Chanin Nantasenamat

List of Publications by Year
in descending order

155	4,894	66315	133188
papers	citations	42 h-index	59 g-index

167	167	167	4835
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Synthesis, biological evaluation and molecular docking of novel chalconeâ€“coumarin hybrids as anticancer and antimalarial agents. European Journal of Medicinal Chemistry, 2014, 85, 65-76.	2.6	175
2	Advances in computational methods to predict the biological activity of compounds. Expert Opinion on Drug Discovery, 2010, 5, 633-654.	2.5	163
3	Copper complexes of pyridine derivatives with superoxide scavenging and antimicrobial activities. European Journal of Medicinal Chemistry, 2009, 44, 3259-3265.	2.6	155
4	ACPred: A Computational Tool for the Prediction and Analysis of Anticancer Peptides. Molecules, 2019, 24, 1973.	1.7	125
5	Towards reproducible computational drug discovery. Journal of Cheminformatics, 2020, 12, 9.	2.8	100
6	Synthesis, anticancer activity and QSAR study of 1,4-naphthoquinone derivatives. European Journal of Medicinal Chemistry, 2014, 84, 247-263.	2.6	84
7	HemoPred: a web server for predicting the hemolytic activity of peptides. Future Medicinal Chemistry, 2017, 9, 275-291.	1.1	84
8	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.	1.8	84
9	BERT4Bitter: a bidirectional encoder representations from transformers (BERT)-based model for improving the prediction of bitter peptides. Bioinformatics, 2021, 37, 2556-2562.	1.8	84
10	StackIL6: a stacking ensemble model for improving the prediction of IL-6 inducing peptides. Briefings in Bioinformatics, 2021, 22, .	3.2	84
11	Quantitative structure-imprinting factor relationship of molecularly imprinted polymers. Biosensors and Bioelectronics, 2007, 22, 3309-3317.	5.3	81
12	Novel 1,4-naphthoquinone-based sulfonamides: Synthesis, QSAR, anticancer and antimalarial studies. European Journal of Medicinal Chemistry, 2015, 103, 446-459.	2.6	80
13	Copper Complexes of Nicotinic-Aromatic Carboxylic Acids as Superoxide Dismutase Mimetics. Molecules, 2008, 13, 3040-3056.	1.7	79
14	iBitter-SCM: Identification and characterization of bitter peptides using a scoring card method with propensity scores of dipeptides. Genomics, 2020, 112, 2813-2822.	1.3	77
15	Molecular Docking of Aromatase Inhibitors. Molecules, 2011, 16, 3597-3617.	1.7	76
16	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.	2.5	76
17	Quantitative prediction of imprinting factor of molecularly imprinted polymers by artificial neural network. Journal of Computer-Aided Molecular Design, 2005, 19, 509-524.	1.3	75
18	Computer-Aided Drug Design of Bioactive Natural Products. Current Topics in Medicinal Chemistry, 2015, 15, 1780-1800.	1.0	71

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19	Unraveling the bioactivity of anticancer peptides as deduced from machine learning. EXCLI Journal, 2018, 17, 734-752.	0.5	71
20	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.	1.8	66
21	Exploring the epigenetic drug discovery landscape. Expert Opinion on Drug Discovery, 2017, 12, 345-362.	2.5	62
22	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.	1.8	61
23	Synthesis and molecular docking of 1,2,3-triazole-based sulfonamides as aromatase inhibitors. Bioorganic and Medicinal Chemistry, 2015, 23, 3472-3480.	1.4	60
24	Prediction of GFP spectral properties using artificial neural network. Journal of Computational Chemistry, 2007, 28, 1275-1289.	1.5	59
25	EDTA-induced Membrane Fluidization and Destabilization: Biophysical Studies on Artificial Lipid Membranes. Acta Biochimica Et Biophysica Sinica, 2007, 39, 901-913.	0.9	59
26	Prediction of bond dissociation enthalpy of antioxidant phenols by support vector machine. Journal of Molecular Graphics and Modelling, 2008, 27, 188-196.	1.3	56
27	THPep: A machine learning-based approach for predicting tumor homing peptides. Computational Biology and Chemistry, 2019, 80, 441-451.	1.1	56
28	Roles of d-Amino Acids on the Bioactivity of Host Defense Peptides. International Journal of Molecular Sciences, 2016, 17, 1023.	1.8	55
29	Maximizing computational tools for successful drug discovery. Expert Opinion on Drug Discovery, 2015, 10, 321-329.	2.5	52
30	Large-scale QSAR study of aromatase inhibitors using SMILES-based descriptors. Chemometrics and Intelligent Laboratory Systems, 2014, 138, 120-126.	1.8	51
31	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.	1.3	51
32	Design, synthesis and molecular docking studies of novel N-benzenesulfonyl-1,2,3,4-tetrahydroisoquinoline-based triazoles with potential anticancer activity. European Journal of Medicinal Chemistry, 2014, 81, 192-203.	2.6	50
33	PAAP: a web server for predicting antihypertensive activity of peptides. Future Medicinal Chemistry, 2018, 10, 1749-1767.	1.1	50
34	Tackling the Antibiotic Resistance Caused by Class A Î²-Lactamases through the Use of Î²-Lactamase Inhibitory Protein. International Journal of Molecular Sciences, 2018, 19, 2222.	1.8	50
35	Discovery of novel 1,2,3-triazole derivatives as anticancer agents using QSAR and in silico structural modification. SpringerPlus, 2015, 4, 571.	1.2	49
36	Identification of metabolic syndrome using decision tree analysis. Diabetes Research and Clinical Practice, 2010, 90, e15-e18.	1.1	48

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37	Improved prediction and characterization of anticancer activities of peptides using a novel flexible scoring card method. Scientific Reports, 2021, 11, 3017.	1.6	48
38	Probing the origins of human acetylcholinesterase inhibition via QSAR modeling and molecular docking. PeerJ, 2016, 4, e2322.	0.9	48
39	Predicting the free radical scavenging activity of curcumin derivatives. Chemometrics and Intelligent Laboratory Systems, 2011, 109, 207-216.	1.8	47
40	Predicting Metabolic Syndrome Using the Random Forest Method. Scientific World Journal, The, 2015, 2015, 1-10.	0.8	47
41	Molecularly imprinted polymer for human viral pathogen detection. Materials Science and Engineering C, 2017, 77, 1341-1348.	3.8	46
42	Synthesis and structureâ€“activity relationship of 2-thiopyrimidine-4-one analogs as antimicrobial and anticancer agents. European Journal of Medicinal Chemistry, 2011, 46, 738-742.	2.6	44
43	Synthesis and Theoretical Study of Molecularly Imprinted Nanospheres for Recognition of Tocopherols. Molecules, 2009, 14, 2985-3002.	1.7	42
44	A Unified Proteochemometric Model for Prediction of Inhibition of Cytochrome P450 Isoforms. PLoS ONE, 2013, 8, e66566.	1.1	42
45	Modeling the activity of furin inhibitors using artificial neural network. European Journal of Medicinal Chemistry, 2009, 44, 1664-1673.	2.6	40
46	iTTCA-Hybrid: Improved and robust identification of tumor T cell antigens by utilizing hybrid feature representation. Analytical Biochemistry, 2020, 599, 113747.	1.1	40
47	Metalloantibiotic Mn(II)â€“bacitracin complex mimicking manganese superoxide dismutase. Biochemical and Biophysical Research Communications, 2006, 341, 925-930.	1.0	37
48	CryoProtect: A Web Server for Classifying Antifreeze Proteins from Nonantifreeze Proteins. Journal of Chemistry, 2017, 2017, 1-15.	0.9	37
49	miR-130a and miR-27b Enhance Osteogenesis in Human Bone Marrow Mesenchymal Stem Cells via Specific Down-Regulation of Peroxisome Proliferator-Activated Receptor Î³. Frontiers in Genetics, 2018, 9, 543.	1.1	37
50	TargetAntiAngio: A Sequence-Based Tool for the Prediction and Analysis of Anti-Angiogenic Peptides. International Journal of Molecular Sciences, 2019, 20, 2950.	1.8	37
51	Trapping of Human Hemoglobin by Haptoglobin: Molecular Mechanisms and Clinical Applications. Antioxidants and Redox Signaling, 2013, 18, 2364-2374.	2.5	36
52	Mechanisms and Neuroprotective Activities of Stigmasterol Against Oxidative Stress-Induced Neuronal Cell Death via Sirtuin Family. Frontiers in Nutrition, 2021, 8, 648995.	1.6	36
53	UMPred-FRL: A New Approach for Accurate Prediction of Umami Peptides Using Feature Representation Learning. International Journal of Molecular Sciences, 2021, 22, 13124.	1.8	35
54	StackDPPIV: A novel computational approach for accurate prediction of dipeptidyl peptidase IV (DPP-IV) inhibitory peptides. Methods, 2022, 204, 189-198.	1.9	34

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55	Antioxidant, cytotoxicity, and QSAR study of 1-adamantylthio derivatives of 3-picoline and phenylpyridines. Medicinal Chemistry Research, 2012, 21, 3514-3522.	1.1	32
56	QSAR Study of H1N1 Neuraminidase Inhibitors from Influenza a Virus. Letters in Drug Design and Discovery, 2014, 11, 420-427.	0.4	32
57	QSAR modeling of aromatase inhibitory activity of 1-substituted 1,2,3-triazole analogs of letrozole. European Journal of Medicinal Chemistry, 2013, 69, 99-114.	2.6	31
58	iAMY-SCM: Improved prediction and analysis of amyloid proteins using a scoring card method with propensity scores of dipeptides. Genomics, 2021, 113, 689-698.	1.3	31
59	Computational Insights on Sulfonamide Imprinted Polymers. Molecules, 2008, 13, 3077-3091.	1.7	30
60	Elucidating the Structure-Activity Relationships of the Vasorelaxation and Antioxidation Properties of Thionicotinic Acid Derivatives. Molecules, 2010, 15, 198-214.	1.7	28
61	Exploring the chemical space of aromatase inhibitors. Molecular Diversity, 2013, 17, 661-677.	2.1	28
62	Predictive QSAR modeling of aldose reductase inhibitors using Monte Carlo feature selection. European Journal of Medicinal Chemistry, 2014, 76, 352-359.	2.6	28
63	Towards Predicting the Cytochrome P450 Modulation: From QSAR to Proteochemometric Modeling. Current Drug Metabolism, 2017, 18, 540-555.	0.7	28
64	osFP: a web server for predicting the oligomeric states of fluorescent proteins. Journal of Cheminformatics, 2016, 8, 72.	2.8	27
65	iBitter-Fuse: A Novel Sequence-Based Bitter Peptide Predictor by Fusing Multi-View Features. International Journal of Molecular Sciences, 2021, 22, 8958.	1.8	27
66	Exploring the chemical space of influenza neuraminidase inhibitors. PeerJ, 2016, 4, e1958.	0.9	27
67	AMYPred-FRL is a novel approach for accurate prediction of amyloid proteins by using feature representation learning. Scientific Reports, 2022, 12, 7697.	1.6	27
68	Probing the origin of estrogen receptor alpha inhibitionvialarge-scale QSAR study. RSC Advances, 2018, 8, 11344-11356.	1.7	25
69	Towards understanding aromatase inhibitory activity via QSAR modeling. EXCLI Journal, 2018, 17, 688-708.	0.5	24
70	A novel sequence-based predictor for identifying and characterizing thermophilic proteins using estimated propensity scores of dipeptides. Scientific Reports, 2021, 11, 23782.	1.6	24
71	Modeling the LPS Neutralization Activity of Anti-Endotoxins. Molecules, 2009, 14, 1869-1888.	1.7	23
72	Quantitative structureâ€“property relationship study of spectral properties of green fluorescent protein with support vector machine. Chemometrics and Intelligent Laboratory Systems, 2013, 120, 42-52.	1.8	23

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73	QSAR study of amidino bis-benzimidazole derivatives as potent anti-malarial agents against Plasmodium falciparum. Chemical Papers, 2013, 67, .	1.0	22
74	AutoWeka: Toward an Automated Data Mining Software for QSAR and QSPR Studies. Methods in Molecular Biology, 2015, 1260, 119-147.	0.4	22
75	Navigating the chemical space of dipeptidyl peptidase-4 inhibitors. Drug Design, Development and Therapy, 2015, 9, 4515.	2.0	20
76	Structural and biochemical characterization of two heme binding sites on Î± 1 -microglobulin using site directed mutagenesis and molecular simulation. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2016, 1864, 29-41.	1.1	20
77	QSAR MODEL OF THE QUORUM-QUENCHING N-ACYL-HOMOSERINE LACTONE LACTONASE ACTIVITY. Journal of Biological Systems, 2008, 16, 279-293.	0.5	19
78	The decreasing prevalence of the thyroid ima artery: A systematic review and machine learning assisted meta-analysis. Annals of Anatomy, 2022, 239, 151803.	1.0	19
79	Rational Design of Analyte Channels of the Green Fluorescent Protein for Biosensor Applications. International Journal of Biological Sciences, 2007, 3, 463-470.	2.6	18
80	Investigation of aromatase inhibitory activity of metal complexes of 8-hydroxyquinoline and uracil derivatives. Drug Design, Development and Therapy, 2014, 8, 1089.	2.0	18
81	Insights into antioxidant activity of 1-adamantylthiopyridine analogs using multiple linear regression. European Journal of Medicinal Chemistry, 2014, 73, 258-264.	2.6	18
82	Large-scale classification of P-glycoprotein inhibitors using SMILES-based descriptors. SAR and QSAR in Environmental Research, 2017, 28, 1-16.	1.0	18
83	In Silico Approaches for the Prediction and Analysis of Antiviral Peptides: A Review. Current Pharmaceutical Design, 2021, 27, 2180-2188.	0.9	18
84	Prediction of aromatase inhibitory activity using the efficient linear method (ELM). EXCLI Journal, 2015, 14, 452-64.	0.5	18
85	ABCpred: a webserver for the discovery of acetyl- and butyryl-cholinesterase inhibitors. Molecular Diversity, 2022, 26, 467-487.	2.1	18
86	Cytotoxicity and QSAR study of (thio)ureas derived from phenylalkylamines and pyridylalkylamines. Medicinal Chemistry Research, 2013, 22, 4016-4029.	1.1	17
87	Towards the Revival of Interpretable QSAR Models. Challenges and Advances in Computational Chemistry and Physics, 2017, , 3-55.	0.6	17
88	HIVCoR: A sequence-based tool for predicting HIV-1 CRF01_AE coreceptor usage. Computational Biology and Chemistry, 2019, 80, 419-432.	1.1	17
89	Molecular Modeling of the Human Hemoglobin-Haptoglobin Complex Sheds Light on the Protective Mechanisms of Haptoglobin. PLoS ONE, 2013, 8, e62996.	1.1	17
90	Rational Design of Colchicine Derivatives as anti-HIV Agents via QSAR and Molecular Docking. Medicinal Chemistry, 2019, 15, 328-340.	0.7	17

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91	Synthesis, cytotoxicity and QSAR study of N-tosyl-1,2,3,4-tetrahydroisoquinoline derivatives. Archives of Pharmacal Research, 2013, 36, 1066-1077.	2.7	16
92	Origin of aromatase inhibitory activity via proteochemometric modeling. PeerJ, 2016, 4, e1979.	0.9	16
93	<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.	1.5	16
94	Aromatase inhibitory activity of 1,4-naphthoquinone derivatives and QSAR study. EXCLI Journal, 2017, 16, 714-726.	0.5	16
95	Data mining for the identification of metabolic syndrome status. EXCLI Journal, 2018, 17, 72-88.	0.5	16
96	Quantitative population-health relationship (QPHR) for assessing metabolic syndrome. EXCLI Journal, 2013, 12, 569-83.	0.5	16
97	The MicroRNA Interaction Network of Lipid Diseases. Frontiers in Genetics, 2017, 8, 116.	1.1	15
98	Computational identification of miRNAs that modulate the differentiation of mesenchymal stem cells to osteoblasts. PeerJ, 2016, 4, e1976.	0.9	15
99	Multidisciplinary approaches for targeting the secretase protein family as a therapeutic route for Alzheimer's disease. Medicinal Research Reviews, 2019, 39, 1730-1778.	5.0	14
100	Lower BMI cutoff for assessing the prevalence of metabolic syndrome in Thai population. Acta Diabetologica, 2010, 47, 91-96.	1.2	13
101	Large-scale structure-activity relationship study of hepatitis C virus NS5B polymerase inhibition using SMILES-based descriptors. Molecular Diversity, 2015, 19, 955-964.	2.1	13
102	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.	1.3	13
103	Predicting antimicrobial activities of benzimidazole derivatives. Medicinal Chemistry Research, 2013, 22, 5418-5430.	1.1	12
104	Proteomic study of in vitro osteogenic differentiation of mesenchymal stem cells in high glucose condition. Molecular Biology Reports, 2020, 47, 7505-7516.	1.0	12
105	Classification of P-glycoprotein-interacting compounds using machine learning methods. EXCLI Journal, 2015, 14, 958-70.	0.5	12
106	QSAR study of anti-prion activity of 2-aminothiazoles. EXCLI Journal, 2012, 11, 453-67.	0.5	12
107	Determining the optimal cutoff points for waist circumference and body mass index for identification of metabolic abnormalities and metabolic syndrome in urban Thai population. Diabetes Research and Clinical Practice, 2012, 98, e16-e21.	1.1	11
108	Genetic algorithm search space splicing particle swarm optimization as general-purpose optimizer. Chemometrics and Intelligent Laboratory Systems, 2013, 128, 153-159.	1.8	11

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109	Proteochemometric model for predicting the inhibition of penicillin-binding proteins. Journal of Computer-Aided Molecular Design, 2015, 29, 127-141.	1.3	11
110	A novel potent autophagy inhibitor ECDD-S27 targets vacuolar ATPase and inhibits cancer cell survival. Scientific Reports, 2019, 9, 9177.	1.6	11
111	A novel peptide isolated from garlic shows anticancer effect against leukemic cell lines via interaction with Bclâ€2 family proteins. Chemical Biology and Drug Design, 2021, 97, 1017-1028.	1.5	11
112	On the Origins of Hepatitis C Virus NS5B Polymerase Inhibitory Activity Using Machine Learning Approaches. Current Topics in Medicinal Chemistry, 2015, 15, 1814-1826.	1.0	11
113	Machine learning approaches for discerning intercorrelation of hematological parameters and glucose level for identification of diabetes mellitus. EXCLI Journal, 2013, 12, 885-93.	0.5	11
114	Oxidative responses and defense mechanism of hyperpigmented as characterized by proteomics and metabolomics. EXCLI Journal, 2018, 17, 544-562.	0.5	10
115	Oxidized regenerated cellulose nanofiber membranes for capturing heavy metals in aqueous solutions. Cellulose, 2021, 28, 11465.	2.4	10
116	Synthesis and computational investigation of molecularly imprinted nanospheres for selective recognition of alpha-tocopherol succinate. EXCLI Journal, 2013, 12, 701-18.	0.5	10
117	SCMTHP: A New Approach for Identifying and Characterizing of Tumor-Homing Peptides Using Estimated Propensity Scores of Amino Acids. Pharmaceutics, 2022, 14, 122.	2.0	10
118	QSAR modeling of aromatase inhibition by flavonoids using machine learning approaches. Chemical Papers, 2014, 68, .	1.0	9
119	Unraveling the origin of splice switching activity of hemoglobin Î²-globin gene modulators via QSAR modeling. Chemometrics and Intelligent Laboratory Systems, 2016, 151, 51-60.	1.8	9
120	Exploring the origin of phosphodiesterase inhibition via proteochemometric modeling. RSC Advances, 2017, 7, 28056-28068.	1.7	9
121	Privileged substructures for anti-sickling activity via cheminformatic analysis. RSC Advances, 2018, 8, 5920-5935.	1.7	9
122	Clinical validation of urine-based XpertÂ® MTB/RIF assay for the diagnosis of urogenital tuberculosis: A systematic review and meta-analysis. International Journal of Infectious Diseases, 2020, 95, 15-21.	1.5	9
123	Beneficial Effects of Cyclic Ether 2-Butoxytetrahydrofuran from Sea Cucumber Holothuria scabra against AÎ² Aggregate Toxicity in Transgenic Caenorhabditis elegans and Potential Chemical Interaction. Molecules, 2021, 26, 2195.	1.7	9
124	Toward insights on determining factors for high activity in antimicrobial peptides via machine learning. PeerJ, 2019, 7, e8265.	0.9	9
125	Pragmatic Applications and Universality of DNA Barcoding for Substantial Organisms at Species Level: A Review to Explore a Way Forward. BioMed Research International, 2022, 2022, 1-19.	0.9	9
126	Solving the barriers to diabetes education through the use of multimedia. Australian Journal of Cancer Nursing, 2010, 12, 58-66.	0.8	8

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127	PepBio: predicting the bioactivity of host defense peptides. RSC Advances, 2017, 7, 35119-35134.	1.7	8
128	Proteochemometric Modeling for Drug Repositioning. , 2019, , 281-302.		7
129	Exploring the Chemical Space of P-Glycoprotein Interacting Compounds. Mini-Reviews in Medicinal Chemistry, 2017, 17, 1332-1345.	1.1	7
130	Probing the origins of aromatase inhibitory activity of disubstituted coumarins via QSAR and molecular docking. EXCLI Journal, 2014, 13, 1259-74.	0.5	7
131	Data mining of magnetocardiograms for prediction of ischemic heart disease. EXCLI Journal, 2010, 9, 82-95.	0.5	7
132	Quantitative Structure-activity Relationship Study of Betulinic Acid Derivatives Against HIV using SMILES-based Descriptors. Current Computer-Aided Drug Design, 2018, 14, 152-159.	0.8	6
133	Rational design of novel sirtuin 1 activators via structure-activity insights from application of QSAR modeling. EXCLI Journal, 2019, 18, 207-222.	0.5	6
134	Exploring the physicochemical properties of templates from molecular imprinting literature using interactive text mining approach. Chemometrics and Intelligent Laboratory Systems, 2012, 116, 128-136.	1.8	5
135	Probing the origins of anticancer activity of chrysin derivatives. Medicinal Chemistry Research, 2015, 24, 1884-1892.	1.1	5
136	Review and Comparative Analysis of Machine Learning-based Predictors for Predicting and Analyzing Anti-angiogenic Peptides. Current Medicinal Chemistry, 2022, 29, 849-864.	1.2	5
137	Bioinformatics and experimental studies of anti-leukemic activity from 6-gingerol demonstrate its role in p53 mediated apoptosis pathway. EXCLI Journal, 2020, 19, 582-595.	0.5	5
138	Illuminating the origins of spectral properties of green fluorescent proteins via proteochemometric and molecular modeling. Journal of Computational Chemistry, 2014, 35, 1951-1966.	1.5	4
139	Probing the origins of 17Î²-hydroxysteroid dehydrogenase type 1 inhibitory activity via QSAR and molecular docking. European Journal of Medicinal Chemistry, 2015, 96, 231-237.	2.6	4
140	Exploring the origins of structureâ€“oxygen affinity relationship of human haemoglobin allosteric effector. Molecular Simulation, 2015, 41, 1283-1291.	0.9	4
141	Extending proteochemometric modeling for unraveling the sorption behavior of compoundâ€“soil interaction. Chemometrics and Intelligent Laboratory Systems, 2016, 151, 219-227.	1.8	4
142	ERpred: a web server for the prediction of subtype-specific estrogen receptor antagonists. PeerJ, 2021, 9, e11716.	0.9	4
143	Toward insights on antimicrobial selectivity of host defense peptides via machine learning model interpretation. Genomics, 2021, 113, 3851-3863.	1.3	4
144	Classification and Morphometric Features of Pterion in Thai Population with Potential Sex Prediction. Medicina (Lithuania), 2021, 57, 1282.	0.8	4

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145	PyBact: an algorithm for bacterial identification. EXCLI Journal, 2011, 10, 240-245.	0.5	3
146	QSAR-driven rational design of novel DNA methyltransferase 1 inhibitors. EXCLI Journal, 2020, 19, 458-475.	0.5	3
147	Computational study on the origin of the cancer immunotherapeutic potential of B and T cell epitope peptides. Molecular BioSystems, 2017, 13, 2310-2322.	2.9	2
148	Synthesis, Plasmodium falciparum Inhibitory Activity, Cytotoxicity and Solubility of N2 ,N4 -Disubstituted Quinazoline-2,4-diamines.. Medicinal Chemistry, 2019, 15, 693-704.	0.7	2
149	Betulinic Acid Modulates the Expression of HSPA and Activates Apoptosis in Two Cell Lines of Human Colorectal Cancer. Molecules, 2021, 26, 6377.	1.7	2
150	Proteomic and bioinformatic discovery of biomarkers for diabetic nephropathy. EXCLI Journal, 2018, 17, 312-330.	0.5	2
151	Large-scale comparative review and assessment of computational methods for phage virion proteins identification.. EXCLI Journal, 2022, 21, 11-29.	0.5	2
152	Towards the design of 3-aminopyrazole pharmacophore of pyrazolopyridine derivatives as novel antioxidants. Medicinal Chemistry Research, 2017, 26, 2699-2706.	1.1	1
153	Development and performance of CUHAS-ROBUST application for pulmonary rifampicin-resistance tuberculosis screening in Indonesia. PLoS ONE, 2021, 16, e0249243.	1.1	1
154	Interpretable SMILES-based QSAR model of inhibitory activity of sirtuins 1 and 2. Combinatorial Chemistry and High Throughput Screening, 2020, 23, .	0.6	1
155	Production and characterization of antibody against Opisthorchis viverrini via phage display and molecular simulation. PLoS ONE, 2021, 16, e0248887.	1.1	0