

# Alessandro Varani

## List of Publications by Year in descending order

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87  
papers

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236833

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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.	1.3	0
2	<i>Bartonella machadoae</i> sp. nov. isolated from wild rodents in the Pantanal wetland. <i>Acta Tropica</i> , 2022, 229, 106368.	0.9	12
3	The complete mitochondrial genome of carnivorous <i>Genlisea tuberosa</i> (Lentibulariaceae): Structure and evolutionary aspects. <i>Gene</i> , 2022, 824, 146391.	1.0	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.	1.0	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.	1.0	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.	1.6	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.	1.6	2
8	The IS6 family, a clinically important group of insertion sequences including IS26. <i>Mobile DNA</i> , 2021, 12, 11.	1.3	58
9	The plasmidome of multidrug-resistant emergent <i>Salmonella</i> serovars isolated from poultry. <i>Infection, Genetics and Evolution</i> , 2021, 89, 104716.	1.0	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.	1.6	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, .	0.8	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.	1.6	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.	1.3	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.	1.6	11
15	TnCentral: a Prokaryotic Transposable Element Database and Web Portal for Transposon Analysis. <i>MBio</i> , 2021, 12, e0206021.	1.8	56
16	An Atlas of Plant Transposable Elements. <i>F1000Research</i> , 2021, 10, 1194.	0.8	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.	1.8	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, .	1.4	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.	1.0	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.	1.6	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, .	1.8	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>	0.9	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.	1.1	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.	1.5	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.	1.2	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>	2.0	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.	1.0	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.	1.1	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.	1.5	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.	0.9	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, .	0.3	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, .	0.3	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, .	0.3	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.	1.6	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.	1.8	23

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37	Detection and identification of <i>Xanthomonas</i> pathotypes associated with citrus diseases using comparative genomics and multiplex PCR. PeerJ, 2019, 7, e7676.	0.9	10
38	Development of microsatellite markers for the carnivorous plant <i>Genlisea aurea</i> (Lentibulariaceae) using genomics data of NGS. Molecular Biology Reports, 2018, 45, 57-61.	1.0	4
39	A Practical Guide for Comparative Genomics of Mobile Genetic Elements in Prokaryotic Genomes. Methods in Molecular Biology, 2018, 1704, 213-242.	0.4	15
40	Closed Genome Sequence of Phytopathogen Biocontrol Agent <i>Bacillus velezensis</i> Strain AGVL-005, Isolated from Soybean. Genome Announcements, 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. Scientific Reports, 2018, 8, 13024.	1.6	18
42	The genome sequence of <i>Dyella jiangningensis</i> FCAV SCS01 from a lignocellulose-decomposing microbial consortium metagenome reveals potential for biotechnological applications. Genetics and Molecular Biology, 2018, 41, 507-513.	0.6	6
43	Genomic and Genotypic Characterization of <i>Cylindrospermopsis raciborskii</i> : Toward an Intraspecific Phylogenetic Evaluation by Comparative Genomics. Frontiers in Microbiology, 2018, 9, 306.	1.5	26
44	Phylogenetic and antimicrobial resistance gene analysis of <i>Salmonella</i> Typhimurium strains isolated in Brazil by whole genome sequencing. PLoS ONE, 2018, 13, e0201882.	1.1	48
45	Comparative genomic analysis of <i>Genlisea</i> (corkscrew plants) chloroplast genomes reveals an increasing loss of the <i>ndh</i> genes. PLoS ONE, 2018, 13, e0190321.	1.1	17
46	Biosynthesis of microcystin hepatotoxins in the cyanobacterial genus <i>Fischerella</i> . Toxicon, 2018, 141, 43-50.	0.8	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. PeerJ, 2018, 6, e6111.	0.9	8
48	Genetic Organization of Anabaenopeptin and Spumigin Biosynthetic Gene Clusters in the Cyanobacterium <i>Sphaerospermopsis torques-reginae</i> ITEP-024. ACS Chemical Biology, 2017, 12, 769-778.	1.6	25
49	The complete chloroplast genome sequence of the leafy bladderwort, <i>Utricularia foliosa</i> L. (Lentibulariaceae). Conservation Genetics Resources, 2017, 9, 213-216.	0.4	5
50	The Chloroplast Genome of <i>Passiflora edulis</i> (Passifloraceae) Assembled from Long Sequence Reads: Structural Organization and Phylogenomic Studies in Malpighiales. Frontiers in Plant Science, 2017, 8, 334.	1.7	79
51	Hepatozoon <i>caimani</i> in <i>Caiman crocodilus yacare</i> (Crocodylia, Alligatoridae) from North Pantanal, Brazil. Brazilian Journal of Veterinary Parasitology, 2017, 26, 352-358.	0.2	11
52	A Metagenomic Approach to Cyanobacterial Genomics. Frontiers in Microbiology, 2017, 8, 809.	1.5	98
53	The mitochondrial genome of the terrestrial carnivorous plant <i>Utricularia reniformis</i> (Lentibulariaceae): Structure, comparative analysis and evolutionary landmarks. PLoS ONE, 2017, 12, e0180484.	1.1	24
54	Metagenomic analysis of soil and freshwater from zoo agricultural area with organic fertilization. PLoS ONE, 2017, 12, e0190178.	1.1	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.	0.9	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.	1.1	57
57	Mechanisms of Evolution in High-Consequence Drug Resistance Plasmids. MBio, 2016, 7, .	1.8	49
58	Evaluating methods for purifying cyanobacterial cultures by qPCR and high-throughput Illumina sequencing. Journal of Microbiological Methods, 2016, 129, 55-60.	0.7	16
59	A Step Forward to Empower Global Microbiome Research Through Local Leadership. Trends in Microbiology, 2016, 24, 767-771.	3.5	12
60	New Small Plasmid Harboring <i>bla</i> <sub>KPC-2</sub> in <i>Pseudomonas aeruginosa</i> . Antimicrobial Agents and Chemotherapy, 2016, 60, 3211-3214.	1.4	12
61	Everyman's Guide to Bacterial Insertion Sequences. Microbiology Spectrum, 2015, 3, MDNA3-0030-2014.	1.2	204
62	Insertion Sequence IS <i>26</i> Reorganizes Plasmids in Clinically Isolated Multidrug-Resistant Bacteria by Replicative Transposition. MBio, 2015, 6, e00762.	1.8	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.	1.8	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.	1.1	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.	4.8	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.	1.2	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.	1.0	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. <i>Annual Review of Phytopathology</i> , 2013, 51, 429-451.	3.5	76
74	Draft Genome Sequence of the Brazilian Toxic Bloom-Forming Cyanobacterium <i>Microcystis aeruginosa</i> Strain SPC777. <i>Genome Announcements</i> , 2013, 1, .	0.8	11
75	Draft Genome Sequence of <i>Bacillus thuringiensis</i> var. <i>thuringiensis</i> Strain T01-328, a Brazilian Isolate That Produces a Soluble Pesticide Protein, Cry11a. <i>Genome Announcements</i> , 2013, 1, .	0.8	7
76	Exploring Bacterial Insertion Sequences with ISfinder: Objectives, Uses, and Future Developments. <i>Methods in Molecular Biology</i> , 2012, 859, 91-103.	0.4	61
77	Analysis of expressed sequence tags from the agarophyte <i>Gracilaria tenuistipitata</i> (Rhodophyta). <i>Journal of Applied Phycology</i> , 2012, 24, 641-647.	1.5	12
78	Strain-specific polyketide synthase genes of <i>Aspergillus niger</i> . <i>International Journal of Food Microbiology</i> , 2012, 155, 137-145.	2.1	32
79	<i>Xylella fastidiosa</i> comparative genomic database is an information resource to explore the annotation, genomic features, and biology of different strains. <i>Genetics and Molecular Biology</i> , 2012, 35, 149-152.	0.6	15
80	ISsaga is an ensemble of web-based methods for high throughput identification and semi-automatic annotation of insertion sequences in prokaryotic genomes. <i>Genome Biology</i> , 2011, 12, R30.	13.9	340
81	NAD Biosynthesis Evolution in Bacteria: Lateral Gene Transfer of Kynurenine Pathway in Xanthomonadales and Flavobacteriales. <i>Molecular Biology and Evolution</i> , 2009, 26, 399-406.	3.5	50
82	Laterally transferred genomic islands in Xanthomonadales related to pathogenicity and primary metabolism. <i>FEMS Microbiology Letters</i> , 2008, 281, 87-97.	0.7	43
83	Origins of the <i>Xylella fastidiosa</i> Prophage-Like Regions and Their Impact in Genome Differentiation. <i>PLoS ONE</i> , 2008, 3, e4059.	1.1	50
84	MudrA-like sequences from rice and sugarcane cluster as two bona fide transposon clades and two domesticated transposases. <i>Gene</i> , 2007, 392, 117-125.	1.0	17
85	<i>Xylella</i> and <i>Xanthomonas</i> Mobil'omics. <i>OMICS A Journal of Integrative Biology</i> , 2005, 9, 146-159.	1.0	46
86	Comparative analysis of Mutator -like transposases in sugarcane. <i>Molecular Genetics and Genomics</i> , 2004, 272, 194-203.	1.0	31
87	Everyman's Guide to Bacterial Insertion Sequences. , 0, , 555-590.		12