

# Noel Malod-Dognin

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5429917/publications.pdf>

Version: 2024-02-01

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	A global genetic interaction network maps a wiring diagram of cellular function. <i>Science</i> , 2016, 353, .	12.6	979
2	Revealing the Hidden Language of Complex Networks. <i>Scientific Reports</i> , 2014, 4, 4547.	3.3	153
3	Integrative methods for analyzing big data in precision medicine. <i>Proteomics</i> , 2016, 16, 741-758.	2.2	149
4	L-GRAAL: Lagrangian graphlet-based network aligner. <i>Bioinformatics</i> , 2015, 31, 2182-2189.	4.1	112
5	Network analytics in the age of big data. <i>Science</i> , 2016, 353, 123-124.	12.6	77
6	Graphlet-based Characterization of Directed Networks. <i>Scientific Reports</i> , 2016, 6, 35098.	3.3	68
7	Topology-function conservation in protein-protein interaction networks. <i>Bioinformatics</i> , 2015, 31, 1632-1639.	4.1	62
8	GR-Align: fast and flexible alignment of protein 3D structures using graphlet degree similarity. <i>Bioinformatics</i> , 2014, 30, 1259-1265.	4.1	55
9	Fuse: multiple network alignment via data fusion. <i>Bioinformatics</i> , 2016, 32, 1195-1203.	4.1	42
10	Unified Alignment of Protein-Protein Interaction Networks. <i>Scientific Reports</i> , 2017, 7, 953.	3.3	40
11	Towards a data-integrated cell. <i>Nature Communications</i> , 2019, 10, 805.	12.8	37
12	Maximum Contact Map Overlap Revisited. <i>Journal of Computational Biology</i> , 2011, 18, 27-41.	1.6	34
13	Higher-order molecular organization as a source of biological function. <i>Bioinformatics</i> , 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. <i>PLoS ONE</i> , 2020, 15, e0231059.	2.5	18
16	CSA: comprehensive comparison of pairwise protein structure alignments. <i>Nucleic Acids Research</i> , 2012, 40, W303-W309.	14.5	17
17	PATIENT-SPECIFIC DATA FUSION FOR CANCER STRATIFICATION AND PERSONALISED TREATMENT. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2016, 21, 321-32.	0.7	15
18	Precision medicine - A promising, yet challenging road lies ahead. <i>Current Opinion in Systems Biology</i> , 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. <i>European Journal of Medicinal Chemistry</i> , 2020, 185, 111833.	5.5	13
20	An Efficient Lagrangian Relaxation for the Contact Map Overlap Problem. <i>Lecture Notes in Computer Science</i> , 2008, , 162-173.	1.3	10
21	Classification in biological networks with hypergraphlet kernels. <i>Bioinformatics</i> , 2021, 37, 1000-1007.	4.1	9
22	Graphlet Laplacians for topology-function and topology-disease relationships. <i>Bioinformatics</i> , 2019, 35, 5226-5234.	4.1	8
23	Characterizing the morphology of protein binding patches. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 2652-2665.	2.6	7
24	Functional geometry of protein interactomes. <i>Bioinformatics</i> , 2019, 35, 3727-3734.	4.1	5
25	Network neighbors of viral targets and differentially expressed genes in COVID-19 are drug target candidates. <i>Scientific Reports</i> , 2021, 11, 18985.	3.3	5
26	Probabilistic graphlets capture biological function in probabilistic molecular networks. <i>Bioinformatics</i> , 2020, 36, i804-i812.	4.1	4
27	Integrative Data Analytic Framework to Enhance Cancer Precision Medicine. <i>Network and Systems Medicine</i> , 2021, 4, 60-73.	2.5	2
28	Using Dominances for Solving the Protein Family Identification Problem. <i>Lecture Notes in Computer Science</i> , 2011, , 201-212.	1.3	2
29	Graphlet eigencentralities capture novel central roles of genes in pathways. <i>PLoS ONE</i> , 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. <i>Bioinformatics</i> , 2017, 33, 1107-1109.	4.1	1
31	Omics Data Complementarity Underlines Functional Cross-Communication in Yeast. <i>Journal of Integrative Bioinformatics</i> , 2017, 14, .	1.5	0