Paolo Ribeca

List of Publications by Year
in descending order

51 papers	**30,171** citations	279487 **23** h-index	233125 **45** g-index
65 all docs	**65** docs citations	**65** times ranked	**53516** citing authors

#	ARTICLE	IF	CITATIONS
1	AI-Based Media Coding Standards. Smpte Motion Imaging Journal, 2022, 131, 10-20.	0.2	1
2	Whole genome sequencing and comparative analysis of a novel Chlamydia psittaci strain. Access Microbiology, 2022, 4, .	0.2	0
3	Whole genome de novo sequencing and comparative genomic analyses suggests that Chlamydia psittaci strain 84/2334 should be reclassified as Chlamydia abortus species. BMC Genomics, 2021, 22, 159.	1.2	14
4	Mutagenesis Mapping of RNA Structures within the Foot-and-Mouth Disease Virus Genome Reveals Functional Elements Localized in the Polymerase (3D^{pol})-Encoding Region. MSphere, 2021, 6, e0001521.	1.3	3
5	Transcriptomic Profiling of Dromedary Camels Immunised with a MERS Vaccine Candidate. Veterinary Sciences, 2021, 8, 156.	0.6	0
6	Engineered Promoter-Switched Viruses Reveal the Role of Poxvirus Maturation Protein A26 as a Negative Regulator of Viral Spread. Journal of Virology, 2021, 95, e0101221.	1.5	3
7	Transposons played a major role in the diversification between the closely related almond and peach genomes: results from the almond genome sequence. Plant Journal, 2020, 101, 455-472.	2.8	94
8	Pervasive within-host recombination and epistasis as major determinants of the molecular evolution of the foot-and-mouth disease virus capsid. PLoS Pathogens, 2020, 16, e1008235.	2.1	14
9	Full genome sequencing of archived wild type and vaccine rinderpest virus isolates prior to their destruction. Scientific Reports, 2020, 10, 6563.	1.6	10
10	A Systematic Evaluation of High-Throughput Sequencing Approaches to Identify Low-Frequency Single Nucleotide Variants in Viral Populations. Viruses, 2020, 12, 1187.	1.5	9
11	Pervasive Differential Splicing in Marek's Disease Virus Can Discriminate CVI-988 Vaccine Strain from RB-1B Very Virulent Strain in Chicken Embryonic Fibroblasts. Viruses, 2020, 12, 329.	1.5	6
12	'Seq & Destroy': the full genome sequencing of archived wild type and vaccine rinderpest virus isolates prior to their destruction. Access Microbiology, 2020, 2, .	0.2	0
13	Mass Die-Off of Saiga Antelopes, Kazakhstan, 2015. Emerging Infectious Diseases, 2019, 25, 1169-1176.	2.0	32
14	SiNPle: Fast and Sensitive Variant Calling for Deep Sequencing Data. Genes, 2019, 10, 561.	1.0	9
15	Bovine Derived in vitro Cultures Generate Heterogeneous Populations of Antigen Presenting Cells. Frontiers in Immunology, 2019, 10, 612.	2.2	14
16	Persistent Infection of African Buffalo (Syncerus caffer) with Foot-and-Mouth Disease Virus: Limited Viral Evolution and No Evidence of Antibody Neutralization Escape. Journal of Virology, 2019, 93, .	1.5	15
17	The Site Frequency/Dosage Spectrum of Autopolyploid Populations. Frontiers in Genetics, 2018, 9, 480.	1.1	8
18	Differential gene regulation underlies variation in melanic plumage coloration in the dark-eyed junco (*Junco hyemalis*). Molecular Ecology, 2018, 27, 4501-4515.	2.0	41

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19	Within-Host Recombination in the Foot-and-Mouth Disease Virus Genome. Viruses, 2018, 10, 221.	1.5	23
20	ChimPipe: accurate detection of fusion genes and transcription-induced chimeras from RNA-seq data. BMC Genomics, 2017, 18, 7.	1.2	30
21	A 3-way hybrid approach to generate a new high-quality chimpanzee reference genome (Pan_tro_3.0). GigaScience, 2017, 6, 1-6.	3.3	17
22	Extreme genomic erosion after recurrent demographic bottlenecks in the highly endangered Iberian lynx. Genome Biology, 2016, 17, 251.	3.8	131
23	CARGO: effective format-free compressed storage of genomic information. Nucleic Acids Research, 2016, 44, e114-e114.	6.5	10
24	Genome sequence of the olive tree, Olea europaea. GigaScience, 2016, 5, 29.	3.3	201
25	Efficient Alignment of Illumina‐Like High‐Throughput Sequencing Reads with the GEnomic Multi‐tool (GEM) Mapper. Current Protocols in Bioinformatics, 2015, 50, 11.13.1-11.13.20.	25.8	11
26	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. Nature Communications, 2015, 6, 10001.	5.8	266
27	Effect of predicted protein-truncating genetic variants on the human transcriptome. Science, 2015, 348, 666-669.	6.0	252
28	Boosting the FM-Index on the GPU: Effective Techniques to Mitigate Random Memory Access. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 1048-1059.	1.9	21
29	Tandem RNA Chimeras Contribute to Transcriptome Diversity in Human Population and Are Associated with Intronic Genetic Variants. PLoS ONE, 2014, 9, e104567.	1.1	31
30	Thread-cooperative, bit-parallel computation of levenshtein distance on GPU. , 2014, , .		25
31	FM-Index on GPU: A Cooperative Scheme to Reduce Memory Footprint. , 2014, , .		6
32	Assessment of transcript reconstruction methods for RNA-seq. Nature Methods, 2013, 10, 1177-1184.	9.0	679
33	Systematic evaluation of spliced alignment programs for RNA-seq data. Nature Methods, 2013, 10, 1185-1191.	9.0	467
34	Reproducibility of high-throughput mRNA and small RNA sequencing across laboratories. Nature Biotechnology, 2013, 31, 1015-1022.	9.4	251
35	Transcriptome and genome sequencing uncovers functional variation in humans. Nature, 2013, 501, 506-511.	13.7	1,857
36	Modelling and simulating generic RNA-Seq experiments with the flux simulator. Nucleic Acids Research, 2012, 40, 10073-10083.	6.5	264

#	Article	IF	Citations
37	An integrated encyclopedia of DNA elements in the human genome. Nature, 2012, 489, 57-74.	13.7	15,516
38	The GEM mapper: fast, accurate and versatile alignment by filtration. Nature Methods, 2012, 9, 1185-1188.	9.0	500
39	The tomato genome sequence provides insights into fleshy fruit evolution. Nature, 2012, 485, 635-641.	13.7	2,860
40	Landscape of transcription in human cells. Nature, 2012, 489, 101-108.	13.7	4,484
41	Evidence for Transcript Networks Composed of Chimeric RNAs in Human Cells. PLoS ONE, 2012, 7, e28213.	1.1	61
42	Fast Computation and Applications of Genome Mappability. PLoS ONE, 2012, 7, e30377.	1.1	458
43	A User's Guide to the Encyclopedia of DNA Elements (ENCODE). PLoS Biology, 2011, 9, e1001046.	2.6	1,257
44	Computational challenges of sequence classification in microbiomic data. Briefings in Bioinformatics, 2011, 12, 614-625.	3.2	15
45	A more precise characterization of chaperonin substrates. Bioinformatics, 2010, 26, 1685-1689.	1.8	25
46	Evolvability of Chaperonin Substrate Proteins. Nature Precedings, 2009, , .	0.1	0
47	Novel determinants describe chaperonin substrate proteins. Nature Precedings, 2009, , .	0.1	0
48	Faster exact Markovian probability functions for motif occurrences: a DFA-only approach. Bioinformatics, 2008, 24, 2839-2848.	1.8	26
49	From useful algorithms for slowly convergent series to physical predictions based on divergent perturbative expansions. Physics Reports, 2007, 446, 1-96.	10.3	103
50	Topology of pseudoknotted homopolymers. Physical Review E, 2006, 73, 031902.	0.8	10
51	Towards a fully automated computation of RG functions for the three-dimensional O(N) vector model: parametrizing amplitudes. Journal of Statistical Mechanics: Theory and Experiment, 2006, 2006, P02007-P02007.	0.9	3