Noel Malod-Dognin

List of Publications by Year
in descending order

31 papers	2,016 citations	623734 14 h-index	454955 30 g-index
35 all docs	35 docs citations	35 times ranked	3282 citing authors

#	Article	IF	Citations
1	Graphlet eigencentralities capture novel central roles of genes in pathways. PLoS ONE, 2022, 17, e0261676.	2.5	2
2	Classification in biological networks with hypergraphlet kernels. Bioinformatics, 2021, 37, 1000-1007.	4.1	9
3	Integrative Data Analytic Framework to Enhance Cancer Precision Medicine. Network and Systems Medicine, 2021, 4, 60-73.	2.5	2
4	Network neighbors of viral targets and differentially expressed genes in COVID-19 are drug target candidates. Scientific Reports, 2021, 11, 18985.	3.3	5
5	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
6	Unveiling new disease, pathway, and gene associations via multi-scale neural network. PLoS ONE, 2020, 15, e0231059.	2.5	18
7	Probabilistic graphlets capture biological function in probabilistic molecular networks. Bioinformatics, 2020, 36, i804-i812.	4.1	4
8	Graphlet Laplacians for topology-function and topology-disease relationships. Bioinformatics, 2019, 35, 5226-5234.	4.1	8
9	Functional geometry of protein interactomes. Bioinformatics, 2019, 35, 3727-3734.	4.1	5
10	Towards a data-integrated cell. Nature Communications, 2019, 10, 805.	12.8	37
11	Precision medicine â€• A promising, yet challenging road lies ahead. Current Opinion in Systems Biology, 2018, 7, 1-7.	2.6	13
12	Higher-order molecular organization as a source of biological function. Bioinformatics, 2018, 34, i944-i953.	4.1	32
13	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
14	Unified Alignment of Protein-Protein Interaction Networks. Scientific Reports, 2017, 7, 953.	3.3	40
15	Omics Data Complementarity Underlines Functional Cross-Communication in Yeast. Journal of Integrative Bioinformatics, 2017, 14, .	1.5	0
16	Network analytics in the age of big data. Science, 2016, 353, 123-124.	12.6	77
17	PATIENT-SPECIFIC DATA FUSION FOR CANCER STRATIFICATION AND PERSONALISED TREATMENT. , 2016, , .		27
18	Graphlet-based Characterization of Directed Networks. Scientific Reports, 2016, 6, 35098.	3.3	68

#	Article	IF	Citations
19	A global genetic interaction network maps a wiring diagram of cellular function. Science, 2016, 353, .	12.6	979
20	Integrative methods for analyzing big data in precision medicine. Proteomics, 2016, 16, 741-758.	2.2	149
21	Fuse: multiple network alignment via data fusion. Bioinformatics, 2016, 32, 1195-1203.	4.1	42
22	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
23	L-GRAAL: Lagrangian graphlet-based network aligner. Bioinformatics, 2015, 31, 2182-2189.	4.1	112
24	Topology-function conservation in protein–protein interaction networks. Bioinformatics, 2015, 31, 1632-1639.	4.1	62
25	GR-Align: fast and flexible alignment of protein 3D structures using graphlet degree similarity. Bioinformatics, 2014, 30, 1259-1265.	4.1	55
26	Revealing the Hidden Language of Complex Networks. Scientific Reports, 2014, 4, 4547.	3.3	153
27	CSA: comprehensive comparison of pairwise protein structure alignments. Nucleic Acids Research, 2012, 40, W303-W309.	14.5	17
28	Characterizing the morphology of protein binding patches. Proteins: Structure, Function and Bioinformatics, 2012, 80, 2652-2665.	2.6	7
29	Maximum Contact Map Overlap Revisited. Journal of Computational Biology, 2011, 18, 27-41.	1.6	34
30	Using Dominances for Solving the Protein Family Identification Problem. Lecture Notes in Computer Science, 2011, , 201-212.	1.3	2
31	An Efficient Lagrangian Relaxation for the Contact Map Overlap Problem. Lecture Notes in Computer Science, 2008, , 162-173.	1.3	10