

François Choulet

List of Publications by Year in descending order

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Version: 2024-02-01

48
papers

9,120
citations

159585

30
h-index

197818

49
g-index

54
all docs

54
docs citations

54
times ranked

7336
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 (<i>Triticum aestivum</i>) genome. Science, 2014, 345, 1251788.	12.6	1,479
3	The transcriptional landscape of polyploid wheat. Science, 2018, 361, .	12.6	768
4	Ancient hybridizations among the ancestral genomes of bread wheat. Science, 2014, 345, 1250092.	12.6	629
5	Structural and functional partitioning of bread wheat chromosome 3B. Science, 2014, 345, 1249721.	12.6	542
6	A Physical Map of the 1-Gigabase Bread Wheat Chromosome 3B. Science, 2008, 322, 101-104.	12.6	356
7	Megabase Level Sequencing Reveals Contrasted Organization and Evolution Patterns of the Wheat Gene and Transposable Element Spaces. Plant Cell, 2010, 22, 1686-1701.	6.6	258
8	Optical maps refine the bread wheat <i>Triticum aestivum</i> cv. Chinese Spring genome assembly. Plant Journal, 2021, 107, 303-314.	5.7	237
9	Linking the International Wheat Genome Sequencing Consortium bread wheat reference genome sequence to wheat genetic and phenomic data. Genome Biology, 2018, 19, 111.	8.8	232
10	Impact of transposable elements on genome structure and evolution in bread wheat. Genome Biology, 2018, 19, 103.	8.8	226
11	High throughput SNP discovery and genotyping in hexaploid wheat. PLoS ONE, 2018, 13, e0186329.	2.5	200
12	Frequent Gene Movement and Pseudogene Evolution Is Common to the Large and Complex Genomes of Wheat, Barley, and Their Relatives. Plant Cell, 2011, 23, 1706-1718.	6.6	190
13	Worldwide phylogeography and history of wheat genetic diversity. Science Advances, 2019, 5, eaav0536.	10.3	118
14	Insertion site-based polymorphism markers open new perspectives for genome saturation and marker-assisted selection in wheat. Plant Biotechnology Journal, 2010, 8, 196-210.	8.3	111
15	Deep transcriptome sequencing provides new insights into the structural and functional organization of the wheat genome. Genome Biology, 2015, 16, 29.	8.8	101
16	Evolution of the Terminal Regions of the Streptomyces Linear Chromosome. Molecular Biology and Evolution, 2006, 23, 2361-2369.	8.9	96
17	Organization and evolution of transposable elements along the bread wheat chromosome 3B. Genome Biology, 2014, 15, 546.	8.8	88
18	Wheat centromeric retrotransposons: the new ones take a major role in centromeric structure. Plant Journal, 2013, 73, 952-965.	5.7	78

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19	Small-scale gene duplications played a major role in the recent evolution of wheat chromosome 3B. <i>Genome Biology</i> , 2015, 16, 188.	8.8	76
20	TriAnnot: A Versatile and High Performance Pipeline for the Automated Annotation of Plant Genomes. <i>Frontiers in Plant Science</i> , 2012, 3, 5.	3.6	73
21	High-Resolution Mapping of Crossover Events in the Hexaploid Wheat Genome Suggests a Universal Recombination Mechanism. <i>Genetics</i> , 2017, 206, 1373-1388.	2.9	72
22	Meiotic Gene Evolution: Can You Teach a New Dog New Tricks?. <i>Molecular Biology and Evolution</i> , 2014, 31, 1724-1727.	8.9	71
23	Conjugative Transfer of the Integrative Conjugative Elements ICES _t 1 and ICES _t 3 from <i>Streptococcus thermophilus</i> . <i>Journal of Bacteriology</i> , 2009, 191, 2764-2775.	2.2	55
24	Variation in crossover rates across a 3-Mb contig of bread wheat (<i>Triticum aestivum</i>) reveals the presence of a meiotic recombination hotspot. <i>Chromosoma</i> , 2011, 120, 185-198.	2.2	55
25	A 3,000-Loci Transcription Map of Chromosome 3B Unravels the Structural and Functional Features of Gene Islands in Hexaploid Wheat. <i>Plant Physiology</i> , 2011, 157, 1596-1608.	4.8	49
26	A high density physical map of chromosome 1BL supports evolutionary studies, map-based cloning and sequencing in wheat. <i>Genome Biology</i> , 2013, 14, R64.	8.8	45
27	Transcriptome and Allele Specificity Associated with a 3BL Locus for Fusarium Crown Rot Resistance in Bread Wheat. <i>PLoS ONE</i> , 2014, 9, e113309.	2.5	42
28	Optical and physical mapping with local finishing enables megabase-scale resolution of agronomically important regions in the wheat genome. <i>Genome Biology</i> , 2018, 19, 112.	8.8	41
29	Fine mapping of a large-effect QTL conferring Fusarium crown rot resistance on the long arm of chromosome 3B in hexaploid wheat. <i>BMC Genomics</i> , 2015, 16, 850.	2.8	40
30	Major Gene for Field Stem Rust Resistance Co-Locates with Resistance Gene Sr12 in ‘Thatcher’ Wheat. <i>PLoS ONE</i> , 2016, 11, e0157029.	2.5	37
31	Intraspecific Variability of the Terminal Inverted Repeats of the Linear Chromosome of <i>Streptomyces ambifaciens</i> . <i>Journal of Bacteriology</i> , 2006, 188, 6599-6610.	2.2	32
32	Whole Genome Profiling provides a robust framework for physical mapping and sequencing in the highly complex and repetitive wheat genome. <i>BMC Genomics</i> , 2012, 13, 47.	2.8	29
33	<i>QTug.sau-3B</i> Is a Major Quantitative Trait Locus for Wheat Hexaploidization. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1943-1953.	1.8	26
34	Long-read and chromosome-scale assembly of the hexaploid wheat genome achieves high resolution for research and breeding. <i>GigaScience</i> , 2022, 11, .	6.4	26
35	Identification, Molecular Cloning, and Functional Characterization of a Wheat UDP-Glucosyltransferase Involved in Resistance to Fusarium Head Blight and to Mycotoxin Accumulation. <i>Frontiers in Plant Science</i> , 2018, 9, 1853.	3.6	22
36	Specific patterns of gene space organisation revealed in wheat by using the combination of barley and wheat genomic resources. <i>BMC Genomics</i> , 2010, 11, 714.	2.8	21

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37	Genotyping by sequencing transcriptomes in an evolutionary pre-breeding durum wheat population. <i>Molecular Breeding</i> , 2014, 34, 1531-1548.	2.1	20
38	Genome-level identification of cell wall invertase genes in wheat for the study of drought tolerance. <i>Functional Plant Biology</i> , 2012, 39, 569.	2.1	18
39	Intraspecific sequence comparisons reveal similar rates of non-collinear gene insertion in the B and D genomes of bread wheat. <i>BMC Plant Biology</i> , 2012, 12, 155.	3.6	18
40	Structural Variations Affecting Genes and Transposable Elements of Chromosome 3B in Wheats. <i>Frontiers in Genetics</i> , 2020, 11, 891.	2.3	16
41	New insights into homoeologous copy number variations in the hexaploid wheat genome. <i>Plant Genome</i> , 2021, 14, e20069.	2.8	16
42	Deciphering carbohydrate metabolism during wheat grain development via integrated transcriptome and proteome dynamics. <i>Molecular Biology Reports</i> , 2020, 47, 5439-5449.	2.3	15
43	Exploiting the Repetitive Fraction of the Wheat Genome for High-Throughput Single-Nucleotide Polymorphism Discovery and Genotyping. <i>Plant Genome</i> , 2016, 9, plantgenome2015.09.0078.	2.8	13
44	Genetic diversity and linkage disequilibrium studies on a 3.1-Mb genomic region of chromosome 3B in European and Asian bread wheat (<i>Triticum aestivum</i> L.) populations. <i>Theoretical and Applied Genetics</i> , 2010, 121, 1209-1225.	3.6	11
45	High-resolution analysis of a QTL for resistance to <i>Stagonospora nodorum</i> glume blotch in wheat reveals presence of two distinct resistance loci in the target interval. <i>Theoretical and Applied Genetics</i> , 2014, 127, 573-586.	3.6	11
46	Annotation, classification, genomic organization and expression of the <i>Vitis vinifera</i> CYPome. <i>PLoS ONE</i> , 2018, 13, e0199902.	2.5	11
47	dbWFA: a web-based database for functional annotation of <i>Triticum aestivum</i> transcripts. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat014.	3.0	9
48	De Novo Annotation of Transposable Elements: Tackling the Fat Genome Issue. <i>Proceedings of the IEEE</i> , 2016, , 1-8.	21.3	8