Nouman Rasool

List of Publications by Year in descending order

65 papers	1,802 citations	218677 26 h-index	289244 40 g-index
65 all docs	65 docs citations	65 times ranked	764 citing authors

#	Article	IF	Citations
1	SPrenylC-PseAAC: A sequence-based model developed via Chou's 5-steps rule and general PseAAC for identifying S-prenylation sites in proteins. Journal of Theoretical Biology, 2019, 468, 1-11.	1.7	115
2	iPhosT-PseAAC: Identify phosphothreonine sites by incorporating sequence statistical moments into PseAAC. Analytical Biochemistry, 2018, 550, 109-116.	2.4	111
3	SPalmitoylC-PseAAC: A sequence-based model developed via Chou's 5-steps rule and general PseAAC for identifying S-palmitoylation sites in proteins. Analytical Biochemistry, 2019, 568, 14-23.	2.4	105
4	Prediction of N-linked glycosylation sites using position relative features and statistical moments. PLoS ONE, 2017, 12, e0181966.	2.5	72
5	iPhosH-PseAAC: Identify Phosphohistidine Sites in Proteins by Blending Statistical Moments and Position Relative Features According to the Chou's 5-Step Rule and General Pseudo Amino Acid Composition. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 596-610.	3.0	70
6	pSSbond-PseAAC: Prediction of disulfide bonding sites by integration of PseAAC and statistical moments. Journal of Theoretical Biology, 2019, 463, 47-55.	1.7	68
7	A Treatise to Computational Approaches Towards Prediction of Membrane Protein and Its Subtypes. Journal of Membrane Biology, 2017, 250, 55-76.	2.1	63
8	iPhosY-PseAAC: identify phosphotyrosine sites by incorporating sequence statistical moments into PseAAC. Molecular Biology Reports, 2018, 45, 2501-2509.	2.3	57
9	A Prediction Model for Membrane Proteins Using Moments Based Features. BioMed Research International, 2016, 2016, 1-7.	1.9	56
10	Computer-aided analysis of phytochemicals as potential dengue virus inhibitors based on molecular docking, ADMET and DFT studies. Journal of Vector Borne Diseases, 2017, 54, 255.	0.4	55
11	Prediction of antioxidant proteins by incorporating statistical moments based features into Chou's PseAAC. Journal of Theoretical Biology, 2019, 473, 1-8.	1.7	53
12	Predicting membrane proteins and their types by extracting various sequence features into Chouâ€™s general PseAAC. Molecular Biology Reports, 2018, 45, 2295-2306.	2.3	51
13	Optimization of serine phosphorylation prediction in proteins by comparing human engineered features and deep representations. Analytical Biochemistry, 2021, 615, 114069.	2.4	50
14	Sequence-based Identification of Arginine Amidation Sites in Proteins Using Deep Representations of Proteins and PseAAC. Current Bioinformatics, 2021, 15, 937-948.	1.5	46
15	pNitro-Tyr-PseAAC: Predict Nitrotyrosine Sites in Proteins by Incorporating Five Features into Chouâ€™s General PseAAC. Current Pharmaceutical Design, 2019, 24, 4034-4043.	1.9	45
16	Identification of Lysine Carboxylation Sites in Proteins by Integrating Statistical Moments and Position Relative Features via General PseAAC. Current Bioinformatics, 2020, 15, 396-407.	1.5	45
17	iPhosS(Deep)-PseAAC: Identify Phosphoserine Sites in Proteins using Deep Learning on General Pseudo Amino Acid Compositions via Modified 5-Steps Rule. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, PP, 1-1.	3.0	40
18	NPalmitoylDeep-PseAAC: A Predictor of N-Palmitoylation Sites in Proteins Using Deep Representations of Proteins and PseAAC via Modified 5-Steps Rule. Current Bioinformatics, 2021, 16, 294-305.	1.5	38

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19	A Sequence-Based Predictor of Zika Virus Proteins Developed by Integration of PseAAC and Statistical Moments. Combinatorial Chemistry and High Throughput Screening, 2020, 23, 797-804.	1.1	38
20	iProtease-PseAAC(2L): A two-layer predictor for identifying proteases and their types using Chou's 5-step-rule and general PseAAC. Analytical Biochemistry, 2020, 588, 113477.	2.4	36
21	Phytochemicals from Selective Plants Have Promising Potential against SARS-CoV-2: Investigation and Corroboration through Molecular Docking, MD Simulations, and Quantum Computations. BioMed Research International, 2020, 2020, 1-15.	1.9	36
22	Insights into Machine Learning-based Approaches for Virtual Screening in Drug Discovery: Existing Strategies and Streamlining Through FP-CADD. Current Drug Discovery Technologies, 2021, 18, 463-472.	1.2	36
23	iTSP-PseAAC: Identifying Tumor Suppressor Proteins by Using Fully Connected Neural Network and PseAAC. Current Bioinformatics, 2021, 16, 700-709.	1.5	35
24	Gene cloning and characterization of a xylanase from a newly isolated Bacillus subtilis strain R5. Journal of Bioscience and Bioengineering, 2009, 107, 360-365.	2.2	34
25	Prediction of Nitrosocysteine Sites Using Position and Composition Variant Features. Letters in Organic Chemistry, 2019, 16, 283-293.	0.5	34
26	Using CHOU'S 5-Steps Rule to Predict O-Linked Serine Glycosylation Sites by Blending Position Relative Features and Statistical Moment. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2045-2056.	3.0	30
27	Computational exploration of antiviral activity of phytochemicals against NS2B/NS3 proteases from dengue virus. Biyokimya Dergisi, 2019, 44, 261-277.	0.5	23
28	Insights into the inhibitory potential of selective phytochemicals against Mpro of 2019-nCoV: a computer-aided study. Structural Chemistry, 2020, 31, 1777-1783.	2.0	21
29	Probing the Pharmacological Binding Properties, and Reactivity of Selective Phytochemicals as Potential HIV-1 protease Inhibitors. Universitas Scientiarum, 2019, 24, 441-464.	0.4	20
30	Virtual Screening of Phytochemicals by Targeting HR1 Domain of SARS-CoV-2 S Protein: Molecular Docking, Molecular Dynamics Simulations, and DFT Studies. BioMed Research International, 2021, 2021, 1-19.	1.9	20
31	In Silico Computations of Selective Phytochemicals as Potential Inhibitors Against Major Biological Targets of Diabetes Mellitus. Current Computer-Aided Drug Design, 2019, 15, 401-408.	1.2	20
32	In silico targeting of non-structural 4B protein from dengue virus 4 with spiropyrazolopyridone: study of molecular dynamics simulation, ADMET and virtual screening. VirusDisease, 2018, 29, 147-156.	2.0	19
33	In Silico Inhibition of BACE-1 by Selective Phytochemicals as Novel Potential Inhibitors: Molecular Docking and DFT Studies. Current Drug Discovery Technologies, 2020, 17, 397-411.	1.2	19
34	Probing the Pharmacological Parameters, Molecular Docking and Quantum Computations of Plant Derived Compounds Exhibiting Strong Inhibitory Potential Against NS5 from Zika Virus. Brazilian Archives of Biology and Technology, 0, 61, .	0.5	17
35	Revelation of enzyme activity of mutant pyrazinamidases from Mycobacterium tuberculosis upon binding with various metals using quantum mechanical approach. Computational Biology and Chemistry, 2019, 83, 107108.	2.3	17
36	Biological perspective of thiazolide derivatives against Mpro and MTase of SARS-CoV-2: Molecular docking, DFT and MD simulation investigations. Chemical Physics Letters, 2021, 771, 138463.	2.6	16

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37	Evaluation of different methods for DNA extraction from human burnt bones and the generation of genetic profiles for identification. Medicine, Science and the Law, 2017, 57, 159-166.	1.0	15
38	Structural and quantum mechanical computations to elucidate the altered binding mechanism of metal and drug with pyrazinamidase from Mycobacterium tuberculosis due to mutagenicity. Journal of Molecular Graphics and Modelling, 2018, 80, 126-131.	2.4	15
39	N-terminal deletion of Tk1689, a subtilisin-like serine protease from Thermococcus kodakaraensis, copes with its cytotoxicity in Escherichia coli. Journal of Bioscience and Bioengineering, 2010, 110, 381-385.	2.2	14
40	Detection of dry bloodstains on different fabrics after washing with commercially available detergents. Australian Journal of Forensic Sciences, 2016, 48, 87-94.	1.2	14
41	Computer-aided study of selective flavonoids against chikungunya virus replication using molecular docking and DFT-based approach. Structural Chemistry, 2020, 31, 1363-1374.	2.0	14
42	Penta-1,4-Diene-3-One Oxime Derivatives Strongly Inhibit the Replicase Domain of Tobacco Mosaic Virus: Elucidation Through Molecular Docking and Density Functional Theory Mechanistic Computations. Journal of Antivirals & Antiretrovirals, 2018, 10, .	0.1	14
43	Three Major Phosphoacceptor Sites in HIV-1 Capsid Protein Enhances its Structural Stability and Resistance Against the Inhibitor: Explication Through Molecular Dynamics Simulation, Molecular Docking and DFT Analysis. Combinatorial Chemistry and High Throughput Screening, 2020, 23, 41-54.	1.1	13
44	Prevalence of thyroid stimulating hormone dysfunction among sofosbuvirâ€treated HCVâ€infected patients: A realâ€world clinical experience. Journal of Medical Virology, 2019, 91, 514-517.	5.0	11
45	Prediction of Protein Solubility using Primary Structure Compositional Features: A Machine Learning Perspective. Journal of Proteomics and Bioinformatics, 2017, 10, .	0.4	10
46	Analysis of Inhibitor Binding Combined with Reactivity Studies to Discover the Potentially Inhibiting Phytochemicals Targeting Chikungunya Viral Replication. Current Drug Discovery Technologies, 2021, 18, 437-450.	1.2	9
47	Identification of sex from footprint dimensions using machine learning: a study on population of Punjab in Pakistan. Egyptian Journal of Forensic Sciences, 2018, 8, .	1.0	7
48	Identification of novel inhibitory candidates against two major Flavivirus pathogens via CADD protocols: in silico analysis of phytochemical binding, reactivity, and pharmacokinetics against NS5 from ZIKV and DENV. Structural Chemistry, 2020, 31, 2189-2204.	2.0	7
49	Forensic science in Pakistan; present and future. Egyptian Journal of Forensic Sciences, 2018, 8, .	1.0	6
50	ForeStatistics: A windows-based feature-rich software program for performing statistics in forensic DNA analysis, paternity and relationship testing. Forensic Science International, 2020, 307, 110142.	2.2	6
51	AEPI: insights into the potential of deep representations for human identification through outer ear images. Multimedia Tools and Applications, 2022, 81, 10427-10443.	3.9	5
52	Recent trends in molecular epidemiology of Hepatitis C virus in Mardan, KPK Pakistan. Infection, Genetics and Evolution, 2018, 66, 66-71.	2.3	4
53	Erroneous calculations of weight of DNA evidence may lead to miscarriage of justice in Pakistan. Egyptian Journal of Forensic Sciences, 2019, 9, .	1.0	4
54	ADVIT: Using the potentials of deep representations incorporated with grid-based features of dorsum vein patterns for human identification. Forensic Science International, 2020, 313, 110345.	2.2	4

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55	Computational Studies of 3D-QSAR on a Highly Active Series of Naturally Occurring Nonnucleoside Inhibitors of HIV-1 RT (NNRTI). Journal of Computational Biophysics and Chemistry, 2021, 20, 3-11.	1.7	4
56	An in silico investigation of phytochemicals as potential inhibitors against non-structural protein 1 from dengue virus 4. Brazilian Journal of Pharmaceutical Sciences, 0, 56, .	1.2	4
57	Molecular Simulation Investigation of Prolyl Oligopeptidase from Pyrobaculum Calidifontis and In Silico Docking With Substrates and Inhibitors. Open Access Journal of Biomedical Engineering and Biosciences, 2018, 2, .	0.4	3
58	Tattooing trend: major cause of HCV transmission among youngsters. Infectious Diseases, 2018, 50, 871-873.	2.8	2
59	Inhibitory role of selective phytochemicals against HIV-2 protease: a study of molecular docking, ADMET and DFT computations. International Journal of Computational Biology and Drug Design, 2020, 13, 390.	0.3	2
60	DNA evidence in sexual assault cases in Pakistan. Medicine, Science and the Law, 2020, 60, 270-277.	1.0	1
61	iDRP-PseAAC: Identification of DNA Replication Proteins Using General PseAAC and Position Dependent Features. International Journal of Peptide Research and Therapeutics, 2021, 27, 1315-1329.	1.9	1
62	A pilot study for the use of coumarin-480 to enhance the fingermarks. Studia Universitatis Babes-Bolyai Chemia, 2019, 64, 185-196.	0.2	1
63	The Role of Lipsticks and Blush Sticks in Genetic Profiling for Human Identification. Arab Journal of Forensic Sciences and Forensic Medicine, 2016, , .	0.1	1
64	Analyzing Phytochemicals as Inhibitors of Diabetes Mellitus 2 Causing Proteins based on Computer-Aided Drug Discovery Protocols. Natural Products Journal, 2021, 11, 383-391.	0.3	0
65	Computational Studies of 3D-QSAR on a Highly Active Series of Naturally Occurring Non-Nucleoside Inhibitors of HIV-1 RT (NNRTI). Journal of Theoretical and Computational Chemistry, 0, , .	1.8	0