

Giorgio Valle

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

118
papers

11,851
citations

44
h-index

108
g-index

121
ext. papers

13,579
ext. citations

6.8
avg, IF

5.25
L-index

#	Paper	IF	Citations
118	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	8.8	1
117	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	3	
116	Mitochondria-rough-ER contacts in the liver regulate systemic lipid homeostasis. <i>Cell Reports</i> , 2021 , 34, 108873	10.6	21
115	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	5.6	
114	Engineering a 3D in vitro model of human skeletal muscle at the single fiber scale. <i>PLoS ONE</i> , 2020 , 15, e0232081	3.7	6
113	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	5.1	8
112	SAMHD1-deficient fibroblasts from Aicardi-Goutières Syndrome patients can escape senescence and accumulate mutations. <i>FASEB Journal</i> , 2020 , 34, 631-647	0.9	7
111	Genetic Analyses in Dent Disease and Characterization of CLCN5 Mutations in Kidney Biopsies. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	5
110	Revealing metabolic mechanisms of interaction in the anaerobic digestion microbiome by flux balance analysis. <i>Metabolic Engineering</i> , 2020 , 62, 138-149	9.7	15
109	Exome Sequencing Reveals Immune Genes as Susceptibility Modifiers in Individuals with Antitrypsin Deficiency. <i>Scientific Reports</i> , 2019 , 9, 13088	4.9	6
108	MicroRNA signatures in cardiac biopsies and detection of allograft rejection. <i>Journal of Heart and Lung Transplantation</i> , 2018 , 37, 1329-1340	5.8	25
107	High-Throughput Sequencing of microRNAs in Glucocorticoid Sensitive Paediatric Inflammatory Bowel Disease Patients. <i>International Journal of Molecular Sciences</i> , 2018 , 19,	6.3	12
106	Scuba: scalable kernel-based gene prioritization. <i>BMC Bioinformatics</i> , 2018 , 19, 23	3.6	10
105	FP698MICRORNA SEQUENCING IN GRAFT PROTOCOL BIOPSIES: NOVEL BIOMARKERS OF GRAFT REJECTION IN PEDIATRIC KIDNEY TRANSPLANTATION. <i>Nephrology Dialysis Transplantation</i> , 2018 , 33, i281-i281	4.3	
104	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	3.6	6
103	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	4.5	26
102	Microbial activity response to hydrogen injection in thermophilic anaerobic digesters revealed by genome-centric metatranscriptomics. <i>Microbiome</i> , 2018 , 6, 194	16.6	18

101	The Accumulation of miRNAs Differentially Modulated by Drought Stress Is Affected by Grafting in Grapevine. <i>Plant Physiology</i> , 2017 , 173, 2180-2195	6.6	58
100	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, 2127-2143	4.4	29
99	QueryOR: a comprehensive web platform for genetic variant analysis and prioritization. <i>BMC Bioinformatics</i> , 2017 , 18, 225	3.6	14
98	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	2.9	58
97	Brain RNA-Seq Profiling of the Mucopolysaccharidosis Type II Mouse Model. <i>International Journal of Molecular Sciences</i> , 2017 , 18,	6.3	20
96	SNP-Discovery by RAD-Sequencing in a Germplasm Collection of Wild and Cultivated Grapevines (<i>V. vinifera</i> L.). <i>PLoS ONE</i> , 2017 , 12, e0170655	3.7	33
95	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	2.2	
94	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	7.8	164
93	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		2
92	Light Remodels Lipid Biosynthesis in <i>Nannochloropsis gaditana</i> by Modulating Carbon Partitioning between Organelles. <i>Plant Physiology</i> , 2016 , 171, 2468-82	6.6	70
91	Transcriptome dynamics in the asexual cycle of the chordate <i>Botryllus schlosseri</i> . <i>BMC Genomics</i> , 2016 , 17, 275	4.5	17
90	Transcriptional Characterization of a Widely-Used Grapevine Rootstock Genotype under Different Iron-Limited Conditions. <i>Frontiers in Plant Science</i> , 2016 , 7, 1994	6.2	13
89	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	6.2	40
88	Differential expression and localization of Ankrd2 isoforms in human skeletal and cardiac muscles. <i>Histochemistry and Cell Biology</i> , 2016 , 146, 569-584	2.4	4
87	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	4.9	56
86	Genomic instability: Crossing pathways at the origin of structural and numerical chromosome changes. <i>Environmental and Molecular Mutagenesis</i> , 2015 , 56, 563-80	3.2	22
85	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, 5739-52	7	87
84	Profiling of skeletal muscle Ankrd2 protein in human cardiac tissue and neonatal rat cardiomyocytes. <i>Histochemistry and Cell Biology</i> , 2015 , 143, 583-97	2.4	8

83	SATRAP: SOLiD Assembler TRANslation Program. <i>PLoS ONE</i> , 2015 , 10, e0137436	3.7	2
82	Chromosome scale genome assembly and transcriptome profiling of <i>Nannochloropsis gaditana</i> in nitrogen depletion. <i>Molecular Plant</i> , 2014 , 7, 323-35	14.4	147
81	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, 4119-35	5.7	28
80	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	5.3	177
79	Adaptations of the Psychrotolerant Piezophile Photobacterium profundum Strain SS9 2014 , 319-337		12
78	ZASP interacts with the mechanosensing protein Ankrd2 and p53 in the signalling network of striated muscle. <i>PLoS ONE</i> , 2014 , 9, e92259	3.7	18
77	PASS-bis: a bisulfite aligner suitable for whole methylome analysis of Illumina and SOLiD reads. <i>Bioinformatics</i> , 2013 , 29, 268-70	7.2	14
76	RNA sequencing of the exercise transcriptome in equine athletes. <i>PLoS ONE</i> , 2013 , 8, e83504	3.7	32
75	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 ²		15
74	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	4.5	24
73	Multi-tasking role of the mechanosensing protein Ankrd2 in the signaling network of striated muscle. <i>PLoS ONE</i> , 2011 , 6, e25519	3.7	26
72	First survey of the wheat chromosome 5A composition through a next generation sequencing approach. <i>PLoS ONE</i> , 2011 , 6, e26421	3.7	52
71	Large-scale detection and analysis of RNA editing in grape mtDNA by RNA deep-sequencing. <i>Nucleic Acids Research</i> , 2010 , 38, 4755-67	20.1	117
70	Correction: 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> , 2010 , 11, 109	4.5	44
69	Physical mapping in highly heterozygous genomes: a physical contig map of the Pinot Noir grapevine cultivar. <i>BMC Genomics</i> , 2010 , 11, 204	4.5	15
68	Combining ontologies and workflows to design formal protocols for biological laboratories. <i>Automated Experimentation</i> , 2010 , 2, 3		5
67	PASS: a program to align short sequences. <i>Bioinformatics</i> , 2009 , 25, 967-8	7.2	99
66	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, 822-34	4.8	73

65	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	4.5	52
64	Muscle Research and Gene Ontology: New standards for improved data integration. <i>BMC Medical Genomics</i> , 2009 , 2, 6	3.7	16
63	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, 463-76	4.2	18
62	A Snapshot of the Emerging Tomato Genome Sequence. <i>Plant Genome</i> , 2009 , 2,	4.4	62
61	CUDA compatible GPU cards as efficient hardware accelerators for Smith-Waterman sequence alignment. <i>BMC Bioinformatics</i> , 2008 , 9 Suppl 2, S10	3.6	263
60	Protein evolution in deep sea bacteria: an analysis of amino acids substitution rates. <i>BMC Evolutionary Biology</i> , 2008 , 8, 313	3	31
59	Annotating genomes with massive-scale RNA sequencing. <i>Genome Biology</i> , 2008 , 9, R175	18.3	186
58	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, 1699-703	3.5	77
57	PABS: an online platform to assist BAC-by-BAC sequencing projects. <i>BioTechniques</i> , 2008 , 44, 60, 62, 64	2.5	4
56	The grapevine genome sequence suggests ancestral hexaploidization in major angiosperm phyla. <i>Nature</i> , 2007 , 449, 463-7	50.4	2675
55	A global gene evolution analysis on Vibrionaceae family using phylogenetic profile. <i>BMC Bioinformatics</i> , 2007 , 8 Suppl 1, S23	3.6	9
54	Genes involved in TGF beta1-driven epithelial-mesenchymal transition of renal epithelial cells are topologically related in the human interactome map. <i>BMC Genomics</i> , 2007 , 8, 383	4.5	16
53	Quantitative proteomic comparison of rat mitochondria from muscle, heart, and liver. <i>Molecular and Cellular Proteomics</i> , 2006 , 5, 608-19	7.6	221
52	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, 564-74	11	156
51	Piezophilic adaptation: a genomic point of view. <i>Journal of Biotechnology</i> , 2006 , 126, 11-25	3.7	142
50	Functional insights from the structural modelling of a small Fe-hydrogenase. <i>Biochemical and Biophysical Research Communications</i> , 2006 , 339, 277-83	3.4	9
49	The LGI1/epitempin gene encodes two protein isoforms differentially expressed in human brain. <i>Journal of Neurochemistry</i> , 2006 , 98, 985-91	6	19
48	Overview of BITS2005, the Second Annual Meeting of the Italian Bioinformatics Society. <i>BMC Bioinformatics</i> , 2005 , 6, S1	3.6	3

47	Laterally transferred elements and high pressure adaptation in <i>Photobacterium profundum</i> strains. <i>BMC Genomics</i> , 2005 , 6, 122	4.5	77
46	RAP: a new computer program for de novo identification of repeated sequences in whole genomes. <i>Bioinformatics</i> , 2005 , 21, 582-8	7.2	32
45	The SSEA server for protein secondary structure alignment. <i>Bioinformatics</i> , 2005 , 21, 393-5	7.2	31
44	The mitochondrial genome of the house centipede scutigera and the monophyly versus paraphyly of myriapods. <i>Molecular Biology and Evolution</i> , 2004 , 21, 770-80	8.3	79
43	Extensive gene order rearrangement in the mitochondrial genome of the centipede <i>Scutigera coleoptrata</i> . <i>Journal of Molecular Evolution</i> , 2004 , 58, 413-23	3.1	40
42	The Ankrd2 protein, a link between the sarcomere and the nucleus in skeletal muscle. <i>Journal of Molecular Biology</i> , 2004 , 339, 313-25	6.5	116
41	PRIMEX: rapid identification of oligonucleotide matches in whole genomes. <i>Bioinformatics</i> , 2003 , 19, 2486-8	7.2	26
40	Autosomal dominant lateral temporal epilepsy: clinical spectrum, new epitempin mutations, and genetic heterogeneity in seven European families. <i>Epilepsia</i> , 2003 , 44, 1289-97	6.4	119
39	Mutations in Cypher/ZASP in patients with dilated cardiomyopathy and left ventricular non-compaction. <i>Journal of the American College of Cardiology</i> , 2003 , 42, 2014-27	15.1	416
38	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, 137-49	6.5	60
37	Simple consensus procedures are effective and sufficient in secondary structure prediction. <i>Protein Engineering, Design and Selection</i> , 2003 , 16, 459-62	1.9	53
36	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, 823-36	5.6	38
35	TRAIT (TRANscript Integrated Table): a knowledgebase of human skeletal muscle transcripts. <i>Bioinformatics</i> , 2003 , 19, 661-2	7.2	4
34	Development and production of an oligonucleotide MuscleChip: use for validation of ambiguous ESTs. <i>BMC Bioinformatics</i> , 2002 , 3, 33	3.6	6
33	Analysis of 22 deletion breakpoints in dystrophin intron 49. <i>Human Genetics</i> , 2002 , 110, 418-21	6.3	48
32	Functional profiling of the <i>Saccharomyces cerevisiae</i> genome. <i>Nature</i> , 2002 , 418, 387-91	50.4	3278
31	Gene expression profiling in dysferlinopathies using a dedicated muscle microarray. <i>Human Molecular Genetics</i> , 2002 , 11, 3283-98	5.6	63
30	A two-step strategy for constructing specifically self-subtracted cDNA libraries. <i>Nucleic Acids Research</i> , 2002 , 30, e38	20.1	11

29	Characterization of 16 novel human genes showing high similarity to yeast sequences. <i>Yeast</i> , 2001 , 18, 69-80	3.4	23
28	Dysferlin protein analysis in limb-girdle muscular dystrophies. <i>Journal of Molecular Neuroscience</i> , 2001 , 17, 71-80	3.3	50
27	Telethonin and other new proteins of the Z-disc of skeletal muscle. <i>IUBMB Life</i> , 2001 , 51, 275-82	4.7	76
26	Immediate early genes induced by H-Ras in thyroid cells. <i>Oncogene</i> , 2001 , 20, 2281-90	9.2	4
25	Characterization of human skeletal muscle Ankrd2. <i>Biochemical and Biophysical Research Communications</i> , 2001 , 285, 378-86	3.4	47
24	Do the four clades of the mtDNA haplogroup L2 evolve at different rates?. <i>American Journal of Human Genetics</i> , 2001 , 69, 1348-56	11	171
23	Characterization of 16 novel human genes showing high similarity to yeast sequences 2001 , 18, 69		1
22	Gene disruption and basic phenotypic analysis of nine novel yeast genes from chromosome XIV. <i>Yeast</i> , 2000 , 16, 1089-97	3.4	10
21	Limb-girdle muscular dystrophy type 2G is caused by mutations in the gene encoding the sarcomeric protein telethonin. <i>Nature Genetics</i> , 2000 , 24, 163-6	36.3	278
20	FATZ, a filamin-, actinin-, and telethonin-binding protein of the Z-disc of skeletal muscle. <i>Journal of Biological Chemistry</i> , 2000 , 275, 41234-42	5.4	118
19	TUBA8: A new tissue-specific isoform of alpha-tubulin that is highly conserved in human and mouse. <i>Biochemical and Biophysical Research Communications</i> , 2000 , 270, 1111-8	3.4	51
18	ZASP: a new Z-band alternatively spliced PDZ-motif protein. <i>Journal of Cell Biology</i> , 1999 , 146, 465-75	7.3	183
17	A comprehensive, high-resolution genomic transcript map of human skeletal muscle. <i>Genome Research</i> , 1998 , 8, 817-25	9.7	65
16	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	7.3	277
15	The preliminary transcript map of a human skeletal muscle. <i>Human Molecular Genetics</i> , 1997 , 6, 1445-50	5.6	14
14	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, 347-50	3.4	48
13	Maturation and translation mechanisms involved in the expression of a myb gene of rice. <i>Plant Molecular Biology</i> , 1997 , 35, 1003-8	4.6	26
12	The DNA sequence of cosmid 14-13b from chromosome XIV of <i>Saccharomyces cerevisiae</i> reveals an unusually high number of overlapping open reading frames. <i>Yeast</i> , 1997 , 13, 261-6	3.4	6

11	Chromosomal localization of the human genes, CPP32, Mch2, Mch3, and Ich-1, involved in cellular apoptosis. <i>Biochemical and Biophysical Research Communications</i> , 1996 , 225, 983-9	3-4	21
10	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	3-4	11
9	Ancestral hemoglobin switching in lampreys. <i>Developmental Biology</i> , 1994 , 164, 402-8	3-1	25
8	Discover 1: a new program to search for unusually represented DNA motifs. <i>Nucleic Acids Research</i> , 1993 , 21, 5152-6	20-1	3
7	TA-repeat microsatellites are closely associated with ARS consensus sequences in yeast chromosome III. <i>Yeast</i> , 1993 , 9, 753-9	3-4	11
6	A putative serine/threonine protein kinase gene on chromosome III of <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 1992 , 8, 71-7	3-4	10
5	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, 981-8	3-4	8
4	Different globin messenger RNAs are present before and after the metamorphosis in <i>Lampetra zanandreaei</i> . <i>Developmental Biology</i> , 1991 , 145, 367-73	3-1	4
3	Post-translational fate of variant MOPC 315 lambda chains in <i>Xenopus</i> oocytes and mouse myeloma cells. <i>FEBS Journal</i> , 1983 , 132, 131-8		22
2	Actin in <i>Xenopus</i> development: indirect immunofluorescence study of actin localization. <i>Differentiation</i> , 1981 , 20, 45-51	3-5	23
1	Synthesis and secretion of mouse immunoglobulin chains from <i>Xenopus</i> oocytes. <i>Nature</i> , 1981 , 291, 338-40	3-4	47