

# Hung Nguyen

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4672541/publications.pdf>

Version: 2024-02-01

19  
papers

479  
citations

933264

10  
h-index

1058333

14  
g-index

20  
all docs

20  
docs citations

20  
times ranked

450  
citing authors

| #  | ARTICLE  | IF  | CITATIONS |
|----|--|-----|-----------|
| 1  | A comprehensive survey of regulatory network inference methods using single cell RNA sequencing data. <i>Briefings in Bioinformatics</i> , 2021, 22, .   | 3.2 | 92        |
| 2  | PINSPlus: a tool for tumor subtype discovery in integrated genomic data. <i>Bioinformatics</i> , 2019, 35, 2843-2846.  | 1.8 | 82        |
| 3  | Fast and precise single-cell data analysis using a hierarchical autoencoder. <i>Nature Communications</i> , 2021, 12, 1029.  | 5.8 | 71        |
| 4  | Functional analysis tools for postâ€translational modification: a postâ€translational modification database for analysis of proteins and metabolic pathways. <i>Plant Journal</i> , 2019, 99, 1003-1013. | 2.8 | 55        |
| 5  | A Comprehensive Survey of Tools and Software for Active Subnetwork Identification. <i>Frontiers in Genetics</i> , 2019, 10, 155.   | 1.1 | 48        |
| 6  | A Multi-Cohort and Multi-Omics Meta-Analysis Framework to Identify Network-Based Gene Signatures. <i>Frontiers in Genetics</i> , 2019, 10, 159.  | 1.1 | 25        |
| 7  | CPA: a web-based platform for consensus pathway analysis and interactive visualization. <i>Nucleic Acids Research</i> , 2021, 49, W114-W124.   | 6.5 | 20        |
| 8  | Multi-Omics Analysis Detects Novel Prognostic Subgroups of Breast Cancer. <i>Frontiers in Genetics</i> , 2020, 11, 574661.   | 1.1 | 18        |
| 9  | Thioesterase enzyme families: Functions, structures, and mechanisms. <i>Protein Science</i> , 2022, 31, 652-676.   | 3.1 | 18        |
| 10 | A Novel Method for Cancer Subtyping and Risk Prediction Using Consensus Factor Analysis. <i>Frontiers in Oncology</i> , 2020, 10, 1052.  | 1.3 | 13        |
| 11 | SMRT: Randomized Data Transformation for Cancer Subtyping and Big Data Analysis. <i>Frontiers in Oncology</i> , 2021, 11, 725133.  | 1.3 | 7         |
| 12 | scCAN: single-cell clustering using autoencoder and network fusion. <i>Scientific Reports</i> , 2022, 12, .  | 1.6 | 7         |
| 13 | A novel method for single-cell data imputation using subspace regression. <i>Scientific Reports</i> , 2022, 12, 2697.  | 1.6 | 6         |
| 14 | MGKA: A genetic algorithm-based clustering technique for genomic data. , 2019, , .   |     | 4         |
| 15 | RIA: a novel Regression-based Imputation Approach for single-cell RNA sequencing. , 2019, , .  |     | 4         |
| 16 | Disease subtyping using community detection from consensus networks. , 2020, , .   |     | 3         |
| 17 | MIA. , 2018, , .   |     | 1         |
| 18 | Single-Cell RNA Sequencing Data Imputation Using Deep Neural Network. <i>Advances in Intelligent Systems and Computing</i> , 2021, , 403-410.  | 0.5 | 1         |

| #  | ARTICLE   | IF | CITATIONS |
|----|---|----|-----------|
| 19 | Single-cell RNA sequencing data imputation using similarity preserving network. , 2021, , . |    | 0         |