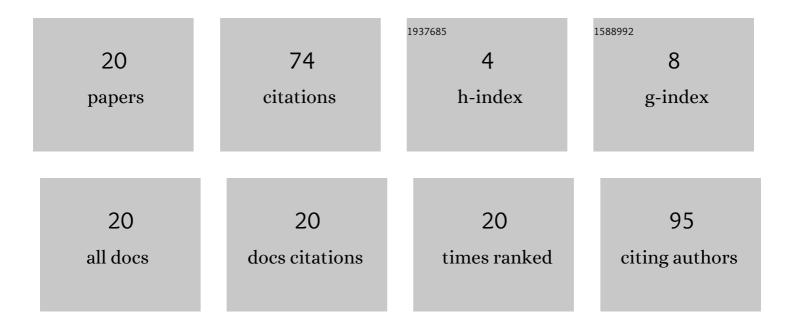
Usha Chouhan

List of Publications by Year in descending order

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Пену Снолнум

#	Article	IF	CITATIONS
1	Relevance of Machine Learning Techniques and Various Protein Features in Protein Fold Classification: A Review. Current Bioinformatics, 2019, 14, 688-697.	1.5	17
2	Identification of novel inhibitors against Cyclin Dependent Kinase 9/Cyclin T1 complex as: Anti cancer agent. Saudi Journal of Biological Sciences, 2017, 24, 1229-1242.	3.8	9
3	An Application of Similarity Measure of Fuzzy Soft Sets in Verndor Selection Problem. Materials Today: Proceedings, 2018, 5, 3987-3993.	1.8	6
4	Comparative study of machine learning approaches for classification and prediction of selective caspase-3 antagonist for Zika virus drugs. Neural Computing and Applications, 2020, 32, 11311-11328.	5.6	5
5	Comparative Study of Machine Learning Techniques for Genome Scale Discrimination of Recombinant HIV-1 Strains. Journal of Medical Imaging and Health Informatics, 2016, 6, 425-430.	0.3	4
6	COMPUTATIONAL APPROACHES FOR THE PREDICTION OF ANTIMICROBIAL POTENTIAL PEPTIDES FROM OCIMUM TENUIFLORUM Asian Journal of Pharmaceutical and Clinical Research, 2018, 11, 398.	0.3	4
7	Chemometric Modelling of PPAR-α and PPAR-γ Dual Agonists for the Treatment of Type-2 Diabetes. Current Science, 2016, 111, 356.	0.8	4
8	Genome-Scale Classification of Recombinant and Non-Recombinant HIV-1 Sequences Using Artificial Neural Network Ensembles. Current Science, 2016, 111, 853.	0.8	4
9	A Review of Various Machine Learning Techniques for Brain Tumor Detection from MRI Images. Current Medical Imaging, 2020, 16, 937-945.	0.8	4
10	Comparative study of artificial neural network for classification of hot and cold recombination regions in Saccharomyces cerevisiae. Neural Computing and Applications, 2018, 29, 529-535.	5.6	3
11	Multilayer Perceptron and Evolutionary Radial Basis Function Neural Network Models for Discrimination of HIV-1 Genomes. Current Science, 2018, 115, 2063.	0.8	3
12	On Support Vector Machine Ensembles for Classification of Recombination Breakpoint Regions in Saccharomyces Cerevisiae. International Journal of Computer Applications, 2014, 108, 44-48.	0.2	3
13	Comparative Analysis of Machine Learning Algorithms for Mycobacterium Tuberculosis Protein Sequences on the Basis of Physicochemical Parameters. Journal of Medical Imaging and Health Informatics, 2014, 4, 212-219.	0.3	2
14	Application of Similarity Measure of Fuzzy Soft Sets in Selection of Manufacturing Method. Materials Today: Proceedings, 2017, 4, 1561-1569.	1.8	2
15	Analysis of Protein-Protein Interaction Network of Laminopathy Based on Topological Properties. Biomedical and Pharmacology Journal, 2018, 11, 1091-1103.	0.5	2
16	In-silico Analysis of Phenyl Propanoic Acid Derivatives to Design Potent Peroxisome Proliferator-activated Receptor (PPAR) Dual Agonists for Type 2 Diabetes mellitus Therapy. Oriental Journal of Chemistry, 2018, 34, 1400-1410.	0.3	1
17	HIV Infection: A Review of their Inhibitors Progression. Biomedical and Pharmacology Journal, 2017, 10, 749-758.	0.5	1
18	Classification of Hot and Cold Recombination Regions in Saccharomyces cerevisiae: Comparative Analysis of Two Machine Learning Techniques. Proceedings of the National Academy of Sciences India Section A - Physical Sciences, 2019, 89, 249-256.	1.2	0

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#	Article	IF	CITATIONS
19	<i>Insilico</i> SSR Mining And Analysis of BAC/PAC Sequences Present Within The Putative Root Related Drought Tolerant QTL Marker Interval of Rice. Vegetos, 2013, 26, 111.	1.5	ο
	Computational analysis of nolymorphisms of which it and an arbour life "tarminal actors of 1 (1) (1) and		

20 Computational analysis of polymorphisms of ubiquitin carboxyl–terminal esterase L1 (UCHL1) gene involved in Parkinson's disease. Bioscience Biotechnology Research Communications, 2016, 9, 503-511.