

Mihaela Pertea

List of Publications by Year in descending order

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Version: 2024-02-01

52
papers

30,301
citations

117625

34
h-index

197818

49
g-index

60
all docs

60
docs citations

60
times ranked

37782
citing authors

#	ARTICLE	IF	CITATIONS
1	StringTie enables improved reconstruction of a transcriptome from RNA-seq reads. <i>Nature Biotechnology</i> , 2015, 33, 290-295.	17.5	8,385
2	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
3	Genome sequence of the human malaria parasite <i>Plasmodium falciparum</i> . <i>Nature</i> , 2002, 419, 498-511.	27.8	3,881
4	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
5	Genomic sequence of the pathogenic and allergenic filamentous fungus <i>Aspergillus fumigatus</i> . <i>Nature</i> , 2005, 438, 1151-1156.	27.8	1,272
6	Genome Sequence of <i>Aedes aegypti</i> , a Major Arbovirus Vector. <i>Science</i> , 2007, 316, 1718-1723.	12.6	1,025
7	The genome of the blood fluke <i>Schistosoma mansoni</i> . <i>Nature</i> , 2009, 460, 352-358.	27.8	945
8	Transcriptome assembly from long-read RNA-seq alignments with StringTie2. <i>Genome Biology</i> , 2019, 20, 278.	8.8	897
9	Draft Genome Sequence of the Sexually Transmitted Pathogen <i>Trichomonas vaginalis</i> . <i>Science</i> , 2007, 315, 207-212.	12.6	731
10	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
11	GFF Utilities: GffRead and GffCompare. <i>F1000Research</i> , 2020, 9, 304.	1.6	579
12	Draft Genome of the Filarial Nematode Parasite <i>Brugia malayi</i> . <i>Science</i> , 2007, 317, 1756-1760.	12.6	571
13	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
14	GFF Utilities: GffRead and GffCompare. <i>F1000Research</i> , 2020, 9, 304.	1.6	469
15	Chromosome Sequence of the Human Malaria Parasite <i>Plasmodium falciparum</i> . , 1998, 282, 1126-1132.		419
16	Genome Sequence of <i>Theileria parva</i> , a Bovine Pathogen That Transforms Lymphocytes. <i>Science</i> , 2005, 309, 134-137.	12.6	309
17	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
18	CHESS: a new human gene catalog curated from thousands of large-scale RNA sequencing experiments reveals extensive transcriptional noise. <i>Genome Biology</i> , 2018, 19, 208.	8.8	263

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19	Interpolated Markov Models for Eukaryotic Gene Finding. <i>Genomics</i> , 1999, 59, 24-31.	2.9	184
20	Between a chicken and a grape: estimating the number of human genes. <i>Genome Biology</i> , 2010, 11, 206.	9.6	182
21	Sequence of Plasmodium falciparum chromosomes 2, 10, 11 and 14. <i>Nature</i> , 2002, 419, 531-534.	27.8	167
22	The Human Transcriptome: An Unfinished Story. <i>Genes</i> , 2012, 3, 344-360.	2.4	121
23	Human contamination in bacterial genomes has created thousands of spurious proteins. <i>Genome Research</i> , 2019, 29, 954-960.	5.5	111
24	Computational Gene Prediction Using Multiple Sources of Evidence. <i>Genome Research</i> , 2003, 14, 142-148.	5.5	110
25	Improved transcriptome assembly using a hybrid of long and short reads with StringTie. <i>PLoS Computational Biology</i> , 2022, 18, e1009730.	3.2	94
26	Genome-wide annotation of microRNA primary transcript structures reveals novel regulatory mechanisms. <i>Genome Research</i> , 2015, 25, 1401-1409.	5.5	91
27	OperonDB: a comprehensive database of predicted operons in microbial genomes. <i>Nucleic Acids Research</i> , 2009, 37, D479-D482.	14.5	83
28	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
29	Single-cell transcriptional landscapes reveal HIV-1-driven aberrant host gene transcription as a potential therapeutic target. <i>Science Translational Medicine</i> , 2020, 12, .	12.4	75
30	JIGSAW, GeneZilla, and GlimmerHMM: puzzling out the features of human genes in the ENCODE regions. <i>Genome Biology</i> , 2006, 7, S9.	9.6	61
31	GlimmerM, Exonomy and Unveil: three ab initio eukaryotic genefinders. <i>Nucleic Acids Research</i> , 2003, 31, 3601-3604.	14.5	60
32	Rapid detection of inter-clade recombination in SARS-CoV-2 with Bolotie. <i>Genetics</i> , 2021, 218, .	2.9	58
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	Rice Bioinformatics. Analysis of Rice Sequence Data and Leveraging the Data to Other Plant Species. <i>Plant Physiology</i> , 2001, 125, 1166-1174.	4.8	46
35	Assembly and annotation of an Ashkenazi human reference genome. <i>Genome Biology</i> , 2020, 21, 129.	8.8	42
36	Computational gene finding in plants. <i>Plant Molecular Biology</i> , 2002, 48, 39-48.	3.9	41

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37	Efficient decoding algorithms for generalized hidden Markov model gene finders. BMC Bioinformatics, 2005, 6, 16.	2.6	34
38	Detection of lineage-specific evolutionary changes among primate species. BMC Bioinformatics, 2011, 12, 274.	2.6	19
39	Finding genes in Plasmodium falciparum. Nature, 2000, 404, 34-34.	27.8	18
40	Sim4cc: a cross-species spliced alignment program. Nucleic Acids Research, 2009, 37, e80-e80.	14.5	16
41	Effects of transcriptional noise on estimates of gene and transcript expression in RNA sequencing experiments. Genome Research, 2021, 31, 301-308.	5.5	13
42	Computational gene finding in plants. Plant Molecular Biology, 2002, 48, 39-48.	3.9	12
43	DIAMUND : Direct Comparison of Genomes to Detect Mutations. Human Mutation, 2014, 35, 283-288.	2.5	9
44	TieBrush: an efficient method for aggregating and summarizing mapped reads across large datasets. Bioinformatics, 2021, 37, 3650-3651.	4.1	9
45	A reference-quality, fully annotated genome from a Puerto Rican individual. Genetics, 2022, 220, .	2.9	7
46	Temozolomide-induced guanine mutations create exploitable vulnerabilities of guanine-rich DNA and RNA regions in drug-resistant gliomas. Science Advances, 2022, 8, .	10.3	7
47	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
48	Using GlimmerM to Find Genes in Eukaryotic Genomes. Current Protocols in Bioinformatics, 2003, 00, Unit 4.4.	25.8	5
49	Genomics of Theileria Parva. World Class Parasites, 2002, , 85-92.	0.3	1
50	Computational gene finding in plants. , 2002, , 39-48.		1
51	Searching for genes and biologically related signals in DNA sequences. , 2005, , .		0
52	Problems and Solutions in Biological Sequence Analysis * Mark Borodovsky, Svetlana Ekisheva. Briefings in Bioinformatics, 2008, 9, 550-551.	6.5	0