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	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
2	ACPred: A Computational Tool for the Prediction and Analysis of Anticancer Peptides. Molecules, 2019, 24, 1973.	3.8	125
3	HemoPred: a web server for predicting the hemolytic activity of peptides. Future Medicinal Chemistry, 2017, 9, 275-291.	2.3	84
4	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
5	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
6	StackIL6: a stacking ensemble model for improving the prediction of IL-6 inducing peptides. Briefings in Bioinformatics, 2021, 22, .	6.5	84
7	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
8	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
9	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
10	Computer-Aided Drug Design of Bioactive Natural Products. Current Topics in Medicinal Chemistry, 2015, 15, 1780-1800.	2.1	71
11	Unraveling the bioactivity of anticancer peptides as deduced from machine learning. EXCLI Journal, 2018, 17, 734-752.	0.7	71
12	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
13	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
14	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
15	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
16	THPep: A machine learning-based approach for predicting tumor homing peptides. Computational Biology and Chemistry, 2019, 80, 441-451.	2.3	56
17	NeuroPred-FRL: an interpretable prediction model for identifying neuropeptide using feature representation learning. Briefings in Bioinformatics, 2021, 22, .	6.5	56
18	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

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19	PAAP: a web server for predicting antihypertensive activity of peptides. Future Medicinal Chemistry, 2018, 10, 1749-1767.	2.3	50
20	Improved prediction and characterization of anticancer activities of peptides using a novel flexible scoring card method. Scientific Reports, 2021, 11, 3017.	3.3	48
21	Probing the origins of human acetylcholinesterase inhibition via QSAR modeling and molecular docking. PeerJ, 2016, 4, e2322.	2.0	48
22	Predicting Metabolic Syndrome Using the Random Forest Method. Scientific World Journal, The, 2015, 2015, 1-10.	2.1	47
23	PVPred-SCM: Improved Prediction and Analysis of Phage Virion Proteins Using a Scoring Card Method. Cells, 2020, 9, 353.	4.1	47
24	iTTCA-Hybrid: Improved and robust identification of tumor T cell antigens by utilizing hybrid feature representation. Analytical Biochemistry, 2020, 599, 113747.	2.4	40
25	CryoProtect: A Web Server for Classifying Antifreeze Proteins from Nonantifreeze Proteins. Journal of Chemistry, 2017, 2017, 1-15.	1.9	37
26	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
27	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
28	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
29	StackDPPIV: A novel computational approach for accurate prediction of dipeptidyl peptidase IV (DPP-IV) inhibitory peptides. Methods, 2022, 204, 189-198.	3.8	34
30	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
31	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
32	Critical evaluation of web-based DNA N6-methyladenine site prediction tools. Briefings in Functional Genomics, 2021, 20, 258-272.	2.7	29
33	Towards Predicting the Cytochrome P450 Modulation: From QSAR to Proteochemometric Modeling. Current Drug Metabolism, 2017, 18, 540-555.	1.2	28
34	osFP: a web server for predicting the oligomeric states of fluorescent proteins. Journal of Cheminformatics, 2016, 8, 72.	6.1	27
35	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
36	Exploring the chemical space of influenza neuraminidase inhibitors. PeerJ, 2016, 4, e1958.	2.0	27

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37	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
38	Probing the origin of estrogen receptor alpha inhibitionvialarge-scale QSAR study. RSC Advances, 2018, 8, 11344-11356.	3.6	25
39	Evolution of Sequence-based Bioinformatics Tools for Protein-protein Interaction Prediction. Current Genomics, 2020, 21, 454-463.	1.6	25
40	Towards understanding aromatase inhibitory activity via QSAR modeling. EXCLI Journal, 2018, 17, 688-708.	0.7	24
41	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
42	AutoWeka: Toward an Automated Data Mining Software for QSAR and QSPR Studies. Methods in Molecular Biology, 2015, 1260, 119-147.	0.9	22
43	SAPPHIRE: A stacking-based ensemble learning framework for accurate prediction of thermophilic proteins. Computers in Biology and Medicine, 2022, 146, 105704.	7.0	22
44	SCORPION is a stacking-based ensemble learning framework for accurate prediction of phage virion proteins. Scientific Reports, 2022, 12, 4106.	3.3	21
45	Navigating the chemical space of dipeptidyl peptidase-4 inhibitors. Drug Design, Development and Therapy, 2015, 9, 4515.	4.3	20
46	In Silico Approaches for the Prediction and Analysis of Antiviral Peptides: A Review. Current Pharmaceutical Design, 2021, 27, 2180-2188.	1.9	18
47	Prediction of aromatase inhibitory activity using the efficient linear method (ELM). EXCLI Journal, 2015, 14, 452-64.	0.7	18
48	Towards the Revival of Interpretable QSAR Models. Challenges and Advances in Computational Chemistry and Physics, 2017, , 3-55.	0.6	17
49	New Bioinformatics-Based Discrimination Formulas for Differentiation of Thalassemia Traits From Iron Deficiency Anemia. Laboratory Medicine, 2017, 48, 230-237.	1.2	17
50	HIVCoR: A sequence-based tool for predicting HIV-1 CRF01_AE coreceptor usage. Computational Biology and Chemistry, 2019, 80, 419-432.	2.3	17
51	PredNTS: Improved and Robust Prediction of Nitrotyrosine Sites by Integrating Multiple Sequence Features. International Journal of Molecular Sciences, 2021, 22, 2704.	4.1	16
52	<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
53	The MicroRNA Interaction Network of Lipid Diseases. Frontiers in Genetics, 2017, 8, 116.	2.3	15
54	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

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55	Classification of P-glycoprotein-interacting compounds using machine learning methods. EXCLI Journal, 2015, 14, 958-70.	0.7	12
56	Prediction of human leukocyte antigen gene using k-nearest neighbour classifier based on spectrum kernel. ScienceAsia, 2013, 39, 42.	0.5	12
57	Sequence based human leukocyte antigen gene prediction using informative physicochemical properties. International Journal of Data Mining and Bioinformatics, 2015, 13, 211.	0.1	11
58	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
59	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
60	Privileged substructures for anti-sickling activity via cheminformatic analysis. RSC Advances, 2018, 8, 5920-5935.	3.6	9
61	Recent Development of Bioinformatics Tools for microRNA Target Prediction. Current Medicinal Chemistry, 2022, 29, 865-880.	2.4	9
62	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
63	PepBio: predicting the bioactivity of host defense peptides. RSC Advances, 2017, 7, 35119-35134.	3.6	8
64	PUP-Fuse: Prediction of Protein Pupylation Sites by Integrating Multiple Sequence Representations. International Journal of Molecular Sciences, 2021, 22, 2120.	4.1	8
65	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
66	iPMI: Machine Learning-Aided Identification of Parametrial Invasion in Women with Early-Stage Cervical Cancer. Diagnostics, 2021, 11, 1454.	2.6	7
67	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
68	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
69	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
70	Exploring the origins of structureâ€“oxygen affinity relationship of human haemoglobin allosteric effector. Molecular Simulation, 2015, 41, 1283-1291.	2.0	4
71	Extending proteochemometric modeling for unraveling the sorption behavior of compoundâ€“soil interaction. Chemometrics and Intelligent Laboratory Systems, 2016, 151, 219-227.	3.5	4
72	Predicting protein crystallization using a simple scoring card method. , 2013, , .		3

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73	Effects of Bacille Calmette Guerin (BCG) vaccination during COVID-19 infection. Computers in Biology and Medicine, 2021, 138, 104891.	7.0	3
74	Large-scale comparative review and assessment of computational methods for phage virion proteins identification.. EXCLI Journal, 2022, 21, 11-29.	0.7	2
75	AnkPlex: algorithmic structure for refinement of near-native ankyrin-protein docking. BMC Bioinformatics, 2017, 18, 220.	2.6	0