Waqar Hussain

List of Publications by Year
in descending order

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59 papers	1,454 citations	361413 20 h-index	345221 36 g-index
59 all docs	59 docs citations	59 times ranked	601 citing authors

#	Article	IF	Citations
1	sAMP-PFPDeep: Improving accuracy of short antimicrobial peptides prediction using three different sequence encodings and deep neural networks. Briefings in Bioinformatics, 2022, 23, .	6.5	17
2	ORI-Deep: improving the accuracy for predicting origin of replication sites by using a blend of features and long short-term memory network. Briefings in Bioinformatics, 2022, 23, .	6.5	9
3	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
4	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
5	Optimization of serine phosphorylation prediction in proteins by comparing human engineered features and deep representations. Analytical Biochemistry, 2021, 615, 114069.	2.4	50
6	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
7	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
8	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
9	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
10	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
11	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
12	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
13	iTSP-PseAAC: Identifying Tumor Suppressor Proteins by Using Fully Connected Neural Network and PseAAC. Current Bioinformatics, 2021, 16, 700-709.	1.5	35
14	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
15	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
16	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
17	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
18	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

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19	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
20	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
21	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
22	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
23	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
24	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
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. Combinatorial Chemistry and High Throughput Screening, 2020, 23, 41-54.	1.1	13
26	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
27	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
28	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
29	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	0
30	Computational exploration of antiviral activity of phytochemicals against NS2B/NS3 proteases from dengue virus. Biyokimya Dergisi, 2019, 44, 261-277.	0.5	23
31	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
32	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
33	Person Fall Recognition by using Deep Learning: Convolutional Neural Networks and Image category classification using bag of feature. , 2019, , .		0
34	A Survey about Efficient Job Scheduling Strategies in Cloud and Large Scale Environments. , 2019, , .		2
35	An exposition on the applications of Locality Aware Scheduling algorithms. , 2019, , .		2
36	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

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37	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
38	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
39	iMethylK-PseAAC: Improving Accuracy of Lysine Methylation Sites Identification by Incorporating Statistical Moments and Position Relative Features into General PseAAC via Chouâ€™s 5-steps Rule. Current Genomics, 2019, 20, 275-292.	1.6	42
40	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
41	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
42	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
43	iPhosT-PseAAC: Identify phosphothreonine sites by incorporating sequence statistical moments into PseAAC. Analytical Biochemistry, 2018, 550, 109-116.	2.4	111
44	iPhosY-PseAAC: identify phosphotyrosine sites by incorporating sequence statistical moments into PseAAC. Molecular Biology Reports, 2018, 45, 2501-2509.	2.3	57
45	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
46	Evaluation of a Heterogeneous Multicore Architecture by Design and Test of an OFDM Receiver. IEEE Transactions on Parallel and Distributed Systems, 2017, 28, 3171-3187.	5.6	15
47	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
48	Prediction of Protein Solubility using Primary Structure Compositional Features: A Machine Learning Perspective. Journal of Proteomics and Bioinformatics, 2017, 10, .	0.4	10
49	Energy and power estimation of Coarse-Grain Reconfigurable Array based Fast Fourier Transform accelerators. , 2012, , .		5
50	Designing Fast Fourier Transform Accelerators for Orthogonal Frequency-Division Multiplexing Systems. Journal of Signal Processing Systems, 2012, 69, 161-171.	2.1	20
51	Application-driven dimensioning of a Coarse-Grain Reconfigurable Array. , 2011, , .		6
52	Exploiting control management to accelerate Radix-4 FFT on a reconfigurable platform. , 2010, , .		9
53	Control Techniques for Coupling a Coarse-Grain Reconfigurable Array with a Generic RISC Core. , 2010, , .		2
54	Evaluation of Radix-2 and Radix-4 FFT processing on a reconfigurable platform. , 2010, , .		14

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55	A reconfigurable SoC tailored to Software Defined Radio applications. , 2009, , .		14
56	CREMA: A coarse-grain reconfigurable array with mapping adaptiveness. , 2009, , .		26
57	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
58	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
59	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