Watshara Shoombuatong

List of Publications by Year
in descending order

75 papers	2,557 citations	172457 29 h-index	223800 46 g-index
79 all docs	79 docs citations	79 times ranked	1466 citing authors

#	Article	IF	Citations
1	Recent Development of Bioinformatics Tools for microRNA Target Prediction. Current Medicinal Chemistry, 2022, 29, 865-880.	2.4	9
2	Review and Comparative Analysis of Machine Learning-based Predictors for Predicting and Analyzing Anti-angiogenic Peptides. Current Medicinal Chemistry, 2022, 29, 849-864.	2.4	5
3	SCMTHP: A New Approach for Identifying and Characterizing of Tumor-Homing Peptides Using Estimated Propensity Scores of Amino Acids. Pharmaceutics, 2022, 14, 122.	4.5	10
4	SCORPION is a stacking-based ensemble learning framework for accurate prediction of phage virion proteins. Scientific Reports, 2022, 12, 4106.	3.3	21
5	DeepDNAbP: A deep learning-based hybrid approach to improve the identification of deoxyribonucleic acid-binding proteins. Computers in Biology and Medicine, 2022, 145, 105433.	7.0	5
6	StackDPPIV: A novel computational approach for accurate prediction of dipeptidyl peptidase IV (DPP-IV) inhibitory peptides. Methods, 2022, 204, 189-198.	3.8	34
7	Large-scale comparative review and assessment of computational methods for phage virion proteins identification.. EXCLI Journal, 2022, 21, 11-29.	0.7	2
8	AMYPred-FRL is a novel approach for accurate prediction of amyloid proteins by using feature representation learning. Scientific Reports, 2022, 12, 7697.	3.3	27
9	NEPTUNE: A novel computational approach for accurate and large-scale identification of tumor homing peptides. Computers in Biology and Medicine, 2022, 148, 105700.	7.0	9
10	SAPPHIRE: A stacking-based ensemble learning framework for accurate prediction of thermophilic proteins. Computers in Biology and Medicine, 2022, 146, 105704.	7.0	22
11	iAMY-SCM: Improved prediction and analysis of amyloid proteins using a scoring card method with propensity scores of dipeptides. Genomics, 2021, 113, 689-698.	2.9	31
12	Critical evaluation of web-based DNA N6-methyladenine site prediction tools. Briefings in Functional Genomics, 2021, 20, 258-272.	2.7	29
13	IRC-Fuse: improved and robust prediction of redox-sensitive cysteine by fusing of multiple feature representations. Journal of Computer-Aided Molecular Design, 2021, 35, 315-323.	2.9	5
14	PUP-Fuse: Prediction of Protein Pupylation Sites by Integrating Multiple Sequence Representations. International Journal of Molecular Sciences, 2021, 22, 2120.	4.1	8
15	Improved prediction and characterization of anticancer activities of peptides using a novel flexible scoring card method. Scientific Reports, 2021, 11, 3017.	3.3	48
16	BERT4Bitter: a bidirectional encoder representations from transformers (BERT)-based model for improving the prediction of bitter peptides. Bioinformatics, 2021, 37, 2556-2562.	4.1	84
17	PredNTS: Improved and Robust Prediction of Nitrotyrosine Sites by Integrating Multiple Sequence Features. International Journal of Molecular Sciences, 2021, 22, 2704.	4.1	16
18	NeuroPred-FRL: an interpretable prediction model for identifying neuropeptide using feature representation learning. Briefings in Bioinformatics, 2021, 22, .	6.5	56

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19	StackIL6: a stacking ensemble model for improving the prediction of IL-6 inducing peptides. Briefings in Bioinformatics, 2021, 22, .	6.5	84
20	In Silico Approaches for the Prediction and Analysis of Antiviral Peptides: A Review. Current Pharmaceutical Design, 2021, 27, 2180-2188.	1.9	18
21	iBitter-Fuse: A Novel Sequence-Based Bitter Peptide Predictor by Fusing Multi-View Features. International Journal of Molecular Sciences, 2021, 22, 8958.	4.1	27
22	iPMI: Machine Learning-Aided Identification of Parametrial Invasion in Women with Early-Stage Cervical Cancer. Diagnostics, 2021, 11, 1454.	2.6	7
23	Effects of Bacille Calmette Guerin (BCG) vaccination during COVID-19 infection. Computers in Biology and Medicine, 2021, 138, 104891.	7.0	3
24	StackHCV: a web-based integrative machine-learning framework for large-scale identification of hepatitis C virus NS5B inhibitors. Journal of Computer-Aided Molecular Design, 2021, 35, 1037-1053.	2.9	13
25	A novel sequence-based predictor for identifying and characterizing thermophilic proteins using estimated propensity scores of dipeptides. Scientific Reports, 2021, 11, 23782.	3.3	24
26	UMPred-FRL: A New Approach for Accurate Prediction of Umami Peptides Using Feature Representation Learning. International Journal of Molecular Sciences, 2021, 22, 13124.	4.1	35
27	iQSP: A Sequence-Based Tool for the Prediction and Analysis of Quorum Sensing Peptides Using Informative Physicochemical Properties. International Journal of Molecular Sciences, 2020, 21, 75.	4.1	61
28	iUmami-SCM: A Novel Sequence-Based Predictor for Prediction and Analysis of Umami Peptides Using a Scoring Card Method with Propensity Scores of Dipeptides. Journal of Chemical Information and Modeling, 2020, 60, 6666-6678.	5.4	76
29	ProIn-Fuse: improved and robust prediction of proinflammatory peptides by fusing of multiple feature representations. Journal of Computer-Aided Molecular Design, 2020, 34, 1229-1236.	2.9	33
30	iDPPIV-SCM: A Sequence-Based Predictor for Identifying and Analyzing Dipeptidyl Peptidase IV (DPP-IV) Inhibitory Peptides Using a Scoring Card Method. Journal of Proteome Research, 2020, 19, 4125-4136.	3.7	66
31	iTTCA-Hybrid: Improved and robust identification of tumor T cell antigens by utilizing hybrid feature representation. Analytical Biochemistry, 2020, 599, 113747.	2.4	40
32	Meta-iPVP: a sequence-based meta-predictor for improving the prediction of phage virion proteins using effective feature representation. Journal of Computer-Aided Molecular Design, 2020, 34, 1105-1116.	2.9	51
33	i6mA-Fuse: improved and robust prediction of DNA 6ÂmA sites in the Rosaceae genome by fusing multiple feature representation. Plant Molecular Biology, 2020, 103, 225-234.	3.9	59
34	HLPpred-Fuse: improved and robust prediction of hemolytic peptide and its activity by fusing multiple feature representation. Bioinformatics, 2020, 36, 3350-3356.	4.1	144
35	PVPred-SCM: Improved Prediction and Analysis of Phage Virion Proteins Using a Scoring Card Method. Cells, 2020, 9, 353.	4.1	47
36	i4mC-Mouse: Improved identification of DNA N4-methylcytosine sites in the mouse genome using multiple encoding schemes. Computational and Structural Biotechnology Journal, 2020, 18, 906-912.	4.1	57

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37	iBitter-SCM: Identification and characterization of bitter peptides using a scoring card method with propensity scores of dipeptides. Genomics, 2020, 112, 2813-2822.	2.9	77
38	<scp>HCVpred</scp>: A web server for predicting the bioactivity of hepatitis C virus <scp>NS5B</scp> inhibitors. Journal of Computational Chemistry, 2020, 41, 1820-1834.	3.3	16
39	Evolution of Sequence-based Bioinformatics Tools for Protein-protein Interaction Prediction. Current Genomics, 2020, 21, 454-463.	1.6	25
40	ACPred: A Computational Tool for the Prediction and Analysis of Anticancer Peptides. Molecules, 2019, 24, 1973.	3.8	125
41	TargetAntiAngio: A Sequence-Based Tool for the Prediction and Analysis of Anti-Angiogenic Peptides. International Journal of Molecular Sciences, 2019, 20, 2950.	4.1	37
42	HIVCoR: A sequence-based tool for predicting HIV-1 CRF01_AE coreceptor usage. Computational Biology and Chemistry, 2019, 80, 419-432.	2.3	17
43	THPep: A machine learning-based approach for predicting tumor homing peptides. Computational Biology and Chemistry, 2019, 80, 441-451.	2.3	56
44	Meta-iAVP: A Sequence-Based Meta-Predictor for Improving the Prediction of Antiviral Peptides Using Effective Feature Representation. International Journal of Molecular Sciences, 2019, 20, 5743.	4.1	84
45	Privileged substructures for anti-sickling activity via cheminformatic analysis. RSC Advances, 2018, 8, 5920-5935.	3.6	9
46	Probing the origin of estrogen receptor alpha inhibitionvialarge-scale QSAR study. RSC Advances, 2018, 8, 11344-11356.	3.6	25
47	PAAP: a web server for predicting antihypertensive activity of peptides. Future Medicinal Chemistry, 2018, 10, 1749-1767.	2.3	50
48	Towards understanding aromatase inhibitory activity via QSAR modeling. EXCLI Journal, 2018, 17, 688-708.	0.7	24
49	Unraveling the bioactivity of anticancer peptides as deduced from machine learning. EXCLI Journal, 2018, 17, 734-752.	0.7	71
50	HemoPred: a web server for predicting the hemolytic activity of peptides. Future Medicinal Chemistry, 2017, 9, 275-291.	2.3	84
51	Towards the Revival of Interpretable QSAR Models. Challenges and Advances in Computational Chemistry and Physics, 2017, , 3-55.	0.6	17
52	PepBio: predicting the bioactivity of host defense peptides. RSC Advances, 2017, 7, 35119-35134.	3.6	8
53	AnkPlex: algorithmic structure for refinement of near-native ankyrin-protein docking. BMC Bioinformatics, 2017, 18, 220.	2.6	0
54	New Bioinformatics-Based Discrimination Formulas for Differentiation of Thalassemia Traits From Iron Deficiency Anemia. Laboratory Medicine, 2017, 48, 230-237.	1.2	17

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55	The MicroRNA Interaction Network of Lipid Diseases. Frontiers in Genetics, 2017, 8, 116.	2.3	15
56	CryoProtect: A Web Server for Classifying Antifreeze Proteins from Nonantifreeze Proteins. Journal of Chemistry, 2017, 2017, 1-15.	1.9	37
57	Towards Predicting the Cytochrome P450 Modulation: From QSAR to Proteochemometric Modeling. Current Drug Metabolism, 2017, 18, 540-555.	1.2	28
58	osFP: a web server for predicting the oligomeric states of fluorescent proteins. Journal of Cheminformatics, 2016, 8, 72.	6.1	27
59	Extending proteochemometric modeling for unraveling the sorption behavior of compoundâ€“soil interaction. Chemometrics and Intelligent Laboratory Systems, 2016, 151, 219-227.	3.5	4
60	Exploring the chemical space of influenza neuraminidase inhibitors. PeerJ, 2016, 4, e1958.	2.0	27
61	Probing the origins of human acetylcholinesterase inhibition via QSAR modeling and molecular docking. PeerJ, 2016, 4, e2322.	2.0	48
62	Sequence based human leukocyte antigen gene prediction using informative physicochemical properties. International Journal of Data Mining and Bioinformatics, 2015, 13, 211.	0.1	11
63	Navigating the chemical space of dipeptidyl peptidase-4 inhibitors. Drug Design, Development and Therapy, 2015, 9, 4515.	4.3	20
64	Predicting Metabolic Syndrome Using the Random Forest Method. Scientific World Journal, The, 2015, 2015, 1-10.	2.1	47
65	Computer-Aided Drug Design of Bioactive Natural Products. Current Topics in Medicinal Chemistry, 2015, 15, 1780-1800.	2.1	71
66	Exploring the origins of structureâ€“oxygen affinity relationship of human haemoglobin allosteric effector. Molecular Simulation, 2015, 41, 1283-1291.	2.0	4
67	AutoWeka: Toward an Automated Data Mining Software for QSAR and QSPR Studies. Methods in Molecular Biology, 2015, 1260, 119-147.	0.9	22
68	Prediction of aromatase inhibitory activity using the efficient linear method (ELM). EXCLI Journal, 2015, 14, 452-64.	0.7	18
69	Classification of P-glycoprotein-interacting compounds using machine learning methods. EXCLI Journal, 2015, 14, 958-70.	0.7	12
70	On the Origins of Hepatitis C Virus NS5B Polymerase Inhibitory Activity Using Machine Learning Approaches. Current Topics in Medicinal Chemistry, 2015, 15, 1814-1826.	2.1	11
71	Predicting protein crystallization using a simple scoring card method. , 2013, , .		3
72	SCMCRYS: Predicting Protein Crystallization Using an Ensemble Scoring Card Method with Estimating Propensity Scores of P-Collocated Amino Acid Pairs. PLoS ONE, 2013, 8, e72368.	2.5	74

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73	Prediction of human leukocyte antigen gene using k-nearest neighbour classifier based on spectrum kernel. ScienceAsia, 2013, 39, 42.	0.5	12
74	HIV-1 CRF01_AE coreceptor usage prediction using kernel methods based logistic model trees. Computers in Biology and Medicine, 2012, 42, 885-889.	7.0	34
75	Prediction of the disulphide bonding state of cysteines in proteins using Conditional Random Fields. International Journal of Data Mining and Bioinformatics, 2011, 5, 449.	0.1	7