Valentina Galata

List of Publications by Year
in descending order

31	1,577	516561	434063
		16	31
papers	citations	h-index	g-index

35	35	35	2725
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	An estimate of the total number of true human miRNAs. Nucleic Acids Research, 2019, 47, 3353-3364.	6.5	400
2	PLSDB: a resource of complete bacterial plasmids. Nucleic Acids Research, 2019, 47, D195-D202.	6.5	336
3	BusyBee Web: metagenomic data analysis by bootstrapped supervised binning and annotation. Nucleic Acids Research, 2017, 45, W171-W179.	6.5	84
4	Evaluating the Use of Circulating MicroRNA Profiles for Lung Cancer Detection in Symptomatic Patients. JAMA Oncology, 2020, 6, 714.	3.4	84
5	PathoFact: a pipeline for the prediction of virulence factors and antimicrobial resistance genes in metagenomic data. Microbiome, 2021, 9, 49.	4.9	81
6	miRNAs can be generally associated with human pathologies as exemplified for miR-144*. BMC Medicine, 2014, 12, 224.	2.3	74
7	High-throughput qRT-PCR validation of blood microRNAs in non-small cell lung cancer. Oncotarget, 2016, 7, 4611-4623.	0.8	65
8	What makes a blood cell based miRNA expression pattern disease specific? - A miRNome analysis of blood cell subsets in lung cancer patients and healthy controls. Oncotarget, 2014, 5, 9484-9497.	0.8	54
9	Validating Alzheimer's disease micro RNAs using next‐generation sequencing. Alzheimer's and Dementia, 2016, 12, 565-576.	0.4	53
10	Prioritizing and selecting likely novel miRNAs from NGS data. Nucleic Acids Research, 2016, 44, e53-e53.	6.5	52
11	Posttranscriptional deregulation of signaling pathways in meningioma subtypes by differential expression of miRNAs. Neuro-Oncology, 2015, 17, 1250-1260.	0.6	31
12	Longitudinal study on circulating miRNAs in patients after lung cancer resection. Oncotarget, 2015, 6, 16674-16685.	0.8	26
13	Effects of Resistant Starch on Symptoms, Fecal Markers, and Gut Microbiota in Parkinson's Disease – The RESISTA-PD Trial. Genomics, Proteomics and Bioinformatics, 2022, 20, 274-287.	3.0	26
14	The composition of the pulmonary microbiota in sarcoidosis – an observational study. Respiratory Research, 2019, 20, 46.	1.4	24
15	Influence of Next-Generation Sequencing and Storage Conditions on miRNA Patterns Generated from PAXgene Blood. Analytical Chemistry, 2015, 87, 8910-8916.	3.2	22
16	Assessing the heterogeneity of in silico plasmid predictions based on whole-genome-sequenced clinical isolates. Briefings in Bioinformatics, 2019, 20, 857-865.	3.2	19
17	MicroRNA signature in spermatozoa and seminal plasma of proven fertile men and in testicular tissue of men with obstructive azoospermia. Andrologia, 2020, 52, e13503.	1.0	18
18	miRNAs in ancient tissue specimens of the Tyrolean Iceman. Molecular Biology and Evolution, 2017, 34, msw291.	3.5	17

#	Article	IF	Citations
19	Deep characterization of blood cell miRNomes by NGS. Cellular and Molecular Life Sciences, 2016, 73, 3169-3181.	2.4	15
20	Clinical Resistome Screening of 1,110 Escherichia coli Isolates Efficiently Recovers Diagnostically Relevant Antibiotic Resistance Biomarkers and Potential Novel Resistance Mechanisms. Frontiers in Microbiology, 2019, 10, 1671.	1.5	14
21	MicroRNA profiling from dried blood samples. Critical Reviews in Clinical Laboratory Sciences, 2019, 56, 111-117.	2.7	13
22	Comparison of initial oral microbiomes of young adults with and without cavitated dentin caries lesions using an in situ biofilm model. Scientific Reports, 2018, 8, 14010.	1.6	12
23	Integrating Culture-based Antibiotic Resistance Profiles with Whole-genome Sequencing Data for 11,087 Clinical Isolates. Genomics, Proteomics and Bioinformatics, 2019, 17, 169-182.	3.0	8
24	The sncRNA Zoo: a repository for circulating small noncoding RNAs in animals. Nucleic Acids Research, 2019, 47, 4431-4441.	6.5	8
25	Secretion and Immunogenicity of the Meningioma-Associated Antigen TXNDC16. Journal of Immunology, 2014, 193, 3146-3154.	0.4	7
26	Comparing genome versus proteome-based identification of clinical bacterial isolates. Briefings in Bioinformatics, 2018, 19, bbw122.	3.2	7
27	Gene amplification in mesenchymal stem cells and during differentiation towards adipocytes or osteoblasts. Oncotarget, 2018, 9, 1803-1812.	0.8	7
28	Functional meta-omics provide critical insights into long- and short-read assemblies. Briefings in Bioinformatics, 2021, 22, .	3.2	6
29	Large-scale validation of miRNAs by disease association, evolutionary conservation and pathway activity. RNA Biology, 2019, 16, 93-103.	1.5	5
30	Small ncRNA-Seq Results of Human Tissues: Variations Depending on Sample Integrity. Clinical Chemistry, 2018, 64, 1074-1084.	1.5	4
31	Prospect and challenge of detecting dynamic gene copy number increases in stem cells by whole genome sequencing. Journal of Molecular Medicine, 2019, 97, 1099-1111.	1.7	2