

Anna Maria D'erchia

List of Publications by Year in descending order

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Version: 2024-02-01

45
papers

2,500
citations

257357

24
h-index

223716

46
g-index

48
all docs

48
docs citations

48
times ranked

5096
citing authors

#	ARTICLE	IF	CITATIONS
1	YAP contributes to DNA methylation remodeling upon mouse embryonic stem cell differentiation. <i>Journal of Biological Chemistry</i> , 2021, 296, 100138.	1.6	25
2	<i>Campylobacter vulpis</i> sp. nov. isolated from wild red foxes. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126204.	1.2	13
3	Accurate detection and quantification of SARS-CoV-2 genomic and subgenomic mRNAs by ddPCR and meta-transcriptomics analysis. <i>Communications Biology</i> , 2021, 4, 1215.	2.0	10
4	VINYL: Variant prioritization by survival analysis. <i>Bioinformatics</i> , 2021, 36, 5590-5599.	1.8	4
5	Accurate quantification of bacterial abundance in metagenomic DNAs accounting for variable DNA integrity levels. <i>Microbial Genomics</i> , 2020, 6, .	1.0	8
6	Enrichment of intestinal <i>Lactobacillus</i> by enhanced secretory IgA coating alters glucose homeostasis in P2rx7 ^{+/+} mice. <i>Scientific Reports</i> , 2019, 9, 9315.	1.6	18
7	No metagenomic evidence of tumorigenic viruses in cancers from a selected cohort of immunosuppressed subjects. <i>Scientific Reports</i> , 2019, 9, 19815.	1.6	3
8	Whole transcriptome profiling of Late-Onset Alzheimer's Disease patients provides insights into the molecular changes involved in the disease. <i>Scientific Reports</i> , 2018, 8, 4282.	1.6	102
9	RNA editing signature during myeloid leukemia cell differentiation. <i>Leukemia</i> , 2017, 31, 2824-2832.	3.3	29
10	T Follicular Helper Cells Promote a Beneficial Gut Ecosystem for Host Metabolic Homeostasis by Sensing Microbiota-Derived Extracellular ATP. <i>Cell Reports</i> , 2017, 18, 2566-2575.	2.9	87
11	Massive transcriptome sequencing of human spinal cord tissues provides new insights into motor neuron degeneration in ALS. <i>Scientific Reports</i> , 2017, 7, 10046.	1.6	99
12	REDportal: a comprehensive database of A-to-I RNA editing events in humans. <i>Nucleic Acids Research</i> , 2017, 45, D750-D757.	6.5	256
13	Targeted next-generation sequencing detects novel gene phenotype associations and expands the mutational spectrum in cardiomyopathies. <i>PLoS ONE</i> , 2017, 12, e0181842.	1.1	28
14	Profile of microbial communities on carbonate stones of the medieval church of San Leonardo di Siponto (Italy) by Illumina-based deep sequencing. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 8537-8548.	1.7	47
15	Reduced levels of protein recoding by A-to-I RNA editing in Alzheimer's disease. <i>Rna</i> , 2016, 22, 290-302.	1.6	122
16	Intestinal microbiota sustains inflammation and autoimmunity induced by hypomorphic <i>RAG</i> defects. <i>Journal of Experimental Medicine</i> , 2016, 213, 355-375.	4.2	61
17	Profiling RNA editing in human tissues: towards the inosinome Atlas. <i>Scientific Reports</i> , 2015, 5, 14941.	1.6	194
18	RAP: RNA-Seq Analysis Pipeline, a new cloud-based NGS web application. <i>BMC Genomics</i> , 2015, 16, S3.	1.2	79

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19	Comparative Genomics of <i>Listeria</i> Sensu Lato: Genus-Wide Differences in Evolutionary Dynamics and the Progressive Gain of Complex, Potentially Pathogenicity-Related Traits through Lateral Gene Transfer. <i>Genome Biology and Evolution</i> , 2015, 7, 2154-2172.	1.1	47
20	The influence of invasive jellyfish blooms on the aquatic microbiome in a coastal lagoon (Varano, SE Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.2	58
21	Using REDIttools to Detect RNA Editing Events in NGS Datasets. <i>Current Protocols in Bioinformatics</i> , 2015, 49, 12.12.1-12.12.15.	25.8	32
22	Epstein-Barr virus genetic variants are associated with multiple sclerosis. <i>Neurology</i> , 2015, 84, 1362-1368.	1.5	44
23	Draft genome sequence of <i>Acinetobacter</i> sp. neg1 capable of degrading ochratoxin A. <i>FEMS Microbiology Letters</i> , 2015, 362, .	0.7	12
24	BALB/c and C57BL/6 Mice Differ in Polyreactive IgA Abundance, which Impacts the Generation of Antigen-Specific IgA and Microbiota Diversity. <i>Immunity</i> , 2015, 43, 527-540.	6.6	247
25	Tissue-specific mtDNA abundance from exome data and its correlation with mitochondrial transcription, mass and respiratory activity. <i>Mitochondrion</i> , 2015, 20, 13-21.	1.6	146
26	Detection of Post-Transcriptional RNA Editing Events. <i>Methods in Molecular Biology</i> , 2015, 1269, 189-205.	0.4	10
27	Exploring the RNA Editing Potential of RNA-Seq Data by ExpEdit. <i>Methods in Molecular Biology</i> , 2015, 1269, 327-338.	0.4	5
28	ASPicDB: A Database Web Tool for Alternative Splicing Analysis. <i>Methods in Molecular Biology</i> , 2015, 1269, 365-378.	0.4	5
29	Draft genome sequence of <i>Sphingobium</i> sp. strain ba1, resistant to kanamycin and nickel ions. <i>FEMS Microbiology Letters</i> , 2014, 361, 8-9.	0.7	14
30	A platform independent RNA-Seq protocol for the detection of transcriptome complexity. <i>BMC Genomics</i> , 2013, 14, 855.	1.2	7
31	SpliceAid-F: a database of human splicing factors and their RNA-binding sites. <i>Nucleic Acids Research</i> , 2013, 41, D125-D131.	6.5	148
32	Genome-Wide Analysis of Differentially Expressed Genes and Splicing Isoforms in Clear Cell Renal Cell Carcinoma. <i>PLoS ONE</i> , 2013, 8, e78452.	1.1	19
33	TRIM8 modulates p53 activity to dictate cell cycle arrest. <i>Cell Cycle</i> , 2012, 11, 511-523.	1.3	78
34	ASPicDB: a database of annotated transcript and protein variants generated by alternative splicing. <i>Nucleic Acids Research</i> , 2011, 39, D80-D85.	6.5	38
35	Identification of tumor-associated cassette exons in human cancer through EST-based computational prediction and experimental validation. <i>Molecular Cancer</i> , 2010, 9, 230.	7.9	5
36	p73 and p63 Sustain Cellular Growth by Transcriptional Activation of Cell Cycle Progression Genes. <i>Cancer Research</i> , 2009, 69, 8563-8571.	0.4	51

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37	Identification and functional characterization of two new transcriptional variants of the human p63 gene. <i>Nucleic Acids Research</i> , 2009, 37, 6092-6104.	6.5	130
38	ASPicDB: A database resource for alternative splicing analysis. <i>Bioinformatics</i> , 2008, 24, 1300-1304.	1.8	40
39	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.	1.2	57
40	Molecular Clock and Gene Function. <i>Journal of Molecular Evolution</i> , 2003, 57, S277-S285.	0.8	31
41	Methods for screening tumors for p53 status and therapeutic exploitation. <i>Expert Review of Molecular Diagnostics</i> , 2003, 3, 289-301.	1.5	14
42	Molecular strategies in Metazoan genomic evolution. <i>Gene</i> , 2002, 300, 195-201.	1.0	18
43	Guinea Pig p53 mRNA: Identification of New Elements in Coding and Untranslated Regions and Their Functional and Evolutionary Implications. <i>Genomics</i> , 1999, 58, 50-64.	1.3	20
44	Detection of novel transcripts in the human mitochondrial DNA region coding for ATPase8-ATPase6 subunits. <i>FEBS Letters</i> , 1994, 344, 10-14.	1.3	13
45	Transcription of rat mitochondrial NADH-dehydrogenase subunits presence of antisense and precursor RNA species. <i>FEBS Letters</i> , 1994, 354, 30-36.	1.3	22