

Andrew Quitadamo

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1796019/publications.pdf>

Version: 2024-02-01

9
papers

2,093
citations

1684188

5
h-index

1872680

6
g-index

9
all docs

9
docs citations

9
times ranked

6178
citing authors

| # | ARTICLE | IF | CITATIONS |
|---|--|------|-----------|
| 1 | Children's rare disease cohorts: an integrative research and clinical genomics initiative. <i>Npj Genomic Medicine</i> , 2020, 5, 29. | 3.8 | 38 |
| 2 | Epistasis analysis of microRNAs on pathological stages in colon cancer based on an Empirical Bayesian Elastic Net method. <i>BMC Genomics</i> , 2017, 18, 756. | 2.8 | 4 |
| 3 | Identifying microRNA and gene expression networks using graph communities. <i>Tsinghua Science and Technology</i> , 2016, 21, 176-195. | 6.1 | 0 |
| 4 | A predictive model of gene expression using a deep learning framework. , 2016, , . | | 5 |
| 5 | A phylogeny of sand flies (<i>Diptera: Phlebotominae</i>), using recent Ethiopian collections and a broad selection of publicly available DNA sequence data. <i>Systematic Entomology</i> , 2015, 40, 733-744. | 3.9 | 15 |
| 6 | An integrated network of microRNA and gene expression in ovarian cancer. <i>BMC Bioinformatics</i> , 2015, 16, S5. | 2.6 | 24 |
| 7 | An integrated map of structural variation in 2,504 human genomes. <i>Nature</i> , 2015, 526, 75-81. | 27.8 | 1,994 |
| 8 | A Graph Community Approach for Constructing microRNA Networks. <i>Lecture Notes in Computer Science</i> , 2015, , 283-293. | 1.3 | 0 |
| 9 | Methods for population-based eQTL analysis in human genetics. <i>Tsinghua Science and Technology</i> , 2014, 19, 624-634. | 6.1 | 13 |