

# Zaynab

## 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.

16  
papers

304  
citations

8  
h-index

17  
g-index

21  
ext. papers

429  
ext. citations

5  
avg, IF

3.69  
L-index

| #  | Paper   | IF  | Citations |
|----|---|-----|-----------|
| 16 | Drug-target interaction prediction via chemogenomic space: learning-based methods. <i>Expert Opinion on Drug Metabolism and Toxicology</i> , <b>2014</b> , 10, 1273-87  | 5.5 | 60        |
| 15 | iDTI-ESBoost: Identification of Drug Target Interaction Using Evolutionary and Structural Features with Boosting. <i>Scientific Reports</i> , <b>2017</b> , 7, 17731  | 4.9 | 58        |
| 14 | Drug-target interaction prediction from PSSM based evolutionary information. <i>Journal of Pharmacological and Toxicological Methods</i> , <b>2016</b> , 78, 42-51  | 1.7 | 45        |
| 13 | Drug-target and disease networks: polypharmacology in the post-genomic era. <i>In Silico Pharmacology</i> , <b>2013</b> , 1, 17   | 4.3 | 31        |
| 12 | Information theory in systems biology. Part II: protein-protein interaction and signaling networks. <i>Seminars in Cell and Developmental Biology</i> , <b>2016</b> , 51, 14-23   | 7.5 | 22        |
| 11 | Information theory in systems biology. Part I: Gene regulatory and metabolic networks. <i>Seminars in Cell and Developmental Biology</i> , <b>2016</b> , 51, 3-13   | 7.5 | 22        |
| 10 | FRnet-DTI: Deep convolutional neural network for drug-target interaction prediction. <i>Heliyon</i> , <b>2020</b> , 6, e03444   | 3.6 | 16        |
| 9  | Network-based expression analysis reveals key genes related to glucocorticoid resistance in infant acute lymphoblastic leukemia. <i>Cellular Oncology (Dordrecht)</i> , <b>2017</b> , 40, 33-45                           | 7.2 | 16        |
| 8  | Comparison of gene co-expression networks in <i>Pseudomonas aeruginosa</i> and <i>Staphylococcus aureus</i> reveals conservation in some aspects of virulence. <i>Gene</i> , <b>2018</b> , 639, 1-10                      | 3.8 | 7         |
| 7  | Differential network analysis and protein-protein interaction study reveals active protein modules in glucocorticoid resistance for infant acute lymphoblastic leukemia. <i>Molecular Medicine</i> , <b>2019</b> , 25, 36 | 6.2 | 7         |
| 6  | Scalable graph analyzing approach for software fault-localization <b>2011</b> ,   |     | 5         |
| 5  | Reconstruction of the genome-scale co-expression network for the Hippo signaling pathway in colorectal cancer. <i>Computers in Biology and Medicine</i> , <b>2018</b> , 99, 76-84   | 7   | 5         |
| 4  | Identification of Key Components in Colon Adenocarcinoma Using Transcriptome to Interactome Multilayer Framework. <i>Scientific Reports</i> , <b>2020</b> , 10, 4991  | 4.9 | 4         |
| 3  | StrongestPath: a Cytoscape application for protein-protein interaction analysis. <i>BMC Bioinformatics</i> , <b>2021</b> , 22, 352  | 3.6 | 3         |
| 2  | CeFunMO: A centrality based method for discovering functional motifs with application in biological networks. <i>Computers in Biology and Medicine</i> , <b>2016</b> , 76, 154-9  | 7   | 1         |
| 1  | A propagation-based seed-centric local community detection for multilayer environment: The case study of colon adenocarcinoma. <i>PLoS ONE</i> , <b>2021</b> , 16, e0255718   | 3.7 | 0         |