

Georgios A Pavlopoulos

List of Publications by Year in descending order

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Version: 2024-02-01

73
papers

5,215
citations

201674
27
h-index

102487
66
g-index

86
all docs

86
docs citations

86
times ranked

8478
citing authors

#	ARTICLE	IF	CITATIONS
1	Uncovering Earth's virome. <i>Nature</i> , 2016, 536, 425-430.	27.8	880
2	Using graph theory to analyze biological networks. <i>BioData Mining</i> , 2011, 4, 10.	4.0	547
3	Protein structure determination using metagenome sequence data. <i>Science</i> , 2017, 355, 294-298.	12.6	456
4	Cultivation and sequencing of rumen microbiome members from the Hungate1000 Collection. <i>Nature Biotechnology</i> , 2018, 36, 359-367.	17.5	414
5	Metagenomics: Tools and Insights for Analyzing Next-Generation Sequencing Data Derived from Biodiversity Studies. <i>Bioinformatics and Biology Insights</i> , 2015, 9, BBI.S12462.	2.0	317
6	1,003 reference genomes of bacterial and archaeal isolates expand coverage of the tree of life. <i>Nature Biotechnology</i> , 2017, 35, 676-683.	17.5	222
7	IMG/VR: a database of cultured and uncultured DNA Viruses and retroviruses. <i>Nucleic Acids Research</i> , 2016, 45, D457-D465.	14.5	177
8	A survey of visualization tools for biological network analysis. <i>BioData Mining</i> , 2008, 1, 12.	4.0	173
9	Large-Scale Analyses of Human Microbiomes Reveal Thousands of Small, Novel Genes. <i>Cell</i> , 2019, 178, 1245-1259.e14.	28.9	163
10	A Guide to Conquer the Biological Network Era Using Graph Theory. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 34.	4.1	149
11	Bipartite graphs in systems biology and medicine: a survey of methods and applications. <i>GigaScience</i> , 2018, 7, 1-31.	6.4	117
12	Nontargeted virus sequence discovery pipeline and virus clustering for metagenomic data. <i>Nature Protocols</i> , 2017, 12, 1673-1682.	12.0	115
13	HipMCL: a high-performance parallel implementation of the Markov clustering algorithm for large-scale networks. <i>Nucleic Acids Research</i> , 2018, 46, e33-e33.	14.5	104
14	Arena3D: visualization of biological networks in 3D. <i>BMC Systems Biology</i> , 2008, 2, 104.	3.0	95
15	Visualizing genome and systems biology: technologies, tools, implementation techniques and trends, past, present and future. <i>GigaScience</i> , 2015, 4, 38.	6.4	84
16	A reference guide for tree analysis and visualization. <i>BioData Mining</i> , 2010, 3, 1.	4.0	81
17	Protein-protein interaction predictions using text mining methods. <i>Methods</i> , 2015, 74, 47-53.	3.8	73
18	Diversity, evolution, and classification of virophages uncovered through global metagenomics. <i>Microbiome</i> , 2019, 7, 157.	11.1	53

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19	Medusa: A tool for exploring and clustering biological networks. BMC Research Notes, 2011, 4, 384.	1.4	49
20	Caipirini: using gene sets to rank literature. BioData Mining, 2012, 5, 1.	4.0	47
21	Empirical Comparison of Visualization Tools for Larger-Scale Network Analysis. Advances in Bioinformatics, 2017, 2017, 1-8.	5.7	44
22	Unraveling genomic variation from next generation sequencing data. BioData Mining, 2013, 6, 13.	4.0	43
23	Arena3D: visualizing time-driven phenotypic differences in biological systems. BMC Bioinformatics, 2012, 13, 45.	2.6	41
24	Apolipoprotein A-I inhibits experimental colitis and colitis-propelled carcinogenesis. Oncogene, 2016, 35, 2496-2505.	5.9	39
25	ProteoSign: an end-user online differential proteomics statistical analysis platform. Nucleic Acids Research, 2017, 45, W300-W306.	14.5	32
26	Network analysis of genes and their association with diseases. Gene, 2016, 590, 68-78.	2.2	31
27	NAP: The Network Analysis Profiler, a web tool for easier topological analysis and comparison of medium-scale biological networks. BMC Research Notes, 2017, 10, 278.	1.4	31
28	Structure determination of the HgcAB complex using metagenome sequence data: insights into microbial mercury methylation. Communications Biology, 2020, 3, 320.	4.4	30
29	Prediction of miRNA Targets. Methods in Molecular Biology, 2015, 1269, 207-229.	0.9	29
30	Annotate-it: a Swiss-knife approach to annotation, analysis and interpretation of single nucleotide variation in human disease. Genome Medicine, 2012, 4, 73.	8.2	28
31	DrugQuest - a text mining workflow for drug association discovery. BMC Bioinformatics, 2016, 17, 182.	2.6	27
32	LAITOR - Literature Assistant for Identification of Terms co-Occurrences and Relationships. BMC Bioinformatics, 2010, 11, 70.	2.6	26
33	Human gene correlation analysis (HGCA): A tool for the identification of transcriptionally co-expressed genes. BMC Research Notes, 2012, 5, 265.	1.4	26
34	Which clustering algorithm is better for predicting protein complexes?. BMC Research Notes, 2011, 4, 549.	1.4	24
35	FLAME: A Web Tool for Functional and Literature Enrichment Analysis of Multiple Gene Lists. Biology, 2021, 10, 665.	2.8	24
36	BioTextQuest + : a knowledge integration platform for literature mining and concept discovery. Bioinformatics, 2014, 30, 3249-3256.	4.1	23

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37	GPCRs, G-proteins, effectors and their interactions: human-gpDB, a database employing visualization tools and data integration techniques. Database: the Journal of Biological Databases and Curation, 2010, 2010, baq019-baq019.	3.0	22
38	Arena3Dweb: interactive 3D visualization of multilayered networks. Nucleic Acids Research, 2021, 49, W36-W45.	14.5	22
39	jClust: a clustering and visualization toolbox. Bioinformatics, 2009, 25, 1994-1996.	4.1	21
40	GIBA: a clustering tool for detecting protein complexes. BMC Bioinformatics, 2009, 10, S11.	2.6	20
41	Biological Information Extraction and Co-occurrence Analysis. Methods in Molecular Biology, 2014, 1159, 77-92.	0.9	19
42	OnTheFly: a tool for automated document-based text annotation, data linking and network generation. Bioinformatics, 2009, 25, 977-978.	4.1	18
43	Biomolecule and Bioentity Interaction Databases in Systems Biology: A Comprehensive Review. Biomolecules, 2021, 11, 1245.	4.0	17
44	Distinct transcriptional profile of blood mononuclear cells in Behçet's disease: insights into the central role of neutrophil chemotaxis. Rheumatology, 2021, 60, 4910-4919.	1.9	16
45	PREGO: A Literature and Data-Mining Resource to Associate Microorganisms, Biological Processes, and Environment Types. Microorganisms, 2022, 10, 293.	3.6	15
46	ProteoSign v2: a faster and evolved user-friendly online tool for statistical analyses of differential proteomics. Nucleic Acids Research, 2021, 49, W573-W577.	14.5	11
47	Blood Transcriptomes of Anti-SARS-CoV-2 Antibody-Positive Healthy Individuals Who Experienced Asymptomatic Versus Clinical Infection. Frontiers in Immunology, 2021, 12, 746203.	4.8	10
48	OnTheFly2.0: a text-mining web application for automated biomedical entity recognition, document annotation, network and functional enrichment analysis. NAR Genomics and Bioinformatics, 2021, 3, lqab090.	3.2	10
49	Distributed Many-to-Many Protein Sequence Alignment using Sparse Matrices. , 2020, , .		9
50	Darling: A Web Application for Detecting Disease-Related Biomedical Entity Associations with Literature Mining. Biomolecules, 2022, 12, 520.	4.0	9
51	An enhanced Markov clustering method for detecting protein complexes. , 2008, , .		8
52	UniProt-Related Documents (UniReD): assisting wet lab biologists in their quest on finding novel counterparts in a protein network. NAR Genomics and Bioinformatics, 2020, 2, lqaa005.	3.2	8
53	NORMA: The Network Makeup Artist – A Web Tool for Network Annotation Visualization. Genomics, Proteomics and Bioinformatics, 2022, 20, 578-586.	6.9	8
54	Molecular Epidemiology of SARS-CoV-2 in Greece Reveals Low Rates of Onward Virus Transmission after Lifting of Travel Restrictions Based on Risk Assessment during Summer 2020. MSphere, 2021, 6, e0018021.	2.9	8

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55	Interpreting the Omics “era” Data. Smart Innovation, Systems and Technologies, 2013, , 79-100.	0.6	7
56	Meander: visually exploring the structural variome using space-filling curves. Nucleic Acids Research, 2013, 41, e118-e118.	14.5	6
57	Exploring Networks in the STRING and Reactome Database. , 2021, , 507-520.		6
58	Bee foraging preferences, microbiota and pathogens revealed by direct shotgun metagenomics of honey. Molecular Ecology Resources, 2022, 22, 2506-2523.	4.8	6
59	ReLiance: a machine learning and literature-based prioritization of receptor–ligand pairings. Bioinformatics, 2012, 28, i569-i574.	4.1	5
60	VICTOR: A visual analytics web application for comparing cluster sets. Computers in Biology and Medicine, 2021, 135, 104557.	7.0	5
61	Visualizing high dimensional datasets using parallel coordinates: Application to gene prioritization. , 2012, , .		4
62	A Simple Genetic Algorithm for Biomarker Mining. Lecture Notes in Computer Science, 2012, , 222-232.	1.3	4
63	How to Cluster Protein Sequences: Tools, Tips and Commands. MOJ Proteomics & Bioinformatics, 2017, 5, .	0.1	4
64	The network makeup artist (NORMA-2.0): distinguishing annotated groups in a network using innovative layout strategies. Bioinformatics Advances, 2022, 2, .	2.4	4
65	Analyzing Protein-Protein Interaction Networks with Web Tools. Current Bioinformatics, 2011, 6, 389-397.	1.5	3
66	Data and programs in support of network analysis of genes and their association with diseases. Data in Brief, 2016, 8, 1036-1039.	1.0	3
67	The Network Analysis Profiler (NAP v2.0): a web tool for visual topological comparison between multiple networks. EMBnet Journal, 2021, 26, e943.	0.6	2
68	Mining Cell Cycle Literature Using Support Vector Machines. Lecture Notes in Computer Science, 2012, , 278-284.	1.3	2
69	A bioinformatics e-dating story: computational prediction and prioritization of receptor-ligand pairs. BMC Bioinformatics, 2012, 13, .	2.6	1
70	OnTheFly 2.0: A tool for automatic annotation of files and biological information extraction. , 2013, , .		1
71	The human GPCR signal transduction network. Network Modeling Analysis in Health Informatics and Bioinformatics, 2021, 10, 1.	2.1	1
72	The Network Analysis Profiler (NAP v2.0): a web tool for visual topological comparison between multiple networks. EMBnet Journal, 0, 26, e943.	0.6	1

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73	Towards Better Prioritization of Epigenetically Modified DNA Regions. Lecture Notes in Computer Science, 2012, , 270-277.	1.3	0