

# Georgios A Pavlopoulos

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	PREGO: A Literature and Data-Mining Resource to Associate Microorganisms, Biological Processes, and Environment Types.. <i>Microorganisms</i> , <b>2022</b> , 10,	4.9	2
73	Darling: A Web Application for Detecting Disease-Related Biomedical Entity Associations with Literature Mining.. <i>Biomolecules</i> , <b>2022</b> , 12,	5.9	1
72	Blood Transcriptomes of Anti-SARS-CoV-2 Antibody-Positive Healthy Individuals Who Experienced Asymptomatic Clinical Infection. <i>Frontiers in Immunology</i> , <b>2021</b> , 12, 746203	8.4	2
71	OnTheFly: a text-mining web application for automated biomedical entity recognition, document annotation, network and functional enrichment analysis. <i>NAR Genomics and Bioinformatics</i> , <b>2021</b> , 3, 190	3.7	3
70	Arena3Dweb: interactive 3D visualization of multilayered networks. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, W36-W45	20.1	5
69	ProteoSign v2: a faster and evolved user-friendly online tool for statistical analyses of differential proteomics. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, W573-W577	20.1	3
68	The Network Analysis Profiler (NAP v2.0): a web tool for visual topological comparison between multiple networks. <i>EMBnet Journal</i> , <b>2021</b> , 26, e943	2.3	2
67	NORMA: The Network Makeup Artist - A Web Tool for Network Annotation Visualization. <i>Genomics, Proteomics and Bioinformatics</i> , <b>2021</b> ,	6.5	4
66	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. <i>MSphere</i> , <b>2021</b> , e018021	5.1	3
65	FLAME: A Web Tool for Functional and Literature Enrichment Analysis of Multiple Gene Lists. <i>Biology</i> , <b>2021</b> , 10,	4.9	4
64	The human GPCR signal transduction network. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , <b>2021</b> , 10, 1	1.6	1
63	Distinct transcriptional profile of blood mononuclear cells in Behçet's disease: insights into the central role of neutrophil chemotaxis. <i>Rheumatology</i> , <b>2021</b> , 60, 4910-4919	3.9	3
62	Exploring Networks in the STRING and Reactome Database <b>2021</b> , 507-520		4
61	VICTOR: A visual analytics web application for comparing cluster sets. <i>Computers in Biology and Medicine</i> , <b>2021</b> , 135, 104557	7	2
60	Biomolecule and Bioentity Interaction Databases in Systems Biology: A Comprehensive Review. <i>Biomolecules</i> , <b>2021</b> , 11,	5.9	4
59	Structure determination of the HgcAB complex using metagenome sequence data: insights into microbial mercury methylation. <i>Communications Biology</i> , <b>2020</b> , 3, 320	6.7	8
58	A Guide to Conquer the Biological Network Era Using Graph Theory. <i>Frontiers in Bioengineering and Biotechnology</i> , <b>2020</b> , 8, 34	5.8	50

57	Distributed Many-to-Many Protein Sequence Alignment using Sparse Matrices <b>2020</b> ,		2
56	UniProt-Related Documents (UniReD): assisting wet lab biologists in their quest on finding novel counterparts in a protein network. <i>NAR Genomics and Bioinformatics</i> , <b>2020</b> , 2, lqaa005	3.7	3
55	Large-Scale Analyses of Human Microbiomes Reveal Thousands of Small, Novel Genes. <i>Cell</i> , <b>2019</b> , 178, 1245-1259.e14	56.2	91
54	Diversity, evolution, and classification of virophages uncovered through global metagenomics. <i>Microbiome</i> , <b>2019</b> , 7, 157	16.6	21
53	Bipartite graphs in systems biology and medicine: a survey of methods and applications. <i>GigaScience</i> , <b>2018</b> , 7, 1-31	7.6	64
52	HipMCL: a high-performance parallel implementation of the Markov clustering algorithm for large-scale networks. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, e33	20.1	48
51	Cultivation and sequencing of rumen microbiome members from the Hungate1000 Collection. <i>Nature Biotechnology</i> , <b>2018</b> , 36, 359-367	44.5	207
50	Protein structure determination using metagenome sequence data. <i>Science</i> , <b>2017</b> , 355, 294-298	33.3	346
49	ProteoSign: an end-user online differential proteomics statistical analysis platform. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, W300-W306	20.1	25
48	1,003 reference genomes of bacterial and archaeal isolates expand coverage of the tree of life. <i>Nature Biotechnology</i> , <b>2017</b> , 35, 676-683	44.5	161
47	NAP: The Network Analysis Profiler, a web tool for easier topological analysis and comparison of medium-scale biological networks. <i>BMC Research Notes</i> , <b>2017</b> , 10, 278	2.3	23
46	IMG/VR: a database of cultured and uncultured DNA Viruses and retroviruses. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, D457-D465	20.1	115
45	Nontargeted virus sequence discovery pipeline and virus clustering for metagenomic data. <i>Nature Protocols</i> , <b>2017</b> , 12, 1673-1682	18.8	71
44	Empirical Comparison of Visualization Tools for Larger-Scale Network Analysis. <i>Advances in Bioinformatics</i> , <b>2017</b> , 2017, 1278932	5.5	32
43	How to Cluster Protein Sequences: Tools, Tips and Commands. <i>MOJ Proteomics &amp; Bioinformatics</i> , <b>2017</b> , 5,	0	2
42	Uncovering Earth's virome. <i>Nature</i> , <b>2016</b> , 536, 425-30	50.4	551
41	Network analysis of genes and their association with diseases. <i>Gene</i> , <b>2016</b> , 590, 68-78	3.8	21
40	Apolipoprotein A-I inhibits experimental colitis and colitis-propelled carcinogenesis. <i>Oncogene</i> , <b>2016</b> , 35, 2496-505	9.2	31

39	DrugQuest - a text mining workflow for drug association discovery. <i>BMC Bioinformatics</i> , <b>2016</b> , 17 Suppl 5, 182	3.6	19
38	Data and programs in support of network analysis of genes and their association with diseases. <i>Data in Brief</i> , <b>2016</b> , 8, 1036-9	1.2	3
37	Visualizing genome and systems biology: technologies, tools, implementation techniques and trends, past, present and future. <i>GigaScience</i> , <b>2015</b> , 4, 38	7.6	60
36	Protein-protein interaction predictions using text mining methods. <i>Methods</i> , <b>2015</b> , 74, 47-53	4.6	53
35	Metagenomics: tools and insights for analyzing next-generation sequencing data derived from biodiversity studies. <i>Bioinformatics and Biology Insights</i> , <b>2015</b> , 9, 75-88	5.3	222
34	Prediction of miRNA targets. <i>Methods in Molecular Biology</i> , <b>2015</b> , 1269, 207-29	1.4	27
33	BioTextQuest(+): a knowledge integration platform for literature mining and concept discovery. <i>Bioinformatics</i> , <b>2014</b> , 30, 3249-56	7.2	14
32	Biological information extraction and co-occurrence analysis. <i>Methods in Molecular Biology</i> , <b>2014</b> , 1159, 77-92	1.4	13
31	Unraveling genomic variation from next generation sequencing data. <i>BioData Mining</i> , <b>2013</b> , 6, 13	4.3	33
30	Interpreting the Omics Era Data. <i>Smart Innovation, Systems and Technologies</i> , <b>2013</b> , 79-100	0.5	7
29	OnTheFly 2.0: A tool for automatic annotation of files and biological information extraction <b>2013</b> ,		1
28	Meander: visually exploring the structural variome using space-filling curves. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, e118	20.1	6
27	Arena3D: visualizing time-driven phenotypic differences in biological systems. <i>BMC Bioinformatics</i> , <b>2012</b> , 13, 45	3.6	37
26	Caipirini: using gene sets to rank literature. <i>BioData Mining</i> , <b>2012</b> , 5, 1	4.3	32
25	Human gene correlation analysis (HGCA): a tool for the identification of transcriptionally co-expressed genes. <i>BMC Research Notes</i> , <b>2012</b> , 5, 265	2.3	20
24	A bioinformatics e-dating story: computational prediction and prioritization of receptor-ligand pairs. <i>BMC Bioinformatics</i> , <b>2012</b> , 13,	3.6	1
23	Annotate-it: a Swiss-knife approach to annotation, analysis and interpretation of single nucleotide variation in human disease. <i>Genome Medicine</i> , <b>2012</b> , 4, 73	14.4	27
22	Visualizing high dimensional datasets using parallel coordinates: Application to gene prioritization <b>2012</b> ,		3

21	ReLIance: a machine learning and literature-based prioritization of receptor--ligand pairings. <i>Bioinformatics</i> , <b>2012</b> , 28, i569-i574	7.2	3
20	Mining Cell Cycle Literature Using Support Vector Machines. <i>Lecture Notes in Computer Science</i> , <b>2012</b> , 278-284	0.9	2
19	A Simple Genetic Algorithm for Biomarker Mining. <i>Lecture Notes in Computer Science</i> , <b>2012</b> , 222-232	0.9	3
18	Towards Better Prioritization of Epigenetically Modified DNA Regions. <i>Lecture Notes in Computer Science</i> , <b>2012</b> , 270-277	0.9	
17	Which clustering algorithm is better for predicting protein complexes?. <i>BMC Research Notes</i> , <b>2011</b> , 4, 549	2.3	21
16	Analyzing Protein-Protein Interaction Networks with Web Tools. <i>Current Bioinformatics</i> , <b>2011</b> , 6, 389-397	4.7	3
15	Medusa: A tool for exploring and clustering biological networks. <i>BMC Research Notes</i> , <b>2011</b> , 4, 384	2.3	44
14	Using graph theory to analyze biological networks. <i>BioData Mining</i> , <b>2011</b> , 4, 10	4.3	357
13	GPCRs, G-proteins, effectors and their interactions: human-gpDB, a database employing visualization tools and data integration techniques. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2010</b> , 2010, baq019	5	18
12	LAITOR--Literature Assistant for Identification of Terms co-Occurrences and Relationships. <i>BMC Bioinformatics</i> , <b>2010</b> , 11, 70	3.6	21
11	A reference guide for tree analysis and visualization. <i>BioData Mining</i> , <b>2010</b> , 3, 1	4.3	55
10	OnTheFly: a tool for automated document-based text annotation, data linking and network generation. <i>Bioinformatics</i> , <b>2009</b> , 25, 977-8	7.2	15
9	jClust: a clustering and visualization toolbox. <i>Bioinformatics</i> , <b>2009</b> , 25, 1994-6	7.2	18
8	GIBA: a clustering tool for detecting protein complexes. <i>BMC Bioinformatics</i> , <b>2009</b> , 10 Suppl 6, S11	3.6	18
7	Arena3D: visualization of biological networks in 3D. <i>BMC Systems Biology</i> , <b>2008</b> , 2, 104	3.5	73
6	An enhanced Markov clustering method for detecting protein complexes <b>2008</b> ,		8
5	A survey of visualization tools for biological network analysis. <i>BioData Mining</i> , <b>2008</b> , 1, 12	4.3	134
4	NORMA-The network makeup artist: a web tool for network annotation visualization		2

3	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
2	OnTheFly2.0: a text-mining web application for automated biomedical entity recognition, document annotation, network and functional enrichment analysis	2
1	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