

# Paolo Ribeca

## List of Publications by Year in descending order

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Version: 2024-02-01

51  
papers

30,171  
citations

279798

23  
h-index

233421

45  
g-index

65  
all docs

65  
docs citations

65  
times ranked

53516  
citing authors

#	ARTICLE	IF	CITATIONS
1	AI-Based Media Coding Standards. <i>Smpte Motion Imaging Journal</i> , 2022, 131, 10-20.	0.2	1
2	Whole genome sequencing and comparative analysis of a novel <i>Chlamydia psittaci</i> strain. <i>Access Microbiology</i> , 2022, 4, .	0.5	0
3	Whole genome de novo sequencing and comparative genomic analyses suggests that <i>Chlamydia psittaci</i> strain 84/2334 should be reclassified as <i>Chlamydia abortus</i> species. <i>BMC Genomics</i> , 2021, 22, 159.	2.8	14
4	Mutagenesis Mapping of RNA Structures within the Foot-and-Mouth Disease Virus Genome Reveals Functional Elements Localized in the Polymerase (3D <sup>pol</sup> )-Encoding Region. <i>MSphere</i> , 2021, 6, e0001521.	2.9	3
5	Transcriptomic Profiling of Dromedary Camels Immunised with a MERS Vaccine Candidate. <i>Veterinary Sciences</i> , 2021, 8, 156.	1.7	0
6	Engineered Promoter-Switched Viruses Reveal the Role of Poxvirus Maturation Protein A26 as a Negative Regulator of Viral Spread. <i>Journal of Virology</i> , 2021, 95, e0101221.	3.4	3
7	Transposons played a major role in the diversification between the closely related almond and peach genomes: results from the almond genome sequence. <i>Plant Journal</i> , 2020, 101, 455-472.	5.7	94
8	Pervasive within-host recombination and epistasis as major determinants of the molecular evolution of the foot-and-mouth disease virus capsid. <i>PLoS Pathogens</i> , 2020, 16, e1008235.	4.7	14
9	Full genome sequencing of archived wild type and vaccine rinderpest virus isolates prior to their destruction. <i>Scientific Reports</i> , 2020, 10, 6563.	3.3	10
10	A Systematic Evaluation of High-Throughput Sequencing Approaches to Identify Low-Frequency Single Nucleotide Variants in Viral Populations. <i>Viruses</i> , 2020, 12, 1187.	3.3	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. <i>Viruses</i> , 2020, 12, 329.	3.3	6
12	â€˜Seq & Destroyâ€™: the full genome sequencing of archived wild type and vaccine rinderpest virus isolates prior to their destruction. <i>Access Microbiology</i> , 2020, 2, .	0.5	0
13	Mass Die-Off of Saiga Antelopes, Kazakhstan, 2015. <i>Emerging Infectious Diseases</i> , 2019, 25, 1169-1176.	4.3	32
14	SiNPLE: Fast and Sensitive Variant Calling for Deep Sequencing Data. <i>Genes</i> , 2019, 10, 561.	2.4	9
15	Bovine Derived in vitro Cultures Generate Heterogeneous Populations of Antigen Presenting Cells. <i>Frontiers in Immunology</i> , 2019, 10, 612.	4.8	14
16	Persistent Infection of African Buffalo ( <i>Syncerus caffer</i> ) with Foot-and-Mouth Disease Virus: Limited Viral Evolution and No Evidence of Antibody Neutralization Escape. <i>Journal of Virology</i> , 2019, 93, .	3.4	15
17	The Site Frequency/Dosage Spectrum of Autopolyploid Populations. <i>Frontiers in Genetics</i> , 2018, 9, 480.	2.3	8
18	Differential gene regulation underlies variation in melanic plumage coloration in the dark-eyed junco ( <i>Junco hyemalis</i> ). <i>Molecular Ecology</i> , 2018, 27, 4501-4515.	3.9	41

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19	Within-Host Recombination in the Foot-and-Mouth Disease Virus Genome. <i>Viruses</i> , 2018, 10, 221.	3.3	23
20	ChimPipe: accurate detection of fusion genes and transcription-induced chimeras from RNA-seq data. <i>BMC Genomics</i> , 2017, 18, 7.	2.8	30
21	A 3-way hybrid approach to generate a new high-quality chimpanzee reference genome (Pan_tro_3.0). <i>GigaScience</i> , 2017, 6, 1-6.	6.4	17
22	Extreme genomic erosion after recurrent demographic bottlenecks in the highly endangered Iberian lynx. <i>Genome Biology</i> , 2016, 17, 251.	8.8	131
23	CARGO: effective format-free compressed storage of genomic information. <i>Nucleic Acids Research</i> , 2016, 44, e114-e114.	14.5	10
24	Genome sequence of the olive tree, <i>Olea europaea</i> . <i>GigaScience</i> , 2016, 5, 29.	6.4	201
25	Efficient Alignment of Illumina-like High-throughput Sequencing Reads with the Genomic Multi-tool (GEM) Mapper. <i>Current Protocols in Bioinformatics</i> , 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. <i>Nature Communications</i> , 2015, 6, 10001.	12.8	266
27	Effect of predicted protein-truncating genetic variants on the human transcriptome. <i>Science</i> , 2015, 348, 666-669.	12.6	252
28	Boosting the FM-Index on the GPU: Effective Techniques to Mitigate Random Memory Access. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015, 12, 1048-1059.	3.0	21
29	Tandem RNA Chimeras Contribute to Transcriptome Diversity in Human Population and Are Associated with Intronic Genetic Variants. <i>PLoS ONE</i> , 2014, 9, e104567.	2.5	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. <i>Nature Methods</i> , 2013, 10, 1177-1184.	19.0	679
33	Systematic evaluation of spliced alignment programs for RNA-seq data. <i>Nature Methods</i> , 2013, 10, 1185-1191.	19.0	467
34	Reproducibility of high-throughput mRNA and small RNA sequencing across laboratories. <i>Nature Biotechnology</i> , 2013, 31, 1015-1022.	17.5	251
35	Transcriptome and genome sequencing uncovers functional variation in humans. <i>Nature</i> , 2013, 501, 506-511.	27.8	1,857
36	Modelling and simulating generic RNA-Seq experiments with the flux simulator. <i>Nucleic Acids Research</i> , 2012, 40, 10073-10083.	14.5	264

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37	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012, 489, 57-74.	27.8	15,516
38	The GEM mapper: fast, accurate and versatile alignment by filtration. <i>Nature Methods</i> , 2012, 9, 1185-1188.	19.0	500
39	The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , 2012, 485, 635-641.	27.8	2,860
40	Landscape of transcription in human cells. <i>Nature</i> , 2012, 489, 101-108.	27.8	4,484
41	Evidence for Transcript Networks Composed of Chimeric RNAs in Human Cells. <i>PLoS ONE</i> , 2012, 7, e28213.	2.5	61
42	Fast Computation and Applications of Genome Mappability. <i>PLoS ONE</i> , 2012, 7, e30377.	2.5	458
43	A User's Guide to the Encyclopedia of DNA Elements (ENCODE). <i>PLoS Biology</i> , 2011, 9, e1001046.	5.6	1,257
44	Computational challenges of sequence classification in microbiomic data. <i>Briefings in Bioinformatics</i> , 2011, 12, 614-625.	6.5	15
45	A more precise characterization of chaperonin substrates. <i>Bioinformatics</i> , 2010, 26, 1685-1689.	4.1	25
46	Evolvability of Chaperonin Substrate Proteins. <i>Nature Precedings</i> , 2009, , .	0.1	0
47	Novel determinants describe chaperonin substrate proteins. <i>Nature Precedings</i> , 2009, , .	0.1	0
48	Faster exact Markovian probability functions for motif occurrences: a DFA-only approach. <i>Bioinformatics</i> , 2008, 24, 2839-2848.	4.1	26
49	From useful algorithms for slowly convergent series to physical predictions based on divergent perturbative expansions. <i>Physics Reports</i> , 2007, 446, 1-96.	25.6	103
50	Topology of pseudoknotted homopolymers. <i>Physical Review E</i> , 2006, 73, 031902.	2.1	10
51	Towards a fully automated computation of RG functions for the three-dimensional O(N) vector model: parametrizing amplitudes. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2006, 2006, P02007-P02007.	2.3	3