

Alessandro Varani

List of Publications by Year in descending order

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Version: 2024-02-01

87
papers

2,777
citations

236925

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214800

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all docs

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docs citations

93
times ranked

4066
citing authors

#	ARTICLE	IF	CITATIONS
1	Response from Varani et al. to "Comment on" the IS6 family, a clinically important group of insertion sequences including IS26™ by Ruth M. Hall, Mobile DNA, 2022, 13, 2.	3.6	0
2	<i>Bartonella machadoae</i> sp. nov. isolated from wild rodents in the Pantanal wetland. <i>Acta Tropica</i> , 2022, 229, 106368.	2.0	12
3	The complete mitochondrial genome of carnivorous <i>Genlisea tuberosa</i> (Lentibulariaceae): Structure and evolutionary aspects. <i>Gene</i> , 2022, 824, 146391.	2.2	3
4	New insights into plant natriuretic peptide evolution: From the lysogenic conversion in <i>Xanthomonas</i> to the lateral transfer to the whitefly <i>Bemisia tabaci</i> . <i>Gene</i> , 2022, 821, 146326.	2.2	2
5	Draft genome sequence of the cyanobacterium <i>Sphaerospermopsis aphanizomenoides</i> BCCUSP55 from the Brazilian semiarid region reveals potential for anti-cancer applications. <i>Archives of Microbiology</i> , 2022, 204, 4.	2.2	0
6	XAC4296 Is a Multifunctional and Exclusive <i>Xanthomonadaceae</i> Gene Containing a Fusion of Lytic Transglycosylase and Epimerase Domains. <i>Microorganisms</i> , 2022, 10, 1008.	3.6	0
7	Riboswitch <i>theo/metE</i> as a Transcription Regulation Tool for <i>Xanthomonas citri</i> subsp. <i>citri</i> . <i>Microorganisms</i> , 2021, 9, 329.	3.6	2
8	The IS6 family, a clinically important group of insertion sequences including IS26. <i>Mobile DNA</i> , 2021, 12, 11.	3.6	58
9	The plasmidome of multidrug-resistant emergent <i>Salmonella</i> serovars isolated from poultry. <i>Infection, Genetics and Evolution</i> , 2021, 89, 104716.	2.3	10
10	Unraveling a Lignocellulose-Decomposing Bacterial Consortium from Soil Associated with Dry Sugarcane Straw by Genomic-Centered Metagenomics. <i>Microorganisms</i> , 2021, 9, 995.	3.6	17
11	<i>Amazonocrinis nigriterrae</i> gen. nov., sp. nov., <i>Atlanticothrix silvestris</i> gen. nov., sp. nov. and <i>Dendronalium phyllosphericum</i> gen. nov., sp. nov., nostocacean cyanobacteria from Brazilian environments. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	1.7	30
12	A genome sequence resource for the genus <i>Passiflora</i> , the genome of the wild diploid species <i>Passiflora organensis</i> . <i>Plant Genome</i> , 2021, 14, e20117.	2.8	8
13	A comparative genomic analysis of <i>Xanthomonas arboricola</i> pv. <i>juglandis</i> strains reveal hallmarks of mobile genetic elements in the adaptation and accelerated evolution of virulence. <i>Genomics</i> , 2021, 113, 2513-2525.	2.9	9
14	Genomic comparisons and phylogenetic analysis of mastitis-related staphylococci with a focus on adhesion, biofilm, and related regulatory genes. <i>Scientific Reports</i> , 2021, 11, 17392.	3.3	11
15	TnCentral: a Prokaryotic Transposable Element Database and Web Portal for Transposon Analysis. <i>MBio</i> , 2021, 12, e0206021.	4.1	56
16	An Atlas of Plant Transposable Elements. <i>F1000Research</i> , 2021, 10, 1194.	1.6	11
17	The Terrestrial Carnivorous Plant <i>Utricularia reniformis</i> Sheds Light on Environmental and Life-Form Genome Plasticity. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3.	4.1	30
18	CitrusKB: a comprehensive knowledge base for transcriptome and interactome of <i>Citrus</i> spp. infected by <i>Xanthomonas citri</i> subsp. <i>citri</i> at different infection stages. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	3.0	2

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19	Exploring the Potential of Two Bacterial Consortia to Degrade Cellulosic Biomass for Biotechnological Applications. <i>Current Microbiology</i> , 2020, 77, 3114-3124.	2.2	6
20	A Genomic and Transcriptomic Overview of MATE, ABC, and MFS Transporters in <i>Citrus sinensis</i> Interaction with <i>Xanthomonas citri</i> subsp. <i>citri</i> . <i>Plants</i> , 2020, 9, 794.	3.5	9
21	Toxin-Antitoxin Gene Pairs Found in Tn <i>3</i> Family Transposons Appear To Be an Integral Part of the Transposition Module. <i>MBio</i> , 2020, 11, .	4.1	25
22	Evaluating Eucalyptus leaf colonization by <i>Brasilonema octagenarum</i> (Cyanobacteria). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 622 Td (Scy</i>	2.0	2
23	Complete genome sequence and analysis of <i>Alcaligenes faecalis</i> strain Mc250, a new potential plant bioinoculant. <i>PLoS ONE</i> , 2020, 15, e0241546.	2.5	9
24	Analyses of Seven New Genomes of <i>Xanthomonas citri</i> pv. <i>aurantifolii</i> Strains, Causative Agents of Citrus Canker B and C, Show a Reduced Repertoire of Pathogenicity-Related Genes. <i>Frontiers in Microbiology</i> , 2019, 10, 2361.	3.5	14
25	Origin and diversification of <i>Xanthomonas citri</i> subsp. <i>citri</i> pathotypes revealed by inclusive phylogenomic, dating, and biogeographic analyses. <i>BMC Genomics</i> , 2019, 20, 700.	2.8	33
26	Genomic signatures and co-occurrence patterns of the ultra-small <i>Saccharimonadia</i> (phylum) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 4</i>	3.9	101
27	Gene expression during the germination of coffee seed. <i>Journal of Seed Science</i> , 2019, 41, 168-179.	0.7	6
28	Transposable element discovery and characterization of LTR-retrotransposon evolutionary lineages in the tropical fruit species <i>Passiflora edulis</i> . <i>Molecular Biology Reports</i> , 2019, 46, 6117-6133.	2.3	8
29	Antibiotic resistance and heavy metal tolerance plasmids: the antimicrobial bulletproof properties of <i>Escherichia fergusonii</i> ; isolated from poultry. <i>Infection and Drug Resistance</i> , 2019, Volume 12, 1029-1033.	2.7	14
30	A Phage-Like Plasmid Carrying blaKPC-2 Gene in Carbapenem-Resistant <i>Pseudomonas aeruginosa</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 572.	3.5	22
31	SPM-1-producing <i>Pseudomonas aeruginosa</i> ST277 carries a chromosomal pack of acquired resistance genes: An example of high-risk clone associated with "intrinsic resistome". <i>Journal of Global Antimicrobial Resistance</i> , 2019, 16, 183-186.	2.2	11
32	Closed Genome Sequence of <i>Bacillus paralicheniformis</i> Strain CBMAI 1303, a Bacterium Applied for Phytopathogen Biocontrol. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	4
33	Draft Genomic Sequences of <i>Streptomyces misionensis</i> ACT66 and <i>Streptomyces albidoflavus</i> ACT77, Bacteria with Potential Application for Phytopathogen Biocontrol. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	3
34	Complete Genome Sequences of 11 <i>Staphylococcus</i> sp. Strains Isolated from Buffalo Milk and Milkers' Hands. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	4
35	<i>Serratia liquefaciens</i> FG3 isolated from a metallophyte plant sheds light on the evolution and mechanisms of adaptive traits in extreme environments. <i>Scientific Reports</i> , 2019, 9, 18006.	3.3	10
36	Intraspecific Variation within the <i>Utricularia amethystina</i> Species Morphotypes Based on Chloroplast Genomes. <i>International Journal of Molecular Sciences</i> , 2019, 20, 6130.	4.1	23

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37	Detection and identification of <i>Xanthomonas</i> pathotypes associated with citrus diseases using comparative genomics and multiplex PCR. <i>PeerJ</i> , 2019, 7, e7676.	2.0	10
38	Development of microsatellite markers for the carnivorous plant <i>Genlisea aurea</i> (Lentibulariaceae) using genomics data of NGS. <i>Molecular Biology Reports</i> , 2018, 45, 57-61.	2.3	4
39	A Practical Guide for Comparative Genomics of Mobile Genetic Elements in Prokaryotic Genomes. <i>Methods in Molecular Biology</i> , 2018, 1704, 213-242.	0.9	15
40	Closed Genome Sequence of Phytopathogen Biocontrol Agent <i>Bacillus velezensis</i> Strain AGVL-005, Isolated from Soybean. <i>Genome Announcements</i> , 2018, 6, .	0.8	1
41	A gene-rich fraction analysis of the <i>Passiflora edulis</i> genome reveals highly conserved microsyntenic regions with two related Malpighiales species. <i>Scientific Reports</i> , 2018, 8, 13024.	3.3	18
42	The genome sequence of <i>Dyella jiangningensis</i> FCAV SCS01 from a lignocellulose-decomposing microbial consortium metagenome reveals potential for biotechnological applications. <i>Genetics and Molecular Biology</i> , 2018, 41, 507-513.	1.3	6
43	Genomic and Genotypic Characterization of <i>Cylindrospermopsis raciborskii</i> : Toward an Intraspecific Phylogenetic Evaluation by Comparative Genomics. <i>Frontiers in Microbiology</i> , 2018, 9, 306.	3.5	26
44	Phylogenetic and antimicrobial resistance gene analysis of <i>Salmonella</i> Typhimurium strains isolated in Brazil by whole genome sequencing. <i>PLoS ONE</i> , 2018, 13, e0201882.	2.5	48
45	Comparative genomic analysis of <i>Genlisea</i> (corkscrew plants) chloroplast genomes reveals an increasing loss of the <i>ndh</i> genes. <i>PLoS ONE</i> , 2018, 13, e0190321.	2.5	17
46	Biosynthesis of microcystin hepatotoxins in the cyanobacterial genus <i>Fischerella</i> . <i>Toxicon</i> , 2018, 141, 43-50.	1.6	15
47	Transposons and pathogenicity in <i>Xanthomonas</i> : acquisition of murein lytic transglycosylases by <i>TnXax1</i> enhances <i>Xanthomonas citri</i> subsp. <i>citri</i> 306 virulence and fitness. <i>PeerJ</i> , 2018, 6, e6111.	2.0	8
48	Genetic Organization of Anabaenopeptin and Spumigin Biosynthetic Gene Clusters in the Cyanobacterium <i>Sphaerospermopsis torques-reginae</i> ITEP-024. <i>ACS Chemical Biology</i> , 2017, 12, 769-778.	3.4	25
49	The complete chloroplast genome sequence of the leafy bladderwort, <i>Utricularia foliosa</i> L. (Lentibulariaceae). <i>Conservation Genetics Resources</i> , 2017, 9, 213-216.	0.8	5
50	The Chloroplast Genome of <i>Passiflora edulis</i> (Passifloraceae) Assembled from Long Sequence Reads: Structural Organization and Phylogenomic Studies in Malpighiales. <i>Frontiers in Plant Science</i> , 2017, 8, 334.	3.6	79
51	Hepatozoon <i>caimani</i> in <i>Caiman crocodilus yacare</i> (Crocodylia, Alligatoridae) from North Pantanal, Brazil. <i>Brazilian Journal of Veterinary Parasitology</i> , 2017, 26, 352-358.	0.7	11
52	A Metagenomic Approach to Cyanobacterial Genomics. <i>Frontiers in Microbiology</i> , 2017, 8, 809.	3.5	98
53	The mitochondrial genome of the terrestrial carnivorous plant <i>Utricularia reniformis</i> (Lentibulariaceae): Structure, comparative analysis and evolutionary landmarks. <i>PLoS ONE</i> , 2017, 12, e0180484.	2.5	24
54	Metagenomic analysis of soil and freshwater from zoo agricultural area with organic fertilization. <i>PLoS ONE</i> , 2017, 12, e0190178.	2.5	23

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55	Unravelling potential virulence factor candidates in <i>Xanthomonas citri</i> subsp. <i>citri</i> by secretome analysis. PeerJ, 2016, 4, e1734.	2.0	35
56	The Chloroplast Genome of <i>Utricularia reniformis</i> Sheds Light on the Evolution of the <i>ndh</i> Gene Complex of Terrestrial Carnivorous Plants from the <i>Lentibulariaceae</i> Family. PLoS ONE, 2016, 11, e0165176.	2.5	57
57	Mechanisms of Evolution in High-Consequence Drug Resistance Plasmids. MBio, 2016, 7, .	4.1	49
58	Evaluating methods for purifying cyanobacterial cultures by qPCR and high-throughput Illumina sequencing. Journal of Microbiological Methods, 2016, 129, 55-60.	1.6	16
59	A Step Forward to Empower Global Microbiome Research Through Local Leadership. Trends in Microbiology, 2016, 24, 767-771.	7.7	12
60	New Small Plasmid Harboring <i>bla</i> _{KPC-2} in <i>Pseudomonas aeruginosa</i> . Antimicrobial Agents and Chemotherapy, 2016, 60, 3211-3214.	3.2	12
61	Everyman's Guide to Bacterial Insertion Sequences. Microbiology Spectrum, 2015, 3, MDNA3-0030-2014.	3.0	204
62	Insertion Sequence IS <i>26</i> Reorganizes Plasmids in Clinically Isolated Multidrug-Resistant Bacteria by Replicative Transposition. MBio, 2015, 6, e00762.	4.1	256
63	A TALE of Transposition: Tn <i>3</i> -Like Transposons Play a Major Role in the Spread of Pathogenicity Determinants of <i>Xanthomonas citri</i> and Other <i>Xanthomonads</i> . MBio, 2015, 6, e02505-14.	4.1	43
64	Genetic diversity and molecular phylogeny of <i>Anaplasma marginale</i> studied longitudinally under natural transmission conditions in Rio de Janeiro, Brazil. Ticks and Tick-borne Diseases, 2015, 6, 499-507.	2.7	23
65	A balanced microbiota efficiently produces methane in a novel high-rate horizontal anaerobic reactor for the treatment of swine wastewater. Bioresource Technology, 2015, 197, 152-160.	9.6	34
66	Draft Genome Sequence of a Novel Culturable Marine Chroococcalean Cyanobacterium from the South Atlantic Ocean. Genome Announcements, 2015, 3, .	0.8	1
67	The Family Rhizobiaceae. , 2014, , 419-437.		39
68	The Family Bradyrhizobiaceae. , 2014, , 135-154.		37
69	Building the sugarcane genome for biotechnology and identifying evolutionary trends. BMC Genomics, 2014, 15, 540.	2.8	136
70	Molecular and phylogenetic characterization based on the complete genome of a virulent pathotype of Newcastle disease virus isolated in the 1970s in Brazil. Infection, Genetics and Evolution, 2014, 26, 160-167.	2.3	11
71	Draft Genome Sequence of <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar <i>Gallinarum</i> Biovar <i>Pullorum</i> Strain FCAV198, a Brazilian Chicken Pathogen. Genome Announcements, 2014, 2, .	0.8	2
72	Microbiological quality assessment of a compost produced from animal waste and vegetables. WIT Transactions on Ecology and the Environment, 2014, , .	0.0	1

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73	The Role of Prophage in Plant-Pathogenic Bacteria. Annual Review of Phytopathology, 2013, 51, 429-451.	7.8	76
74	Draft Genome Sequence of the Brazilian Toxic Bloom-Forming Cyanobacterium Microcystis aeruginosa Strain SPC777. Genome Announcements, 2013, 1, .	0.8	11
75	Draft Genome Sequence of Bacillus thuringiensis var. thuringiensis Strain T01-328, a Brazilian Isolate That Produces a Soluble Pesticide Protein, Cry1Ia. Genome Announcements, 2013, 1, .	0.8	7
76	Exploring Bacterial Insertion Sequences with ISfinder: Objectives, Uses, and Future Developments. Methods in Molecular Biology, 2012, 859, 91-103.	0.9	61
77	Analysis of expressed sequence tags from the agarophyte Gracilaria tenuistipitata (Rhodophyta). Journal of Applied Phycology, 2012, 24, 641-647.	2.8	12
78	Strain-specific polyketide synthase genes of Aspergillus niger. International Journal of Food Microbiology, 2012, 155, 137-145.	4.7	32
79	Xylella fastidiosa comparative genomic database is an information resource to explore the annotation, genomic features, and biology of different strains. Genetics and Molecular Biology, 2012, 35, 149-152.	1.3	15
80	ISsaga is an ensemble of web-based methods for high throughput identification and semi-automatic annotation of insertion sequences in prokaryotic genomes. Genome Biology, 2011, 12, R30.	9.6	340
81	NAD Biosynthesis Evolution in Bacteria: Lateral Gene Transfer of Kynurenine Pathway in Xanthomonadales and Flavobacteriales. Molecular Biology and Evolution, 2009, 26, 399-406.	8.9	50
82	Laterally transferred genomic islands in Xanthomonadales related to pathogenicity and primary metabolism. FEMS Microbiology Letters, 2008, 281, 87-97.	1.8	43
83	Origins of the Xylella fastidiosa Prophage-Like Regions and Their Impact in Genome Differentiation. PLoS ONE, 2008, 3, e4059.	2.5	50
84	MudrA-like sequences from rice and sugarcane cluster as two bona fide transposon clades and two domesticated transposases. Gene, 2007, 392, 117-125.	2.2	17
85	Xylella and Xanthomonas Mobil'omics. OMICS A Journal of Integrative Biology, 2005, 9, 146-159.	2.0	46
86	Comparative analysis of Mutator -like transposases in sugarcane. Molecular Genetics and Genomics, 2004, 272, 194-203.	2.1	31
87	Everyman's Guide to Bacterial Insertion Sequences. , 0, , 555-590.		12