

# Ernesto Picardi

## List of Publications by Citations

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**Version:** 2024-04-20

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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.

87  
papers

2,867  
citations

31  
h-index

51  
g-index

101  
ext. papers

3,686  
ext. citations

6.5  
avg, IF

5.38  
L-index

#	Paper	IF	Citations
87	UTRdb and UTRsite (RELEASE 2010): a collection of sequences and regulatory motifs of the untranslated regions of eukaryotic mRNAs. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, D75-80	20.1	247
86	REDIportal: a comprehensive database of A-to-I RNA editing events in humans. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, D750-D757	20.1	166
85	REDItools: high-throughput RNA editing detection made easy. <i>Bioinformatics</i> , <b>2013</b> , 29, 1813-4	7.2	157
84	Profiling RNA editing in human tissues: towards the inosinome Atlas. <i>Scientific Reports</i> , <b>2015</b> , 5, 14941	4.9	137
83	MToolBox: a highly automated pipeline for heteroplasmy annotation and prioritization analysis of human mitochondrial variants in high-throughput sequencing. <i>Bioinformatics</i> , <b>2014</b> , 30, 3115-7	7.2	132
82	Bioinformatics approaches for genomics and post genomics applications of next-generation sequencing. <i>Briefings in Bioinformatics</i> , <b>2010</b> , 11, 181-97	13.4	120
81	Large-scale detection and analysis of RNA editing in grape mtDNA by RNA deep-sequencing. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, 4755-67	20.1	117
80	Tissue-specific mtDNA abundance from exome data and its correlation with mitochondrial transcription, mass and respiratory activity. <i>Mitochondrion</i> , <b>2015</b> , 20, 13-21	4.9	94
79	Mitochondrial genomes gleaned from human whole-exome sequencing. <i>Nature Methods</i> , <b>2012</b> , 9, 523-4	21.6	87
78	SpliceAid-F: a database of human splicing factors and their RNA-binding sites. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, D125-31	20.1	87
77	Reduced levels of protein recoding by A-to-I RNA editing in Alzheimer's disease. <i>Rna</i> , <b>2016</b> , 22, 290-302	5.8	77
76	Phylogenetic comparison of huntingtin homologues reveals the appearance of a primitive polyQ in sea urchin. <i>Molecular Biology and Evolution</i> , <b>2008</b> , 25, 330-8	8.3	65
75	Massive transcriptome sequencing of human spinal cord tissues provides new insights into motor neuron degeneration in ALS. <i>Scientific Reports</i> , <b>2017</b> , 7, 10046	4.9	59
74	RAP: RNA-Seq Analysis Pipeline, a new cloud-based NGS web application. <i>BMC Genomics</i> , <b>2015</b> , 16, S3	4.5	58
73	<i>Lactobacillus rossiae</i> , a vitamin B12 producer, represents a metabolically versatile species within the Genus <i>Lactobacillus</i> . <i>PLoS ONE</i> , <b>2014</b> , 9, e107232	3.7	50
72	Whole transcriptome profiling of Late-Onset Alzheimer's Disease patients provides insights into the molecular changes involved in the disease. <i>Scientific Reports</i> , <b>2018</b> , 8, 4282	4.9	46
71	Differences in gene expression and cytokine release profiles highlight the heterogeneity of distinct subsets of adipose tissue-derived stem cells in the subcutaneous and visceral adipose tissue in humans. <i>PLoS ONE</i> , <b>2013</b> , 8, e57892	3.7	46

70	Single-cell transcriptomics reveals specific RNA editing signatures in the human brain. <i>Rna</i> , <b>2017</b> , 23, 860-865	5.8	45
69	REDIdb: the RNA editing database. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, D173-7	20.1	45
68	The influence of invasive jellyfish blooms on the aquatic microbiome in a coastal lagoon (Varano, SE Italy) detected by an Illumina-based deep sequencing strategy. <i>Biological Invasions</i> , <b>2015</b> , 17, 923-940	2.7	43
67	Elucidating the editome: bioinformatics approaches for RNA editing detection. <i>Briefings in Bioinformatics</i> , <b>2019</b> , 20, 436-447	13.4	43
66	MitoZoa: a curated mitochondrial genome database of metazoans for comparative genomics studies. <i>Mitochondrion</i> , <b>2010</b> , 10, 192-9	4.9	41
65	WEP: a high-performance analysis pipeline for whole-exome data. <i>BMC Bioinformatics</i> , <b>2013</b> , 14 Suppl 7, S11	3.6	38
64	ASPicDB: a database resource for alternative splicing analysis. <i>Bioinformatics</i> , <b>2008</b> , 24, 1300-4	7.2	36
63	Investigating RNA editing in deep transcriptome datasets with REDIttools and REDIportal. <i>Nature Protocols</i> , <b>2020</b> , 15, 1098-1131	18.8	35
62	A high resolution A-to-I editing map in the mouse identifies editing events controlled by pre-mRNA splicing. <i>Genome Research</i> , <b>2019</b> , 29, 1453-1463	9.7	35
61	ASPicDB: a database of annotated transcript and protein variants generated by alternative splicing. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, D80-5	20.1	35
60	Uncovering RNA Editing Sites in Long Non-Coding RNAs. <i>Frontiers in Bioengineering and Biotechnology</i> , <b>2014</b> , 2, 64	5.8	34
59	Computational methods for ab initio and comparative gene finding. <i>Methods in Molecular Biology</i> , <b>2010</b> , 609, 269-84	1.4	33
58	Dynamic inosinome profiles reveal novel patient stratification and gender-specific differences in glioblastoma. <i>Genome Biology</i> , <b>2019</b> , 20, 33	18.3	32
57	Epstein-Barr virus genetic variants are associated with multiple sclerosis. <i>Neurology</i> , <b>2015</b> , 84, 1362-8	6.5	29
56	ExpEdit: a webserver to explore human RNA editing in RNA-Seq experiments. <i>Bioinformatics</i> , <b>2011</b> , 27, 1311-2	7.2	24
55	Using REDIttools to Detect RNA Editing Events in NGS Datasets. <i>Current Protocols in Bioinformatics</i> , <b>2015</b> , 49, 12.12.1-12.12.15	24.2	23
54	RNEntropy: an entropy-based tool for the detection of significant variation of gene expression across multiple RNA-Seq experiments. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, e46	20.1	23
53	Geographic Population Structure in Epstein-Barr Virus Revealed by Comparative Genomics. <i>Genome Biology and Evolution</i> , <b>2016</b> , 8, 3284-3291	3.9	23

52	Detecting alternative gene structures from spliced ESTs: a computational approach. <i>Journal of Computational Biology</i> , <b>2009</b> , 16, 43-66	1.7	22
51	Transcriptional Analysis of sp. Capable of Degrading Ochratoxin A. <i>Frontiers in Microbiology</i> , <b>2016</b> , 7, 2162	5.7	21
50	Rhodobacter sphaeroides adaptation to high concentrations of cobalt ions requires energetic metabolism changes. <i>FEMS Microbiology Ecology</i> , <b>2014</b> , 88, 345-57	4.3	20
49	REDIportal: millions of novel A-to-I RNA editing events from thousands of RNAseq experiments. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, D1012-D1019	20.1	19
48	RNA editing in plants: A comprehensive survey of bioinformatics tools and databases. <i>Plant Physiology and Biochemistry</i> , <b>2019</b> , 137, 53-61	5.4	18
47	REDIdb: an upgraded bioinformatics resource for organellar RNA editing sites. <i>Mitochondrion</i> , <b>2011</b> , 11, 360-5	4.9	18
46	The cell line A-to-I RNA editing catalogue. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, 5849-5858	20.1	17
45	RNA editing signature during myeloid leukemia cell differentiation. <i>Leukemia</i> , <b>2017</b> , 31, 2824-2832	10.7	16
44	REDIdb 3.0: A Comprehensive Collection of RNA Editing Events in Plant Organellar Genomes. <i>Frontiers in Plant Science</i> , <b>2018</b> , 9, 482	6.2	16
43	A novel computational strategy to identify A-to-I RNA editing sites by RNA-Seq data: de novo detection in human spinal cord tissue. <i>PLoS ONE</i> , <b>2012</b> , 7, e44184	3.7	15
42	RNA editing has been lost in the mitochondrial cox3 and rps13 mRNAs in Asparagales. <i>Biochimie</i> , <b>2007</b> , 89, 159-67	4.6	15
41	A novel additional group II intron distinguishes the mitochondrial rps3 gene in gymnosperms. <i>Journal of Molecular Evolution</i> , <b>2005</b> , 60, 196-206	3.1	15
40	Genome-wide analysis of differentially expressed genes and splicing isoforms in clear cell renal cell carcinoma. <i>PLoS ONE</i> , <b>2013</b> , 8, e78452	3.7	14
39	A polygalacturonase-inhibiting protein with a role in pea defence against the cyst nematode <i>Heterodera goettingiana</i> . <i>Molecular Plant Pathology</i> , <b>2011</b> , 12, 275-87	5.7	14
38	CoVaCS: a consensus variant calling system. <i>BMC Genomics</i> , <b>2018</b> , 19, 120	4.5	14
37	Changes in gene expression and metabolic profile of drupes of <i>Olea europaea</i> L. cv Carolea in relation to maturation stage and cultivation area. <i>BMC Plant Biology</i> , <b>2019</b> , 19, 428	5.3	12
36	Quantifying RNA Editing in Deep Transcriptome Datasets. <i>Frontiers in Genetics</i> , <b>2020</b> , 11, 194	4.5	11
35	EasyCluster: a fast and efficient gene-oriented clustering tool for large-scale transcriptome data. <i>BMC Bioinformatics</i> , <b>2009</b> , 10 Suppl 6, S10	3.6	11

34	Detection of A-to-I RNA Editing in SARS-COV-2.. <i>Genes</i> , <b>2021</b> , 13,	4.2	11
33	Molecular characterization and functional analysis of four E1,4-endoglucanases from the root-lesion nematode <i>Pratylenchus vulnus</i> . <i>Plant Pathology</i> , <b>2014</b> , 63, 1436-1445	2.8	9
32	Striking differences in RNA editing requirements to express the rps4 gene in magnolia and sunflower mitochondria. <i>Gene</i> , <b>2002</b> , 286, 33-41	3.8	9
31	Plntron: a fast method for detecting the gene structure due to alternative splicing via maximal pairings of a pattern and a text. <i>BMC Bioinformatics</i> , <b>2012</b> , 13 Suppl 5, S2	3.6	8
30	HPC-REDIttools: a novel HPC-aware tool for improved large scale RNA-editing analysis. <i>BMC Bioinformatics</i> , <b>2020</b> , 21, 353	3.6	8
29	Transcriptomic analysis of nickel exposure in <i>Sphingobium</i> sp. ba1 cells using RNA-seq. <i>Scientific Reports</i> , <b>2017</b> , 7, 8262	4.9	7
28	EdiPy: a resource to simulate the evolution of plant mitochondrial genes under the RNA editing. <i>Computational Biology and Chemistry</i> , <b>2006</b> , 30, 77-80	3.6	7
27	Detection of post-transcriptional RNA editing events. <i>Methods in Molecular Biology</i> , <b>2015</b> , 1269, 189-205	1.4	7
26	Investigating Human Mitochondrial Genomes in Single Cells. <i>Genes</i> , <b>2020</b> , 11,	4.2	6
25	ASPic-GenelD: a lightweight pipeline for gene prediction and alternative isoforms detection. <i>BioMed Research International</i> , <b>2013</b> , 2013, 502827	3	6
24	BCR/ABL1 fusion transcripts generated from alternative splicing: implications for future targeted therapies in Ph+ leukaemias. <i>Current Molecular Medicine</i> , <b>2012</b> , 12, 547-65	2.5	6
23	ELIXIR-IT HPC@CINECA: high performance computing resources for the bioinformatics community. <i>BMC Bioinformatics</i> , <b>2020</b> , 21, 352	3.6	6
22	A-GAME: improving the assembly of pooled functional metagenomics sequence data. <i>BMC Genomics</i> , <b>2018</b> , 19, 44	4.5	6
21	A platform independent RNA-Seq protocol for the detection of transcriptome complexity. <i>BMC Genomics</i> , <b>2013</b> , 14, 855	4.5	4
20	Is plant mitochondrial RNA editing a source of phylogenetic incongruence? An answer from in silico and in vivo data sets. <i>BMC Bioinformatics</i> , <b>2008</b> , 9 Suppl 2, S14	3.6	4
19	Critical assessment of bioinformatics methods for the characterization of pathological repeat expansions with single-molecule sequencing data. <i>Briefings in Bioinformatics</i> , <b>2020</b> , 21, 1971-1986	13.4	4
18	In <i>Arabidopsis thaliana</i> Cd differentially impacts on hormone genetic pathways in the methylation defective ddc mutant compared to wild type. <i>Scientific Reports</i> , <b>2021</b> , 11, 10965	4.9	4
17	EasyCluster2: an improved tool for clustering and assembling long transcriptome reads. <i>BMC Bioinformatics</i> , <b>2014</b> , 15 Suppl 15, S7	3.6	3

16	Exploring the RNA editing potential of RNA-Seq data by ExpEdit. <i>Methods in Molecular Biology</i> , <b>2015</b> , 1269, 327-38	1.4	3
15	ASPicDB: a database web tool for alternative splicing analysis. <i>Methods in Molecular Biology</i> , <b>2015</b> , 1269, 365-78	1.4	3
14	HPC-REDIttools: a Novel HPC-aware Tool for Improved Large Scale RNA-editing Analysis		3
13	High-Throughput Sequencing to Detect DNA-RNA Changes. <i>Methods in Molecular Biology</i> , <b>2021</b> , 2181, 193-212	1.4	3
12	A Machine Learning Approach to Parkinson's Disease Blood Transcriptomics. <i>Genes</i> , <b>2022</b> , 13, 727	4.2	3
11	An improved procedure for clustering and assembly of large transcriptome data. <i>EMBnet Journal</i> , <b>2012</b> , 18, 134	2.3	2
10	A Novel Approach to Clustering and Assembly of Large-Scale Roche 454 Transcriptome Data for Gene Validation and Alternative Splicing Analysis. <i>Lecture Notes in Computer Science</i> , <b>2012</b> , 641-648	0.9	2
9	A-to-I RNA editing in SARS-COV-2: real or artifact?		2
8	Transcriptome assembly and alternative splicing analysis. <i>Methods in Molecular Biology</i> , <b>2015</b> , 1269, 173-88		1
7	Clustering and Assembling Large Transcriptome Datasets by EasyCluster2. <i>Communications in Computer and Information Science</i> , <b>2013</b> , 231-236	0.3	1
6	Databases for RNA Editing Collections. <i>Methods in Molecular Biology</i> , <b>2021</b> , 2284, 467-480	1.4	1
5	A primer on machine learning techniques for genomic applications. <i>Computational and Structural Biotechnology Journal</i> , <b>2021</b> , 19, 4345-4359	6.8	1
4	RNA Editing Detection in HPC Infrastructures. <i>Methods in Molecular Biology</i> , <b>2021</b> , 2284, 253-270	1.4	1
3	Bioinformatics Resources for RNA Editing. <i>Methods in Molecular Biology</i> , <b>2021</b> , 2181, 177-191	1.4	1
2	New Tools for Expression Alternative Splicing Validation. <i>Communications in Computer and Information Science</i> , <b>2010</b> , 222-231	0.3	
1	RAP: A Web Tool for RNA-Seq Data Analysis. <i>Methods in Molecular Biology</i> , <b>2021</b> , 2284, 393-415	1.4	