Georgios A Pavlopoulos

List of Publications by Citations

74 papers	3,324 citations
26 h-index	57 g-index
86 ext. papers	4,450 ext. citations
9.1 avg, IF	5.3 L-index

#	Paper	IF	Citations
74	Uncovering Earth's virome. *Nature*, **2016**, 536, 425-30	50.4	551
73	Using graph theory to analyze biological networks. *BioData Mining*, **2011**, 4, 10	4.3	357
72	Protein structure determination using metagenome sequence data. *Science*, **2017**, 355, 294-298	33.3	346
71	Metagenomics: tools and insights for analyzing next-generation sequencing data derived from biodiversity studies. *Bioinformatics and Biology Insights*, **2015**, 9, 75-88	5.3	222
70	Cultivation and sequencing of rumen microbiome members from the Hungate1000 Collection. *Nature Biotechnology*, **2018**, 36, 359-367	44.5	207
69	1,003 reference genomes of bacterial and archaeal isolates expand coverage of the tree of life. *Nature Biotechnology*, **2017**, 35, 676-683	44.5	161
68	A survey of visualization tools for biological network analysis. *BioData Mining*, **2008**, 1, 12	4.3	134
67	IMG/VR: a database of cultured and uncultured DNA Viruses and retroviruses. *Nucleic Acids Research*, **2017**, 45, D457-D465	20.1	115
66	Large-Scale Analyses of Human Microbiomes Reveal Thousands of Small, Novel Genes. *Cell*, **2019**, 178, 1245-1259.e14	56.2	91
65	Arena3D: visualization of biological networks in 3D. *BMC Systems Biology*, **2008**, 2, 104	3.5	73
64	Nontargeted virus sequence discovery pipeline and virus clustering for metagenomic data. *Nature Protocols*, **2017**, 12, 1673-1682	18.8	71
63	Bipartite graphs in systems biology and medicine: a survey of methods and applications. *GigaScience*, **2018**, 7, 1-31	7.6	64
62	Visualizing genome and systems biology: technologies, tools, implementation techniques and trends, past, present and future. *GigaScience*, **2015**, 4, 38	7.6	60
61	A reference guide for tree analysis and visualization. *BioData Mining*, **2010**, 3, 1	4.3	55
60	Protein-protein interaction predictions using text mining methods. *Methods*, **2015**, 74, 47-53	4.6	53
59	A Guide to Conquer the Biological Network Era Using Graph Theory. *Frontiers in Bioengineering and Biotechnology*, **2020**, 8, 34	5.8	50
58	HipMCL: a high-performance parallel implementation of the Markov clustering algorithm for large-scale networks. *Nucleic Acids Research*, **2018**, 46, e33	20.1	48

57	Medusa: A tool for exploring and clustering biological networks. *BMC Research Notes*, **2011**, 4, 384	2.3	44
56	Arena3D: visualizing time-driven phenotypic differences in biological systems. *BMC Bioinformatics*, **2012**, 13, 45	3.6	37
55	Unraveling genomic variation from next generation sequencing data. *BioData Mining*, **2013**, 6, 13	4.3	33
54	Empirical Comparison of Visualization Tools for Larger-Scale Network Analysis. *Advances in Bioinformatics*, **2017**, 2017, 1278932	5.5	32
53	Caipirini: using gene sets to rank literature. *BioData Mining*, **2012**, 5, 1	4.3	32
52	Apolipoprotein A-I inhibits experimental colitis and colitis-propelled carcinogenesis. *Oncogene*, **2016**, 35, 2496-505	9.2	31
51	Global BioID-based SARS-CoV-2 proteins proximal interactome unveils novel ties between viral polypeptides and host factors involved in multiple COVID19-associated mechanisms		29
50	Annotate-it: a Swiss-knife approach to annotation, analysis and interpretation of single nucleotide variation in human disease. *Genome Medicine*, **2012**, 4, 73	14.4	27
49	Prediction of miRNA targets. *Methods in Molecular Biology*, **2015**, 1269, 207-29	1.4	27
48	ProteoSign: an end-user online differential proteomics statistical analysis platform. *Nucleic Acids Research*, **2017**, 45, W300-W306	20.1	25
47	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	2.3	23
46	Network analysis of genes and their association with diseases. *Gene*, **2016**, 590, 68-78	3.8	21
45	Which clustering algorithm is better for predicting protein complexes?. *BMC Research Notes*, **2011**, 4, 549	2.3	21
44	LAITOR--Literature Assistant for Identification of Terms co-Occurrences and Relationships. *BMC Bioinformatics*, **2010**, 11, 70	3.6	21
43	Diversity, evolution, and classification of virophages uncovered through global metagenomics. *Microbiome*, **2019**, 7, 157	16.6	21
42	Human gene correlation analysis (HGCA): a tool for the identification of transcriptionally co-expressed genes. *BMC Research Notes*, **2012**, 5, 265	2.3	20
41	DrugQuest - a text mining workflow for drug association discovery. *BMC Bioinformatics*, **2016**, 17 Suppl 5, 182	3.6	19
40	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	5	18

No.	Title	IF	Cit.
39	jClust: a clustering and visualization toolbox. *Bioinformatics*, **2009**, 25, 1994-6	7.2	18
38	GIBA: a clustering tool for detecting protein complexes. *BMC Bioinformatics*, **2009**, 10 Suppl 6, S11	3.6	18
37	OnTheFly: a tool for automated document-based text annotation, data linking and network generation. *Bioinformatics*, **2009**, 25, 977-8	7.2	15
36	BioTextQuest(+): a knowledge integration platform for literature mining and concept discovery. *Bioinformatics*, **2014**, 30, 3249-56	7.2	14
35	Biological information extraction and co-occurrence analysis. *Methods in Molecular Biology*, **2014**, 1159, 77-92	1.4	13
34	Structure determination of the HgcAB complex using metagenome sequence data: insights into microbial mercury methylation. *Communications Biology*, **2020**, 3, 320	6.7	8
33	An enhanced Markov clustering method for detecting protein complexes **2008**,		8
32	Interpreting the Omics Era Data. *Smart Innovation, Systems and Technologies*, **2013**, 79-100	0.5	7
31	Meander: visually exploring the structural variome using space-filling curves. *Nucleic Acids Research*, **2013**, 41, e118	20.1	6
30	Arena3Dweb: interactive 3D visualization of multilayered networks. *Nucleic Acids Research*, **2021**, 49, W36-W45	20.1	5
29	NORMA: The Network Makeup Artist - A Web Tool for Network Annotation Visualization. *Genomics, Proteomics and Bioinformatics*, **2021**,	6.5	4
28	FLAME: A Web Tool for Functional and Literature Enrichment Analysis of Multiple Gene Lists. *Biology*, **2021**, 10,	4.9	4
27	Exploring Networks in the STRING and Reactome Database **2021**, 507-520		4
26	Biomolecule and Bioentity Interaction Databases in Systems Biology: A Comprehensive Review. *Biomolecules*, **2021**, 11,	5.9	4
25	Analyzing Protein-Protein Interaction Networks with Web Tools. *Current Bioinformatics*, **2011**, 6, 389-397	4.7	3
24	Visualizing high dimensional datasets using parallel coordinates: Application to gene prioritization **2012**,		3
23	ReLiance: a machine learning and literature-based prioritization of receptor--ligand pairings. *Bioinformatics*, **2012**, 28, i569-i574	7.2	3
22	OnTheFly: a text-mining web application for automated biomedical entity recognition, document annotation, network and functional enrichment analysis. *NAR Genomics and Bioinformatics*, **2021**, 3, lqab090	2.7	3

21	A Simple Genetic Algorithm for Biomarker Mining. *Lecture Notes in Computer Science*, **2012**, 222-232	0.9	3
20	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	3.7	3
19	ProteoSign v2: a faster and evolved user-friendly online tool for statistical analyses of differential proteomics. *Nucleic Acids Research*, **2021**, 49, W573-W577	20.1	3
18	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**, e0018021	5	3
17	Data and programs in support of network analysis of genes and their association with diseases. *Data in Brief*, **2016**, 8, 1036-9	1.2	3
16	Distinct transcriptional profile of blood mononuclear cells in Behçet's disease: insights into the central role of neutrophil chemotaxis. *Rheumatology*, **2021**, 60, 4910-4919	3.9	3
15	PREGO: A Literature and Data-Mining Resource to Associate Microorganisms, Biological Processes, and Environment Types.. *Microorganisms*, **2022**, 10,	4.9	2
14	Distributed Many-to-Many Protein Sequence Alignment using Sparse Matrices **2020**,		2
13	How to Cluster Protein Sequences: Tools, Tips and Commands. *MOJ Proteomics & Bioinformatics*, **2017**, 5,	0	2
12	Blood Transcriptomes of Anti-SARS-CoV-2 Antibody-Positive Healthy Individuals Who Experienced Asymptomatic Clinical Infection. *Frontiers in Immunology*, **2021**, 12, 746203	8.4	2
11	Mining Cell Cycle Literature Using Support Vector Machines. *Lecture Notes in Computer Science*, **2012**, 278-284	0.9	2
10	NORMA-The network makeup artist: a web tool for network annotation visualization		2
9	OnTheFly2.0: a text-mining web application for automated biomedical entity recognition, document annotation, network and functional enrichment analysis		2
8	The Network Analysis Profiler (NAP v2.0): a web tool for visual topological comparison between multiple networks. *EMBnet Journal*, **2021**, 26, e943	2.3	2
7	VICTOR: A visual analytics web application for comparing cluster sets. *Computers in Biology and Medicine*, **2021**, 135, 104557	7	2
6	OnTheFly 2.0: A tool for automatic annotation of files and biological information extraction **2013**,		1
5	A bioinformatics e-dating story: computational prediction and prioritization of receptor-ligand pairs. *BMC Bioinformatics*, **2012**, 13,	3.6	1
4	The human GPCR signal transduction network. *Network Modeling Analysis in Health Informatics and Bioinformatics*, **2021**, 10, 1	1.6	1

3	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		1
2	Darling: A Web Application for Detecting Disease-Related Biomedical Entity Associations with Literature Mining.. *Biomolecules*, **2022**, 12,	5.9	1
1	Towards Better Prioritization of Epigenetically Modified DNA Regions. *Lecture Notes in Computer Science*, **2012**, 270-277	0.9	