# Feixiong Cheng

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/2994228/publications.pdf

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|---|---|---|---|
| 145 papers | 12,267 citations | 38742 50 h-index | 29157 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. Journal of Chemical Information and Modeling, 2012, 52, 3099-3105. | 5.4 | 1,439 |
| 2 | Network-based drug repurposing for novel coronavirus 2019-nCoV/SARS-CoV-2. Cell Discovery, 2020, 6, 14. | 6.7 | 1,258 |
| 3 | Prediction of Drug-Target Interactions and Drug Repositioning via Network-Based Inference. PLoS Computational Biology, 2012, 8, e1002503. | 3.2 | 674 |
| 4 | Network-based prediction of drug combinations. Nature Communications, 2019, 10, 1197. | 12.8 | 437 |
| 5 | Artificial intelligence in COVID-19 drug repurposing. The Lancet Digital Health, 2020, 2, e667-e676. | 12.3 | 349 |
| 6 | deepDR: a network-based deep learning approach toin silicodrug repositioning. Bioinformatics, 2019, 35, 5191-5198. | 4.1 | 343 |
| 7 | SoNar, a Highly Responsive NAD+/NADH Sensor, Allows High-Throughput Metabolic Screening of Anti-tumor Agents. Cell Metabolism, 2015, 21, 777-789. | 16.2 | 311 |
| 8 | New insights into genetic susceptibility of COVID-19: an ACE2 and TMPRSS2 polymorphism analysis. BMC Medicine, 2020, 18, 216. | 5.5 | 304 |
| 9 | Estimation of ADME Properties with Substructure Pattern Recognition. Journal of Chemical Information and Modeling, 2010, 50, 1034-1041. | 5.4 | 266 |
| 10 | 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. | 4.4 | 264 |
| 11 | Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. Cell Reports, 2018, 23, 255-269.e4. | 6.4 | 204 |
| 12 | Suppression of the SLC7A11/glutathione axis causes synthetic lethality in KRAS-mutant lung adenocarcinoma. Journal of Clinical Investigation, 2020, 130, 1752-1766. | 8.2 | 200 |
| 13 | Target identification among known drugs by deep learning from heterogeneous networks. Chemical Science, 2020, 11, 1775-1797. | 7.4 | 193 |
| 14 | Repurpose Open Data to Discover Therapeutics for COVID-19 Using Deep Learning. Journal of Proteome Research, 2020, 19, 4624-4636. | 3.7 | 183 |
| 15 | In Silico ADMET Prediction: Recent Advances, Current Challenges and Future Trends. Current Topics in Medicinal Chemistry, 2013, 13, 1273-1289. | 2.1 | 181 |
| 16 | In silico Prediction of Chemical Ames Mutagenicity. Journal of Chemical Information and Modeling, 2012, 52, 2840-2847. | 5.4 | 163 |
| 17 | Classification of Cytochrome P450 Inhibitors and Noninhibitors Using Combined Classifiers. Journal of Chemical Information and Modeling, 2011, 51, 996-1011. | 5.4 | 155 |
| 18 | In Silico Prediction of Chemical Acute Oral Toxicity Using Multi-Classification Methods. Journal of Chemical Information and Modeling, 2014, 54, 1061-1069. | 5.4 | 140 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | A network medicine approach to investigation and population-based validation of disease manifestations and drug repurposing for COVID-19. PLoS Biology, 2020, 18, e3000970. | 5.6 | 139 |
| 20 | A genome-wide positioning systems network algorithm for in silico drug repurposing. Nature Communications, 2019, 10, 3476. | 12.8 | 134 |
| 21 | Computational network biology: Data, models, and applications. Physics Reports, 2020, 846, 1-66. | 25.6 | 126 |
| 22 | Deep Learning-Based Prediction of Drug-Induced Cardiotoxicity. Journal of Chemical Information and Modeling, 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. Nature Neuroscience, 2019, 22, 691-699. | 14.8 | 118 |
| 24 | Adverse Drug Events: Database Construction and in Silico Prediction. Journal of Chemical Information and Modeling, 2013, 53, 744-752. | 5.4 | 116 |
| 25 | Comprehensive characterization of proteinâ€“protein interactions perturbed by disease mutations. Nature Genetics, 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. Alzheimer's Research and Therapy, 2021, 13, 110. | 6.2 | 108 |
| 27 | SDTNBI: an integrated network and chemoinformatics tool for systematic prediction of drugâ€“target interactions and drug repositioning. Briefings in Bioinformatics, 2017, 18, bbw012. | 6.5 | 102 |
| 28 | Network-based prediction of drugâ€“target interactions using an arbitrary-order proximity embedded deep forest. Bioinformatics, 2020, 36, 2805-2812. | 4.1 | 101 |
| 29 | Prediction of chemicalâ€“protein interactions: multitarget-QSAR versus computational chemogenomic methods. Molecular BioSystems, 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. Oncotarget, 2014, 5, 3697-3710. | 1.8 | 96 |
| 31 | In silico polypharmacology of natural products. Briefings in Bioinformatics, 2018, 19, 1153-1171. | 6.5 | 95 |
| 32 | Reducing acetylated tau is neuroprotective in brain injury. Cell, 2021, 184, 2715-2732.e23. | 28.9 | 91 |
| 33 | In Silico Assessment of Chemical Biodegradability. Journal of Chemical Information and Modeling, 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 Alzheimerâ€™s disease. Nature Aging, 2021, 1, 1175-1188. | 11.6 | 87 |
| 35 | Prediction of Chemical-Protein Interactions Network with Weighted Network-Based Inference Method. PLoS ONE, 2012, 7, e41064. | 2.5 | 86 |
| 36 | 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. | 5.4 | 86 |

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|---|---|---|---|
| 37 | Network-based identification of microRNAs as potential pharmacogenomic biomarkers for anticancer drugs. Oncotarget, 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. PLoS Computational Biology, 2019, 15, e1006658. | 3.2 | 83 |
| 39 | Studying Tumorigenesis through Network Evolution and Somatic Mutational Perturbations in the Cancer Interactome. Molecular Biology and Evolution, 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. Cancer Research, 2017, 77, 3280-3292. | 0.9 | 76 |
| 41 | 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. | 5.4 | 76 |
| 42 | In silico prediction of Tetrahymena pyriformis toxicity for diverse industrial chemicals with substructure pattern recognition and machine learning methods. Chemosphere, 2011, 82, 1636-1643. | 8.2 | 75 |
| 43 | In silico Prediction of Drug Induced Liver Toxicity Using Substructure Pattern Recognition Method. Molecular Informatics, 2016, 35, 136-144. | 2.5 | 75 |
| 44 | Suppression of KRas-mutant cancer through the combined inhibition of KRAS with PLK1 and ROCK. Nature Communications, 2016, 7, 11363. | 12.8 | 74 |
| 45 | In silico prediction of chemical mechanism of action via an improved networkâ€based inference method. British Journal of Pharmacology, 2016, 173, 3372-3385. | 5.4 | 73 |
| 46 | 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. | 6.2 | 72 |
| 47 | Drug Repurposing: New Treatments for Zika Virus Infection?. Trends in Molecular Medicine, 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. PLoS Computational Biology, 2015, 11, e1004497. | 3.2 | 65 |
| 49 | Harnessing endophenotypes and network medicine for Alzheimer's drug repurposing. Medicinal Research Reviews, 2020, 40, 2386-2426. | 10.5 | 61 |
| 50 | Insights into Molecular Basis of Cytochrome P450 Inhibitory Promiscuity of Compounds. Journal of Chemical Information and Modeling, 2011, 51, 2482-2495. | 5.4 | 60 |
| 51 | Reprogramming immunosuppressive myeloid cells facilitates immunotherapy for colorectal cancer. EMBO Molecular Medicine, 2021, 13, e12798. | 6.9 | 59 |
| 52 | Individualized network-based drug repositioning infrastructure for precision oncology in the panomics era. Briefings in Bioinformatics, 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. Journal of Proteome Research, 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. Cell Chemical Biology, 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. Genome Research, 2021, 31, 1900-1912. | 5.5 | 53 |
| 56 | Systems Biology-Based Investigation of Cellular Antiviral Drug Targets Identified by Gene-Trap Insertional Mutagenesis. PLoS Computational Biology, 2016, 12, e1005074. | 3.2 | 52 |
| 57 | Computational prediction of microRNA networks incorporating environmental toxicity and disease etiology. Scientific Reports, 2014, 4, 5576. | 3.3 | 51 |
| 58 | Repurposing sertraline sensitizes nonâ€“small cell lung cancer cells to erlotinib by inducing autophagy. JCI Insight, 2018, 3, . | 5.0 | 51 |
| 59 | iDrug: Integration of drug repositioning and drug-target prediction via cross-network embedding. PLoS Computational Biology, 2020, 16, e1008040. | 3.2 | 51 |
| 60 | Computational models to predict endocrine-disrupting chemical binding with androgen or oestrogen receptors. Ecotoxicology and Environmental Safety, 2014, 110, 280-287. | 6.0 | 50 |
| 61 | In Silico Oncology Drug Repositioning and Polypharmacology. Methods in Molecular Biology, 2019, 1878, 243-261. | 0.9 | 48 |
| 62 | Deep learning for drug repurposing: Methods, databases, and applications. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2022, 12, . | 14.6 | 48 |
| 63 | Personal Mutanomes Meet Modern Oncology Drug Discovery and Precision Health. Pharmacological Reviews, 2019, 71, 1-19. | 16.0 | 47 |
| 64 | Epilepsy subtype-specific copy number burden observed in a genome-wide study of 17â€‰458 subjects. Brain, 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. Journal of the American Medical Informatics Association: JAMIA, 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. American Journal of Human Genetics, 2019, 104, 861-878. | 6.2 | 45 |
| 67 | FXR antagonism of NSAIDs contributes to drug-induced liver injury identified by systems pharmacology approach. Scientific Reports, 2015, 5, 8114. | 3.3 | 44 |
| 68 | AlzGPS: a genome-wide positioning systems platform to catalyze multi-omics for Alzheimerâ€™s drug discovery. Alzheimer's Research and Therapy, 2021, 13, 24. | 6.2 | 44 |
| 69 | Systematic Prioritization of Druggable Mutations in â¼5000 Genomes Across 16 Cancer Types Using a Structural Genomics-based Approach. Molecular and Cellular Proteomics, 2016, 15, 642-656. | 3.8 | 43 |
| 70 | Precision medicine review: rare driver mutations and their biophysical classification. Biophysical Reviews, 2019, 11, 5-19. | 3.2 | 43 |
| 71 | Artificial intelligence framework identifies candidate targets for drug repurposing in Alzheimerâ€™s disease. Alzheimer's Research and Therapy, 2022, 14, 7. | 6.2 | 42 |
| 72 | In silico prediction of chemical toxicity on avian species using chemical category approaches. Chemosphere, 2015, 122, 280-287. | 8.2 | 41 |

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| 73 | ccmGDB: a database for cancer cell metabolism genes. Nucleic Acids Research, 2016, 44, D959-D968. | 14.5 | 41 |
| 74 | Applications of artificial intelligence in multimodality cardiovascular imaging: A state-of-the-art review. Progress in Cardiovascular Diseases, 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. Frontiers in Pharmacology, 2017, 8, 747. | 3.5 | 38 |
| 76 | Comprehensive germline genomic profiles of children, adolescents and young adults with solid tumors. Nature Communications, 2020, 11, 2206. | 12.8 | 38 |
| 77 | In Silico Pharmacoepidemiologic Evaluation of Drug-Induced Cardiovascular Complications Using Combined Classifiers. Journal of Chemical Information and Modeling, 2018, 58, 943-956. | 5.4 | 37 |
| 78 | Investigating cellular network heterogeneity and modularity in cancer: a network entropy and unbalanced motif approach. BMC Systems Biology, 2016, 10, 65. | 3.0 | 36 |
| 79 | Inhibition of histone deacetylases sensitizes EGF receptorâ€TK inhibitorâ€resistant nonâ€smallâ€cell lung cancer cells to erlotinib <scp>in vitro</scp> and <scp>in vivo</scp>. British Journal of Pharmacology, 2017, 174, 3608-3622. | 5.4 | 34 |
| 80 | Mechanical forces induce an asthma gene signature in healthy airway epithelial cells. Scientific Reports, 2020, 10, 966. | 3.3 | 34 |
| 81 | Investigation of Indazole Unbinding Pathways in CYP2E1 by Molecular Dynamics Simulations. PLoS ONE, 2012, 7, e33500. | 2.5 | 32 |
| 82 | Autoimmune Cardiotoxicity of Cancer Immunotherapy. Trends in Immunology, 2017, 38, 77-78. | 6.8 | 32 |
| 83 | Individualized genetic network analysis reveals new therapeutic vulnerabilities in 6,700 cancer genomes. PLoS Computational Biology, 2020, 16, e1007701. | 3.2 | 32 |
| 84 | Functional consequences of somatic mutations in cancer using protein pocket-based prioritization approach. Genome Medicine, 2014, 6, 81. | 8.2 | 31 |
| 85 | A new precision medicine initiative at the dawn of exascale computing. Signal Transduction and Targeted Therapy, 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. Journal of Medicinal Chemistry, 2017, 60, 1817-1828. | 6.4 | 30 |
| 87 | Insights into binding modes of adenosine A2B antagonists with ligand-based and receptor-based methods. European Journal of Medicinal Chemistry, 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. Cancer Research, 2017, 77, 2810-2821. | 0.9 | 29 |
| 89 | An integrative functional genomics framework for effective identification of novel regulatory variants in genomeâ€“phenome studies. Genome Medicine, 2018, 10, 7. | 8.2 | 29 |
| 90 | Prediction of human genes and diseases targeted by xenobiotics using predictive toxicogenomic-derived models (PTDMs). Molecular BioSystems, 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. Biomarkers in Medicine, 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. Pharmacological Research, 2018, 129, 400-413. | 7.1 | 28 |
| 93 | Quantitative and systems pharmacology 4. Network-based analysis of drug pleiotropy on coronary artery disease. European Journal of Medicinal Chemistry, 2019, 161, 192-204. | 5.5 | 25 |
| 94 | A network-based approach to uncover microRNA-mediated disease comorbidities and potential pathobiological implications. Npj Systems Biology and Applications, 2019, 5, 41. | 3.0 | 24 |
| 95 | 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. | 5.4 | 22 |
| 96 | COVID-19 treatment: Combining anti-inflammatory and antiviral therapeutics using a network-based approach. Cleveland Clinic Journal of Medicine, 2020, , . | 1.3 | 21 |
| 97 | PTEN Mutations Trigger Resistance to Immunotherapy. Trends in Molecular Medicine, 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. Scientific Reports, 2015, 5, 12063. | 3.3 | 19 |
| 99 | Cardiac risk stratification in cancer patients: A longitudinal patientâ€“patient network analysis. PLoS Medicine, 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. Scientific Reports, 2021, 11, 6985. | 3.3 | 18 |
| 101 | KRAS Activating Signaling Triggers Arteriovenous Malformations. Trends in Biochemical Sciences, 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. Journal of Biomolecular Structure and Dynamics, 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. PLoS Computational Biology, 2019, 15, e1006772. | 3.2 | 14 |
| 104 | A retrospective analysis of cardiovascular adverse events associated with immune checkpoint inhibitors. Cardio-Oncology, 2021, 7, 19. | 1.7 | 14 |
| 105 | Systemic Administration of Tempol Attenuates the Cardiorespiratory Depressant Effects of Fentanyl. Frontiers in Pharmacology, 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. Frontiers in Pharmacology, 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. Breast Cancer Research and Treatment, 2016, 160, 457-474. | 2.5 | 13 |
| 108 | In Silico Insights into Proteinâ€“Protein Interaction Disruptive Mutations in the PCSK9-LDLR Complex. International Journal of Molecular Sciences, 2020, 21, 1550. | 4.1 | 13 |

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|---|---|---|---|
| 109 | 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. | 17.1 | 13 |
| 110 | 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. | 5.7 | 13 |
| 111 | Pharmacophore modeling of human adenosine receptor A2A antagonists. Journal of Molecular Modeling, 2010, 16, 1867-1876. | 1.8 | 12 |
| 112 | Pik3c3 deficiency in myeloid cells imparts partial resistance to experimental autoimmune encephalomyelitis associated with reduced IL-1Î² production. Cellular and Molecular Immunology, 2021, 18, 2024-2039. | 10.5 | 12 |
| 113 | Identifying miRNAs in multiple sclerosis gray matter lesions that correlate with atrophy measures. Annals of Clinical and Translational Neurology, 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. Genome Biology, 2021, 22, 53. | 8.8 | 11 |
| 115 | Agingâ€related cell typeâ€specific pathophysiologic immune responses that exacerbate disease severity in aged COVIDâ€19 patients. Aging Cell, 2022, 21, e13544. | 6.7 | 11 |
| 116 | Computational Insights into Ligand Selectivity of Estrogen Receptors from Pharmacophore Modeling. Molecular Informatics, 2011, 30, 539-549. | 2.5 | 10 |
| 117 | Importance of scientific collaboration in contemporary drug discovery and development: a detailed network analysis. BMC Biology, 2020, 18, 138. | 3.8 | 10 |
| 118 | A network-based deep learning methodology for stratification of tumor mutations. Bioinformatics, 2021, 37, 82-88. | 4.1 | 10 |
| 119 | A cross-cancer differential co-expression network reveals microRNA-regulated oncogenic functional modules. Molecular BioSystems, 2015, 11, 3244-3252. | 2.9 | 9 |
| 120 | Pulmonary Comorbidity in Lung Cancer. Trends in Molecular Medicine, 2018, 24, 239-241. | 6.7 | 8 |
| 121 | Phosphorylation of PLCÎ³1 by EphA2 Receptor Tyrosine Kinase Promotes Tumor Growth in Lung Cancer. Molecular Cancer Research, 2020, 18, 1735-1743. | 3.4 | 8 |
| 122 | Establishing an interdisciplinary research team for cardio-oncology artificial intelligence informatics precision and health equity. American Heart Journal Plus, 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. Systems Medicine (New Rochelle, N Y ), 2020, 3, 22-35. | 1.1 | 7 |
| 124 | Pharmacogenomics for immunotherapy and immune-related cardiotoxicity. Human Molecular Genetics, 2020, 29, R186-R196. | 2.9 | 7 |
| 125 | Open Structural Data in Precision Medicine. Annual Review of Biomedical Data Science, 2022, 5, 95-117. | 6.5 | 7 |
| 126 | Gender Dimorphism Creates Divergent Cancer Susceptibilities. Trends in Cancer, 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. Frontiers in Neuroscience, 2021, 15, 606926. | 2.8 | 6 |
| 128 | Shape shifting: The multiple conformational substates of the <scp>PTEN</scp> Nâ€terminal <scp>PIP<sub>2</sub></scp>â€binding domain. Protein Science, 2022, 31, e4308. | 7.6 | 6 |
| 129 | Temporal Trends of Cardiac Outcomes and Impact on Survival in Patients With Cancer. American Journal of Cardiology, 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. Open Heart, 2020, 7, e001412. | 2.3 | 3 |
| 131 | Target Identification Among Known Drugs by Deep Learning from Heterogeneous Networks. SSRN Electronic Journal, 0, , . | 0.4 | 3 |
| 132 | Editorial overview: Artificial intelligence (AI) methodologies in structural biology. Current Opinion in Structural Biology, 2022, , 102387. | 5.7 | 3 |
| 133 | Comparative pharmacophore modeling of human adenosine receptor A1 and A3 antagonists. Science China Chemistry, 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. Journal of Immunology, 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. Circulation: Cardiovascular Imaging, 2022, 15, e013829. | 2.6 | 2 |
| 137 | Cardio-oncology: Network-Based Prediction of Cancer Therapy-Induced Cardiotoxicity. Challenges and Advances in Computational Chemistry and Physics, 2019, , 75-97. | 0.6 | 1 |
| 138 | Pharmacogenomics meets precision cardio-oncology: is there synergistic potential?. Human Molecular Genetics, 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 |
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| 145 | Title is missing!. , 2020, 18, e3000970. | | 0 |