# Xing Chen

List of Publications by Year
in descending order



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|---|---|---|---|
| 143 papers | 14,364 citations | 23567 58 h-index | 20358 116 g-index |
| 145 all docs | 145 docs citations | 145 times ranked | 6501 citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | LncRNADisease: a database for long-non-coding RNA-associated diseases. Nucleic Acids Research, 2012, 41, D983-D986. | 14.5 | 869 |
| 2 | Novel human lncRNAâ€"disease association inference based on lncRNA expression profiles. Bioinformatics, 2013, 29, 2617-2624. | 4.1 | 558 |
| 3 | MicroRNAs and complex diseases: from experimental results to computational models. Briefings in Bioinformatics, 2019, 20, 515-539. | 6.5 | 507 |
| 4 | Drugâ€"target interaction prediction: databases, web servers and computational models. Briefings in Bioinformatics, 2016, 17, 696-712. | 6.5 | 496 |
| 5 | Long non-coding RNAs and complex diseases: from experimental results to computational models. Briefings in Bioinformatics, 2017, 18, bbw060. | 6.5 | 477 |
| 6 | Predicting miRNAâ€"disease association based on inductive matrix completion. Bioinformatics, 2018, 34, 4256-4265. | 4.1 | 448 |
| 7 | Drugâ€"target interaction prediction by random walk on the heterogeneous network. Molecular BioSystems, 2012, 8, 1970. | 2.9 | 442 |
| 8 | RWRMDA: predicting novel human microRNAâ€"disease associations. Molecular BioSystems, 2012, 8, 2792. | 2.9 | 389 |
| 9 | PBMDA: A novel and effective path-based computational model for miRNA-disease association prediction. PLoS Computational Biology, 2017, 13, e1005455. | 3.2 | 387 |
| 10 | Semi-supervised learning for potential human microRNA-disease associations inference. Scientific Reports, 2014, 4, 5501. | 3.3 | 324 |
| 11 | MDHGI: Matrix Decomposition and Heterogeneous Graph Inference for miRNA-disease association prediction. PLoS Computational Biology, 2018, 14, e1006418. | 3.2 | 323 |
| 12 | WBSMDA: Within and Between Score for MiRNA-Disease Association prediction. Scientific Reports, 2016, 6, 21106. | 3.3 | 314 |
| 13 | BNPMDA: Bipartite Network Projection for MiRNAâ€"Disease Association prediction. Bioinformatics, 2018, 34, 3178-3186. | 4.1 | 307 |
| 14 | EGBMMDA: Extreme Gradient Boosting Machine for MiRNA-Disease Association prediction. Cell Death and Disease, 2018, 9, 3. | 6.3 | 256 |
| 15 | LRSSLMDA: Laplacian Regularized Sparse Subspace Learning for MiRNA-Disease Association prediction. PLoS Computational Biology, 2017, 13, e1005912. | 3.2 | 254 |
| 16 | NLLSS: Predicting Synergistic Drug Combinations Based on Semi-supervised Learning. PLoS Computational Biology, 2016, 12, e1004975. | 3.2 | 250 |
| 17 | A novel approach based on KATZ measure to predict associations of human microbiota with non-infectious diseases. Bioinformatics, 2017, 33, 733-739. | 4.1 | 222 |
| 18 | HGIMDA: Heterogeneous graph inference for miRNA-disease association prediction. Oncotarget, 2016, 7, 65257-65269. | 1.8 | 219 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | Predicting lncRNA-disease associations and constructing lncRNA functional similarity network based on the information of miRNA. Scientific Reports, 2015, 5, 13186. | 3.3 | 207 |
| 20 | KATZLDA: KATZ measure for the lncRNA-disease association prediction. Scientific Reports, 2015, 5, 16840. | 3.3 | 205 |
| 21 | IRWRLDA: improved random walk with restart for lncRNA-disease association prediction. Oncotarget, 2016, 7, 57919-57931. | 1.8 | 200 |
| 22 | Constructing lncRNA functional similarity network based on lncRNA-disease associations and disease semantic similarity. Scientific Reports, 2015, 5, 11338. | 3.3 | 195 |
| 23 | MCMDA: Matrix completion for MiRNA-disease association prediction. Oncotarget, 2017, 8, 21187-21199. | 1.8 | 189 |
| 24 | Feasibility and cardiac synchrony of permanent left bundle branch pacing through the interventricular septum. Europace, 2019, 21, 1694-1702. | 1.7 | 173 |
| 25 | Ensemble of decision tree reveals potential miRNA-disease associations. PLoS Computational Biology, 2019, 15, e1007209. | 3.2 | 166 |
| 26 | RBMMMDA: predicting multiple types of disease-microRNA associations. Scientific Reports, 2015, 5, 13877. | 3.3 | 154 |
| 27 | RKNNMDA: Ranking-based KNN for MiRNA-Disease Association prediction. RNA Biology, 2017, 14, 952-962. | 3.1 | 152 |
| 28 | NCMCMDA: miRNAâ€"disease association prediction through neighborhood constraint matrix completion. Briefings in Bioinformatics, 2021, 22, 485-496. | 6.5 | 148 |
| 29 | DroidDet: Effective and robust detection of android malware using static analysis along with rotation forest model. Neurocomputing, 2018, 272, 638-646. | 5.9 | 146 |
| 30 | Computational models for lncRNA function prediction and functional similarity calculation. Briefings in Functional Genomics, 2019, 18, 58-82. | 2.7 | 141 |
| 31 | A Computational-Based Method for Predicting Drugâ€"Target Interactions by Using Stacked Autoencoder Deep Neural Network. Journal of Computational Biology, 2018, 25, 361-373. | 1.6 | 140 |
| 32 | A Computational Framework to Infer Human Disease-Associated Long Noncoding RNAs. PLoS ONE, 2014, 9, e84408. | 2.5 | 130 |
| 33 | Sequence-based prediction of protein-protein interactions using weighted sparse representation model combined with global encoding. BMC Bioinformatics, 2016, 17, 184. | 2.6 | 125 |
| 34 | Adaptive boosting-based computational model for predicting potential miRNA-disease associations. Bioinformatics, 2019, 35, 4730-4738. | 4.1 | 125 |
| 35 | ILNCSIM: improved lncRNA functional similarity calculation model. Oncotarget, 2016, 7, 25902-25914. | 1.8 | 122 |
| 36 | Circular RNAs and complex diseases: from experimental results to computational models. Briefings in Bioinformatics, 2021, 22, . | 6.5 | 116 |

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|---|---|---|---|
| 37 | MeT-DB V2.0: elucidating context-specific functions of N6-methyl-adenosine methyltranscriptome. Nucleic Acids Research, 2018, 46, D281-D287. | 14.5 | 115 |
| 38 | Predicting proteinâ€"protein interactions from protein sequences by a stacked sparse autoencoder deep neural network. Molecular BioSystems, 2017, 13, 1336-1344. | 2.9 | 114 |
| 39 | LRLSHMDA: Laplacian Regularized Least Squares for Human Microbeâ€"Disease Association prediction. Scientific Reports, 2017, 7, 7601. | 3.3 | 112 |
| 40 | LMTRDA: Using logistic model tree to predict MiRNA-disease associations by fusing multi-source information of sequences and similarities. PLoS Computational Biology, 2019, 15, e1006865. | 3.2 | 111 |
| 41 | Prediction of microbeâ€"disease association from the integration of neighbor and graph with collaborative recommendation model. Journal of Translational Medicine, 2017, 15, 209. | 4.4 | 105 |
| 42 | MicroRNA-small molecule association identification: from experimental results to computational models. Briefings in Bioinformatics, 2018, , . | 6.5 | 105 |
| 43 | FMLNCSIM: fuzzy measure-based lncRNA functional similarity calculation model. Oncotarget, 2016, 7, 45948-45958. | 1.8 | 103 |
| 44 | Deep-belief network for predicting potential miRNA-disease associations. Briefings in Bioinformatics, 2021, 22, . | 6.5 | 101 |
| 45 | PBHMDA: Path-Based Human Microbe-Disease Association Prediction. Frontiers in Microbiology, 2017, 8, 233. | 3.5 | 97 |
| 46 | Novel Human miRNA-Disease Association Inference Based on Random Forest. Molecular Therapy - Nucleic Acids, 2018, 13, 568-579. | 5.1 | 97 |
| 47 | Smartphone-based sensing system using ZnO and graphene modified electrodes for VOCs detection. Biosensors and Bioelectronics, 2017, 93, 94-101. | 10.1 | 95 |
| 48 | RFDT: A Rotation Forest-based Predictor for Predicting Drug-Target Interactions Using Drug Structure and Protein Sequence Information. Current Protein and Peptide Science, 2018, 19, 445-454. | 1.4 | 94 |
| 49 | MicroRNA-34a overcomes HGF-mediated gefitinib resistance in EGFR mutant lung cancer cells partly by targeting MET. Cancer Letters, 2014, 351, 265-271. | 7.2 | 75 |
| 50 | DRMDA: deep representationsâ€based miRNAâ€"disease association prediction. Journal of Cellular and Molecular Medicine, 2018, 22, 472-485. | 3.6 | 75 |
| 51 | RNA methylation and diseases: experimental results, databases, Web servers and computational models. Briefings in Bioinformatics, 2019, 20, 896-917. | 6.5 | 74 |
| 52 | A Systematic Prediction of Drug-Target Interactions Using Molecular Fingerprints and Protein Sequences. Current Protein and Peptide Science, 2018, 19, 468-478. | 1.4 | 69 |
| 53 | FGF15 Activates Hippo Signaling to Suppress Bile Acid Metabolism and Liver Tumorigenesis. Developmental Cell, 2019, 48, 460-474.e9. | 7.0 | 68 |
| 54 | Prediction of Disease-Related Interactions between MicroRNAs and Environmental Factors Based on a Semi-Supervised Classifier. PLoS ONE, 2012, 7, e43425. | 2.5 | 66 |

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|---|---|---|---|
| 55 | VEGF stimulated the angiogenesis by promoting the mitochondrial functions. Oncotarget, 2017, 8, 77020-77027. | 1.8 | 66 |
| 56 | Inferring potential small moleculeâ€"miRNA association based on triple layer heterogeneous network. Journal of Cheminformatics, 2018, 10, 30. | 6.1 | 65 |
| 57 | ASDCD: Antifungal Synergistic Drug Combination Database. PLoS ONE, 2014, 9, e86499. | 2.5 | 65 |
| 58 | In silico prediction of drug-target interaction networks based on drug chemical structure and protein sequences. Scientific Reports, 2017, 7, 11174. | 3.3 | 62 |
| 59 | Anticancer Drug Response Prediction in Cell Lines Using Weighted Graph Regularized Matrix Factorization. Molecular Therapy - Nucleic Acids, 2019, 17, 164-174. | 5.1 | 62 |
| 60 | Prediction of Drugâ€"Target Interaction Networks from the Integration of Protein Sequences and Drug Chemical Structures. Molecules, 2017, 22, 1119. | 3.8 | 61 |
| 61 | PCVMZM: Using the Probabilistic Classification Vector Machines Model Combined with a Zernike Moments Descriptor to Predict Proteinâ€"Protein Interactions from Protein Sequences. International Journal of Molecular Sciences, 2017, 18, 1029. | 4.1 | 61 |
| 62 | NRDTD: a database for clinically or experimentally supported non-coding RNAs and drug targets associations. Database: the Journal of Biological Databases and Curation, 2017, 2017, . | 3.0 | 60 |
| 63 | ELLPMDA: Ensemble learning and link prediction for miRNA-disease association prediction. RNA Biology, 2018, 15, 1-12. | 3.1 | 58 |
| 64 | Quercetin ameliorates ischemia/reperfusion-induced cognitive deficits by inhibiting ASK1/JNK3/caspase-3 by enhancing the Akt signaling pathway. Biochemical and Biophysical Research Communications, 2016, 478, 199-205. | 2.1 | 57 |
| 65 | MDAD: A Special Resource for Microbe-Drug Associations. Frontiers in Cellular and Infection Microbiology, 2018, 8, 424. | 3.9 | 57 |
| 66 | PSPEL: In Silico Prediction of Self-Interacting Proteins from Amino Acids Sequences Using Ensemble Learning. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 1165-1172. | 3.0 | 56 |
| 67 | Anti-cancer Drug Response Prediction Using Neighbor-Based Collaborative Filtering with Global Effect Removal. Molecular Therapy - Nucleic Acids, 2018, 13, 303-311. | 5.1 | 56 |
| 68 | miREFRWR: a novel disease-related microRNA-environmental factor interactions prediction method. Molecular BioSystems, 2016, 12, 624-633. | 2.9 | 55 |
| 69 | Prediction of subcellular location of apoptosis proteins by incorporating PsePSSM and DCCA coefficient based on LFDA dimensionality reduction. BMC Genomics, 2018, 19, 478. | 2.8 | 55 |
| 70 | Comparison of [68ÂGa]Ga-FAPI-04 and [18F]-FDG for the detection of primary and metastatic lesions in patients with gastric cancer: a bicentric retrospective study. European Journal of Nuclear Medicine and Molecular Imaging, 2022, 49, 732-742. | 6.4 | 55 |
| 71 | In Silico Prediction of Small Molecule-miRNA Associations Based on the HeteSim Algorithm. Molecular Therapy - Nucleic Acids, 2019, 14, 274-286. | 5.1 | 54 |
| 72 | Formulation and Delivery Mode Affect Disposition and Activity of Tyrphostin-Loaded Nanoparticles in the Rat Carotid Model. Arteriosclerosis, Thrombosis, and Vascular Biology, 2001, 21, 1434-1439. | 2.4 | 53 |

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|---|---|---|---|
| 73 | Detection of Interactions between Proteins through Rotation Forest and Local Phase Quantization Descriptors. International Journal of Molecular Sciences, 2016, 17, 21. | 4.1 | 51 |
| 74 | Advancing the prediction accuracy of protein-protein interactions by utilizing evolutionary information from position-specific scoring matrix and ensemble classifier. Journal of Theoretical Biology, 2017, 418, 105-110. | 1.7 | 50 |
| 75 | SNMFSMMA: using symmetric nonnegative matrix factorization and Kronecker regularized least squares to predict potential small molecule-microRNA association. RNA Biology, 2020, 17, 281-291. | 3.1 | 50 |
| 76 | A novel computational model based on super-disease and miRNA for potential miRNAâ€"disease association prediction. Molecular BioSystems, 2017, 13, 1202-1212. | 2.9 | 47 |
| 77 | HAMDA: Hybrid Approach for MiRNA-Disease Association prediction. Journal of Biomedical Informatics, 2017, 76, 50-58. | 4.3 | 47 |
| 78 | Prediction of Potential miRNAâ€"Disease Associations Through a Novel Unsupervised Deep Learning Framework with Variational Autoencoder. Cells, 2019, 8, 1040. | 4.1 | 47 |
| 79 | Construction of reliable proteinâ€"protein interaction networks using weighted sparse representation based classifier with pseudo substitution matrix representation features. Neurocomputing, 2016, 218, 131-138. | 5.9 | 45 |
| 80 | RFSMMA: A New Computational Model to Identify and Prioritize Potential Small Moleculeâ€"MiRNA Associations. Journal of Chemical Information and Modeling, 2019, 59, 1668-1679. | 5.4 | 45 |
| 81 | Predicting potential small moleculeâ€"miRNA associations based on bounded nuclear norm regularization. Briefings in Bioinformatics, 2021, 22, . | 6.5 | 44 |
| 82 | MKRMDA: multiple kernel learning-based Kronecker regularized least squares for MiRNAâ€"disease association prediction. Journal of Translational Medicine, 2017, 15, 251. | 4.4 | 43 |
| 83 | Modeling of signaling crosstalk-mediated drug resistance and its implications on drug combination. Oncotarget, 2016, 7, 63995-64006. | 1.8 | 43 |
| 84 | A heterogeneous label propagation approach to explore the potential associations between miRNA and disease. Journal of Translational Medicine, 2018, 16, 348. | 4.4 | 41 |
| 85 | An ensemble approach for large-scale identification of protein-protein interactions using the alignments of multiple sequences. Oncotarget, 2017, 8, 5149-5159. | 1.8 | 40 |
| 86 | A Hybrid Interpolation Weighted Collaborative Filtering Method for Anti-cancer Drug Response Prediction. Frontiers in Pharmacology, 2018, 9, 1017. | 3.5 | 38 |
| 87 | Prediction of Small Moleculeâ€"MicroRNA Associations by Sparse Learning and Heterogeneous Graph Inference. Molecular Pharmaceutics, 2019, 16, 3157-3166. | 4.6 | 38 |
| 88 | Therapeutic Angiogenesis of Chinese Herbal Medicines in Ischemic Heart Disease: A Review. Frontiers in Pharmacology, 2018, 9, 428. | 3.5 | 37 |
| 89 | A Computational Study of Potential miRNA-Disease Association Inference Based on Ensemble Learning and Kernel Ridge Regression. Frontiers in Bioengineering and Biotechnology, 2020, 8, 40. | 4.1 | 37 |
| 90 | Accurate prediction of protein-protein interactions by integrating potential evolutionary information embedded in PSSM profile and discriminative vector machine classifier. Oncotarget, 2017, 8, 23638-23649. | 1.8 | 36 |

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|---|---|---|---|
| 91 | Highly Accurate Prediction of Protein-Protein Interactions via Incorporating Evolutionary Information and Physicochemical Characteristics. International Journal of Molecular Sciences, 2016, 17, 1396. | 4.1 | 35 |
| 92 | A Novel Computational Method for the Identification of Potential miRNA-Disease Association Based on Symmetric Non-negative Matrix Factorization and Kronecker Regularized Least Square. Frontiers in Genetics, 2018, 9, 324. | 2.3 | 35 |
| 93 | An integrated framework for the identification of potential miRNA-disease association based on novel negative samples extraction strategy. RNA Biology, 2019, 16, 257-269. | 3.1 | 35 |
| 94 | NDAMDA: Network distance analysis for Mi<scp>RNA</scp>â€disease association prediction. Journal of Cellular and Molecular Medicine, 2018, 22, 2884-2895. | 3.6 | 34 |
| 95 | An improved efficient rotation forest algorithm to predict the interactions among proteins. Soft Computing, 2018, 22, 3373-3381. | 3.6 | 34 |
| 96 | Prediction of Potential Small Molecule-Associated MicroRNAs Using Graphlet Interaction. Frontiers in Pharmacology, 2018, 9, 1152. | 3.5 | 33 |
| 97 | PRMDA: personalized recommendation-based MiRNA-disease association prediction. Oncotarget, 2017, 8, 85568-85583. | 1.8 | 32 |
| 98 | Predicting microRNA-disease associations using bipartite local models and hubness-aware regression. RNA Biology, 2018, 15, 1192-1205. | 3.1 | 32 |
| 99 | Potential miRNA-disease association prediction based on kernelized Bayesian matrix factorization. Genomics, 2020, 112, 809-819. | 2.9 | 32 |
| 100 | Improving proteinâ€"protein interactions prediction accuracy using protein evolutionary information and relevance vector machine model. Protein Science, 2016, 25, 1825-1833. | 7.6 | 31 |
| 101 | Prediction of potential miRNAâ€"disease associations based on stacked autoencoder. Briefings in Bioinformatics, 2022, 23, . | 6.5 | 31 |
| 102 | GRMDA: Graph Regression for MiRNA-Disease Association Prediction. Frontiers in Physiology, 2018, 9, 92. | 2.8 | 30 |
| 103 | Integrating random walk and binary regression to identify novel miRNA-disease association. BMC Bioinformatics, 2019, 20, 59. | 2.6 | 30 |
| 104 | Drug-pathway association prediction: from experimental results to computational models. Briefings in Bioinformatics, 2021, 22, . | 6.5 | 30 |
| 105 | Microbes and complex diseases: from experimental results to computational models. Briefings in Bioinformatics, 2021, 22, . | 6.5 | 29 |
| 106 | TLHNMDA: Triple Layer Heterogeneous Network Based Inference for MiRNA-Disease Association Prediction. Frontiers in Genetics, 2018, 9, 234. | 2.3 | 27 |
| 107 | A Novel Candidate Disease Genes Prioritization Method Based on Module Partition and Rank Fusion. OMICS A Journal of Integrative Biology, 2010, 14, 337-356. | 2.0 | 25 |
| 108 | Improved protein-protein interactions prediction via weighted sparse representation model combining continuous wavelet descriptor and PseAA composition. BMC Systems Biology, 2016, 10, 120. | 3.0 | 25 |

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| 109 | GIMDA: Graphlet interactionâ€based MiRNAâ€disease association prediction. Journal of Cellular and Molecular Medicine, 2018, 22, 1548-1561. | 3.6 | 25 |
| 110 | Identification of self-interacting proteins by exploring evolutionary information embedded in PSI-BLAST-constructed position specific scoring matrix. Oncotarget, 2016, 7, 82440-82449. | 1.8 | 24 |
| 111 | Prediction of potential miRNA-disease associations using matrix decomposition and label propagation. Knowledge-Based Systems, 2019, 186, 104963. | 7.1 | 24 |
| 112 | Ensemble of kernel ridge regression-based small moleculeâ€“miRNA association prediction in human disease. Briefings in Bioinformatics, 2022, 23, . | 6.5 | 24 |
| 113 | Distributed image understanding with semantic dictionary and semantic expansion. Neurocomputing, 2016, 174, 384-392. | 5.9 | 23 |
| 114 | NARRMDA: negative-aware and rating-based recommendation algorithm for miRNAâ€“disease association prediction. Molecular BioSystems, 2017, 13, 2650-2659. | 2.9 | 23 |
| 115 | Computational Model Development of Drug-Target Interaction Prediction: A Review. Current Protein and Peptide Science, 2019, 20, 492-494. | 1.4 | 23 |
| 116 | A Unified Framework for the Prediction of Small Moleculeâ€“MicroRNA Association Based on Cross-Layer Dependency Inference on Multilayered Networks. Journal of Chemical Information and Modeling, 2019, 59, 5281-5293. | 5.4 | 22 |
| 117 | HNMDA: heterogeneous network-based miRNAâ€“disease association prediction. Molecular Genetics and Genomics, 2018, 293, 983-995. | 2.1 | 19 |
| 118 | Robust and accurate prediction of protein self-interactions from amino acids sequence using evolutionary information. Molecular BioSystems, 2016, 12, 3702-3710. | 2.9 | 17 |
| 119 | Prediction of protein-protein interactions by label propagation with protein evolutionary and chemical information derived from heterogeneous network. Journal of Theoretical Biology, 2017, 430, 9-20. | 1.7 | 17 |
| 120 | Identification of miRNAâ€“disease associations via multiple information integration with Bayesian ranking. Briefings in Bioinformatics, 2021, 22, . | 6.5 | 17 |
| 121 | Engineering Onâ€Demand Magnetic Coreâ€“Shell Composite Wound Dressing Matrices via Electrohydrodynamic Microâ€Scale Printing. Advanced Engineering Materials, 2019, 21, 1900699. | 3.5 | 16 |
| 122 | Dual-Network Collaborative Matrix Factorization for predicting small molecule-miRNA associations. Briefings in Bioinformatics, 2022, 23, . | 6.5 | 15 |
| 123 | DLREFD: a database providing associations of long non-coding RNAs, environmental factors and phenotypes. Database: the Journal of Biological Databases and Curation, 2017, 2017, . | 3.0 | 12 |
| 124 | Computational Methods for the Prediction of Drug-Target Interactions from Drug Fingerprints and Protein Sequences by Stacked Auto-Encoder Deep Neural Network. Lecture Notes in Computer Science, 2017, , 46-58. | 1.3 | 12 |
| 125 | SSCMDA: spy and super cluster strategy for MiRNA-disease association prediction. Oncotarget, 2018, 9, 1826-1842. | 1.8 | 10 |
| 126 | Computational Models in Non-Coding RNA and Human Disease. International Journal of Molecular Sciences, 2020, 21, 1557. | 4.1 | 9 |

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|---|---|---|---|
| 127 | Crosstalk between hypoxia-sensing ULK1/2 and YAP-driven glycolysis fuels pancreatic ductal adenocarcinoma development. International Journal of Biological Sciences, 2021, 17, 2772-2794. | 6.4 | 9 |
| 128 | Stochastic modeling suggests that noise reduces differentiation efficiency by inducing a heterogeneous drug response in glioma differentiation therapy. BMC Systems Biology, 2016, 10, 73. | 3.0 | 8 |
| 129 | A potential target gene for the host-directed therapy of mycobacterial infection in murine macrophages. International Journal of Molecular Medicine, 2016, 38, 823-833. | 4.0 | 7 |
| 130 | Editorial: Bioinformatics in Microbiota. Frontiers in Microbiology, 2020, 11, 100. | 3.5 | 5 |
| 131 | Physiological Left Bundle Branch Pacing Validated by Ultra-High Density Ventricular Mapping in a Swine Model. Circulation: Arrhythmia and Electrophysiology, 2020, 13, e007898. | 4.8 | 5 |
| 132 | Comparative evaluation of the wound-healing potency of recombinant bFGF and ski gene therapy in rats. Growth Factors, 2016, 34, 119-127. | 1.7 | 4 |
| 133 | Increased plasma prothrombin time is associated with poor prognosis in patients with paraquat poisoning. Journal of Clinical Laboratory Analysis, 2018, 32, e22597. | 2.1 | 4 |
| 134 | Large scale image understanding with non-convex multi-task learning. , 2014, , . | | 3 |
| 135 | Current Computational Models for Prediction of the Varied Interactions Related to Noncoding RNAs. BioMed Research International, 2016, 2016, 1-2. | 1.9 | 3 |
| 136 | Highly Pathogenic Porcine Reproductive and Respiratory Syndrome Virus Modulates Interferon-Î² Expression Mainly Through Attenuating Interferon-Regulatory Factor 3 Phosphorylation. DNA and Cell Biology, 2016, 35, 489-497. | 1.9 | 3 |
| 137 | Enterovirus 71 infection impairs the reproductive capacity of female mice. Experimental and Therapeutic Medicine, 2017, 14, 403-409. | 1.8 | 2 |
| 138 | Developing Novel Computational Techniques for Medicine and Pharmacy. Current Topics in Medicinal Chemistry, 2018, 18, 947-948. | 2.1 | 2 |
| 139 | Editorial: Identifying Drug-target Interactions Based on Heterogeneous Biological Data - PART 1. Current Protein and Peptide Science, 2018, 19, 428-429. | 1.4 | 1 |
| 140 | A two-stage cardiac PET and late gadolinium enhancement MRI co-registration method for improved assessment of non-ischemic cardiomyopathies using integrated PET/MR. European Journal of Nuclear Medicine and Molecular Imaging, 2022, 49, 2199-2208. | 6.4 | 1 |
| 141 | Current Computational Models for Prediction of the Varied Interactions Related to Protein - PART 1. Protein and Peptide Letters, 2018, 25, 806-806. | 0.9 | 0 |
| 142 | Editorial: Identifying Drug-target Interactions Based on Heterogeneous Biological Data - PART 2. Current Protein and Peptide Science, 2018, 19, 524-524. | 1.4 | 0 |
| 143 | Current Computational Models for Prediction of the Varied Interactions Related to Protein - Part 2. Protein and Peptide Letters, 2020, 27, 347-347. | 0.9 | 0 |