Anastasis Oulas

List of Publications by Year
in descending order

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	Metagenomics: Tools and Insights for Analyzing Next-Generation Sequencing Data Derived from Biodiversity Studies. Bioinformatics and Biology Insights, 2015, 9, BBI.S12462.	2.0	317
2	Systems Bioinformatics: increasing precision of computational diagnostics and therapeutics through network-based approaches. Briefings in Bioinformatics, 2019, 20, 806-824.	6.5	87
3	Improved grading and survival prediction of human astrocytic brain tumors by artificial neural network analysis of gene expression microarray data. Molecular Cancer Therapeutics, 2008, 7, 1013-1024.	4.1	72
4	Prediction of novel microRNA genes in cancer-associated genomic regions—a combined computational and experimental approach. Nucleic Acids Research, 2009, 37, 3276-3287.	14.5	60
5	Impaired clearance of apoptotic cells leads to HMGB1 release in the bone marrow of patients with myelodysplastic syndromes and induces TLR4-mediated cytokine production. Haematologica, 2013, 98, 1206-1215.	3.5	50
6	Unraveling genomic variation from next generation sequencing data. BioData Mining, 2013, 6, 13.	4.0	43
7	Sediment microbial taxonomic and functional diversity in a natural salinity gradient challenge Remane's "species minimum" concept. PeerJ, 2017, 5, e3687.	2.0	43
8	Metagenomic investigation of the geologically unique Hellenic Volcanic Arc reveals a distinctive ecosystem with unexpected physiology. Environmental Microbiology, 2016, 18, 1122-1136.	3.8	37
9	Integrating multi-source information on a single network to detect disease-related clusters of molecular mechanisms. Journal of Proteomics, 2018, 188, 15-29.	2.4	37
10	PathwayConnector: finding complementary pathways to enhance functional analysis. Bioinformatics, 2019, 35, 889-891.	4.1	37
11	Prediction of miRNA Targets. Methods in Molecular Biology, 2015, 1269, 207-229.	0.9	29
12	Seqenv: linking sequences to environments through text mining. PeerJ, 2016, 4, e2690.	2.0	26
13	Generalized linear models provide a measure of virulence for specific mutations in SARS-CoV-2 strains. PLoS ONE, 2021, 16, e0238665.	2.5	23
14	A new microRNA target prediction tool identifies a novel interaction of a putative miRNA with CCND2. RNA Biology, 2012, 9, 1196-1207.	3.1	22
15	Salinity is the major factor influencing the sediment bacterial communities in a Mediterranean lagoonal complex (Amvrakikos Gulf, Ionian Sea). Marine Genomics, 2016, 28, 71-81.	1.1	22
16	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. Frontiers in Endocrinology, 2020, 11, 626.	3.5	20
17	DCL-suppressed *Nicotiana benthamiana* plants: valuable tools in research and biotechnology. Molecular Plant Pathology, 2019, 20, 432-446.	4.2	19
18	MicroRNAs and Cancer—The Search Begins!. IEEE Transactions on Information Technology in Biomedicine, 2009, 13, 67-77.	3.2	18

#	Article	IF	Citations
19	Positioning Europe for the EPITRANSCRIPTOMICS challenge. RNA Biology, 2018, 15, 1-3.	3.1	18
20	Selecting variants of unknown significance through network-based gene-association significantly improves risk prediction for disease-control cohorts. Scientific Reports, 2019, 9, 3266.	3.3	18
21	Multi-omics data integration and network-based analysis drives a multiplex drug repurposing approach to a shortlist of candidate drugs against COVID-19. Briefings in Bioinformatics, 2021, 22, .	6.5	18
22	Pyrosequencing analysis of microbial communities reveals dominant cosmopolitan phylotypes in deep-sea sediments of the eastern Mediterranean Sea. Research in Microbiology, 2015, 166, 448-457.	2.1	15
23	Optimized R functions for analysis of ecological community data using the R virtual laboratory (RvLab). Biodiversity Data Journal, 2016, 4, e8357.	0.8	13
24	Metagenomic 16s rRNA investigation of microbial communities in the Black Sea estuaries in South-West of Ukraine.. Acta Biochimica Polonica, 2016, 63, 315-9.	0.5	12
25	In Silico Identification of Antimicrobial Peptides in the Proteomes of Goat and Sheep Milk and Feta Cheese. Proteomes, 2019, 7, 32.	3.5	12
26	Utilization of SSCprofiler to Predict a New miRNA Gene. Methods in Molecular Biology, 2011, 676, 243-252.	0.9	8
27	Finding Cancer-Associated miRNAs: Methods and Tools. Molecular Biotechnology, 2011, 49, 97-107.	2.4	7
28	PathWalks: identifying pathway communities using a disease-related map of integrated information. Bioinformatics, 2020, 36, 4070-4079.	4.1	7
29	miR-223-3p and miR-24-3p as novel serum-based biomarkers for myotonic dystrophy type 1. Molecular Therapy - Methods and Clinical Development, 2021, 23, 169-183.	4.1	6
30	Computational Identification of miRNAs Involved in Cancer. Methods in Molecular Biology, 2011, 676, 23-41.	0.9	5
31	Serum miRNAs as biomarkers for the rare types of muscular dystrophy. Neuromuscular Disorders, 2022, 32, 332-346.	0.6	5
32	In depth analysis of Cyprus-specific mutations of SARS-CoV-2 strains using computational approaches. BMC Genomic Data, 2021, 22, 48.	1.7	4
33	High genetic diversity and variability of microbial communities in near-surface atmosphere of Crete island, Greece. Aerobiologia, 2020, 36, 341-353.	1.7	3
34	Putative Antimicrobial Peptides Within Bacterial Proteomes Affect Bacterial Predominance: A Network Analysis Perspective. Frontiers in Microbiology, 2021, 12, 752674.	3.5	3
35	Transcriptomic characterization of tissues from patients and subsequent pathway analyses reveal biological pathways that are implicated in spastic ataxia. Cell and Bioscience, 2022, 12, 29.	4.8	1
36	Circulating small RNA signatures differentiate accurately the subtypes of muscular dystrophies: small-RNA next-generation sequencing analytics and functional insights. RNA Biology, 2022, 19, 507-518.	3.1	1

#	ARTICLE	IF	CITATIONS
37	A45â€¦Clusters of connected pathways through multisource data integration in huntingtons disease. , 2018, , .		0