

Nouman Rasool

List of Publications by Year in descending order

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Version: 2024-02-01

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	AEPI: insights into the potential of deep representations for human identification through outer ear images. <i>Multimedia Tools and Applications</i> , 2022, 81, 10427-10443.	3.9	5
2	Using CHOU'S 5-Steps Rule to Predict O-Linked Serine Glycosylation Sites by Blending Position Relative Features and Statistical Moment. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 2045-2056.	3.0	30
3	Optimization of serine phosphorylation prediction in proteins by comparing human engineered features and deep representations. <i>Analytical Biochemistry</i> , 2021, 615, 114069.	2.4	50
4	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. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 596-610.	3.0	70
5	Sequence-based Identification of Arginine Amidation Sites in Proteins Using Deep Representations of Proteins and PseAAC. <i>Current Bioinformatics</i> , 2021, 15, 937-948.	1.5	46
6	iDRP-PseAAC: Identification of DNA Replication Proteins Using General PseAAC and Position Dependent Features. <i>International Journal of Peptide Research and Therapeutics</i> , 2021, 27, 1315-1329.	1.9	1
7	NPalmitoylDeep-PseAAC: A Predictor of N-Palmitoylation Sites in Proteins Using Deep Representations of Proteins and PseAAC via Modified 5-Steps Rule. <i>Current Bioinformatics</i> , 2021, 16, 294-305.	1.5	38
8	Biological perspective of thiazolide derivatives against Mpro and MTase of SARS-CoV-2: Molecular docking, DFT and MD simulation investigations. <i>Chemical Physics Letters</i> , 2021, 771, 138463.	2.6	16
9	Virtual Screening of Phytochemicals by Targeting HR1 Domain of SARS-CoV-2 S Protein: Molecular Docking, Molecular Dynamics Simulations, and DFT Studies. <i>BioMed Research International</i> , 2021, 2021, 1-19.	1.9	20
10	Analysis of Inhibitor Binding Combined with Reactivity Studies to Discover the Potentially Inhibiting Phytochemicals Targeting Chikungunya Viral Replication. <i>Current Drug Discovery Technologies</i> , 2021, 18, 437-450.	1.2	9
11	iTSP-PseAAC: Identifying Tumor Suppressor Proteins by Using Fully Connected Neural Network and PseAAC. <i>Current Bioinformatics</i> , 2021, 16, 700-709.	1.5	35
12	Analyzing Phytochemicals as Inhibitors of Diabetes Mellitus 2 Causing Proteins based on Computer-Aided Drug Discovery Protocols. <i>Natural Products Journal</i> , 2021, 11, 383-391.	0.3	0
13	Computational Studies of 3D-QSAR on a Highly Active Series of Naturally Occurring Nonnucleoside Inhibitors of HIV-1 RT (NNRTI). <i>Journal of Computational Biophysics and Chemistry</i> , 2021, 20, 3-11.	1.7	4
14	Insights into Machine Learning-based Approaches for Virtual Screening in Drug Discovery: Existing Strategies and Streamlining Through FP-CADD. <i>Current Drug Discovery Technologies</i> , 2021, 18, 463-472.	1.2	36
15	iProtease-PseAAC(2L): A two-layer predictor for identifying proteases and their types using Chou's 5-step-rule and general PseAAC. <i>Analytical Biochemistry</i> , 2020, 588, 113477.	2.4	36
16	ForeStatistics: A windows-based feature-rich software program for performing statistics in forensic DNA analysis, paternity and relationship testing. <i>Forensic Science International</i> , 2020, 307, 110142.	2.2	6
17	Phytochemicals from Selective Plants Have Promising Potential against SARS-CoV-2: Investigation and Corroboration through Molecular Docking, MD Simulations, and Quantum Computations. <i>BioMed Research International</i> , 2020, 2020, 1-15.	1.9	36
18	ADVIT: Using the potentials of deep representations incorporated with grid-based features of dorsum vein patterns for human identification. <i>Forensic Science International</i> , 2020, 313, 110345.	2.2	4

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19	DNA evidence in sexual assault cases in Pakistan. <i>Medicine, Science and the Law</i> , 2020, 60, 270-277.	1.0	1
20	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. <i>Structural Chemistry</i> , 2020, 31, 2189-2204.	2.0	7
21	Computer-aided study of selective flavonoids against chikungunya virus replication using molecular docking and DFT-based approach. <i>Structural Chemistry</i> , 2020, 31, 1363-1374.	2.0	14
22	Insights into the inhibitory potential of selective phytochemicals against Mpro of 2019-nCoV: a computer-aided study. <i>Structural Chemistry</i> , 2020, 31, 1777-1783.	2.0	21
23	iPhosS(Deep)-PseAAC: Identify Phosphoserine Sites in Proteins using Deep Learning on General Pseudo Amino Acid Compositions via Modified 5-Steps Rule. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, PP, 1-1.	3.0	40
24	Inhibitory role of selective phytochemicals against HIV-2 protease: a study of molecular docking, ADMET and DFT computations. <i>International Journal of Computational Biology and Drug Design</i> , 2020, 13, 390.	0.3	2
25	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. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2020, 23, 41-54.	1.1	13
26	A Sequence-Based Predictor of Zika Virus Proteins Developed by Integration of PseAAC and Statistical Moments. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2020, 23, 797-804.	1.1	38
27	In Silico Inhibition of BACE-1 by Selective Phytochemicals as Novel Potential Inhibitors: Molecular Docking and DFT Studies. <i>Current Drug Discovery Technologies</i> , 2020, 17, 397-411.	1.2	19
28	Identification of Lysine Carboxylation Sites in Proteins by Integrating Statistical Moments and Position Relative Features via General PseAAC. <i>Current Bioinformatics</i> , 2020, 15, 396-407.	1.5	45
29	Computational exploration of antiviral activity of phytochemicals against NS2B/NS3 proteases from dengue virus. <i>Biyokimya Dergisi</i> , 2019, 44, 261-277.	0.5	23
30	Erroneous calculations of weight of DNA evidence may lead to miscarriage of justice in Pakistan. <i>Egyptian Journal of Forensic Sciences</i> , 2019, 9, .	1.0	4
31	Revelation of enzyme activity of mutant pyrazinamidases from <i>Mycobacterium tuberculosis</i> upon binding with various metals using quantum mechanical approach. <i>Computational Biology and Chemistry</i> , 2019, 83, 107108.	2.3	17
32	Prediction of antioxidant proteins by incorporating statistical moments based features into Chou's PseAAC. <i>Journal of Theoretical Biology</i> , 2019, 473, 1-8.	1.7	53
33	SPrenylC-PseAAC: A sequence-based model developed via Chou's 5-steps rule and general PseAAC for identifying S-prenylation sites in proteins. <i>Journal of Theoretical Biology</i> , 2019, 468, 1-11.	1.7	115
34	Probing the Pharmacological Binding Properties, and Reactivity of Selective Phytochemicals as Potential HIV-1 protease Inhibitors. <i>Universitas Scientiarum</i> , 2019, 24, 441-464.	0.4	20
35	Prevalence of thyroid stimulating hormone dysfunction among sofosbuvir-treated HCV-infected patients: A real-world clinical experience. <i>Journal of Medical Virology</i> , 2019, 91, 514-517.	5.0	11
36	SPalmitoylC-PseAAC: A sequence-based model developed via Chou's 5-steps rule and general PseAAC for identifying S-palmitoylation sites in proteins. <i>Analytical Biochemistry</i> , 2019, 568, 14-23.	2.4	105

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37	pSSbond-PseAAC: Prediction of disulfide bonding sites by integration of PseAAC and statistical moments. <i>Journal of Theoretical Biology</i> , 2019, 463, 47-55.	1.7	68
38	pNitro-Tyr-PseAAC: Predict Nitrotyrosine Sites in Proteins by Incorporating Five Features into Chou's General PseAAC. <i>Current Pharmaceutical Design</i> , 2019, 24, 4034-4043.	1.9	45
39	Prediction of Nitrosocysteine Sites Using Position and Composition Variant Features. <i>Letters in Organic Chemistry</i> , 2019, 16, 283-293.	0.5	34
40	In Silico Computations of Selective Phytochemicals as Potential Inhibitors Against Major Biological Targets of Diabetes Mellitus. <i>Current Computer-Aided Drug Design</i> , 2019, 15, 401-408.	1.2	20
41	A pilot study for the use of coumarin-480 to enhance the fingermarks. <i>Studia Universitatis Babeş-Bolyai Chemia</i> , 2019, 64, 185-196.	0.2	1
42	In silico targeting of non-structural 4B protein from dengue virus 4 with spiropyrazolopyridone: study of molecular dynamics simulation, ADMET and virtual screening. <i>VirusDisease</i> , 2018, 29, 147-156.	2.0	19
43	Structural and quantum mechanical computations to elucidate the altered binding mechanism of metal and drug with pyrazinamidase from <i>Mycobacterium tuberculosis</i> due to mutagenicity. <i>Journal of Molecular Graphics and Modelling</i> , 2018, 80, 126-131.	2.4	15
44	iPhosT-PseAAC: Identify phosphothreonine sites by incorporating sequence statistical moments into PseAAC. <i>Analytical Biochemistry</i> , 2018, 550, 109-116.	2.4	111
45	Forensic science in Pakistan; present and future. <i>Egyptian Journal of Forensic Sciences</i> , 2018, 8, .	1.0	6
46	Identification of sex from footprint dimensions using machine learning: a study on population of Punjab in Pakistan. <i>Egyptian Journal of Forensic Sciences</i> , 2018, 8, .	1.0	7
47	Predicting membrane proteins and their types by extracting various sequence features into Chou's general PseAAC. <i>Molecular Biology Reports</i> , 2018, 45, 2295-2306.	2.3	51
48	iPhosY-PseAAC: identify phosphotyrosine sites by incorporating sequence statistical moments into PseAAC. <i>Molecular Biology Reports</i> , 2018, 45, 2501-2509.	2.3	57
49	Tattooing trend: major cause of HCV transmission among youngsters. <i>Infectious Diseases</i> , 2018, 50, 871-873.	2.8	2
50	Recent trends in molecular epidemiology of Hepatitis C virus in Mardan, KPK Pakistan. <i>Infection, Genetics and Evolution</i> , 2018, 66, 66-71.	2.3	4
51	Molecular Simulation Investigation of Prolyl Oligopeptidase from <i>Pyrobaculum Calidifontis</i> and In Silico Docking With Substrates and Inhibitors. <i>Open Access Journal of Biomedical Engineering and Biosciences</i> , 2018, 2, .	0.4	3
52	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. <i>Journal of Antivirals & Antiretrovirals</i> , 2018, 10, .	0.1	14
53	Evaluation of different methods for DNA extraction from human burnt bones and the generation of genetic profiles for identification. <i>Medicine, Science and the Law</i> , 2017, 57, 159-166.	1.0	15
54	A Treatise to Computational Approaches Towards Prediction of Membrane Protein and Its Subtypes. <i>Journal of Membrane Biology</i> , 2017, 250, 55-76.	2.1	63

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55	Prediction of N-linked glycosylation sites using position relative features and statistical moments. PLoS ONE, 2017, 12, e0181966.	2.5	72
56	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
57	Prediction of Protein Solubility using Primary Structure Compositional Features: A Machine Learning Perspective. Journal of Proteomics and Bioinformatics, 2017, 10, .	0.4	10
58	A Prediction Model for Membrane Proteins Using Moments Based Features. BioMed Research International, 2016, 2016, 1-7.	1.9	56
59	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
60	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
61	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
62	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
63	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
64	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
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