Ricardo Ramirez-Gonzalez

List of Publications by Year
in descending order

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	Shifting the limits in wheat research and breeding using a fully annotated reference genome. Science, 2018, 361, .	12.6	2,424
2	A chromosome-based draft sequence of the hexaploid bread wheat (*Triticum aestivum*) genome. Science, 2014, 345, 1251788.	12.6	1,479
3	Analyses of pig genomes provide insight into porcine demography and evolution. Nature, 2012, 491, 393-398.	27.8	1,190
4	The transcriptional landscape of polyploid wheat. Science, 2018, 361, .	12.6	768
5	Ancient hybridizations among the ancestral genomes of bread wheat. Science, 2014, 345, 1250092.	12.6	629
6	Uncovering hidden variation in polyploid wheat. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E913-E921.	7.1	554
7	Multiple wheat genomes reveal global variation in modern breeding. Nature, 2020, 588, 277-283.	27.8	513
8	An improved assembly and annotation of the allohexaploid wheat genome identifies complete families of agronomic genes and provides genomic evidence for chromosomal translocations. Genome Research, 2017, 27, 885-896.	5.5	464
9	Assemblathon 1: A competitive assessment of de novo short read assembly methods. Genome Research, 2011, 21, 2224-2241.	5.5	443
10	expVIP: a Customizable RNA-seq Data Analysis and Visualization Platform. Plant Physiology, 2016, 170, 2172-2186.	4.8	403
11	Genome interplay in the grain transcriptome of hexaploid bread wheat. Science, 2014, 345, 1250091.	12.6	318
12	Speed breeding in growth chambers and glasshouses for crop breeding and model plant research. Nature Protocols, 2018, 13, 2944-2963.	12.0	286
13	Impact of transposable elements on genome structure and evolution in bread wheat. Genome Biology, 2018, 19, 103.	8.8	226
14	PolyMarker: A fast polyploid primer design pipeline. Bioinformatics, 2015, 31, 2038-2039.	4.1	202
15	<scp>RNA</scp>‐<scp>S</scp>eq bulked segregant analysis enables the identification of high‐resolution genetic markers for breeding in hexaploid wheat. Plant Biotechnology Journal, 2015, 13, 613-624.	8.3	202
16	Field pathogenomics reveals the emergence of a diverse wheat yellow rust population. Genome Biology, 2015, 16, 23.	8.8	185
17	Genome sequence and genetic diversity of European ash trees. Nature, 2017, 541, 212-216.	27.8	166
18	Sequencing quality assessment tools to enable data-driven informatics for high throughput genomics. Frontiers in Genetics, 2013, 4, 288.	2.3	163

#	Article	IF	Citations
19	The NLR-Annotator Tool Enables Annotation of the Intracellular Immune Receptor Repertoire. Plant Physiology, 2020, 183, 468-482.	4.8	147
20	Enabling reusability of plant phenomic datasets with MIAPPE 1.1. New Phytologist, 2020, 227, 260-273.	7.3	84
21	BrAPIâ€"an application programming interface for plant breeding applications. Bioinformatics, 2019, 35, 4147-4155.	4.1	82
22	Evolution of an Eurasian Avian-like Influenza Virus in NaÃ¯ve and Vaccinated Pigs. PLoS Pathogens, 2012, 8, e1002730.	4.7	79
23	A roadmap for gene functional characterisation in crops with large genomes: Lessons from polyploid wheat. ELife, 2020, 9, .	6.0	78
24	A haplotype-led approach to increase the precision of wheat breeding. Communications Biology, 2020, 3, 712.	4.4	68
25	Bio-samtools: Ruby bindings for SAMtools, a library for accessing BAM files containing high-throughput sequence alignments. Source Code for Biology and Medicine, 2012, 7, 6.	1.7	65
26	Mutation Scanning in Wheat by Exon Capture and Next-Generation Sequencing. PLoS ONE, 2015, 10, e0137549.	2.5	65
27	Optimizing <i>Rhizobium-</i> legume symbioses by simultaneous measurement of rhizobial competitiveness and N ₂ fixation in nodules. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 9822-9831.	7.1	63
28	bio-samtools 2: a package for analysis and visualization of sequence and alignment data with SAMtools in Ruby. Bioinformatics, 2015, 31, 2565-2567.	4.1	61
29	Host Subtraction, Filtering and Assembly Validations for Novel Viral Discovery Using Next Generation Sequencing Data. PLoS ONE, 2015, 10, e0129059.	2.5	44
30	Genome-Wide Transcription During Early Wheat Meiosis Is Independent of Synapsis, Ploidy Level, and the Ph1 Locus. Frontiers in Plant Science, 2018, 9, 1791.	3.6	44
31	Hotspots in the genomic architecture of field drought responses in wheat as breeding targets. Functional and Integrative Genomics, 2019, 19, 295-309.	3.5	40
32	A carbohydrate-binding protein, B-GRANULE CONTENT 1, influences starch granule size distribution in a dose-dependent manner in polyploid wheat. Journal of Experimental Botany, 2020, 71, 105-115.	4.8	36
33	Pathogen-induced biosynthetic pathways encode defense-related molecules in bread wheat. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2123299119.	7.1	30
34	Biogem: an effective tool-based approach for scaling up open source software development in bioinformatics. Bioinformatics, 2012, 28, 1035-1037.	4.1	27
35	RNA-seq, de novo transcriptome assembly and flavonoid gene analysis in 13 wild and cultivated berry fruit species with high content of phenolics. BMC Genomics, 2019, 20, 995.	2.8	27
36	Identifying and Classifying Trait Linked Polymorphisms in Non-Reference Species by Walking Coloured de Bruijn Graphs. PLoS ONE, 2013, 8, e60058.	2.5	26

#	Article	IF	Citations
37	A Co-Expression Network in Hexaploid Wheat Reveals Mostly Balanced Expression and Lack of Significant Gene Loss of Homeologous Meiotic Genes Upon Polyploidization. Frontiers in Plant Science, 2019, 10, 1325.	3.6	24
38	PyroClean: Denoising Pyrosequences from Protein-Coding Amplicons for the Recovery of Interspecific and Intraspecific Genetic Variation. PLoS ONE, 2013, 8, e57615.	2.5	19
39	New insights into homoeologous copy number variations in the hexaploid wheat genome. Plant Genome, 2021, 14, e20069.	2.8	16
40	Global transcriptome analysis uncovers the gene co-expression regulation network and key genes involved in grain development of wheat (Triticum aestivum L.). Functional and Integrative Genomics, 2019, 19, 853-866.	3.5	14
41	StatsDB: platform-agnostic storage and understanding of next generation sequencing run metrics. F1000Research, 2013, 2, 248.	1.6	14
42	StatsDB: platform-agnostic storage and understanding of next generation sequencing run metrics. F1000Research, 2013, 2, 248.	1.6	12
43	Wheat in vivo RNA structure landscape reveals a prevalent role of RNA structure in modulating translational subgenome expression asymmetry. Genome Biology, 2021, 22, 326.	8.8	12
44	Mapping a Type 1 FHB resistance on chromosome 4AS of Triticum macha and deployment in combination with two Type 2 resistances. Theoretical and Applied Genetics, 2015, 128, 1725-1738.	3.6	10
45	Rust expression browser: an open source database for simultaneous analysis of host and pathogen gene expression profiles with expVIP. BMC Genomics, 2021, 22, 166.	2.8	10
46	transPLANT Resources for Triticeae Genomic Data. Plant Genome, 2016, 9, plantgenome2015.06.0038.	2.8	8
47	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. Electronics (Switzerland), 2021, 10, 1069.	3.1	8
48	Gee Fu: a sequence version and web-services database tool for genomic assembly, genome feature and NGS data. Bioinformatics, 2011, 27, 2754-2755.	4.1	2
49	Next Generation Sequencing Enabled Genetics in Hexaploid Wheat. , 2015, , 201-209.		0