

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

150 papers	6,162 citations	41 h-index	74 g-index
162 ext. papers	8,796 ext. citations	8.5 avg, IF	6.09 L-index

#	Paper	IF	Citations
150	Mechanisms of drug combinations: interaction and network perspectives. <i>Nature Reviews Drug Discovery</i> , 2009 , 8, 111-28	64.1	603
149	Therapeutic target database update 2012: a resource for facilitating target-oriented drug discovery. <i>Nucleic Acids Research</i> , 2012 , 40, D1128-36	20.1	359
148	Therapeutic target database update 2018: enriched resource for facilitating bench-to-clinic research of targeted therapeutics. <i>Nucleic Acids Research</i> , 2018 , 46, D1121-D1127	20.1	322
147	Therapeutic target database 2020: enriched resource for facilitating research and early development of targeted therapeutics. <i>Nucleic Acids Research</i> , 2020 , 48, D1031-D1041	20.1	286
146	Therapeutic target database update 2016: enriched resource for bench to clinical drug target and targeted pathway information. <i>Nucleic Acids Research</i> , 2016 , 44, D1069-74	20.1	193
145	NOREVA: normalization and evaluation of MS-based metabolomics data. <i>Nucleic Acids Research</i> , 2017 , 45, W162-W170	20.1	190
144	Update of TTD: Therapeutic Target Database. <i>Nucleic Acids Research</i> , 2010 , 38, D787-91	20.1	190
143	Clustered patterns of species origins of nature-derived drugs and clues for future bioprospecting. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 12943-8	11.5	177
142	Assessing the performance of MM/PBSA and MM/GBSA methods. 7. Entropy effects on the performance of end-point binding free energy calculation approaches. <i>Physical Chemistry Chemical Physics</i> , 2018 , 20, 14450-14460	3.6	149
141	HawkDock: a web server to predict and analyze the protein-protein complex based on computational docking and MM/GBSA. <i>Nucleic Acids Research</i> , 2019 , 47, W322-W330	20.1	139
140	What Contributes to Serotonin-Norepinephrine Reuptake Inhibitors Dual-Targeting Mechanism? The Key Role of Transmembrane Domain 6 in Human Serotonin and Norepinephrine Transporters Revealed by Molecular Dynamics Simulation. <i>ACS Chemical Neuroscience</i> , 2018 , 9, 1128-1140	5.7	139
139	A combination of humanised anti-CD19 and anti-BCMA CAR T cells in patients with relapsed or refractory multiple myeloma: a single-arm, phase 2 trial. <i>Lancet Haematology</i> , 2019 , 6, e521-e529	14.6	138
138	Therapeutic target database update 2014: a resource for targeted therapeutics. <i>Nucleic Acids Research</i> , 2014 , 42, D1118-23	20.1	97
137	Performance Evaluation and Online Realization of Data-driven Normalization Methods Used in LC/MS based Untargeted Metabolomics Analysis. <i>Scientific Reports</i> , 2016 , 6, 38881	4.9	84
136	ANPELA: analysis and performance assessment of the label-free quantification workflow for metaproteomic studies. <i>Briefings in Bioinformatics</i> , 2020 , 21, 621-636	13.4	83
135	Computational identification of the binding mechanism of a triple reuptake inhibitor amitifadine for the treatment of major depressive disorder. <i>Physical Chemistry Chemical Physics</i> , 2018 , 20, 6606-6616	3.6	79
134	Consistent gene signature of schizophrenia identified by a novel feature selection strategy from comprehensive sets of transcriptomic data. <i>Briefings in Bioinformatics</i> , 2020 , 21, 1058-1068	13.4	74

133	VARIDT1.0: variability of drug transporter database. <i>Nucleic Acids Research</i> , 2020 , 48, D1042-D1050	20.1	74
132	Simultaneous Improvement in the Precision, Accuracy, and Robustness of Label-free Proteome Quantification by Optimizing Data Manipulation Chains. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 1683-1699	7.6	70
131	Clinical trials, progression-speed differentiating features and swiftness rule of the innovative targets of first-in-class drugs. <i>Briefings in Bioinformatics</i> , 2020 , 21, 649-662	13.4	67
130	NOREVA: enhanced normalization and evaluation of time-course and multi-class metabolomic data. <i>Nucleic Acids Research</i> , 2020 , 48, W436-W448	20.1	66
129	SVM-Prot 2016: A Web-Server for Machine Learning Prediction of Protein Functional Families from Sequence Irrespective of Similarity. <i>PLoS ONE</i> , 2016 , 11, e0155290	3.7	66
128	Exploring the Binding Mechanism of Metabotropic Glutamate Receptor 5 Negative Allosteric Modulators in Clinical Trials by Molecular Dynamics Simulations. <i>ACS Chemical Neuroscience</i> , 2018 , 9, 1492-1502	5.7	65
127	Support vector machines approach for predicting druggable proteins: recent progress in its exploration and investigation of its usefulness. <i>Drug Discovery Today</i> , 2007 , 12, 304-13	8.8	58
126	Age Related Multiple Sclerosis Severity Score: Disability ranked by age. <i>Multiple Sclerosis Journal</i> , 2017 , 23, 1938-1946	5	55
125	Protein functional annotation of simultaneously improved stability, accuracy and false discovery rate achieved by a sequence-based deep learning. <i>Briefings in Bioinformatics</i> , 2020 , 21, 1437-1447	13.4	53
124	Clinical Success of Drug Targets Prospectively Predicted by In Silico Study. <i>Trends in Pharmacological Sciences</i> , 2018 , 39, 229-231	13.2	52
123	Discovery of the Consistently Well-Performed Analysis Chain for SWATH-MS Based Pharmacoproteomic Quantification. <i>Frontiers in Pharmacology</i> , 2018 , 9, 681	5.6	52
122	Infection-related health care utilization among people with and without multiple sclerosis. <i>Multiple Sclerosis Journal</i> , 2017 , 23, 1506-1516	5	51
121	Assessing the performance of MM/PBSA and MM/GBSA methods. 8. Predicting binding free energies and poses of protein-RNA complexes. <i>Rna</i> , 2018 , 24, 1183-1194	5.8	51
120	Differentiating Physicochemical Properties between Addictive and Nonaddictive ADHD Drugs Revealed by Molecular Dynamics Simulation Studies. <i>ACS Chemical Neuroscience</i> , 2017 , 8, 1416-1428	5.7	49
119	How Does Chirality Determine the Selective Inhibition of Histone Deacetylase 6? A Lesson from Trichostatin A Enantiomers Based on Molecular Dynamics. <i>ACS Chemical Neuroscience</i> , 2019 , 10, 2467-2480	5.7	49
118	Identification of the inhibitory mechanism of FDA approved selective serotonin reuptake inhibitors: an insight from molecular dynamics simulation study. <i>Physical Chemistry Chemical Physics</i> , 2016 , 18, 3260-3271	3.6	47
117	Comparative analysis of machine learning methods in ligand-based virtual screening of large compound libraries. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2009 , 12, 344-57	1.3	47
116	ADMET Evaluation in Drug Discovery. 18. Reliable Prediction of Chemical-Induced Urinary Tract Toxicity by Boosting Machine Learning Approaches. <i>Molecular Pharmaceutics</i> , 2017 , 14, 3935-3953	5.6	46

115	The novel EZH2 inhibitor, GSK126, suppresses cell migration and angiogenesis via down-regulating VEGF-A. <i>Cancer Chemotherapy and Pharmacology</i> , 2016 , 77, 757-65	3.5	44
114	What are next generation innovative therapeutic targets? Clues from genetic, structural, physicochemical, and systems profiles of successful targets. <i>Journal of Pharmacology and Experimental Therapeutics</i> , 2009 , 330, 304-15	4.7	43
113	Drug discovery prospect from untapped species: indications from approved natural product drugs. <i>PLoS ONE</i> , 2012 , 7, e39782	3.7	43
112	Convolutional neural network-based annotation of bacterial type IV secretion system effectors with enhanced accuracy and reduced false discovery. <i>Briefings in Bioinformatics</i> , 2020 , 21, 1825-1836	13.4	43
111	Co-targeting cancer drug escape pathways confers clinical advantage for multi-target anticancer drugs. <i>Pharmacological Research</i> , 2015 , 102, 123-31	10.2	41
110	Assessing the performance of the MM/PBSA and MM/GBSA methods. 10. Impacts of enhanced sampling and variable dielectric model on protein-protein Interactions. <i>Physical Chemistry Chemical Physics</i> , 2019 , 21, 18958-18969	3.6	41
109	Differentiating physicochemical properties between NDRIs and sNRIs clinically important for the treatment of ADHD. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017 , 1861, 2766-2777	4	40
108	Therapeutic target database update 2022: facilitating drug discovery with enriched comparative data of targeted agents. <i>Nucleic Acids Research</i> , 2021 ,	20.1	40
107	The miRNA: a small but powerful RNA for COVID-19. <i>Briefings in Bioinformatics</i> , 2021 , 22, 1137-1149	13.4	40
106	The Human Kinome Targeted by FDA Approved Multi-Target Drugs and Combination Products: A Comparative Study from the Drug-Target Interaction Network Perspective. <i>PLoS ONE</i> , 2016 , 11, e0165737	3.7	39
105	Discovery of Novel and Selective Adenosine A Receptor Antagonists for Treating Parkinson's Disease through Comparative Structure-Based Virtual Screening. <i>Journal of Chemical Information and Modeling</i> , 2017 , 57, 1474-1487	6.1	35
104	Five years before multiple sclerosis onset: Phenotyping the prodrome. <i>Multiple Sclerosis Journal</i> , 2019 , 25, 1092-1101	5	35
103	Exploring the Inhibitory Mechanism of Approved Selective Norepinephrine Reuptake Inhibitors and Reboxetine Enantiomers by Molecular Dynamics Study. <i>Scientific Reports</i> , 2016 , 6, 26883	4.9	33
102	farPPI: a webserver for accurate prediction of protein-ligand binding structures for small-molecule PPI inhibitors by MM/PB(GB)SA methods. <i>Bioinformatics</i> , 2019 , 35, 1777-1779	7.2	33
101	Predicting risk of secondary progression in multiple sclerosis: A nomogram. <i>Multiple Sclerosis Journal</i> , 2019 , 25, 1102-1112	5	32
100	Cheminformatic Insight into the Differences between Terrestrial and Marine Originated Natural Products. <i>Journal of Chemical Information and Modeling</i> , 2018 , 58, 1182-1193	6.1	32
99	Revealing vilazodone's binding mechanism underlying its partial agonism to the 5-HT receptor in the treatment of major depressive disorder. <i>Physical Chemistry Chemical Physics</i> , 2017 , 19, 28885-28896	3.6	31
98	HawkRank: a new scoring function for protein-protein docking based on weighted energy terms. <i>Journal of Cheminformatics</i> , 2017 , 9, 66	8.6	31

97	Effective degradation of 2,4-dihydroxybenzophenone by zero-valent iron powder (Fe)-activated persulfate in aqueous solution: Kinetic study, product identification and theoretical calculations. <i>Science of the Total Environment</i> , 2021 , 771, 144743	10.2	31
96	Combating Drug-Resistant Mutants of Anaplastic Lymphoma Kinase with Potent and Selective Type-I Inhibitors by Stabilizing Unique DFG-Shifted Loop Conformation. <i>ACS Central Science</i> , 2017 , 3, 1208-1220	16.8	30
95	Comparison of FDA Approved Kinase Targets to Clinical Trial Ones: Insights from Their System Profiles and Drug-Target Interaction Networks. <i>BioMed Research International</i> , 2016 , 2016, 2509385	3	30
94	A novel bioinformatics approach to identify the consistently well-performing normalization strategy for current metabolomic studies. <i>Briefings in Bioinformatics</i> , 2020 , 21, 2142-2152	13.4	29
93	Prognostic Value of Bone Mineral Density on Curve Progression: A Longitudinal Cohort Study of 513 Girls with Adolescent Idiopathic Scoliosis. <i>Scientific Reports</i> , 2016 , 6, 39220	4.9	29
92	INTEDE: interactome of drug-metabolizing enzymes. <i>Nucleic Acids Research</i> , 2021 , 49, D1233-D1243	20.1	29
91	SSizer: Determining the Sample Sufficiency for Comparative Biological Study. <i>Journal of Molecular Biology</i> , 2020 , 432, 3411-3421	6.5	28
90	Computational characterization of the selective inhibition of human norepinephrine and serotonin transporters by an escitalopram scaffold. <i>Physical Chemistry Chemical Physics</i> , 2018 , 20, 29513-29527	3.6	27
89	A protein network descriptor server and its use in studying protein, disease, metabolic and drug targeted networks. <i>Briefings in Bioinformatics</i> , 2017 , 18, 1057-1070	13.4	26
88	Identification of novel immune-relevant drug target genes for Alzheimer's Disease by combining ontology inference with network analysis. <i>CNS Neuroscience and Therapeutics</i> , 2018 , 24, 1253-1263	6.8	26
87	Nature's contribution to today's pharmacopeia. <i>Nature Biotechnology</i> , 2014 , 32, 979-80	44.5	26
86	The Effects of Hashimoto Thyroiditis on Lymph Node Metastases in Unifocal and Multifocal Papillary Thyroid Carcinoma: A Retrospective Chinese Cohort Study. <i>Medicine (United States)</i> , 2016 , 95, e2674	1.8	26
85	Assessing the Performances of Protein Function Prediction Algorithms from the Perspectives of Identification Accuracy and False Discovery Rate. <i>International Journal of Molecular Sciences</i> , 2018 , 19,	6.3	25
84	Optimization of metabolomic data processing using NOREVA.. <i>Nature Protocols</i> , 2021 ,	18.8	24
83	Insight into the selective binding mechanism of DNMT1 and DNMT3A inhibitors: a molecular simulation study. <i>Physical Chemistry Chemical Physics</i> , 2019 , 21, 12931-12947	3.6	23
82	Importance of protein flexibility in molecular recognition: a case study on Type-11/2 inhibitors of ALK. <i>Physical Chemistry Chemical Physics</i> , 2018 , 20, 4851-4863	3.6	21
81	Prediction of the binding mode and resistance profile for a dual-target pyrrolyl diketo acid scaffold against HIV-1 integrase and reverse-transcriptase-associated ribonuclease H. <i>Physical Chemistry Chemical Physics</i> , 2018 , 20, 23873-23884	3.6	21
80	A critical assessment of the feature selection methods used for biomarker discovery in current metaproteomics studies. <i>Briefings in Bioinformatics</i> , 2020 , 21, 1378-1390	13.4	21

79	MMEASE: Online meta-analysis of metabolomic data by enhanced metabolite annotation, marker selection and enrichment analysis. <i>Journal of Proteomics</i> , 2021 , 232, 104023	3.9	21
78	Identification of dual active agents targeting 5-HT1A and SERT by combinatorial virtual screening methods. <i>Bio-Medical Materials and Engineering</i> , 2015 , 26 Suppl 1, S2233-9	1	19
77	Determining the Balance Between Drug Efficacy and Safety by the Network and Biological System Profile of Its Therapeutic Target. <i>Frontiers in Pharmacology</i> , 2018 , 9, 1245	5.6	19
76	Structure-Based Drug Design and Identification of HO-Soluble and Low Toxic Hexacyclic Camptothecin Derivatives with Improved Efficacy in Cancer and Lethal Inflammation Models in Vivo. <i>Journal of Medicinal Chemistry</i> , 2018 , 61, 8613-8624	8.3	19
75	Metformin inhibits proliferation and growth hormone secretion of GH3 pituitary adenoma cells. <i>Oncotarget</i> , 2017 , 8, 37538-37549	3.3	18
74	DNA polymerase zeta: new insight into eukaryotic mutagenesis and mammalian embryonic development. <i>World Journal of Gastroenterology</i> , 2003 , 9, 1165-9	5.6	18
73	Biomarker Discovery for Immunotherapy of Pituitary Adenomas: Enhanced Robustness and Prediction Ability by Modern Computational Tools. <i>International Journal of Molecular Sciences</i> , 2019 , 20,	6.3	18
72	Recent Advances and Challenges of the Drugs Acting on Monoamine Transporters. <i>Current Medicinal Chemistry</i> , 2020 , 27, 3830-3876	4.3	18
71	Comparison of computational model and X-ray crystal structure of human serotonin transporter: potential application for the pharmacology of human monoamine transporters. <i>Molecular Simulation</i> , 2017 , 43, 1089-1098	2	17
70	Response of human REV3 gene to gastric cancer inducing carcinogen N-methyl-N-nitro-N-nitrosoguanidine and its role in mutagenesis. <i>World Journal of Gastroenterology</i> , 2003 , 9, 888-93	5.6	17
69	Assessing the Effectiveness of Direct Data Merging Strategy in Long-Term and Large-Scale Pharmacometabonomics. <i>Frontiers in Pharmacology</i> , 2019 , 10, 127	5.6	17
68	Reliability of Docking-Based Virtual Screening for GPCR Ligands with Homology Modeled Structures: A Case Study of the Angiotensin II Type I Receptor. <i>ACS Chemical Neuroscience</i> , 2019 , 10, 677-689	5.7	17
67	MetaFS: Performance assessment of biomarker discovery in metaproteomics. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	17
66	Clustered distribution of natural product leads of drugs in the chemical space as influenced by the privileged target-sites. <i>Scientific Reports</i> , 2015 , 5, 9325	4.9	16
65	VARIDT 2.0: structural variability of drug transporter. <i>Nucleic Acids Research</i> , 2021 ,	20.1	16
64	How Does the L884P Mutation Confer Resistance to Type-II Inhibitors of JAK2 Kinase: A Comprehensive Molecular Modeling Study. <i>Scientific Reports</i> , 2017 , 7, 9088	4.9	15
63	Identification of the gene signature reflecting schizophrenia's etiology by constructing artificial intelligence-based method of enhanced reproducibility. <i>CNS Neuroscience and Therapeutics</i> , 2019 , 25, 1054-1063	6.8	15
62	The Therapeutic Target Database: an internet resource for the primary targets of approved, clinical trial and experimental drugs. <i>Expert Opinion on Therapeutic Targets</i> , 2011 , 15, 903-12	6.4	15

61	Molecular Mechanism for the Allosteric Inhibition of the Human Serotonin Transporter by Antidepressant Escitalopram.. <i>ACS Chemical Neuroscience</i> , 2022 ,	5.7	15
60	Computational advances of tumor marker selection and sample classification in cancer proteomics. <i>Computational and Structural Biotechnology Journal</i> , 2020 , 18, 2012-2025	6.8	15
59	The binding mode of vilazodone in the human serotonin transporter elucidated by ligand docking and molecular dynamics simulations. <i>Physical Chemistry Chemical Physics</i> , 2020 , 22, 5132-5144	3.6	14
58	Modelling disease progression in relapsing-remitting onset multiple sclerosis using multilevel models applied to longitudinal data from two natural history cohorts and one treated cohort. <i>Health Technology Assessment</i> , 2016 , 20, 1-48	4.4	14
57	Out-of-the-box deep learning prediction of pharmaceutical properties by broadly learned knowledge-based molecular representations. <i>Nature Machine Intelligence</i> , 2021 , 3, 334-343	22.5	14
56	Akt Inhibitor Perifosine Prevents Epileptogenesis in a Rat Model of Temporal Lobe Epilepsy. <i>Neuroscience Bulletin</i> , 2018 , 34, 283-290	4.3	14
55	Databases for the targeted COVID-19 therapeutics. <i>British Journal of Pharmacology</i> , 2020 , 177, 4999-5008	16	12
54	Computational design and modeling of nanobodies toward SARS-CoV-2 receptor binding domain. <i>Chemical Biology and Drug Design</i> , 2021 , 98, 1-18	2.9	12
53	Computational Advances in the Label-free Quantification of Cancer Proteomics Data. <i>Current Pharmaceutical Design</i> , 2018 , 24, 3842-3858	3.3	12
52	Disability progression in aggressive multiple sclerosis. <i>Multiple Sclerosis Journal</i> , 2017 , 23, 456-463	5	11
51	Identification of Key Long Non-Coding RNAs in the Pathology of Alzheimer's Disease and their Functions Based on Genome-Wide Associations Study, Microarray, and RNA-seq Data. <i>Journal of Alzheimer's Disease</i> , 2019 , 68, 339-355	4.3	11
50	Genome-wide identification and analysis of the eQTL lncRNAs in multiple sclerosis based on RNA-seq data. <i>Briefings in Bioinformatics</i> , 2020 , 21, 1023-1037	13.4	11
49	What Makes Species Productive of Anti-Cancer Drugs? Clues from Drugs' Species Origin, Druglikeness, Target and Pathway. <i>Anti-Cancer Agents in Medicinal Chemistry</i> , 2019 , 19, 194-203	2.2	10
48	Regeneration of a Bioengineered Thyroid Using Decellularized Thyroid Matrix. <i>Thyroid</i> , 2019 , 29, 142-153	3.2	10
47	Oxidation of benzophenone-3 in aqueous solution by potassium permanganate: kinetics, degradation products, reaction pathways, and toxicity assessment. <i>Environmental Science and Pollution Research</i> , 2021 , 28, 31301-31311	5.1	10
46	Analysis of bypass signaling in EGFR pathway and profiling of bypass genes for predicting response to anticancer EGFR tyrosine kinase inhibitors. <i>Molecular BioSystems</i> , 2012 , 8, 2645-56		9
45	Pharmacometabonomics: data processing and statistical analysis. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	9
44	Evidence for possible role of toll-like receptor 3 mediating virus-induced progression of pituitary adenomas. <i>Molecular and Cellular Endocrinology</i> , 2016 , 426, 22-32	4.4	9

43	Prediction of GluN2B-CT/DAPK1 Interaction by Protein?Peptide Docking and Molecular Dynamics Simulation. <i>Molecules</i> , 2018 , 23,	4.8	9
42	RNA-RNA interactions between SARS-CoV-2 and host benefit viral development and evolution during COVID-19 infection. <i>Briefings in Bioinformatics</i> , 2021 ,	13.4	9
41	SYNBIP: synthetic binding proteins for research, diagnosis and therapy. <i>Nucleic Acids Research</i> , 2021 ,	20.1	8
40	CYP2J2/EET reduces vulnerability to atrial fibrillation in chronic pressure overload mice. <i>Journal of Cellular and Molecular Medicine</i> , 2020 , 24, 862-874	5.6	8
39	GIMICA: host genetic and immune factors shaping human microbiota. <i>Nucleic Acids Research</i> , 2021 , 49, D715-D722	20.1	8
38	Comprehensive assessment of nine docking programs on type II kinase inhibitors: prediction accuracy of sampling power, scoring power and screening power. <i>Briefings in Bioinformatics</i> , 2018 ,	13.4	8
37	In silico identification of human pregnane X receptor activators from molecular descriptors by machine learning approaches. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2012 , 118, 271-279	3.8	7
36	THE DISCRIMINATION OF LEARNING STYLES BY BAYES-BASED STATISTICS: AN EXTENDED STUDY ON ILS SYSTEM. <i>Control and Intelligent Systems</i> , 2015 , 43,		6
35	Subtype-selective mechanisms of negative allosteric modulators binding to group I metabotropic glutamate receptors. <i>Acta Pharmacologica Sinica</i> , 2021 , 42, 1354-1367	8	6
34	The mechanistic, diagnostic and therapeutic novel nucleic acids for hepatocellular carcinoma emerging in past score years. <i>Briefings in Bioinformatics</i> , 2021 , 22, 1860-1883	13.4	6
33	SCP2-mediated cholesterol membrane trafficking promotes the growth of pituitary adenomas via Hedgehog signaling activation. <i>Journal of Experimental and Clinical Cancer Research</i> , 2019 , 38, 404	12.8	5
32	Selective Inhibition of HDAC1 by Macrocyclic Polypeptide for the Treatment of Glioblastoma: A Binding Mechanistic Analysis Based on Molecular Dynamics. <i>Frontiers in Molecular Biosciences</i> , 2020 , 7, 41	5.6	5
31	Discovery of novel antagonists targeting the DNA binding domain of androgen receptor by integrated docking-based virtual screening and bioassays. <i>Acta Pharmacologica Sinica</i> , 2021 ,	8	5
30	Understanding the Polypharmacological Profiles of Triple Reuptake Inhibitors by Molecular Simulation. <i>ACS Chemical Neuroscience</i> , 2021 , 12, 2013-2026	5.7	5
29	Advances in Current Diabetes Proteomics: From the Perspectives of Label- free Quantification and Biomarker Selection. <i>Current Drug Targets</i> , 2020 , 21, 34-54	3	5
28	Adherence to laboratory monitoring among people taking oral drugs for multiple sclerosis: A Canadian population-based study. <i>Multiple Sclerosis Journal</i> , 2021 , 27, 239-249	5	4
27	Discovery of a novel nonsteroidal selective glucocorticoid receptor modulator by virtual screening and bioassays.. <i>Acta Pharmacologica Sinica</i> , 2022 ,	8	4
26	Epoxyeicosatrienoic acid prevents maladaptive remodeling in pressure overload by targeting calcineurin/NFAT and Smad-7. <i>Experimental Cell Research</i> , 2020 , 386, 111716	4.2	4

25	Integrating the Ribonucleic Acid Sequencing Data From Various Studies for Exploring the Multiple Sclerosis-Related Long Noncoding Ribonucleic Acids and Their Functions. <i>Frontiers in Genetics</i> , 2019 , 10, 1136	4.5	4
24	Sp1 Targeted PARP1 Inhibition Protects Cardiomyocytes From Myocardial Ischemia-Reperfusion Injury via Downregulation of Autophagy. <i>Frontiers in Cell and Developmental Biology</i> , 2021 , 9, 621906	5.7	3
23	Inhibition of RhoA/Rho kinase signaling pathway by fasudil protects against kainic acid-induced neurite injury. <i>Brain and Behavior</i> , 2021 , 11, e2266	3.4	3
22	Neural Progenitor Cells Rptor Ablation Impairs Development but Benefits to Seizure-Induced Behavioral Abnormalities. <i>CNS Neuroscience and Therapeutics</i> , 2016 , 22, 1000-1008	6.8	3
21	NPCDR: natural product-based drug combination and its disease-specific molecular regulation. <i>Nucleic Acids Research</i> , 2021 ,	20.1	3
20	Comment on: "MicroRNA Mimics or Inhibitors as Antiviral Therapeutic Approaches Against COVID-19". <i>Drugs</i> , 2021 , 81, 1691-1692	12.1	3
19	PFmulDL: a novel strategy enabling multi-class and multi-label protein function annotation by integrating diverse deep learning methods.. <i>Computers in Biology and Medicine</i> , 2022 , 145, 105465	7	3
18	High iodine induces DNA damage in autoimmune thyroiditis partially by inhibiting the DNA repair protein MTH1. <i>Cellular Immunology</i> , 2019 , 344, 103948	4.4	2
17	Gut microbiota signatures in Schistosoma japonicum infection-induced liver cirrhosis patients: a case-control study. <i>Infectious Diseases of Poverty</i> , 2021 , 10, 43	10.4	2
16	Identification of the key target profiles underlying the drugs of narrow therapeutic index for treating cancer and cardiovascular disease. <i>Computational and Structural Biotechnology Journal</i> , 2021 , 19, 2318-2328	6.8	2
15	POSREG: proteomic signature discovered by simultaneously optimizing its reproducibility and generalizability.. <i>Briefings in Bioinformatics</i> , 2022 ,	13.4	2
14	Infiltration of nanocarbon suspension into the tracheal cavity during surgical treatment of papillary thyroid carcinoma: a case report. <i>Journal of International Medical Research</i> , 2020 , 48, 300060520919251	1.4	1
13	Papillary Thyroid Carcinoma Landscape and Its Immunological Link With Hashimoto Thyroiditis at Single-Cell Resolution. <i>Frontiers in Cell and Developmental Biology</i> , 2021 , 9, 758339	5.7	1
12	Effectiveness of low dose of rapamycin in preventing seizure-induced anxiety-like behaviour, cognitive impairment, and defects in neurogenesis in developing rats. <i>International Journal of Neuroscience</i> , 2020 , 130, 9-18	2	1
11	Feature, Function, and Information of Drug Transporter Related Databases. <i>Drug Metabolism and Disposition</i> , 2021 ,	4	1
10	Dysregulation of miR-411 in cancer: Causative factor for pathogenesis, diagnosis and prognosis.. <i>Biomedicine and Pharmacotherapy</i> , 2022 , 149, 112896	7.5	1
9	Recent Technological Advances in the Mass Spectrometry-based Nanomedicine Studies: An Insight from Nanoproteomics. <i>Current Pharmaceutical Design</i> , 2019 , 25, 1536-1553	3.3	0
8	The effects of sample size on omics study: from the perspective of robustness and diagnostic accuracy. <i>IOP Conference Series: Earth and Environmental Science</i> , 2019 , 252, 022127	0.3	0

7	Identification of DNA adduct formation of small molecules by molecular descriptors and machine learning methods. <i>Molecular Simulation</i> , 2012 , 38, 259-273	2	o
6	LncRNA functional annotation with improved false discovery rate achieved by disease associations.. <i>Computational and Structural Biotechnology Journal</i> , 2022 , 20, 322-332	6.8	o
5	The effect of data integration on LC-MS-based metabolomics data: evaluation on the comparative classification capacities. <i>IOP Conference Series: Earth and Environmental Science</i> , 2019 , 252, 032166	0.3	
4	Combining kinase inhibitors for optimally co-targeting cancer and drug escape by exploitation of drug target promiscuities. <i>Drug Development Research</i> , 2021 , 82, 133-142	5.1	
3	Stability of the gut microbiota in persons with paediatric-onset multiple sclerosis and related demyelinating diseases.. <i>Multiple Sclerosis Journal</i> , 2022 , 13524585221079533	5	
2	LINC00520: A Potential Diagnostic and Prognostic Biomarker in Cancer.. <i>Frontiers in Immunology</i> , 2022 , 13, 845418	8.4	
1	Emergency department use by persons with MS: A population-based descriptive study with a focus on infection-related visits.. <i>Multiple Sclerosis Journal</i> , 2022 , 13524585221078497	5	