

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3226761/publications.pdf>

Version: 2024-02-01

137
papers

12,854
citations

34076

52
h-index

27389

106
g-index

154
all docs

154
docs citations

154
times ranked

15772
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Network-based drug repurposing for novel coronavirus 2019-nCoV/SARS-CoV-2. <i>Cell Discovery</i> , 2020, 6, 14.	3.1	1,258
3	Prediction of Drug-Target Interactions and Drug Repositioning via Network-Based Inference. <i>PLoS Computational Biology</i> , 2012, 8, e1002503.	1.5	674
4	Network-based prediction of drug combinations. <i>Nature Communications</i> , 2019, 10, 1197.	5.8	437
5	Network-based approach to prediction and population-based validation of in silico drug repurposing. <i>Nature Communications</i> , 2018, 9, 2691.	5.8	351
6	Artificial intelligence in COVID-19 drug repurposing. <i>The Lancet Digital Health</i> , 2020, 2, e667-e676.	5.9	349
7	deepDR: a network-based deep learning approach to in silico drug repositioning. <i>Bioinformatics</i> , 2019, 35, 5191-5198.	1.8	343
8	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
9	New insights into genetic susceptibility of COVID-19: an ACE2 and TMPRSS2 polymorphism analysis. <i>BMC Medicine</i> , 2020, 18, 216.	2.3	304
10	Estimation of ADME Properties with Substructure Pattern Recognition. <i>Journal of Chemical Information and Modeling</i> , 2010, 50, 1034-1041.	2.5	266
11	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
12	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
13	Target identification among known drugs by deep learning from heterogeneous networks. <i>Chemical Science</i> , 2020, 11, 1775-1797.	3.7	193
14	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
15	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
16	In silico Prediction of Chemical Ames Mutagenicity. <i>Journal of Chemical Information and Modeling</i> , 2012, 52, 2840-2847.	2.5	163
17	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
18	In Silico 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

#	ARTICLE	IF	CITATIONS
19	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
20	Myeloid-Derived Suppressor Cell Subsets Drive Glioblastoma Growth in a Sex-Specific Manner. <i>Cancer Discovery</i> , 2020, 10, 1210-1225.	7.7	138
21	A genome-wide positioning systems network algorithm for in silico drug repurposing. <i>Nature Communications</i> , 2019, 10, 3476.	5.8	134
22	Computational network biology: Data, models, and applications. <i>Physics Reports</i> , 2020, 846, 1-66.	10.3	126
23	Deep Learning-Based Prediction of Drug-Induced Cardiotoxicity. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 1073-1084.	2.5	123
24	Advances in computational approaches for prioritizing driver mutations and significantly mutated genes in cancer genomes. <i>Briefings in Bioinformatics</i> , 2016, 17, 642-656.	3.2	120
25	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
26	Adverse Drug Events: Database Construction and in Silico Prediction. <i>Journal of Chemical Information and Modeling</i> , 2013, 53, 744-752.	2.5	116
27	Comprehensive characterization of protein-protein interactions perturbed by disease mutations. <i>Nature Genetics</i> , 2021, 53, 342-353.	9.4	109
28	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
29	SDTNBI: an integrated network and cheminformatics tool for systematic prediction of drug-target interactions and drug repositioning. <i>Briefings in Bioinformatics</i> , 2017, 18, bbw012.	3.2	102
30	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
31	Prediction of chemical-protein interactions: multitarget-QSAR versus computational chemogenomic methods. <i>Molecular BioSystems</i> , 2012, 8, 2373.	2.9	100
32	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
33	In silico polypharmacology of natural products. <i>Briefings in Bioinformatics</i> , 2018, 19, 1153-1171.	3.2	95
34	Reducing acetylated tau is neuroprotective in brain injury. <i>Cell</i> , 2021, 184, 2715-2732.e23.	13.5	91
35	In Silico Assessment of Chemical Biodegradability. <i>Journal of Chemical Information and Modeling</i> , 2012, 52, 655-669.	2.5	87
36	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

#	ARTICLE	IF	CITATIONS
37	Prediction of Chemical-Protein Interactions Network with Weighted Network-Based Inference Method. PLoS ONE, 2012, 7, e41064.	1.1	86
38	Prediction of Polypharmacological Profiles of Drugs by the Integration of Chemical, Side Effect, and Therapeutic Space. Journal of Chemical Information and Modeling, 2013, 53, 753-762.	2.5	86
39	Network-based identification of microRNAs as potential pharmacogenomic biomarkers for anticancer drugs. Oncotarget, 2016, 7, 45584-45596.	0.8	85
40	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
41	Studying Tumorigenesis through Network Evolution and Somatic Mutational Perturbations in the Cancer Interactome. Molecular Biology and Evolution, 2014, 31, 2156-2169.	3.5	79
42	Quantitative and Systems Pharmacology. 1. <i>In Silico</i> Prediction of Drug-Target Interactions of Natural Products Enables New Targeted Cancer Therapy. Journal of Chemical Information and Modeling, 2017, 57, 2657-2671.	2.5	76
43	<i>In silico</i> prediction of <i>Tetrahymena pyriformis</i> toxicity for diverse industrial chemicals with substructure pattern recognition and machine learning methods. Chemosphere, 2011, 82, 1636-1643.	4.2	75
44	<i>In silico</i> Prediction of Drug Induced Liver Toxicity Using Substructure Pattern Recognition Method. Molecular Informatics, 2016, 35, 136-144.	1.4	75
45	Suppression of KRas-mutant cancer through the combined inhibition of KRAS with PLK1 and ROCK. Nature Communications, 2016, 7, 11363.	5.8	74
46	<i>In silico</i> prediction of chemical mechanism of action via an improved network-based inference method. British Journal of Pharmacology, 2016, 173, 3372-3385.	2.7	73
47	Entropy-based consensus clustering for patient stratification. Bioinformatics, 2017, 33, 2691-2698.	1.8	73
48	Proteome-Scale Investigation of Protein Allosteric Regulation Perturbed by Somatic Mutations in 7,000 Cancer Genomes. American Journal of Human Genetics, 2017, 100, 5-20.	2.6	72
49	Drug Repurposing: New Treatments for Zika Virus Infection?. Trends in Molecular Medicine, 2016, 22, 919-921.	3.5	71
50	Pharmacological inhibition of dihydroorotate dehydrogenase induces apoptosis and differentiation in acute myeloid leukemia cells. Haematologica, 2018, 103, 1472-1483.	1.7	66
51	A Gene Gravity Model for the Evolution of Cancer Genomes: A Study of 3,000 Cancer Genomes across 9 Cancer Types. PLoS Computational Biology, 2015, 11, e1004497.	1.5	65
52	Harnessing endophenotypes and network medicine for Alzheimer's drug repurposing. Medicinal Research Reviews, 2020, 40, 2386-2426.	5.0	61
53	Insights into Molecular Basis of Cytochrome P450 Inhibitory Promiscuity of Compounds. Journal of Chemical Information and Modeling, 2011, 51, 2482-2495.	2.5	60
54	Reprogramming immunosuppressive myeloid cells facilitates immunotherapy for colorectal cancer. EMBO Molecular Medicine, 2021, 13, e12798.	3.3	59

#	ARTICLE	IF	CITATIONS
55	Individualized network-based drug repositioning infrastructure for precision oncology in the panomics era. <i>Briefings in Bioinformatics</i> , 2016, 18, bbw051.	3.2	57
56	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
57	Systematic dissection of dysregulated transcription factorâ€“miRNA feed-forward loops across tumor types. <i>Briefings in Bioinformatics</i> , 2016, 17, 996-1008.	3.2	54
58	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
59	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
60	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
61	Computational prediction of microRNA networks incorporating environmental toxicity and disease etiology. <i>Scientific Reports</i> , 2014, 4, 5576.	1.6	51
62	Repurposing sertraline sensitizes nonâ€“small cell lung cancer cells to erlotinib by inducing autophagy. <i>JCI Insight</i> , 2018, 3, .	2.3	51
63	iDrug: Integration of drug repositioning and drug-target prediction via cross-network embedding. <i>PLoS Computational Biology</i> , 2020, 16, e1008040.	1.5	51
64	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
65	In Silico Oncology Drug Repositioning and Polypharmacology. <i>Methods in Molecular Biology</i> , 2019, 1878, 243-261.	0.4	48
66	Deep learning for drug repurposing: Methods, databases, and applications. <i>Wiley Interdisciplinary Reviews: Computational Molecular Science</i> , 2022, 12, .	6.2	48
67	Personal Mutanomes Meet Modern Oncology Drug Discovery and Precision Health. <i>Pharmacological Reviews</i> , 2019, 71, 1-19.	7.1	47
68	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
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	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
71	AlzGPS: a genome-wide positioning systems platform to catalyze multi-omics for Alzheimerâ€™s drug discovery. <i>Alzheimer's Research and Therapy</i> , 2021, 13, 24.	3.0	44
72	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

#	ARTICLE	IF	CITATIONS
73	Precision medicine review: rare driver mutations and their biophysical classification. <i>Biophysical Reviews</i> , 2019, 11, 5-19.	1.5	43
74	Integrative proteomics and phosphoproteomics in pulmonary arterial hypertension. <i>Scientific Reports</i> , 2019, 9, 18623.	1.6	42
75	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
76	In silico prediction of chemical toxicity on avian species using chemical category approaches. <i>Chemosphere</i> , 2015, 122, 280-287.	4.2	41
77	ccmGDB: a database for cancer cell metabolism genes. <i>Nucleic Acids Research</i> , 2016, 44, D959-D968.	6.5	41
78	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
79	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
80	<i>In Silico</i> Pharmacoepidemiologic Evaluation of Drug-Induced Cardiovascular Complications Using Combined Classifiers. <i>Journal of Chemical Information and Modeling</i> , 2018, 58, 943-956.	2.5	37
81	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
82	Mechanical forces induce an asthma gene signature in healthy airway epithelial cells. <i>Scientific Reports</i> , 2020, 10, 966.	1.6	34
83	Machine Learning-Based Risk Assessment for Cancer Therapy-Related Cardiac Dysfunction in 4300 Longitudinal Oncology Patients. <i>Journal of the American Heart Association</i> , 2020, 9, e019628.	1.6	33
84	Investigation of Indazole Unbinding Pathways in CYP2E1 by Molecular Dynamics Simulations. <i>PLoS ONE</i> , 2012, 7, e33500.	1.1	32
85	Autoimmune Cardiotoxicity of Cancer Immunotherapy. <i>Trends in Immunology</i> , 2017, 38, 77-78.	2.9	32
86	Individualized genetic network analysis reveals new therapeutic vulnerabilities in 6,700 cancer genomes. <i>PLoS Computational Biology</i> , 2020, 16, e1007701.	1.5	32
87	Functional consequences of somatic mutations in cancer using protein pocket-based prioritization approach. <i>Genome Medicine</i> , 2014, 6, 81.	3.6	31
88	A new precision medicine initiative at the dawn of exascale computing. <i>Signal Transduction and Targeted Therapy</i> , 2021, 6, 3.	7.1	31
89	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. <i>Journal of Medicinal Chemistry</i> , 2017, 60, 1817-1828.	2.9	30
90	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

#	ARTICLE	IF	CITATIONS
91	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
92	An integrative functional genomics framework for effective identification of novel regulatory variants in genome-wide phenome studies. <i>Genome Medicine</i> , 2018, 10, 7.	3.6	29
93	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
94	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
95	Quantitative and systems pharmacology 2. In silico polypharmacology of G protein-coupled receptor ligands via network-based approaches. <i>Pharmacological Research</i> , 2018, 129, 400-413.	3.1	28
96	Clinical Validation of a Blood-Based Predictive Test for Stratification of Response to Tumor Necrosis Factor Inhibitor Therapies in Rheumatoid Arthritis Patients. <i>Network and Systems Medicine</i> , 2020, 3, 91-104.	2.7	26
97	Quantitative and systems pharmacology 4. Network-based analysis of drug pleiotropy on coronary artery disease. <i>European Journal of Medicinal Chemistry</i> , 2019, 161, 192-204.	2.6	25
98	A network-based approach to uncover microRNA-mediated disease comorbidities and potential pathobiological implications. <i>Npj Systems Biology and Applications</i> , 2019, 5, 41.	1.4	24
99	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
100	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
101	PTEN Mutations Trigger Resistance to Immunotherapy. <i>Trends in Molecular Medicine</i> , 2019, 25, 461-463.	3.5	20
102	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
103	Cardiac risk stratification in cancer patients: A longitudinal patient-patient network analysis. <i>PLoS Medicine</i> , 2021, 18, e1003736.	3.9	19
104	KRAS Activating Signaling Triggers Arteriovenous Malformations. <i>Trends in Biochemical Sciences</i> , 2018, 43, 481-483.	3.7	17
105	Heterogeneous DNA methylation contributes to tumorigenesis through inducing the loss of coexpression connectivity in colorectal cancer. <i>Genes Chromosomes and Cancer</i> , 2015, 54, 110-121.	1.5	15
106	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
107	A component overlapping attribute clustering (COAC) algorithm for single-cell RNA sequencing data analysis and potential pathobiological implications. <i>PLoS Computational Biology</i> , 2019, 15, e1006772.	1.5	14
108	A retrospective analysis of cardiovascular adverse events associated with immune checkpoint inhibitors. <i>Cardio-Oncology</i> , 2021, 7, 19.	0.8	14

#	ARTICLE	IF	CITATIONS
109	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
110	NHLBI-CMREF Workshop Report on Pulmonary Vascular Disease Classification. <i>Journal of the American College of Cardiology</i> , 2021, 77, 2040-2052.	1.2	13
111	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
112	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
113	Pharmacophore modeling of human adenosine receptor A2A antagonists. <i>Journal of Molecular Modeling</i> , 2010, 16, 1867-1876.	0.8	12
114	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
115	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
116	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
117	Computational Insights into Ligand Selectivity of Estrogen Receptors from Pharmacophore Modeling. <i>Molecular Informatics</i> , 2011, 30, 539-549.	1.4	10
118	Importance of scientific collaboration in contemporary drug discovery and development: a detailed network analysis. <i>BMC Biology</i> , 2020, 18, 138.	1.7	10
119	A network-based deep learning methodology for stratification of tumor mutations. <i>Bioinformatics</i> , 2021, 37, 82-88.	1.8	10
120	A cross-cancer differential co-expression network reveals microRNA-regulated oncogenic functional modules. <i>Molecular BioSystems</i> , 2015, 11, 3244-3252.	2.9	9
121	Single-cell network biology characterizes cell type gene regulation for drug repurposing and phenotype prediction in Alzheimer's disease. <i>PLoS Computational Biology</i> , 2022, 18, e1010287.	1.5	9
122	Pulmonary Comorbidity in Lung Cancer. <i>Trends in Molecular Medicine</i> , 2018, 24, 239-241.	3.5	8
123	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
124	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
125	Pharmacogenomics for immunotherapy and immune-related cardiotoxicity. <i>Human Molecular Genetics</i> , 2020, 29, R186-R196.	1.4	7
126	Open Structural Data in Precision Medicine. <i>Annual Review of Biomedical Data Science</i> , 2022, 5, 95-117.	2.8	7

#	ARTICLE	IF	CITATIONS
127	Gender Dimorphism Creates Divergent Cancer Susceptibilities. Trends in Cancer, 2016, 2, 325-326.	3.8	6
128	The Epidemiological and Mechanistic Understanding of the Neurological Manifestations of COVID-19: A Comprehensive Meta-Analysis and a Network Medicine Observation. Frontiers in Neuroscience, 2021, 15, 606926.	1.4	6
129	Metabolic endophenotype associated with right ventricular glucose uptake in pulmonary hypertension. Pulmonary Circulation, 2021, 11, 1-12.	0.8	5
130	Temporal Trends of Cardiac Outcomes and Impact on Survival in Patients With Cancer. American Journal of Cardiology, 2020, 137, 118-124.	0.7	4
131	Impact of timing of atrial fibrillation, CHA2DS2-VASc score and cancer therapeutics on mortality in oncology patients. Open Heart, 2020, 7, e001412.	0.9	3
132	Target Identification Among Known Drugs by Deep Learning from Heterogeneous Networks. SSRN Electronic Journal, 0, , .	0.4	3
133	Editorial overview: Artificial intelligence (AI) methodologies in structural biology. Current Opinion in Structural Biology, 2022, , 102387.	2.6	3
134	Comparative pharmacophore modeling of human adenosine receptor A1 and A3 antagonists. Science China Chemistry, 2012, 55, 2407-2418.	4.2	2
135	Artificial Intelligence in Alzheimer's Drug Discovery. , 2022, , 62-72.		2
136	Cardio-oncology: Network-Based Prediction of Cancer Therapy-Induced Cardiotoxicity. Challenges and Advances in Computational Chemistry and Physics, 2019, , 75-97.	0.6	1
137	Pharmacogenomics meets precision cardio-oncology: is there synergistic potential?. Human Molecular Genetics, 2020, 29, R177-R185.	1.4	1