Philippa Borrill

List of Publications by Year
in descending order

29 papers	6,297 citations	304743 22 h-index	454955 30 g-index
47 all docs	47 docs citations	47 times ranked	5975 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	The transcriptional landscape of polyploid wheat. Science, 2018, 361, .	12.6	768
3	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
4	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
5	expVIP: a Customizable RNA-seq Data Analysis and Visualization Platform. Plant Physiology, 2016, 170, 2172-2186.	4.8	403
6	Impact of transposable elements on genome structure and evolution in bread wheat. Genome Biology, 2018, 19, 103.	8.8	226
7	Biofortification of wheat grain with iron and zinc: integrating novel genomic resources and knowledge from model crops. Frontiers in Plant Science, 2014, 5, 53.	3.6	171
8	Chaperonins Facilitate KNOTTED1 Cell-to-Cell Trafficking and Stem Cell Function. Science, 2011, 333, 1141-1144.	12.6	154
9	Genomics as the key to unlocking the polyploid potential of wheat. New Phytologist, 2015, 208, 1008-1022.	7.3	151
10	Arabidopsis plants perform arithmetic division to prevent starvation at night. ELife, 2013, 2, e00669.	6.0	134
11	Applying the latest advances in genomics and phenomics for trait discovery in polyploid wheat. Plant Journal, 2019, 97, 56-72.	5.7	83
12	A roadmap for gene functional characterisation in crops with large genomes: Lessons from polyploid wheat. ELife, 2020, 9, .	6.0	78
13	Identification of Transcription Factors Regulating Senescence in Wheat through Gene Regulatory Network Modelling. Plant Physiology, 2019, 180, 1740-1755.	4.8	73
14	Wheat Grain Filling Is Limited by Grain Filling Capacity rather than the Duration of Flag Leaf Photosynthesis: A Case Study Using NAM RNAi Plants. PLoS ONE, 2015, 10, e0134947.	2.5	73
15	Multiple Arabidopsis genes primed for recruitment into C₄ photosynthesis. Plant Journal, 2012, 69, 47-56.	5.7	63
16	Genome-Wide Sequence and Expression Analysis of the NAC Transcription Factor Family in Polyploid Wheat. G3: Genes, Genomes, Genetics, 2017, 7, 3019-3029.	1.8	59
17	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
18	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

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19	Final grain weight is not limited by the activity of key starch-synthesising enzymes during grain filling in wheat. Journal of Experimental Botany, 2018, 69, 5461-5475.	4.8	38
20	Systematic Investigation of FLOWERING LOCUS T-Like Poaceae Gene Families Identifies the Short-Day Expressed Flowering Pathway Gene, TaFT3 in Wheat (Triticum aestivum L.). Frontiers in Plant Science, 2016, 7, 857.	3.6	37
21	Applying genomic resources to accelerate wheat biofortification. Heredity, 2020, 125, 386-395.	2.6	32
22	Blurring the boundaries between cereal crops and model plants. New Phytologist, 2020, 228, 1721-1727.	7.3	30
23	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
24	Overgrowth mutants determine the causal role of gibberellin GA2oxidaseA13 in Rht12 dwarfism of wheat. Journal of Experimental Botany, 2020, 71, 7171-7178.	4.8	28
25	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
26	Conserved residues in the wheat (Triticum aestivum) NAM-A1 NAC domain are required for protein binding and when mutated lead to delayed peduncle and flag leaf senescence. BMC Plant Biology, 2019, 19, 407.	3.6	19
27	Identification of a Dominant Chlorosis Phenotype Through a Forward Screen of the Triticum turgidum cv. Kronos TILLING Population. Frontiers in Plant Science, 2019, 10, 963.	3.6	18
28	LYS3 encodes a prolamin-box-binding transcription factor that controls embryo growth in barley and wheat. Journal of Cereal Science, 2020, 93, 102965.	3.7	14
29	A heat-shock inducible system for flexible gene expression in cereals. Plant Methods, 2020, 16, 137.	4.3	5