

# Cristobal Uauy

## List of Publications by Year in descending order

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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  | 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         |
| 2  | 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         |
| 3  | 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       |
| 4  | Characterization of wheat lacking B-type starch granules. <i>Journal of Cereal Science</i> , 2022, 104, 103398.  | 3.7  | 8         |
| 5  | 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        |
| 6  | 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         |
| 7  | 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        |
| 8  | 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        |
| 9  | 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         |
| 10 | 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        |
| 11 | New insights into homoeologous copy number variations in the hexaploid wheat genome. <i>Plant Genome</i> , 2021, 14, e20069.   | 2.8  | 16        |
| 12 | Identification of <i>Fusarium</i> head blight resistance loci in two Brazilian wheat mapping populations. <i>PLoS ONE</i> , 2021, 16, e0248184.  | 2.5  | 7         |
| 13 | 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         |
| 14 | Wheat root systems as a breeding target for climate resilience. <i>Theoretical and Applied Genetics</i> , 2021, 134, 1645-1662.  | 3.6  | 74        |
| 15 | The membrane-localized protein kinase MAP4K4/TOT3 regulates thermomorphogenesis. <i>Nature Communications</i> , 2021, 12, 2842.  | 12.8 | 30        |
| 16 | Genome-wide association mapping identifies yellow rust resistance loci in Ethiopian durum wheat germplasm. <i>PLoS ONE</i> , 2021, 16, e0243675.   | 2.5  | 12        |
| 17 | Ectopic expression of <i>Triticum polonicum</i> <i>VRT-A2</i> underlies elongated glumes and grains in hexaploid wheat in a dosage-dependent manner. <i>Plant Cell</i> , 2021, 33, 2296-2319.                                  | 6.6  | 36        |
| 18 | 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         |

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|----|--|------|-----------|
| 19 | <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        |
| 20 | 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        |
| 21 | 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        |
| 22 | <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        |
| 23 | 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         |
| 24 | 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         |
| 25 | A heat-shock inducible system for flexible gene expression in cereals. <i>Plant Methods</i> , 2020, 16, 137.   | 4.3  | 5         |
| 26 | 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        |
| 27 | 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         |
| 28 | Multiple wheat genomes reveal global variation in modern breeding. <i>Nature</i> , 2020, 588, 277-283.   | 27.8 | 513       |
| 29 | A haplotype-led approach to increase the precision of wheat breeding. <i>Communications Biology</i> , 2020, 3, 712.  | 4.4  | 68        |
| 30 | Comparative Genomics and Functional Studies of Wheat BED-NLR Loci. <i>Genes</i> , 2020, 11, 1406.  | 2.4  | 7         |
| 31 | The Wheat GENIE3 Network Provides Biologically-Relevant Information in Polyploid Wheat. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3675-3686.   | 1.8  | 21        |
| 32 | 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        |
| 33 | 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        |
| 34 | Diversity analysis of 80,000 wheat accessions reveals consequences and opportunities of selection footprints. <i>Nature Communications</i> , 2020, 11, 4572.   | 12.8 | 129       |
| 35 | Strategies to improve wheat for human health. <i>Nature Food</i> , 2020, 1, 475-480.   | 14.0 | 54        |
| 36 | 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        |

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|----|---|-----|-----------|
| 37 | 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        |
| 38 | The NLR-Annotator Tool Enables Annotation of the Intracellular Immune Receptor Repertoire. <i>Plant Physiology</i> , 2020, 183, 468-482.  | 4.8 | 147       |
| 39 | Enabling reusability of plant phenomic datasets with MIAPPE 1.1. <i>New Phytologist</i> , 2020, 227, 260-273.   | 7.3 | 84        |
| 40 | Agricultural Selection of Wheat Has Been Shaped by Plant-Microbe Interactions. <i>Frontiers in Microbiology</i> , 2020, 11, 132.  | 3.5 | 53        |
| 41 | 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        |
| 42 | 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        |
| 43 | A roadmap for gene functional characterisation in crops with large genomes: Lessons from polyploid wheat. <i>ELife</i> , 2020, 9, .   | 6.0 | 78        |
| 44 | 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        |
| 45 | 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        |
| 46 | 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        |
| 47 | 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        |
| 48 | 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        |
| 49 | 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        |
| 50 | 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         |
| 51 | 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        |
| 52 | Identification of Transcription Factors Regulating Senescence in Wheat through Gene Regulatory Network Modelling. <i>Plant Physiology</i> , 2019, 180, 1740-1755.   | 4.8 | 73        |
| 53 | Improving wheat as a source of iron and zinc for global nutrition. <i>Nutrition Bulletin</i> , 2019, 44, 53-59.   | 1.8 | 69        |
| 54 | 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        |

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|----|---|------|-----------|
| 55 | 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       |
| 56 | 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        |
| 57 | Wheat receptor-kinase-like protein <i>Stb6</i> controls gene-for-gene resistance to fungal pathogen <i>Zymoseptoria tritici</i> . <i>Nature Genetics</i> , 2018, 50, 368-374.   | 21.4 | 215       |
| 58 | Speed breeding is a powerful tool to accelerate crop research and breeding. <i>Nature Plants</i> , 2018, 4, 23-29.  | 9.3  | 770       |
| 59 | <i>Rht18</i> Semidwarfism in Wheat Is Due to Increased <i>GA 2-oxidase9</i> Expression and Reduced GA Content. <i>Plant Physiology</i> , 2018, 177, 168-180.  | 4.8  | 128       |
| 60 | 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       |
| 61 | Genome-Wide Transcription During Early Wheat Meiosis Is Independent of Synapsis, Ploidy Level, and the <i>Ph1</i> Locus. <i>Frontiers in Plant Science</i> , 2018, 9, 1791.   | 3.6  | 44        |
| 62 | Heat in Wheat: Exploit Reverse Genetic Techniques to Discover New Alleles Within the <i>Triticum durum</i> <i>sHsp26</i> Family. <i>Frontiers in Plant Science</i> , 2018, 9, 1337.   | 3.6  | 38        |
| 63 | 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        |
| 64 | 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        |
| 65 | Barley <i>lys3</i> 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        |
| 66 | Gene editing and mutagenesis reveal inter-cultivar differences and additivity in the contribution of <i>TaGW2</i> homologues to grain size and weight in wheat. <i>Theoretical and Applied Genetics</i> , 2018, 131, 2463-2475. | 3.6  | 142       |
| 67 | BED-domain-containing immune receptors confer diverse resistance spectra to yellow rust. <i>Nature Plants</i> , 2018, 4, 662-668.   | 9.3  | 194       |
| 68 | The transcriptional landscape of polyploid wheat. <i>Science</i> , 2018, 361, .   | 12.6 | 768       |
| 69 | Shifting the limits in wheat research and breeding using a fully annotated reference genome. <i>Science</i> , 2018, 361, .  | 12.6 | 2,424     |
| 70 | Impact of transposable elements on genome structure and evolution in bread wheat. <i>Genome Biology</i> , 2018, 19, 103.  | 8.8  | 226       |
| 71 | 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       |
| 72 | 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       |

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|----|--|------|-----------|
| 73 | 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       |
| 74 | Wheat genomics comes of age. <i>Current Opinion in Plant Biology</i> , 2017, 36, 142-148.  | 7.1  | 103       |
| 75 | Genomic innovation for crop improvement. <i>Nature</i> , 2017, 543, 346-354.   | 27.8 | 301       |
| 76 | Genome sequence and genetic diversity of European ash trees. <i>Nature</i> , 2017, 541, 212-216.   | 27.8 | 166       |
| 77 | Plant Genomics: Unlocking the Genome of Wheat's Progenitor. <i>Current Biology</i> , 2017, 27, R1122-R1124.  | 3.9  | 6         |
| 78 | 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       |
| 79 | 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       |
| 80 | Genome-Wide Sequence and Expression Analysis of the NAC Transcription Factor Family in Polyploid Wheat. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3019-3029.  | 1.8  | 59        |
| 81 | 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       |
| 82 | 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        |
| 83 | 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        |
| 84 | 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       |
| 85 | 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        |
| 86 | 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        |
| 87 | 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       |
| 88 | 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       |
| 89 | 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         |
| 90 | 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        |

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|-----|--|-----|-----------|
| 91  | The <i>Cer-cqu</i> gene cluster determines three key players in a $\beta^2$ -diketone synthase polyketide pathway synthesizing aliphatics in epicuticular waxes. <i>Journal of Experimental Botany</i> , 2016, 67, 2715-2730.      | 4.8 | 81        |
| 92  | The wheat <i>Phs-A1</i> pre-harvest sprouting resistance locus delays the rate of seed dormancy loss and maps 0.3 cM distal to the <i>PM19</i> genes in UK germplasm. <i>Journal of Experimental Botany</i> , 2016, 67, 4169-4178. | 4.8 | 53        |
| 93  | A splice acceptor site mutation in <i>TaGW2-A1</i> 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       |
| 94  | expVIP: a Customizable RNA-seq Data Analysis and Visualization Platform. <i>Plant Physiology</i> , 2016, 170, 2172-2186.   | 4.8 | 403       |
| 95  | Genomics as the key to unlocking the polyploid potential of wheat. <i>New Phytologist</i> , 2015, 208, 1008-1022.  | 7.3 | 151       |
| 96  | The Genetic Basis of Composite Spike Form in Barley and "Miracle-Wheat"™. <i>Genetics</i> , 2015, 201, 155-165.  | 2.9 | 109       |
| 97  | Mutation Scanning in Wheat by Exon Capture and Next-Generation Sequencing. <i>PLoS ONE</i> , 2015, 10, e0137549.   | 2.5 | 65        |
| 98  | Induction of targeted, heritable mutations in barley and <i>Brassica oleracea</i> using RNA-guided Cas9 nuclease. <i>Genome Biology</i> , 2015, 16, 258.   | 8.8 | 490       |
| 99  | PolyMarker: A fast polyploid primer design pipeline. <i>Bioinformatics</i> , 2015, 31, 2038-2039.  | 4.1 | 202       |
| 100 | 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       |
| 101 | Field pathogenomics reveals the emergence of a diverse wheat yellow rust population. <i>Genome Biology</i> , 2015, 16, 23.   | 8.8 | 185       |
| 102 | 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       |
| 103 | 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        |
| 104 | Next Generation Sequencing Enabled Genetics in Hexaploid Wheat. , 2015, , 201-209.   |     | 0         |
| 105 | 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       |
| 106 | A change in temperature modulates defence to yellow (stripe) rust in wheat line UC1041 independently of resistance gene <i>Yr36</i> . <i>BMC Plant Biology</i> , 2014, 14, 10.   | 3.6 | 41        |
| 107 | Functional characterization of <i>GPC-1</i> genes in hexaploid wheat. <i>Planta</i> , 2014, 239, 313-324.  | 3.2 | 85        |
| 108 | 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       |

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|-----|---|-----|-----------|
| 109 | <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        |
| 110 | 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       |
| 111 | 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        |
| 112 | Genomics reveals new landscapes for crop improvement. <i>Genome Biology</i> , 2013, 14, 206.  | 8.8 | 99        |
| 113 | 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       |
| 114 | Application of TILLING for Orphan Crop Improvement. , 2013, , 83-113.   |     | 20        |
| 115 | The inhibitor of wax 1 locus ( <i>W1</i> ) prevents formation of $\alpha$ - and $\beta$ -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        |
| 116 | Separating homeologs by phasing in the tetraploid wheat transcriptome. <i>Genome Biology</i> , 2013, 14, R66.   | 8.8 | 126       |
| 117 | Reduced height alleles ( <i>Rht</i> ) and Hagberg falling number of wheat. <i>Journal of Cereal Science</i> , 2012, 55, 305-311.  | 3.7 | 39        |
| 118 | TILLING in <i>extremis</i> . <i>Plant Biotechnology Journal</i> , 2012, 10, 761-772.  | 8.3 | 109       |
| 119 | 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       |
| 120 | Divergent functions of orthologous NAC transcription factors in wheat and rice. <i>Plant Molecular Biology</i> , 2012, 78, 515-524.   | 3.9 | 70        |
| 121 | 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        |
| 122 | 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        |
| 123 | Discovery of Rare Mutations in Populations: TILLING by Sequencing $\hat{A} \hat{A}$ . <i>Plant Physiology</i> , 2011, 156, 1257-1268.   | 4.8 | 266       |
| 124 | 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        |
| 125 | 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        |
| 126 | A modified TILLING approach to detect induced mutations in tetraploid and hexaploid wheat. <i>BMC Plant Biology</i> , 2009, 9, 115.   | 3.6 | 323       |

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|-----|--|------|-----------|
| 127 | 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       |
| 128 | A Kinase-START Gene Confers Temperature-Dependent Resistance to Wheat Stripe Rust. <i>Science</i> , 2009, 323, 1357-1360.  | 12.6 | 625       |
| 129 | Colinearity between the barley grain protein content (GPC) QTL on chromosome arm 6HS and the wheat Gpc-B1 region. <i>Molecular Breeding</i> , 2008, 22, 25-38.   | 2.1  | 70        |
| 130 | RNA interference for wheat functional gene analysis. <i>Transgenic Research</i> , 2007, 16, 689-701.   | 2.4  | 76        |
| 131 | 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     |
| 132 | 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       |
| 133 | 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       |
| 134 | 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       |
| 135 | Microcolinearity between a 2-cM region encompassing the grain protein content locus Gpc-6B1 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       |