization. <i>Expert Systems With Applications</i> , 2011 , 38, 13367-13377 | 7.8 | 54 |
| 179 | Chemical composition and antibacterial activities of Illicium verum against antibiotic-resistant pathogens. <i>Journal of Medicinal Food</i> , 2010 , 13, 1254-62 | 2.8 | 50 |
| 178 | Antibacterial Activities and Antibacterial Mechanism of Polygonum cuspidatum Extracts against Nosocomial Drug-Resistant Pathogens. <i>Molecules</i> , 2015 , 20, 11119-30 | 4.8 | 49 |
| 177 | Biofilm Formation in : Genotype-Phenotype Correlation. <i>Molecules</i> , 2019 , 24, | 4.8 | 48 |
| 176 | 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 |
| 175 | Chaotic catfish particle swarm optimization for solving global numerical optimization problems. <i>Applied Mathematics and Computation</i> , 2011 , 217, 6900-6916 | 2.7 | 41 |
| 174 | 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 |
| 173 | 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 |

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|-----|--|-----|----|
| 172 | An improved PSO algorithm for generating protective SNP barcodes in breast cancer. <i>PLoS ONE</i> , 2012 , 7, e37018 | 3.7 | 38 |
| 171 | SNP-RFLPing: restriction enzyme mining for SNPs in genomes. <i>BMC Genomics</i> , 2006 , 7, 30 | 4.5 | 35 |
| 170 | Specific primer design for the polymerase chain reaction. <i>Biotechnology Letters</i> , 2013 , 35, 1541-9 | 3 | 32 |
| 169 | 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 |
| 168 | Chaotic maps in binary particle swarm optimization for feature selection 2008 , | | 31 |
| 167 | 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 |
| 166 | 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 |
| 165 | CMDR based differential evolution identifies the epistatic interaction in genome-wide association studies. <i>Bioinformatics</i> , 2017 , 33, 2354-2362 | 7.2 | 28 |
| 164 | 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 |
| 163 | SNP-RFLPing 2: an updated and integrated PCR-RFLP tool for SNP genotyping. <i>BMC Bioinformatics</i> , 2010 , 11, 173 | 3.6 | 28 |
| 162 | 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 |
| 161 | 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 |
| 160 | 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 |
| 159 | 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 |
| 158 | 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 |
| 157 | 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 |
| 156 | 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 |
| 155 | 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 |

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|-----|---|------|----|
| 154 | Binary particle swarm optimization for operon prediction. <i>Nucleic Acids Research</i> , 2010 , 38, e128 | 20.1 | 21 |
| 153 | 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 |
| 152 | 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 |
| 151 | Restriction enzyme mining for SNPs in genomes. <i>Anticancer Research</i> , 2008 , 28, 2001-7 | 2.3 | 21 |
| 150 | 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 |
| 149 | Prim-SNPing: a primer designer for cost-effective SNP genotyping. <i>BioTechniques</i> , 2009 , 46, 421-31 | 2.5 | 19 |
| 148 | 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 |
| 147 | Specific PCR product primer design using memetic algorithm. <i>Biotechnology Progress</i> , 2009 , 25, 745-53 | 2.8 | 18 |
| 146 | Boolean binary particle swarm optimization for feature selection 2008 , | | 18 |
| 145 | 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 |
| 144 | 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 |
| 143 | Identifying association model for single-nucleotide polymorphisms of ORAI1 gene for breast cancer. <i>Cancer Cell International</i> , 2014 , 14, 29 | 6.4 | 17 |
| 142 | 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 |
| 141 | The importance of integrating SNP and cheminformatics resources to pharmacogenomics. <i>Current Drug Metabolism</i> , 2012 , 13, 991-9 | 3.5 | 16 |
| 140 | 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 | | 16 |
| 139 | Particle Swarm Optimization-Based Support Vector Regression for Tourist Arrivals Forecasting. <i>Computational Intelligence and Neuroscience</i> , 2018 , 2018, 6076475 | 3 | 16 |
| 138 | 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 |
| 137 | Fuzzy support vector machines for adaptive Morse code recognition. <i>Medical Engineering and Physics</i> , 2006 , 28, 925-31 | 2.4 | 15 |

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|-----|--|-----|----|
| 136 | Multiobjective multifactor dimensionality reduction to detect SNP-SNP interactions. <i>Bioinformatics</i> , 2018 , 34, 2228-2236 | 7.2 | 14 |
| 135 | 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 |
| 134 | Genetic algorithm-generated SNP barcodes of the mitochondrial D-loop for chronic dialysis susceptibility. <i>Mitochondrial DNA</i> , 2014 , 25, 231-7 | | 14 |
| 133 | Operon prediction using chaos embedded particle swarm optimization. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013 , 10, 1299-309 | 3 | 14 |
| 132 | Features for computational operon prediction in prokaryotes. <i>Briefings in Functional Genomics</i> , 2012 , 11, 291-9 | 4.9 | 14 |
| 131 | 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 |
| 130 | Feature Selection Using Memetic Algorithms 2008 , | | 14 |
| 129 | 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 |
| 128 | Morse code application for wireless environmental control systems for severely disabled individuals. <i>IEEE Transactions on Neural Systems and Rehabilitation Engineering</i> , 2003 , 11, 463-9 | 4.8 | 14 |
| 127 | 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 |
| 126 | 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 |
| 125 | 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 |
| 124 | Improved branch and bound algorithm for detecting SNP-SNP interactions in breast cancer. <i>Journal of Clinical Bioinformatics</i> , 2013 , 3, 4 | | 13 |
| 123 | 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 |
| 122 | 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 |
| 121 | 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 |
| 120 | V-MitoSNP: visualization of human mitochondrial SNPs. <i>BMC Bioinformatics</i> , 2006 , 7, 379 | 3.6 | 13 |
| 119 | URPD: a specific product primer design tool. <i>BMC Research Notes</i> , 2012 , 5, 306 | 2.3 | 12 |

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|-----|---|------|----|
| 118 | 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 |
| 117 | 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 |
| 116 | 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 |
| 115 | Impact of risk factors on functional status in maintenance hemodialysis patients. <i>European Journal of Medical Research</i> , 2017 , 22, 54 | 4.8 | 11 |
| 114 | The Combinational Polymorphisms of ORA1 Gene Are Associated with Preventive Models of Breast Cancer in the Taiwanese. <i>BioMed Research International</i> , 2015 , 2015, 281263 | 3 | 11 |
| 113 | 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 |
| 112 | A mobile communication aid system for persons with physical disabilities. <i>Mathematical and Computer Modelling</i> , 2008 , 47, 318-327 | | 11 |
| 111 | SNP-Flankplus: SNP ID-centric retrieval for SNP flanking sequences. <i>Bioinformatics</i> , 2008 , 3, 147-9 | 1.1 | 11 |
| 110 | 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 |
| 109 | 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 |
| 108 | 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 |
| 107 | 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 |
| 106 | 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 |
| 105 | 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 |
| 104 | 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 |
| 103 | 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 |
| 102 | . <i>IEEE Access</i> , 2020 , 8, 159389-159401 | 3.5 | 8 |
| 101 | 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 |

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|-----|---|-----|---|
| 100 | 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 |
| 99 | CpGPAP: CpG island predictor analysis platform. <i>BMC Genetics</i> , 2012 , 13, 13 | 2.6 | 7 |
| 98 | 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 |
| 97 | 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 |
| 96 | Chaotic genetic algorithm for gene selection and classification problems. <i>OMICS A Journal of Integrative Biology</i> , 2009 , 13, 407-20 | 3.8 | 7 |
| 95 | Methyl-Typing: an improved and visualized COBRA software for epigenomic studies. <i>FEBS Letters</i> , 2010 , 584, 739-44 | 3.8 | 7 |
| 94 | Catfish particle swarm optimization 2008 , | | 7 |
| 93 | An interactive morse code emulation management system. <i>Computers and Mathematics With Applications</i> , 2003 , 46, 479-492 | 2.7 | 7 |
| 92 | 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 |
| 91 | Identification of SNP-SNP interaction for chronic dialysis patients. <i>Computers in Biology and Medicine</i> , 2017 , 83, 94-101 | 7 | 6 |
| 90 | 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 |
| 89 | Multiobjective differential evolution-based multifactor dimensionality reduction for detecting gene-gene interactions. <i>Scientific Reports</i> , 2017 , 7, 12869 | 4.9 | 6 |
| 88 | 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 |
| 87 | Factors Associated with Functional Performance among Patients on Hemodialysis in Taiwan. <i>Blood Purification</i> , 2018 , 46, 12-18 | 3.1 | 6 |
| 86 | 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 |
| 85 | A Hybrid Approach for CpG Island Detection in the Human Genome. <i>PLoS ONE</i> , 2016 , 11, e0144748 | 3.7 | 6 |
| 84 | 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 |
| 83 | 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 |

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|----|--|-----|---|
| 82 | 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 |
| 81 | 2011 , | | 5 |
| 80 | SNP ID-info: SNP ID searching and visualization platform. <i>OMICS A Journal of Integrative Biology</i> , 2008 , 12, 217-26 | 3.8 | 5 |
| 79 | 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 |
| 78 | Effective multinational trade forecasting using LSTM recurrent neural network. <i>Expert Systems With Applications</i> , 2021 , 182, 115199 | 7.8 | 5 |
| 77 | 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 |
| 76 | 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 |
| 75 | PPO: predictor for prokaryotic operons. <i>Bioinformatics</i> , 2010 , 26, 3127-8 | 7.2 | 4 |
| 74 | A Novel Chaotic Inertia Weight Particle Swarm Optimization for PCR Primer Design 2010 , | | 4 |
| 73 | Operon Prediction Using Particle Swarm Optimization and Reinforcement Learning 2010 , | | 4 |
| 72 | A Hybrid Feature Selection Method Using Gene Expression Data 2009 , | | 4 |
| 71 | An improved fuzzy set-based multifactor dimensionality reduction for detecting epistasis. <i>Artificial Intelligence in Medicine</i> , 2020 , 102, 101768 | 7.4 | 4 |
| 70 | Analyzing the Performance of Machine Learning Techniques in Disease Prediction. <i>Journal of Food Quality</i> , 2022 , 2022, 1-9 | 2.7 | 4 |
| 69 | . <i>IEEE Access</i> , 2020 , 8, 82382-82390 | 3.5 | 3 |
| 68 | 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 |
| 67 | An Interactive Digital Somatosensory Game System That Implements a Decision Tree Algorithm. <i>IEEE Access</i> , 2019 , 7, 140190-140196 | 3.5 | 3 |
| 66 | 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 |
| 65 | Tag SNP selection using particle swarm optimization. <i>Biotechnology Progress</i> , 2010 , 26, 580-8 | 2.8 | 3 |

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|----|--|-----|---|
| 64 | LD2SNPing: linkage disequilibrium plotter and RFLP enzyme mining for tag SNPs. <i>BMC Genetics</i> , 2009 , 10, 26 | 2.6 | 3 |
| 63 | A NOVEL APPROACH TO MANDARIN MORSE CODE RECOGNITION. <i>Biomedical Engineering - Applications, Basis and Communications</i> , 2005 , 17, 267-274 | 0.6 | 3 |
| 62 | Immersive Virtual Reality-Based Cardiopulmonary Resuscitation Interactive Learning Support System. <i>IEEE Access</i> , 2020 , 8, 120870-120880 | 3.5 | 3 |
| 61 | An Effective Hybrid Approach for Forecasting Currency Exchange Rates. <i>Sustainability</i> , 2021 , 13, 2761 | 3.6 | 3 |
| 60 | 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 |
| 59 | PCR-CTPP design for enzyme-free SNP genotyping using memetic algorithm. <i>IEEE Transactions on Nanobioscience</i> , 2015 , 14, 13-23 | 3.4 | 2 |
| 58 | Fuzzy Logic System Application for Detecting SNP-SNP Interaction. <i>IEEE Access</i> , 2020 , 8, 49951-49960 | 3.5 | 2 |
| 57 | 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 |
| 56 | 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 |
| 55 | 2014 , | | 2 |
| 54 | The expert system application for diagnosing human vitamin deficiency through forward chaining method 2015 , | | 2 |
| 53 | Improved candidate drug mining for Alzheimer's disease. <i>BioMed Research International</i> , 2014 , 2014, 897653 | 3 | 2 |
| 52 | A wireless internet interface for person with physical disability. <i>Mathematical and Computer Modelling</i> , 2009 , 50, 72-80 | | 2 |
| 51 | Genetic Algorithm for the Design of Confronting Two-Pair Primers 2009 , | | 2 |
| 50 | 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 |
| 49 | SNP barcodes generated using particle swarm optimization to detect susceptibility to breast cancer. <i>Natural Science</i> , 2013 , 05, 359-367 | 0.5 | 2 |
| 48 | 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 |
| 47 | Confronting Two-Pair Primer Design Using Particle Swarm Optimization. <i>Lecture Notes in Computer Science</i> , 2010 , 448-456 | 0.9 | 2 |

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|----|---|-----|---|
| 46 | 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 |
| 45 | 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 |
| 44 | Forecasting outbound student mobility: A machine learning approach. <i>PLoS ONE</i> , 2020 , 15, e0238129 | 3.7 | 2 |
| 43 | 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 |
| 42 | Forecasting of the Prevalence of Dementia Using the LSTM Neural Network in Taiwan. <i>Mathematics</i> , 2021 , 9, 488 | 2.3 | 2 |
| 41 | Effect of Money Supply, Population, and Rent on Real Estate: A Clustering Analysis in Taiwan. <i>Mathematics</i> , 2022 , 10, 1155 | 2.3 | 2 |
| 40 | 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 |
| 39 | Relationship between Clinicopathologic Variables in Breast Cancer Overall Survival Using Biogeography-Based Optimization Algorithm. <i>BioMed Research International</i> , 2019 , 2019, 2304128 | 3 | 1 |
| 38 | Decision Theory-Based COI-SNP Tagging Approach for 126 Scombriformes Species Tagging. <i>Frontiers in Genetics</i> , 2019 , 10, 259 | 4.5 | 1 |
| 37 | . <i>IEEE Access</i> , 2019 , 7, 143036-143045 | 3.5 | 1 |
| 36 | A Quantum Genetic Algorithm for Operon Prediction 2012 , | | 1 |
| 35 | Fuzzy adaptive particle swarm optimization for a specific primer design problem 2009 , | | 1 |
| 34 | 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 |
| 33 | A hybrid approach for selecting gene subsets using gene expression data 2008 , | | 1 |
| 32 | Hybrid feature selection method using gene expression data 2008 , | | 1 |
| 31 | Comparative Particle Swarm Optimization (CPSO) for solving optimization problems 2008 , | | 1 |
| 30 | Improved tag SNP selection using binary particle swarm optimization 2008 , | | 1 |
| 29 | 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 |

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|----|--|-----|---|
| 28 | A wireless emulation management system for learning Mandarin phonetic and chanjei Morse code 2005, | | 1 |
| 27 | Deep Hybrid Convolutional Neural Network for Segmentation of Melanoma Skin Lesion. <i>Computational Intelligence and Neuroscience</i> , 2021 , 2021, 9409508 | 3 | 1 |
| 26 | 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 |
| 25 | Improved Classification Method for Detecting Potential Interactions Between Genes. <i>Advances in Intelligent Systems and Computing</i> , 2019 , 394-403 | 0.4 | 1 |
| 24 | An introduction to mitochondrial informatics. <i>Methods in Molecular Biology</i> , 2010 , 628, 259-74 | 1.4 | 1 |
| 23 | Student Enrollment and Teacher Statistics Forecasting Based on Time-Series Analysis. <i>Computational Intelligence and Neuroscience</i> , 2020 , 2020, 1246920 | 3 | 1 |
| 22 | Associations between Circulating Markers of Cholesterol Homeostasis and Macrovascular Events among Patients Undergoing Hemodialysis. <i>Nutrients</i> , 2021 , 13, | 6.7 | 1 |
| 21 | 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 |
| 20 | Machine Learning Data Imputation and Prediction of Foraging Group Size in a Kleptoparasitic Spider. <i>Mathematics</i> , 2021 , 9, 415 | 2.3 | 1 |
| 19 | 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 |
| 18 | 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 |
| 17 | AN INTELLIGENT CHINESE PHONETIC ON-SCREEN VIRTUAL KEYBOARD SYSTEM. <i>Biomedical Engineering - Applications, Basis and Communications</i> , 2006 , 18, 178-184 | 0.6 | 0 |
| 16 | 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 |
| 15 | 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 |
| 14 | Deep Learning for Imputation and Forecasting Tidal Level. <i>IEEE Journal of Oceanic Engineering</i> , 2021 , 1-11 | 3.3 | 0 |
| 13 | AIS-Based Intelligent Vessel Trajectory Prediction Using Bi-LSTM. <i>IEEE Access</i> , 2022 , 10, 24302-24315 | 3.5 | 0 |
| 12 | 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 |
| 11 | 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 | |

- 10 0138 The association of blood lead levels and bone density in different combinational SNP polymorphisms among Taiwan lead workers. *Occupational and Environmental Medicine*, **2014**, 71, A77.3-A78 2.1
- 9 Prevalence and molecular characterization of plasmidmediated beta-lactamase genes among nosocomial *Staphylococcus aureus* isolated in Taiwan. *Tropical Journal of Pharmaceutical Research*, **2017**, 16, 155 0.8
- 8 Complementary distribution BPSO for feature selection. *Intelligent Data Analysis*, **2012**, 16, 183-198 1.1
- 7 hSAGEing: an improved SAGE-based software for identification of human tissue-specific or common tumor markers and suppressors. *PLoS ONE*, **2010**, 5, e14369 3.7
- 6 COMBAT GA-BASED GENE SELECTION FOR CLASSIFICATION OF MICROARRAY DATA. *Biomedical Engineering - Applications, Basis and Communications*, **2008**, 20, 345-352 0.6
- 5 VSA-TOOL: A TOOL FOR DATA VISUALIZATION IN SEQUENCE ALIGNMENT. *Biomedical Engineering - Applications, Basis and Communications*, **2004**, 16, 68-72 0.6
- 4 Effect of clinical factors on trajectory of functional performance in patients undergoing hemodialysis. *Renal Failure*, **2021**, 43, 90-96 2.9
- 3 An Interactive Wireless Morse Code Learning System **2009**, 3361-3367
- 2 A combined bisulfite restriction analysis bioinformatics tool: methyl-typing. *Methods in Molecular Biology*, **2011**, 791, 73-88 1.4
- 1 Hybrid High Exploration Particle Swarm Optimization Algorithm Improves the Prediction of the 2-Dimensional Hydrophobic-Polar Model for Protein Folding. *Current Bioinformatics*, **2018**, 13, 182-192 4.7