Anna Maria D'erchia

List of Publications by Year
in descending order

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	REDIportal: a comprehensive database of A-to-I RNA editing events in humans. Nucleic Acids Research, 2017, 45, D750-D757.	6.5	256
2	BALB/c and C57BL/6 Mice Differ in Polyreactive IgA Abundance, which Impacts the Generation of Antigen-Specific IgA and Microbiota Diversity. Immunity, 2015, 43, 527-540.	6.6	247
3	Profiling RNA editing in human tissues: towards the inosinome Atlas. Scientific Reports, 2015, 5, 14941.	1.6	194
4	SpliceAid-F: a database of human splicing factors and their RNA-binding sites. Nucleic Acids Research, 2013, 41, D125-D131.	6.5	148
5	Tissue-specific mtDNA abundance from exome data and its correlation with mitochondrial transcription, mass and respiratory activity. Mitochondrion, 2015, 20, 13-21.	1.6	146
6	Identification and functional characterization of two new transcriptional variants of the human p63 gene. Nucleic Acids Research, 2009, 37, 6092-6104.	6.5	130
7	Reduced levels of protein recoding by A-to-I RNA editing in Alzheimer's disease. Rna, 2016, 22, 290-302.	1.6	122
8	Whole transcriptome profiling of Late-Onset Alzheimer's Disease patients provides insights into the molecular changes involved in the disease. Scientific Reports, 2018, 8, 4282.	1.6	102
9	Massive transcriptome sequencing of human spinal cord tissues provides new insights into motor neuron degeneration in ALS. Scientific Reports, 2017, 7, 10046.	1.6	99
10	T Follicular Helper Cells Promote a Beneficial Gut Ecosystem for Host Metabolic Homeostasis by Sensing Microbiota-Derived Extracellular ATP. Cell Reports, 2017, 18, 2566-2575.	2.9	87
11	RAP: RNA-Seq Analysis Pipeline, a new cloud-based NGS web application. BMC Genomics, 2015, 16, S3.	1.2	79
12	TRIM8 modulates p53 activity to dictate cell cycle arrest. Cell Cycle, 2012, 11, 511-523.	1.3	78
13	Intestinal microbiota sustains inflammation and autoimmunity induced by hypomorphic *RAG* defects. Journal of Experimental Medicine, 2016, 213, 355-375.	4.2	61
14	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
15	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.	1.2	57
16	p73 and p63 Sustain Cellular Growth by Transcriptional Activation of Cell Cycle Progression Genes. Cancer Research, 2009, 69, 8563-8571.	0.4	51
17	Comparative Genomics of *Listeria* Sensu Lato: Genus-Wide Differences in Evolutionary Dynamics and the Progressive Gain of Complex, Potentially Pathogenicity-Related Traits through Lateral Gene Transfer. Genome Biology and Evolution, 2015, 7, 2154-2172.	1.1	47
18	Profile of microbial communities on carbonate stones of the medieval church of San Leonardo di Siponto (Italy) by Illumina-based deep sequencing. Applied Microbiology and Biotechnology, 2016, 100, 8537-8548.	1.7	47

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19	Epstein-Barr virus genetic variants are associated with multiple sclerosis. Neurology, 2015, 84, 1362-1368.	1.5	44
20	ASPicDB: A database resource for alternative splicing analysis. Bioinformatics, 2008, 24, 1300-1304.	1.8	40
21	ASPicDB: a database of annotated transcript and protein variants generated by alternative splicing. Nucleic Acids Research, 2011, 39, D80-D85.	6.5	38
22	Using REDItools to Detect RNA Editing Events in NGS Datasets. Current Protocols in Bioinformatics, 2015, 49, 12.12.1-12.12.15.	25.8	32
23	Molecular Clock and Gene Function. Journal of Molecular Evolution, 2003, 57, S277-S285.	0.8	31
24	RNA editing signature during myeloid leukemia cell differentiation. Leukemia, 2017, 31, 2824-2832.	3.3	29
25	Targeted next-generation sequencing detects novel gene–phenotype associations and expands the mutational spectrum in cardiomyopathies. PLoS ONE, 2017, 12, e0181842.	1.1	28
26	YAP contributes to DNA methylation remodeling upon mouse embryonic stem cell differentiation. Journal of Biological Chemistry, 2021, 296, 100138.	1.6	25
27	Transcription of rat mitochondrial NADH-dehydrogenase subunits presence of antisense and precursor RNA species. FEBS Letters, 1994, 354, 30-36.	1.3	22
28	Guinea Pig p53 mRNA: Identification of New Elements in Coding and Untranslated Regions and Their Functional and Evolutionary Implications. Genomics, 1999, 58, 50-64.	1.3	20
29	Genome-Wide Analysis of Differentially Expressed Genes and Splicing Isoforms in Clear Cell Renal Cell Carcinoma. PLoS ONE, 2013, 8, e78452.	1.1	19
30	Molecular strategies in Metazoan genomic evolution. Gene, 2002, 300, 195-201.	1.0	18
31	Enrichment of intestinal Lactobacillus by enhanced secretory IgA coating alters glucose homeostasis in P2rx7ˉ/ˉ mice. Scientific Reports, 2019, 9, 9315.	1.6	18
32	Methods for screening tumors for p53 status and therapeutic exploitation. Expert Review of Molecular Diagnostics, 2003, 3, 289-301.	1.5	14
33	Draft genome sequence ofSphingobiumsp. strain ba1, resistant to kanamycin and nickel ions. FEMS Microbiology Letters, 2014, 361, 8-9.	0.7	14
34	Detection of novel transcripts in the human mitochondrial DNA region coding for ATPase8-ATPase6 subunits. FEBS Letters, 1994, 344, 10-14.	1.3	13
35	Campylobacter vulpis sp. nov. isolated from wild red foxes. Systematic and Applied Microbiology, 2021, 44, 126204.	1.2	13
36	Draft genome sequence of Acinetobacter sp. neg1 capable of degrading ochratoxin A. FEMS Microbiology Letters, 2015, 362, .	0.7	12

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37	Detection of Post-Transcriptional RNA Editing Events. Methods in Molecular Biology, 2015, 1269, 189-205.	0.4	10
38	Accurate detection and quantification of SARS-CoV-2 genomic and subgenomic mRNAs by ddPCR and meta-transcriptomics analysis. Communications Biology, 2021, 4, 1215.	2.0	10
39	Accurate quantification of bacterial abundance in metagenomic DNAs accounting for variable DNA integrity levels. Microbial Genomics, 2020, 6, .	1.0	8
40	A platform independent RNA-Seq protocol for the detection of transcriptome complexity. BMC Genomics, 2013, 14, 855.	1.2	7
41	Identification of tumor-associated cassette exons in human cancer through EST-based computational prediction and experimental validation. Molecular Cancer, 2010, 9, 230.	7.9	5
42	Exploring the RNA Editing Potential of RNA-Seq Data by ExpEdit. Methods in Molecular Biology, 2015, 1269, 327-338.	0.4	5
43	ASPicDB: A Database Web Tool for Alternative Splicing Analysis. Methods in Molecular Biology, 2015, 1269, 365-378.	0.4	5
44	VINYL: Variant prIoritizatioN bY survivaL analysis. Bioinformatics, 2021, 36, 5590-5599.	1.8	4
45	No metagenomic evidence of tumorigenic viruses in cancers from a selected cohort of immunosuppressed subjects. Scientific Reports, 2019, 9, 19815.	1.6	3