

Vito Flavio Licciulli

List of Publications by Year in descending order

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Version: 2024-02-01

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	Structural and functional features of eukaryotic mRNA untranslated regions. <i>Gene</i> , 2001, 276, 73-81.	2.2	365
2	UTRdb and UTRsite (RELEASE 2010): a collection of sequences and regulatory motifs of the untranslated regions of eukaryotic mRNAs. <i>Nucleic Acids Research</i> , 2010, 38, D75-D80.	14.5	285
3	UTRdb and UTRsite: specialized databases of sequences and functional elements of 5' and 3' untranslated regions of eukaryotic mRNAs. Update 2002. <i>Nucleic Acids Research</i> , 2002, 30, 335-340.	14.5	176
4	UTRdb and UTRsite: specialized databases of sequences and functional elements of 5' and 3' untranslated regions of eukaryotic mRNAs. <i>Nucleic Acids Research</i> , 2000, 28, 193-196.	14.5	155
5	UTRdb and UTRsite: a collection of sequences and regulatory motifs of the untranslated regions of eukaryotic mRNAs. <i>Nucleic Acids Research</i> , 2004, 33, D141-D146.	14.5	140
6	PLANT-PIs: a database for plant protease inhibitors and their genes. <i>Nucleic Acids Research</i> , 2002, 30, 347-348.	14.5	131
7	PatSearch: a program for the detection of patterns and structural motifs in nucleotide sequences. <i>Nucleic Acids Research</i> , 2003, 31, 3608-3612.	14.5	101
8	Dysregulation of MicroRNAs and Target Genes Networks in Peripheral Blood of Patients With Sporadic Amyotrophic Lateral Sclerosis. <i>Frontiers in Molecular Neuroscience</i> , 2018, 11, 288.	2.9	93
9	Reference databases for taxonomic assignment in metagenomics. <i>Briefings in Bioinformatics</i> , 2012, 13, 682-695.	6.5	82
10	Analysis of oligonucleotide AUG start codon context in eukariotic mRNAs. <i>Gene</i> , 2000, 261, 85-91.	2.2	70
11	Combined microRNA and mRNA expression analysis in pediatric multiple sclerosis: an integrated approach to uncover novel pathogenic mechanisms of the disease. <i>Human Molecular Genetics</i> , 2018, 27, 66-79.	2.9	65
12	p53FamTaG: a database resource of human p53, p63 and p73 direct target genes combining in silico prediction and microarray data. <i>BMC Bioinformatics</i> , 2007, 8, S20.	2.6	57
13	MitoDrome: a database of <i>Drosophila melanogaster</i> nuclear genes encoding proteins targeted to the mitochondrion. <i>Nucleic Acids Research</i> , 2003, 31, 322-324.	14.5	49
14	ASPicDB: A database resource for alternative splicing analysis. <i>Bioinformatics</i> , 2008, 24, 1300-1304.	4.1	40
15	ASPicDB: a database of annotated transcript and protein variants generated by alternative splicing. <i>Nucleic Acids Research</i> , 2011, 39, D80-D85.	14.5	38
16	ITSoneDB: a comprehensive collection of eukaryotic ribosomal RNA Internal Transcribed Spacer 1 (ITS1) sequences. <i>Nucleic Acids Research</i> , 2018, 46, D127-D132.	14.5	31
17	MitoRes: a resource of nuclear-encoded mitochondrial genes and their products in Metazoa. <i>BMC Bioinformatics</i> , 2006, 7, 36.	2.6	28
18	Statistical assessment of functional categories of genes deregulated in pathological conditions by using microarray data. <i>Bioinformatics</i> , 2007, 23, 2063-2072.	4.1	22

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19	Integrated Analysis of microRNA and mRNA Expression Profiles: An Attempt to Disentangle the Complex Interaction Network in Attention Deficit Hyperactivity Disorder. <i>Brain Sciences</i> , 2019, 9, 288.	2.3	22
20	The MitoDrome database annotates and compares the OXPHOS nuclear genes of <i>Drosophila melanogaster</i> , <i>Drosophila pseudoobscura</i> and <i>Anopheles gambiae</i> . <i>Mitochondrion</i> , 2006, 6, 252-257.	3.4	21
21	MitBASE : a comprehensive and integrated mitochondrial DNA database. The present status. <i>Nucleic Acids Research</i> , 2000, 28, 148-152.	14.5	18
22	Update of AMmtDB: a database of multi-aligned metazoa mitochondrial DNA sequences. <i>Nucleic Acids Research</i> , 1999, 27, 134-137.	14.5	17
23	Arena-Idb: a platform to build human non-coding RNA interaction networks. <i>BMC Bioinformatics</i> , 2018, 19, 350.	2.6	17
24	WoPPER: Web server for Position Related data analysis of gene Expression in Prokaryotes. <i>Nucleic Acids Research</i> , 2017, 45, W109-W115.	14.5	16
25	Update of AMmtDB: a database of multi-aligned Metazoa mitochondrial DNA sequences. <i>Nucleic Acids Research</i> , 2002, 30, 174-175.	14.5	14
26	MitoNuc: a database of nuclear genes coding for mitochondrial proteins. Update 2002. <i>Nucleic Acids Research</i> , 2002, 30, 172-173.	14.5	12
27	Update of AMmtDB: a database of multi-aligned Metazoa mitochondrial DNA sequences. <i>Nucleic Acids Research</i> , 2000, 28, 153-154.	14.5	11
28	PlantPls “ An Interactive Web Resource on Plant Protease Inhibitors. <i>Current Protein and Peptide Science</i> , 2011, 12, 448-454.	1.4	10
29	Explaining Ovarian Cancer Gene Expression Profiles with Fuzzy Rules and Genetic Algorithms. <i>Electronics (Switzerland)</i> , 2021, 10, 375.	3.1	10
30	GIDL: a rule based expert system for GenBank Intelligent Data Loading into the Molecular Biodiversity database. <i>BMC Bioinformatics</i> , 2012, 13, S4.	2.6	9
31	PLMitRNA, a database on the heterogeneous genetic origin of mitochondrial tRNA genes and tRNAs in photosynthetic eukaryotes. <i>Nucleic Acids Research</i> , 2003, 31, 436-438.	14.5	8
32	MitoNuc and MitoAln: two related databases of nuclear genes coding for mitochondrial proteins. <i>Nucleic Acids Research</i> , 2000, 28, 163-165.	14.5	7
33	A platform independent RNA-Seq protocol for the detection of transcriptome complexity. <i>BMC Genomics</i> , 2013, 14, 855.	2.8	7
34	InteractomeSeq: a web server for the identification and profiling of domains and epitopes from phage display and next generation sequencing data. <i>Nucleic Acids Research</i> , 2020, 48, W200-W207.	14.5	7
35	KEYnet: a keywords database for biosequences functional organization. <i>Nucleic Acids Research</i> , 1999, 27, 365-367.	14.5	6
36	DNAfan: a software tool for automated extraction and analysis of user-defined sequence regions. <i>Bioinformatics</i> , 2004, 20, 3676-3679.	4.1	6

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37	Gene analogue finder: a GRID solution for finding functionally analogous gene products. BMC Bioinformatics, 2007, 8, 329.	2.6	6
38	Tackling critical parameters in metazoan meta-barcoding experiments: a preliminary study based on <i>cox1</i> DNA barcode. PeerJ, 2018, 6, e4845.	2.0	6
39	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
40	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
41	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
42	The mitBASE human dataset structure. Nucleic Acids Research, 1998, 26, 116-119.	14.5	4
43	PLMItRNA, a database for tRNAs and tRNA genes in plant mitochondria: enlargement and updating. Nucleic Acids Research, 2000, 28, 159-162.	14.5	4
44	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
45	PLMItRNA, a database for higher plant mitochondrial tRNAs and tRNA genes. Nucleic Acids Research, 1999, 27, 156-157.	14.5	3
46	Update of KEYnet: a gene and protein names database for biosequences functional organisation. Nucleic Acids Research, 2000, 28, 372-373.	14.5	2
47	A Pilot Longitudinal Evaluation of MicroRNAs for Monitoring the Cognitive Impairment in Pediatric Multiple Sclerosis. Applied Sciences (Switzerland), 2020, 10, 8274.	2.5	2
48	PLMItRNA, a database for mitochondrial tRNA genes and tRNAs in photosynthetic eukaryotes. Nucleic Acids Research, 2001, 29, 167-168.	14.5	1
49	ITSoneWB: profiling global taxonomic diversity of eukaryotic communities on Galaxy. Bioinformatics, 2021, 37, 4253-4254.	4.1	1
50	MBLabDB: a social database for molecular biodiversity data. EMBnet Journal, 2012, 18, 121.	0.6	1
51	The NonCode aReNA DB: a non-redundant and integrated collection of non-coding RNAs. EMBnet Journal, 2016, 21, 834.	0.6	1
52	A high performance grid-web service framework for the identification of conserved sequence tags™. Future Generation Computer Systems, 2007, 23, 371-381.	7.5	0