

# Mihaela Pertea

## List of Publications by Year in Descending Order

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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.

35  
papers

13,138  
citations

19  
h-index

41  
g-index

41  
ext. papers

19,225  
ext. citations

16  
avg, IF

6.45  
L-index

#	Paper	IF	Citations
35	Reducing Capsular Contracture Formation in Breast Augmentation with Silicone Implants: Experimental Study on Rats. <i>Applied Sciences (Switzerland)</i> , <b>2022</b> , 12, 4056	2.6	
34	Schwannoma of the Upper Limb: Retrospective Study of a Rare Tumor with Uncommon Locations. <i>Diagnostics</i> , <b>2022</b> , 12, 1319	3.8	1
33	Omega plate for the treatment of acetabular fractures involving the quadrilateral plate. <i>Experimental and Therapeutic Medicine</i> , <b>2021</b> , 22, 1064	2.1	1
32	Efficiency of Bromelain-Enriched Enzyme Mixture (NexoBrid) in the Treatment of Burn Wounds. <i>Applied Sciences (Switzerland)</i> , <b>2021</b> , 11, 8134	2.6	2
31	GFF Utilities: GffRead and GffCompare. <i>F1000Research</i> , <b>2020</b> , 9, 304	3.6	185
30	New insights into human hair: SAXS, SEM, TEM and EDX for Alopecia Areata investigations. <i>PeerJ</i> , <b>2020</b> , 8, e8376	3.1	3
29	Effectiveness and Safety of Wide Awake Local Anesthesia no Tourniquet (WALANT) Technique in Hand Surgery. <i>Revista De Chimie (discontinued)</i> , <b>2019</b> , 70, 3587-3591	1.8	4
28	Study on Epinephrine Used in Local Anesthesia Controversy and certainty. <i>Revista De Chimie (discontinued)</i> , <b>2018</b> , 69, 169-171	1.8	4
27	Defective HIV-1 Proviruses Are Expressed and Can Be Recognized by Cytotoxic T Lymphocytes, which Shape the Proviral Landscape. <i>Cell Host and Microbe</i> , <b>2017</b> , 21, 494-506.e4	23.4	176
26	Transcript-level expression analysis of RNA-seq experiments with HISAT, StringTie and Ballgown. <i>Nature Protocols</i> , <b>2016</b> , 11, 1650-67	18.8	2264
25	Genome-wide annotation of microRNA primary transcript structures reveals novel regulatory mechanisms. <i>Genome Research</i> , <b>2015</b> , 25, 1401-9	9.7	62
24	Broad CTL response is required to clear latent HIV-1 due to dominance of escape mutations. <i>Nature</i> , <b>2015</b> , 517, 381-5	50.4	377
23	StringTie enables improved reconstruction of a transcriptome from RNA-seq reads. <i>Nature Biotechnology</i> , <b>2015</b> , 33, 290-5	44.5	3679
22	DIAMUND: direct comparison of genomes to detect mutations. <i>Human Mutation</i> , <b>2014</b> , 35, 283-8	4.7	6
21	The human transcriptome: an unfinished story. <i>Genes</i> , <b>2012</b> , 3, 344-60	4.2	80
20	Detection of lineage-specific evolutionary changes among primate species. <i>BMC Bioinformatics</i> , <b>2011</b> , 12, 274	3.6	15
19	Do-it-yourself genetic testing. <i>Genome Biology</i> , <b>2010</b> , 11, 404	18.3	12

18	OperonDB: a comprehensive database of predicted operons in microbial genomes. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, D479-82	20.1	75
17	Sim4cc: a cross-species spliced alignment program. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, e80	20.1	14
16	The genome of the blood fluke <i>Schistosoma mansoni</i> . <i>Nature</i> , <b>2009</b> , 460, 352-8	50.4	822
15	Automated eukaryotic gene structure annotation using EVIDENCEModeler and the Program to Assemble Spliced Alignments. <i>Genome Biology</i> , <b>2008</b> , 9, R7	18.3	1212
14	Genome sequence of <i>Aedes aegypti</i> , a major arbovirus vector. <i>Science</i> , <b>2007</b> , 316, 1718-23	33.3	867
13	A computational survey of candidate exonic splicing enhancer motifs in the model plant <i>Arabidopsis thaliana</i> . <i>BMC Bioinformatics</i> , <b>2007</b> , 8, 159	3.6	60
12	Draft genome sequence of the sexually transmitted pathogen <i>Trichomonas vaginalis</i> . <i>Science</i> , <b>2007</b> , 315, 207-12	33.3	622
11	Draft genome of the filarial nematode parasite <i>Brugia malayi</i> . <i>Science</i> , <b>2007</b> , 317, 1756-60	33.3	513
10	Using Protein Domains to Improve the Accuracy of Ab Initio Gene Finding. <i>Lecture Notes in Computer Science</i> , <b>2007</b> , 208-215	0.9	
9	Genomic sequence of the pathogenic and allergenic filamentous fungus <i>Aspergillus fumigatus</i> . <i>Nature</i> , <b>2005</b> , 438, 1151-6	50.4	1114
8	Insight into the genome of <i>Aspergillus fumigatus</i> : analysis of a 922 kb region encompassing the nitrate assimilation gene cluster. <i>Fungal Genetics and Biology</i> , <b>2004</b> , 41, 443-53	3.9	50
7	Sequence of <i>Plasmodium falciparum</i> chromosomes 2, 10, 11 and 14. <i>Nature</i> , <b>2002</b> , 419, 531-4	50.4	146
6	Genome sequence and comparative analysis of the model rodent malaria parasite <i>Plasmodium yoelii yoelii</i> . <i>Nature</i> , <b>2002</b> , 419, 512-9	50.4	591
5	Using GlimmerM to find genes in eukaryotic genomes. <i>Current Protocols in Bioinformatics</i> , <b>2002</b> , Chapter 4, Unit 4.4	24.2	4
4	Computational gene finding in plants <b>2002</b> , 39-48		1
3	A Method to Improve the Performance of Translation Start Site Detection and Its Application for Gene Finding. <i>Lecture Notes in Computer Science</i> , <b>2002</b> , 210-219	0.9	5
2	Genomics of <i>Theileria Parva</i> . <i>World Class Parasites</i> , <b>2002</b> , 85-92		1
1	Interpolated Markov models for eukaryotic gene finding. <i>Genomics</i> , <b>1999</b> , 59, 24-31	4.3	163

