

Hong Yan

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.

442
papers

6,850
citations

40
h-index

63
g-index

543
ext. papers

8,483
ext. citations

4.6
avg, IF

6.41
L-index

#	Paper	IF	Citations
442	Patch-Aware Deep Hyperspectral and Multispectral Image Fusion by Unfolding Subspace-Based Optimization Model. <i>IEEE Journal of Selected Topics in Applied Earth Observations and Remote Sensing</i> , 2022 , 15, 1024-1038	4.7	1
441	Elastic Net Constraint-Based Tensor Model for High-Order Graph Matching. <i>IEEE Transactions on Cybernetics</i> , 2021 , 51, 4062-4074	10.2	5
440	Time-Varying Differential Network Analysis for Revealing Network Rewiring over Cancer Progression. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021 , 18, 1632-1642	3	1
439	Structure-based protein-ligand interaction fingerprints for binding affinity prediction.. <i>Computational and Structural Biotechnology Journal</i> , 2021 , 19, 6291-6300	6.8	2
438	Exploiting higher-order patterns for community detection in attributed graphs. <i>Integrated Computer-Aided Engineering</i> , 2021 , 28, 207-218	5.2	8
437	WDNE: an integrative graphical model for inferring differential networks from multi-platform gene expression data with missing values. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	2
436	An Efficient Randomized Algorithm for Computing the Approximate Tucker Decomposition. <i>Journal of Scientific Computing</i> , 2021 , 88, 1	2.3	1
435	Genotype-determined EGFR-RTK heterodimerization and its effects on drug resistance in lung Cancer treatment revealed by molecular dynamics simulations. <i>BMC Molecular and Cell Biology</i> , 2021 , 22, 34	2.7	0
434	Differential network analysis by simultaneously considering changes in gene interactions and gene expression. <i>Bioinformatics</i> , 2021 ,	7.2	2
433	Multi-deep features fusion for high-resolution remote sensing image scene classification. <i>Neural Computing and Applications</i> , 2021 , 33, 2047-2063	4.8	11
432	Computationally predicting binding affinity in protein-ligand complexes: free energy-based simulations and machine learning-based scoring functions. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	14
431	Joint Transformation Learning via the L-Norm Metric for Robust Graph Matching. <i>IEEE Transactions on Cybernetics</i> , 2021 , 51, 521-533	10.2	4
430	Learning Kernel for Conditional Moment-Matching Discrepancy-Based Image Classification. <i>IEEE Transactions on Cybernetics</i> , 2021 , 51, 2006-2018	10.2	4
429	Visualization of Protein-Drug Interactions for the Analysis of Drug Resistance in Lung Cancer. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2021 , 25, 1839-1848	7.2	0
428	Fuzzy SLIC: Fuzzy Simple Linear Iterative Clustering. <i>IEEE Transactions on Circuits and Systems for Video Technology</i> , 2021 , 31, 2114-2124	6.4	4
427	HiSCF: leveraging higher-order structures for clustering analysis in biological networks. <i>Bioinformatics</i> , 2021 , 37, 542-550	7.2	27
426	A Joint Graphical Model for Inferring Gene Networks Across Multiple Subpopulations and Data Types. <i>IEEE Transactions on Cybernetics</i> , 2021 , 51, 1043-1055	10.2	4

425	. <i>IEEE Access</i> , 2021 , 9, 96964-96974	3.5	11
424	. <i>IEEE Transactions on Multimedia</i> , 2021 , 23, 2902-2916	6.6	8
423	Proteo-chemometrics interaction fingerprints of protein-ligand complexes predict binding affinity. <i>Bioinformatics</i> , 2021 ,	7.2	3
422	An Efficient Parallel Processor for Dense Tensor Computation. <i>IEEE Transactions on Very Large Scale Integration (VLSI) Systems</i> , 2021 , 29, 1335-1347	2.6	0
421	Mechanism of Actions of Dexamethasone Against COVID-19 Predicted by Alpha Shape Analysis of Binding Sites. <i>Current Bioinformatics</i> , 2021 , 16, 682-690	4.7	
420	Deep center-based dual-constrained hashing for discriminative face image retrieval. <i>Pattern Recognition</i> , 2021 , 117, 107976	7.7	5
419	A Novel Regularized Model for Third-Order Tensor Completion. <i>IEEE Transactions on Signal Processing</i> , 2021 , 1-1	4.8	3
418	Establishment of a morphological atlas of the <i>Caenorhabditis elegans</i> embryo using deep-learning-based 4D segmentation. <i>Nature Communications</i> , 2020 , 11, 6254	17.4	17
417	Correlated Motions and Dynamics in Different Domains of EGFR with L858R and T790M Mutations. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020 , PP,	3	2
416	Predicting the impacts of mutations on protein-ligand binding affinity based on molecular dynamics simulations and machine learning methods. <i>Computational and Structural Biotechnology Journal</i> , 2020 , 18, 439-454	6.8	15
415	Saliency detection via multiple-morphological and superpixel based fast fuzzy C-mean clustering network. <i>Expert Systems With Applications</i> , 2020 , 161, 113654	7.8	8
414	scTSSR: gene expression recovery for single-cell RNA sequencing using two-side sparse self-representation. <i>Bioinformatics</i> , 2020 , 36, 3131-3138	7.2	10
413	Joint reconstruction of multiple gene networks by simultaneously capturing inter-tumor and intra-tumor heterogeneity. <i>Bioinformatics</i> , 2020 , 36, 2755-2762	7.2	4
412	Learning Multiple Parameters for Kernel Collaborative Representation Classification. <i>IEEE Transactions on Neural Networks and Learning Systems</i> , 2020 , 31, 5068-5078	10.3	11
411	Superpixel Based Hierarchical Segmentation for Color Image. <i>IEICE Transactions on Information and Systems</i> , 2020 , E103.D, 2246-2249	0.6	0
410	Stability Analysis at Key Positions of EGFR Related to Non-small Cell Lung Cancer. <i>Current Bioinformatics</i> , 2020 , 15, 260-267	4.7	5
409	Generalized Tensor Regression for Hyperspectral Image Classification. <i>IEEE Transactions on Geoscience and Remote Sensing</i> , 2020 , 58, 1244-1258	8.1	25
408	Hypergraph Clustering Using a New Laplacian Tensor with Applications in Image Processing. <i>SIAM Journal on Imaging Sciences</i> , 2020 , 13, 1157-1178	1.9	3

407	A Truncated Matrix Decomposition for Hyperspectral Image Super-Resolution. <i>IEEE Transactions on Image Processing</i> , 2020 , 29, 8028-8042	8.7	27
406	Unsupervised Domain Adaptation via Discriminative Manifold Propagation. <i>IEEE Transactions on Pattern Analysis and Machine Intelligence</i> , 2020 , PP,	13.3	7
405	Contour and region harmonic features for sub-local facial expression recognition. <i>Journal of Visual Communication and Image Representation</i> , 2020 , 73, 102949	2.7	5
404	Co-Clustering to Reveal Salient Facial Features for Expression Recognition. <i>IEEE Transactions on Affective Computing</i> , 2020 , 11, 348-360	5.7	9
403	Generalized Conditional Domain Adaptation: A Causal Perspective With Low-Rank Translators. <i>IEEE Transactions on Cybernetics</i> , 2020 , 50, 821-834	10.2	12
402	MCNF: A Novel Method for Cancer Subtyping by Integrating Multi-Omics and Clinical Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020 , 17, 1682-1690	3	4
401	Deep Class-Wise Hashing: Semantics-Preserving Hashing via Class-Wise Loss. <i>IEEE Transactions on Neural Networks and Learning Systems</i> , 2020 , 31, 1681-1695	10.3	9
400	Image Correspondence With CUR Decomposition-Based Graph Completion and Matching. <i>IEEE Transactions on Circuits and Systems for Video Technology</i> , 2020 , 30, 3054-3067	6.4	5
399	Differential Network Analysis via Weighted Fused Conditional Gaussian Graphical Model. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020 , 17, 2162-2169	3	1
398	DiffNetFDR: differential network analysis with false discovery rate control. <i>Bioinformatics</i> , 2019 , 35, 3184-3186		
397	EnImpute: imputing dropout events in single-cell RNA-sequencing data via ensemble learning. <i>Bioinformatics</i> , 2019 , 35, 4827-4829	7.2	15
396	Multiscale co-clustering for tensor data based on canonical polyadic decomposition and slice-wise factorization. <i>Information Sciences</i> , 2019 , 503, 72-91	7.7	4
395	A unified formulation of a class of graph matching techniques. <i>Pattern Recognition</i> , 2019 , 95, 223-234	7.7	
394	3DMMS: robust 3D Membrane Morphological Segmentation of <i>C. elegans</i> embryo. <i>BMC Bioinformatics</i> , 2019 , 20, 176	3.6	8
393	Joint Learning of Multiple Differential Networks With Latent Variables. <i>IEEE Transactions on Cybernetics</i> , 2019 , 49, 3494-3506	10.2	10
392	Parametric Models for Understanding Atomic Trajectories in Different Domains of Lung Cancer Causing Protein. <i>IEEE Access</i> , 2019 , 7, 67551-67563	3.5	7
391	Multimodal Co-clustering Analysis of Big Data Based on Matrix and Tensor Decomposition 2019 , 95-124		
390	Superpixel Tensor Pooling for Visual Tracking Using Multiple Midlevel Visual Cues Fusion. <i>IEEE Access</i> , 2019 , 7, 147462-147469	3.5	1

389	Discriminative Residual Analysis for Image Set Classification with Posture and Age Variations. <i>IEEE Transactions on Image Processing</i> , 2019 ,	8.7	6
388	Computational Analysis of Structural Dynamics of EGFR and its Mutants 2019 ,		2
387	Singular value decomposition based recommendation using imputed data. <i>Knowledge-Based Systems</i> , 2019 , 163, 485-494	7.3	30
386	Hydrogen bond analysis of the EGFR-ErbB3 heterodimer related to non-small cell lung cancer and drug resistance. <i>Journal of Theoretical Biology</i> , 2019 , 464, 63-71	2.3	10
385	. <i>IEEE Transactions on Systems, Man, and Cybernetics: Systems</i> , 2019 , 49, 71-80	7.3	17
384	EmDL: Extracting miRNA-Drug Interactions from Literature. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019 , 16, 1722-1728	3	6
383	Molecular subtyping of cancer: current status and moving toward clinical applications. <i>Briefings in Bioinformatics</i> , 2019 , 20, 572-584	13.4	35
382	DrPOCS: Drug Repositioning Based on Projection Onto Convex Sets. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019 , 16, 154-162	3	10
381	Establishment of Signaling Interactions with Cellular Resolution for Every Cell Cycle of Embryogenesis. <i>Genetics</i> , 2018 , 209, 37-49	4	11
380	DiffGraph: an R package for identifying gene network rewiring using differential graphical models. <i>Bioinformatics</i> , 2018 , 34, 1571-1573	7.2	9
379	Prediction of sensitivity to gefitinib/erlotinib for EGFR mutations in NSCLC based on structural interaction fingerprints and multilinear principal component analysis. <i>BMC Bioinformatics</i> , 2018 , 19, 88	3.6	14
378	Tensor Decomposition of Gait Dynamics in Parkinson's Disease. <i>IEEE Transactions on Biomedical Engineering</i> , 2018 , 65, 1820-1827	5	21
377	Bayes Saliency-Based Object Proposal Generator for Nighttime Traffic Images. <i>IEEE Transactions on Intelligent Transportation Systems</i> , 2018 , 19, 814-825	6.1	17
376	Some inequalities for the Hadamard product of tensors. <i>Linear and Multilinear Algebra</i> , 2018 , 66, 1199-1214		11
375	Gene expression profiling of 1200 pancreatic ductal adenocarcinoma reveals novel subtypes. <i>BMC Cancer</i> , 2018 , 18, 603	4.8	35
374	Analysis of the Relative Movements Between EGFR and Drug Inhibitors Based on Molecular Dynamics Simulation. <i>Current Bioinformatics</i> , 2018 , 13, 299-309	4.7	3
373	Cascade feature selection and coarse-to-fine mechanism for nighttime multiclass vehicle detection. <i>Journal of Electronic Imaging</i> , 2018 , 27, 1	0.7	1
372	A quadratic penalty method for hypergraph matching. <i>Journal of Global Optimization</i> , 2018 , 70, 237-259	1.5	4

371	Spatial-dependence recurrence sample entropy. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2018 , 494, 581-590	3.3	13
370	Computing the p-Spectral Radii of Uniform Hypergraphs with Applications. <i>Journal of Scientific Computing</i> , 2018 , 75, 1-25	2.3	7
369	Accurate Cell Segmentation Based on Biological Morphology Features 2018 ,		1
368	Tagrec-CMTF: Coupled Matrix and Tensor Factorization for Tag Recommendation. <i>IEEE Access</i> , 2018 , 6, 64142-64152	3.5	4
367	Constructing Dynamic Topic Models Based on Variational Autoencoder and Factor Graph. <i>IEEE Access</i> , 2018 , 6, 53102-53111	3.5	2
366	An Eigen-Binding Site Based Method for the Analysis of Anti-EGFR Drug Resistance in Lung Cancer Treatment. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017 , 14, 1187-1194	3	7
365	Sliced Inverse Regression With Adaptive Spectral Sparsity for Dimension Reduction. <i>IEEE Transactions on Cybernetics</i> , 2017 , 47, 759-771	10.2	2
364	Incorporating prior information into differential network analysis using non-paranormal graphical models. <i>Bioinformatics</i> , 2017 , 33, 2436-2445	7.2	31
363	Coclustering of Multidimensional Big Data: A Useful Tool for Genomic, Financial, and Other Data Analysis. <i>IEEE Systems, Man, and Cybernetics Magazine</i> , 2017 , 3, 23-30	1.6	12
362	mTD: A database of microRNAs affecting therapeutic effects of drugs. <i>Journal of Genetics and Genomics</i> , 2017 , 44, 269-271	4	13
361	Node-based differential network analysis in genomics. <i>Computational Biology and Chemistry</i> , 2017 , 69, 194-201	3.6	8
360	An online spatio-temporal tensor learning model for visual tracking and its applications to facial expression recognition. <i>Expert Systems With Applications</i> , 2017 , 90, 427-438	7.8	8
359	Deciphering mechanisms of acquired T790M mutation after EGFR inhibitors for NSCLC by computational simulations. <i>Scientific Reports</i> , 2017 , 7, 6595	4.9	20
358	Nighttime Vehicle Detection Based on Bio-Inspired Image Enhancement and Weighted Score-Level Feature Fusion. <i>IEEE Transactions on Intelligent Transportation Systems</i> , 2017 , 18, 927-936	6.1	35
357	Predicting new indications of compounds with a network pharmacology approach: Liuwei Dihuang Wan as a case study. <i>Oncotarget</i> , 2017 , 8, 93957-93968	3.3	8
356	Inference of cellular level signaling networks using single-cell gene expression data in <i>Caenorhabditis elegans</i> reveals mechanisms of cell fate specification. <i>Bioinformatics</i> , 2017 , 33, 1528-1535	7.2	3
355	Comparative analysis of housekeeping and tissue-specific driver nodes in human protein interaction networks. <i>BMC Bioinformatics</i> , 2016 , 17, 358	3.6	10
354	Differential network analysis from cross-platform gene expression data. <i>Scientific Reports</i> , 2016 , 6, 34112.9		24

353	Identifying EGFR mutation-induced drug resistance based on alpha shape model analysis of the dynamics. <i>Proteome Science</i> , 2016 , 14, 12	2.6	9
352	Analysis of the relationship between lung cancer drug response level and atom connectivity dynamics based on trimmed Delaunay triangulation. <i>Chemical Physics Letters</i> , 2016 , 652, 117-122	2.5	6
351	A two-layer integration framework for protein complex detection. <i>BMC Bioinformatics</i> , 2016 , 17, 100	3.6	15
350	Regularized logistic regression with network-based pairwise interaction for biomarker identification in breast cancer. <i>BMC Bioinformatics</i> , 2016 , 17, 108	3.6	17
349	Fruit classification based on weighted score-level feature fusion. <i>Journal of Electronic Imaging</i> , 2016 , 25, 013009	0.7	7
348	Text-Independent Phoneme Segmentation Combining EGG and Speech Data. <i>IEEE/ACM Transactions on Audio Speech and Language Processing</i> , 2016 , 24, 1029-1037	3.6	10
347	Combining Region-of-Interest Extraction and Image Enhancement for Nighttime Vehicle Detection. <i>IEEE Intelligent Systems</i> , 2016 , 31, 57-65	4.2	38
346	Selectivity profile of afatinib for EGFR-mutated non-small-cell lung cancer. <i>Molecular BioSystems</i> , 2016 , 12, 1552-63		4
345	A study on the discriminating characteristics of Gabor phase-face and an improved method for face recognition. <i>International Journal of Machine Learning and Cybernetics</i> , 2016 , 7, 1115-1130	3.8	5
344	An integrative C. elegans protein-protein interaction network with reliability assessment based on a probabilistic graphical model. <i>Molecular BioSystems</i> , 2016 , 12, 85-92		9
343	A Probabilistic Relaxation Labeling (PRL) Based Method for C. elegans Cell Tracking in Microscopic Image Sequences. <i>IEEE Journal on Selected Topics in Signal Processing</i> , 2016 , 10, 185-192	7.5	5
342	Identifying differential networks based on multi-platform gene expression data. <i>Molecular BioSystems</i> , 2016 , 13, 183-192		11
341	Identifying Multi-Dimensional Co-Clusters in Tensors Based on Hyperplane Detection in Singular Vector Spaces. <i>PLoS ONE</i> , 2016 , 11, e0162293	3.7	7
340	Identifying protein complexes via multi-network clustering 2016 ,		1
339	Feature selection based on co-clustering for effective facial expression recognition 2016 ,		5
338	Protein complex detection based on partially shared multi-view clustering. <i>BMC Bioinformatics</i> , 2016 , 17, 371	3.6	6
337	Support System Using Microsoft Kinect and Mobile Phone for Daily Activity of Visually Impaired 2015 , 425-440		4
336	Adaptive Cockroach Colony Optimization for Rod-Like Robot Navigation. <i>Journal of Bionic Engineering</i> , 2015 , 12, 324-337	2.7	8

335	EGFR Mutant Structural Database: computationally predicted 3D structures and the corresponding binding free energies with gefitinib and erlotinib. <i>BMC Bioinformatics</i> , 2015 , 16, 85	3.6	23
334	Decoding the EGFR mutation-induced drug resistance in lung cancer treatment by local surface geometric properties. <i>Computers in Biology and Medicine</i> , 2015 , 63, 293-300	7	8
333	Sample Weighting: An Inherent Approach for Outlier Suppressing Discriminant Analysis. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2015 , 27, 3070-3083	4.2	10
332	Mining of protein-protein interfacial residues from massive protein sequential and spatial data. <i>Fuzzy Sets and Systems</i> , 2015 , 258, 101-116	3.7	4
331	Recommender systems based on social networks. <i>Journal of Systems and Software</i> , 2015 , 99, 109-119	3.3	101
330	Computational Evaluation of EGFR Dynamic Characteristics in Mutation-Induced Drug Resistance Prediction 2015 ,		1
329	Systems-level quantification of division timing reveals a common genetic architecture controlling asynchrony and fate asymmetry. <i>Molecular Systems Biology</i> , 2015 , 11, 814	12.2	19
328	Local Topology Preserved Tensor Models for Graph Matching 2015 ,		3
327	Contribution of EGFR and ErbB-3 Heterodimerization to the EGFR Mutation-Induced Gefitinib- and Erlotinib-Resistance in Non-Small-Cell Lung Carcinoma Treatments. <i>PLoS ONE</i> , 2015 , 10, e0128360	3.7	13
326	Bicluster Analysis for Coherent Pattern Discovery 2015 , 1665-1674		1
325	Design Exploration of Geometric Biclustering for Microarray Data Analysis in Data Mining. <i>IEEE Transactions on Parallel and Distributed Systems</i> , 2014 , 25, 2540-2550	3.7	9
324	Detecting overlapping protein complexes based on a generative model with functional and topological properties. <i>BMC Bioinformatics</i> , 2014 , 15, 186	3.6	33
323	Dimensionality reduction and topographic mapping of binary tensors. <i>Pattern Analysis and Applications</i> , 2014 , 17, 497-515	2.3	4
322	A machine learning approach to improve contactless heart rate monitoring using a webcam. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2014 , 18, 1153-60	7.2	96
321	GPU-based biclustering for microarray data analysis in neurocomputing. <i>Neurocomputing</i> , 2014 , 134, 239-246	5.4	10
320	Fast prediction of protein-protein interaction sites based on Extreme Learning Machines. <i>Neurocomputing</i> , 2014 , 128, 258-266	5.4	54
319	An FPGA based scalable architecture of a stochastic state point process filter (SSPPF) to track the nonlinear dynamics underlying neural spiking. <i>Microelectronics Journal</i> , 2014 , 45, 690-701	1.8	4
318	Genome-wide nucleosome detection based on the dinucleotide position frequencies. <i>International Journal of Data Mining and Bioinformatics</i> , 2014 , 10, 285-99	0.5	

317	Chapter 2: Identification of Genes and their Regulatory Regions Based on Multiple Physical and Structural Properties of a DNA Sequence. <i>Science, Engineering, and Biology Informatics</i> , 2014 , 33-65		
316	A bicluster-based Bayesian principal component analysis method for microarray missing value estimation. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2014 , 18, 863-71	7.2	13
315	Alpha shape and Delaunay triangulation in studies of protein-related interactions. <i>Briefings in Bioinformatics</i> , 2014 , 15, 54-64	13.4	22
314	Retina based biometric authentication using phase congruency. <i>International Journal of Machine Learning and Cybernetics</i> , 2014 , 5, 933-945	3.8	7
313	Recognizing Bangladeshi Currency for Visually Impaired. <i>Communications in Computer and Information Science</i> , 2014 , 129-135	0.3	3
312	Identification of DNA-binding and protein-binding proteins using enhanced graph wavelet features. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013 , 10, 1017-31	3	2
311	Autoregressive and iterative hidden Markov models for periodicity detection and solenoid structure recognition in protein sequences. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2013 , 17, 436-41	7.2	6
310	A graph spectrum based geometric biclustering algorithm. <i>Journal of Theoretical Biology</i> , 2013 , 317, 200-214	2.1	8
309	2013 ,		4
308	Prediction of Protein-Protein Interactions Based on Molecular Interface Features and the Support Vector Machine. <i>Current Bioinformatics</i> , 2013 , 8, 3-8	4.7	1
307	Boolean genetic network model for the control of C. elegans early embryonic cell cycles. <i>BioMedical Engineering OnLine</i> , 2013 , 12 Suppl 1, S1	4.1	10
306	A Flexible and Customizable Architecture for the Relaxation Labeling Algorithm. <i>IEEE Transactions on Circuits and Systems II: Express Briefs</i> , 2013 , 60, 106-110	3.5	2
305	Personalized prediction of EGFR mutation-induced drug resistance in lung cancer. <i>Scientific Reports</i> , 2013 , 3, 2855	4.9	25
304	A novel cell nuclei segmentation method for 3D C. elegans embryonic time-lapse images. <i>BMC Bioinformatics</i> , 2013 , 14, 328	3.6	9
303	A Survey on Structural Analysis of Nucleosome Core Particles. <i>Current Bioinformatics</i> , 2013 , 8, 112-132	4.7	
302	Transcriptional protein-protein cooperativity in POU/HMG/DNA complexes revealed by normal mode analysis. <i>Computational and Mathematical Methods in Medicine</i> , 2013 , 2013, 854710	2.8	1
301	Prediction of Protein-Protein Interactions Based on Molecular Interface Features and the Support Vector Machine. <i>Current Bioinformatics</i> , 2013 , 8, 3-8	4.7	3
300	A Hierarchical Multilevel Image Thresholding Method Based on the Maximum Fuzzy Entropy Principle 2013 , 241-272		

299	Image Processing and Reconstruction of Cultured Neuron Skeletons. <i>Studies in Computational Intelligence</i> , 2013 , 43-78	0.8	
298	Exon prediction using empirical mode decomposition and Fourier transform of structural profiles of DNA sequences. <i>Pattern Recognition</i> , 2012 , 45, 947-955	7.7	20
297	Robust classification using ℓ_1 -norm based regression model. <i>Pattern Recognition</i> , 2012 , 45, 2708-2718	7.7	67
296	Biomarker identification and cancer classification based on microarray data using Laplace naive Bayes model with mean shrinkage. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012 , 9, 1649-62	3	33
295	The relationship between geometric patterns of hydrogen bonds and periodic dinucleotides in nucleosome structures. <i>Journal of Theoretical Biology</i> , 2012 , 313, 136-41	2.3	3
294	A hierarchical multilevel thresholding method for edge information extraction using fuzzy entropy. <i>International Journal of Machine Learning and Cybernetics</i> , 2012 , 3, 297-305	3.8	10
293	Analysis of surface structures of hydrogen bonding in protein-ligand interactions using the alpha shape model. <i>Chemical Physics Letters</i> , 2012 , 545, 125-131	2.5	16
292	Analysis of DNA deformation patterns in nucleosome core particles based on isometric feature mapping and continuous wavelet transform. <i>Chemical Physics Letters</i> , 2012 , 547, 73-81	2.5	2
291	Dermatological disease diagnosis using color-skin images 2012 ,		16
290	Hypergraph based geometric biclustering algorithm. <i>Pattern Recognition Letters</i> , 2012 , 33, 1656-1665	4.7	11
289	Hybrid method for the analysis of time series gene expression data. <i>Knowledge-Based Systems</i> , 2012 , 35, 14-20	7.3	4
288	Coupled kernel embedding for low resolution face image recognition. <i>IEEE Transactions on Image Processing</i> , 2012 , 21, 3770-83	8.7	66
287	PRL-Dock: protein-ligand docking based on hydrogen bond matching and probabilistic relaxation labeling. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012 , 80, 2137-53	4.2	14
286	Noise reduction in microarray gene expression data based on spectral analysis. <i>International Journal of Machine Learning and Cybernetics</i> , 2012 , 3, 51-57	3.8	17
285	Biclustering Analysis for Pattern Discovery: Current Techniques, Comparative Studies and Applications. <i>Current Bioinformatics</i> , 2012 , 7, 43-55	4.7	28
284	Measurement of retinal arteriolar diameters from auto scale phase congruency with fuzzy weighting and L1 regularization. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference</i> , 2012 , 2012, 1434-7	0.9	
283	Selection and mapping of DNA structural features for short gene recognition. <i>International Journal of Data Mining and Bioinformatics</i> , 2012 , 6, 675-91	0.5	1
282	Detection and 2-dimensional display of short tandem repeats based on signal decomposition. <i>International Journal of Data Mining and Bioinformatics</i> , 2011 , 5, 661-90	0.5	3

281	Rapid feature extraction for Bangla handwritten digit recognition 2011 ,		12
280	Face recognition accuracy of Gabor phase representations at different scales and orientations 2011 ,		2
279	An Improved Position Weight Matrix method based on an entropy measure for the recognition of prokaryotic promoters. <i>International Journal of Data Mining and Bioinformatics</i> , 2011 , 5, 22-37	0.5	11
278	Short Exon Detection in DNA Sequences Based on Multifeature Spectral Analysis. <i>Eurasip Journal on Advances in Signal Processing</i> , 2011 , 2011,	1.9	8
277	Recent patents on biclustering algorithms for gene expression data analysis. <i>Recent Patents on DNA & Gene Sequences</i> , 2011 , 5, 117-25		3
276	Integration of clustering and biclustering procedures for analysis of large DNA microarray datasets. <i>International Journal of Computational Biology and Drug Design</i> , 2011 , 4, 179-93	0.4	1
275	High speed detection of retinal blood vessels in fundus image using phase congruency. <i>Soft Computing</i> , 2011 , 15, 1217-1230	3.5	38
274	Correlation between the flexibility and periodic dinucleotide patterns in yeast nucleosomal DNA sequences. <i>Journal of Theoretical Biology</i> , 2011 , 284, 92-8	2.3	4
273	Unified formulation of linear discriminant analysis methods and optimal parameter selection. <i>Pattern Recognition</i> , 2011 , 44, 307-319	7.7	5
272	Performance evaluation and comparison of PCA Based human face recognition methods for distorted images. <i>International Journal of Machine Learning and Cybernetics</i> , 2011 , 2, 245-259	3.8	34
271	Prediction of DNA-binding protein based on statistical and geometric features and support vector machines. <i>Proteome Science</i> , 2011 , 9 Suppl 1, S1	2.6	16
270	Searching for coexpressed genes in three-color cDNA microarray data using a probabilistic model-based Hough Transform. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011 , 8, 1093-107	3	5
269	Blood cell image segmentation based on the Hough transform and fuzzy curve tracing 2011 ,		12
268	Finding Correlated Biclusters from Gene Expression Data. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2011 , 23, 568-584	4.2	52
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