Feng Zhu

List of Publications by Year in Descending Order

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	Molecular Mechanism for the Allosteric Inhibition of the Human Serotonin Transporter by Antidepressant Escitalopram.. *ACS Chemical Neuroscience*, **2022**,	5.7	15
149	Discovery of a novel nonsteroidal selective glucocorticoid receptor modulator by virtual screening and bioassays.. *Acta Pharmacologica Sinica*, **2022**,	8	4
148	LncRNA functional annotation with improved false discovery rate achieved by disease associations.. *Computational and Structural Biotechnology Journal*, **2022**, 20, 322-332	6.8	0
147	POSREG: proteomic signature discovered by simultaneously optimizing its reproducibility and generalizability.. *Briefings in Bioinformatics*, **2022**,	13.4	2
146	Stability of the gut microbiota in persons with paediatric-onset multiple sclerosis and related demyelinating diseases.. *Multiple Sclerosis Journal*, **2022**, 13524585221079533	5	
145	LINC00520: A Potential Diagnostic and Prognostic Biomarker in Cancer.. *Frontiers in Immunology*, **2022**, 13, 845418	8.4	
144	Emergency department use by persons with MS: A population-based descriptive study with a focus on infection-related visits.. *Multiple Sclerosis Journal*, **2022**, 13524585221078497	5	
143	Dysregulation of miR-411 in cancer: Causative factor for pathogenesis, diagnosis and prognosis.. *Biomedicine and Pharmacotherapy*, **2022**, 149, 112896	7.5	1
142	PFmulDL: a novel strategy enabling multi-class and multi-label protein function annotation by integrating diverse deep learning methods.. *Computers in Biology and Medicine*, **2022**, 145, 105465	7	3
141	Adherence to laboratory monitoring among people taking oral drugs for multiple sclerosis: A Canadian population-based study. *Multiple Sclerosis Journal*, **2021**, 27, 239-249	5	4
140	Optimization of metabolomic data processing using NOREVA.. *Nature Protocols*, **2021**,	18.8	24
139	Papillary Thyroid Carcinoma Landscape and Its Immunological Link With Hashimoto Thyroiditis at Single-Cell Resolution. *Frontiers in Cell and Developmental Biology*, **2021**, 9, 758339	5.7	1
138	Combining kinase inhibitors for optimally co-targeting cancer and drug escape by exploitation of drug target promiscuities. *Drug Development Research*, **2021**, 82, 133-142	5.1	
137	VARIDT 2.0: structural variability of drug transporter. *Nucleic Acids Research*, **2021**,	20.1	16
136	Therapeutic target database update 2022: facilitating drug discovery with enriched comparative data of targeted agents. *Nucleic Acids Research*, **2021**,	20.1	40
135	SYNBIP: synthetic binding proteins for research, diagnosis and therapy. *Nucleic Acids Research*, **2021** ,	20.1	8
134	Subtype-selective mechanisms of negative allosteric modulators binding to group I metabotropic glutamate receptors. *Acta Pharmacologica Sinica*, **2021**, 42, 1354-1367	8	6

133	The miRNA: a small but powerful RNA for COVID-19. *Briefings in Bioinformatics*, **2021**, 22, 1137-1149	13.4	40
132	Discovery of novel antagonists targeting the DNA binding domain of androgen receptor by integrated docking-based virtual screening and bioassays. *Acta Pharmacologica Sinica*, **2021**,	8	5
131	Gut microbiota signatures in Schistosoma japonicum infection-induced liver cirrhosis patients: a case-control study. *Infectious Diseases of Poverty*, **2021**, 10, 43	10.4	2
130	Out-of-the-box deep learning prediction of pharmaceutical properties by broadly learned knowledge-based molecular representations. *Nature Machine Intelligence*, **2021**, 3, 334-343	22.5	14
129	Pharmacometabonomics: data processing and statistical analysis. *Briefings in Bioinformatics*, **2021**, 22,	13.4	9
128	Sp1 Targeted PARP1 Inhibition Protects Cardiomyocytes From Myocardial Ischemia-Reperfusion Injury via Downregulation of Autophagy. *Frontiers in Cell and Developmental Biology*, **2021**, 9, 621906	5.7	3
127	Computational design and modeling of nanobodies toward SARS-CoV-2 receptor binding domain. *Chemical Biology and Drug Design*, **2021**, 98, 1-18	2.9	12
126	Understanding the Polypharmacological Profiles of Triple Reuptake Inhibitors by Molecular Simulation. *ACS Chemical Neuroscience*, **2021**, 12, 2013-2026	5.7	5
125	Inhibition of RhoA/Rho kinase signaling pathway by fasudil protects against kainic acid-induced neurite injury. *Brain and Behavior*, **2021**, 11, e2266	3.4	3
124	Effective degradation of 2,4-dihydroxybenzophenone by zero-valent iron powder (Fe)-activated persulfate in aqueous solution: Kinetic study, product identification and theoretical calculations. *Science of the Total Environment*, **2021**, 771, 144743	10.2	31
123	The mechanistic, diagnostic and therapeutic novel nucleic acids for hepatocellular carcinoma emerging in past score years. *Briefings in Bioinformatics*, **2021**, 22, 1860-1883	13.4	6
122	MetaFS: Performance assessment of biomarker discovery in metaproteomics. *Briefings in Bioinformatics*, **2021**, 22,	13.4	17
121	MMEASE: Online meta-analysis of metabolomic data by enhanced metabolite annotation, marker selection and enrichment analysis. *Journal of Proteomics*, **2021**, 232, 104023	3.9	21
120	INTEDE: interactome of drug-metabolizing enzymes. *Nucleic Acids Research*, **2021**, 49, D1233-D1243	20.1	29
119	GIMICA: host genetic and immune factors shaping human microbiota. *Nucleic Acids Research*, **2021**, 49, D715-D722	20.1	8
118	Identification of the key target profiles underlying the drugs of narrow therapeutic index for treating cancer and cardiovascular disease. *Computational and Structural Biotechnology Journal*, **2021**, 19, 2318-2328	6.8	2
117	NPCDR: natural product-based drug combination and its disease-specific molecular regulation. *Nucleic Acids Research*, **2021**,	20.1	3
116	Oxidation of benzophenone-3 in aqueous solution by potassium permanganate: kinetics, degradation products, reaction pathways, and toxicity assessment. *Environmental Science and Pollution Research*, **2021**, 28, 31301-31311	5.1	10

115	Comment on: "MicroRNA Mimics or Inhibitors as Antiviral Therapeutic Approaches Against COVID-19". *Drugs*, **2021**, 81, 1691-1692	12.1	3
114	Feature, Function, and Information of Drug Transporter Related Databases. *Drug Metabolism and Disposition*, **2021**,	4	1
113	RNA-RNA interactions between SARS-CoV-2 and host benefit viral development and evolution during COVID-19 infection. *Briefings in Bioinformatics*, **2021**,	13.4	9
112	Consistent gene signature of schizophrenia identified by a novel feature selection strategy from comprehensive sets of transcriptomic data. *Briefings in Bioinformatics*, **2020**, 21, 1058-1068	13.4	74
111	The binding mode of vilazodone in the human serotonin transporter elucidated by ligand docking and molecular dynamics simulations. *Physical Chemistry Chemical Physics*, **2020**, 22, 5132-5144	3.6	14
110	Selective Inhibition of HDAC1 by Macrocyclic Polypeptide for the Treatment of Glioblastoma: A Binding Mechanistic Analysis Based on Molecular Dynamics. *Frontiers in Molecular Biosciences*, **2020**, 7, 41	5.6	5
109	NOREVA: enhanced normalization and evaluation of time-course and multi-class metabolomic data. *Nucleic Acids Research*, **2020**, 48, W436-W448	20.1	66
108	Infiltration of nanocarbon suspension into the tracheal cavity during surgical treatment of papillary thyroid carcinoma: a case report. *Journal of International Medical Research*, **2020**, 48, 300060520919251	1.4	1
107	Therapeutic target database 2020: enriched resource for facilitating research and early development of targeted therapeutics. *Nucleic Acids Research*, **2020**, 48, D1031-D1041	20.1	286
106	Databases for the targeted COVID-19 therapeutics. *British Journal of Pharmacology*, **2020**, 177, 4999-5008	8.6	12
105	SSizer: Determining the Sample Sufficiency for Comparative Biological Study. *Journal of Molecular Biology*, **2020**, 432, 3411-3421	6.5	28
104	Convolutional neural network-based annotation of bacterial type IV secretion system effectors with enhanced accuracy and reduced false discovery. *Briefings in Bioinformatics*, **2020**, 21, 1825-1836	13.4	43
103	Epoxyeicosatrienoic acid prevents maladaptive remodeling in pressure overload by targeting calcineurin/NFAT and Smad-7. *Experimental Cell Research*, **2020**, 386, 111716	4.2	4
102	A novel bioinformatics approach to identify the consistently well-performing normalization strategy for current metabolomic studies. *Briefings in Bioinformatics*, **2020**, 21, 2142-2152	13.4	29
101	CYP2J2/EET reduces vulnerability to atrial fibrillation in chronic pressure overload mice. *Journal of Cellular and Molecular Medicine*, **2020**, 24, 862-874	5.6	8
100	Computational advances of tumor marker selection and sample classification in cancer proteomics. *Computational and Structural Biotechnology Journal*, **2020**, 18, 2012-2025	6.8	15
99	Advances in Current Diabetes Proteomics: From the Perspectives of Label- free Quantification and Biomarker Selection. *Current Drug Targets*, **2020**, 21, 34-54	3	5
98	Recent Advances and Challenges of the Drugs Acting on Monoamine Transporters. *Current Medicinal Chemistry*, **2020**, 27, 3830-3876	4.3	18

97	ANPELA: analysis and performance assessment of the label-free quantification workflow for metaproteomic studies. *Briefings in Bioinformatics*, **2020**, 21, 621-636	13.4	83
96	Clinical trials, progression-speed differentiating features and swiftness rule of the innovative targets of first-in-class drugs. *Briefings in Bioinformatics*, **2020**, 21, 649-662	13.4	67
95	A critical assessment of the feature selection methods used for biomarker discovery in current metaproteomics studies. *Briefings in Bioinformatics*, **2020**, 21, 1378-1390	13.4	21
94	Genome-wide identification and analysis of the eQTL lncRNAs in multiple sclerosis based on RNA-seq data. *Briefings in Bioinformatics*, **2020**, 21, 1023-1037	13.4	11
93	Effectiveness of low dose of rapamycin in preventing seizure-induced anxiety-like behaviour, cognitive impairment, and defects in neurogenesis in developing rats. *International Journal of Neuroscience*, **2020**, 130, 9-18	2	1
92	Protein functional annotation of simultaneously improved stability, accuracy and false discovery rate achieved by a sequence-based deep learning. *Briefings in Bioinformatics*, **2020**, 21, 1437-1447	13.4	53
91	VARIDT 1.0: variability of drug transporter database. *Nucleic Acids Research*, **2020**, 48, D1042-D1050	20.1	74
90	Recent Technological Advances in the Mass Spectrometry-based Nanomedicine Studies: An Insight from Nanoproteomics. *Current Pharmaceutical Design*, **2019**, 25, 1536-1553	3.3	0
89	The effect of data integration on LC-MS-based metabolomics data: evaluation on the comparative classification capacities. *IOP Conference Series: Earth and Environmental Science*, **2019**, 252, 032166	0.3	
88	SCP2-mediated cholesterol membrane trafficking promotes the growth of pituitary adenomas via Hedgehog signaling activation. *Journal of Experimental and Clinical Cancer Research*, **2019**, 38, 404	12.8	5
87	Simultaneous Improvement in the Precision, Accuracy, and Robustness of Label-free Proteome Quantification by Optimizing Data Manipulation Chains. *Molecular and Cellular Proteomics*, **2019**, 18, 1683-1699	7.6	70
86	Insight into the selective binding mechanism of DNMT1 and DNMT3A inhibitors: a molecular simulation study. *Physical Chemistry Chemical Physics*, **2019**, 21, 12931-12947	3.6	23
85	HawkDock: a web server to predict and analyze the protein-protein complex based on computational docking and MM/GBSA. *Nucleic Acids Research*, **2019**, 47, W322-W330	20.1	139
84	Predicting risk of secondary progression in multiple sclerosis: A nomogram. *Multiple Sclerosis Journal*, **2019**, 25, 1102-1112	5	32
83	Five years before multiple sclerosis onset: Phenotyping the prodrome. *Multiple Sclerosis Journal*, **2019**, 25, 1092-1101	5	35
82	Assessing the performance of the MM/PBSA and MM/GBSA methods. 10. Impacts of enhanced sampling and variable dielectric model on protein-protein Interactions. *Physical Chemistry Chemical Physics*, **2019**, 21, 18958-18969	3.6	41
81	The effects of sample size on omics study: from the perspective of robustness and diagnostic accuracy. *IOP Conference Series: Earth and Environmental Science*, **2019**, 252, 022127	0.3	0
80	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. *Lancet Haematology,the*, **2019**, 6, e521-e529	14.6	138

79	High iodine induces DNA damage in autoimmune thyroiditis partially by inhibiting the DNA repair protein MTH1. *Cellular Immunology*, **2019**, 344, 103948	4.4	2
78	Identification of the gene signature reflecting schizophrenia's etiology by constructing artificial intelligence-based method of enhanced reproducibility. *CNS Neuroscience and Therapeutics*, **2019**, 25, 1054-1063	6.8	15
77	What Makes Species Productive of Anti-Cancer Drugs? Clues from Drugs' Species Origin, Druglikeness, Target and Pathway. *Anti-Cancer Agents in Medicinal Chemistry*, **2019**, 19, 194-203	2.2	10
76	Assessing the Effectiveness of Direct Data Merging Strategy in Long-Term and Large-Scale Pharmacometabonomics. *Frontiers in Pharmacology*, **2019**, 10, 127	5.6	17
75	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. *Journal of Alzheimer's Disease*, **2019**, 68, 339-355	4.3	11
74	How Does Chirality Determine the Selective Inhibition of Histone Deacetylase 6? A Lesson from Trichostatin A Enantiomers Based on Molecular Dynamics. *ACS Chemical Neuroscience*, **2019**, 10, 2467-2480	5.7	49
73	Integrating the Ribonucleic Acid Sequencing Data From Various Studies for Exploring the Multiple Sclerosis-Related Long Noncoding Ribonucleic Acids and Their Functions. *Frontiers in Genetics*, **2019**, 10, 1136	4.5	4
72	Biomarker Discovery for Immunotherapy of Pituitary Adenomas: Enhanced Robustness and Prediction Ability by Modern Computational Tools. *International Journal of Molecular Sciences*, **2019**, 20,	6.3	18
71	farPPI: a webserver for accurate prediction of protein-ligand binding structures for small-molecule PPI inhibitors by MM/PB(GB)SA methods. *Bioinformatics*, **2019**, 35, 1777-1779	7.2	33
70	Regeneration of a Bioengineered Thyroid Using Decellularized Thyroid Matrix. *Thyroid*, **2019**, 29, 142-152	5.2	10
69	Reliability of Docking-Based Virtual Screening for GPCR Ligands with Homology Modeled Structures: A Case Study of the Angiotensin II Type I Receptor. *ACS Chemical Neuroscience*, **2019**, 10, 677-689	5.7	17
68	Computational identification of the binding mechanism of a triple reuptake inhibitor amitifadine for the treatment of major depressive disorder. *Physical Chemistry Chemical Physics*, **2018**, 20, 6606-6616	3.6	79
67	Importance of protein flexibility in molecular recognition: a case study on Type-I1/2 inhibitors of ALK. *Physical Chemistry Chemical Physics*, **2018**, 20, 4851-4863	3.6	21
66	Clinical Success of Drug Targets Prospectively Predicted by In Silico Study. *Trends in Pharmacological Sciences*, **2018**, 39, 229-231	13.2	52
65	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. *ACS Chemical Neuroscience*, **2018**, 9, 1128-1140	5.7	139
64	Assessing the performance of MM/PBSA and MM/GBSA methods. 7. Entropy effects on the performance of end-point binding free energy calculation approaches. *Physical Chemistry Chemical Physics*, **2018**, 20, 14450-14460	3.6	149
63	Exploring the Binding Mechanism of Metabotropic Glutamate Receptor 5 Negative Allosteric Modulators in Clinical Trials by Molecular Dynamics Simulations. *ACS Chemical Neuroscience*, **2018**, 9, 1492-1502	5.7	65
62	Assessing the performance of MM/PBSA and MM/GBSA methods. 8. Predicting binding free energies and poses of protein-RNA complexes. *Rna*, **2018**, 24, 1183-1194	5.8	51

61	Discovery of the Consistently Well-Performed Analysis Chain for SWATH-MS Based Pharmacoproteomic Quantification. *Frontiers in Pharmacology*, **2018**, 9, 681	5.6	52
60	Assessing the Performances of Protein Function Prediction Algorithms from the Perspectives of Identification Accuracy and False Discovery Rate. *International Journal of Molecular Sciences*, **2018**, 19,	6.3	25
59	Identification of novel immune-relevant drug target genes for Alzheimer?s Disease by combining ontology inference with network analysis. *CNS Neuroscience and Therapeutics*, **2018**, 24, 1253-1263	6.8	26
58	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. *Physical Chemistry Chemical Physics*, **2018**, 20, 23873-23884	3.6	21
57	Computational Advances in the Label-free Quantification of Cancer Proteomics Data. *Current Pharmaceutical Design*, **2018**, 24, 3842-3858	3.3	12
56	Akt Inhibitor Perifosine Prevents Epileptogenesis in a Rat Model of Temporal Lobe Epilepsy. *Neuroscience Bulletin*, **2018**, 34, 283-290	4.3	14
55	Computational characterization of the selective inhibition of human norepinephrine and serotonin transporters by an escitalopram scaffold. *Physical Chemistry Chemical Physics*, **2018**, 20, 29513-29527	3.6	27
54	Determining the Balance Between Drug Efficacy and Safety by the Network and Biological System Profile of Its Therapeutic Target. *Frontiers in Pharmacology*, **2018**, 9, 1245	5.6	19
53	Prediction of GluN2B-CT/DAPK1 Interaction by Protein?Peptide Docking and Molecular Dynamics Simulation. *Molecules*, **2018**, 23,	4.8	9
52	Comprehensive assessment of nine docking programs on type II kinase inhibitors: prediction accuracy of sampling power, scoring power and screening power. *Briefings in Bioinformatics*, **2018**,	13.4	8
51	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. *Journal of Medicinal Chemistry*, **2018**, 61, 8613-8624	8.3	19
50	Therapeutic target database update 2018: enriched resource for facilitating bench-to-clinic research of targeted therapeutics. *Nucleic Acids Research*, **2018**, 46, D1121-D1127	20.1	322
49	Cheminformatic Insight into the Differences between Terrestrial and Marine Originated Natural Products. *Journal of Chemical Information and Modeling*, **2018**, 58, 1182-1193	6.1	32
48	Disability progression in aggressive multiple sclerosis. *Multiple Sclerosis Journal*, **2017**, 23, 456-463	5	11
47	Infection-related health care utilization among people with and without multiple sclerosis. *Multiple Sclerosis Journal*, **2017**, 23, 1506-1516	5	51
46	Discovery of Novel and Selective Adenosine A Receptor Antagonists for Treating Parkinson?s Disease through Comparative Structure-Based Virtual Screening. *Journal of Chemical Information and Modeling*, **2017**, 57, 1474-1487	6.1	35
45	Age Related Multiple Sclerosis Severity Score: Disability ranked by age. *Multiple Sclerosis Journal*, **2017**, 23, 1938-1946	5	55
44	Comparison of computational model and X-ray crystal structure of human serotonin transporter: potential application for the pharmacology of human monoamine transporters. *Molecular Simulation*, **2017**, 43, 1089-1098	2	17

43	NOREVA: normalization and evaluation of MS-based metabolomics data. *Nucleic Acids Research*, **2017**, 45, W162-W170	20.1	190
42	Differentiating Physicochemical Properties between Addictive and Nonaddictive ADHD Drugs Revealed by Molecular Dynamics Simulation Studies. *ACS Chemical Neuroscience*, **2017**, 8, 1416-1428	5.7	49
41	Revealing vilazodone's binding mechanism underlying its partial agonism to the 5-HT receptor in the treatment of major depressive disorder. *Physical Chemistry Chemical Physics*, **2017**, 19, 28885-28896	3.6	31
40	ADMET Evaluation in Drug Discovery. 18. Reliable Prediction of Chemical-Induced Urinary Tract Toxicity by Boosting Machine Learning Approaches. *Molecular Pharmaceutics*, **2017**, 14, 3935-3953	5.6	46
39	HawkRank: a new scoring function for protein-protein docking based on weighted energy terms. *Journal of Cheminformatics*, **2017**, 9, 66	8.6	31
38	How Does the L884P Mutation Confer Resistance to Type-II Inhibitors of JAK2 Kinase: A Comprehensive Molecular Modeling Study. *Scientific Reports*, **2017**, 7, 9088	4.9	15
37	Metformin inhibits proliferation and growth hormone secretion of GH3 pituitary adenoma cells. *Oncotarget*, **2017**, 8, 37538-37549	3.3	18
36	A protein network descriptor server and its use in studying protein, disease, metabolic and drug targeted networks. *Briefings in Bioinformatics*, **2017**, 18, 1057-1070	13.4	26
35	Differentiating physicochemical properties between NDRIs and sNRIs clinically important for the treatment of ADHD. *Biochimica Et Biophysica Acta - General Subjects*, **2017**, 1861, 2766-2777	4	40
34	Combating Drug-Resistant Mutants of Anaplastic Lymphoma Kinase with Potent and Selective Type-I Inhibitors by Stabilizing Unique DFG-Shifted Loop Conformation. *ACS Central Science*, **2017**, 3, 1208-1220	16.8	30
33	Exploring the Inhibitory Mechanism of Approved Selective Norepinephrine Reuptake Inhibitors and Reboxetine Enantiomers by Molecular Dynamics Study. *Scientific Reports*, **2016**, 6, 26883	4.9	33
32	Identification of the inhibitory mechanism of FDA approved selective serotonin reuptake inhibitors: an insight from molecular dynamics simulation study. *Physical Chemistry Chemical Physics*, **2016**, 18, 3260-71	3.6	47
31	Therapeutic target database update 2016: enriched resource for bench to clinical drug target and targeted pathway information. *Nucleic Acids Research*, **2016**, 44, D1069-74	20.1	193
30	The novel EZH2 inhibitor, GSK126, suppresses cell migration and angiogenesis via down-regulating VEGF-A. *Cancer Chemotherapy and Pharmacology*, **2016**, 77, 757-65	3.5	44
29	SVM-Prot 2016: A Web-Server for Machine Learning Prediction of Protein Functional Families from Sequence Irrespective of Similarity. *PLoS ONE*, **2016**, 11, e0155290	3.7	66
28	The Human Kinome Targeted by FDA Approved Multi-Target Drugs and Combination Products: A Comparative Study from the Drug-Target Interaction Network Perspective. *PLoS ONE*, **2016**, 11, e0165737	3.7	39
27	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. *Health Technology Assessment*, **2016**, 20, 1-48	4.4	14
26	Comparison of FDA Approved Kinase Targets to Clinical Trial Ones: Insights from Their System Profiles and Drug-Target Interaction Networks. *BioMed Research International*, **2016**, 2016, 2509385	3	30

25	The Effects of Hashimoto Thyroiditis on Lymph Node Metastases in Unifocal and Multifocal Papillary Thyroid Carcinoma: A Retrospective Chinese Cohort Study. *Medicine (United States)*, **2016**, 95, e2674	1.8	26
24	Prognostic Value of Bone Mineral Density on Curve Progression: A Longitudinal Cohort Study of 513 Girls with Adolescent Idiopathic Scoliosis. *Scientific Reports*, **2016**, 6, 39220	4.9	29
23	Performance Evaluation and Online Realization of Data-driven Normalization Methods Used in LC/MS based Untargeted Metabolomics Analysis. *Scientific Reports*, **2016**, 6, 38881	4.9	84
22	Evidence for possible role of toll-like receptor 3 mediating virus-induced progression of pituitary adenomas. *Molecular and Cellular Endocrinology*, **2016**, 426, 22-32	4.4	9
21	Neural Progenitor Cells Rptor Ablation Impairs Development but Benefits to Seizure-Induced Behavioral Abnormalities. *CNS Neuroscience and Therapeutics*, **2016**, 22, 1000-1008	6.8	3
20	Clustered distribution of natural product leads of drugs in the chemical space as influenced by the privileged target-sites. *Scientific Reports*, **2015**, 5, 9325	4.9	16
19	Co-targeting cancer drug escape pathways confers clinical advantage for multi-target anticancer drugs. *Pharmacological Research*, **2015**, 102, 123-31	10.2	41
18	Identification of dual active agents targeting 5-HT1A and SERT by combinatorial virtual screening methods. *Bio-Medical Materials and Engineering*, **2015**, 26 Suppl 1, S2233-9	1	19
17	THE DISCRIMINATION OF LEARNING STYLES BY BAYES-BASED STATISTICS: AN EXTENDED STUDY ON ILS SYSTEM. *Control and Intelligent Systems*, **2015**, 43,		6
16	Nature's contribution to today's pharmacopeia. *Nature Biotechnology*, **2014**, 32, 979-80	44.5	26
15	Therapeutic target database update 2014: a resource for targeted therapeutics. *Nucleic Acids Research*, **2014**, 42, D1118-23	20.1	97
14	In silico identification of human pregnane X receptor activators from molecular descriptors by machine learning approaches. *Chemometrics and Intelligent Laboratory Systems*, **2012**, 118, 271-279	3.8	7
13	Analysis of bypass signaling in EGFR pathway and profiling of bypass genes for predicting response to anticancer EGFR tyrosine kinase inhibitors. *Molecular BioSystems*, **2012**, 8, 2645-56		9
12	Therapeutic target database update 2012: a resource for facilitating target-oriented drug discovery. *Nucleic Acids Research*, **2012**, 40, D1128-36	20.1	359
11	Identification of DNA adduct formation of small molecules by molecular descriptors and machine learning methods. *Molecular Simulation*, **2012**, 38, 259-273	2	0
10	Drug discovery prospect from untapped species: indications from approved natural product drugs. *PLoS ONE*, **2012**, 7, e39782	3.7	43
9	The Therapeutic Target Database: an internet resource for the primary targets of approved, clinical trial and experimental drugs. *Expert Opinion on Therapeutic Targets*, **2011**, 15, 903-12	6.4	15
8	Clustered patterns of species origins of nature-derived drugs and clues for future bioprospecting. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 12943-8	11.5	177

7	Update of TTD: Therapeutic Target Database. *Nucleic Acids Research*, **2010**, 38, D787-91	20.1	190
6	What are next generation innovative therapeutic targets? Clues from genetic, structural, physicochemical, and systems profiles of successful targets. *Journal of Pharmacology and Experimental Therapeutics*, **2009**, 330, 304-15	4.7	43
5	Comparative analysis of machine learning methods in ligand-based virtual screening of large compound libraries. *Combinatorial Chemistry and High Throughput Screening*, **2009**, 12, 344-57	1.3	47
4	Mechanisms of drug combinations: interaction and network perspectives. *Nature Reviews Drug Discovery*, **2009**, 8, 111-28	64.1	603
3	Support vector machines approach for predicting druggable proteins: recent progress in its exploration and investigation of its usefulness. *Drug Discovery Today*, **2007**, 12, 304-13	8.8	58
2	Response of human REV3 gene to gastric cancer inducing carcinogen N-methyl-NRnitro-N-nitrosoguanidine and its role in mutagenesis. *World Journal of Gastroenterology*, **2003**, 9, 888-93	5.6	17
1	DNA polymerase zeta: new insight into eukaryotic mutagenesis and mammalian embryonic development. *World Journal of Gastroenterology*, **2003**, 9, 1165-9	5.6	18