

Feixiong Cheng

List of Publications by Year in descending order

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Version: 2024-02-01

145
papers

12,267
citations

38738

50
h-index

29154

104
g-index

159
all docs

159
docs citations

159
times ranked

15678
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.	5.4	1,439
2	Network-based drug repurposing for novel coronavirus 2019-nCoV/SARS-CoV-2. <i>Cell Discovery</i> , 2020, 6, 14.	6.7	1,258
3	Prediction of Drug-Target Interactions and Drug Repositioning via Network-Based Inference. <i>PLoS Computational Biology</i> , 2012, 8, e1002503.	3.2	674
4	Network-based prediction of drug combinations. <i>Nature Communications</i> , 2019, 10, 1197.	12.8	437
5	Artificial intelligence in COVID-19 drug repurposing. <i>The Lancet Digital Health</i> , 2020, 2, e667-e676.	12.3	349
6	deepDR: a network-based deep learning approach to <i>in silico</i> drug repositioning. <i>Bioinformatics</i> , 2019, 35, 5191-5198.	4.1	343
7	SoNar, a Highly Responsive NAD ⁺ /NADH Sensor, Allows High-Throughput Metabolic Screening of Anti-tumor Agents. <i>Cell Metabolism</i> , 2015, 21, 777-789.	16.2	311
8	New insights into genetic susceptibility of COVID-19: an ACE2 and TMPRSS2 polymorphism analysis. <i>BMC Medicine</i> , 2020, 18, 216.	5.5	304
9	Estimation of ADME Properties with Substructure Pattern Recognition. <i>Journal of Chemical Information and Modeling</i> , 2010, 50, 1034-1041.	5.4	266
10	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.	4.4	264
11	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. <i>Cell Reports</i> , 2018, 23, 255-269.e4.	6.4	204
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.	8.2	200
13	Target identification among known drugs by deep learning from heterogeneous networks. <i>Chemical Science</i> , 2020, 11, 1775-1797.	7.4	193
14	Repurpose Open Data to Discover Therapeutics for COVID-19 Using Deep Learning. <i>Journal of Proteome Research</i> , 2020, 19, 4624-4636.	3.7	183
15	In Silico ADMET Prediction: Recent Advances, Current Challenges and Future Trends. <i>Current Topics in Medicinal Chemistry</i> , 2013, 13, 1273-1289.	2.1	181
16	In silico Prediction of Chemical Ames Mutagenicity. <i>Journal of Chemical Information and Modeling</i> , 2012, 52, 2840-2847.	5.4	163
17	Classification of Cytochrome P450 Inhibitors and Noninhibitors Using Combined Classifiers. <i>Journal of Chemical Information and Modeling</i> , 2011, 51, 996-1011.	5.4	155
18	<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.	5.4	140

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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.	5.6	139
20	A genome-wide positioning systems network algorithm for in silico drug repurposing. <i>Nature Communications</i> , 2019, 10, 3476.	12.8	134
21	Computational network biology: Data, models, and applications. <i>Physics Reports</i> , 2020, 846, 1-66.	25.6	126
22	Deep Learning-Based Prediction of Drug-Induced Cardiotoxicity. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 1073-1084.	5.4	123
23	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.	14.8	118
24	Adverse Drug Events: Database Construction and in Silico Prediction. <i>Journal of Chemical Information and Modeling</i> , 2013, 53, 744-752.	5.4	116
25	Comprehensive characterization of protein-protein interactions perturbed by disease mutations. <i>Nature Genetics</i> , 2021, 53, 342-353.	21.4	109
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.	6.2	108
27	SDTNBI: an integrated network and chemoinformatics tool for systematic prediction of drug-target interactions and drug repositioning. <i>Briefings in Bioinformatics</i> , 2017, 18, bbw012.	6.5	102
28	Network-based prediction of drug-target interactions using an arbitrary-order proximity embedded deep forest. <i>Bioinformatics</i> , 2020, 36, 2805-2812.	4.1	101
29	Prediction of chemical-protein interactions: multitarget-QSAR versus computational chemogenomic methods. <i>Molecular BioSystems</i> , 2012, 8, 2373.	2.9	100
30	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.	1.8	96
31	In silico polypharmacology of natural products. <i>Briefings in Bioinformatics</i> , 2018, 19, 1153-1171.	6.5	95
32	Reducing acetylated tau is neuroprotective in brain injury. <i>Cell</i> , 2021, 184, 2715-2732.e23.	28.9	91
33	In Silico Assessment of Chemical Biodegradability. <i>Journal of Chemical Information and Modeling</i> , 2012, 52, 655-669.	5.4	87
34	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.	11.6	87
35	Prediction of Chemical-Protein Interactions Network with Weighted Network-Based Inference Method. <i>PLoS ONE</i> , 2012, 7, e41064.	2.5	86
36	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.	5.4	86

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37	Network-based identification of microRNAs as potential pharmacogenomic biomarkers for anticancer drugs. <i>Oncotarget</i> , 2016, 7, 45584-45596.	1.8	85
38	Review: Precision medicine and driver mutations: Computational methods, functional assays and conformational principles for interpreting cancer drivers. <i>PLoS Computational Biology</i> , 2019, 15, e1006658.	3.2	83
39	Studying Tumorigenesis through Network Evolution and Somatic Mutational Perturbations in the Cancer Interactome. <i>Molecular Biology and Evolution</i> , 2014, 31, 2156-2169.	8.9	79
40	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.	0.9	76
41	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.	5.4	76
42	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.	8.2	75
43	<i>In silico</i> Prediction of Drug Induced Liver Toxicity Using Substructure Pattern Recognition Method. <i>Molecular Informatics</i> , 2016, 35, 136-144.	2.5	75
44	Suppression of KRas-mutant cancer through the combined inhibition of KRAS with PLK1 and ROCK. <i>Nature Communications</i> , 2016, 7, 11363.	12.8	74
45	<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.	5.4	73
46	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.	6.2	72
47	Drug Repurposing: New Treatments for Zika Virus Infection?. <i>Trends in Molecular Medicine</i> , 2016, 22, 919-921.	6.7	71
48	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.	3.2	65
49	Harnessing endophenotypes and network medicine for Alzheimer's drug repurposing. <i>Medicinal Research Reviews</i> , 2020, 40, 2386-2426.	10.5	61
50	Insights into Molecular Basis of Cytochrome P450 Inhibitory Promiscuity of Compounds. <i>Journal of Chemical Information and Modeling</i> , 2011, 51, 2482-2495.	5.4	60
51	Reprogramming immunosuppressive myeloid cells facilitates immunotherapy for colorectal cancer. <i>EMBO Molecular Medicine</i> , 2021, 13, e12798.	6.9	59
52	Individualized network-based drug repositioning infrastructure for precision oncology in the panomics era. <i>Briefings in Bioinformatics</i> , 2016, 18, bbw051.	6.5	57
53	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.	3.7	55
54	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.	5.2	53

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55	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.	5.5	53
56	Systems Biology-Based Investigation of Cellular Antiviral Drug Targets Identified by Gene-Trap Insertional Mutagenesis. <i>PLoS Computational Biology</i> , 2016, 12, e1005074.	3.2	52
57	Computational prediction of microRNA networks incorporating environmental toxicity and disease etiology. <i>Scientific Reports</i> , 2014, 4, 5576.	3.3	51
58	Repurposing sertraline sensitizes non-small cell lung cancer cells to erlotinib by inducing autophagy. <i>JCI Insight</i> , 2018, 3, .	5.0	51
59	iDrug: Integration of drug repositioning and drug-target prediction via cross-network embedding. <i>PLoS Computational Biology</i> , 2020, 16, e1008040.	3.2	51
60	Computational models to predict endocrine-disrupting chemical binding with androgen or oestrogen receptors. <i>Ecotoxicology and Environmental Safety</i> , 2014, 110, 280-287.	6.0	50
61	In Silico Oncology Drug Repositioning and Polypharmacology. <i>Methods in Molecular Biology</i> , 2019, 1878, 243-261.	0.9	48
62	Deep learning for drug repurposing: Methods, databases, and applications. <i>Wiley Interdisciplinary Reviews: Computational Molecular Science</i> , 2022, 12, .	14.6	48
63	Personal Mutanomes Meet Modern Oncology Drug Discovery and Precision Health. <i>Pharmacological Reviews</i> , 2019, 71, 1-19.	16.0	47
64	Epilepsy subtype-specific copy number burden observed in a genome-wide study of 17,458 subjects. <i>Brain</i> , 2020, 143, 2106-2118.	7.6	47
65	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.	4.4	46
66	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.	6.2	45
67	FXR antagonism of NSAIDs contributes to drug-induced liver injury identified by systems pharmacology approach. <i>Scientific Reports</i> , 2015, 5, 8114.	3.3	44
68	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.	6.2	44
69	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.	3.8	43
70	Precision medicine review: rare driver mutations and their biophysical classification. <i>Biophysical Reviews</i> , 2019, 11, 5-19.	3.2	43
71	Artificial intelligence framework identifies candidate targets for drug repurposing in Alzheimer's disease. <i>Alzheimer's Research and Therapy</i> , 2022, 14, 7.	6.2	42
72	In silico prediction of chemical toxicity on avian species using chemical category approaches. <i>Chemosphere</i> , 2015, 122, 280-287.	8.2	41

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73	ccmGDB: a database for cancer cell metabolism genes. <i>Nucleic Acids Research</i> , 2016, 44, D959-D968.	14.5	41
74	Applications of artificial intelligence in multimodality cardiovascular imaging: A state-of-the-art review. <i>Progress in Cardiovascular Diseases</i> , 2020, 63, 367-376.	3.1	40
75	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.	3.5	38
76	Comprehensive germline genomic profiles of children, adolescents and young adults with solid tumors. <i>Nature Communications</i> , 2020, 11, 2206.	12.8	38
77	<i>In Silico</i> Pharmacoeconomic Evaluation of Drug-Induced Cardiovascular Complications Using Combined Classifiers. <i>Journal of Chemical Information and Modeling</i> , 2018, 58, 943-956.	5.4	37
78	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
79	Inhibition of histone deacetylases sensitizes EGF receptor- TK 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.	5.4	34
80	Mechanical forces induce an asthma gene signature in healthy airway epithelial cells. <i>Scientific Reports</i> , 2020, 10, 966.	3.3	34
81	Investigation of Indazole Unbinding Pathways in CYP2E1 by Molecular Dynamics Simulations. <i>PLoS ONE</i> , 2012, 7, e33500.	2.5	32
82	Autoimmune Cardiotoxicity of Cancer Immunotherapy. <i>Trends in Immunology</i> , 2017, 38, 77-78.	6.8	32
83	Individualized genetic network analysis reveals new therapeutic vulnerabilities in 6,700 cancer genomes. <i>PLoS Computational Biology</i> , 2020, 16, e1007701.	3.2	32
84	Functional consequences of somatic mutations in cancer using protein pocket-based prioritization approach. <i>Genome Medicine</i> , 2014, 6, 81.	8.2	31
85	A new precision medicine initiative at the dawn of exascale computing. <i>Signal Transduction and Targeted Therapy</i> , 2021, 6, 3.	17.1	31
86	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.	6.4	30
87	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.	5.5	29
88	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.	0.9	29
89	An integrative functional genomics framework for effective identification of novel regulatory variants in genome-phenome studies. <i>Genome Medicine</i> , 2018, 10, 7.	8.2	29
90	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

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91	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.	1.4	28
92	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.	7.1	28
93	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.	5.5	25
94	A network-based approach to uncover microRNA-mediated disease comorbidities and potential pathobiological implications. <i>Npj Systems Biology and Applications</i> , 2019, 5, 41.	3.0	24
95	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.	5.4	22
96	COVID-19 treatment: Combining anti-inflammatory and antiviral therapeutics using a network-based approach. <i>Cleveland Clinic Journal of Medicine</i> , 2020, , .	1.3	21
97	PTEN Mutations Trigger Resistance to Immunotherapy. <i>Trends in Molecular Medicine</i> , 2019, 25, 461-463.	6.7	20
98	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.	3.3	19
99	Cardiac risk stratification in cancer patients: A longitudinal patientâ€‘patient network analysis. <i>PLoS Medicine</i> , 2021, 18, e1003736.	8.4	19
100	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.	3.3	18
101	KRAS Activating Signaling Triggers Arteriovenous Malformations. <i>Trends in Biochemical Sciences</i> , 2018, 43, 481-483.	7.5	17
102	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.	3.5	15
103	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.	3.2	14
104	A retrospective analysis of cardiovascular adverse events associated with immune checkpoint inhibitors. <i>Cardio-Oncology</i> , 2021, 7, 19.	1.7	14
105	Systemic Administration of Tempol Attenuates the Cardiorespiratory Depressant Effects of Fentanyl. <i>Frontiers in Pharmacology</i> , 2021, 12, 690407.	3.5	14
106	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.	3.5	14
107	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.	2.5	13
108	In Silico Insights into Proteinâ€‘Protein Interaction Disruptive Mutations in the PCSK9-LDLR Complex. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1550.	4.1	13

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109	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.	17.1	13
110	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.	5.7	13
111	Pharmacophore modeling of human adenosine receptor A2A antagonists. <i>Journal of Molecular Modeling</i> , 2010, 16, 1867-1876.	1.8	12
112	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.	10.5	12
113	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.	3.7	12
114	My personal mutanome: a computational genomic medicine platform for searching network perturbing alleles linking genotype to phenotype. <i>Genome Biology</i> , 2021, 22, 53.	8.8	11
115	Aging-related cell type-specific pathophysiologic immune responses that exacerbate disease severity in aged COVID-19 patients. <i>Aging Cell</i> , 2022, 21, e13544.	6.7	11
116	Computational Insights into Ligand Selectivity of Estrogen Receptors from Pharmacophore Modeling. <i>Molecular Informatics</i> , 2011, 30, 539-549.	2.5	10
117	Importance of scientific collaboration in contemporary drug discovery and development: a detailed network analysis. <i>BMC Biology</i> , 2020, 18, 138.	3.8	10
118	A network-based deep learning methodology for stratification of tumor mutations. <i>Bioinformatics</i> , 2021, 37, 82-88.	4.1	10
119	A cross-cancer differential co-expression network reveals microRNA-regulated oncogenic functional modules. <i>Molecular BioSystems</i> , 2015, 11, 3244-3252.	2.9	9
120	Pulmonary Comorbidity in Lung Cancer. <i>Trends in Molecular Medicine</i> , 2018, 24, 239-241.	6.7	8
121	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.	3.4	8
122	Establishing an interdisciplinary research team for cardio-oncology artificial intelligence informatics precision and health equity. <i>American Heart Journal Plus</i> , 2022, 13, 100094.	0.6	8
123	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.	1.1	7
124	Pharmacogenomics for immunotherapy and immune-related cardiotoxicity. <i>Human Molecular Genetics</i> , 2020, 29, R186-R196.	2.9	7
125	Open Structural Data in Precision Medicine. <i>Annual Review of Biomedical Data Science</i> , 2022, 5, 95-117.	6.5	7
126	Gender Dimorphism Creates Divergent Cancer Susceptibilities. <i>Trends in Cancer</i> , 2016, 2, 325-326.	7.4	6

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127	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.	2.8	6
128	Shape shifting: The multiple conformational substates of the <scp>PTEN</scp> Nâ€terminal <scp>PIP₂</scp>â€binding domain. <i>Protein Science</i> , 2022, 31, e4308.	7.6	6
129	Temporal Trends of Cardiac Outcomes and Impact on Survival in Patients With Cancer. <i>American Journal of Cardiology</i> , 2020, 137, 118-124.	1.6	4
130	Impact of timing of atrial fibrillation, CHA2DS2-VASc score and cancer therapeutics on mortality in oncology patients. <i>Open Heart</i> , 2020, 7, e001412.	2.3	3
131	Target Identification Among Known Drugs by Deep Learning from Heterogeneous Networks. <i>SSRN Electronic Journal</i> , 0, , .	0.4	3
132	Editorial overview: Artificial intelligence (AI) methodologies in structural biology. <i>Current Opinion in Structural Biology</i> , 2022, , 102387.	5.7	3
133	Comparative pharmacophore modeling of human adenosine receptor A1 and A3 antagonists. <i>Science China Chemistry</i> , 2012, 55, 2407-2418.	8.2	2
134	Artificial Intelligence in Alzheimerâ€™s Drug Discovery. , 2022, , 62-72.		2
135	Peripheral sTREM2-Related Inflammatory Activity Alterations in Early-Stage Alzheimerâ€™s Disease. <i>Journal of Immunology</i> , 2022, 208, 2283-2299.	0.8	2
136	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.	2.6	2
137	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
138	Pharmacogenomics meets precision cardio-oncology: is there synergistic potential?. <i>Human Molecular Genetics</i> , 2020, 29, R177-R185.	2.9	1
139	Title is missing!. , 2020, 18, e3000970.		0
140	Title is missing!. , 2020, 18, e3000970.		0
141	Title is missing!. , 2020, 18, e3000970.		0
142	Title is missing!. , 2020, 18, e3000970.		0
143	Title is missing!. , 2020, 18, e3000970.		0
144	Title is missing!. , 2020, 18, e3000970.		0

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145	Title is missing!. , 2020, 18, e3000970.		0