Yu Zong Chen

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/5016405/publications.pdf

Version: 2024-02-01

149 papers	8,897 citations	44069 48 h-index	45317 90 g-index
150 all docs	150 docs citations	150 times ranked	10452 citing authors

#	Article	IF	Citations
1	Therapeutic target database update 2022: facilitating drug discovery with enriched comparative data of targeted agents. Nucleic Acids Research, 2022, 50, D1398-D1407.	14.5	310
2	AggMapNet: enhanced and explainable low-sample omics deep learning with feature-aggregated multi-channel networks. Nucleic Acids Research, 2022, 50, e45-e45.	14.5	9
3	Fluorescence Analysis of Circulating Exosomes for Breast Cancer Diagnosis Using a Sensor Array and Deep Learning. ACS Sensors, 2022, 7, 1524-1532.	7.8	27
4	ConSIG: consistent discovery of molecular signature from OMIC data. Briefings in Bioinformatics, 2022, 23, .	6.5	37
5	MASI: microbiotaâ€"active substance interactions database. Nucleic Acids Research, 2021, 49, D776-D782.	14.5	28
6	Histopathology classification and localization of colorectal cancer using global labels by weakly supervised deep learning. Computerized Medical Imaging and Graphics, 2021, 88, 101861.	5.8	41
7	Out-of-the-box deep learning prediction of pharmaceutical properties by broadly learned knowledge-based molecular representations. Nature Machine Intelligence, 2021, 3, 334-343.	16.0	66
8	Immunometabolism and potential targets in severe COVID-19 peripheral immune responses. Asian Journal of Pharmaceutical Sciences, 2021, 16, 665-667.	9.1	3
9	Protein music of enhanced musicality by music style guided exploration of diverse amino acid properties. Heliyon, 2021, 7, e07933.	3.2	3
10	Combining kinase inhibitors for optimally coâ€targeting cancer and drug escape by exploitation of drug target promiscuities. Drug Development Research, 2021, 82, 133-142.	2.9	0
11	Therapeutic target database 2020: enriched resource for facilitating research and early development of targeted therapeutics. Nucleic Acids Research, 2020, 48, D1031-D1041.	14.5	488
12	ANPELA: analysis and performance assessment of the label-free quantification workflow for metaproteomic studies. Briefings in Bioinformatics, 2020, 21, 621-636.	6.5	151
13	Clinical trials, progression-speed differentiating features and swiftness rule of the innovative targets of first-in-class drugs. Briefings in Bioinformatics, 2020, 21, 649-662.	6.5	139
14	The pros and cons of traditional Chinese medicines in the treatment of COVID-19. Pharmacological Research, 2020, 157, 104873.	7.1	12
15	East meets West in COVID-19 therapeutics. Pharmacological Research, 2020, 159, 105008.	7.1	5
16	Databases for facilitating mechanistic investigations of traditional Chinese medicines against COVID-19. Pharmacological Research, 2020, 159, 104989.	7.1	11
17	Consistent gene signature of schizophrenia identified by a novel feature selection strategy from comprehensive sets of transcriptomic data. Briefings in Bioinformatics, 2020, 21, 1058-1068.	6.5	177
18	Expression signature of sixâ€snoRNA serves as novel nonâ€invasive biomarker for diagnosis and prognosis prediction of renal clear cell carcinoma. Journal of Cellular and Molecular Medicine, 2020, 24, 2215-2228.	3.6	32

#	Article	IF	Citations
19	The Antipsychotic Agent Sertindole Exhibited Antiproliferative Activities by Inhibiting the STAT3 Signaling Pathway in Human Gastric Cancer Cells. Journal of Cancer, 2020, 11, 849-857.	2.5	14
20	Databases for the targeted COVIDâ€19 therapeutics. British Journal of Pharmacology, 2020, 177, 4999-5001.	5.4	16
21	SNORD89 promotes stemness phenotype of ovarian cancer cells by regulating Notch1-c-Myc pathway. Journal of Translational Medicine, 2019, 17, 259.	4.4	43
22	Design, Synthesis and Evaluation of New Indolylpyrimidylpiperazines for Gastrointestinal Cancer Therapy. Molecules, 2019, 24, 3661.	3.8	0
23	Cover Image, Volume 80, Issue 2. Drug Development Research, 2019, 80, i.	2.9	0
24	Simultaneous Improvement in the Precision, Accuracy, and Robustness of Label-free Proteome Quantification by Optimizing Data Manipulation Chains*. Molecular and Cellular Proteomics, 2019, 18, 1683-1699.	3.8	113
25	Development of a versatile DNMT and HDAC inhibitor C02S modulating multiple cancer hallmarks for breast cancer therapy. Bioorganic Chemistry, 2019, 87, 200-208.	4.1	37
26	Metabolic Profiling of Amino Acids by Liquid Chromatographyâ€“Tandem Mass Spectrometry (LCâ€“MS) to Characterize the Significance of Glutamine in Triple-Negative Breast Cancer (TNBC). Analytical Letters, 2019, 52, 1068-1082.	1.8	1
27	Naphthalimide-containing conjugated polyelectrolytes with different chain configurations. Organic and Biomolecular Chemistry, 2019, 17, 2635-2639.	2.8	3
28	Drug sales confirm clinical advantage of multiâ€target inhibition of drug escapes by anticancer kinase inhibitors. Drug Development Research, 2019, 80, 246-252.	2.9	1
29	CMAUP: a database of collective molecular activities of useful plants. Nucleic Acids Research, 2019, 47, D1118-D1127.	14.5	68
30	Prognostic relevance of miRâ€137 and its liver microenvironment regulatory target gene AFM in hepatocellular carcinoma. Journal of Cellular Physiology, 2019, 234, 11888-11899.	4.1	11
31	NPASS: natural product activity and species source database for natural product research, discovery and tool development. Nucleic Acids Research, 2018, 46, D1217-D1222.	14.5	177
32	Computational identification of the binding mechanism of a triple reuptake inhibitor amitifadine for the treatment of major depressive disorder. Physical Chemistry Chemical Physics, 2018, 20, 6606-6616.	2.8	125
33	Clinical Success of Drug Targets Prospectively Predicted by In Silico Study. Trends in Pharmacological Sciences, 2018, 39, 229-231.	8.7	97
34	What Contributes to Serotoninâ€“Norepinephrine Reuptake Inhibitorsâ€™ Dual-Targeting Mechanism? The Key Role of Transmembrane Domain 6 in Human Serotonin and Norepinephrine Transporters Revealed by Molecular Dynamics Simulation. ACS Chemical Neuroscience, 2018, 9, 1128-1140.	3.5	225
35	Phthalimide conjugations for the degradation of oncogenic PI3K. European Journal of Medicinal Chemistry, 2018, 151, 237-247.	5.5	73
36	Exploring the Binding Mechanism of Metabotropic Glutamate Receptor 5 Negative Allosteric Modulators in Clinical Trials by Molecular Dynamics Simulations. ACS Chemical Neuroscience, 2018, 9, 1492-1502.	3.5	108

#	Article	IF	Citations
37	Computational characterization of the selective inhibition of human norepinephrine and serotonin transporters by an escitalopram scaffold. Physical Chemistry Chemical Physics, 2018, 20, 29513-29527.	2.8	37
38	Antiproliferative activities of the second-generation antipsychotic drug sertindole against breast cancers with a potential application for treatment of breast-to-brain metastases. Scientific Reports, 2018, 8, 15753.	3.3	21
39	Therapeutic target database update 2018: enriched resource for facilitating bench-to-clinic research of targeted therapeutics. Nucleic Acids Research, 2018, 46, D1121-D1127.	14.5	462
40	Discovery of the Consistently Well-Performed Analysis Chain for SWATH-MS Based Pharmacoproteomic Quantification. Frontiers in Pharmacology, 2018, 9, 681.	3.5	69
41	A benchmarking study on virtual ligand screening against homology models of human GPCRs. Proteins: Structure, Function and Bioinformatics, 2018, 86, 978-989.	2.6	13
42	Assessing the Performances of Protein Function Prediction Algorithms from the Perspectives of Identification Accuracy and False Discovery Rate. International Journal of Molecular Sciences, 2018, 19, 183.	4.1	35
43	Development of Ligandâ€based Big Data Deep Neural Network Models for Virtual Screening of Large Compound Libraries. Molecular Informatics, 2018, 37, e1800031.	2.5	16
44	Discovery of indolylpiperazinylpyrimidines with dual-target profiles at adenosine A2A and dopamine D2 receptors for Parkinson's disease treatment. PLoS ONE, 2018, 13, e0188212.	2.5	23
45	Predicting Drug Combination Index and Simulating the Network-Regulation Dynamics by Mathematical Modeling of Drug-Targeted EGFR-ERK Signaling Pathway. Scientific Reports, 2017, 7, 40752.	3.3	46
46	Novel multi-substituted benzyl acridone derivatives as survivin inhibitors for hepatocellular carcinoma treatment. European Journal of Medicinal Chemistry, 2017, 129, 337-348.	5.5	38
47	Design, synthesis and anticancer potential of NSC-319745 hydroxamic acid derivatives as DNMT and HDAC inhibitors. European Journal of Medicinal Chemistry, 2017, 134, 281-292.	5.5	47
48	Synthesis and biological research of novel azaacridine derivatives as potent DNA-binding ligands and topoisomerase II inhibitors. Bioorganic and Medicinal Chemistry, 2017, 25, 3437-3446.	3.0	16
49	Design, synthesis and evaluation of azaacridine derivatives as dual-target EGFR and Src kinase inhibitors for antitumor treatment. European Journal of Medicinal Chemistry, 2017, 136, 372-381.	5.5	31
50	Predicting the Enzymatic Hydrolysis Halfâ€lives of New Chemicals Using Support Vector Regression Models Based on Stepwise Feature Elimination. Molecular Informatics, 2017, 36, 1600153.	2.5	3
51	NOREVA: normalization and evaluation of MS-based metabolomics data. Nucleic Acids Research, 2017, 45, W162-W170.	14.5	305
52	Differentiating Physicochemical Properties between Addictive and Nonaddictive ADHD Drugs Revealed by Molecular Dynamics Simulation Studies. ACS Chemical Neuroscience, 2017, 8, 1416-1428.	3.5	61
53	Olaparib hydroxamic acid derivatives as dual PARP and HDAC inhibitors for cancer therapy. Bioorganic and Medicinal Chemistry, 2017, 25, 4100-4109.	3.0	64
54	Discovery of novel dual VEGFR2 and Src inhibitors using a multistep virtual screening approach. Future Medicinal Chemistry, 2017, 9, 7-24.	2.3	11

#	Article	IF	Citations
55	Discovery of 1-(3-aryl-4-chlorophenyl)-3-(p -aryl)urea derivatives against breast cancer by inhibiting PI3K/Akt/mTOR and Hedgehog signalings. European Journal of Medicinal Chemistry, 2017, 141, 721-733.	5.5	14
56	Revealing vilazodone's binding mechanism underlying its partial agonism to the 5-HT_{1A} receptor in the treatment of major depressive disorder. Physical Chemistry Chemical Physics, 2017, 19, 28885-28896.	2.8	41
57	Database and Bioinformatics Studies of Probiotics. Journal of Agricultural and Food Chemistry, 2017, 65, 7599-7606.	5.2	18
58	Pharmacological relationships and ligand discovery of G protein-coupled receptors revealed by simultaneous ligand and receptor clustering. Journal of Molecular Graphics and Modelling, 2017, 76, 136-142.	2.4	1
59	Differentiating physicochemical properties between NDRIs and sNRIs clinically important for the treatment of ADHD. Biochimica Et Biophysica Acta - General Subjects, 2017, 1861, 2766-2777.	2.4	56
60	Synthesis and investigation of novel 6-(1,2,3-triazol-4-yl)-4-aminoquinazolin derivatives possessing hydroxamic acid moiety for cancer therapy. Bioorganic and Medicinal Chemistry, 2017, 25, 27-37.	3.0	45
61	HEROD: a human ethnic and regional specific omics database. Bioinformatics, 2017, 33, 3276-3282.	4.1	3
62	Fluorescence array-based sensing of nitroaromatics using conjugated polyelectrolytes. Analyst, The, 2016, 141, 3242-3245.	3.5	12
63	A sensitive polymeric dark quencher-based sensing platform for fluorescence â€œturn onâ€•detection of proteins. RSC Advances, 2016, 6, 42443-42446.	3.6	6
64	Towards cheminformatics-based estimation of drug therapeutic index: Predicting the protective index of anticonvulsants using a new quantitative structure-index relationship approach. Journal of Molecular Graphics and Modelling, 2016, 67, 102-110.	2.4	3
65	Identification of the inhibitory mechanism of FDA approved selective serotonin reuptake inhibitors: an insight from molecular dynamics simulation study. Physical Chemistry Chemical Physics, 2016, 18, 3260-3271.	2.8	66
66	Molecularly imprinted polymer microprobes for manipulating neurological function by regulating temperature-dependent molecular interactions. Process Biochemistry, 2016, 51, 142-157.	3.7	3
67	Design, synthesis and evaluation of acridine derivatives as multi-target Src and MEK kinase inhibitors for anti-tumor treatment. Bioorganic and Medicinal Chemistry, 2016, 24, 261-269.	3.0	45
68	Therapeutic target database update 2016: enriched resource for bench to clinical drug target and targeted pathway information. Nucleic Acids Research, 2016, 44, D1069-D1074.	14.5	278
69	SVM-Prot 2016: A Web-Server for Machine Learning Prediction of Protein Functional Families from Sequence Irrespective of Similarity. PLoS ONE, 2016, 11, e0155290.	2.5	98
70	The Assessment of the Readiness of Molecular Biomarker-Based Mobile Health Technologies for Healthcare Applications. Scientific Reports, 2015, 5, 17854.	3.3	15
71	Physicochemical Profiles of the Marketed Agrochemicals and Clues for Agrochemical Lead Discovery and Screening Library Development. Molecular Informatics, 2015, 34, 331-338.	2.5	19
72	Molecular design, synthesis and biological research of novel pyridyl acridones as potent DNA-binding and apoptosis-inducing agents. European Journal of Medicinal Chemistry, 2015, 93, 214-226.	5.5	25

#	Article	IF	Citations
73	CFam: a chemical families database based on iterative selection of functional seeds and seed-directed compound clustering. Nucleic Acids Research, 2015, 43, D558-D565.	14.5	6
74	Clustered Distribution of Natural Product Leads of Drugs in the Chemical Space as Influenced by the Privileged Target-Sites. Scientific Reports, 2015, 5, 9325.	3.3	20
75	Fluorescence Array-Based Sensing of Metal Ions Using Conjugated Polyelectrolytes. ACS Applied Materials & Interfaces, 2015, 7, 6882-6888.	8.0	82
76	Co-targeting cancer drug escape pathways confers clinical advantage for multi-target anticancer drugs. Pharmacological Research, 2015, 102, 123-131.	7.1	51
77	An imprinted dopamine receptor for discovery of highly potent and selective D 3 analogues with neuroprotective effects. Process Biochemistry, 2015, 50, 1537-1556.	3.7	5
78	A Preclinical Evaluation of SKLB261, a Multikinase Inhibitor of EGFR/Src/VEGFR2, as a Therapeutic Agent against Pancreatic Cancer. Molecular Cancer Therapeutics, 2015, 14, 407-418.	4.1	27
79	Multitarget inhibitors derived from crosstalk mechanism involving VEGFR2. Future Medicinal Chemistry, 2014, 6, 1771-1789.	2.3	13
80	Therapeutic target database update 2014: a resource for targeted therapeutics. Nucleic Acids Research, 2014, 42, D1118-D1123.	14.5	116
81	Nature's contribution to today's pharmacopeia. Nature Biotechnology, 2014, 32, 979-980.	17.5	32
82	Exploration of N-(2-aminoethyl)piperidine-4-carboxamide as a potential scaffold for development of VEGFR-2, ERK-2 and Abl-1 multikinase inhibitor. Bioorganic and Medicinal Chemistry, 2013, 21, 5694-5706.	3.0	17
83	Novel synthetic acridine derivatives as potent DNA-binding and apoptosis-inducing antitumor agents. Bioorganic and Medicinal Chemistry, 2013, 21, 4170-4177.	3.0	66
84	Exploration of 1-(3-chloro-4-(4-oxo-4H-chromen-2-yl)phenyl)-3-phenylurea derivatives as selective dual inhibitors of Raf1 and JNK1 kinases for anti-tumor treatment. Bioorganic and Medicinal Chemistry, 2013, 21, 824-831.	3.0	19
85	In Silico Prediction of Adverse Drug Reactions and Toxicities Based on Structural, Biological and Clinical Data. Current Drug Safety, 2012, 7, 225-237.	0.6	1
86	Therapeutic target database update 2012: a resource for facilitating target-oriented drug discovery. Nucleic Acids Research, 2012, 40, D1128-D1136.	14.5	459
87	Identification of DNA adduct formation of small molecules by molecular descriptors and machine learning methods. Molecular Simulation, 2012, 38, 259-273.	2.0	5
88	Metabolic network analysis revealed distinct routes of deletion effects between essential and non-essential genes. Molecular BioSystems, 2012, 8, 1179.	2.9	5
89	Analysis of bypass signaling in EGFR pathway and profiling of bypass genes for predicting response to anticancer EGFR tyrosine kinase inhibitors. Molecular BioSystems, 2012, 8, 2645.	2.9	11
90	Development and experimental test of support vector machines virtual screening method for searching Src inhibitors from large compound libraries. Chemistry Central Journal, 2012, 6, 139.	2.6	3

#	Article	IF	Citations
91	A Two-Step Target Binding and Selectivity Support Vector Machines Approach for Virtual Screening of Dopamine Receptor Subtype-Selective Ligands. PLoS ONE, 2012, 7, e39076.	2.5	22
92	Synthesis and Cytotoxic Activity of Some Novel N-Pyridinyl-2-(6-phenylimidazo[2,1-b]thiazol-3-yl)acetamide Derivatives. Molecules, 2012, 17, 4703-4716.	3.8	25
93	The interprotein scoring noises in glide docking scores. Proteins: Structure, Function and Bioinformatics, 2012, 80, 169-183.	2.6	24
94	Prediction of human major histocompatibility complex class II binding peptides by continuous kernel discrimination method. Artificial Intelligence in Medicine, 2012, 55, 107-115.	6.5	3
95	Drug Discovery Prospect from Untapped Species: Indications from Approved Natural Product Drugs. PLoS ONE, 2012, 7, e39782.	2.5	53
96	What Does It Take to Synergistically Combine Sub-Potent Natural Products into Drug-Level Potent Combinations?. PLoS ONE, 2012, 7, e49969.	2.5	17
97	Toxicogenomic Analysis Suggests Chemical-Induced Sexual Dimorphism in the Expression of Metabolic Genes in Zebrafish Liver. PLoS ONE, 2012, 7, e51971.	2.5	4
98	The Therapeutic Target Database: an Internet resource for the primary targets of approved, clinical trial and experimental drugs. Expert Opinion on Therapeutic Targets, 2011, 15, 903-912.	3.4	20
99	Effect of training data size and noise level on support vector machines virtual screening of genotoxic compounds from large compound libraries. Journal of Computer-Aided Molecular Design, 2011, 25, 455-467.	2.9	3
100	Dispersive transport of biomolecules in periodic energy landscapes with application to nanofilter sieving arrays. Electrophoresis, 2011, 32, 506-517.	2.4	5
101	Exploration of acridine scaffold as a potentially interesting scaffold for discovering novel multi-target VEGFR-2 and Src kinase inhibitors. Bioorganic and Medicinal Chemistry, 2011, 19, 3312-3319.	3.0	62
102	Discovery of benzimidazole derivatives as novel multi-target EGFR, VEGFR-2 and PDGFR kinase inhibitors. Bioorganic and Medicinal Chemistry, 2011, 19, 4529-4535.	3.0	97
103	Exploration of (S)-3-aminopyrrolidine as a potentially interesting scaffold for discovery of novel Abl and PI3K dual inhibitors. European Journal of Medicinal Chemistry, 2011, 46, 1404-1414.	5.5	45
104	Clustered patterns of species origins of nature-derived drugs and clues for future bioprospecting. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 12943-12948.	7.1	223
105	Simulating EGFR-ERK Signaling Control by Scaffold Proteins KSR and MP1 Reveals Differential Ligand-Sensitivity Co-Regulated by Cbl-CIN85 and Endophilin. PLoS ONE, 2011, 6, e22933.	2.5	9
106	Identification of small molecule aggregators from large compound libraries by support vector machines. Journal of Computational Chemistry, 2010, 31, 752-763.	3.3	26
107	An insight into the opening path to semi-open conformation of HIV-1 protease by molecular dynamics simulation. Aids, 2010, 24, 1121-1125.	2.2	3
108	In-Silico Approaches to Multi-target Drug Discovery. Pharmaceutical Research, 2010, 27, 739-749.	3.5	135

#	Article	IF	Citations
109	Virtual screening prediction of new potential organocatalysts for direct aldol reactions. Journal of Molecular Catalysis A, 2010, 319, 114-118.	4.8	1
110	Update of TTD: Therapeutic Target Database. Nucleic Acids Research, 2010, 38, D787-D791.	14.5	243
111	Computational model of VEGF, thrombin and histamine signalling network. , 2010, , .		0
112	Cancer informatics for the clinician: An interaction database for chemotherapy regimens and antiepileptic drugs. Seizure: the Journal of the British Epilepsy Association, 2010, 19, 59-67.	2.0	8
113	Analytical description of Ogston-regime biomolecule separation using nanofilters and nanopores. Physical Review E, 2009, 80, 041911.	2.1	7
114	What Are Next Generation Innovative Therapeutic Targets? Clues from Genetic, Structural, Physicochemical, and Systems Profiles of Successful Targets. Journal of Pharmacology and Experimental Therapeutics, 2009, 330, 304-315.	2.5	47
115	Simulation of crosstalk between small GTPase RhoA and EGFR-ERK signaling pathway via MEKK1. Bioinformatics, 2009, 25, 358-364.	4.1	29
116	Pathway sensitivity analysis for detecting proâ€proliferation activities of oncogenes and tumor suppressors of epidermal growth factor receptorâ€extracellular signalâ€regulated protein kinase pathway at altered protein levels. Cancer, 2009, 115, 4246-4263.	4.1	7
117	Transport of biomolecules in asymmetric nanofilter arrays. Analytical and Bioanalytical Chemistry, 2009, 394, 427-435.	3.7	14
118	Mechanisms of drug combinations: interaction and network perspectives. Nature Reviews Drug Discovery, 2009, 8, 111-128.	46.4	779
119	Genome-scale search of tumor-specific antigens by collective analysis of mutations, expressions and T-cell recognition. Molecular Immunology, 2009, 46, 1824-1829.	2.2	7
120	Dissipative particle dynamics simulations of electroosmotic flow in nano-fluidic devices. Microfluidics and Nanofluidics, 2008, 4, 219-225.	2.2	47
121	Continuum transport model of Ogston sieving in patterned nanofilter arrays for separation of rodâ€like biomolecules. Electrophoresis, 2008, 29, 329-339.	2.4	21
122	Realistic simulations of combined DNA electrophoretic flow and EOF in nanoâ€fluidic devices. Electrophoresis, 2008, 29, 4880-4886.	2.4	27
123	Simulation of the regulation of EGFR endocytosis and EGFRâ€ERK signaling by endophilinâ€mediated RhoAâ€EGFR crosstalk. FEBS Letters, 2008, 582, 2283-2290.	2.8	31
124	Advances in Machine Learning Prediction of Toxicological Properties and Adverse Drug Reactions of Pharmaceutical Agents. Current Drug Safety, 2008, 3, 100-114.	0.6	5
125	Advances in Exploration of Machine Learning Methods for Predicting Functional Class and Interaction Profiles of Proteins and Peptides Irrespective of Sequence Homology. Current Bioinformatics, 2007, 2, 95-112.	1.5	7
126	Are herb-pairs of traditional Chinese medicine distinguishable from others? Pattern analysis and artificial intelligence classification study of traditionally defined herbal properties. Journal of Ethnopharmacology, 2007, 111, 371-377.	4.1	82

#	Article	IF	Citations
127	Computer prediction of allergen proteins from sequence-derived protein structural and physicochemical properties. Molecular Immunology, 2007, 44, 514-520.	2.2	69
128	Prediction of Functional Class of Proteins and Peptides Irrespective of Sequence Homology by Support Vector Machines. Bioinformatics and Biology Insights, 2007, 1, BBI.S315.	2.0	8
129	Does Drug-target Have a Likeness?. Methods of Information in Medicine, 2007, 46, 360-366.	1.2	13
130	Learning the drug targetâ€likeness of a protein. Proteomics, 2007, 7, 4255-4263.	2.2	29
131	Efficacy of different protein descriptors in predicting protein functional families. BMC Bioinformatics, 2007, 8, 300.	2.6	66
132	Support vector machines approach for predicting druggable proteins: recent progress in its exploration and investigation of its usefulness. Drug Discovery Today, 2007, 12, 304-313.	6.4	69
133	In silico search of putative adverse drug reaction related proteins as a potential tool for facilitating drug adverse effect prediction. Toxicology Letters, 2006, 164, 104-112.	0.8	49
134	Recent progresses in the application of machine learning approach for predicting protein functional class independent of sequence similarity. Proteomics, 2006, 6, 4023-4037.	2.2	72
135	Super Paramagnetic Clustering of DNA Sequences. Journal of Biological Physics, 2006, 32, 11-25.	1.5	2
136	MHC-BPS: MHC-binder prediction server for identifying peptides of flexible lengths from sequence-derived physicochemical properties. Immunogenetics, 2006, 58, 607-613.	2.4	27
137	Progress and problems in the exploration of therapeutic targets. Drug Discovery Today, 2006, 11, 412-420.	6.4	60
138	Tannic Acid, a Potent Inhibitor of Epidermal Growth Factor Receptor Tyrosine Kinase. Journal of Biochemistry, 2006, 139, 495-502.	1.7	31
139	MILITARY VEHICLE CLASSIFICATION VIA ACOUSTIC AND SEISMIC SIGNALS USING STATISTICAL LEARNING METHODS. International Journal of Modern Physics C, 2006, 17, 197-212.	1.7	6
140	Computer prediction of drug resistance mutations in proteins. Drug Discovery Today, 2005, 10, 521-529.	6.4	58
141	Effect of training datasets on support vector machine prediction of protein-protein interactions. Proteomics, 2005, 5, 876-884.	2.2	73
142	Prediction of Putative Adverse Drug Reaction-Related Proteins from Primary Sequence by Support Vector Machines. Pharmaceutical Medicine, 2005, 19, 317-322.	0.4	1
143	Effect of Selection of Molecular Descriptors on the Prediction of Bloodâ^'Brain Barrier Penetrating and Nonpenetrating Agents by Statistical Learning Methods. Journal of Chemical Information and Modeling, 2005, 45, 1376-1384.	5.4	145
144	Prediction of RNA-binding proteins from primary sequence by a support vector machine approach. Rna, 2004, 10, 355-368.	3.5	109

#	Article	IF	Citations
145	Density Functional Theory Studies on Structure, Spectra, and Electronic Properties of 3,7-Dinitrodibenzobromolium Cation and Chloride. Journal of Physical Chemistry A, 2004, 108, 7596-7602.	2.5	1
146	Drug Adverse Reaction Target Database (DART). Drug Safety, 2003, 26, 685-690.	3.2	67
147	Can an in silico drug-target search method be used to probe potential mechanisms of medicinal plant ingredients?. Natural Product Reports, 2003, 20, 432.	10.3	70
148	Inhibition of epidermal growth factor receptor tyrosine kinase by chalcone derivatives. BBA - Proteins and Proteomics, 2001, 1550, 144-152.	2.1	86
149	Current QSAR Techniques for Toxicology. , 0, , 217-238.		5