Pugalenthi Ganesan

List of Publications by Year
in descending order

39 papers	1,342 citations	331259 21 h-index	344852 36 g-index
39 all docs	39 docs citations	39 times ranked	1811 citing authors

#	Article	IF	Citations
1	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
2	An approach for classification of highly imbalanced data using weighting and undersampling. Amino Acids, 2010, 39, 1385-1391.	1.2	134
3	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
4	Prediction of Apoptosis Protein Locations with Genetic Algorithms and Support Vector Machines Through a New Mode of Pseudo Amino Acid Composition. Protein and Peptide Letters, 2010, 17, 1473-1479.	0.4	75
5	Identification of structurally conserved residues of proteins in absence of structural homologs using neural network ensemble. Bioinformatics, 2009, 25, 204-210.	1.8	70
6	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
7	RSARF: Prediction of Residue Solvent Accessibility from Protein Sequence Using Random Forest Method. Protein and Peptide Letters, 2012, 19, 50-56.	0.4	47
8	Isolation and Characterization of NDM-Positive Escherichia coli from Municipal Wastewater in Jeddah, Saudi Arabia. Antimicrobial Agents and Chemotherapy, 2016, 60, 5223-5231.	1.4	44
9	HARMONY: a server for the assessment of protein structures. Nucleic Acids Research, 2006, 34, W231-W234.	6.5	37
10	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
11	PASS2: an automated database of protein alignments organised as structural superfamilies. BMC Bioinformatics, 2004, 5, 35.	1.2	34
12	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
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	Identification and Analysis of Red Sea Mangrove (Avicennia marina) microRNAs by High-Throughput Sequencing and Their Association with Stress Responses. PLoS ONE, 2013, 8, e60774.	1.1	33
15	BLProt: prediction of bioluminescent proteins based on support vector machine and relieff feature selection. BMC Bioinformatics, 2011, 12, 345.	1.2	31
16	3DSwap: curated knowledgebase of proteins involved in 3D domain swapping. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar042-bar042.	1.4	28
17	3dswap-pred: Prediction of 3D Domain Swapping from Protein Sequence Using Random Forest Approach. Protein and Peptide Letters, 2011, 18, 1010-1020.	0.4	26
18	DIAL: a web-based server for the automatic identification of structural domains in proteins. Nucleic Acids Research, 2005, 33, W130-W132.	6.5	25

#	Article	IF	Citations
19	MegaMotifBase: a database of structural motifs in protein families and superfamilies. Nucleic Acids Research, 2007, 36, D218-D221.	6.5	25
20	Native and modeled disulfide bonds in proteins: Knowledge-based approaches toward structure prediction of disulfide-rich polypeptides. Proteins: Structure, Function and Bioinformatics, 2005, 58, 866-879.	1.5	23
21	A machine learning approach for the identification of odorant binding proteins from sequence-derived properties. BMC Bioinformatics, 2007, 8, 351.	1.2	23
22	Structural analysis and dimerization profile of the SCAN domain of the pluripotency factor Zfp206. Nucleic Acids Research, 2012, 40, 8721-8732.	6.5	21
23	EcmPred: Prediction of extracellular matrix proteins based on random forest with maximum relevance minimum redundancy feature selection. Journal of Theoretical Biology, 2013, 317, 377-383.	0.8	21
24	Gelsolin-Cu/ZnSOD interaction alters intracellular reactive oxygen species levels to promote cancer cell invasion. Oncotarget, 2016, 7, 52832-52848.	0.8	18
25	GenDiS: Genomic Distribution of protein structural domain Superfamilies. Nucleic Acids Research, 2004, 33, D252-D255.	6.5	16
26	Subtractive hybridization–mediated analysis of genes and <i>in silico</i> prediction of associated microRNAs under waterlogged conditions in sugarcane (<i>Saccharum</i> spp.). FEBS Open Bio, 2014, 4, 533-541.	1.0	16
27	SMotif: a server for structural motifs in proteins. Bioinformatics, 2007, 23, 637-638.	1.8	15
28	Nglyc: A Random Forest Method for Prediction of N-Glycosylation Sites in Eukaryotic Protein Sequence. Protein and Peptide Letters, 2020, 27, 178-186.	0.4	15
29	Insights into Protein Sequence and Structure-Derived Features Mediating 3D Domain Swapping Mechanism using Support Vector Machine Based Approach. Bioinformatics and Biology Insights, 2010, 4, BBI.S4464.	1.0	13
30	SCANMOT: searching for similar sequences using a simultaneous scan of multiple sequence motifs. Nucleic Acids Research, 2005, 33, W274-W276.	6.5	11
31	Identification of functionally diverse lipocalin proteins from sequence information using support vector machine. Amino Acids, 2010, 39, 777-783.	1.2	11
32	iMOT: an interactive package for the selection of spatially interacting motifs. Nucleic Acids Research, 2004, 32, W602-W605.	6.5	9
33	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
34	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
35	iMOTdb--a comprehensive collection of spatially interacting motifs in proteins. Nucleic Acids Research, 2006, 34, D285-D286.	6.5	3
36	SSToSS--sequence-structural templates of single-member superfamilies. In Silico Biology, 2006, 6, 311-9.	0.4	3

#	Article	IF	Citations
37	Identification and analysis of transcription factor family-specific features derived from DNA and protein information. Pattern Recognition Letters, 2010, 31, 2097-2102.	2.6	2
38	Prediction of Transcription Factor Families Using DNA Sequence Features. Lecture Notes in Computer Science, 2008, , 154-164.	1.0	1
39	Molecular cloning, sequencing and structural studies of granulocyteâ€"macrophage colonyâ€"stimulating factor (<scp>GM</scp>â€‹<scp>CSF</scp>) from <scp>I</scp>ndian water buffalo (<i><scp>B</scp>ubalus bubalis</i>). International Journal of Immunogenetics, 2014, 41, 74-80.	0.8	0