

Anastasis Oulas

List of Publications by Year in descending order

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Version: 2024-02-01

37
papers

1,121
citations

516710

16
h-index

414414

32
g-index

41
all docs

41
docs citations

41
times ranked

2225
citing authors

#	ARTICLE	IF	CITATIONS
1	Serum miRNAs as biomarkers for the rare types of muscular dystrophy. <i>Neuromuscular Disorders</i> , 2022, 32, 332-346.	0.6	5
2	Transcriptomic characterization of tissues from patients and subsequent pathway analyses reveal biological pathways that are implicated in spastic ataxia. <i>Cell and Bioscience</i> , 2022, 12, 29.	4.8	1
3	Circulating small RNA signatures differentiate accurately the subtypes of muscular dystrophies: small-RNA next-generation sequencing analytics and functional insights. <i>RNA Biology</i> , 2022, 19, 507-518.	3.1	1
4	Generalized linear models provide a measure of virulence for specific mutations in SARS-CoV-2 strains. <i>PLoS ONE</i> , 2021, 16, e0238665.	2.5	23
5	Multi-omics data integration and network-based analysis drives a multiplex drug repurposing approach to a shortlist of candidate drugs against COVID-19. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	18
6	miR-223-3p and miR-24-3p as novel serum-based biomarkers for myotonic dystrophy type 1. <i>Molecular Therapy - Methods and Clinical Development</i> , 2021, 23, 169-183.	4.1	6
7	Putative Antimicrobial Peptides Within Bacterial Proteomes Affect Bacterial Predominance: A Network Analysis Perspective. <i>Frontiers in Microbiology</i> , 2021, 12, 752674.	3.5	3
8	In depth analysis of Cyprus-specific mutations of SARS-CoV-2 strains using computational approaches. <i>BMC Genomic Data</i> , 2021, 22, 48.	1.7	4
9	GnRH Deficient Patients With Congenital Hypogonadotropic Hypogonadism: Novel Genetic Findings in ANOS1, RNF216, WDR11, FGFR1, CHD7, and POLR3A Genes in a Case Series and Review of the Literature. <i>Frontiers in Endocrinology</i> , 2020, 11, 626.	3.5	20
10	PathWalks: identifying pathway communities using a disease-related map of integrated information. <i>Bioinformatics</i> , 2020, 36, 4070-4079.	4.1	7
11	High genetic diversity and variability of microbial communities in near-surface atmosphere of Crete island, Greece. <i>Aerobiologia</i> , 2020, 36, 341-353.	1.7	3
12	PathwayConnector: finding complementary pathways to enhance functional analysis. <i>Bioinformatics</i> , 2019, 35, 889-891.	4.1	37
13	In Silico Identification of Antimicrobial Peptides in the Proteomes of Goat and Sheep Milk and Feta Cheese. <i>Proteomes</i> , 2019, 7, 32.	3.5	12
14	Selecting variants of unknown significance through network-based gene-association significantly improves risk prediction for disease-control cohorts. <i>Scientific Reports</i> , 2019, 9, 3266.	3.3	18
15	DCL-suppressed <i>Nicotiana benthamiana</i> plants: valuable tools in research and biotechnology. <i>Molecular Plant Pathology</i> , 2019, 20, 432-446.	4.2	19
16	Systems Bioinformatics: increasing precision of computational diagnostics and therapeutics through network-based approaches. <i>Briefings in Bioinformatics</i> , 2019, 20, 806-824.	6.5	87
17	Positioning Europe for the EPITRANSCRIPTOMICS challenge. <i>RNA Biology</i> , 2018, 15, 1-3.	3.1	18
18	A45...Clusters of connected pathways through multisource data integration in huntingtons disease. , 2018, , .		0

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19	Integrating multi-source information on a single network to detect disease-related clusters of molecular mechanisms. <i>Journal of Proteomics</i> , 2018, 188, 15-29.	2.4	37
20	Sediment microbial taxonomic and functional diversity in a natural salinity gradient challenge Remane's "species minimum" concept. <i>PeerJ</i> , 2017, 5, e3687.	2.0	43
21	Metagenomic 16s rRNA investigation of microbial communities in the Black Sea estuaries in South-West of Ukraine.. <i>Acta Biochimica Polonica</i> , 2016, 63, 315-9.	0.5	12
22	Salinity is the major factor influencing the sediment bacterial communities in a Mediterranean lagoonal complex (Amvrakikos Gulf, Ionian Sea). <i>Marine Genomics</i> , 2016, 28, 71-81.	1.1	22
23	Metagenomic investigation of the geologically unique Hellenic Volcanic Arc reveals a distinctive ecosystem with unexpected physiology. <i>Environmental Microbiology</i> , 2016, 18, 1122-1136.	3.8	37
24	Optimized R functions for analysis of ecological community data using the R virtual laboratory (RvLab). <i>Biodiversity Data Journal</i> , 2016, 4, e8357.	0.8	13
25	Seqenv: linking sequences to environments through text mining. <i>PeerJ</i> , 2016, 4, e2690.	2.0	26
26	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
27	Pyrosequencing analysis of microbial communities reveals dominant cosmopolitan phylotypes in deep-sea sediments of the eastern Mediterranean Sea. <i>Research in Microbiology</i> , 2015, 166, 448-457.	2.1	15
28	Prediction of miRNA Targets. <i>Methods in Molecular Biology</i> , 2015, 1269, 207-229.	0.9	29
29	Unraveling genomic variation from next generation sequencing data. <i>BioData Mining</i> , 2013, 6, 13.	4.0	43
30	Impaired clearance of apoptotic cells leads to HMGB1 release in the bone marrow of patients with myelodysplastic syndromes and induces TLR4-mediated cytokine production. <i>Haematologica</i> , 2013, 98, 1206-1215.	3.5	50
31	A new microRNA target prediction tool identifies a novel interaction of a putative miRNA with CCND2. <i>RNA Biology</i> , 2012, 9, 1196-1207.	3.1	22
32	Utilization of SSCprofiler to Predict a New miRNA Gene. <i>Methods in Molecular Biology</i> , 2011, 676, 243-252.	0.9	8
33	Finding Cancer-Associated miRNAs: Methods and Tools. <i>Molecular Biotechnology</i> , 2011, 49, 97-107.	2.4	7
34	Computational Identification of miRNAs Involved in Cancer. <i>Methods in Molecular Biology</i> , 2011, 676, 23-41.	0.9	5
35	Prediction of novel microRNA genes in cancer-associated genomic regions—a combined computational and experimental approach. <i>Nucleic Acids Research</i> , 2009, 37, 3276-3287.	14.5	60
36	MicroRNAs and Cancer—The Search Begins!. <i>IEEE Transactions on Information Technology in Biomedicine</i> , 2009, 13, 67-77.	3.2	18

#	ARTICLE	IF	CITATIONS
37	Improved grading and survival prediction of human astrocytic brain tumors by artificial neural network analysis of gene expression microarray data. <i>Molecular Cancer Therapeutics</i> , 2008, 7, 1013-1024.	4.1	72