

Mihaela Pertea

List of Publications by Year in descending order

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Version: 2024-02-01

40
papers

23,071
citations

394421

19
h-index

330143

37
g-index

41
all docs

41
docs citations

41
times ranked

32561
citing authors

#	ARTICLE	IF	CITATIONS
1	Pain Intensity and Degree of Disability after Fragility Fractures of the Pelvis. <i>Medicina (Lithuania)</i> , 2022, 58, 477.	2.0	2
2	Reducing Capsular Contracture Formation in Breast Augmentation with Silicone Implants: Experimental Study on Rats. <i>Applied Sciences (Switzerland)</i> , 2022, 12, 4056.	2.5	1
3	Schwannoma of the Upper Limb: Retrospective Study of a Rare Tumor with Uncommon Locations. <i>Diagnostics</i> , 2022, 12, 1319.	2.6	2
4	Raman Spectroscopy, X-ray Diffraction, and Scanning Electron Microscopy as Noninvasive Methods for Microstructural Alterations in Psoriatic Nails. <i>Molecules</i> , 2021, 26, 280.	3.8	5
5	Omega plate for the treatment of acetabular fractures involving the quadrilateral plate. <i>Experimental and Therapeutic Medicine</i> , 2021, 22, 1064.	1.8	5
6	Efficiency of Bromelain-Enriched Enzyme Mixture (NexoBrid®, [®]) in the Treatment of Burn Wounds. <i>Applied Sciences (Switzerland)</i> , 2021, 11, 8134.	2.5	8
7	Mechanical Testing Following the Application of Polymers on Different Types of Screws Used to Fix Osteoporotic Bone. , 2021, , .		0
8	GFF Utilities: GffRead and GffCompare. <i>F1000Research</i> , 2020, 9, 304.	1.6	579
9	New insights into human hair: SAXS, SEM, TEM and EDX for Alopecia Areata investigations. <i>PeerJ</i> , 2020, 8, e8376.	2.0	7
10	Effectiveness and Safety of Wide Awake Local Anesthesia no Tourniquet (WALANT) Technique in Hand Surgery. <i>Revista De Chimie (discontinued)</i> , 2019, 70, 3587-3591.	0.4	10
11	Efficacy of Negative Pressure Therapy (NPWT) in the Management of Wounds of Different Etiologies. <i>Revista De Chimie (discontinued)</i> , 2018, 69, 1980-1986.	0.4	3
12	Study on Epinephrine Used in Local Anesthesia Controversy and certainty. <i>Revista De Chimie (discontinued)</i> , 2018, 69, 169-171.	0.4	9
13	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> , 2017, 21, 494-506.e4.	11.0	289
14	Transcript-level expression analysis of RNA-seq experiments with HISAT, StringTie and Ballgown. <i>Nature Protocols</i> , 2016, 11, 1650-1667.	12.0	4,743
15	Broad CTL response is required to clear latent HIV-1 due to dominance of escape mutations. <i>Nature</i> , 2015, 517, 381-385.	27.8	469
16	StringTie enables improved reconstruction of a transcriptome from RNA-seq reads. <i>Nature Biotechnology</i> , 2015, 33, 290-295.	17.5	8,385
17	Genome-wide annotation of microRNA primary transcript structures reveals novel regulatory mechanisms. <i>Genome Research</i> , 2015, 25, 1401-1409.	5.5	91
18	DIAMUND : Direct Comparison of Genomes to Detect Mutations. <i>Human Mutation</i> , 2014, 35, 283-288.	2.5	9

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19	The Human Transcriptome: An Unfinished Story. <i>Genes</i> , 2012, 3, 344-360.	2.4	121
20	Detection of lineage-specific evolutionary changes among primate species. <i>BMC Bioinformatics</i> , 2011, 12, 274.	2.6	19
21	Do-it-yourself genetic testing. <i>Genome Biology</i> , 2010, 11, 404.	8.8	16
22	OperonDB: a comprehensive database of predicted operons in microbial genomes. <i>Nucleic Acids Research</i> , 2009, 37, D479-D482.	14.5	83
23	Sim4cc: a cross-species spliced alignment program. <i>Nucleic Acids Research</i> , 2009, 37, e80-e80.	14.5	16
24	The genome of the blood fluke <i>Schistosoma mansoni</i> . <i>Nature</i> , 2009, 460, 352-358.	27.8	945
25	Automated eukaryotic gene structure annotation using EvidenceModeler and the Program to Assemble Spliced Alignments. <i>Genome Biology</i> , 2008, 9, R7.	9.6	2,484
26	Draft Genome Sequence of the Sexually Transmitted Pathogen <i>Trichomonas vaginalis</i> . <i>Science</i> , 2007, 315, 207-212.	12.6	731
27	Draft Genome of the Filarial Nematode Parasite <i>Brugia malayi</i> . <i>Science</i> , 2007, 317, 1756-1760.	12.6	571
28	Genome Sequence of <i>Aedes aegypti</i> , a Major Arbovirus Vector. <i>Science</i> , 2007, 316, 1718-1723.	12.6	1,025
29	A computational survey of candidate exonic splicing enhancer motifs in the model plant <i>Arabidopsis thaliana</i> . <i>BMC Bioinformatics</i> , 2007, 8, 159.	2.6	81
30	Using Protein Domains to Improve the Accuracy of Ab Initio Gene Finding. <i>Lecture Notes in Computer Science</i> , 2007, , 208-215.	1.3	0
31	Genomic sequence of the pathogenic and allergenic filamentous fungus <i>Aspergillus fumigatus</i> . <i>Nature</i> , 2005, 438, 1151-1156.	27.8	1,272
32	Searching for genes and biologically related signals in DNA sequences. , 2005, , .		0
33	Insight into the genome of <i>Aspergillus fumigatus</i> : analysis of a 922kb region encompassing the nitrate assimilation gene cluster. <i>Fungal Genetics and Biology</i> , 2004, 41, 443-453.	2.1	55
34	Using GlimmerM to Find Genes in Eukaryotic Genomes. <i>Current Protocols in Bioinformatics</i> , 2003, 00, Unit 4.4.	25.8	5
35	Sequence of <i>Plasmodium falciparum</i> chromosomes 2, 10, 11 and 14. <i>Nature</i> , 2002, 419, 531-534.	27.8	167
36	Genome sequence and comparative analysis of the model rodent malaria parasite <i>Plasmodium yoelii yoelii</i> . <i>Nature</i> , 2002, 419, 512-519.	27.8	666

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37	A Method to Improve the Performance of Translation Start Site Detection and Its Application for Gene Finding. Lecture Notes in Computer Science, 2002, , 210-219.	1.3	6
38	Genomics of Theileria Parva. World Class Parasites, 2002, , 85-92.	0.3	1
39	Computational gene finding in plants. , 2002, , 39-48.		1
40	Interpolated Markov Models for Eukaryotic Gene Finding. Genomics, 1999, 59, 24-31.	2.9	184