

Valentina Galata

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4569783/publications.pdf>

Version: 2024-02-01

31
papers

1,577
citations

516561

16
h-index

434063

31
g-index

35
all docs

35
docs citations

35
times ranked

2725
citing authors

#	ARTICLE	IF	CITATIONS
1	Effects of Resistant Starch on Symptoms, Fecal Markers, and Gut Microbiota in Parkinson's Disease – The RESISTA-PD Trial. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 274-287.	3.0	26
2	PathoFact: a pipeline for the prediction of virulence factors and antimicrobial resistance genes in metagenomic data. <i>Microbiome</i> , 2021, 9, 49.	4.9	81
3	Functional meta-omics provide critical insights into long- and short-read assemblies. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	6
4	MicroRNA signature in spermatozoa and seminal plasma of proven fertile men and in testicular tissue of men with obstructive azoospermia. <i>Andrologia</i> , 2020, 52, e13503.	1.0	18
5	Evaluating the Use of Circulating MicroRNA Profiles for Lung Cancer Detection in Symptomatic Patients. <i>JAMA Oncology</i> , 2020, 6, 714.	3.4	84
6	Clinical Resistome Screening of 1,110 Escherichia coli Isolates Efficiently Recovers Diagnostically Relevant Antibiotic Resistance Biomarkers and Potential Novel Resistance Mechanisms. <i>Frontiers in Microbiology</i> , 2019, 10, 1671.	1.5	14
7	MicroRNA profiling from dried blood samples. <i>Critical Reviews in Clinical Laboratory Sciences</i> , 2019, 56, 111-117.	2.7	13
8	Prospect and challenge of detecting dynamic gene copy number increases in stem cells by whole genome sequencing. <i>Journal of Molecular Medicine</i> , 2019, 97, 1099-1111.	1.7	2
9	Integrating Culture-based Antibiotic Resistance Profiles with Whole-genome Sequencing Data for 11,087 Clinical Isolates. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 169-182.	3.0	8
10	The composition of the pulmonary microbiota in sarcoidosis – an observational study. <i>Respiratory Research</i> , 2019, 20, 46.	1.4	24
11	An estimate of the total number of true human miRNAs. <i>Nucleic Acids Research</i> , 2019, 47, 3353-3364.	6.5	400
12	The sncRNA Zoo: a repository for circulating small noncoding RNAs in animals. <i>Nucleic Acids Research</i> , 2019, 47, 4431-4441.	6.5	8
13	PLSDB: a resource of complete bacterial plasmids. <i>Nucleic Acids Research</i> , 2019, 47, D195-D202.	6.5	336
14	Large-scale validation of miRNAs by disease association, evolutionary conservation and pathway activity. <i>RNA Biology</i> , 2019, 16, 93-103.	1.5	5
15	Assessing the heterogeneity of in silico plasmid predictions based on whole-genome-sequenced clinical isolates. <i>Briefings in Bioinformatics</i> , 2019, 20, 857-865.	3.2	19
16	Comparing genome versus proteome-based identification of clinical bacterial isolates. <i>Briefings in Bioinformatics</i> , 2018, 19, bbw122.	3.2	7
17	Small ncRNA-Seq Results of Human Tissues: Variations Depending on Sample Integrity. <i>Clinical Chemistry</i> , 2018, 64, 1074-1084.	1.5	4
18	Gene amplification in mesenchymal stem cells and during differentiation towards adipocytes or osteoblasts. <i>Oncotarget</i> , 2018, 9, 1803-1812.	0.8	7

#	ARTICLE	IF	CITATIONS
19	Comparison of initial oral microbiomes of young adults with and without cavitated dentin caries lesions using an in situ biofilm model. <i>Scientific Reports</i> , 2018, 8, 14010.	1.6	12
20	miRNAs in ancient tissue specimens of the Tyrolean Iceman. <i>Molecular Biology and Evolution</i> , 2017, 34, msw291.	3.5	17
21	BusyBee Web: metagenomic data analysis by bootstrapped supervised binning and annotation. <i>Nucleic Acids Research</i> , 2017, 45, W171-W179.	6.5	84
22	Validating Alzheimer's disease micro RNAs using next-generation sequencing. <i>Alzheimer's and Dementia</i> , 2016, 12, 565-576.	0.4	53
23	Deep characterization of blood cell miRNomes by NGS. <i>Cellular and Molecular Life Sciences</i> , 2016, 73, 3169-3181.	2.4	15
24	Prioritizing and selecting likely novel miRNAs from NGS data. <i>Nucleic Acids Research</i> , 2016, 44, e53-e53.	6.5	52
25	High-throughput qRT-PCR validation of blood microRNAs in non-small cell lung cancer. <i>Oncotarget</i> , 2016, 7, 4611-4623.	0.8	65
26	Influence of Next-Generation Sequencing and Storage Conditions on miRNA Patterns Generated from PAXgene Blood. <i>Analytical Chemistry</i> , 2015, 87, 8910-8916.	3.2	22
27	Posttranscriptional deregulation of signaling pathways in meningioma subtypes by differential expression of miRNAs. <i>Neuro-Oncology</i> , 2015, 17, 1250-1260.	0.6	31
28	Longitudinal study on circulating miRNAs in patients after lung cancer resection. <i>Oncotarget</i> , 2015, 6, 16674-16685.	0.8	26
29	miRNAs can be generally associated with human pathologies as exemplified for miR-144*. <i>BMC Medicine</i> , 2014, 12, 224.	2.3	74
30	Secretion and Immunogenicity of the Meningioma-Associated Antigen TXNDC16. <i>Journal of Immunology</i> , 2014, 193, 3146-3154.	0.4	7
31	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. <i>Oncotarget</i> , 2014, 5, 9484-9497.	0.8	54