Fotis E Psomopoulos

List of Publications by Year
in descending order

75 papers	862 citations	623574 14 h-index	580701 25 g-index
86 all docs	86 docs citations	86 times ranked	1477 citing authors

#	Article	IF	Citations
1	Towards FAIR principles for research software. Data Science, 2020, 3, 37-59.	0.7	144
2	DOME: recommendations for supervised machine learning validation in biology. Nature Methods, 2021, 18, 1122-1127.	9.0	105
3	Bacterial communities and potential spoilage markers of whole blue crab (Callinectes sapidus) stored under commercial simulated conditions. Food Microbiology, 2019, 82, 325-333.	2.1	47
4	Microbial spoilage investigation of thawed common cuttlefish (Sepia officinalis) stored at 2â€¯Â°C using next generation sequencing and volatilome analysis. Food Microbiology, 2018, 76, 518-525.	2.1	44
5	Pretransplant Genetic Susceptibility: Clinical Relevance in Transplant-Associated Thrombotic Microangiopathy. Thrombosis and Haemostasis, 2020, 120, 638-646.	1.8	33
6	Reinforcement Learning based scheduling in a workflow management system. Engineering Applications of Artificial Intelligence, 2019, 81, 94-106.	4.3	30
7	De novo comparative transcriptome analysis of genes involved in fruit morphology of pumpkin cultivars with extreme size difference and development of EST-SSR markers. Gene, 2017, 622, 50-66.	1.0	29
8	Towards an integrated robotics architecture for social inclusion â€" The RAPP paradigm. Cognitive Systems Research, 2017, 43, 157-173.	1.9	27
9	Integrated epigenomic and transcriptomic analysis reveals <i>TP63</i> as a novel player in clinically aggressive chronic lymphocytic leukemia. International Journal of Cancer, 2019, 144, 2695-2706.	2.3	24
10	Ten simple rules for making training materials FAIR. PLoS Computational Biology, 2020, 16, e1007854.	1.5	24
11	Variable structure robot control systems: The RAPP approach. Robotics and Autonomous Systems, 2017, 94, 226-244.	3.0	22
12	Higher-order immunoglobulin repertoire restrictions in CLL: the illustrative case of stereotyped subsets 2 and 169. Blood, 2021, 137, 1895-1904.	0.6	21
13	T-Cell Dynamics in Chronic Lymphocytic Leukemia under Different Treatment Modalities. Clinical Cancer Research, 2020, 26, 4958-4969.	3.2	18
14	Stereotyped B Cell Receptor Immunoglobulins in B Cell Lymphomas. Methods in Molecular Biology, 2019, 1956, 139-155.	0.4	17
15	Detecting SARS-CoV-2 lineages and mutational load in municipal wastewater and a use-case in the metropolitan area of Thessaloniki, Greece. Scientific Reports, 2022, 12, 2659.	1.6	17
16	Detection of Genomic Idiosyncrasies Using Fuzzy Phylogenetic Profiles. PLoS ONE, 2013, 8, e52854.	1.1	16
17	De novo transcriptome assembly of two contrasting pumpkin cultivars. Genomics Data, 2016, 7, 200-201.	1.3	14
18	Nuclear inclusions of pathogenic ataxin-1 induce oxidative stress and perturb the protein synthesis machinery. Redox Biology, 2020, 32, 101458.	3.9	14

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19	RAPP: A Robotic-Oriented Ecosystem for Delivering Smart User Empowering Applications for Older People. International Journal of Social Robotics, 2016, 8, 539-552.	3.1	13
20	<i>RPS15</i> mutations rewire RNA translation in chronic lymphocytic leukemia. Blood Advances, 2021, 5, 2788-2792.	2.5	12
21	Chronic lymphocytic leukemias with trisomy 12 show a distinct DNA methylation profile linked to altered chromatin activation. Haematologica, 2020, 105, 2864-2867.	1.7	11
22	Fostering global data sharing: highlighting the recommendations of the Research Data Alliance COVID-19 working group. Wellcome Open Research, 2020, 5, 267.	0.9	11
23	TRIP - T cell receptor/immunoglobulin profiler. BMC Bioinformatics, 2020, 21, 422.	1.2	11
24	Data Discovery Paradigms: User Requirements and Recommendations for Data Repositories. Data Science Journal, 2019, 18, .	0.6	11
25	The Chlamydiales Pangenome Revisited: Structural Stability and Functional Coherence. Genes, 2012, 3, 291-319.	1.0	9
26	Hermes: Seamless delivery of containerized bioinformatics workflows in hybrid cloud (HTC) environments. SoftwareX, 2017, 6, 217-224.	1.2	9
27	UMIc: A Preprocessing Method for UMI Deduplication and Reads Correction. Frontiers in Genetics, 2021, 12, 660366.	1.1	9
28	Future opportunities and trends for e-infrastructures and life sciences: going beyond the grid to enable life science data analysis. Frontiers in Genetics, 2015, 6, 197.	1.1	8
29	Infrequent â€œchronic lymphocytic leukemia-specificâ€•immunoglobulin stereotypes in aged individuals with or without low-count monoclonal B-cell lymphocytosis. Haematologica, 2021, 106, 1178-1181.	1.7	8
30	A framework to assess the quality and impact of bioinformatics training across ELIXIR. PLoS Computational Biology, 2020, 16, e1007976.	1.5	7
31	Fostering global data sharing: highlighting the recommendations of the Research Data Alliance COVID-19 working group. Wellcome Open Research, 2020, 5, 267.	0.9	6
32	BioPAXViz: a cytoscape application for the visual exploration of metabolic pathway evolution. Bioinformatics, 2017, 33, 1418-1420.	1.8	5
33	Eleven quick tips for finding research data. PLoS Computational Biology, 2018, 14, e1006038.	1.5	5
34	Remarkable Functional Constraints on the Antigen Receptors of CLL Stereotyped Subset #2: High-Throughput Immunogenetic Evidence. Blood, 2018, 132, 1839-1839.	0.6	5
35	A dockerized framework for hierarchical frequency-based document clustering on cloud computing infrastructures. Journal of Cloud Computing: Advances, Systems and Applications, 2020, 9, .	2.1	5
36	Comparative Genomics of Botrytis cinerea Strains with Differential Multi-Drug Resistance. Frontiers in Plant Science, 2016, 7, 554.	1.7	4

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37	Comparative metagenomics reveals alterations in the soil bacterial community driven by N-fertilizer and Amino 16® application in lettuce. Genomics Data, 2017, 14, 14-17.	1.3	4
38	Dynamics of a Protein Interaction Network Associated to the Aggregation of polyQ-Expanded Ataxin-1. Genes, 2020, 11, 1129.	1.0	4
39	Combining Multiple RNA-Seq Data Analysis Algorithms Using Machine Learning Improves Differential Isoform Expression Analysis. Methods and Protocols, 2021, 4, 68.	0.9	4
40	In silico analysis of the LRR receptor-like serine threonine kinases subfamily in Morus notabilis. Plant OMICS, 2016, 9, 319-326.	0.4	4
41	Bioinformatics algorithm development for Grid environments. Journal of Systems and Software, 2010, 83, 1249-1257.	3.3	3
42	High-throughput analysis of the T cell receptor gene repertoire in low-count monoclonal B cell lymphocytosis reveals a distinct profile from chronic lymphocytic leukemia. Haematologica, 2020, 105, e515.	1.7	3
43	The Calcitriol/Vitamin D Receptor System Regulates Key Immune Signaling Pathways in Chronic Lymphocytic Leukemia. Cancers, 2021, 13, 285.	1.7	3
44	Exploring plant diversity through soil DNA in Thai national parks for influencing land reform and agriculture planning. PeerJ, 2021, 9, e11753.	0.9	3
45	VH CDR3-Focused Somatic Hypermutation in CLL IGHV-IGHD-IGHJ Gene Rearrangements with 100% IGHV Germline Identity. Blood, 2019, 134, 4277-4277.	0.6	3
46	Ancestral state reconstruction of metabolic pathways across pangenome ensembles. Microbial Genomics, 2020, 6, .	1.0	3
47	Multi Level Clustering of Phylogenetic Profiles. , 2010, , .		2
48	Data-aware optimization of bioinformatics workflows in hybrid clouds. Journal of Big Data, 2016, 3, .	6.9	2
49	A Hierarchical Multi-Metric Framework for Item Clustering. , 2018, , .		2
50	Evidence for Epitope-Specific T Cell Responses in HIV-Associated Non Neoplastic Lymphadenopathy: High-Throughput Immunogenetic Evidence. Blood, 2018, 132, 1117-1117.	0.6	2
51	PS1131 HIGH‐THROUGHPUT B‐CELL IMMUNOPROFILING AT DIAGNOSIS AND RELAPSE OFFERS FURTHER EVIDENCE OF FUNCTIONAL SELECTION THROUGHOUT THE NATURAL HISTORY OF CHRONIC LYMPHOCYTIC LEUKEMIA. HemaSphere, 2019, 3, 512.	1.2	2
52	InterTADs: integration of multi-omics data on topologically associated domains, application to chronic lymphocytic leukemia. NAR Genomics and Bioinformatics, 2022, 4, lqab121.	1.5	2
53	MULTI-LEVEL CLUSTERING OF PHYLOGENETIC PROFILES. International Journal on Artificial Intelligence Tools, 2012, 21, 1240023.	0.7	1
54	Multi-genome Core Pathway Identification through Gene Clustering. International Federation for Information Processing, 2012, , 545-555.	0.4	1

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55	RPS15 mutations Repress mRNA Translation in Chronic Lymphocytic Leukemia Cells. Blood, 2018, 132, 1843-1843.	0.6	1
56	Higher Order Restrictions of the Immunoglobulin Repertoire in CLL: The Illustrative Case of Stereotyped Subsets #2 and #169. Blood, 2019, 134, 5453-5453.	0.6	1
57	The TΊp63/BCL2 axis represents a novel mechanism of clinical aggressiveness in chronic lymphocytic leukemia. Blood Advances, 2022, 6, 2646-2656.	2.5	1
58	A grid-enabled algorithm yields figure-eight molecular knot. Molecular Simulation, 2009, 35, 725-736.	0.9	0
59	Inference of Pathway Decomposition Across Multiple Species Through Gene Clustering. International Journal on Artificial Intelligence Tools, 2015, 24, 1540003.	0.7	0
60	A Scalable Grid Computing Framework for Extensible Phylogenetic Profile Construction. IFIP Advances in Information and Communication Technology, 2016, , 455-462.	0.5	0
61	Lesson Development for Open Source Software Best Practices Adoption. , 2018, , .		0
62	A Computational Framework for Pattern Detection on Unaligned Sequences: An Application on SARS-CoV-2 Data. Frontiers in Genetics, 2021, 12, 618170.	1.1	0
63	miRkit: R framework analyzing miRNA PCR array data. BMC Research Notes, 2021, 14, 376.	0.6	0
64	Data Mining in Proteomics Using Grid Computing. , 2009, , 245-267.		0
65	Data Mining in Proteomics Using Grid Computing. , 2012, , 918-940.		0
66	Algebraic Interpretations Towards Clustering Protein Homology Data. Lecture Notes in Computer Science, 2014, , 136-145.	1.0	0
67	Pre-Transplant Genetic Susceptibility in Adult Allogeneic Hematopoietic Cell Transplant Recipients: Incidence and Clinical Relevance in Transplant-Associated Thrombotic Microangiopathy. Blood, 2018, 132, 3401-3401.	0.6	0
68	Longitudinal High-Throughput T Cell Repertoire Profiling of Chronic Lymphocytic Leukemia Patients Under Different Types of Treatment: Implications for Combination Strategies. Blood, 2018, 132, 4400-4400.	0.6	0
69	A Dockerized String Analysis Workflow for Big Data. Communications in Computer and Information Science, 2019, , 564-569.	0.4	0
70	ELIXIR Europe on the Road to Sustainable Research Software. Biodiversity Information Science and Standards, 0, 3, .	0.0	0
71	Genome-Wide Histone Acetylation Profiling in Chronic Lymphocytic Leukemia Reveals a Distinctive Signature in Stereotyped Subset #8. Blood, 2019, 134, 1241-1241.	0.6	0
72	Functional Calcitriol/Vitamin D Receptor Signaling in Chronic Lymphocytic Leukemia. Blood, 2019, 134, 3019-3019.	0.6	0

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73	Specific T Cell Receptor Gene Repertoire Profiles in Subgroups of CLL Patients with Distinct Genomic Aberrations. Blood, 2021, 138, 3749-3749.	0.6	0
74	Distinct Modes of Ongoing Antigen Interactions Shape Intraclonal Dynamics in Splenic Marginal Zone Lymphoma. Blood, 2021, 138, 1330-1330.	0.6	0
75	DNA coding and GÃ¶del numbering. Physica A: Statistical Mechanics and Its Applications, 2022, 594, 127053.	1.2	0