

Chanin Nantasenamat

List of Publications by Year in descending order

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155
papers

4,894
citations

66315

42
h-index

133188

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all docs

167
docs citations

167
times ranked

4835
citing authors

#	ARTICLE	IF	CITATIONS
1	Review and Comparative Analysis of Machine Learning-based Predictors for Predicting and Analyzing Anti-angiogenic Peptides. <i>Current Medicinal Chemistry</i> , 2022, 29, 849-864.	1.2	5
2	The decreasing prevalence of the thyroid ima artery: A systematic review and machine learning assisted meta-analysis. <i>Annals of Anatomy</i> , 2022, 239, 151803.	1.0	19
3	ABCpred: a webserver for the discovery of acetyl- and butyryl-cholinesterase inhibitors. <i>Molecular Diversity</i> , 2022, 26, 467-487.	2.1	18
4	SCMTHP: A New Approach for Identifying and Characterizing of Tumor-Homing Peptides Using Estimated Propensity Scores of Amino Acids. <i>Pharmaceutics</i> , 2022, 14, 122.	2.0	10
5	Pragmatic Applications and Universality of DNA Barcoding for Substantial Organisms at Species Level: A Review to Explore a Way Forward. <i>BioMed Research International</i> , 2022, 2022, 1-19.	0.9	9
6	StackDPPiV: A novel computational approach for accurate prediction of dipeptidyl peptidase IV (DPP-IV) inhibitory peptides. <i>Methods</i> , 2022, 204, 189-198.	1.9	34
7	Large-scale comparative review and assessment of computational methods for phage virion proteins identification.. <i>EXCLI Journal</i> , 2022, 21, 11-29.	0.5	2
8	AMYPred-FRL is a novel approach for accurate prediction of amyloid proteins by using feature representation learning. <i>Scientific Reports</i> , 2022, 12, 7697.	1.6	27
9	iAMY-SCM: Improved prediction and analysis of amyloid proteins using a scoring card method with propensity scores of dipeptides. <i>Genomics</i> , 2021, 113, 689-698.	1.3	31
10	Improved prediction and characterization of anticancer activities of peptides using a novel flexible scoring card method. <i>Scientific Reports</i> , 2021, 11, 3017.	1.6	48
11	BERT4Bitter: a bidirectional encoder representations from transformers (BERT)-based model for improving the prediction of bitter peptides. <i>Bioinformatics</i> , 2021, 37, 2556-2562.	1.8	84
12	Production and characterization of antibody against <i>Opisthorchis viverrini</i> via phage display and molecular simulation. <i>PLoS ONE</i> , 2021, 16, e0248887.	1.1	0
13	A novel peptide isolated from garlic shows anticancer effect against leukemic cell lines via interaction with Bcl-2 family proteins. <i>Chemical Biology and Drug Design</i> , 2021, 97, 1017-1028.	1.5	11
14	Development and performance of CUHAS-ROBUST application for pulmonary rifampicin-resistance tuberculosis screening in Indonesia. <i>PLoS ONE</i> , 2021, 16, e0249243.	1.1	1
15	Beneficial Effects of Cyclic Ether 2-Butoxytetrahydrofuran from Sea Cucumber <i>Holothuria scabra</i> against Al ³⁺ Aggregate Toxicity in Transgenic <i>Caenorhabditis elegans</i> and Potential Chemical Interaction. <i>Molecules</i> , 2021, 26, 2195.	1.7	9
16	Mechanisms and Neuroprotective Activities of Stigmasterol Against Oxidative Stress-Induced Neuronal Cell Death via Sirtuin Family. <i>Frontiers in Nutrition</i> , 2021, 8, 648995.	1.6	36
17	StackIL6: a stacking ensemble model for improving the prediction of IL-6 inducing peptides. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	84
18	In Silico Approaches for the Prediction and Analysis of Antiviral Peptides: A Review. <i>Current Pharmaceutical Design</i> , 2021, 27, 2180-2188.	0.9	18

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19	ERpred: a web server for the prediction of subtype-specific estrogen receptor antagonists. PeerJ, 2021, 9, e11716.	0.9	4
20	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
21	Toward insights on antimicrobial selectivity of host defense peptides via machine learning model interpretation. Genomics, 2021, 113, 3851-3863.	1.3	4
22	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
23	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
24	Oxidized regenerated cellulose nanofiber membranes for capturing heavy metals in aqueous solutions. Cellulose, 2021, 28, 11465.	2.4	10
25	Classification and Morphometric Features of Pterion in Thai Population with Potential Sex Prediction. Medicina (Lithuania), 2021, 57, 1282.	0.8	4
26	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
27	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
28	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
29	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
30	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
31	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
32	iTTCA-Hybrid: Improved and robust identification of tumor T cell antigens by utilizing hybrid feature representation. Analytical Biochemistry, 2020, 599, 113747.	1.1	40
33	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
34	Towards reproducible computational drug discovery. Journal of Cheminformatics, 2020, 12, 9.	2.8	100
35	Clinical validation of urine-based Xpert [®] 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
36	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

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37	<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
38	QSAR-driven rational design of novel DNA methyltransferase 1 inhibitors. EXCLI Journal, 2020, 19, 458-475.	0.5	3
39	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
40	Interpretable SMILES-based QSAR model of inhibitory activity of sirtuins 1 and 2. Combinatorial Chemistry and High Throughput Screening, 2020, 23, .	0.6	1
41	A novel potent autophagy inhibitor ECDD-S27 targets vacuolar ATPase and inhibits cancer cell survival. Scientific Reports, 2019, 9, 9177.	1.6	11
42	ACPred: A Computational Tool for the Prediction and Analysis of Anticancer Peptides. Molecules, 2019, 24, 1973.	1.7	125
43	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
44	HIVCoR: A sequence-based tool for predicting HIV-1 CRF01_AE coreceptor usage. Computational Biology and Chemistry, 2019, 80, 419-432.	1.1	17
45	THPep: A machine learning-based approach for predicting tumor homing peptides. Computational Biology and Chemistry, 2019, 80, 441-451.	1.1	56
46	Proteochemometric Modeling for Drug Repositioning. , 2019, , 281-302.		7
47	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
48	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
49	Rational Design of Colchicine Derivatives as anti-HIV Agents via QSAR and Molecular Docking. Medicinal Chemistry, 2019, 15, 328-340.	0.7	17
50	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
51	Toward insights on determining factors for high activity in antimicrobial peptides via machine learning. PeerJ, 2019, 7, e8265.	0.9	9
52	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
53	Privileged substructures for anti-sickling activity <i>via</i> cheminformatic analysis. RSC Advances, 2018, 8, 5920-5935.	1.7	9
54	Probing the origin of estrogen receptor alpha inhibition <i>via</i> large-scale QSAR study. RSC Advances, 2018, 8, 11344-11356.	1.7	25

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55	miR-130a and miR-27b Enhance Osteogenesis in Human Bone Marrow Mesenchymal Stem Cells via Specific Down-Regulation of Peroxisome Proliferator-Activated Receptor β . <i>Frontiers in Genetics</i> , 2018, 9, 543.	1.1	37
56	PAAP: a web server for predicting antihypertensive activity of peptides. <i>Future Medicinal Chemistry</i> , 2018, 10, 1749-1767.	1.1	50
57	Tackling the Antibiotic Resistance Caused by Class A β -Lactamases through the Use of β -Lactamase Inhibitory Protein. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2222.	1.8	50
58	Oxidative responses and defense mechanism of hyperpigmented as characterized by proteomics and metabolomics. <i>EXCLI Journal</i> , 2018, 17, 544-562.	0.5	10
59	Towards understanding aromatase inhibitory activity via QSAR modeling. <i>EXCLI Journal</i> , 2018, 17, 688-708.	0.5	24
60	Unraveling the bioactivity of anticancer peptides as deduced from machine learning. <i>EXCLI Journal</i> , 2018, 17, 734-752.	0.5	71
61	Quantitative Structure-activity Relationship Study of Betulinic Acid Derivatives Against HIV using SMILES-based Descriptors. <i>Current Computer-Aided Drug Design</i> , 2018, 14, 152-159.	0.8	6
62	Data mining for the identification of metabolic syndrome status. <i>EXCLI Journal</i> , 2018, 17, 72-88.	0.5	16
63	Proteomic and bioinformatic discovery of biomarkers for diabetic nephropathy. <i>EXCLI Journal</i> , 2018, 17, 312-330.	0.5	2
64	Large-scale classification of P-glycoprotein inhibitors using SMILES-based descriptors. <i>SAR and QSAR in Environmental Research</i> , 2017, 28, 1-16.	1.0	18
65	Exploring the epigenetic drug discovery landscape. <i>Expert Opinion on Drug Discovery</i> , 2017, 12, 345-362.	2.5	62
66	HemoPred: a web server for predicting the hemolytic activity of peptides. <i>Future Medicinal Chemistry</i> , 2017, 9, 275-291.	1.1	84
67	Towards the Revival of Interpretable QSAR Models. <i>Challenges and Advances in Computational Chemistry and Physics</i> , 2017, , 3-55.	0.6	17
68	Exploring the origin of phosphodiesterase inhibition via proteochemometric modeling. <i>RSC Advances</i> , 2017, 7, 28056-28068.	1.7	9
69	Molecularly imprinted polymer for human viral pathogen detection. <i>Materials Science and Engineering C</i> , 2017, 77, 1341-1348.	3.8	46
70	Computational study on the origin of the cancer immunotherapeutic potential of B and T cell epitope peptides. <i>Molecular BioSystems</i> , 2017, 13, 2310-2322.	2.9	2
71	PepBio: predicting the bioactivity of host defense peptides. <i>RSC Advances</i> , 2017, 7, 35119-35134.	1.7	8
72	Towards the design of 3-aminopyrazole pharmacophore of pyrazolopyridine derivatives as novel antioxidants. <i>Medicinal Chemistry Research</i> , 2017, 26, 2699-2706.	1.1	1

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73	The MicroRNA Interaction Network of Lipid Diseases. <i>Frontiers in Genetics</i> , 2017, 8, 116.	1.1	15
74	CryoProtect: A Web Server for Classifying Antifreeze Proteins from Nonantifreeze Proteins. <i>Journal of Chemistry</i> , 2017, 2017, 1-15.	0.9	37
75	Aromatase inhibitory activity of 1,4-naphthoquinone derivatives and QSAR study. <i>EXCLI Journal</i> , 2017, 16, 714-726.	0.5	16
76	Towards Predicting the Cytochrome P450 Modulation: From QSAR to Proteochemometric Modeling. <i>Current Drug Metabolism</i> , 2017, 18, 540-555.	0.7	28
77	Exploring the Chemical Space of P-Glycoprotein Interacting Compounds. <i>Mini-Reviews in Medicinal Chemistry</i> , 2017, 17, 1332-1345.	1.1	7
78	Roles of d-Amino Acids on the Bioactivity of Host Defense Peptides. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1023.	1.8	55
79	Origin of aromatase inhibitory activity via proteochemometric modeling. <i>PeerJ</i> , 2016, 4, e1979.	0.9	16
80	osFP: a web server for predicting the oligomeric states of fluorescent proteins. <i>Journal of Cheminformatics</i> , 2016, 8, 72.	2.8	27
81	Extending proteochemometric modeling for unraveling the sorption behavior of compoundâ€™soil interaction. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2016, 151, 219-227.	1.8	4
82	Unraveling the origin of splice switching activity of hemoglobin $\hat{1}^2$ -globin gene modulators via QSAR modeling. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2016, 151, 51-60.	1.8	9
83	Structural and biochemical characterization of two heme binding sites on $\hat{1}^{\pm}$ 1 -microglobulin using site directed mutagenesis and molecular simulation. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016, 1864, 29-41.	1.1	20
84	Exploring the chemical space of influenza neuraminidase inhibitors. <i>PeerJ</i> , 2016, 4, e1958.	0.9	27
85	Computational identification of miRNAs that modulate the differentiation of mesenchymal stem cells to osteoblasts. <i>PeerJ</i> , 2016, 4, e1976.	0.9	15
86	Probing the origins of human acetylcholinesterase inhibition via QSAR modeling and molecular docking. <i>PeerJ</i> , 2016, 4, e2322.	0.9	48
87	Navigating the chemical space of dipeptidyl peptidase-4 inhibitors. <i>Drug Design, Development and Therapy</i> , 2015, 9, 4515.	2.0	20
88	Predicting Metabolic Syndrome Using the Random Forest Method. <i>Scientific World Journal</i> , The, 2015, 2015, 1-10.	0.8	47
89	Computer-Aided Drug Design of Bioactive Natural Products. <i>Current Topics in Medicinal Chemistry</i> , 2015, 15, 1780-1800.	1.0	71
90	Discovery of novel 1,2,3-triazole derivatives as anticancer agents using QSAR and in silico structural modification. <i>SpringerPlus</i> , 2015, 4, 571.	1.2	49

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91	Proteochemometric model for predicting the inhibition of penicillin-binding proteins. <i>Journal of Computer-Aided Molecular Design</i> , 2015, 29, 127-141.	1.3	11
92	Maximizing computational tools for successful drug discovery. <i>Expert Opinion on Drug Discovery</i> , 2015, 10, 321-329.	2.5	52
93	Probing the origins of anticancer activity of chrysin derivatives. <i>Medicinal Chemistry Research</i> , 2015, 24, 1884-1892.	1.1	5
94	Large-scale structure-activity relationship study of hepatitis C virus NS5B polymerase inhibition using SMILES-based descriptors. <i>Molecular Diversity</i> , 2015, 19, 955-964.	2.1	13
95	Probing the origins of 17 β -hydroxysteroid dehydrogenase type 1 inhibitory activity via QSAR and molecular docking. <i>European Journal of Medicinal Chemistry</i> , 2015, 96, 231-237.	2.6	4
96	Synthesis and molecular docking of 1,2,3-triazole-based sulfonamides as aromatase inhibitors. <i>Bioorganic and Medicinal Chemistry</i> , 2015, 23, 3472-3480.	1.4	60
97	Exploring the origins of structure-oxygen affinity relationship of human haemoglobin allosteric effector. <i>Molecular Simulation</i> , 2015, 41, 1283-1291.	0.9	4
98	Novel 1,4-naphthoquinone-based sulfonamides: Synthesis, QSAR, anticancer and antimalarial studies. <i>European Journal of Medicinal Chemistry</i> , 2015, 103, 446-459.	2.6	80
99	AutoWeka: Toward an Automated Data Mining Software for QSAR and QSPR Studies. <i>Methods in Molecular Biology</i> , 2015, 1260, 119-147.	0.4	22
100	Prediction of aromatase inhibitory activity using the efficient linear method (ELM). <i>EXCLI Journal</i> , 2015, 14, 452-64.	0.5	18
101	Classification of P-glycoprotein-interacting compounds using machine learning methods. <i>EXCLI Journal</i> , 2015, 14, 958-70.	0.5	12
102	On the Origins of Hepatitis C Virus NS5B Polymerase Inhibitory Activity Using Machine Learning Approaches. <i>Current Topics in Medicinal Chemistry</i> , 2015, 15, 1814-1826.	1.0	11
103	Investigation of aromatase inhibitory activity of metal complexes of 8-hydroxyquinoline and uracil derivatives. <i>Drug Design, Development and Therapy</i> , 2014, 8, 1089.	2.0	18
104	Predictive QSAR modeling of aldose reductase inhibitors using Monte Carlo feature selection. <i>European Journal of Medicinal Chemistry</i> , 2014, 76, 352-359.	2.6	28
105	Insights into antioxidant activity of 1-adamantylthiopyridine analogs using multiple linear regression. <i>European Journal of Medicinal Chemistry</i> , 2014, 73, 258-264.	2.6	18
106	Synthesis, anticancer activity and QSAR study of 1,4-naphthoquinone derivatives. <i>European Journal of Medicinal Chemistry</i> , 2014, 84, 247-263.	2.6	84
107	Synthesis, biological evaluation and molecular docking of novel chalcone-coumarin hybrids as anticancer and antimalarial agents. <i>European Journal of Medicinal Chemistry</i> , 2014, 85, 65-76.	2.6	175
108	Large-scale QSAR study of aromatase inhibitors using SMILES-based descriptors. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2014, 138, 120-126.	1.8	51

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109	Illuminating the origins of spectral properties of green fluorescent proteins via proteochemometric and molecular modeling. <i>Journal of Computational Chemistry</i> , 2014, 35, 1951-1966.	1.5	4
110	QSAR modeling of aromatase inhibition by flavonoids using machine learning approaches. <i>Chemical Papers</i> , 2014, 68, .	1.0	9
111	Design, synthesis and molecular docking studies of novel N-benzenesulfonyl-1,2,3,4-tetrahydroisoquinoline-based triazoles with potential anticancer activity. <i>European Journal of Medicinal Chemistry</i> , 2014, 81, 192-203.	2.6	50
112	QSAR Study of H1N1 Neuraminidase Inhibitors from Influenza a Virus. <i>Letters in Drug Design and Discovery</i> , 2014, 11, 420-427.	0.4	32
113	Probing the origins of aromatase inhibitory activity of disubstituted coumarins via QSAR and molecular docking. <i>EXCLI Journal</i> , 2014, 13, 1259-74.	0.5	7
114	Exploring the chemical space of aromatase inhibitors. <i>Molecular Diversity</i> , 2013, 17, 661-677.	2.1	28
115	Cytotoxicity and QSAR study of (thio)ureas derived from phenylalkylamines and pyridylalkylamines. <i>Medicinal Chemistry Research</i> , 2013, 22, 4016-4029.	1.1	17
116	QSAR modeling of aromatase inhibitory activity of 1-substituted 1,2,3-triazole analogs of letrozole. <i>European Journal of Medicinal Chemistry</i> , 2013, 69, 99-114.	2.6	31
117	QSAR study of amidino bis-benzimidazole derivatives as potent anti-malarial agents against <i>Plasmodium falciparum</i> . <i>Chemical Papers</i> , 2013, 67, .	1.0	22
118	Quantitative structureâ€“property relationship study of spectral properties of green fluorescent protein with support vector machine. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2013, 120, 42-52.	1.8	23
119	Trapping of Human Hemoglobin by Haptoglobin: Molecular Mechanisms and Clinical Applications. <i>Antioxidants and Redox Signaling</i> , 2013, 18, 2364-2374.	2.5	36
120	Genetic algorithm search space splicing particle swarm optimization as general-purpose optimizer. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2013, 128, 153-159.	1.8	11
121	Predicting antimicrobial activities of benzimidazole derivatives. <i>Medicinal Chemistry Research</i> , 2013, 22, 5418-5430.	1.1	12
122	Synthesis, cytotoxicity and QSAR study of N-tosyl-1,2,3,4-tetrahydroisoquinoline derivatives. <i>Archives of Pharmacal Research</i> , 2013, 36, 1066-1077.	2.7	16
123	A Unified Proteochemometric Model for Prediction of Inhibition of Cytochrome P450 Isoforms. <i>PLoS ONE</i> , 2013, 8, e66566.	1.1	42
124	Molecular Modeling of the Human Hemoglobin-Haptoglobin Complex Sheds Light on the Protective Mechanisms of Haptoglobin. <i>PLoS ONE</i> , 2013, 8, e62996.	1.1	17
125	Synthesis and computational investigation of molecularly imprinted nanospheres for selective recognition of alpha-tocopherol succinate. <i>EXCLI Journal</i> , 2013, 12, 701-18.	0.5	10
126	Quantitative population-health relationship (QPHR) for assessing metabolic syndrome. <i>EXCLI Journal</i> , 2013, 12, 569-83.	0.5	16

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127	Machine learning approaches for discerning intercorrelation of hematological parameters and glucose level for identification of diabetes mellitus. <i>EXCLI Journal</i> , 2013, 12, 885-93.	0.5	11
128	Antioxidant, cytotoxicity, and QSAR study of 1-adamantylthio derivatives of 3-picoline and phenylpyridines. <i>Medicinal Chemistry Research</i> , 2012, 21, 3514-3522.	1.1	32
129	Determining the optimal cutoff points for waist circumference and body mass index for identification of metabolic abnormalities and metabolic syndrome in urban Thai population. <i>Diabetes Research and Clinical Practice</i> , 2012, 98, e16-e21.	1.1	11
130	Exploring the physicochemical properties of templates from molecular imprinting literature using interactive text mining approach. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2012, 116, 128-136.	1.8	5
131	QSAR study of anti-prion activity of 2-aminothiazoles. <i>EXCLI Journal</i> , 2012, 11, 453-67.	0.5	12
132	Molecular Docking of Aromatase Inhibitors. <i>Molecules</i> , 2011, 16, 3597-3617.	1.7	76
133	Synthesis and structure-activity relationship of 2-thiopyrimidine-4-one analogs as antimicrobial and anticancer agents. <i>European Journal of Medicinal Chemistry</i> , 2011, 46, 738-742.	2.6	44
134	Predicting the free radical scavenging activity of curcumin derivatives. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2011, 109, 207-216.	1.8	47
135	PyBact: an algorithm for bacterial identification. <i>EXCLI Journal</i> , 2011, 10, 240-245.	0.5	3
136	Elucidating the Structure-Activity Relationships of the Vasorelaxation and Antioxidation Properties of Thionicotinic Acid Derivatives. <i>Molecules</i> , 2010, 15, 198-214.	1.7	28
137	Lower BMI cutoff for assessing the prevalence of metabolic syndrome in Thai population. <i>Acta Diabetologica</i> , 2010, 47, 91-96.	1.2	13
138	Solving the barriers to diabetes education through the use of multimedia. <i>Australian Journal of Cancer Nursing</i> , 2010, 12, 58-66.	0.8	8
139	Identification of metabolic syndrome using decision tree analysis. <i>Diabetes Research and Clinical Practice</i> , 2010, 90, e15-e18.	1.1	48
140	Advances in computational methods to predict the biological activity of compounds. <i>Expert Opinion on Drug Discovery</i> , 2010, 5, 633-654.	2.5	163
141	Data mining of magnetocardiograms for prediction of ischemic heart disease. <i>EXCLI Journal</i> , 2010, 9, 82-95.	0.5	7
142	Modeling the LPS Neutralization Activity of Anti-Endotoxins. <i>Molecules</i> , 2009, 14, 1869-1888.	1.7	23
143	Modeling the activity of furin inhibitors using artificial neural network. <i>European Journal of Medicinal Chemistry</i> , 2009, 44, 1664-1673.	2.6	40
144	Copper complexes of pyridine derivatives with superoxide scavenging and antimicrobial activities. <i>European Journal of Medicinal Chemistry</i> , 2009, 44, 3259-3265.	2.6	155

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145	Synthesis and Theoretical Study of Molecularly Imprinted Nanospheres for Recognition of Tocopherols. <i>Molecules</i> , 2009, 14, 2985-3002.	1.7	42
146	Prediction of bond dissociation enthalpy of antioxidant phenols by support vector machine. <i>Journal of Molecular Graphics and Modelling</i> , 2008, 27, 188-196.	1.3	56
147	QSAR MODEL OF THE QUORUM-QUENCHING N-ACYL-HOMOSERINE LACTONE LACTONASE ACTIVITY. <i>Journal of Biological Systems</i> , 2008, 16, 279-293.	0.5	19
148	Computational Insights on Sulfonamide Imprinted Polymers. <i>Molecules</i> , 2008, 13, 3077-3091.	1.7	30
149	Copper Complexes of Nicotinic-Aromatic Carboxylic Acids as Superoxide Dismutase Mimetics. <i>Molecules</i> , 2008, 13, 3040-3056.	1.7	79
150	Rational Design of Analyte Channels of the Green Fluorescent Protein for Biosensor Applications. <i>International Journal of Biological Sciences</i> , 2007, 3, 463-470.	2.6	18
151	Prediction of GFP spectral properties using artificial neural network. <i>Journal of Computational Chemistry</i> , 2007, 28, 1275-1289.	1.5	59
152	Quantitative structure-imprinting factor relationship of molecularly imprinted polymers. <i>Biosensors and Bioelectronics</i> , 2007, 22, 3309-3317.	5.3	81
153	EDTA-induced Membrane Fluidization and Destabilization: Biophysical Studies on Artificial Lipid Membranes. <i>Acta Biochimica Et Biophysica Sinica</i> , 2007, 39, 901-913.	0.9	59
154	Metalloantibiotic Mn(II)â€“bacitracin complex mimicking manganese superoxide dismutase. <i>Biochemical and Biophysical Research Communications</i> , 2006, 341, 925-930.	1.0	37
155	Quantitative prediction of imprinting factor of molecularly imprinted polymers by artificial neural network. <i>Journal of Computer-Aided Molecular Design</i> , 2005, 19, 509-524.	1.3	75