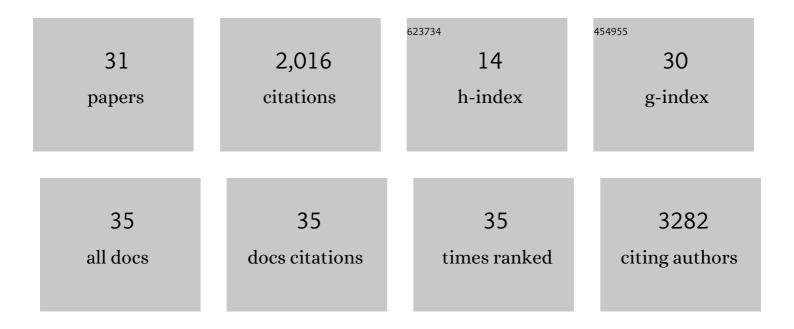
Noel Malod-Dognin

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5429917/publications.pdf Version: 2024-02-01



| # | Article | IF | CITATIONS |
|----|---|------|-----------|
| 1 | A global genetic interaction network maps a wiring diagram of cellular function. Science, 2016, 353, . | 12.6 | 979 |
| 2 | Revealing the Hidden Language of Complex Networks. Scientific Reports, 2014, 4, 4547. | 3.3 | 153 |
| 3 | Integrative methods for analyzing big data in precision medicine. Proteomics, 2016, 16, 741-758. | 2.2 | 149 |
| 4 | L-GRAAL: Lagrangian graphlet-based network aligner. Bioinformatics, 2015, 31, 2182-2189. | 4.1 | 112 |
| 5 | Network analytics in the age of big data. Science, 2016, 353, 123-124. | 12.6 | 77 |
| 6 | Graphlet-based Characterization of Directed Networks. Scientific Reports, 2016, 6, 35098. | 3.3 | 68 |
| 7 | Topology-function conservation in protein–protein interaction networks. Bioinformatics, 2015, 31, 1632-1639. | 4.1 | 62 |
| 8 | GR-Align: fast and flexible alignment of protein 3D structures using graphlet degree similarity. Bioinformatics, 2014, 30, 1259-1265. | 4.1 | 55 |
| 9 | Fuse: multiple network alignment via data fusion. Bioinformatics, 2016, 32, 1195-1203. | 4.1 | 42 |
| 10 | Unified Alignment of Protein-Protein Interaction Networks. Scientific Reports, 2017, 7, 953. | 3.3 | 40 |
| 11 | Towards a data-integrated cell. Nature Communications, 2019, 10, 805. | 12.8 | 37 |
| 12 | Maximum Contact Map Overlap Revisited. Journal of Computational Biology, 2011, 18, 27-41. | 1.6 | 34 |
| 13 | Higher-order molecular organization as a source of biological function. Bioinformatics, 2018, 34, i944-i953. | 4.1 | 32 |
| 14 | PATIENT-SPECIFIC DATA FUSION FOR CANCER STRATIFICATION AND PERSONALISED TREATMENT. , 2016, , . | | 27 |
| 15 | Unveiling new disease, pathway, and gene associations via multi-scale neural network. PLoS ONE, 2020, 15, e0231059. | 2.5 | 18 |
| 16 | CSA: comprehensive comparison of pairwise protein structure alignments. Nucleic Acids Research, 2012, 40, W303-W309. | 14.5 | 17 |
| 17 | PATIENT-SPECIFIC DATA FUSION FOR CANCER STRATIFICATION AND PERSONALISED TREATMENT. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2016, 21, 321-32. | 0.7 | 15 |
| 18 | Precision medicine ― A promising, yet challenging road lies ahead. Current Opinion in Systems Biology, 2018, 7, 1-7. | 2.6 | 13 |

| # | Article | IF | CITATIONS |
|----|--|-----|-----------|
| 19 | Antiproliferative activity and mode of action analysis of novel amino and amido substituted phenantrene and naphtho[2,1-b]thiophene derivatives. European Journal of Medicinal Chemistry, 2020, 185, 111833. | 5.5 | 13 |
| 20 | An Efficient Lagrangian Relaxation for the Contact Map Overlap Problem. Lecture Notes in Computer Science, 2008, , 162-173. | 1.3 | 10 |
| 21 | Classification in biological networks with hypergraphlet kernels. Bioinformatics, 2021, 37, 1000-1007. | 4.1 | 9 |
| 22 | Graphlet Laplacians for topology-function and topology-disease relationships. Bioinformatics, 2019, 35, 5226-5234. | 4.1 | 8 |
| 23 | Characterizing the morphology of protein binding patches. Proteins: Structure, Function and Bioinformatics, 2012, 80, 2652-2665. | 2.6 | 7 |
| 24 | Functional geometry of protein interactomes. Bioinformatics, 2019, 35, 3727-3734. | 4.1 | 5 |
| 25 | Network neighbors of viral targets and differentially expressed genes in COVID-19 are drug target candidates. Scientific Reports, 2021, 11, 18985. | 3.3 | 5 |
| 26 | Probabilistic graphlets capture biological function in probabilistic molecular networks. Bioinformatics, 2020, 36, i804-i812. | 4.1 | 4 |
| 27 | Integrative Data Analytic Framework to Enhance Cancer Precision Medicine. Network and Systems Medicine, 2021, 4, 60-73. | 2.5 | 2 |
| 28 | Using Dominances for Solving the Protein Family Identification Problem. Lecture Notes in Computer Science, 2011, , 201-212. | 1.3 | 2 |
| 29 | Graphlet eigencentralities capture novel central roles of genes in pathways. PLoS ONE, 2022, 17, e0261676. | 2.5 | 2 |
| 30 | Rebuttal to the Letter to the Editor in response to the paper: proper evaluation of alignment-free network comparison methods. Bioinformatics, 2017, 33, 1107-1109. | 4.1 | 1 |
| 31 | Omics Data Complementarity Underlines Functional Cross-Communication in Yeast. Journal of Integrative Bioinformatics, 2017, 14, . | 1.5 | О |