

Feixiong Cheng

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2994228/publications.pdf>

Version: 2024-02-01

145
papers

12,267
citations

44444

50
h-index

33145

104
g-index

159
all docs

159
docs citations

159
times ranked

17267
citing authors

#	ARTICLE	IF	CITATIONS
1	A rational design of a multi-epitope vaccine against SARS-CoV-2 which accounts for the glycan shield of the spike glycoprotein. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 7099-7113.	2.0	15
2	Interpretable artificial intelligence and exascale molecular dynamics simulations to reveal kinetics: Applications to Alzheimer's disease. <i>Current Opinion in Structural Biology</i> , 2022, 72, 103-113.	2.6	13
3	Aging-related cell type-specific pathophysiologic immune responses that exacerbate disease severity in aged COVID-19 patients. <i>Aging Cell</i> , 2022, 21, e13544.	3.0	11
4	Artificial intelligence framework identifies candidate targets for drug repurposing in Alzheimer's disease. <i>Alzheimer's Research and Therapy</i> , 2022, 14, 7.	3.0	42
5	Establishing an interdisciplinary research team for cardio-oncology artificial intelligence informatics precision and health equity. <i>American Heart Journal Plus</i> , 2022, 13, 100094.	0.3	8
6	Deep learning for drug repurposing: Methods, databases, and applications. <i>Wiley Interdisciplinary Reviews: Computational Molecular Science</i> , 2022, 12, .	6.2	48
7	Artificial Intelligence in Alzheimer's Drug Discovery. , 2022, , 62-72.		2
8	Shape shifting: The multiple conformational substates of the <sc>PTEN</sc> N-terminal <sc>PIP₂</sc> binding domain. <i>Protein Science</i> , 2022, 31, e4308.	3.1	6
9	Peripheral sTREM2-Related Inflammatory Activity Alterations in Early-Stage Alzheimer's Disease. <i>Journal of Immunology</i> , 2022, 208, 2283-2299.	0.4	2
10	Open Structural Data in Precision Medicine. <i>Annual Review of Biomedical Data Science</i> , 2022, 5, 95-117.	2.8	7
11	Association Between Atrial Uptake on Cardiac Scintigraphy With Technetium-99m-Pyrophosphate Labeled Bone-Seeking Tracers and Atrial Fibrillation. <i>Circulation: Cardiovascular Imaging</i> , 2022, 15, e013829.	1.3	2
12	Editorial overview: Artificial intelligence (AI) methodologies in structural biology. <i>Current Opinion in Structural Biology</i> , 2022, , 102387.	2.6	3
13	Pik3c3 deficiency in myeloid cells imparts partial resistance to experimental autoimmune encephalomyelitis associated with reduced IL-1 β production. <i>Cellular and Molecular Immunology</i> , 2021, 18, 2024-2039.	4.8	12
14	Reprogramming immunosuppressive myeloid cells facilitates immunotherapy for colorectal cancer. <i>EMBO Molecular Medicine</i> , 2021, 13, e12798.	3.3	59
15	A new precision medicine initiative at the dawn of exascale computing. <i>Signal Transduction and Targeted Therapy</i> , 2021, 6, 3.	7.1	31
16	A network-based deep learning methodology for stratification of tumor mutations. <i>Bioinformatics</i> , 2021, 37, 82-88.	1.8	10
17	AlzGPS: a genome-wide positioning systems platform to catalyze multi-omics for Alzheimer's drug discovery. <i>Alzheimer's Research and Therapy</i> , 2021, 13, 24.	3.0	44
18	Comprehensive characterization of protein-protein interactions perturbed by disease mutations. <i>Nature Genetics</i> , 2021, 53, 342-353.	9.4	109

#	ARTICLE	IF	CITATIONS
19	The Epidemiological and Mechanistic Understanding of the Neurological Manifestations of COVID-19: A Comprehensive Meta-Analysis and a Network Medicine Observation. <i>Frontiers in Neuroscience</i> , 2021, 15, 606926.	1.4	6
20	Multimodal single-cell/nucleus RNA sequencing data analysis uncovers molecular networks between disease-associated microglia and astrocytes with implications for drug repurposing in Alzheimer's disease. <i>Genome Research</i> , 2021, 31, 1900-1912.	2.4	53
21	Glutathione ethyl ester reverses the deleterious effects of fentanyl on ventilation and arterial blood-gas chemistry while prolonging fentanyl-induced analgesia. <i>Scientific Reports</i> , 2021, 11, 6985.	1.6	18
22	Reducing acetylated tau is neuroprotective in brain injury. <i>Cell</i> , 2021, 184, 2715-2732.e23.	13.5	91
23	Identifying miRNAs in multiple sclerosis gray matter lesions that correlate with atrophy measures. <i>Annals of Clinical and Translational Neurology</i> , 2021, 8, 1279-1291.	1.7	12
24	A retrospective analysis of cardiovascular adverse events associated with immune checkpoint inhibitors. <i>Cardio-Oncology</i> , 2021, 7, 19.	0.8	14
25	Systemic Administration of Tempol Attenuates the Cardiorespiratory Depressant Effects of Fentanyl. <i>Frontiers in Pharmacology</i> , 2021, 12, 690407.	1.6	14
26	Network medicine links SARS-CoV-2/COVID-19 infection to brain microvascular injury and neuroinflammation in dementia-like cognitive impairment. <i>Alzheimer's Research and Therapy</i> , 2021, 13, 110.	3.0	108
27	Multimodal single-cell omics analysis identifies epithelium-immune cell interactions and immune vulnerability associated with sex differences in COVID-19. <i>Signal Transduction and Targeted Therapy</i> , 2021, 6, 292.	7.1	13
28	Cardiac risk stratification in cancer patients: A longitudinal patient-patient network analysis. <i>PLoS Medicine</i> , 2021, 18, e1003736.	3.9	19
29	Tempol Reverses the Negative Effects of Morphine on Arterial Blood-Gas Chemistry and Tissue Oxygen Saturation in Freely-Moving Rats. <i>Frontiers in Pharmacology</i> , 2021, 12, 749084.	1.6	14
30	My personal mutanome: a computational genomic medicine platform for searching network perturbing alleles linking genotype to phenotype. <i>Genome Biology</i> , 2021, 22, 53.	3.8	11
31	Endophenotype-based in silico network medicine discovery combined with insurance record data mining identifies sildenafil as a candidate drug for Alzheimer's disease. <i>Nature Aging</i> , 2021, 1, 1175-1188.	5.3	87
32	Computational network biology: Data, models, and applications. <i>Physics Reports</i> , 2020, 846, 1-66.	10.3	126
33	Temporal Trends of Cardiac Outcomes and Impact on Survival in Patients With Cancer. <i>American Journal of Cardiology</i> , 2020, 137, 118-124.	0.7	4
34	Importance of scientific collaboration in contemporary drug discovery and development: a detailed network analysis. <i>BMC Biology</i> , 2020, 18, 138.	1.7	10
35	New insights into genetic susceptibility of COVID-19: an ACE2 and TMPRSS2 polymorphism analysis. <i>BMC Medicine</i> , 2020, 18, 216.	2.3	304
36	iDrug: Integration of drug repositioning and drug-target prediction via cross-network embedding. <i>PLoS Computational Biology</i> , 2020, 16, e1008040.	1.5	51

#	ARTICLE	IF	CITATIONS
37	Repurpose Open Data to Discover Therapeutics for COVID-19 Using Deep Learning. <i>Journal of Proteome Research</i> , 2020, 19, 4624-4636.	1.8	183
38	Harnessing endophenotypes and network medicine for Alzheimer's drug repurposing. <i>Medicinal Research Reviews</i> , 2020, 40, 2386-2426.	5.0	61
39	Impact of timing of atrial fibrillation, CHA2DS2-VASc score and cancer therapeutics on mortality in oncology patients. <i>Open Heart</i> , 2020, 7, e001412.	0.9	3
40	Phosphorylation of PLC β 1 by EphA2 Receptor Tyrosine Kinase Promotes Tumor Growth in Lung Cancer. <i>Molecular Cancer Research</i> , 2020, 18, 1735-1743.	1.5	8
41	Artificial intelligence in COVID-19 drug repurposing. <i>The Lancet Digital Health</i> , 2020, 2, e667-e676.	5.9	349
42	Repurposing of FDA-Approved Toremifene to Treat COVID-19 by Blocking the Spike Glycoprotein and NSP14 of SARS-CoV-2. <i>Journal of Proteome Research</i> , 2020, 19, 4670-4677.	1.8	55
43	Comprehensive germline genomic profiles of children, adolescents and young adults with solid tumors. <i>Nature Communications</i> , 2020, 11, 2206.	5.8	38
44	Epilepsy subtype-specific copy number burden observed in a genome-wide study of 17,458 subjects. <i>Brain</i> , 2020, 143, 2106-2118.	3.7	47
45	Recent Advances in Systems and Network Medicine: Meeting Report from the First International Conference in Systems and Network Medicine. <i>Systems Medicine (New Rochelle, N Y)</i> , 2020, 3, 22-35.	1.4	7
46	Network-based drug repurposing for novel coronavirus 2019-nCoV/SARS-CoV-2. <i>Cell Discovery</i> , 2020, 6, 14.	3.1	1,258
47	Applications of artificial intelligence in multimodality cardiovascular imaging: A state-of-the-art review. <i>Progress in Cardiovascular Diseases</i> , 2020, 63, 367-376.	1.6	40
48	Pharmacogenomics meets precision cardio-oncology: is there synergistic potential?. <i>Human Molecular Genetics</i> , 2020, 29, R177-R185.	1.4	1
49	Pharmacogenomics for immunotherapy and immune-related cardiotoxicity. <i>Human Molecular Genetics</i> , 2020, 29, R186-R196.	1.4	7
50	Individualized genetic network analysis reveals new therapeutic vulnerabilities in 6,700 cancer genomes. <i>PLoS Computational Biology</i> , 2020, 16, e1007701.	1.5	32
51	In Silico Insights into Protein-Protein Interaction Disruptive Mutations in the PCSK9-LDLR Complex. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1550.	1.8	13
52	Target identification among known drugs by deep learning from heterogeneous networks. <i>Chemical Science</i> , 2020, 11, 1775-1797.	3.7	193
53	Network-based prediction of drug-target interactions using an arbitrary-order proximity embedded deep forest. <i>Bioinformatics</i> , 2020, 36, 2805-2812.	1.8	101
54	Mechanical forces induce an asthma gene signature in healthy airway epithelial cells. <i>Scientific Reports</i> , 2020, 10, 966.	1.6	34

#	ARTICLE	IF	CITATIONS
55	Suppression of the SLC7A11/glutathione axis causes synthetic lethality in KRAS-mutant lung adenocarcinoma. <i>Journal of Clinical Investigation</i> , 2020, 130, 1752-1766.	3.9	200
56	A network medicine approach to investigation and population-based validation of disease manifestations and drug repurposing for COVID-19. <i>PLoS Biology</i> , 2020, 18, e3000970.	2.6	139
57	COVID-19 treatment: Combining anti-inflammatory and antiviral therapeutics using a network-based approach. <i>Cleveland Clinic Journal of Medicine</i> , 2020, , .	0.6	21
58	Title is missing!. , 2020, 18, e3000970.		0
59	Title is missing!. , 2020, 18, e3000970.		0
60	Title is missing!. , 2020, 18, e3000970.		0
61	Title is missing!. , 2020, 18, e3000970.		0
62	Title is missing!. , 2020, 18, e3000970.		0
63	Title is missing!. , 2020, 18, e3000970.		0
64	Title is missing!. , 2020, 18, e3000970.		0
65	A genome-wide positioning systems network algorithm for in silico drug repurposing. <i>Nature Communications</i> , 2019, 10, 3476.	5.8	134
66	A Systems Pharmacology Approach Uncovers Wogonoside as an Angiogenesis Inhibitor of Triple-Negative Breast Cancer by Targeting Hedgehog Signaling. <i>Cell Chemical Biology</i> , 2019, 26, 1143-1158.e6.	2.5	53
67	Cardio-oncology: Network-Based Prediction of Cancer Therapy-Induced Cardiotoxicity. <i>Challenges and Advances in Computational Chemistry and Physics</i> , 2019, , 75-97.	0.6	1
68	deepDR: a network-based deep learning approach to <i>in silico</i> drug repositioning. <i>Bioinformatics</i> , 2019, 35, 5191-5198.	1.8	343
69	Conformational Dynamics and Allosteric Regulation Landscapes of Germline PTEN Mutations Associated with Autism Compared to Those Associated with Cancer. <i>American Journal of Human Genetics</i> , 2019, 104, 861-878.	2.6	45
70	PTEN Mutations Trigger Resistance to Immunotherapy. <i>Trends in Molecular Medicine</i> , 2019, 25, 461-463.	3.5	20
71	Network-based prediction of drug combinations. <i>Nature Communications</i> , 2019, 10, 1197.	5.8	437
72	A Bayesian framework that integrates multi-omics data and gene networks predicts risk genes from schizophrenia GWAS data. <i>Nature Neuroscience</i> , 2019, 22, 691-699.	7.1	118

#	ARTICLE	IF	CITATIONS
73	Review: Precision medicine and driver mutations: Computational methods, functional assays and conformational principles for interpreting cancer drivers. PLoS Computational Biology, 2019, 15, e1006658.	1.5	83
74	A component overlapping attribute clustering (COAC) algorithm for single-cell RNA sequencing data analysis and potential pathobiological implications. PLoS Computational Biology, 2019, 15, e1006772.	1.5	14
75	Deep Learning-Based Prediction of Drug-Induced Cardiotoxicity. Journal of Chemical Information and Modeling, 2019, 59, 1073-1084.	2.5	123
76	A network-based approach to uncover microRNA-mediated disease comorbidities and potential pathobiological implications. Npj Systems Biology and Applications, 2019, 5, 41.	1.4	24
77	Precision medicine review: rare driver mutations and their biophysical classification. Biophysical Reviews, 2019, 11, 5-19.	1.5	43
78	In Silico Oncology Drug Repositioning and Polypharmacology. Methods in Molecular Biology, 2019, 1878, 243-261.	0.4	48
79	Quantitative and systems pharmacology 4. Network-based analysis of drug pleiotropy on coronary artery disease. European Journal of Medicinal Chemistry, 2019, 161, 192-204.	2.6	25
80	Personal Mutanomes Meet Modern Oncology Drug Discovery and Precision Health. Pharmacological Reviews, 2019, 71, 1-19.	7.1	47
81	In silico polypharmacology of natural products. Briefings in Bioinformatics, 2018, 19, 1153-1171.	3.2	95
82	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. Cell Reports, 2018, 23, 255-269.e4.	2.9	204
83	Pulmonary Comorbidity in Lung Cancer. Trends in Molecular Medicine, 2018, 24, 239-241.	3.5	8
84	<i>In Silico</i> Pharmacoeconomic Evaluation of Drug-Induced Cardiovascular Complications Using Combined Classifiers. Journal of Chemical Information and Modeling, 2018, 58, 943-956.	2.5	37
85	Quantitative and systems pharmacology 2. In silico polypharmacology of G protein-coupled receptor ligands via network-based approaches. Pharmacological Research, 2018, 129, 400-413.	3.1	28
86	Repurposing sertraline sensitizes non-small cell lung cancer cells to erlotinib by inducing autophagy. JCI Insight, 2018, 3, .	2.3	51
87	KRAS Activating Signaling Triggers Arteriovenous Malformations. Trends in Biochemical Sciences, 2018, 43, 481-483.	3.7	17
88	An integrative functional genomics framework for effective identification of novel regulatory variants in genome-phenome studies. Genome Medicine, 2018, 10, 7.	3.6	29
89	SDTNBI: an integrated network and chemoinformatics tool for systematic prediction of drug-target interactions and drug repositioning. Briefings in Bioinformatics, 2017, 18, bbw012.	3.2	102
90	Drug Repurposing of Histone Deacetylase Inhibitors That Alleviate Neutrophilic Inflammation in Acute Lung Injury and Idiopathic Pulmonary Fibrosis via Inhibiting Leukotriene A4 Hydrolase and Blocking LTB4 Biosynthesis. Journal of Medicinal Chemistry, 2017, 60, 1817-1828.	2.9	30

#	ARTICLE	IF	CITATIONS
91	Extracellular Matrix/Integrin Signaling Promotes Resistance to Combined Inhibition of HER2 and PI3K in HER2+ Breast Cancer. <i>Cancer Research</i> , 2017, 77, 3280-3292.	0.4	76
92	Tissue-Specific Signaling Networks Rewired by Major Somatic Mutations in Human Cancer Revealed by Proteome-Wide Discovery. <i>Cancer Research</i> , 2017, 77, 2810-2821.	0.4	29
93	Autoimmune Cardiotoxicity of Cancer Immunotherapy. <i>Trends in Immunology</i> , 2017, 38, 77-78.	2.9	32
94	Proteome-Scale Investigation of Protein Allosteric Regulation Perturbed by Somatic Mutations in 7,000 Cancer Genomes. <i>American Journal of Human Genetics</i> , 2017, 100, 5-20.	2.6	72
95	Quantitative and Systems Pharmacology. 1. <i>In Silico</i> Prediction of Drug-Target Interactions of Natural Products Enables New Targeted Cancer Therapy. <i>Journal of Chemical Information and Modeling</i> , 2017, 57, 2657-2671.	2.5	76
96	Inhibition of histone deacetylases sensitizes EGF receptor-tyrosine kinase inhibitor-resistant non-small cell lung cancer cells to erlotinib <i>in vitro</i> and <i>in vivo</i> . <i>British Journal of Pharmacology</i> , 2017, 174, 3608-3622.	2.7	34
97	Quantitative and Systems Pharmacology 3. Network-Based Identification of New Targets for Natural Products Enables Potential Uses in Aging-Associated Disorders. <i>Frontiers in Pharmacology</i> , 2017, 8, 747.	1.6	38
98	<i>In silico</i> Prediction of Drug Induced Liver Toxicity Using Substructure Pattern Recognition Method. <i>Molecular Informatics</i> , 2016, 35, 136-144.	1.4	75
99	Suppression of KRas-mutant cancer through the combined inhibition of KRAS with PLK1 and ROCK. <i>Nature Communications</i> , 2016, 7, 11363.	5.8	74
100	A network-based drug repositioning infrastructure for precision cancer medicine through targeting significantly mutated genes in the human cancer genomes. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2016, 23, 681-691.	2.2	46
101	Drug Repurposing: New Treatments for Zika Virus Infection?. <i>Trends in Molecular Medicine</i> , 2016, 22, 919-921.	3.5	71
102	<i>In silico</i> prediction of chemical mechanism of action via an improved network-based inference method. <i>British Journal of Pharmacology</i> , 2016, 173, 3372-3385.	2.7	73
103	Transcriptome- and proteome-oriented identification of dysregulated eIF4G, STAT3, and Hippo pathways altered by PIK3CA H1047R in HER2/ER-positive breast cancer. <i>Breast Cancer Research and Treatment</i> , 2016, 160, 457-474.	1.1	13
104	Investigating cellular network heterogeneity and modularity in cancer: a network entropy and unbalanced motif approach. <i>BMC Systems Biology</i> , 2016, 10, 65.	3.0	36
105	Gender Dimorphism Creates Divergent Cancer Susceptibilities. <i>Trends in Cancer</i> , 2016, 2, 325-326.	3.8	6
106	Individualized network-based drug repositioning infrastructure for precision oncology in the panomics era. <i>Briefings in Bioinformatics</i> , 2016, 18, bbw051.	3.2	57
107	Systematic Prioritization of Druggable Mutations in ~45000 Genomes Across 16 Cancer Types Using a Structural Genomics-based Approach. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 642-656.	2.5	43
108	ccmGDB: a database for cancer cell metabolism genes. <i>Nucleic Acids Research</i> , 2016, 44, D959-D968.	6.5	41

#	ARTICLE	IF	CITATIONS
109	Systems Biology-Based Investigation of Cellular Antiviral Drug Targets Identified by Gene-Trap Insertional Mutagenesis. <i>PLoS Computational Biology</i> , 2016, 12, e1005074.	1.5	52
110	Network-based identification of microRNAs as potential pharmacogenomic biomarkers for anticancer drugs. <i>Oncotarget</i> , 2016, 7, 45584-45596.	0.8	85
111	Regulation rewiring analysis reveals mutual regulation between STAT1 and miR-155-5p in tumor immunosurveillance in seven major cancers. <i>Scientific Reports</i> , 2015, 5, 12063.	1.6	19
112	FXR antagonism of NSAIDs contributes to drug-induced liver injury identified by systems pharmacology approach. <i>Scientific Reports</i> , 2015, 5, 8114.	1.6	44
113	In silico prediction of chemical toxicity on avian species using chemical category approaches. <i>Chemosphere</i> , 2015, 122, 280-287.	4.2	41
114	SoNar, a Highly Responsive NAD ⁺ /NADH Sensor, Allows High-Throughput Metabolic Screening of Anti-tumor Agents. <i>Cell Metabolism</i> , 2015, 21, 777-789.	7.2	311
115	Biomarker-based drug safety assessment in the age of systems pharmacology: from foundational to regulatory science. <i>Biomarkers in Medicine</i> , 2015, 9, 1241-1252.	0.6	28
116	A cross-cancer differential co-expression network reveals microRNA-regulated oncogenic functional modules. <i>Molecular BioSystems</i> , 2015, 11, 3244-3252.	2.9	9
117	A Gene Gravity Model for the Evolution of Cancer Genomes: A Study of 3,000 Cancer Genomes across 9 Cancer Types. <i>PLoS Computational Biology</i> , 2015, 11, e1004497.	1.5	65
118	Functional consequences of somatic mutations in cancer using protein pocket-based prioritization approach. <i>Genome Medicine</i> , 2014, 6, 81.	3.6	31
119	Machine learning-based prediction of drug-drug interactions by integrating drug phenotypic, therapeutic, chemical, and genomic properties. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2014, 21, e278-e286.	2.2	264
120	Computational models to predict endocrine-disrupting chemical binding with androgen or oestrogen receptors. <i>Ecotoxicology and Environmental Safety</i> , 2014, 110, 280-287.	2.9	50
121	Studying Tumorigenesis through Network Evolution and Somatic Mutational Perturbations in the Cancer Interactome. <i>Molecular Biology and Evolution</i> , 2014, 31, 2156-2169.	3.5	79
122	<i>In Silico</i> Prediction of Chemical Acute Oral Toxicity Using Multi-Classification Methods. <i>Journal of Chemical Information and Modeling</i> , 2014, 54, 1061-1069.	2.5	140
123	Computational prediction of microRNA networks incorporating environmental toxicity and disease etiology. <i>Scientific Reports</i> , 2014, 4, 5576.	1.6	51
124	Quantitative network mapping of the human kinome interactome reveals new clues for rational kinase inhibitor discovery and individualized cancer therapy. <i>Oncotarget</i> , 2014, 5, 3697-3710.	0.8	96
125	Prediction of human genes and diseases targeted by xenobiotics using predictive toxicogenomic-derived models (PTDMs). <i>Molecular BioSystems</i> , 2013, 9, 1316.	2.9	28
126	Adverse Drug Events: Database Construction and in Silico Prediction. <i>Journal of Chemical Information and Modeling</i> , 2013, 53, 744-752.	2.5	116

#	ARTICLE	IF	CITATIONS
127	Prediction of Polypharmacological Profiles of Drugs by the Integration of Chemical, Side Effect, and Therapeutic Space. <i>Journal of Chemical Information and Modeling</i> , 2013, 53, 753-762.	2.5	86
128	In Silico ADMET Prediction: Recent Advances, Current Challenges and Future Trends. <i>Current Topics in Medicinal Chemistry</i> , 2013, 13, 1273-1289.	1.0	181
129	In Silico Assessment of Chemical Biodegradability. <i>Journal of Chemical Information and Modeling</i> , 2012, 52, 655-669.	2.5	87
130	Unbinding Pathways of GW4064 from Human Farnesoid X Receptor As Revealed by Molecular Dynamics Simulations. <i>Journal of Chemical Information and Modeling</i> , 2012, 52, 3043-3052.	2.5	22
131	In silico Prediction of Chemical Ames Mutagenicity. <i>Journal of Chemical Information and Modeling</i> , 2012, 52, 2840-2847.	2.5	163
132	admetSAR: A Comprehensive Source and Free Tool for Assessment of Chemical ADMET Properties. <i>Journal of Chemical Information and Modeling</i> , 2012, 52, 3099-3105.	2.5	1,439
133	Comparative pharmacophore modeling of human adenosine receptor A1 and A3 antagonists. <i>Science China Chemistry</i> , 2012, 55, 2407-2418.	4.2	2
134	Prediction of Drug-Target Interactions and Drug Repositioning via Network-Based Inference. <i>PLoS Computational Biology</i> , 2012, 8, e1002503.	1.5	674
135	Investigation of Indazole Unbinding Pathways in CYP2E1 by Molecular Dynamics Simulations. <i>PLoS ONE</i> , 2012, 7, e33500.	1.1	32
136	Prediction of Chemical-Protein Interactions Network with Weighted Network-Based Inference Method. <i>PLoS ONE</i> , 2012, 7, e41064.	1.1	86
137	Prediction of chemical-protein interactions: multitarget-QSAR versus computational chemogenomic methods. <i>Molecular BioSystems</i> , 2012, 8, 2373.	2.9	100
138	Insights into Molecular Basis of Cytochrome P450 Inhibitory Promiscuity of Compounds. <i>Journal of Chemical Information and Modeling</i> , 2011, 51, 2482-2495.	2.5	60
139	Classification of Cytochrome P450 Inhibitors and Noninhibitors Using Combined Classifiers. <i>Journal of Chemical Information and Modeling</i> , 2011, 51, 996-1011.	2.5	155
140	In silico prediction of <i>Tetrahymena pyriformis</i> toxicity for diverse industrial chemicals with substructure pattern recognition and machine learning methods. <i>Chemosphere</i> , 2011, 82, 1636-1643.	4.2	75
141	Computational Insights into Ligand Selectivity of Estrogen Receptors from Pharmacophore Modeling. <i>Molecular Informatics</i> , 2011, 30, 539-549.	1.4	10
142	Insights into binding modes of adenosine A2B antagonists with ligand-based and receptor-based methods. <i>European Journal of Medicinal Chemistry</i> , 2010, 45, 3459-3471.	2.6	29
143	Pharmacophore modeling of human adenosine receptor A2A antagonists. <i>Journal of Molecular Modeling</i> , 2010, 16, 1867-1876.	0.8	12
144	Estimation of ADME Properties with Substructure Pattern Recognition. <i>Journal of Chemical Information and Modeling</i> , 2010, 50, 1034-1041.	2.5	266

#	ARTICLE	IF	CITATIONS
145	Target Identification Among Known Drugs by Deep Learning from Heterogeneous Networks. SSRN Electronic Journal, 0, , .	0.4	3