

Matteo Chiara

List of Publications by Year in descending order

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Version: 2024-02-01

55
papers

4,194
citations

331259

21
h-index

155451

55
g-index

64
all docs

64
docs citations

64
times ranked

5646
citing authors

#	ARTICLE	IF	CITATIONS
1	VirusClust: direct comparison of SARS-CoV-2 genomes and genetic variants in space and time. <i>Bioinformatics</i> , 2022, 38, 1988-1994.	1.8	9
2	The barley mutant happy under the sun 1 (hus1): An additional contribution to pale green crops. <i>Environmental and Experimental Botany</i> , 2022, 196, 104795.	2.0	6
3	Lack of ApoA-I in ApoEKO Mice Causes Skin Xanthomas, Worsening of Inflammation, and Increased Coronary Atherosclerosis in the Absence of Hyperlipidemia. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2022, 42, 839-856.	1.1	6
4	Transcriptome analysis reveals rice MADS13 as an important repressor of the carpel development pathway in ovules. <i>Journal of Experimental Botany</i> , 2021, 72, 398-414.	2.4	7
5	Next generation sequencing of SARS-CoV-2 genomes: challenges, applications and opportunities. <i>Briefings in Bioinformatics</i> , 2021, 22, 616-630.	3.2	143
6	Aortic Gene Expression Profiles Show How ApoA-I Levels Modulate Inflammation, Lysosomal Activity, and Sphingolipid Metabolism in Murine Atherosclerosis. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2021, 41, 651-667.	1.1	12
7	Comparative Genomics Suggests a Taxonomic Revision of the <i>Staphylococcus cohnii</i> Species Complex. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	6
8	Comparative Genomics Reveals Early Emergence and Biased Spatiotemporal Distribution of SARS-CoV-2. <i>Molecular Biology and Evolution</i> , 2021, 38, 2547-2565.	3.5	31
9	Complete vertebrate mitogenomes reveal widespread repeats and gene duplications. <i>Genome Biology</i> , 2021, 22, 120.	3.8	69
10	aScan: A Novel Method for the Study of Allele Specific Expression in Single Individuals. <i>Journal of Molecular Biology</i> , 2021, 433, 166829.	2.0	1
11	<i>Campylobacter vulpis</i> sp. nov. isolated from wild red foxes. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126204.	1.2	13
12	Alginate coating modifies the biological effects of cerium oxide nanoparticles to the freshwater bivalve <i>Dreissena polymorpha</i> . <i>Science of the Total Environment</i> , 2021, 773, 145612.	3.9	11
13	Sox2 Controls Neural Stem Cell Self-Renewal Through a Fos-Centered Gene Regulatory Network. <i>Stem Cells</i> , 2021, 39, 1107-1119.	1.4	36
14	CorGAT: a tool for the functional annotation of SARS-CoV-2 genomes. <i>Bioinformatics</i> , 2021, 36, 5522-5523.	1.8	12
15	VINYL: Variant prioritization by survival analysis. <i>Bioinformatics</i> , 2021, 36, 5590-5599.	1.8	4
16	Laniakea@ReCaS: exploring the potential of customisable Galaxy on-demand instances as a cloud-based service. <i>BMC Bioinformatics</i> , 2021, 22, 544.	1.2	4
17	<i>VID22</i> counteracts G-quadruplex-induced genome instability. <i>Nucleic Acids Research</i> , 2021, 49, 12785-12804.	6.5	5
18	Targeted resequencing of FECH locus reveals that a novel deep intronic pathogenic variant and eQTLs may cause erythropoietic protoporphyria (EPP) through a methylation-dependent mechanism. <i>Genetics in Medicine</i> , 2020, 22, 35-43.	1.1	12

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19	BPC transcription factors and a Polycomb Group protein confine the expression of the ovule identity gene <i><i>SEEDSTICK</i></i> in Arabidopsis. <i>Plant Journal</i> , 2020, 102, 582-599.	2.8	34
20	Critical assessment of bioinformatics methods for the characterization of pathological repeat expansions with single-molecule sequencing data. <i>Briefings in Bioinformatics</i> , 2020, 21, 1971-1986.	3.2	5
21	Drought-Responsive <i><i>ZmFDL1/MYB94</i></i> Regulates Cuticle Biosynthesis and Cuticle-Dependent Leaf Permeability. <i>Plant Physiology</i> , 2020, 184, 266-282.	2.3	27
22	Laniakea: an open solution to provide Galaxy "on-demand" instances over heterogeneous cloud infrastructures. <i>GigaScience</i> , 2020, 9, .	3.3	10
23	ELIXIR-IT HPC@CINECA: high performance computing resources for the bioinformatics community. <i>BMC Bioinformatics</i> , 2020, 21, 352.	1.2	25
24	MADS-Box and bHLH Transcription Factors Coordinate Transmitting Tract Development in Arabidopsis thaliana. <i>Frontiers in Plant Science</i> , 2020, 11, 526.	1.7	25
25	Genes of the <i><i>RAV</i></i> Family Control Heading Date and Carpel Development in Rice. <i>Plant Physiology</i> , 2020, 183, 1663-1680.	2.3	25
26	The Plant NF-Y DNA Matrix In Vitro and In Vivo. <i>Plants</i> , 2019, 8, 406.	1.6	7
27	Staphylococcus arlettae Genomics: Novel Insights on Candidate Antibiotic Resistance and Virulence Genes in an Emerging Opportunistic Pathogen. <i>Microorganisms</i> , 2019, 7, 580.	1.6	10
28	SMRT long reads and Direct Label and Stain optical maps allow the generation of a high-quality genome assembly for the European barn swallow (<i>Hirundo rustica rustica</i>). <i>GigaScience</i> , 2019, 8, .	3.3	23
29	Whole transcriptome profiling of Late-Onset Alzheimer's Disease patients provides insights into the molecular changes involved in the disease. <i>Scientific Reports</i> , 2018, 8, 4282.	1.6	102
30	Draft Genome Sequences of Three Novel Staphylococcus arlettae Strains Isolated from a Disused Biological Safety Cabinet. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	5
31	IS26 mediated antimicrobial resistance gene shuffling from the chromosome to a mosaic conjugative FII plasmid. <i>Plasmid</i> , 2018, 100, 22-30.	0.4	19
32	A-GAME: improving the assembly of pooled functional metagenomics sequence data. <i>BMC Genomics</i> , 2018, 19, 44.	1.2	7
33	CoVaCS: a consensus variant calling system. <i>BMC Genomics</i> , 2018, 19, 120.	1.2	29
34	CONSTANS Imparts DNA Sequence Specificity to the Histone Fold NF-YB/NF-YC Dimer. <i>Plant Cell</i> , 2017, 29, 1516-1532.	3.1	108
35	A novel group of IncQ1 plasmids conferring multidrug resistance. <i>Plasmid</i> , 2017, 89, 22-26.	0.4	52
36	Massive transcriptome sequencing of human spinal cord tissues provides new insights into motor neuron degeneration in ALS. <i>Scientific Reports</i> , 2017, 7, 10046.	1.6	99

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37	Evaluation of Quality Assessment Protocols for High Throughput Genome Resequencing Data. <i>Frontiers in Genetics</i> , 2017, 8, 94.	1.1	10
38	Role of the long non-coding RNA PVT1 in the dysregulation of the ceRNA-ceRNA network in human breast cancer. <i>PLoS ONE</i> , 2017, 12, e0171661.	1.1	92
39	Targeted next-generation sequencing detects novel gene-phenotype associations and expands the mutational spectrum in cardiomyopathies. <i>PLoS ONE</i> , 2017, 12, e0181842.	1.1	28
40	Metagenomics Reveals Dysbiosis and a Potentially Pathogenic <i>N. flavescens</i> Strain in Duodenum of Adult Celiac Patients. <i>American Journal of Gastroenterology</i> , 2016, 111, 879-890.	0.2	128
41	Geographic Population Structure in Epstein-Barr Virus Revealed by Comparative Genomics. <i>Genome Biology and Evolution</i> , 2016, 8, 3284-3291.	1.1	29
42	No Change in the Mucosal Gut Microbiome is Associated With Celiac Disease-Specific Microbiome Alteration in Adult Patients. <i>American Journal of Gastroenterology</i> , 2016, 111, 1659-1661.	0.2	18
43	Comparative Genomics of <i>Listeria</i> Sensu Lato: Genus-Wide Differences in Evolutionary Dynamics and the Progressive Gain of Complex, Potentially Pathogenicity-Related Traits through Lateral Gene Transfer. <i>Genome Biology and Evolution</i> , 2015, 7, 2154-2172.	1.1	47
44	Draft genome sequence of <i>Acinetobacter</i> sp. neg1 capable of degrading ochratoxin A. <i>FEMS Microbiology Letters</i> , 2015, 362, .	0.7	12
45	Genome Sequencing of Multiple Isolates Highlights Subtelomeric Genomic Diversity within <i>Fusarium fujikuroi</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 3062-3069.	1.1	36
46	Tissue-specific mtDNA abundance from exome data and its correlation with mitochondrial transcription, mass and respiratory activity. <i>Mitochondrion</i> , 2015, 20, 13-21.	1.6	146
47	Draft Genome Sequences of Six <i>Listeria monocytogenes</i> Strains Isolated from Dairy Products from a Processing Plant in Southern Italy. <i>Genome Announcements</i> , 2014, 2, .	0.8	11
48	Draft genome sequence of <i>Sphingobium</i> sp. strain ba1, resistant to kanamycin and nickel ions. <i>FEMS Microbiology Letters</i> , 2014, 361, 8-9.	0.7	14
49	Gene coexpression patterns during early development of the native <i>Arabidopsis</i> reproductive meristem: novel candidate developmental regulators and patterns of functional redundancy. <i>Plant Journal</i> , 2014, 79, 861-877.	2.8	29
50	De Novo Assembly of the Transcriptome of the Non-Model Plant <i>Streptocarpus rexii</i> Employing a Novel Heuristic to Recover Locus-Specific Transcript Clusters. <i>PLoS ONE</i> , 2013, 8, e80961.	1.1	20
51	SVM 2 : an improved paired-end-based tool for the detection of small genomic structural variations using high-throughput single-genome resequencing data. <i>Nucleic Acids Research</i> , 2012, 40, e145-e145.	6.5	21
52	Large-scale detection and analysis of RNA editing in grape mtDNA by RNA deep-sequencing. <i>Nucleic Acids Research</i> , 2010, 38, 4755-4767.	6.5	135
53	The SEP4 Gene of <i>Arabidopsis thaliana</i> Functions in Floral Organ and Meristem Identity. <i>Current Biology</i> , 2004, 14, 1935-1940.	1.8	747
54	APETALA1 and SEPALLATA3 interact to promote flower development. <i>Plant Journal</i> , 2001, 26, 385-394.	2.8	290

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55	B and C floral organ identity functions require SEPALLATA MADS-box genes. Nature, 2000, 405, 200-203.	13.7	1,337