P N Suganthan

List of Publications by Year
in descending order

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31
papers

5,310
citations

331259
21
h-index

500791
28
g-index

31
all docs

31
docs citations

31
times ranked

4796
citing authors

#	ARTICLE	IF	CITATIONS
1	Discrete harmony search algorithm for flexible job shop scheduling problem with multiple objectives. Journal of Intelligent Manufacturing, 2016, 27, 363-374.	4.4	131
2	Gaussian adaptation based parameter adaptation for differential evolution. , 2014, , .		16
3	Instance based random forest with rotated feature space. , 2013, , .		4
4	Differential Evolution With Neighborhood Mutation for Multimodal Optimization. IEEE Transactions on Evolutionary Computation, 2012, 16, 601-614.	7.5	440
5	Solving Fuzzy Job-Shop Scheduling Problem by a Hybrid PSO Algorithm. Lecture Notes in Computer Science, 2012, , 275-282.	1.0	9
6	ROBUST ADAPTIVE BEAMFORMING BASED ON COVARIANCE MATRIX RECONSTRUCTION FOR LOOK DIRECTION MISMATCH. Progress in Electromagnetics Research Letters, 2011, 25, 37-46.	0.4	35
7	NEAR OPTIMAL ROBUST ADAPTIVE BEAMFORMING APPROACH BASED ON EVOLUTIONARY ALGORITHM. Progress in Electromagnetics Research B, 2011, 29, 157-174.	0.7	17
8	A hybrid tabu search algorithm with an efficient neighborhood structure for the flexible job shop scheduling problem. International Journal of Advanced Manufacturing Technology, 2011, 52, 683-697.	1.5	137
9	AFP-Pred: A random forest approach for predicting antifreeze proteins from sequence-derived properties. Journal of Theoretical Biology, 2011, 270, 56-62.	0.8	226
10	SVMCRYS: An SVM Approach for the Prediction of Protein Crystallization Propensity from Protein Sequence. Protein and Peptide Letters, 2010, 17, 423-430.	0.4	34
11	Identification of functionally diverse lipocalin proteins from sequence information using support vector machine. Amino Acids, 2010, 39, 777-783.	1.2	11
12	An approach for classification of highly imbalanced data using weighting and undersampling. Amino Acids, 2010, 39, 1385-1391.	1.2	134
13	SPRED: A machine learning approach for the identification of classical and non-classical secretory proteins in mammalian genomes. Biochemical and Biophysical Research Communications, 2010, 391, 1306-1311.	1.0	33
14	SMpred: A Support Vector Machine Approach to Identify Structural Motifs in Protein Structure Without Using Evolutionary Information. Journal of Biomolecular Structure and Dynamics, 2010, 28, 405-414.	2.0	5
15	Identification of structurally conserved residues of proteins in absence of structural homologs using neural network ensemble. Bioinformatics, 2009, 25, 204-210.	1.8	70
16	Differential Evolution Algorithm With Strategy Adaptation for Global Numerical Optimization. IEEE Transactions on Evolutionary Computation, 2009, 13, 398-417.	7.5	3,183
17	Multiclass cancer classification by support vector machines with class-wise optimized genes and probability estimates. Journal of Theoretical Biology, 2009, 259, 533-540.	0.8	35
18	Prediction of functionally important sites from protein sequences using sparse kernel least squares classifiers. Biochemical and Biophysical Research Communications, 2009, 384, 155-159.	1.0	6

#	ARTICLE	IF	CITATIONS
19	DNA-Prot: Identification of DNA Binding Proteins from Protein Sequence Information using Random Forest. Journal of Biomolecular Structure and Dynamics, 2009, 26, 679-686.	2.0	117
20	Predicting protein structural class by SVM with class-wise optimized features and decision probabilities. Journal of Theoretical Biology, 2008, 253, 375-380.	0.8	55
21	Identification of catalytic residues from protein structure using support vector machine with sequence and structural features. Biochemical and Biophysical Research Communications, 2008, 367, 630-634.	1.0	36
22	Prediction of Transcription Factor Families Using DNA Sequence Features. Lecture Notes in Computer Science, 2008, , 154-164.	1.0	1
23	SMotif: a server for structural motifs in proteins. Bioinformatics, 2007, 23, 637-638.	1.8	15
24	MegaMotifBase: a database of structural motifs in protein families and superfamilies. Nucleic Acids Research, 2007, 36, D218-D221.	6.5	25
25	A machine learning approach for the identification of odorant binding proteins from sequence-derived properties. BMC Bioinformatics, 2007, 8, 351.	1.2	23
26	An analysis of diversity measures. Machine Learning, 2006, 65, 247-271.	3.4	343
27	Gene selection algorithms for microarray data based on least squares support vector machine. BMC Bioinformatics, 2006, 7, 95.	1.2	77
28	Shape indexing using self-organizing maps. IEEE Transactions on Neural Networks, 2002, 13, 835-840.	4.8	23
29	Shapesom. , 2001, , 110-117.		0
30	Hierarchical overlapped SOM's for pattern classification. IEEE Transactions on Neural Networks, 1999, 10, 193-196.	4.8	40
31	Hopfield network with constraint parameter adaptation for overlapped shape recognition. IEEE Transactions on Neural Networks, 1999, 10, 444-449.	4.8	29