

Nicola Vitulo

List of Publications by Year in descending order

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Version: 2024-02-01

71
papers

9,872
citations

159525

30
h-index

91828

69
g-index

73
all docs

73
docs citations

73
times ranked

14049
citing authors

#	ARTICLE	IF	CITATIONS
1	The grapevine genome sequence suggests ancestral hexaploidization in major angiosperm phyla. <i>Nature</i> , 2007, 449, 463-467.	13.7	3,384
2	The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , 2012, 485, 635-641.	13.7	2,860
3	Systematic evaluation of spliced alignment programs for RNA-seq data. <i>Nature Methods</i> , 2013, 10, 1185-1191.	9.0	467
4	Life at Depth: <i>Photobacterium profundum</i> Genome Sequence and Expression Analysis. <i>Science</i> , 2005, 307, 1459-1461.	6.0	266
5	A deep survey of alternative splicing in grape reveals changes in the splicing machinery related to tissue, stress condition and genotype. <i>BMC Plant Biology</i> , 2014, 14, 99.	1.6	254
6	Chromosome Scale Genome Assembly and Transcriptome Profiling of <i>Nannochloropsis gaditana</i> in Nitrogen Depletion. <i>Molecular Plant</i> , 2014, 7, 323-335.	3.9	178
7	Piezophilic adaptation: a genomic point of view. <i>Journal of Biotechnology</i> , 2006, 126, 11-25.	1.9	169
8	Comprehensive transcript profiling of two grapevine rootstock genotypes contrasting in drought susceptibility links the phenylpropanoid pathway to enhanced tolerance. <i>Journal of Experimental Botany</i> , 2015, 66, 5739-5752.	2.4	133
9	PASS: a program to align short sequences. <i>Bioinformatics</i> , 2009, 25, 967-968.	1.8	108
10	Light Remodels Lipid Biosynthesis in <i>Nannochloropsis gaditana</i> by Modulating Carbon Partitioning between Organelles. <i>Plant Physiology</i> , 2016, 171, 2468-2482.	2.3	106
11	The Accumulation of miRNAs Differentially Modulated by Drought Stress Is Affected by Grafting in Grapevine. <i>Plant Physiology</i> , 2017, 173, 2180-2195.	2.3	95
12	Large-Scale Transposon Mutagenesis of <i>Photobacterium profundum</i> SS9 Reveals New Genetic Loci Important for Growth at Low Temperature and High Pressure. <i>Journal of Bacteriology</i> , 2008, 190, 1699-1709.	1.0	92
13	Laterally transferred elements and high pressure adaptation in <i>Photobacterium profundum</i> strains. <i>BMC Genomics</i> , 2005, 6, 122.	1.2	91
14	Direct 16S rRNA-seq from bacterial communities: a PCR-independent approach to simultaneously assess microbial diversity and functional activity potential of each taxon. <i>Scientific Reports</i> , 2016, 6, 32165.	1.6	90
15	A single polyploidization event at the origin of the tetraploid genome of <i>Coffea arabica</i> is responsible for the extremely low genetic variation in wild and cultivated germplasm. <i>Scientific Reports</i> , 2020, 10, 4642.	1.6	86
16	Timing and Order of the Molecular Events Marking the Onset of Berry Ripening in Grapevine. <i>Plant Physiology</i> , 2018, 178, 1187-1206.	2.3	84
17	Genomic analysis of <i>Sparus aurata</i> reveals the evolutionary dynamics of sex-biased genes in a sequential hermaphrodite fish. <i>Communications Biology</i> , 2018, 1, 119.	2.0	84
18	Transcriptome analysis of the regenerating tail vs. the scarring limb in lizard reveals pathways leading to successful vs. unsuccessful organ regeneration in amniotes. <i>Developmental Dynamics</i> , 2017, 246, 116-134.	0.8	77

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19	Bark and Grape Microbiome of <i>Vitis vinifera</i> : Influence of Geographic Patterns and Agronomic Management on Bacterial Diversity. <i>Frontiers in Microbiology</i> , 2018, 9, 3203.	1.5	69
20	Microbiota changes induced by microencapsulated sodium butyrate in patients with inflammatory bowel disease. <i>Neurogastroenterology and Motility</i> , 2020, 32, e13914.	1.6	68
21	Grapevine Rootstocks Differentially Affect the Rate of Ripening and Modulate Auxin-Related Genes in Cabernet Sauvignon Berries. <i>Frontiers in Plant Science</i> , 2016, 7, 69.	1.7	67
22	Assessment of statistical methods from single cell, bulk RNA-seq, and metagenomics applied to microbiome data. <i>Genome Biology</i> , 2020, 21, 191.	3.8	67
23	First Survey of the Wheat Chromosome 5A Composition through a Next Generation Sequencing Approach. <i>PLoS ONE</i> , 2011, 6, e26421.	1.1	57
24	Development and validation of a gene expression oligo microarray for the gilthead sea bream (<i>Sparus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.2	55
25	RNA Sequencing of the Exercise Transcriptome in Equine Athletes. <i>PLoS ONE</i> , 2013, 8, e83504.	1.1	55
26	Biocontrol traits of <i>Bacillus licheniformis</i> GL174, a culturable endophyte of <i>Vitis vinifera</i> cv. Glera. <i>BMC Microbiology</i> , 2018, 18, 133.	1.3	45
27	Supplementation with <i>Bifidobacterium breve</i> BR03 and B632 strains improved insulin sensitivity in children and adolescents with obesity in a cross-over, randomized double-blind placebo-controlled trial. <i>Clinical Nutrition</i> , 2021, 40, 4585-4594.	2.3	43
28	Downregulation of lizard immuno-genes in the regenerating tail and myogenes in the scarring limb suggests that tail regeneration occurs in an immuno-privileged organ. <i>Protoplasma</i> , 2017, 254, 2127-2141.	1.0	42
29	RAP: a new computer program for de novo identification of repeated sequences in whole genomes. <i>Bioinformatics</i> , 2005, 21, 582-588.	1.8	41
30	MIDAW: a web tool for statistical analysis of microarray data. <i>Nucleic Acids Research</i> , 2005, 33, W644-W649.	6.5	41
31	Development of an oligo DNA microarray for the European sea bass and its application to expression profiling of jaw deformity. <i>BMC Genomics</i> , 2010, 11, 354.	1.2	37
32	Remission in Crohn's disease is accompanied by alterations in the gut microbiota and mucins production. <i>Scientific Reports</i> , 2019, 9, 13263.	1.6	30
33	ZASP Interacts with the Mechanosensing Protein Ankrd2 and p53 in the Signalling Network of Striated Muscle. <i>PLoS ONE</i> , 2014, 9, e92259.	1.1	29
34	Draft genome assembly and transcriptome data of the icefish <i>Chionodraco myersi</i> reveal the key role of mitochondria for a life without hemoglobin at subzero temperatures. <i>Communications Biology</i> , 2019, 2, 443.	2.0	26
35	A leukemia-enriched cDNA microarray platform identifies new transcripts with relevance to the biology of pediatric acute lymphoblastic leukemia. <i>Haematologica</i> , 2005, 90, 890-8.	1.7	26
36	First draft genome sequencing of fennel (<i>Foeniculum vulgare</i> Mill.): identification of simple sequence repeats and their application in marker-assisted breeding. <i>Molecular Breeding</i> , 2018, 38, 1.	1.0	24

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37	A draft genome of sweet cherry (<i>Prunus avium</i> L.) reveals genome-wide and local effects of domestication. <i>Plant Journal</i> , 2020, 103, 1420-1432.	2.8	23
38	Transcription of LINE-derived sequences in exercise-induced stress in horses. <i>Animal Genetics</i> , 2010, 41, 23-27.	0.6	22
39	High mortality of juvenile gilthead sea bream (<i>Sparus aurata</i>) from photobacteriosis is associated with alternative macrophage activation and anti-inflammatory response: Results of gene expression profiling of early responses in the head kidney. <i>Fish and Shellfish Immunology</i> , 2013, 34, 1269-1278.	1.6	22
40	Transcriptional Characterization of a Widely-Used Grapevine Rootstock Genotype under Different Iron-Limited Conditions. <i>Frontiers in Plant Science</i> , 2016, 7, 1994.	1.7	21
41	Transcriptome dynamics in the asexual cycle of the chordate <i>Botryllus schlosseri</i> . <i>BMC Genomics</i> , 2016, 17, 275.	1.2	20
42	QueryOR: a comprehensive web platform for genetic variant analysis and prioritization. <i>BMC Bioinformatics</i> , 2017, 18, 225.	1.2	20
43	Fast genetic identification of the Beluga sturgeon and its sought-after caviar to stem illegal trade. <i>Food Control</i> , 2017, 75, 145-152.	2.8	19
44	Different Phylogenomic Approaches to Resolve the Evolutionary Relationships among Model Fish Species. <i>Molecular Biology and Evolution</i> , 2010, 27, 2757-2774.	3.5	18
45	Engineering a 3D in vitro model of human skeletal muscle at the single fiber scale. <i>PLoS ONE</i> , 2020, 15, e0232081.	1.1	18
46	Acclimation of photosynthesis and lipids biosynthesis to prolonged nitrogen and phosphorus limitation in <i>Nannochloropsis gaditana</i> . <i>Algal Research</i> , 2021, 58, 102368.	2.4	18
47	VviNAC33 promotes organ de-greening and represses vegetative growth during the vegetative to mature phase transition in grapevine. <i>New Phytologist</i> , 2021, 231, 726-746.	3.5	16
48	High Carotenoid Mutants of <i>Chlorella vulgaris</i> Show Enhanced Biomass Yield under High Irradiance. <i>Plants</i> , 2021, 10, 911.	1.6	16
49	Ecotype Diversity and Conversion in <i>Photobacterium profundum</i> Strains. <i>PLoS ONE</i> , 2014, 9, e96953.	1.1	15
50	High-Throughput Sequencing of microRNAs in Glucocorticoid Sensitive Paediatric Inflammatory Bowel Disease Patients. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1399.	1.8	15
51	PASS-bis: a bisulfite aligner suitable for whole methylome analysis of Illumina and SOLiD reads. <i>Bioinformatics</i> , 2013, 29, 268-270.	1.8	14
52	The leaf transcriptome of fennel (<i>Foeniculum vulgare</i> Mill.) enables characterization of the t-anethole pathway and the discovery of microsatellites and single-nucleotide variants. <i>Scientific Reports</i> , 2018, 8, 10459.	1.6	14
53	Inhibition of Virulence-Related Traits in <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> by Gunpowder Green Tea Extracts. <i>Frontiers in Microbiology</i> , 2019, 10, 2362.	1.5	14
54	Profiling of skeletal muscle Ankrd2 protein in human cardiac tissue and neonatal rat cardiomyocytes. <i>Histochemistry and Cell Biology</i> , 2015, 143, 583-597.	0.8	13

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55	Genome-Wide Transcriptional Changes and Lipid Profile Modifications Induced by <i>Medicago truncatula</i> N5 Overexpression at an Early Stage of the Symbiotic Interaction with <i>Sinorhizobium meliloti</i> . <i>Genes</i> , 2017, 8, 396.	1.0	13
56	Physical Mapping of Bread Wheat Chromosome 5A: An Integrated Approach. <i>Plant Genome</i> , 2015, 8, eplantgenome2015.03.0011.	1.6	11
57	A global gene evolution analysis on Vibrionaceae family using phylogenetic profile. <i>BMC Bioinformatics</i> , 2007, 8, S23.	1.2	10
58	Microbial metabarcoding highlights different bacterial and fungal populations in honey samples from local beekeepers and market in north-eastern Italy. <i>International Journal of Food Microbiology</i> , 2020, 334, 108806.	2.1	10
59	The Mitochondrial Genome Assembly of Fennel (<i>Foeniculum vulgare</i>) Reveals Two Different <i>atp6</i> Gene Sequences in Cytoplasmic Male Sterile Accessions. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4664.	1.8	10
60	Multilevel comparative bioinformatics to investigate evolutionary relationships and specificities in gene annotations: an example for tomato and grapevine. <i>BMC Bioinformatics</i> , 2018, 19, 435.	1.2	9
61	Salivary microbiota composition may discriminate between patients with eosinophilic oesophagitis (<sc>EoE</sc>) and <sc>nonâ€EoE</sc> subjects. <i>Alimentary Pharmacology and Therapeutics</i> , 2022, 56, 450-462.	1.9	8
62	Pangenome analyses of LuxS-coding genes and enzymatic repertoires in cocoa-related lactic acid bacteria. <i>Genomics</i> , 2021, 113, 1659-1670.	1.3	7
63	Natural contaminants in bee pollen: DNA metabarcoding as a tool to identify floral sources of pyrrolizidine alkaloids and fungal diversity. <i>Food Research International</i> , 2021, 146, 110438.	2.9	6
64	Comparative analysis identifies microâ€RNA associated with nutrient homeostasis, development and stress response in <i>Arabidopsis thaliana</i> upon high Zn and metal hyperaccumulator <i>Arabidopsis halleri</i> . <i>Physiologia Plantarum</i> , 2021, 173, 920-934.	2.6	5
65	The Grapevine E3 Ubiquitin Ligase VriATL156 Confers Resistance against the Downy Mildew Pathogen <i>Plasmopara viticola</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 940.	1.8	5
66	Assessing Gut Microbiota in an Infant with Congenital Propionic Acidemia before and after Probiotic Supplementation. <i>Microorganisms</i> , 2021, 9, 2599.	1.6	5
67	SATRAP: SOLiD Assembler TRAnslation Program. <i>PLoS ONE</i> , 2015, 10, e0137436.	1.1	3
68	Mo1232 CHARACTERIZATION OF SALIVARY, GASTRIC AND ESOPHAGEAL MICROBIOTA IN PATIENTS WITH EOSINOPHILIC ESOPHAGITIS. <i>Gastroenterology</i> , 2020, 158, S-837.	0.6	2
69	Su2003 â€“ Microencapsulated Sodium Butyrate Significantly Modifies the Microbiota in Patients with Inflammatory Bowel Disease Mimicking Prebiotic Activity and Proving Effects on the Treatment of the Disease. <i>Gastroenterology</i> , 2019, 156, S-687.	0.6	1
70	P.07.33 MICROENCAPSULATED SODIUM BUTYRATE SIGNIFICANTLY MODIFIES THE MICROBIOTA IN PATIENTS WITH INFLAMMATORY BOWEL DISEASE MIMICKING PREBIOTIC ACTIVITY AND PROVING EFFECTS ON THE TREATMENT OF THE DISEASE. <i>Digestive and Liver Disease</i> , 2019, 51, e236-e238.	0.4	0
71	Supplementation with <i>Bifidobacterium breve</i> BR03 and <i>Bifidobacterium breve</i> B632 favoured weight loss and improved insulin metabolism in children and adolescents with obesity in the BIFI-OBESE cross-over, randomized placebo-controlled trial. <i>Endocrine Abstracts</i> , 0, , .	0.0	0