

Alessandro Varani

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6642980/publications.pdf>

Version: 2024-02-01

87
papers

2,777
citations

236925

25
h-index

214800

47
g-index

93
all docs

93
docs citations

93
times ranked

4066
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	9.6	340
2	Insertion Sequence IS <i>IS26</i> Reorganizes Plasmids in Clinically Isolated Multidrug-Resistant Bacteria by Replicative Transposition. <i>MBio</i> , 2015, 6, e00762.	4.1	256
3	Everyman's Guide to Bacterial Insertion Sequences. <i>Microbiology Spectrum</i> , 2015, 3, MDNA3-0030-2014.	3.0	204
4	Building the sugarcane genome for biotechnology and identifying evolutionary trends. <i>BMC Genomics</i> , 2014, 15, 540.	2.8	136
5	Genomic signatures and co-occurrence patterns of the ultra-small <i>Saccharimonadia</i> (phylum) Tj ETQq1 1 0.784314 rgBT /Overlock 101	3.5	101
6	A Metagenomic Approach to Cyanobacterial Genomics. <i>Frontiers in Microbiology</i> , 2017, 8, 809.	3.5	98
7	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
8	The Role of Prophage in Plant-Pathogenic Bacteria. <i>Annual Review of Phytopathology</i> , 2013, 51, 429-451.	7.8	76
9	Exploring Bacterial Insertion Sequences with ISfinder: Objectives, Uses, and Future Developments. <i>Methods in Molecular Biology</i> , 2012, 859, 91-103.	0.9	61
10	The IS6 family, a clinically important group of insertion sequences including IS26. <i>Mobile DNA</i> , 2021, 12, 11.	3.6	58
11	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 Lentibulariaceae Family. <i>PLoS ONE</i> , 2016, 11, e0165176.	2.5	57
12	TnCentral: a Prokaryotic Transposable Element Database and Web Portal for Transposon Analysis. <i>MBio</i> , 2021, 12, e0206021.	4.1	56
13	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.	8.9	50
14	Origins of the <i>Xylella fastidiosa</i> Prophage-Like Regions and Their Impact in Genome Differentiation. <i>PLoS ONE</i> , 2008, 3, e4059.	2.5	50
15	Mechanisms of Evolution in High-Consequence Drug Resistance Plasmids. <i>MBio</i> , 2016, 7, .	4.1	49
16	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
17	<i>Xylella</i> and <i>Xanthomonas</i> Mobil'omics. <i>OMICS A Journal of Integrative Biology</i> , 2005, 9, 146-159.	2.0	46
18	Laterally transferred genomic islands in Xanthomonadales related to pathogenicity and primary metabolism. <i>FEMS Microbiology Letters</i> , 2008, 281, 87-97.	1.8	43

#	ARTICLE	IF	CITATIONS
19	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> . <i>MBio</i> , 2015, 6, e02505-14.	4.1	43
20	The Family Rhizobiaceae. , 2014, , 419-437.		39
21	The Family Bradyrhizobiaceae. , 2014, , 135-154.		37
22	Unravelling potential virulence factor candidates in <i>Xanthomonas citri</i> subsp. <i>citri</i> by secretome analysis. <i>PeerJ</i> , 2016, 4, e1734.	2.0	35
23	A balanced microbiota efficiently produces methane in a novel high-rate horizontal anaerobic reactor for the treatment of swine wastewater. <i>Bioresource Technology</i> , 2015, 197, 152-160.	9.6	34
24	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
25	Strain-specific polyketide synthase genes of <i>Aspergillus niger</i> . <i>International Journal of Food Microbiology</i> , 2012, 155, 137-145.	4.7	32
26	Comparative analysis of Mutator-like transposases in sugarcane. <i>Molecular Genetics and Genomics</i> , 2004, 272, 194-203.	2.1	31
27	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
28	<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
29	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
30	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
31	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
32	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
33	Genetic diversity and molecular phylogeny of <i>Anaplasma marginale</i> studied longitudinally under natural transmission conditions in Rio de Janeiro, Brazil. <i>Ticks and Tick-borne Diseases</i> , 2015, 6, 499-507.	2.7	23
34	Metagenomic analysis of soil and freshwater from zoo agricultural area with organic fertilization. <i>PLoS ONE</i> , 2017, 12, e0190178.	2.5	23
35	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
36	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

#	ARTICLE	IF	CITATIONS
37	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
38	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.	2.2	17
39	Comparative genomic analysis of <i>Genlisea</i> (corkscrew plants "Lentibulariaceae) chloroplast genomes reveals an increasing loss of the <i>ndh</i> genes. <i>PLoS ONE</i> , 2018, 13, e0190321.	2.5	17
40	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
41	Evaluating methods for purifying cyanobacterial cultures by qPCR and high-throughput Illumina sequencing. <i>Journal of Microbiological Methods</i> , 2016, 129, 55-60.	1.6	16
42	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
43	Biosynthesis of microcystin hepatotoxins in the cyanobacterial genus <i>Fischerella</i> . <i>Toxicon</i> , 2018, 141, 43-50.	1.6	15
44	<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.	1.3	15
45	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
46	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
47	Analysis of expressed sequence tags from the agarophyte <i>Gracilaria tenuistipitata</i> (Rhodophyta). <i>Journal of Applied Phycology</i> , 2012, 24, 641-647.	2.8	12
48	Everyman's Guide to Bacterial Insertion Sequences. , 0, , 555-590.		12
49	A Step Forward to Empower Global Microbiome Research Through Local Leadership. <i>Trends in Microbiology</i> , 2016, 24, 767-771.	7.7	12
50	New Small Plasmid Harboring <i>bla</i> KPC-2 in <i>Pseudomonas aeruginosa</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 3211-3214.	3.2	12
51	<i>Bartonella machadoae</i> sp. nov. isolated from wild rodents in the Pantanal wetland. <i>Acta Tropica</i> , 2022, 229, 106368.	2.0	12
52	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
53	Molecular and phylogenetic characterization based on the complete genome of a virulent pathotype of Newcastle disease virus isolated in the 1970s in Brazil. <i>Infection, Genetics and Evolution</i> , 2014, 26, 160-167.	2.3	11
54	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

#	ARTICLE	IF	CITATIONS
55	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
56	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
57	An Atlas of Plant Transposable Elements. <i>F1000Research</i> , 2021, 10, 1194.	1.6	11
58	<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
59	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
60	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
61	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
62	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
63	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
64	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
65	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
66	Transposons and pathogenicity in <i>Xanthomonas</i> : acquisition of murein lytic transglycosylases by Tn <i>Xax1</i> enhances <i>Xanthomonas citri</i> subsp. <i>citri</i> 306 virulence and fitness. <i>PeerJ</i> , 2018, 6, e6111.	2.0	8
67	Draft Genome Sequence of <i>Bacillus thuringiensis</i> var. <i>thuringiensis</i> Strain T01-328, a Brazilian Isolate That Produces a Soluble Pesticide Protein, Cry1Ia. <i>Genome Announcements</i> , 2013, 1, .	0.8	7
68	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
69	Gene expression during the germination of coffee seed. <i>Journal of Seed Science</i> , 2019, 41, 168-179.	0.7	6
70	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
71	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
72	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

#	ARTICLE	IF	CITATIONS
73	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
74	Complete Genome Sequences of 11 <i>Staphylococcus</i> sp. Strains Isolated from Buffalo Milk and Milkersâ€™ Hands. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	4
75	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
76	The complete mitochondrial genome of carnivorous <i>Genlisea tuberosa</i> (Lentibulariaceae): Structure and evolutionary aspects. <i>Gene</i> , 2022, 824, 146391.	2.2	3
77	Draft Genome Sequence of <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Gallinarum Biovar Pullorum Strain FCAV198, a Brazilian Chicken Pathogen. <i>Genome Announcements</i> , 2014, 2, .	0.8	2
78	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
79	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
80	Evaluating Eucalyptus leaf colonization by <i>Brasilonema octagenarum</i> (Cyanobacteria,) Tj ETQq0 0 0 rgBT /Overlock_10 Tf 50 462 Td (Scy	2.0	2
81	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
82	Draft Genome Sequence of a Novel Culturable Marine Chroococcalean Cyanobacterium from the South Atlantic Ocean. <i>Genome Announcements</i> , 2015, 3, .	0.8	1
83	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
84	Microbiological quality assessment of a compost produced from animal waste and vegetables. <i>WIT Transactions on Ecology and the Environment</i> , 2014, , .	0.0	1
85	Response from Varani et al. to â€œComment on â€˜the IS6 family, a clinically important group of insertion sequences including IS26â€™ by Ruth M. Hallâ€™, <i>Mobile DNA</i> , 2022, 13, 2.	3.6	0
86	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
87	XAC4296 Is a Multifunctional and Exclusive Xanthomonadaceae Gene Containing a Fusion of Lytic Transglycosylase and Epimerase Domains. <i>Microorganisms</i> , 2022, 10, 1008.	3.6	0