

Ricardo Ramirez-Gonzalez

List of Publications by Year in descending order

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Version: 2024-02-01

49
papers

11,889
citations

147801

31
h-index

206112

48
g-index

59
all docs

59
docs citations

59
times ranked

12559
citing authors

#	ARTICLE	IF	CITATIONS
1	Pathogen-induced biosynthetic pathways encode defense-related molecules in bread wheat. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2123299119.	7.1	30
2	New insights into homoeologous copy number variations in the hexaploid wheat genome. <i>Plant Genome</i> , 2021, 14, e20069.	2.8	16
3	Rust expression browser: an open source database for simultaneous analysis of host and pathogen gene expression profiles with expVIP. <i>BMC Genomics</i> , 2021, 22, 166.	2.8	10
4	Kinematic of the Position and Orientation Synchronization of the Posture of a n DoF Upper-Limb Exoskeleton with a Virtual Object in an Immersive Virtual Reality Environment. <i>Electronics (Switzerland)</i> , 2021, 10, 1069.	3.1	8
5	Wheat in vivo RNA structure landscape reveals a prevalent role of RNA structure in modulating translational subgenome expression asymmetry. <i>Genome Biology</i> , 2021, 22, 326.	8.8	12
6	A carbohydrate-binding protein, B-GRANULE CONTENT 1, influences starch granule size distribution in a dose-dependent manner in polyploid wheat. <i>Journal of Experimental Botany</i> , 2020, 71, 105-115.	4.8	36
7	Multiple wheat genomes reveal global variation in modern breeding. <i>Nature</i> , 2020, 588, 277-283.	27.8	513
8	A haplotype-led approach to increase the precision of wheat breeding. <i>Communications Biology</i> , 2020, 3, 712.	4.4	68
9	The NLR-Annotator Tool Enables Annotation of the Intracellular Immune Receptor Repertoire. <i>Plant Physiology</i> , 2020, 183, 468-482.	4.8	147
10	Enabling reusability of plant phenomic datasets with MIAPPE 1.1. <i>New Phytologist</i> , 2020, 227, 260-273.	7.3	84
11	Optimizing <i>Rhizobium</i> legume symbioses by simultaneous measurement of rhizobial competitiveness and N ₂ fixation in nodules. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 9822-9831.	7.1	63
12	A roadmap for gene functional characterisation in crops with large genomes: Lessons from polyploid wheat. <i>ELife</i> , 2020, 9, .	6.0	78
13	BrAPI" an application programming interface for plant breeding applications. <i>Bioinformatics</i> , 2019, 35, 4147-4155.	4.1	82
14	A Co-Expression Network in Hexaploid Wheat Reveals Mostly Balanced Expression and Lack of Significant Gene Loss of Homeologous Meiotic Genes Upon Polyploidization. <i>Frontiers in Plant Science</i> , 2019, 10, 1325.	3.6	24
15	Global transcriptome analysis uncovers the gene co-expression regulation network and key genes involved in grain development of wheat (<i>Triticum aestivum</i> L.). <i>Functional and Integrative Genomics</i> , 2019, 19, 853-866.	3.5	14
16	RNA-seq, de novo transcriptome assembly and flavonoid gene analysis in 13 wild and cultivated berry fruit species with high content of phenolics. <i>BMC Genomics</i> , 2019, 20, 995.	2.8	27
17	Hotspots in the genomic architecture of field drought responses in wheat as breeding targets. <i>Functional and Integrative Genomics</i> , 2019, 19, 295-309.	3.5	40
18	Speed breeding in growth chambers and glasshouses for crop breeding and model plant research. <i>Nature Protocols</i> , 2018, 13, 2944-2963.	12.0	286

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19	Genome-Wide Transcription During Early Wheat Meiosis Is Independent of Synapsis, Ploidy Level, and the Ph1 Locus. <i>Frontiers in Plant Science</i> , 2018, 9, 1791.	3.6	44
20	The transcriptional landscape of polyploid wheat. <i>Science</i> , 2018, 361, .	12.6	768
21	Shifting the limits in wheat research and breeding using a fully annotated reference genome. <i>Science</i> , 2018, 361, .	12.6	2,424
22	Impact of transposable elements on genome structure and evolution in bread wheat. <i>Genome Biology</i> , 2018, 19, 103.	8.8	226
23	Uncovering hidden variation in polyploid wheat. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E913-E921.	7.1	554
24	An improved assembly and annotation of the allohexaploid wheat genome identifies complete families of agronomic genes and provides genomic evidence for chromosomal translocations. <i>Genome Research</i> , 2017, 27, 885-896.	5.5	464
25	Genome sequence and genetic diversity of European ash trees. <i>Nature</i> , 2017, 541, 212-216.	27.8	166
26	transPLANT Resources for Triticeae Genomic Data. <i>Plant Genome</i> , 2016, 9, plantgenome2015.06.0038.	2.8	8
27	expVIP: a Customizable RNA-seq Data Analysis and Visualization Platform. <i>Plant Physiology</i> , 2016, 170, 2172-2186.	4.8	403
28	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
29	Mutation Scanning in Wheat by Exon Capture and Next-Generation Sequencing. <i>PLoS ONE</i> , 2015, 10, e0137549.	2.5	65
30	PolyMarker: A fast polyploid primer design pipeline. <i>Bioinformatics</i> , 2015, 31, 2038-2039.	4.1	202
31	Field pathogenomics reveals the emergence of a diverse wheat yellow rust population. <i>Genome Biology</i> , 2015, 16, 23.	8.8	185
32	bio-samtools 2: a package for analysis and visualization of sequence and alignment data with SAMtools in Ruby. <i>Bioinformatics</i> , 2015, 31, 2565-2567.	4.1	61
33	Mapping a Type 1 FHB resistance on chromosome 4AS of <i>Triticum macha</i> and deployment in combination with two Type 2 resistances. <i>Theoretical and Applied Genetics</i> , 2015, 128, 1725-1738.	3.6	10
34	High-resolution genetic markers for breeding in hexaploid wheat. <i>Plant Biotechnology Journal</i> , 2015, 13, 613-624.	8.3	202
35	Next Generation Sequencing Enabled Genetics in Hexaploid Wheat. , 2015, , 201-209.		0
36	A chromosome-based draft sequence of the hexaploid bread wheat (<i>Triticum aestivum</i>) genome. <i>Science</i> , 2014, 345, 1251788.	12.6	1,479

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37	Genome interplay in the grain transcriptome of hexaploid bread wheat. <i>Science</i> , 2014, 345, 1250091.	12.6	318
38	Ancient hybridizations among the ancestral genomes of bread wheat. <i>Science</i> , 2014, 345, 1250092.	12.6	629
39	Sequencing quality assessment tools to enable data-driven informatics for high throughput genomics. <i>Frontiers in Genetics</i> , 2013, 4, 288.	2.3	163
40	StatsDB: platform-agnostic storage and understanding of next generation sequencing run metrics. <i>F1000Research</i> , 2013, 2, 248.	1.6	14
41	StatsDB: platform-agnostic storage and understanding of next generation sequencing run metrics. <i>F1000Research</i> , 2013, 2, 248.	1.6	12
42	PyroClean: Denoising Pyrosequences from Protein-Coding Amplicons for the Recovery of Interspecific and Intraspecific Genetic Variation. <i>PLoS ONE</i> , 2013, 8, e57615.	2.5	19
43	Identifying and Classifying Trait Linked Polymorphisms in Non-Reference Species by Walking Coloured de Bruijn Graphs. <i>PLoS ONE</i> , 2013, 8, e60058.	2.5	26
44	Biogem: an effective tool-based approach for scaling up open source software development in bioinformatics. <i>Bioinformatics</i> , 2012, 28, 1035-1037.	4.1	27
45	Evolution of an Eurasian Avian-like Influenza Virus in Naïve and Vaccinated Pigs. <i>PLoS Pathogens</i> , 2012, 8, e1002730.	4.7	79
46	Analyses of pig genomes provide insight into porcine demography and evolution. <i>Nature</i> , 2012, 491, 393-398.	27.8	1,190
47	Bio-samtools: Ruby bindings for SAMtools, a library for accessing BAM files containing high-throughput sequence alignments. <i>Source Code for Biology and Medicine</i> , 2012, 7, 6.	1.7	65
48	Assemblathon 1: A competitive assessment of de novo short read assembly methods. <i>Genome Research</i> , 2011, 21, 2224-2241.	5.5	443
49	Gee Fu: a sequence version and web-services database tool for genomic assembly, genome feature and NGS data. <i>Bioinformatics</i> , 2011, 27, 2754-2755.	4.1	2