

# Fotis E Psomopoulos

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2501119/publications.pdf>

Version: 2024-02-01

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	InterTADs: integration of multi-omics data on topologically associated domains, application to chronic lymphocytic leukemia. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, lqab121.	1.5	2
2	DNA coding and GÅrdel numbering. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2022, 594, 127053.	1.2	0
3	Detecting SARS-CoV-2 lineages and mutational load in municipal wastewater and a use-case in the metropolitan area of Thessaloniki, Greece. <i>Scientific Reports</i> , 2022, 12, 2659.	1.6	17
4	The TÎp63/BCL2 axis represents a novel mechanism of clinical aggressiveness in chronic lymphocytic leukemia. <i>Blood Advances</i> , 2022, 6, 2646-2656.	2.5	1
5	Infrequent âœchronic lymphocytic leukemia-specificâœimmunoglobulin stereotypes in aged individuals with or without low-count monoclonal B-cell lymphocytosis. <i>Haematologica</i> , 2021, 106, 1178-1181.	1.7	8
6	Higher-order immunoglobulin repertoire restrictions in CLL: the illustrative case of stereotyped subsets 2 and 169. <i>Blood</i> , 2021, 137, 1895-1904.	0.6	21
7	The Calcitriol/Vitamin D Receptor System Regulates Key Immune Signaling Pathways in Chronic Lymphocytic Leukemia. <i>Cancers</i> , 2021, 13, 285.	1.7	3
8	UMIc: A Preprocessing Method for UMI Deduplication and Reads Correction. <i>Frontiers in Genetics</i> , 2021, 12, 660366.	1.1	9
9	A Computational Framework for Pattern Detection on Unaligned Sequences: An Application on SARS-CoV-2 Data. <i>Frontiers in Genetics</i> , 2021, 12, 618170.	1.1	0
10	<i>RPS15</i> mutations rewire RNA translation in chronic lymphocytic leukemia. <i>Blood Advances</i> , 2021, 5, 2788-2792.	2.5	12
11	DOME: recommendations for supervised machine learning validation in biology. <i>Nature Methods</i> , 2021, 18, 1122-1127.	9.0	105
12	Exploring plant diversity through soil DNA in Thai national parks for influencing land reform and agriculture planning. <i>PeerJ</i> , 2021, 9, e11753.	0.9	3
13	Combining Multiple RNA-Seq Data Analysis Algorithms Using Machine Learning Improves Differential Isoform Expression Analysis. <i>Methods and Protocols</i> , 2021, 4, 68.	0.9	4
14	miRkit: R framework analyzing miRNA PCR array data. <i>BMC Research Notes</i> , 2021, 14, 376.	0.6	0
15	Specific T Cell Receptor Gene Repertoire Profiles in Subgroups of CLL Patients with Distinct Genomic Aberrations. <i>Blood</i> , 2021, 138, 3749-3749.	0.6	0
16	Distinct Modes of Ongoing Antigen Interactions Shape Intraclonal Dynamics in Splenic Marginal Zone Lymphoma. <i>Blood</i> , 2021, 138, 1330-1330.	0.6	0
17	Towards FAIR principles forÂresearchÂsoftware. <i>Data Science</i> , 2020, 3, 37-59.	0.7	144
18	Dynamics of a Protein Interaction Network Associated to the Aggregation of polyQ-Expanded Ataxin-1. <i>Genes</i> , 2020, 11, 1129.	1.0	4

#	ARTICLE	IF	CITATIONS
19	A framework to assess the quality and impact of bioinformatics training across ELIXIR. PLoS Computational Biology, 2020, 16, e1007976.	1.5	7
20	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
21	Nuclear inclusions of pathogenic ataxin-1 induce oxidative stress and perturb the protein synthesis machinery. Redox Biology, 2020, 32, 101458.	3.9	14
22	T-Cell Dynamics in Chronic Lymphocytic Leukemia under Different Treatment Modalities. Clinical Cancer Research, 2020, 26, 4958-4969.	3.2	18
23	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
24	Pretransplant Genetic Susceptibility: Clinical Relevance in Transplant-Associated Thrombotic Microangiopathy. Thrombosis and Haemostasis, 2020, 120, 638-646.	1.8	33
25	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
26	TRIP - T cell receptor/immunoglobulin profiler. BMC Bioinformatics, 2020, 21, 422.	1.2	11
27	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
28	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
29	Ten simple rules for making training materials FAIR. PLoS Computational Biology, 2020, 16, e1007854.	1.5	24
30	Ancestral state reconstruction of metabolic pathways across pangenome ensembles. Microbial Genomics, 2020, 6, .	1.0	3
31	Bacterial communities and potential spoilage markers of whole blue crab ( <i>Callinectes sapidus</i> ) stored under commercial simulated conditions. Food Microbiology, 2019, 82, 325-333.	2.1	47
32	Reinforcement Learning based scheduling in a workflow management system. Engineering Applications of Artificial Intelligence, 2019, 81, 94-106.	4.3	30
33	Stereotyped B Cell Receptor Immunoglobulins in B Cell Lymphomas. Methods in Molecular Biology, 2019, 1956, 139-155.	0.4	17
34	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
35	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
36	Data Discovery Paradigms: User Requirements and Recommendations for Data Repositories. Data Science Journal, 2019, 18, .	0.6	11

#	ARTICLE	IF	CITATIONS
37	A Dockerized String Analysis Workflow for Big Data. <i>Communications in Computer and Information Science</i> , 2019, , 564-569.	0.4	0
38	PS1131 HIGH-THROUGHPUT B-CELL IMMUNOPROFILING AT DIAGNOSIS AND RELAPSE OFFERS FURTHER EVIDENCE OF FUNCTIONAL SELECTION THROUGHOUT THE NATURAL HISTORY OF CHRONIC LYMPHOCYTIC LEUKEMIA. <i>HemaSphere</i> , 2019, 3, 512.	1.2	2
39	Genome-Wide Histone Acetylation Profiling in Chronic Lymphocytic Leukemia Reveals a Distinctive Signature in Stereotyped Subset #8. <i>Blood</i> , 2019, 134, 1241-1241.	0.6	0
40	Higher Order Restrictions of the Immunoglobulin Repertoire in CLL: The Illustrative Case of Stereotyped Subsets #2 and #169. <i>Blood</i> , 2019, 134, 5453-5453.	0.6	1
41	Functional Calcitriol/Vitamin D Receptor Signaling in Chronic Lymphocytic Leukemia. <i>Blood</i> , 2019, 134, 3019-3019.	0.6	0
42	Lesson Development for Open Source Software Best Practices Adoption. , 2018, , .		0
43	A Hierarchical Multi-Metric Framework for Item Clustering. , 2018, , .		2
44	Eleven quick tips for finding research data. <i>PLoS Computational Biology</i> , 2018, 14, e1006038.	1.5	5
45	Microbial spoilage investigation of thawed common cuttlefish ( <i>Sepia officinalis</i> ) stored at 2°C using next generation sequencing and volatilome analysis. <i>Food Microbiology</i> , 2018, 76, 518-525.	2.1	44
46	RPS15 mutations Repress mRNA Translation in Chronic Lymphocytic Leukemia Cells. <i>Blood</i> , 2018, 132, 1843-1843.	0.6	1
47	Remarkable Functional Constraints on the Antigen Receptors of CLL Stereotyped Subset #2: High-Throughput Immunogenetic Evidence. <i>Blood</i> , 2018, 132, 1839-1839.	0.6	5
48	Evidence for Epitope-Specific T Cell Responses in HIV-Associated Non Neoplastic Lymphadenopathy: High-Throughput Immunogenetic Evidence. <i>Blood</i> , 2018, 132, 1117-1117.	0.6	2
49	Pre-Transplant Genetic Susceptibility in Adult Allogeneic Hematopoietic Cell Transplant Recipients: Incidence and Clinical Relevance in Transplant-Associated Thrombotic Microangiopathy. <i>Blood</i> , 2018, 132, 3401-3401.	0.6	0
50	Longitudinal High-Throughput T Cell Repertoire Profiling of Chronic Lymphocytic Leukemia Patients Under Different Types of Treatment: Implications for Combination Strategies. <i>Blood</i> , 2018, 132, 4400-4400.	0.6	0
51	De novo comparative transcriptome analysis of genes involved in fruit morphology of pumpkin cultivars with extreme size difference and development of EST-SSR markers. <i>Gene</i> , 2017, 622, 50-66.	1.0	29
52	Variable structure robot control systems: The RAPP approach. <i>Robotics and Autonomous Systems</i> , 2017, 94, 226-244.	3.0	22
53	BioPAXViz: a cytoscape application for the visual exploration of metabolic pathway evolution. <i>Bioinformatics</i> , 2017, 33, 1418-1420.	1.8	5
54	Comparative metagenomics reveals alterations in the soil bacterial community driven by N-fertilizer and Amino 16® application in lettuce. <i>Genomics Data</i> , 2017, 14, 14-17.	1.3	4

#	ARTICLE	IF	CITATIONS
55	Hermes: Seamless delivery of containerized bioinformatics workflows in hybrid cloud (HTC) environments. <i>SoftwareX</i> , 2017, 6, 217-224.	1.2	9
56	Towards an integrated robotics architecture for social inclusion – The RAPP paradigm. <i>Cognitive Systems Research</i> , 2017, 43, 157-173.	1.9	27
57	Comparative Genomics of <i>Botrytis cinerea</i> Strains with Differential Multi-Drug Resistance. <i>Frontiers in Plant Science</i> , 2016, 7, 554.	1.7	4
58	A Scalable Grid Computing Framework for Extensible Phylogenetic Profile Construction. <i>IFIP Advances in Information and Communication Technology</i> , 2016, , 455-462.	0.5	0
59	RAPP: A Robotic-Oriented Ecosystem for Delivering Smart User Empowering Applications for Older People. <i>International Journal of Social Robotics</i> , 2016, 8, 539-552.	3.1	13
60	Data-aware optimization of bioinformatics workflows in hybrid clouds. <i>Journal of Big Data</i> , 2016, 3, .	6.9	2
61	De novo transcriptome assembly of two contrasting pumpkin cultivars. <i>Genomics Data</i> , 2016, 7, 200-201.	1.3	14
62	In silico analysis of the LRR receptor-like serine threonine kinases subfamily in <i>Morus notabilis</i> . <i>Plant OMICS</i> , 2016, 9, 319-326.	0.4	4
63	Future opportunities and trends for e-infrastructures and life sciences: going beyond the grid to enable life science data analysis. <i>Frontiers in Genetics</i> , 2015, 6, 197.	1.1	8
64	Inference of Pathway Decomposition Across Multiple Species Through Gene Clustering. <i>International Journal on Artificial Intelligence Tools</i> , 2015, 24, 1540003.	0.7	0
65	Algebraic Interpretations Towards Clustering Protein Homology Data. <i>Lecture Notes in Computer Science</i> , 2014, , 136-145.	1.0	0
66	Detection of Genomic Idiosyncrasies Using Fuzzy Phylogenetic Profiles. <i>PLoS ONE</i> , 2013, 8, e52854.	1.1	16
67	MULTI-LEVEL CLUSTERING OF PHYLOGENETIC PROFILES. <i>International Journal on Artificial Intelligence Tools</i> , 2012, 21, 1240023.	0.7	1
68	The Chlamydiales Pangenome Revisited: Structural Stability and Functional Coherence. <i>Genes</i> , 2012, 3, 291-319.	1.0	9
69	Multi-genome Core Pathway Identification through Gene Clustering. <i>International Federation for Information Processing</i> , 2012, , 545-555.	0.4	1
70	Data Mining in Proteomics Using Grid Computing. , 2012, , 918-940.		0
71	Bioinformatics algorithm development for Grid environments. <i>Journal of Systems and Software</i> , 2010, 83, 1249-1257.	3.3	3
72	Multi Level Clustering of Phylogenetic Profiles. , 2010, , .		2

#	ARTICLE	IF	CITATIONS
73	A grid-enabled algorithm yields figure-eight molecular knot. <i>Molecular Simulation</i> , 2009, 35, 725-736.	0.9	0
74	Data Mining in Proteomics Using Grid Computing. , 2009, , 245-267.		0
75	ELIXIR Europe on the Road to Sustainable Research Software. <i>Biodiversity Information Science and Standards</i> , 0, 3, .	0.0	0