

# Frédéric Choulet

## List of Publications by Year in descending order

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Version: 2024-02-01

48  
papers

9,120  
citations

159358

30  
h-index

197535

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. <i>Science</i> , 2018, 361, .	6.0	2,424
2	A chromosome-based draft sequence of the hexaploid bread wheat ( <i>Triticum aestivum</i> ) genome. <i>Science</i> , 2014, 345, 1251788.	6.0	1,479
3	The transcriptional landscape of polyploid wheat. <i>Science</i> , 2018, 361, .	6.0	768
4	Ancient hybridizations among the ancestral genomes of bread wheat. <i>Science</i> , 2014, 345, 1250092.	6.0	629
5	Structural and functional partitioning of bread wheat chromosome 3B. <i>Science</i> , 2014, 345, 1249721.	6.0	542
6	A Physical Map of the 1-Gigabase Bread Wheat Chromosome 3B. <i>Science</i> , 2008, 322, 101-104.	6.0	356
7	Megabase Level Sequencing Reveals Contrasted Organization and Evolution Patterns of the Wheat Gene and Transposable Element Spaces. <i>Plant Cell</i> , 2010, 22, 1686-1701.	3.1	258
8	Optical maps refine the bread wheat <i>Triticum aestivum</i> cv. Chinese Spring genome assembly. <i>Plant Journal</i> , 2021, 107, 303-314.	2.8	237
9	Linking the International Wheat Genome Sequencing Consortium bread wheat reference genome sequence to wheat genetic and phenomic data. <i>Genome Biology</i> , 2018, 19, 111.	3.8	232
10	Impact of transposable elements on genome structure and evolution in bread wheat. <i>Genome Biology</i> , 2018, 19, 103.	3.8	226
11	High throughput SNP discovery and genotyping in hexaploid wheat. <i>PLoS ONE</i> , 2018, 13, e0186329.	1.1	200
12	Frequent Gene Movement and Pseudogene Evolution Is Common to the Large and Complex Genomes of Wheat, Barley, and Their Relatives. <i>Plant Cell</i> , 2011, 23, 1706-1718.	3.1	190
13	Worldwide phylogeography and history of wheat genetic diversity. <i>Science Advances</i> , 2019, 5, eaav0536.	4.7	118
14	Insertion site-based polymorphism markers open new perspectives for genome saturation and marker-assisted selection in wheat. <i>Plant Biotechnology Journal</i> , 2010, 8, 196-210.	4.1	111
15	Deep transcriptome sequencing provides new insights into the structural and functional organization of the wheat genome. <i>Genome Biology</i> , 2015, 16, 29.	3.8	101
16	Evolution of the Terminal Regions of the Streptomyces Linear Chromosome. <i>Molecular Biology and Evolution</i> , 2006, 23, 2361-2369.	3.5	96
17	Organization and evolution of transposable elements along the bread wheat chromosome 3B. <i>Genome Biology</i> , 2014, 15, 546.	3.8	88
18	Wheat centromeric retrotransposons: the new ones take a major role in centromeric structure. <i>Plant Journal</i> , 2013, 73, 952-965.	2.8	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.	3.8	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.	1.7	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.	1.2	72
22	Meiotic Gene Evolution: Can You Teach a New Dog New Tricks?. <i>Molecular Biology and Evolution</i> , 2014, 31, 1724-1727.	3.5	71
23	Conjugative Transfer of the Integrative Conjugative Elements ICeSt1 and ICeSt3 from <i>Streptococcus thermophilus</i> . <i>Journal of Bacteriology</i> , 2009, 191, 2764-2775.	1.0	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.	1.0	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.	2.3	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.	3.8	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.	1.1	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.	3.8	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.	1.2	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.	1.1	37
31	Intraspecific Variability of the Terminal Inverted Repeats of the Linear Chromosome of <i>Streptomyces ambofaciens</i> . <i>Journal of Bacteriology</i> , 2006, 188, 6599-6610.	1.0	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.	1.2	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.	0.8	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, .	3.3	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.	1.7	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.	1.2	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.	1.0	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.	1.1	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.	1.6	18
40	Structural Variations Affecting Genes and Transposable Elements of Chromosome 3B in Wheats. <i>Frontiers in Genetics</i> , 2020, 11, 891.	1.1	16
41	New insights into homoeologous copy number variations in the hexaploid wheat genome. <i>Plant Genome</i> , 2021, 14, e20069.	1.6	16
42	Deciphering carbohydrate metabolism during wheat grain development via integrated transcriptome and proteome dynamics. <i>Molecular Biology Reports</i> , 2020, 47, 5439-5449.	1.0	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.	1.6	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.	1.8	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.	1.8	11
46	Annotation, classification, genomic organization and expression of the <i>Vitis vinifera</i> CYPome. <i>PLoS ONE</i> , 2018, 13, e0199902.	1.1	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.	1.4	9
48	De Novo Annotation of Transposable Elements: Tackling the Fat Genome Issue. <i>Proceedings of the IEEE</i> , 2016, , 1-8.	16.4	8