

Natasa Przulj

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3013300/publications.pdf>

Version: 2024-02-01

100
papers

7,335
citations

81900

39
h-index

62596

80
g-index

106
all docs

106
docs citations

106
times ranked

9296
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	Evidence for Network Evolution in an <i>Arabidopsis</i> Interactome Map. <i>Science</i> , 2011, 333, 601-607.	12.6	838
3	High-Throughput Mapping of a Dynamic Signaling Network in Mammalian Cells. <i>Science</i> , 2005, 307, 1621-1625.	12.6	651
4	Biological network comparison using graphlet degree distribution. <i>Bioinformatics</i> , 2007, 23, e177-e183.	4.1	612
5	Topological network alignment uncovers biological function and phylogeny. <i>Journal of the Royal Society Interface</i> , 2010, 7, 1341-1354.	3.4	281
6	Integrative network alignment reveals large regions of global network similarity in yeast and human. <i>Bioinformatics</i> , 2011, 27, 1390-1396.	4.1	217
7	Uncovering Biological Network Function via Graphlet Degree Signatures. <i>Cancer Informatics</i> , 2008, 6, CIN.S680.	1.9	200
8	Methods for biological data integration: perspectives and challenges. <i>Journal of the Royal Society Interface</i> , 2015, 12, 20150571.	3.4	196
9	Geometric De-noising of Protein-Protein Interaction Networks. <i>PLoS Computational Biology</i> , 2009, 5, e1000454.	3.2	158
10	Revealing the Hidden Language of Complex Networks. <i>Scientific Reports</i> , 2014, 4, 4547.	3.3	153
11	Optimal Network Alignment with Graphlet Degree Vectors. <i>Cancer Informatics</i> , 2010, 9, CIN.S4744.	1.9	149
12	Integrative methods for analyzing big data in precision medicine. <i>Proteomics</i> , 2016, 16, 741-758.	2.2	149
13	Critical Review on Zeolite Clinoptilolite Safety and Medical Applications in vivo. <i>Frontiers in Pharmacology</i> , 2018, 9, 1350.	3.5	137
14	Characterization of the proteasome interaction network using a QTAX-based tag-team strategy and protein interaction network analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 13333-13338.	7.1	129
15	L-GRAAL: Lagrangian graphlet-based network aligner. <i>Bioinformatics</i> , 2015, 31, 2182-2189.	4.1	112
16	Fitting a geometric graph to a protein-protein interaction network. <i>Bioinformatics</i> , 2008, 24, 1093-1099.	4.1	109
17	Discovering disease-disease associations by fusing systems-level molecular data. <i>Scientific Reports</i> , 2013, 3, 3202.	3.3	96
18	Uncovering biological network function via graphlet degree signatures. <i>Cancer Informatics</i> , 2008, 6, 257-73.	1.9	96

#	ARTICLE	IF	CITATIONS
19	Systems-level cancer gene identification from protein interaction network topology applied to melanogenesis-related functional genomics data. <i>Journal of the Royal Society Interface</i> , 2010, 7, 423-437.	3.4	95
20	GraphCrunch: A tool for large network analyses. <i>BMC Bioinformatics</i> , 2008, 9, 70.	2.6	93
21	Predicting disease associations via biological network analysis. <i>BMC Bioinformatics</i> , 2014, 15, 304.	2.6	86
22	Dominating Biological Networks. <i>PLoS ONE</i> , 2011, 6, e23016.	2.5	85
23	C-GRAAL: Common-neighbors-based global GRAPh ALignment of biological networks. <i>Integrative Biology (United Kingdom)</i> , 2012, 4, 734.	1.3	79
24	Not All Scale-Free Networks Are Born Equal: The Role of the Seed Graph in PPI Network Evolution. <i>PLoS Computational Biology</i> , 2007, 3, e118.	3.2	77
25	Network analytics in the age of big data. <i>Science</i> , 2016, 353, 123-124.	12.6	77
26	Modelling protein-protein interaction networks via a stickiness index. <i>Journal of the Royal Society Interface</i> , 2006, 3, 711-716.	3.4	76
27	Graphlet-based measures are suitable for biological network comparison. <i>Bioinformatics</i> , 2013, 29, 483-491.	4.1	71
28	Graphlet-based Characterization of Directed Networks. <i>Scientific Reports</i> , 2016, 6, 35098.	3.3	68
29	Protein-protein interactions: Making sense of networks via graph-theoretic modeling. <i>BioEssays</i> , 2011, 33, 115-123.	2.5	66
30	GraphCrunch 2: Software tool for network modeling, alignment and clustering. <i>BMC Bioinformatics</i> , 2011, 12, 24.	2.6	63
31	Systematic protein-protein interaction mapping for clinically relevant human GPCR's. <i>Molecular Systems Biology</i> , 2017, 13, 918.	7.2	63
32	Topology-function conservation in protein-protein interaction networks. <i>Bioinformatics</i> , 2015, 31, 1632-1639.	4.1	62
33	GR-Align: fast and flexible alignment of protein 3D structures using graphlet degree similarity. <i>Bioinformatics</i> , 2014, 30, 1259-1265.	4.1	55
34	Characterization of Cell Cycle Specific Protein Interaction Networks of the Yeast 26S Proteasome Complex by the QTAX Strategy. <i>Journal of Proteome Research</i> , 2010, 9, 2016-2029.	3.7	51
35	Proper evaluation of alignment-free network comparison methods. <i>Bioinformatics</i> , 2015, 31, 2697-2704.	4.1	46
36	Biological function through network topology: a survey of the human diseaseome. <i>Briefings in Functional Genomics</i> , 2012, 11, 522-532.	2.7	45

#	ARTICLE	IF	CITATIONS
37	Network Topology Reveals Key Cardiovascular Disease Genes. PLoS ONE, 2013, 8, e71537.	2.5	44
38	Fuse: multiple network alignment via data fusion. Bioinformatics, 2016, 32, 1195-1203.	4.1	42
39	The Core Diseasesome. Molecular BioSystems, 2012, 8, 2614.	2.9	40
40	Unified Alignment of Protein-Protein Interaction Networks. Scientific Reports, 2017, 7, 953.	3.3	40
41	Bridging the gaps in systems biology. Molecular Genetics and Genomics, 2014, 289, 727-734.	2.1	38
42	Towards a data-integrated cell. Nature Communications, 2019, 10, 805.	12.8	37
43	Optimized Null Model for Protein Structure Networks. PLoS ONE, 2009, 4, e5967.	2.5	34
44	A framework for FPGA acceleration of large graph problems: Graphlet counting case study. , 2011, , .		33
45	Protein interaction network topology uncovers melanogenesis regulatory network components within functional genomics datasets. BMC Systems Biology, 2010, 4, 84.	3.0	32
46	Higher-order molecular organization as a source of biological function. Bioinformatics, 2018, 34, i944-i953.	4.1	32
47	Integration of molecular network data reconstructs Gene Ontology. Bioinformatics, 2014, 30, i594-i600.	4.1	30
48	GEOMETRIC EVOLUTIONARY DYNAMICS OF PROTEIN INTERACTION NETWORKS. , 2009, , 178-189.		29
49	The integrated disease network. Integrative Biology (United Kingdom), 2014, 6, 1069-1079.	1.3	28
50	PATIENT-SPECIFIC DATA FUSION FOR CANCER STRATIFICATION AND PERSONALISED TREATMENT. , 2016, , .		27
51	Anti-nicestrin monoclonal antibodies elicit pleiotropic anti-tumour pharmacological effects in invasive breast cancer cells. Breast Cancer Research and Treatment, 2014, 148, 455-462.	2.5	22
52	Biological network comparison using graphlet degree distribution. Bioinformatics, 2010, 26, 853-854.	4.1	21
53	Complementarity of network and sequence information in homologous proteins. Journal of Integrative Bioinformatics, 2010, 7, 275-289.	1.5	20
54	Unveiling new disease, pathway, and gene associations via multi-scale neural network. PLoS ONE, 2020, 15, e0231059.	2.5	18

#	ARTICLE	IF	CITATIONS
55	Complementarity of network and sequence information in homologous proteins. Journal of Integrative Bioinformatics, 2010, 7, .	1.5	17
56	Protein Complex Prediction with RNSC. Methods in Molecular Biology, 2012, 804, 297-312.	0.9	15
57	PATIENT-SPECIFIC DATA FLUSION FOR CANCER STRATIFICATION AND PERSONALISED TREATMENT. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2016, 21, 321-32.	0.7	15
58	An integrative approach to modeling biological networks. Journal of Integrative Bioinformatics, 2010, 7, .	1.5	14
59	Modelling the Yeast Interactome. Scientific Reports, 2014, 4, 4273.	3.3	14
60	Precision medicine – A promising, yet challenging road lies ahead. Current Opinion in Systems Biology, 2018, 7, 1-7.	2.6	13
61	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
62	<code>ergm.graphlets</code> : A Package for ERG Modeling Based on Graphlet Statistics. Journal of Statistical Software, 2015, 65, .	3.7	13
63	2-Tree probe interval graphs have a large obstruction set. Discrete Applied Mathematics, 2005, 150, 216-231.	0.9	10
64	Classification in biological networks with hypergraphlet kernels. Bioinformatics, 2021, 37, 1000-1007.	4.1	9
65	LEARNING THE STRUCTURE OF PROTEIN-PROTEIN INTERACTION NETWORKS. , 2008, , .		8
66	Survey of Network-Based Approaches to Research of Cardiovascular Diseases. BioMed Research International, 2014, 2014, 1-10.	1.9	8
67	Graphlet Laplacians for topology-function and topology-disease relationships. Bioinformatics, 2019, 35, 5226-5234.	4.1	8
68	An integrative approach to modeling biological networks. Journal of Integrative Bioinformatics, 2010, 7, .	1.5	8
69	Topological network alignment uncovers biological function and phylogeny. Nature Precedings, 2009, , .	0.1	7
70	Network wiring of pleiotropic kinases yields insight into protective role of diabetes on aneurysm. Integrative Biology (United Kingdom), 2014, 6, 1049-1057.	1.3	6
71	The role of genes co-amplified with nicastrin in breast invasive carcinoma. Breast Cancer Research and Treatment, 2014, 143, 393-401.	2.5	6
72	Learning the structure of protein-protein interaction networks. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2009, , 39-50.	0.7	6

#	ARTICLE	IF	CITATIONS
73	Structure of brain functional networks. , 2009, 2009, 4166-70.		5
74	The Topology of the Growing Human Interactome Data. Journal of Integrative Bioinformatics, 2014, 11, 27-42.	1.5	5
75	Functional geometry of protein interactomes. Bioinformatics, 2019, 35, 3727-3734.	4.1	5
76	Network neighbors of viral targets and differentially expressed genes in COVID-19 are drug target candidates. Scientific Reports, 2021, 11, 18985.	3.3	5
77	Topological Characteristics of Molecular Networks. , 2012, , 15-48.		5
78	The topology of the growing human interactome data. Journal of Integrative Bioinformatics, 2014, 11, 238.	1.5	5
79	Hereditary dominating pair graphs. Discrete Applied Mathematics, 2004, 134, 239-261.	0.9	4
80	Probabilistic graphlets capture biological function in probabilistic molecular networks. Bioinformatics, 2020, 36, i804-i812.	4.1	4
81	Geometric Local Structure in Biological Networks. , 2007, , .		2
82	Introduction to the Special Issue on Biological Networks. Internet Mathematics, 2011, 7, 207-208.	0.7	2
83	Computational Methods for Integration of Biological Data. Europeanization and Globalization, 2016, , 137-178.	0.1	2
84	Graphlets in Network Science and Computational Biology. , 2019, , 193-240.		2
85	Integrative Data Analytic Framework to Enhance Cancer Precision Medicine. Network and Systems Medicine, 2021, 4, 60-73.	2.5	2
86	Graphlet eigencentralities capture novel central roles of genes in pathways. PLoS ONE, 2022, 17, e0261676.	2.5	2
87	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
88	Network Alignment. , 2019, , 369-413.		1
89	Four algorithms to solve symmetric multi-type non-negative matrix tri-factorization problem. Journal of Global Optimization, 0, , 1.	1.8	1
90	From Topology to Phenotype in Protein-Protein Interaction Networks. , 2010, , 31-49.		1

#	ARTICLE	IF	CITATIONS
91	Minimum Average Time Broadcast Graphs. Parallel Processing Letters, 1998, 08, 139-147.	0.6	0
92	Biological networks uncover evolution, disease, and gene functions. , 0, , 291-314.		0
93	Omics Data Complementarity Underlines Functional Cross-Communication in Yeast. Journal of Integrative Bioinformatics, 2017, 14, .	1.5	0
94	Introduction to Graph and Network Theory. , 2019, , 111-150.		0
95	Machine Learning for Data Integration in Cancer Precision Medicine: Matrix Factorization Approaches. , 2019, , 286-312.		0
96	Not All Scale Free Networks Are Born Equal: The Role of the Seed Graph in PPI Network Emulation. Lecture Notes in Computer Science, 2006, , 1-13.	1.3	0
97	Unveiling new disease, pathway, and gene associations via multi-scale neural network. , 2020, 15, e0231059.		0
98	Unveiling new disease, pathway, and gene associations via multi-scale neural network. , 2020, 15, e0231059.		0
99	Unveiling new disease, pathway, and gene associations via multi-scale neural network. , 2020, 15, e0231059.		0
100	Unveiling new disease, pathway, and gene associations via multi-scale neural network. , 2020, 15, e0231059.		0