

Giorgio Valle

List of Publications by Year in descending order

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119
papers

14,629
citations

44069

48
h-index

20358

116
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121
all docs

121
docs citations

121
times ranked

19633
citing authors

#	ARTICLE	IF	CITATIONS
1	A specific microbiota signature is associated to various degrees of ulcerative colitis as assessed by a machine learning approach. <i>Gut Microbes</i> , 2022, 14, 2028366.	9.8	26
2	Identification of Known and Novel <i>Arundo donax</i> L. MicroRNAs and Their Targets Using High-Throughput Sequencing and Degradome Analysis. <i>Life</i> , 2022, 12, 651.	2.4	1
3	Genetic Layout of Melanoma Lesions Is Associated with BRAF/MEK-Targeted Therapy Resistance and Transcriptional Profiles. <i>Journal of Investigative Dermatology</i> , 2022, 142, 3030-3040.e5.	0.7	6
4	Salivary microbiota composition may discriminate between patients with eosinophilic oesophagitis (<sc>EoE</sc>) and <sc>non-EoE</sc> subjects. <i>Alimentary Pharmacology and Therapeutics</i> , 2022, 56, 450-462.	3.7	8
5	BVVL/ FL: features caused by SLC52A3 mutations; WDFY4 and TNFSF13B may be novel causative genes. <i>Neurobiology of Aging</i> , 2021, 99, 102.e1-102.e10.	3.1	3
6	Mitochondria-rough-ER contacts in the liver regulate systemic lipid homeostasis. <i>Cell Reports</i> , 2021, 34, 108873.	6.4	76
7	Revealing metabolic mechanisms of interaction in the anaerobic digestion microbiome by flux balance analysis. <i>Metabolic Engineering</i> , 2020, 62, 138-149.	7.0	45
8	Engineering a 3D in vitro model of human skeletal muscle at the single fiber scale. <i>PLoS ONE</i> , 2020, 15, e0232081.	2.5	18
9	Setup and Validation of a Targeted Next-Generation Sequencing Approach for the Diagnosis of Lysosomal Storage Disorders. <i>Journal of Molecular Diagnostics</i> , 2020, 22, 488-502.	2.8	15
10	SAMHD1-deficient fibroblasts from Aicardi-Goutières Syndrome patients can escape senescence and accumulate mutations. <i>FASEB Journal</i> , 2020, 34, 631-647.	0.5	12
11	Genetic Analyses in Dent Disease and Characterization of CLCN5 Mutations in Kidney Biopsies. <i>International Journal of Molecular Sciences</i> , 2020, 21, 516.	4.1	17
12	Exome Sequencing Reveals Immune Genes as Susceptibility Modifiers in Individuals with α 1-Antitrypsin Deficiency. <i>Scientific Reports</i> , 2019, 9, 13088.	3.3	7
13	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.	2.6	9
14	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.	3.3	45
15	Microbial activity response to hydrogen injection in thermophilic anaerobic digesters revealed by genome-centric metatranscriptomics. <i>Microbiome</i> , 2018, 6, 194.	11.1	39
16	MicroRNA signatures in cardiac biopsies and detection of allograft rejection. <i>Journal of Heart and Lung Transplantation</i> , 2018, 37, 1329-1340.	0.6	34
17	High-Throughput Sequencing of microRNAs in Glucocorticoid Sensitive Paediatric Inflammatory Bowel Disease Patients. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1399.	4.1	15
18	Scuba: scalable kernel-based gene prioritization. <i>BMC Bioinformatics</i> , 2018, 19, 23.	2.6	16

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19	FP698MICRORNA SEQUENCING IN GRAFT PROTOCOL BIOPSIES: NOVEL BIOMARKERS OF GRAFT REJECTION IN PEDIATRIC KIDNEY TRANSPLANTATION. <i>Nephrology Dialysis Transplantation</i> , 2018, 33, i281-i281.	0.7	0
20	The Accumulation of miRNAs Differentially Modulated by Drought Stress Is Affected by Grafting in Grapevine. <i>Plant Physiology</i> , 2017, 173, 2180-2195.	4.8	95
21	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.	2.1	42
22	QueryOR: a comprehensive web platform for genetic variant analysis and prioritization. <i>BMC Bioinformatics</i> , 2017, 18, 225.	2.6	20
23	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.	1.8	77
24	Brain RNA-Seq Profiling of the Mucopolysaccharidosis Type II Mouse Model. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1072.	4.1	28
25	SNP-Discovery by RAD-Sequencing in a Germplasm Collection of Wild and Cultivated Grapevines (<i>V. Tj</i> ETQq1 1 0.784314 rgBT /Over 2.5 59		
26	Whole-exome sequencing in radically resected gastric cancer (GC): Analysis of patients (pts) with poor prognostic factors from the Italian Trial of Adjuvant Chemotherapy Adenocarcinoma (ITACA-S) trial. <i>Journal of Clinical Oncology</i> , 2017, 35, 64-64.	1.6	0
27	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.	3.6	67
28	Differential expression and localization of Ankrd2 isoforms in human skeletal and cardiac muscles. <i>Histochemistry and Cell Biology</i> , 2016, 146, 569-584.	1.7	6
29	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.	3.3	90
30	Metagenomic analysis and functional characterization of the biogas microbiome using high throughput shotgun sequencing and a novel binning strategy. <i>Biotechnology for Biofuels</i> , 2016, 9, 26.	6.2	248
31	Whole exome sequencing and single nucleotide polymorphism array analyses to identify germline alterations in genes associated with testosterone metabolism in a patient with androgen insensitivity syndrome and early-onset colorectal cancer. <i>Chinese Journal of Cancer</i> , 2016, 35, 51.	4.9	3
32	Light Remodels Lipid Biosynthesis in <i>Nannochloropsis gaditana</i> by Modulating Carbon Partitioning between Organelles. <i>Plant Physiology</i> , 2016, 171, 2468-2482.	4.8	106
33	Transcriptome dynamics in the asexual cycle of the chordate <i>Botryllus schlosseri</i> . <i>BMC Genomics</i> , 2016, 17, 275.	2.8	20
34	Transcriptional Characterization of a Widely-Used Grapevine Rootstock Genotype under Different Iron-Limited Conditions. <i>Frontiers in Plant Science</i> , 2016, 7, 1994.	3.6	21
35	Profiling of skeletal muscle Ankrd2 protein in human cardiac tissue and neonatal rat cardiomyocytes. <i>Histochemistry and Cell Biology</i> , 2015, 143, 583-597.	1.7	13
36	Genomic instability: Crossing pathways at the origin of structural and numerical chromosome changes. <i>Environmental and Molecular Mutagenesis</i> , 2015, 56, 563-580.	2.2	29

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37	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.	4.8	133
38	SATRAP: SOLiD Assembler TRANslation Program. <i>PLoS ONE</i> , 2015, 10, e0137436.	2.5	3
39	Chromosome Scale Genome Assembly and Transcriptome Profiling of <i>Nannochloropsis gaditana</i> in Nitrogen Depletion. <i>Molecular Plant</i> , 2014, 7, 323-335.	8.3	178
40	Oxidative stress response and nitrogen utilization are strongly variable in <i>Saccharomyces cerevisiae</i> wine strains with different fermentation performances. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 4119-4135.	3.6	38
41	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.	3.6	254
42	Adaptations of the Psychrotolerant Piezophile Photobacterium profundum Strain SS9. , 2014, , 319-337.		15
43	ZASP Interacts with the Mechanosensing Protein Ankrd2 and p53 in the Signalling Network of Striated Muscle. <i>PLoS ONE</i> , 2014, 9, e92259.	2.5	29
44	PASS-bis: a bisulfite aligner suitable for whole methylome analysis of Illumina and SOLiD reads. <i>Bioinformatics</i> , 2013, 29, 268-270.	4.1	14
45	RNA Sequencing of the Exercise Transcriptome in Equine Athletes. <i>PLoS ONE</i> , 2013, 8, e83504.	2.5	55
46	The transcriptional landscape of the deep-sea bacterium <i>Photobacterium profundum</i> in both a <i>toxR</i> mutant and its parental strain. <i>BMC Genomics</i> , 2012, 13, 567.	2.8	28
47	Genome-wide analysis of plastome sequence variation and development of plastidial CAPS markers in common potato and related <i>Solanum</i> species. <i>Genetic Resources and Crop Evolution</i> , 2012, 59, 419-430.	1.6	17
48	Multi-Tasking Role of the Mechanosensing Protein Ankrd2 in the Signaling Network of Striated Muscle. <i>PLoS ONE</i> , 2011, 6, e25519.	2.5	31
49	First Survey of the Wheat Chromosome 5A Composition through a Next Generation Sequencing Approach. <i>PLoS ONE</i> , 2011, 6, e26421.	2.5	57
50	Physical mapping in highly heterozygous genomes: a physical contig map of the Pinot Noir grapevine cultivar. <i>BMC Genomics</i> , 2010, 11, 204.	2.8	15
51	Combining ontologies and workflows to design formal protocols for biological laboratories. <i>Automated Experimentation</i> , 2010, 2, 3.	2.0	9
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.	14.5	135
53	A Snapshot of the Emerging Tomato Genome Sequence. <i>Plant Genome</i> , 2009, 2, .	2.8	73
54	PASS: a program to align short sequences. <i>Bioinformatics</i> , 2009, 25, 967-968.	4.1	108

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55	A Class III PDZ Binding Motif in the Myotilin and FATZ Families Binds Enigma Family Proteins: a Common Link for Z-Disc Myopathies. <i>Molecular and Cellular Biology</i> , 2009, 29, 822-834.	2.3	87
56	High throughput approaches reveal splicing of primary microRNA transcripts and tissue specific expression of mature microRNAs in <i>Vitis vinifera</i> . <i>BMC Genomics</i> , 2009, 10, 558.	2.8	62
57	Muscle Research and Gene Ontology: New standards for improved data integration. <i>BMC Medical Genomics</i> , 2009, 2, 6.	1.5	16
58	Post-transcriptional silencing of the <i>Drosophila</i> homolog of human ZASP: a molecular and functional analysis. <i>Cell and Tissue Research</i> , 2009, 337, 463-476.	2.9	18
59	CUDA compatible GPU cards as efficient hardware accelerators for Smith-Waterman sequence alignment. <i>BMC Bioinformatics</i> , 2008, 9, S10.	2.6	344
60	Protein evolution in deep sea bacteria: an analysis of amino acids substitution rates. <i>BMC Evolutionary Biology</i> , 2008, 8, 313.	3.2	37
61	Annotating genomes with massive-scale RNA sequencing. <i>Genome Biology</i> , 2008, 9, R175.	9.6	210
62	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.	2.2	92
63	PABS: An online platform to assist BAC-by-BAC sequencing projects. <i>BioTechniques</i> , 2008, 44, 60-64.	1.8	4
64	The grapevine genome sequence suggests ancestral hexaploidization in major angiosperm phyla. <i>Nature</i> , 2007, 449, 463-467.	27.8	3,384
65	A global gene evolution analysis on <i>Vibrionaceae</i> family using phylogenetic profile. <i>BMC Bioinformatics</i> , 2007, 8, S23.	2.6	10
66	Genes involved in TGF β 1-driven epithelial-mesenchymal transition of renal epithelial cells are topologically related in the human interactome map. <i>BMC Genomics</i> , 2007, 8, 383.	2.8	20
67	Quantitative Proteomic Comparison of Rat Mitochondria from Muscle, Heart, and Liver. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 608-619.	3.8	250
68	Haplogroup Effects and Recombination of Mitochondrial DNA: Novel Clues from the Analysis of Leber Hereditary Optic Neuropathy Pedigrees. <i>American Journal of Human Genetics</i> , 2006, 78, 564-574.	6.2	166
69	Piezophilic adaptation: a genomic point of view. <i>Journal of Biotechnology</i> , 2006, 126, 11-25.	3.8	169
70	Functional insights from the structural modelling of a small Fe-hydrogenase. <i>Biochemical and Biophysical Research Communications</i> , 2006, 339, 277-283.	2.1	10
71	The LGI1/Epitempin gene encodes two protein isoforms differentially expressed in human brain. <i>Journal of Neurochemistry</i> , 2006, 98, 985-991.	3.9	24
72	Overview of BITS2005, the Second Annual Meeting of the Italian Bioinformatics Society. <i>BMC Bioinformatics</i> , 2005, 6, S1.	2.6	8

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73	Laterally transferred elements and high pressure adaptation in <i>Photobacterium profundum</i> strains. <i>BMC Genomics</i> , 2005, 6, 122.	2.8	91
74	RAP: a new computer program for de novo identification of repeated sequences in whole genomes. <i>Bioinformatics</i> , 2005, 21, 582-588.	4.1	41
75	The SSEA server for protein secondary structure alignment. <i>Bioinformatics</i> , 2005, 21, 393-395.	4.1	35
76	The Mitochondrial Genome of the House Centipede <i>Scutigera</i> and the Monophyly Versus Paraphyly of Myriapods. <i>Molecular Biology and Evolution</i> , 2004, 21, 770-780.	8.9	98
77	Extensive Gene Order Rearrangement in the Mitochondrial Genome of the Centipede <i>Scutigera coleoptrata</i> . <i>Journal of Molecular Evolution</i> , 2004, 58, 413-423.	1.8	43
78	The Ankrd2 Protein, a Link Between the Sarcomere and the Nucleus in Skeletal Muscle. <i>Journal of Molecular Biology</i> , 2004, 339, 313-325.	4.2	125
79	Autosomal Dominant Lateral Temporal Epilepsy: Clinical Spectrum, New Epitempin Mutations, and Genetic Heterogeneity in Seven European Families. <i>Epilepsia</i> , 2003, 44, 1289-1297.	5.1	134
80	Mutations in Cypher/ZASPin patients with dilated cardiomyopathy and left ventricular non-compaction. <i>Journal of the American College of Cardiology</i> , 2003, 42, 2014-2027.	2.8	479
81	Human MYO18B, a Novel Unconventional Myosin Heavy Chain Expressed in Striated Muscles Moves into the Myonuclei upon Differentiation. <i>Journal of Molecular Biology</i> , 2003, 326, 137-149.	4.2	66
82	Simple consensus procedures are effective and sufficient in secondary structure prediction. <i>Protein Engineering, Design and Selection</i> , 2003, 16, 459-462.	2.1	63
83	Pattern recognition in gene expression profiling using DNA array: a comparative study of different statistical methods applied to cancer classification. <i>Human Molecular Genetics</i> , 2003, 12, 823-836.	2.9	51
84	TRAIT (TRANscript Integrated Table): a knowledgebase of human skeletal muscle transcripts. <i>Bioinformatics</i> , 2003, 19, 661-662.	4.1	4
85	PRIMEX: rapid identification of oligonucleotide matches in whole genomes. <i>Bioinformatics</i> , 2003, 19, 2486-2488.	4.1	31
86	Gene expression profiling in dysferlinopathies using a dedicated muscle microarray. <i>Human Molecular Genetics</i> , 2002, 11, 3283-3298.	2.9	70
87	A two-step strategy for constructing specifically self-subtracted cDNA libraries. <i>Nucleic Acids Research</i> , 2002, 30, 38e-38.	14.5	13
88	Development and production of an oligonucleotide MuscleChip: use for validation of ambiguous ESTs. <i>BMC Bioinformatics</i> , 2002, 3, 33.	2.6	8
89	Analysis of 22 deletion breakpoints in dystrophin intron 49. <i>Human Genetics</i> , 2002, 110, 418-421.	3.8	53
90	Functional profiling of the <i>Saccharomyces cerevisiae</i> genome. <i>Nature</i> , 2002, 418, 387-391.	27.8	3,938

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91	Characterization of Human Skeletal Muscle Ankrd2. <i>Biochemical and Biophysical Research Communications</i> , 2001, 285, 378-386.	2.1	51
92	Do the Four Clades of the mtDNA Haplogroup L2 Evolve at Different Rates?. <i>American Journal of Human Genetics</i> , 2001, 69, 1348-1356.	6.2	185
93	Characterization of 16 novel human genes showing high similarity to yeast sequences. <i>Yeast</i> , 2001, 18, 69-80.	1.7	25
94	Dysferlin Protein Analysis in Limb-Girdle Muscular Dystrophies. <i>Journal of Molecular Neuroscience</i> , 2001, 17, 71-80.	2.3	67
95	Telethonin and Other New Proteins of the Z-Disc of Skeletal Muscle. <i>IUBMB Life</i> , 2001, 51, 275-282.	3.4	86
96	Immediate early genes induced by H-Ras in thyroid cells. <i>Oncogene</i> , 2001, 20, 2281-2290.	5.9	5
97	Characterization of 16 novel human genes showing high similarity to yeast sequences. <i>Yeast</i> , 2001, 18, 69-80.	1.7	1
98	Gene disruption and basic phenotypic analysis of nine novel yeast genes from chromosome XIV. <i>Yeast</i> , 2000, 16, 1089-1097.	1.7	11
99	Limb-girdle muscular dystrophy type 2G is caused by mutations in the gene encoding the sarcomeric protein telethonin. <i>Nature Genetics</i> , 2000, 24, 163-166.	21.4	312
100	FATZ, a Filamin-, Actinin-, and Telethonin-binding Protein of the Z-disc of Skeletal Muscle. <i>Journal of Biological Chemistry</i> , 2000, 275, 41234-41242.	3.4	147
101	TUBA8: A New Tissue-Specific Isoform of β -Tubulin That Is Highly Conserved in Human and Mouse. <i>Biochemical and Biophysical Research Communications</i> , 2000, 270, 1111-1118.	2.1	55
102	ZASP: A New Z-band Alternatively Spliced PDZ-motif Protein. <i>Journal of Cell Biology</i> , 1999, 146, 465-475.	5.2	208
103	A Comprehensive, High-Resolution Genomic Transcript Map of Human Skeletal Muscle. <i>Genome Research</i> , 1998, 8, 817-825.	5.5	69
104	A Septin-based Hierarchy of Proteins Required for Localized Deposition of Chitin in the <i>Saccharomyces cerevisiae</i> Cell Wall. <i>Journal of Cell Biology</i> , 1997, 139, 75-93.	5.2	301
105	The preliminary transcript map of a human skeletal muscle. <i>Human Molecular Genetics</i> , 1997, 6, 1445-1450.	2.9	14
106	Fine Mapping of Five Human Skeletal Muscle Genes: Alpha-Tropomyosin, Beta-Tropomyosin, Troponin-I Slow-Twitch, Troponin-I Fast-Twitch, and Troponin-C Fast. <i>Biochemical and Biophysical Research Communications</i> , 1997, 230, 347-350.	2.1	52
107	Maturation and translation mechanisms involved in the expression of a myb gene of rice. <i>Plant Molecular Biology</i> , 1997, 35, 1003-1008.	3.9	28
108	The DNA Sequence of Cosmid 14â€“13b from Chromosome XIV of <i>Saccharomyces cerevisiae</i> Reveals an Unusually High Number of Overlapping Open Reading Frames. , 1997, 13, 261-266.		6

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109	Chromosomal Localization of the Human Genes, CPP32, Mch2, Mch3, and lch-1, Involved in Cellular Apoptosis. <i>Biochemical and Biophysical Research Communications</i> , 1996, 225, 983-989.	2.1	23
110	The DNA sequence of cosmid 14-5 from chromosome XIV reveals 21 open reading frames including a novel gene encoding a globin-like domain. <i>Yeast</i> , 1996, 12, 1071-1076.	1.7	12
111	Ancestral hemoglobin switching in lampreys. <i>Developmental Biology</i> , 1994, 164, 402-408.	2.0	27
112	TA-repeat microsatellites are closely associated with ARS consensus sequences in yeast chromosome III. <i>Yeast</i> , 1993, 9, 753-759.	1.7	12
113	Discover 1: a new program to search for unusually represented DNA motifs. <i>Nucleic Acids Research</i> , 1993, 21, 5152-5156.	14.5	4
114	A putative serine/threonine protein kinase gene on chromosome III of <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 1992, 8, 71-77.	1.7	10
115	Different globin messenger RNAs are present before and after the metamorphosis in <i>Lampetra zanandreaei</i> . <i>Developmental Biology</i> , 1991, 145, 367-373.	2.0	4
116	The sequence of a 6.3 kb segment of yeast chromosome III reveals an open reading frame coding for a putative mismatch binding protein. <i>Yeast</i> , 1991, 7, 981-988.	1.7	10
117	Post-Translational Fate of Variant MOPC 315 lambda Chains in <i>Xenopus</i> Oocytes and Mouse Myeloma Cells. <i>FEBS Journal</i> , 1983, 132, 131-138.	0.2	22
118	Actin in <i>Xenopus</i> Development: Indirect Immunofluorescence Study of Actin Localization. <i>Differentiation</i> , 1981, 20, 45-51.	1.9	24
119	Synthesis and secretion of mouse immunoglobulin chains from <i>Xenopus</i> oocytes. <i>Nature</i> , 1981, 291, 338-340.	27.8	48