Vito Flavio Licciulli

List of Publications by Year
in descending order

52 papers	2,198 citations	394421 19 h-index	223800 46 g-index
53 all docs	53 docs citations	53 times ranked	3718 citing authors

#	Article	IF	Citations
1	Analysis of Faecal Microbiota and Small ncRNAs in Autism: Detection of miRNAs and piRNAs with Possible Implications in Host–Gut Microbiota Cross-Talk. Nutrients, 2022, 14, 1340.	4.1	6
2	Explaining Ovarian Cancer Gene Expression Profiles with Fuzzy Rules and Genetic Algorithms. Electronics (Switzerland), 2021, 10, 375.	3.1	10
3	ITSoneWB: profiling global taxonomic diversity of eukaryotic communities on Galaxy. Bioinformatics, 2021, 37, 4253-4254.	4.1	1
4	A Pilot Longitudinal Evaluation of MicroRNAs for Monitoring the Cognitive Impairment in Pediatric Multiple Sclerosis. Applied Sciences (Switzerland), 2020, 10, 8274.	2.5	2
5	InteractomeSeq: a web server for the identification and profiling of domains and epitopes from phage display and next generation sequencing data. Nucleic Acids Research, 2020, 48, W200-W207.	14.5	7
6	Integrated Analysis of microRNA and mRNA Expression Profiles: An Attempt to Disentangle the Complex Interaction Network in Attention Deficit Hyperactivity Disorder. Brain Sciences, 2019, 9, 288.	2.3	22
7	ITSoneDB: a comprehensive collection of eukaryotic ribosomal RNA Internal Transcribed Spacer 1 (ITS1) sequences. Nucleic Acids Research, 2018, 46, D127-D132.	14.5	31
8	Combined microRNA and mRNA expression analysis in pediatric multiple sclerosis: an integrated approach to uncover novel pathogenic mechanisms of the disease. Human Molecular Genetics, 2018, 27, 66-79.	2.9	65
9	Arena-Idb: a platform to build human non-coding RNA interaction networks. BMC Bioinformatics, 2018, 19, 350.	2.6	17
10	Interactome-Seq: A Protocol for Domainome Library Construction, Validation and Selection by Phage Display and Next Generation Sequencing. Journal of Visualized Experiments, 2018, , .	0.3	5
11	Dysregulation of MicroRNAs and Target Genes Networks in Peripheral Blood of Patients With Sporadic Amyotrophic Lateral Sclerosis. Frontiers in Molecular Neuroscience, 2018, 11, 288.	2.9	93
12	Tackling critical parameters in metazoan meta-barcoding experiments: a preliminary study based on $coxI$ DNA barcode. PeerJ, 2018, 6, e4845.	2.0	6
13	WoPPER: Web server for Position Related data analysis of gene Expression in Prokaryotes. Nucleic Acids Research, 2017, 45, W109-W115.	14.5	16
14	Molecular Characterization of Peripheral Extracellular Vesicles in Clinically Isolated Syndrome: Preliminary Suggestions from a Pilot Study. Medical Sciences (Basel, Switzerland), 2017, 5, 19.	2.9	4
15	The NonCode aReNA DB: a non-redundant and integrated collection of non-coding RNAs. EMBnet Journal, 2016, 21, 834.	0.6	1
16	A platform independent RNA-Seq protocol for the detection of transcriptome complexity. BMC Genomics, 2013, 14, 855.	2.8	7
17	Reference databases for taxonomic assignment in metagenomics. Briefings in Bioinformatics, 2012, 13, 682-695.	6.5	82
18	BEAT: Bioinformatics Exon Array Tool to store, analyze and visualize Affymetrix GeneChip Human Exon Array data from disease experiments. BMC Bioinformatics, 2012, 13, S21.	2.6	5

#	Article	IF	Citations
19	GIDL: a rule based expert system for GenBank Intelligent Data Loading into the Molecular Biodiversity database. BMC Bioinformatics, 2012, 13, S4.	2.6	9
20	MBLabDB: a social database for molecular biodiversity data. EMBnet Journal, 2012, 18, 121.	0.6	1
21	PlantPIs â€" An Interactive Web Resource on Plant Protease Inhibitors. Current Protein and Peptide Science, 2011, 12, 448-454.	1.4	10
22	ASPicDB: a database of annotated transcript and protein variants generated by alternative splicing. Nucleic Acids Research, 2011, 39, D80-D85.	14.5	38
23	UTRdb and UTRsite (RELEASE 2010): a collection of sequences and regulatory motifs of the untranslated regions of eukaryotic mRNAs. Nucleic Acids Research, 2010, 38, D75-D80.	14.5	285
24	ASPicDB: A database resource for alternative splicing analysis. Bioinformatics, 2008, 24, 1300-1304.	4.1	40
25	Statistical assessment of functional categories of genes deregulated in pathological conditions by using microarray data. Bioinformatics, 2007, 23, 2063-2072.	4.1	22
26	A high performance grid-web service framework for the identification of â€˜conserved sequence tagsâ€™. Future Generation Computer Systems, 2007, 23, 371-381.	7.5	0
27	Gene analogue finder: a GRID solution for finding functionally analogous gene products. BMC Bioinformatics, 2007, 8, 329.	2.6	6
28	p53FamTaG: a database resource of human p53, p63 and p73 direct target genes combining in silico prediction and microarray data. BMC Bioinformatics, 2007, 8, S20.	2.6	57
29	The MitoDrome database annotates and compares the OXPHOS nuclear genes of Drosophila melanogaster, Drosophila pseudoobscura and Anopheles gambiae. Mitochondrion, 2006, 6, 252-257.	3.4	21
30	MitoRes: a resource of nuclear-encoded mitochondrial genes and their products in Metazoa. BMC Bioinformatics, 2006, 7, 36.	2.6	28
31	DNAfan: a software tool for automated extraction and analysis of user-defined sequence regions. Bioinformatics, 2004, 20, 3676-3679.	4.1	6
32	UTRdb and UTRsite: a collection of sequences and regulatory motifs of the untranslated regions of eukaryotic mRNAs. Nucleic Acids Research, 2004, 33, D141-D146.	14.5	140
33	PatSearch: a program for the detection of patterns and structural motifs in nucleotide sequences. Nucleic Acids Research, 2003, 31, 3608-3612.	14.5	101
34	PLMItRNA, a database on the heterogeneous genetic origin of mitochondrial tRNA genes and tRNAs in photosynthetic eukaryotes. Nucleic Acids Research, 2003, 31, 436-438.	14.5	8
35	MitoDrome: a database of Drosophila melanogaster nuclear genes encoding proteins targeted to the mitochondrion. Nucleic Acids Research, 2003, 31, 322-324.	14.5	49
36	Update of AMmtDB: a database of multi-aligned Metazoa mitochondrial DNA sequences. Nucleic Acids Research, 2002, 30, 174-175.	14.5	14

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37	UTRdb and UTRsite: specialized databases of sequences and functional elements of 5' and 3' untranslated regions of eukaryotic mRNAs. Update 2002. Nucleic Acids Research, 2002, 30, 335-340.	14.5	176
38	MitoNuc: a database of nuclear genes coding for mitochondrial proteins. Update 2002. Nucleic Acids Research, 2002, 30, 172-173.	14.5	12
39	PLANT-PIs: a database for plant protease inhibitors and their genes. Nucleic Acids Research, 2002, 30, 347-348.	14.5	131
40	Structural and functional features of eukaryotic mRNA untranslated regions. Gene, 2001, 276, 73-81.	2.2	365
41	PLMItRNA, a database for mitochondrial tRNA genes and tRNAs in photosynthetic eukaryotes. Nucleic Acids Research, 2001, 29, 167-168.	14.5	1
42	PLMItRNA, a database for tRNAs and tRNA genes in plant mitochondria: enlargement and updating. Nucleic Acids Research, 2000, 28, 159-162.	14.5	4
43	Update of AMmtDB: a database of multi-aligned Metazoa mitochondrial DNA sequences. Nucleic Acids Research, 2000, 28, 153-154.	14.5	11
44	MitoNuc and MitoAln: two related databases of nuclear genes coding for mitochondrial proteins. Nucleic Acids Research, 2000, 28, 163-165.	14.5	7
45	Update of KEYnet: a gene and protein names database for biosequences functional organisation. Nucleic Acids Research, 2000, 28, 372-373.	14.5	2
46	MitBASE : a comprehensive and integrated mitochondrial DNA database. The present status. Nucleic Acids Research, 2000, 28, 148-152.	14.5	18
47	UTRdb and UTRsite: specialized databases of sequences and functional elements of 5' and 3' untranslated regions of eukaryotic mRNAs. Nucleic Acids Research, 2000, 28, 193-196.	14.5	155
48	Analysis of oligonucleotide AUG start codon context in eukariotic mRNAs. Gene, 2000, 261, 85-91.	2.2	70
49	KEYnet: a keywords database for biosequences functional organization. Nucleic Acids Research, 1999, 27, 365-367.	14.5	6
50	Update of AMmtDB: a database of multi-aligned metazoa mitochondrial DNA sequences. Nucleic Acids Research, 1999, 27, 134-137.	14.5	17
51	PLMItRNA, a database for higher plant mitochondrial tRNAs and tRNA genes. Nucleic Acids Research, 1999, 27, 156-157.	14.5	3
52	The mitBASE human dataset structure. Nucleic Acids Research, 1998, 26, 116-119.	14.5	4