

Mario Caccamo

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10966373/publications.pdf>

Version: 2024-02-01

24
papers

12,961
citations

361413

20
h-index

580821

25
g-index

26
all docs

26
docs citations

26
times ranked

20842
citing authors

#	ARTICLE	IF	CITATIONS
1	The zebrafish reference genome sequence and its relationship to the human genome. <i>Nature</i> , 2013, 496, 498-503.	27.8	3,708
2	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004, 428, 493-521.	27.8	1,943
3	Control of Treg and TH17 cell differentiation by the aryl hydrocarbon receptor. <i>Nature</i> , 2008, 453, 65-71.	27.8	1,544
4	A chromosome conformation capture ordered sequence of the barley genome. <i>Nature</i> , 2017, 544, 427-433.	27.8	1,365
5	Analyses of pig genomes provide insight into porcine demography and evolution. <i>Nature</i> , 2012, 491, 393-398.	27.8	1,190
6	De novo assembly and genotyping of variants using colored de Bruijn graphs. <i>Nature Genetics</i> , 2012, 44, 226-232.	21.4	564
7	Assemblathon 1: A competitive assessment of de novo short read assembly methods. <i>Genome Research</i> , 2011, 21, 2224-2241.	5.5	443
8	An Overview of Ensembl. <i>Genome Research</i> , 2004, 14, 925-928.	5.5	391
9	Conservation and divergence of gene families encoding components of innate immune response systems in zebrafish. <i>Genome Biology</i> , 2007, 8, R251.	9.6	384
10	gEVAL—a web-based browser for evaluating genome assemblies. <i>Bioinformatics</i> , 2016, 32, 2508-2510.4.1		319
11	RNA-seq bulked segregant analysis enables the identification of high-resolution genetic markers for breeding in hexaploid wheat. <i>Plant Biotechnology Journal</i> , 2015, 13, 613-624.	8.3	202
12	A synteny-based draft genome sequence of the forage grass <i>Lolium perenne</i> . <i>Plant Journal</i> , 2015, 84, 816-826.	5.7	166
13	Red clover (<i>Trifolium pratense</i> L.) draft genome provides a platform for trait improvement. <i>Scientific Reports</i> , 2015, 5, 17394.	3.3	136
14	Construction of a map-based reference genome sequence for barley, <i>Hordeum vulgare</i> L.. <i>Scientific Data</i> , 2017, 4, 170044.	5.3	130
15	Metagenomic study of the viruses of African straw-coloured fruit bats: Detection of a chiropteran poxvirus and isolation of a novel adenovirus. <i>Virology</i> , 2013, 441, 95-106.	2.4	121
16	Adaptive Autoimmunity and Foxp3-Based Immunoregulation in Zebrafish. <i>PLoS ONE</i> , 2010, 5, e9478.	2.5	83
17	ESTGenes: Alternative Splicing From ESTs in Ensembl. <i>Genome Research</i> , 2004, 14, 976-987.	5.5	76
18	Host Subtraction, Filtering and Assembly Validations for Novel Viral Discovery Using Next Generation Sequencing Data. <i>PLoS ONE</i> , 2015, 10, e0129059.	2.5	44

#	ARTICLE	IF	CITATIONS
19	CerealsDB 3.0: expansion of resources and data integration. BMC Bioinformatics, 2016, 17, 256.	2.6	42
20	Primula vulgaris (primrose) genome assembly, annotation and gene expression, with comparative genomics on the heterostyly supergene. Scientific Reports, 2018, 8, 17942.	3.3	40
21	Identifying and Classifying Trait Linked Polymorphisms in Non-Reference Species by Walking Coloured de Bruijn Graphs. PLoS ONE, 2013, 8, e60058.	2.5	26
22	StatsDB: platform-agnostic storage and understanding of next generation sequencing run metrics. F1000Research, 2013, 2, 248.	1.6	14
23	Yerba mate (Ilex paraguariensis, A. St.-Hil.) de novo transcriptome assembly based on tissue specific genomic expression profiles. BMC Genomics, 2018, 19, 891.	2.8	9
24	Whole-Genome Characteristics and Polymorphic Analysis of Vietnamese Rice Landraces as a Comprehensive Information Resource for Marker-Assisted Selection. International Journal of Genomics, 2017, 2017, 1-11.	1.6	6