Mihaela Pertea

List of Publications by Year
in descending order

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	A reference-quality, fully annotated genome from a Puerto Rican individual. Genetics, 2022, 220, .	2.9	7
2	Improved transcriptome assembly using a hybrid of long and short reads with StringTie. PLoS Computational Biology, 2022, 18, e1009730.	3.2	94
3	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
4	Effects of transcriptional noise on estimates of gene and transcript expression in RNA sequencing experiments. Genome Research, 2021, 31, 301-308.	5.5	13
5	TieBrush: an efficient method for aggregating and summarizing mapped reads across large datasets. Bioinformatics, 2021, 37, 3650-3651.	4.1	9
6	Rapid detection of inter-clade recombination in SARS-CoV-2 with Bolotie. Genetics, 2021, 218, .	2.9	58
7	Single-cell transcriptional landscapes reveal HIV-1â€"driven aberrant host gene transcription as a potential therapeutic target. Science Translational Medicine, 2020, 12, .	12.4	75
8	Assembly and annotation of an Ashkenazi human reference genome. Genome Biology, 2020, 21, 129.	8.8	42
9	GFF Utilities: GffRead and GffCompare. F1000Research, 2020, 9, 304.	1.6	579
10	GFF Utilities: GffRead and GffCompare. F1000Research, 2020, 9, 304.	1.6	469
11	Human contamination in bacterial genomes has created thousands of spurious proteins. Genome Research, 2019, 29, 954-960.	5.5	111
12	Transcriptome assembly from long-read RNA-seq alignments with StringTie2. Genome Biology, 2019, 20, 278.	8.8	897
13	CHESS: a new human gene catalog curated from thousands of large-scale RNA sequencing experiments reveals extensive transcriptional noise. Genome Biology, 2018, 19, 208.	8.8	263
14	Defective HIV-1 Proviruses Are Expressed and Can Be Recognized by Cytotoxic T Lymphocytes, which Shape the Proviral Landscape. Cell Host and Microbe, 2017, 21, 494-506.e4.	11.0	289
15	Transcript-level expression analysis of RNA-seq experiments with HISAT, StringTie and Ballgown. Nature Protocols, 2016, 11, 1650-1667.	12.0	4,743
16	Broad CTL response is required to clear latent HIV-1 due to dominance of escape mutations. Nature, 2015, 517, 381-385.	27.8	469
17	StringTie enables improved reconstruction of a transcriptome from RNA-seq reads. Nature Biotechnology, 2015, 33, 290-295.	17.5	8,385
18	Genome-wide annotation of microRNA primary transcript structures reveals novel regulatory mechanisms. Genome Research, 2015, 25, 1401-1409.	5.5	91

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19	DIAMUND : Direct Comparison of Genomes to Detect Mutations. Human Mutation, 2014, 35, 283-288.	2.5	9
20	The Human Transcriptome: An Unfinished Story. Genes, 2012, 3, 344-360.	2.4	121
21	Detection of lineage-specific evolutionary changes among primate species. BMC Bioinformatics, 2011, 12, 274.	2.6	19
22	Between a chicken and a grape: estimating the number of human genes. Genome Biology, 2010, 11, 206.	9.6	182
23	OperonDB: a comprehensive database of predicted operons in microbial genomes. Nucleic Acids Research, 2009, 37, D479-D482.	14.5	83
24	Sim4cc: a cross-species spliced alignment program. Nucleic Acids Research, 2009, 37, e80-e80.	14.5	16
25	The genome of the blood fluke Schistosoma mansoni. Nature, 2009, 460, 352-358.	27.8	945
26	Automated eukaryotic gene structure annotation using EVidenceModeler and the Program to Assemble Spliced Alignments. Genome Biology, 2008, 9, R7.	9.6	2,484
27	Problems and Solutions in Biological Sequence Analysis * Mark Borodovsky, Svetlana Ekisheva. Briefings in Bioinformatics, 2008, 9, 550-551.	6.5	0
28	Draft Genome Sequence of the Sexually Transmitted Pathogen *Trichomonas vaginalis*. Science, 2007, 315, 207-212.	12.6	731
29	Draft Genome of the Filarial Nematode Parasite *Brugia malayi*. Science, 2007, 317, 1756-1760.	12.6	571
30	Genome Sequence of Aedes aegypti, a Major Arbovirus Vector. Science, 2007, 316, 1718-1723.	12.6	1,025
31	A computational survey of candidate exonic splicing enhancer motifs in the model plant Arabidopsis thaliana. BMC Bioinformatics, 2007, 8, 159.	2.6	81
32	JIGSAW, GeneZilla, and GlimmerHMM: puzzling out the features of human genes in the ENCODE regions. Genome Biology, 2006, 7, S9.	9.6	61
33	Genomic sequence of the pathogenic and allergenic filamentous fungus Aspergillus fumigatus. Nature, 2005, 438, 1151-1156.	27.8	1,272
34	Efficient decoding algorithms for generalized hidden Markov model gene finders. BMC Bioinformatics, 2005, 6, 16.	2.6	34
35	Searching for genes and biologically related signals in DNA sequences. , 2005, , .		0
36	Genome Sequence of Theileria parva, a Bovine Pathogen That Transforms Lymphocytes. Science, 2005, 309, 134-137.	12.6	309

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37	Insight into the genome of Aspergillus fumigatus: analysis of a 922kb region encompassing the nitrate assimilation gene cluster. Fungal Genetics and Biology, 2004, 41, 443-453.	2.1	55
38	GlimmerM, Exonomy and Unveil: three ab initio eukaryotic genefinders. Nucleic Acids Research, 2003, 31, 3601-3604.	14.5	60
39	Using GlimmerM to Find Genes in Eukaryotic Genomes. Current Protocols in Bioinformatics, 2003, 00, Unit 4.4.	25.8	5
40	Computational Gene Prediction Using Multiple Sources of Evidence. Genome Research, 2003, 14, 142-148.	5.5	110
41	Sequence of Plasmodium falciparum chromosomes 2, 10, 11 and 14. Nature, 2002, 419, 531-534.	27.8	167
42	Genome sequence of the human malaria parasite Plasmodium falciparum. Nature, 2002, 419, 498-511.	27.8	3,881
43	Genome sequence and comparative analysis of the model rodent malaria parasite Plasmodium yoelii yoelii. Nature, 2002, 419, 512-519.	27.8	666
44	Computational gene finding in plants. Plant Molecular Biology, 2002, 48, 39-48.	3.9	41
45	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
46	Genomics of Theileria Parva. World Class Parasites, 2002, , 85-92.	0.3	1
47	Computational gene finding in plants. , 2002, , 39-48.		1
48	Computational gene finding in plants. Plant Molecular Biology, 2002, 48, 39-48.	3.9	12
49	Rice Bioinformatics. Analysis of Rice Sequence Data and Leveraging the Data to Other Plant Species. Plant Physiology, 2001, 125, 1166-1174.	4.8	46
50	Finding genes in Plasmodium falciparum. Nature, 2000, 404, 34-34.	27.8	18
51	Interpolated Markov Models for Eukaryotic Gene Finding. Genomics, 1999, 59, 24-31.	2.9	184
52	Chromosome 2 Sequence of the Human Malaria Parasite Plasmodium falciparum. , 1998, 282, 1126-1132.		419