

Cristobal Uauy

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7091952/publications.pdf>

Version: 2024-02-01

135
papers

18,659
citations

16451

64
h-index

14759

127
g-index

179
all docs

179
docs citations

179
times ranked

12668
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, .	12.6	2,424
2	A NAC Gene Regulating Senescence Improves Grain Protein, Zinc, and Iron Content in Wheat. <i>Science</i> , 2006, 314, 1298-1301.	12.6	1,408
3	Speed breeding is a powerful tool to accelerate crop research and breeding. <i>Nature Plants</i> , 2018, 4, 23-29.	9.3	770
4	The transcriptional landscape of polyploid wheat. <i>Science</i> , 2018, 361, .	12.6	768
5	A Kinase-START Gene Confers Temperature-Dependent Resistance to Wheat Stripe Rust. <i>Science</i> , 2009, 323, 1357-1360.	12.6	625
6	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
7	Multiple wheat genomes reveal global variation in modern breeding. <i>Nature</i> , 2020, 588, 277-283.	27.8	513
8	Induction of targeted, heritable mutations in barley and Brassica oleracea using RNA-guided Cas9 nuclease. <i>Genome Biology</i> , 2015, 16, 258.	8.8	490
9	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
10	expVIP: a Customizable RNA-seq Data Analysis and Visualization Platform. <i>Plant Physiology</i> , 2016, 170, 2172-2186.	4.8	403
11	A modified TILLING approach to detect induced mutations in tetraploid and hexaploid wheat. <i>BMC Plant Biology</i> , 2009, 9, 115.	3.6	323
12	Genomic innovation for crop improvement. <i>Nature</i> , 2017, 543, 346-354.	27.8	301
13	Wheat (<i>Triticum aestivum</i>) NAM proteins regulate the translocation of iron, zinc, and nitrogen compounds from vegetative tissues to grain. <i>Journal of Experimental Botany</i> , 2009, 60, 4263-4274.	4.8	300
14	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
15	Discovery of Rare Mutations in Populations: TILLING by Sequencing $\hat{A} \hat{A}$. <i>Plant Physiology</i> , 2011, 156, 1257-1268.	4.8	266
16	Combining SNP discovery from next-generation sequencing data with bulked segregant analysis (BSA) to fine-map genes in polyploid wheat. <i>BMC Plant Biology</i> , 2012, 12, 14.	3.6	265
17	The high grain protein content gene Gpc-B1 accelerates senescence and has pleiotropic effects on protein content in wheat. <i>Journal of Experimental Botany</i> , 2006, 57, 2785-2794.	4.8	252
18	Genome analyses of the wheat yellow (stripe) rust pathogen <i>Puccinia striiformis</i> f. sp. <i>tritici</i> reveal polymorphic and haustorial expressed secreted proteins as candidate effectors. <i>BMC Genomics</i> , 2013, 14, 270.	2.8	235

#	ARTICLE	IF	CITATIONS
19	Impact of transposable elements on genome structure and evolution in bread wheat. <i>Genome Biology</i> , 2018, 19, 103.	8.8	226
20	Wheat receptor-kinase-like protein Stb6 controls gene-for-gene resistance to fungal pathogen <i>Zymoseptoria tritici</i> . <i>Nature Genetics</i> , 2018, 50, 368-374.	21.4	215
21	High-temperature adult-plant (HTAP) stripe rust resistance gene Yr36 from <i>Triticum turgidum</i> ssp. <i>dicoccoides</i> is closely linked to the grain protein content locus Gpc-B1. <i>Theoretical and Applied Genetics</i> , 2005, 112, 97-105.	3.6	208
22	Wheat Vacuolar Iron Transporter TaVIT2 Transports Fe and Mn and Is Effective for Biofortification. <i>Plant Physiology</i> , 2017, 174, 2434-2444.	4.8	206
23	PolyMarker: A fast polyploid primer design pipeline. <i>Bioinformatics</i> , 2015, 31, 2038-2039.	4.1	202
24	RNA-seq bulked segregant analysis enables the identification of high-resolution genetic markers for breeding in hexaploid wheat. <i>Plant Biotechnology Journal</i> , 2015, 13, 613-624.	8.3	202
25	BED-domain-containing immune receptors confer diverse resistance spectra to yellow rust. <i>Nature Plants</i> , 2018, 4, 662-668.	9.3	194
26	Field pathogenomics reveals the emergence of a diverse wheat yellow rust population. <i>Genome Biology</i> , 2015, 16, 23.	8.8	185
27	A splice acceptor site mutation in TaGW2-A1 increases thousand grain weight in tetraploid and hexaploid wheat through wider and longer grains. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1099-1112.	3.6	179
28	Biofortification of wheat grain with iron and zinc: integrating novel genomic resources and knowledge from model crops. <i>Frontiers in Plant Science</i> , 2014, 5, 53.	3.6	171
29	Genome sequence and genetic diversity of European ash trees. <i>Nature</i> , 2017, 541, 212-216.	27.8	166
30	Discovery and development of exome-based, co-dominant single nucleotide polymorphism markers in hexaploid wheat (<i>Triticum aestivum</i> L.). <i>Plant Biotechnology Journal</i> , 2013, 11, 279-295.	8.3	161
31	Identification and independent validation of a stable yield and thousand grain weight QTL on chromosome 6A of hexaploid wheat (<i>Triticum aestivum</i> L.). <i>BMC Plant Biology</i> , 2014, 14, 191.	3.6	161
32	Genomics as the key to unlocking the polyploid potential of wheat. <i>New Phytologist</i> , 2015, 208, 1008-1022.	7.3	151
33	Physical map of the wheat high-grain protein content gene Gpc-B1 and development of a high-throughput molecular marker. <i>New Phytologist</i> , 2006, 169, 753-763.	7.3	150
34	The NLR-Annotator Tool Enables Annotation of the Intracellular Immune Receptor Repertoire. <i>Plant Physiology</i> , 2020, 183, 468-482.	4.8	147
35	Gene editing and mutagenesis reveal inter-cultivar differences and additivity in the contribution of TaGW2 homoeologues to grain size and weight in wheat. <i>Theoretical and Applied Genetics</i> , 2018, 131, 2463-2475.	3.6	142
36	Wheat Stripe Rust Resistance Protein WKS1 Reduces the Ability of the Thylakoid-Associated Ascorbate Peroxidase to Detoxify Reactive Oxygen Species. <i>Plant Cell</i> , 2015, 27, 1755-1770.	6.6	133

#	ARTICLE	IF	CITATIONS
37	Diversity analysis of 80,000 wheat accessions reveals consequences and opportunities of selection footprints. <i>Nature Communications</i> , 2020, 11, 4572.	12.8	129
38	<i>Rht18</i> Semidwarfism in Wheat Is Due to Increased <i>GA 2-oxidaseA9</i> Expression and Reduced GA Content. <i>Plant Physiology</i> , 2018, 177, 168-180.	4.8	128
39	Separating homeologs by phasing in the tetraploid wheat transcriptome. <i>Genome Biology</i> , 2013, 14, R66.	8.8	126
40	Exploiting the ZIP4 homologue within the wheat Ph1 locus has identified two lines exhibiting homoeologous crossover in wheat-wild relative hybrids. <i>Molecular Breeding</i> , 2017, 37, 95.	2.1	126
41	A Metabolic Gene Cluster in the Wheat <i>W1</i> and the Barley <i>Cer-cqu</i> Loci Determines Î²-Diketone Biosynthesis and Glaucousness. <i>Plant Cell</i> , 2016, 28, 1440-1460.	6.6	123
42	A reductionist approach to dissecting grain weight and yield in wheat. <i>Journal of Integrative Plant Biology</i> , 2019, 61, 337-358.	8.5	122
43	Genome-Wide Association Study of Grain Architecture in Wild Wheat <i>Aegilops tauschii</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 886.	3.6	114
44	Microcolinearity between a 2-cM region encompassing the grain protein content locus <i>Gpc-6B1</i> on wheat chromosome 6B and a 350-kb region on rice chromosome 2. <i>Functional and Integrative Genomics</i> , 2004, 4, 59-66.	3.5	109
45	TILLING <i>in extremis</i> . <i>Plant Biotechnology Journal</i> , 2012, 10, 761-772.	8.3	109
46	The Genetic Basis of Composite Spike Form in Barley and "Miracle-Wheat". <i>Genetics</i> , 2015, 201, 155-165.	2.9	109
47	The host-pathogen interaction between wheat and yellow rust induces temporally coordinated waves of gene expression. <i>BMC Genomics</i> , 2016, 17, 380.	2.8	105
48	Increased pericarp cell length underlies a major quantitative trait locus for grain weight in hexaploid wheat. <i>New Phytologist</i> , 2017, 215, 1026-1038.	7.3	103
49	Wheat genomics comes of age. <i>Current Opinion in Plant Biology</i> , 2017, 36, 142-148.	7.1	103
50	Population genomic analysis of <i>Aegilops tauschii</i> identifies targets for bread wheat improvement. <i>Nature Biotechnology</i> , 2022, 40, 422-431.	17.5	102
51	Combining Traditional Mutagenesis with New High-Throughput Sequencing and Genome Editing to Reveal Hidden Variation in Polyploid Wheat. <i>Annual Review of Genetics</i> , 2017, 51, 435-454.	7.6	100
52	Genomics reveals new landscapes for crop improvement. <i>Genome Biology</i> , 2013, 14, 206.	8.8	99
53	Induced Mutations in the <i>Starch Branching Enzyme II</i> (<i>SBEII</i>) Genes Increase Amylose and Resistant Starch Content in Durum Wheat. <i>Crop Science</i> , 2012, 52, 1754-1766.	1.8	97
54	Down-regulation of four putative arabinoxylan feruloyl transferase genes from family PF02458 reduces ester-linked ferulate content in rice cell walls. <i>Planta</i> , 2010, 231, 677-691.	3.2	90

#	ARTICLE	IF	CITATIONS
55	Functional characterization of GPC-1 genes in hexaploid wheat. <i>Planta</i> , 2014, 239, 313-324.	3.2	85
56	Enabling reusability of plant phenomic datasets with MIAPPE 1.1. <i>New Phytologist</i> , 2020, 227, 260-273.	7.3	84
57	Applying the latest advances in genomics and phenomics for trait discovery in polyploid wheat. <i>Plant Journal</i> , 2019, 97, 56-72.	5.7	83
58	The <i>W1</i> inhibitor of wax 1 locus (<i>W1</i>) prevents formation of β -diketones in wheat cuticular waxes and maps to a sub-M interval on chromosome arm 2BS. <i>Plant Journal</i> , 2013, 74, 989-1002.	5.7	82
59	The <i>Cer-cqu</i> gene cluster determines three key players in a β -diketone synthase polyketide pathway synthesizing aliphatics in epicuticular waxes. <i>Journal of Experimental Botany</i> , 2016, 67, 2715-2730.	4.8	81
60	A roadmap for gene functional characterisation in crops with large genomes: Lessons from polyploid wheat. <i>ELife</i> , 2020, 9, .	6.0	78
61	RNA interference for wheat functional gene analysis. <i>Transgenic Research</i> , 2007, 16, 689-701.	2.4	76
62	Effect of the down-regulation of the high Grain Protein Content (GPC) genes on the wheat transcriptome during monocarpic senescence. <i>BMC Genomics</i> , 2011, 12, 492.	2.8	75
63	Wheat root systems as a breeding target for climate resilience. <i>Theoretical and Applied Genetics</i> , 2021, 134, 1645-1662.	3.6	74
64	Identification of Transcription Factors Regulating Senescence in Wheat through Gene Regulatory Network Modelling. <i>Plant Physiology</i> , 2019, 180, 1740-1755.	4.8	73
65	Wheat Grain Filling Is Limited by Grain Filling Capacity rather than the Duration of Flag Leaf Photosynthesis: A Case Study Using NAM RNAi Plants. <i>PLoS ONE</i> , 2015, 10, e0134947.	2.5	73
66	Colinearity between the barley grain protein content (GPC) QTL on chromosome arm 6HS and the wheat <i>Gpc-B1</i> region. <i>Molecular Breeding</i> , 2008, 22, 25-38.	2.1	70
67	Divergent functions of orthologous NAC transcription factors in wheat and rice. <i>Plant Molecular Biology</i> , 2012, 78, 515-524.	3.9	70
68	Improving wheat as a source of iron and zinc for global nutrition. <i>Nutrition Bulletin</i> , 2019, 44, 53-59.	1.8	69
69	A haplotype-led approach to increase the precision of wheat breeding. <i>Communications Biology</i> , 2020, 3, 712.	4.4	68
70	Mutation Scanning in Wheat by Exon Capture and Next-Generation Sequencing. <i>PLoS ONE</i> , 2015, 10, e0137549.	2.5	65
71	Strategy for exploiting exotic germplasm using genetic, morphological, and environmental diversity: the <i>Aegilops tauschii</i> Coss. example. <i>Theoretical and Applied Genetics</i> , 2013, 126, 1793-1808.	3.6	62
72	Identification of a major QTL controlling the content of B-type starch granules in <i>Aegilops</i> . <i>Journal of Experimental Botany</i> , 2011, 62, 2217-2228.	4.8	59

#	ARTICLE	IF	CITATIONS
73	Genome-Wide Sequence and Expression Analysis of the NAC Transcription Factor Family in Polyploid Wheat. <i>C3: Genes, Genomes, Genetics</i> , 2017, 7, 3019-3029.	1.8	59
74	Strategies to improve wheat for human health. <i>Nature Food</i> , 2020, 1, 475-480.	14.0	54
75	The wheatPhs-A1pre-harvest sprouting resistance locus delays the rate of seed dormancy loss and maps 0.3 cM distal to thePM19genes in UK germplasm. <i>Journal of Experimental Botany</i> , 2016, 67, 4169-4178.	4.8	53
76	Agricultural Selection of Wheat Has Been Shaped by Plant-Microbe Interactions. <i>Frontiers in Microbiology</i> , 2020, 11, 132.	3.5	53
77	Haplotype Analysis of the Pre-harvest Sprouting Resistance Locus Phs-A1 Reveals a Causal Role of TaMKK3-A in Global Germplasm. <i>Frontiers in Plant Science</i> , 2017, 8, 1555.	3.6	50
78	Genome-Wide Association Mapping of Grain Micronutrients Concentration in <i>Aegilops tauschii</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 54.	3.6	45
79	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
80	A change in temperature modulates defence to yellow (stripe) rust in wheat line UC1041 independently of resistance gene Yr36. <i>BMC Plant Biology</i> , 2014, 14, 10.	3.6	41
81	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
82	Reduced height alleles (Rht) and Hagberg falling number of wheat. <i>Journal of Cereal Science</i> , 2012, 55, 305-311.	3.7	39
83	Heat in Wheat: Exploit Reverse Genetic Techniques to Discover New Alleles Within the <i>Triticum durum</i> sHsp26 Family. <i>Frontiers in Plant Science</i> , 2018, 9, 1337.	3.6	38
84	Final grain weight is not limited by the activity of key starch-synthesising enzymes during grain filling in wheat. <i>Journal of Experimental Botany</i> , 2018, 69, 5461-5475.	4.8	38
85	Systematic Investigation of FLOWERING LOCUS T-Like Poaceae Gene Families Identifies the Short-Day Expressed Flowering Pathway Gene, TaFT3 in Wheat (<i>Triticum aestivum</i> L.). <i>Frontiers in Plant Science</i> , 2016, 7, 857.	3.6	37
86	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
87	Ectopic expression of <i>Triticum polonicum</i> VRT-A2 underlies elongated glumes and grains in hexaploid wheat in a dosage-dependent manner. <i>Plant Cell</i> , 2021, 33, 2296-2319.	6.6	36
88	Copy number variation of <i>TdDof</i> controls solid-stemmed architecture in wheat. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 28708-28718.	7.1	33
89	<i>ENHANCED GRAVITROPISM 2</i> encodes a STERILE ALPHA MOTIF-containing protein that controls root growth angle in barley and wheat. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	32
90	Dissecting the genetic basis of wheat blast resistance in the Brazilian wheat cultivar BR 18-Terena. <i>BMC Plant Biology</i> , 2020, 20, 398.	3.6	30

#	ARTICLE	IF	CITATIONS
91	The membrane-localized protein kinase MAP4K4/TOT3 regulates thermomorphogenesis. <i>Nature Communications</i> , 2021, 12, 2842.	12.8	30
92	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
93	Ubiquitin-related genes are differentially expressed in isogenic lines contrasting for pericarp cell size and grain weight in hexaploid wheat. <i>BMC Plant Biology</i> , 2018, 18, 22.	3.6	29
94	<i>Aegilops umbellulata</i> introgression carrying leaf rust and stripe rust resistance genes Lr76 and Yr70 located to 9.47-Mb region on 5DS telomeric end through a combination of chromosome sorting and sequencing. <i>Theoretical and Applied Genetics</i> , 2020, 133, 903-915.	3.6	26
95	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
96	Transfer of a starch phenotype from wild wheat to bread wheat by deletion of a locus controlling B-type starch granule content. <i>Journal of Experimental Botany</i> , 2017, 68, 5497-5509.	4.8	22
97	The Wheat GENIE3 Network Provides Biologically-Relevant Information in Polyploid Wheat. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3675-3686.	1.8	21
98	FANCM promotes class I interfering crossovers and suppresses class II non-interfering crossovers in wheat meiosis. <i>Nature Communications</i> , 2022, 13, .	12.8	21
99	Application of TILLING for Orphan Crop Improvement. , 2013, , 83-113.		20
100	Conserved residues in the wheat (<i>Triticum aestivum</i>) NAM-A1 NAC domain are required for protein binding and when mutated lead to delayed peduncle and flag leaf senescence. <i>BMC Plant Biology</i> , 2019, 19, 407.	3.6	19
101	MicroRNA-resistant alleles of <i>HOMEBOX DOMAIN-2</i> modify inflorescence branching and increase grain protein content of wheat. <i>Science Advances</i> , 2022, 8, eabn5907.	10.3	19
102	Barley lys3 mutants are unique amongst shrunken-endosperm mutants in having abnormally large embryos. <i>Journal of Cereal Science</i> , 2018, 82, 16-24.	3.7	18
103	Identification of a Dominant Chlorosis Phenotype Through a Forward Screen of the <i>Triticum turgidum</i> cv. Kronos TILLING Population. <i>Frontiers in Plant Science</i> , 2019, 10, 963.	3.6	18
104	Crossover-active regions of the wheat genome are distinguished by DMC1, the chromosome axis, H3K27me3, and signatures of adaptation. <i>Genome Research</i> , 2021, 31, 1614-1628.	5.5	18
105	Genetic Screening for Mutants with Altered Seminal Root Numbers in Hexaploid Wheat Using a High-Throughput Root Phenotyping Platform. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2799-2809.	1.8	17
106	Exome sequencing of bulked segregants identified a novel TaMKK3-A allele linked to the wheat ERA8 ABA-hypersensitive germination phenotype. <i>Theoretical and Applied Genetics</i> , 2020, 133, 719-736.	3.6	17
107	High expression of the MADS-box gene <i>VRT2</i> increases the number of rudimentary basal spikelets in wheat. <i>Plant Physiology</i> , 2022, 189, 1536-1552.	4.8	17
108	Development of mlo-based resistance in tetraploid wheat against wheat powdery mildew. <i>Theoretical and Applied Genetics</i> , 2019, 132, 3009-3022.	3.6	16

#	ARTICLE	IF	CITATIONS
109	New insights into homoeologous copy number variations in the hexaploid wheat genome. <i>Plant Genome</i> , 2021, 14, e20069.	2.8	16
110	A saturated SNP linkage map for the orange wheat blossom midge resistance gene Sm1. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1507-1517.	3.6	15
111	The eyespot resistance genes Pch1 and Pch2 of wheat are not homoeoloci. <i>Theoretical and Applied Genetics</i> , 2017, 130, 91-107.	3.6	15
112	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
113	LYS3 encodes a prolamins-box-binding transcription factor that controls embryo growth in barley and wheat. <i>Journal of Cereal Science</i> , 2020, 93, 102965.	3.7	14
114	Discovery and characterisation of a new leaf rust resistance gene introgressed in wheat from wild wheat <i>Aegilops peregrina</i> . <i>Scientific Reports</i> , 2020, 10, 7573.	3.3	13
115	Genetic Characterization of a Wheat Association Mapping Panel Relevant to Brazilian Breeding Using a High-Density Single Nucleotide Polymorphism Array. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2229-2239.	1.8	12
116	Genome-wide association mapping identifies yellow rust resistance loci in Ethiopian durum wheat germplasm. <i>PLoS ONE</i> , 2021, 16, e0243675.	2.5	12
117	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
118	<i>Yr36</i> Confers Partial Resistance at Temperatures Below 18°C to U.K. Isolates of <i>Puccinia striiformis</i> . <i>Phytopathology</i> , 2014, 104, 871-878.	2.2	11
119	Fine mapping of <i>Aegilops peregrina</i> co-segregating leaf and stripe rust resistance genes to distal-most end of 5DS. <i>Theoretical and Applied Genetics</i> , 2019, 132, 1473-1485.	3.6	8
120	Characterization of wheat lacking B-type starch granules. <i>Journal of Cereal Science</i> , 2022, 104, 103398.	3.7	8
121	Comparative Genomics and Functional Studies of Wheat BED-NLR Loci. <i>Genes</i> , 2020, 11, 1406.	2.4	7
122	Identification of Fusarium head blight resistance loci in two Brazilian wheat mapping populations. <i>PLoS ONE</i> , 2021, 16, e0248184.	2.5	7
123	Plant Genomics: Unlocking the Genome of Wheat's Progenitor. <i>Current Biology</i> , 2017, 27, R1122-R1124.	3.9	6
124	Insights into the resistance of a synthetically-derived wheat to <i>Septoria tritici</i> blotch disease: less is more. <i>BMC Plant Biology</i> , 2020, 20, 407.	3.6	6
125	A heat-shock inducible system for flexible gene expression in cereals. <i>Plant Methods</i> , 2020, 16, 137.	4.3	5
126	Pathogenomic analyses of <i>Puccinia striiformis</i> f. sp. <i>tritici</i> supports a close genetic relationship between South and East Africa. <i>Plant Pathology</i> , 2022, 71, 279-288.	2.4	5

#	ARTICLE	IF	CITATIONS
127	Trend, population structure, and trait mapping from 15 years of national varietal trials of UK winter wheat. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	5
128	Yield reduction historically associated with the <i>Aegilops ventricosa</i> 7DV introgression is genetically and physically distinct from the eyespot resistance gene Pch1. <i>Theoretical and Applied Genetics</i> , 2020, 133, 707-717.	3.6	4
129	Allelic diversity study of functional genes in East Africa bread wheat highlights opportunities for genetic improvement. <i>Molecular Breeding</i> , 2020, 40, 1.	2.1	4
130	The <i>Triticum ispahanicum</i> elongated glume locus P2 maps to chromosome 6A and is associated with the ectopic expression of SVP-A1. <i>Theoretical and Applied Genetics</i> , 2022, , .	3.6	4
131	Distribution of <i>Puccinia striiformis</i> f. sp. <i>tritici</i> Races and Virulence in Wheat Growing Regions of Kenya from 1970 to 2014. <i>Plant Disease</i> , 2022, 106, 701-710.	1.4	3
132	Identification and mapping of resistance to stem rust in the European winter wheat cultivars Spark and Rialto. <i>Molecular Breeding</i> , 2016, 36, 1.	2.1	2
133	Evaluation of the susceptibility of modern, wild, ancestral, and mutational wheat lines to <i>Septoria tritici</i> blotch disease. <i>Plant Pathology</i> , 2021, 70, 1123-1137.	2.4	2
134	A robust KASP marker for selection of four pairs of linked leaf rust and stripe rust resistance genes introgressed on chromosome arm 5DS from different wheat genomes. <i>Molecular Biology Reports</i> , 2021, 48, 5209-5216.	2.3	2
135	Next Generation Sequencing Enabled Genetics in Hexaploid Wheat. , 2015, , 201-209.		0