List of Publications by Year in descending order

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	A rational design of a multi-epitope vaccine against SARS-CoV-2 which accounts for the glycan shield of the spike glycoprotein. Journal of Biomolecular Structure and Dynamics, 2022, 40, 7099-7113.	2.0	15
2	Interpretable artificial intelligence and exascale molecular dynamics simulations to reveal kinetics: Applications to Alzheimer's disease. Current Opinion in Structural Biology, 2022, 72, 103-113.	2.6	13
3	Agingâ€related cell typeâ€specific pathophysiologic immune responses that exacerbate disease severity in aged COVIDâ€19 patients. Aging Cell, 2022, 21, e13544.	3.0	11
4	Artificial intelligence framework identifies candidate targets for drug repurposing in Alzheimerâ€™s disease. Alzheimer's Research and Therapy, 2022, 14, 7.	3.0	42
5	Establishing an interdisciplinary research team for cardio-oncology artificial intelligence informatics precision and health equity. American Heart Journal Plus, 2022, 13, 100094.	0.3	8
6	Deep learning for drug repurposing: Methods, databases, and applications. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2022, 12, .	6.2	48
7	Artificial Intelligence in Alzheimerâ€™s Drug Discovery. , 2022, , 62-72.		2
8	Open Structural Data in Precision Medicine. Annual Review of Biomedical Data Science, 2022, 5, 95-117.	2.8	7
9	Editorial overview: Artificial intelligence (AI) methodologies in structural biology. Current Opinion in Structural Biology, 2022, , 102387.	2.6	3
10	Single-cell network biology characterizes cell type gene regulation for drug repurposing and phenotype prediction in Alzheimerâ€™s disease. PLoS Computational Biology, 2022, 18, e1010287.	1.5	9
11	Reprogramming immunosuppressive myeloid cells facilitates immunotherapy for colorectal cancer. EMBO Molecular Medicine, 2021, 13, e12798.	3.3	59
12	A new precision medicine initiative at the dawn of exascale computing. Signal Transduction and Targeted Therapy, 2021, 6, 3.	7.1	31
13	A network-based deep learning methodology for stratification of tumor mutations. Bioinformatics, 2021, 37, 82-88.	1.8	10
14	AlzGPS: a genome-wide positioning systems platform to catalyze multi-omics for Alzheimerâ€™s drug discovery. Alzheimer's Research and Therapy, 2021, 13, 24.	3.0	44
15	Comprehensive characterization of proteinâ€“protein interactions perturbed by disease mutations. Nature Genetics, 2021, 53, 342-353.	9.4	109
16	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
17	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. Genome Research, 2021, 31, 1900-1912.	2.4	53
18	NHLBI-CMREF Workshop Report on Pulmonary Vascular DiseaseÂClassification. Journal of the American College of Cardiology, 2021, 77, 2040-2052.	1.2	13

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19	Reducing acetylated tau is neuroprotective in brain injury. Cell, 2021, 184, 2715-2732.e23.	13.5	91
20	Identifying miRNAs in multiple sclerosis gray matter lesions that correlate with atrophy measures. Annals of Clinical and Translational Neurology, 2021, 8, 1279-1291.	1.7	12
21	A retrospective analysis of cardiovascular adverse events associated with immune checkpoint inhibitors. Cardio-Oncology, 2021, 7, 19.	0.8	14
22	Network medicine links SARS-CoV-2/COVID-19 infection to brain microvascular injury and neuroinflammation in dementia-like cognitive impairment. Alzheimer's Research and Therapy, 2021, 13, 110.	3.0	108
23	Multimodal single-cell omics analysis identifies epitheliumâ€“immune cell interactions and immune vulnerability associated with sex differences in COVID-19. Signal Transduction and Targeted Therapy, 2021, 6, 292.	7.1	13
24	Cardiac risk stratification in cancer patients: A longitudinal patientâ€“patient network analysis. PLoS Medicine, 2021, 18, e1003736.	3.9	19
25	My personal mutanome: a computational genomic medicine platform for searching network perturbing alleles linking genotype to phenotype. Genome Biology, 2021, 22, 53.	3.8	11
26	Metabolic endophenotype associated with right ventricular glucose uptake in pulmonary hypertension. Pulmonary Circulation, 2021, 11, 1-12.	0.8	5
27	Endophenotype-based in silico network medicine discovery combined with insurance record data mining identifies sildenafil as a candidate drug for Alzheimerâ€™s disease. Nature Aging, 2021, 1, 1175-1188.	5.3	87
28	Computational network biology: Data, models, and applications. Physics Reports, 2020, 846, 1-66.	10.3	126
29	Clinical Validation of a Blood-Based Predictive Test for Stratification of Response to Tumor Necrosis Factor Inhibitor Therapies in Rheumatoid Arthritis Patients. Network and Systems Medicine, 2020, 3, 91-104.	2.7	26
30	Temporal Trends of Cardiac Outcomes and Impact on Survival in Patients With Cancer. American Journal of Cardiology, 2020, 137, 118-124.	0.7	4
31	Importance of scientific collaboration in contemporary drug discovery and development: a detailed network analysis. BMC Biology, 2020, 18, 138.	1.7	10
32	New insights into genetic susceptibility of COVID-19: an ACE2 and TMPRSS2 polymorphism analysis. BMC Medicine, 2020, 18, 216.	2.3	304
33	iDrug: Integration of drug repositioning and drug-target prediction via cross-network embedding. PLoS Computational Biology, 2020, 16, e1008040.	1.5	51
34	Repurpose Open Data to Discover Therapeutics for COVID-19 Using Deep Learning. Journal of Proteome Research, 2020, 19, 4624-4636.	1.8	183
35	Harnessing endophenotypes and network medicine for Alzheimer's drug repurposing. Medicinal Research Reviews, 2020, 40, 2386-2426.	5.0	61
36	Machine Learningâ€“Based Risk Assessment for Cancer Therapyâ€“Related Cardiac Dysfunction in 4300 Longitudinal Oncology Patients. Journal of the American Heart Association, 2020, 9, e019628.	1.6	33

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37	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
38	Phosphorylation of PLCÎ³1 by EphA2 Receptor Tyrosine Kinase Promotes Tumor Growth in Lung Cancer. Molecular Cancer Research, 2020, 18, 1735-1743.	1.5	8
39	Artificial intelligence in COVID-19 drug repurposing. The Lancet Digital Health, 2020, 2, e667-e676.	5.9	349
40	Repurposing of FDA-Approved Toremifene to Treat COVID-19 by Blocking the Spike Glycoprotein and NSP14 of SARS-CoV-2. Journal of Proteome Research, 2020, 19, 4670-4677.	1.8	55
41	Network-based drug repurposing for novel coronavirus 2019-nCoV/SARS-CoV-2. Cell Discovery, 2020, 6, 14.	3.1	1,258
42	Applications of artificial intelligence in multimodality cardiovascular imaging: A state-of-the-art review. Progress in Cardiovascular Diseases, 2020, 63, 367-376.	1.6	40
43	Pharmacogenomics meets precision cardio-oncology: is there synergistic potential?. Human Molecular Genetics, 2020, 29, R177-R185.	1.4	1
44	Pharmacogenomics for immunotherapy and immune-related cardiotoxicity. Human Molecular Genetics, 2020, 29, R186-R196.	1.4	7
45	Individualized genetic network analysis reveals new therapeutic vulnerabilities in 6,700 cancer genomes. PLoS Computational Biology, 2020, 16, e1007701.	1.5	32
46	Target identification among known drugs by deep learning from heterogeneous networks. Chemical Science, 2020, 11, 1775-1797.	3.7	193
47	Network-based prediction of drugâ€“target interactions using an arbitrary-order proximity embedded deep forest. Bioinformatics, 2020, 36, 2805-2812.	1.8	101
48	Myeloid-Derived Suppressor Cell Subsets Drive Glioblastoma Growth in a Sex-Specific Manner. Cancer Discovery, 2020, 10, 1210-1225.	7.7	138
49	Mechanical forces induce an asthma gene signature in healthy airway epithelial cells. Scientific Reports, 2020, 10, 966.	1.6	34
50	Suppression of the SLC7A11/glutathione axis causes synthetic lethality in KRAS-mutant lung adenocarcinoma. Journal of Clinical Investigation, 2020, 130, 1752-1766.	3.9	200
51	A network medicine approach to investigation and population-based validation of disease manifestations and drug repurposing for COVID-19. PLoS Biology, 2020, 18, e3000970.	2.6	139
52	COVID-19 treatment: Combining anti-inflammatory and antiviral therapeutics using a network-based approach. Cleveland Clinic Journal of Medicine, 2020, , .	0.6	21
53	A genome-wide positioning systems network algorithm for in silico drug repurposing. Nature Communications, 2019, 10, 3476.	5.8	134
54	A Systems Pharmacology Approach Uncovers Wogonoside as an Angiogenesis Inhibitor of Triple-Negative Breast Cancer by Targeting Hedgehog Signaling. Cell Chemical Biology, 2019, 26, 1143-1158.e6.	2.5	53

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55	Cardio-oncology: Network-Based Prediction of Cancer Therapy-Induced Cardiotoxicity. Challenges and Advances in Computational Chemistry and Physics, 2019, , 75-97.	0.6	1
56	deepDR: a network-based deep learning approach toin silicodrug repositioning. Bioinformatics, 2019, 35, 5191-5198.	1.8	343
57	Conformational Dynamics and Allosteric Regulation Landscapes of Germline PTEN Mutations Associated with Autism Compared to Those Associated with Cancer. American Journal of Human Genetics, 2019, 104, 861-878.	2.6	45
58	PTEN Mutations Trigger Resistance to Immunotherapy. Trends in Molecular Medicine, 2019, 25, 461-463.	3.5	20
59	Network-based prediction of drug combinations. Nature Communications, 2019, 10, 1197.	5.8	437
60	A Bayesian framework that integrates multi-omics data and gene networks predicts risk genes from schizophrenia GWAS data. Nature Neuroscience, 2019, 22, 691-699.	7.1	118
61	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
62	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
63	Deep Learning-Based Prediction of Drug-Induced Cardiotoxicity. Journal of Chemical Information and Modeling, 2019, 59, 1073-1084.	2.5	123
64	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
65	Integrative proteomics and phosphoproteomics in pulmonary arterial hypertension. Scientific Reports, 2019, 9, 18623.	1.6	42
66	Precision medicine review: rare driver mutations and their biophysical classification. Biophysical Reviews, 2019, 11, 5-19.	1.5	43
67	In Silico Oncology Drug Repositioning and Polypharmacology. Methods in Molecular Biology, 2019, 1878, 243-261.	0.4	48
68	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
69	Personal Mutanomes Meet Modern Oncology Drug Discovery and Precision Health. Pharmacological Reviews, 2019, 71, 1-19.	7.1	47
70	In silico polypharmacology of natural products. Briefings in Bioinformatics, 2018, 19, 1153-1171.	3.2	95
71	Pulmonary Comorbidity in Lung Cancer. Trends in Molecular Medicine, 2018, 24, 239-241.	3.5	8
72	In Silico Pharmacoepidemiologic Evaluation of Drug-Induced Cardiovascular Complications Using Combined Classifiers. Journal of Chemical Information and Modeling, 2018, 58, 943-956.	2.5	37

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73	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
74	Repurposing sertraline sensitizes nonâ€“small cell lung cancer cells to erlotinib by inducing autophagy. JCI Insight, 2018, 3, .	2.3	51
75	Network-based approach to prediction and population-based validation of in silico drug repurposing. Nature Communications, 2018, 9, 2691.	5.8	351
76	KRAS Activating Signaling Triggers Arteriovenous Malformations. Trends in Biochemical Sciences, 2018, 43, 481-483.	3.7	17
77	An integrative functional genomics framework for effective identification of novel regulatory variants in genomeâ€“phenome studies. Genome Medicine, 2018, 10, 7.	3.6	29
78	Pharmacological inhibition of dihydroorotate dehydrogenase induces apoptosis and differentiation in acute myeloid leukemia cells. Haematologica, 2018, 103, 1472-1483.	1.7	66
79	SDTNBI: an integrated network and chemoinformatics tool for systematic prediction of drugâ€“target interactions and drug repositioning. Briefings in Bioinformatics, 2017, 18, bbw012.	3.2	102
80	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
81	Entropy-based consensus clustering for patient stratification. Bioinformatics, 2017, 33, 2691-2698.	1.8	73
82	Tissue-Specific Signaling Networks Rewired by Major Somatic Mutations in Human Cancer Revealed by Proteome-Wide Discovery. Cancer Research, 2017, 77, 2810-2821.	0.4	29
83	Autoimmune Cardiotoxicity of Cancer Immunotherapy. Trends in Immunology, 2017, 38, 77-78.	2.9	32
84	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
85	Quantitative and Systems Pharmacology. 1. In Silico Prediction of Drugâ€“Target Interactions of Natural Products Enables New Targeted Cancer Therapy. Journal of Chemical Information and Modeling, 2017, 57, 2657-2671.	2.5	76
86	Quantitative and Systems Pharmacology 3. Network-Based Identification of New Targets for Natural Products Enables Potential Uses in Aging-Associated Disorders. Frontiers in Pharmacology, 2017, 8, 747.	1.6	38
87	In silico Prediction of Drug Induced Liver Toxicity Using Substructure Pattern Recognition Method. Molecular Informatics, 2016, 35, 136-144.	1.4	75
88	Suppression of KRas-mutant cancer through the combined inhibition of KRAS with PLK1 and ROCK. Nature Communications, 2016, 7, 11363.	5.8	74
89	A network-based drug repositioning infrastructure for precision cancer medicine through targeting significantly mutated genes in the human cancer genomes. Journal of the American Medical Informatics Association: JAMIA, 2016, 23, 681-691.	2.2	46
90	Drug Repurposing: New Treatments for Zika Virus Infection?. Trends in Molecular Medicine, 2016, 22, 919-921.	3.5	71

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91	In silico prediction of chemical mechanism of action via an improved networkâ€based inference method. British Journal of Pharmacology, 2016, 173, 3372-3385.	2.7	73
92	Transcriptome- and proteome-oriented identification of dysregulated eIF4G, STAT3, and Hippo pathways altered by PIK3CA H1047R in HER2/ER-positive breast cancer. Breast Cancer Research and Treatment, 2016, 160, 457-474.	1.1	13
93	Investigating cellular network heterogeneity and modularity in cancer: a network entropy and unbalanced motif approach. BMC Systems Biology, 2016, 10, 65.	3.0	36
94	Gender Dimorphism Creates Divergent Cancer Susceptibilities. Trends in Cancer, 2016, 2, 325-326.	3.8	6
95	Individualized network-based drug repositioning infrastructure for precision oncology in the panomics era. Briefings in Bioinformatics, 2016, 18, bbw051.	3.2	57
96	Systematic Prioritization of Druggable Mutations in â^¼45000 Genomes Across 16 Cancer Types Using a Structural Genomics-based Approach. Molecular and Cellular Proteomics, 2016, 15, 642-656.	2.5	43
97	Systematic dissection of dysregulated transcription factorâ€“miRNA feed-forward loops across tumor types. Briefings in Bioinformatics, 2016, 17, 996-1008.	3.2	54
98	ccmGDB: a database for cancer cell metabolism genes. Nucleic Acids Research, 2016, 44, D959-D968.	6.5	41
99	Advances in computational approaches for prioritizing driver mutations and significantly mutated genes in cancer genomes. Briefings in Bioinformatics, 2016, 17, 642-656.	3.2	120
100	Systems Biology-Based Investigation of Cellular Antiviral Drug Targets Identified by Gene-Trap Insertional Mutagenesis. PLoS Computational Biology, 2016, 12, e1005074.	1.5	52
101	Network-based identification of microRNAs as potential pharmacogenomic biomarkers for anticancer drugs. Oncotarget, 2016, 7, 45584-45596.	0.8	85
102	Regulation rewiring analysis reveals mutual regulation between STAT1 and miR-155-5p in tumor immunosurveillance in seven major cancers. Scientific Reports, 2015, 5, 12063.	1.6	19
103	FXR antagonism of NSAIDs contributes to drug-induced liver injury identified by systems pharmacology approach. Scientific Reports, 2015, 5, 8114.	1.6	44
104	In silico prediction of chemical toxicity on avian species using chemical category approaches. Chemosphere, 2015, 122, 280-287.	4.2	41
105	SoNar, a Highly Responsive NAD+/NADH Sensor, Allows High-Throughput Metabolic Screening of Anti-tumor Agents. Cell Metabolism, 2015, 21, 777-789.	7.2	311
106	Biomarker-based drug safety assessment in the age of systems pharmacology: from foundational to regulatory science. Biomarkers in Medicine, 2015, 9, 1241-1252.	0.6	28
107	A cross-cancer differential co-expression network reveals microRNA-regulated oncogenic functional modules. Molecular BioSystems, 2015, 11, 3244-3252.	2.9	9
108	Heterogeneous DNA methylation contributes to tumorigenesis through inducing the loss of coexpression connectivity in colorectal cancer. Genes Chromosomes and Cancer, 2015, 54, 110-121.	1.5	15

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109	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
110	Functional consequences of somatic mutations in cancer using protein pocket-based prioritization approach. Genome Medicine, 2014, 6, 81.	3.6	31
111	Machine learning-based prediction of drugâ€“drug interactions by integrating drug phenotypic, therapeutic, chemical, and genomic properties. Journal of the American Medical Informatics Association: JAMIA, 2014, 21, e278-e286.	2.2	264
112	Computational models to predict endocrine-disrupting chemical binding with androgen or oestrogen receptors. Ecotoxicology and Environmental Safety, 2014, 110, 280-287.	2.9	50
113	Studying Tumorigenesis through Network Evolution and Somatic Mutational Perturbations in the Cancer Interactome. Molecular Biology and Evolution, 2014, 31, 2156-2169.	3.5	79
114	In Silico Prediction of Chemical Acute Oral Toxicity Using Multi-Classification Methods. Journal of Chemical Information and Modeling, 2014, 54, 1061-1069.	2.5	140
115	Computational prediction of microRNA networks incorporating environmental toxicity and disease etiology. Scientific Reports, 2014, 4, 5576.	1.6	51
116	Quantitative network mapping of the human kinome interactome reveals new clues for rational kinase inhibitor discovery and individualized cancer therapy. Oncotarget, 2014, 5, 3697-3710.	0.8	96
117	Prediction of human genes and diseases targeted by xenobiotics using predictive toxicogenomic-derived models (PTDMs). Molecular BioSystems, 2013, 9, 1316.	2.9	28
118	Adverse Drug Events: Database Construction and in Silico Prediction. Journal of Chemical Information and Modeling, 2013, 53, 744-752.	2.5	116
119	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
120	In Silico ADMET Prediction: Recent Advances, Current Challenges and Future Trends. Current Topics in Medicinal Chemistry, 2013, 13, 1273-1289.	1.0	181
121	In Silico Assessment of Chemical Biodegradability. Journal of Chemical Information and Modeling, 2012, 52, 655-669.	2.5	87
122	Unbinding Pathways of GW4064 from Human Farnesoid X Receptor As Revealed by Molecular Dynamics Simulations. Journal of Chemical Information and Modeling, 2012, 52, 3043-3052.	2.5	22
123	In silico Prediction of Chemical Ames Mutagenicity. Journal of Chemical Information and Modeling, 2012, 52, 2840-2847.	2.5	163
124	admetSAR: A Comprehensive Source and Free Tool for Assessment of Chemical ADMET Properties. Journal of Chemical Information and Modeling, 2012, 52, 3099-3105.	2.5	1,439
125	Comparative pharmacophore modeling of human adenosine receptor A1 and A3 antagonists. Science China Chemistry, 2012, 55, 2407-2418.	4.2	2
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127	Investigation of Indazole Unbinding Pathways in CYP2E1 by Molecular Dynamics Simulations. PLoS ONE, 2012, 7, e33500.	1.1	32
128	Prediction of Chemical-Protein Interactions Network with Weighted Network-Based Inference Method. PLoS ONE, 2012, 7, e41064.	1.1	86
129	Prediction of chemicalâ€“protein interactions: multitarget-QSAR versus computational chemogenomic methods. Molecular BioSystems, 2012, 8, 2373.	2.9	100
130	Insights into Molecular Basis of Cytochrome P450 Inhibitory Promiscuity of Compounds. Journal of Chemical Information and Modeling, 2011, 51, 2482-2495.	2.5	60
131	Classification of Cytochrome P450 Inhibitors and Noninhibitors Using Combined Classifiers. Journal of Chemical Information and Modeling, 2011, 51, 996-1011.	2.5	155
132	In silico prediction of Tetrahymena pyriformis toxicity for diverse industrial chemicals with substructure pattern recognition and machine learning methods. Chemosphere, 2011, 82, 1636-1643.	4.2	75
133	Computational Insights into Ligand Selectivity of Estrogen Receptors from Pharmacophore Modeling. Molecular Informatics, 2011, 30, 539-549.	1.4	10
134	Insights into binding modes of adenosine A2B antagonists with ligand-based and receptor-based methods. European Journal of Medicinal Chemistry, 2010, 45, 3459-3471.	2.6	29
135	Pharmacophore modeling of human adenosine receptor A2A antagonists. Journal of Molecular Modeling, 2010, 16, 1867-1876.	0.8	12
136	Estimation of ADME Properties with Substructure Pattern Recognition. Journal of Chemical Information and Modeling, 2010, 50, 1034-1041.	2.5	266
137	Target Identification Among Known Drugs by Deep Learning from Heterogeneous Networks. SSRN Electronic Journal, 0, , .	0.4	3