# CITATION REPORT
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# GAPIT: genome association and prediction integrated tool

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| 1014 | Multi-Locus Genome-Wide Association Studies Reveal Fruit Quality Hotspots in Peach Genome. **2021**, 12, 644799 | 3 |
| 1013 | Identification of SNPs associated with magnesium and sodium uptake and the effect of their accumulation on micro and macro nutrient levels in. **2021**, 9, e10773 | 2 |
| 1012 | Genome-wide association improves genomic selection for ammonia tolerance in the orange-spotted grouper (Epinephelus coioides). **2021**, 533, 736214 | 7 |

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| 1011 | An Integrated Approach of QTL Mapping and Genome-Wide Association Analysis Identifies Candidate Genes for Phytophthora Blight Resistance in Sesame ( L.). **2021**, 12, 604709 | 8 |
| 1010 | Population genetics and genome-wide association studies provide insights into the influence of selective breeding on genetic variation in lettuce. **2021**, 14, e20086 | 3 |
| 1009 | Application of Genomics to Understand Salt Tolerance in Lentil. **2021**, 12, | 2 |
| 1008 | Nuclear and Chloroplast Genome Diversity Revealed by Low-Coverage Whole-Genome Shotgun Sequence in 44 Brassica oleracea Breeding Lines. **2021**, 7, 539-539 | 2 |
| 1007 | Uncovering candidate genes involved in photosynthetic capacity using unexplored genetic variation in Spring Wheat. **2021**, 19, 1537-1552 | 8 |
| 1006 | Associative transcriptomics study dissects the genetic architecture of seedling biomass-related traits in rapeseed (Brassica napus L.). **2021**, 140, 285-293 | |
| 1005 | Combination of Genome-Wide Association Study and QTL Mapping Reveals the Genetic Architecture of Fusarium Stalk Rot in Maize. **2021**, 2, | 0 |
| 1004 | TheParastagonospora nodorumnecrotrophic effector SnTox5 targets the wheat geneSnn5and facilitates entry into the leaf mesophyll. | 1 |
| 1003 | An epigenetic pathway in rice connects genetic variation to anaerobic germination and seedling establishment. **2021**, 186, 1042-1059 | 6 |
| 1002 | Genome wide association analyses to understand genetic basis of flowering and plant height under three levels of nitrogen application in´Brassica juncea´(L.) Czern & Coss. **2021**, 11, 4278 | 8 |
| 1001 | Sorghum pan-genome explores the functional utility to accelerate the genetic gain. | 1 |
| 1000 | Genome-Wide Association Study of Topsoil Root System Architecture in Field-Grown Soybean [ (L.) Merr.]. **2020**, 11, 590179 | 2 |
| 999 | Genome-wide association study in hexaploid wheat identifies novel genomic regions associated with resistance to root lesion nematode (Pratylenchus thornei). **2021**, 11, 3572 | 4 |
| 998 | Genome-wide association study suggests an independent genetic basis of zinc and cadmium concentrations in fresh sweet corn kernels. | 0 |
| 997 | A classic approach for determining genomic prediction accuracy under terminal drought stress and well-watered conditions in wheat landraces and cultivars. **2021**, 16, e0247824 | 1 |
| 996 | Association Mapping and Transcriptome Analysis Reveal the Genetic Architecture of Maize Kernel Size. **2021**, 12, 632788 | 1 |
| 995 | Genetic Architecture of Kernel Compositional Variation in a Maize Diversity Panel. | 1 |
| 994 | Genome-wide association study reveals the genetic basis of yield- and quality-related traits in wheat. **2021**, 21, 144 | 3 |

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| 993 | Genome-wide association study and gene network analyses reveal potential candidate genes for high night temperature tolerance in rice. **2021**, 11, 6747 | 4 |
| 992 | Genome-wide association study of drought tolerance in cassava. **2021**, 217, 1 | 2 |
| 991 | High-resolution genome-wide association study pinpoints metal transporter and chelator genes involved in the genetic control of element levels in maize grain. **2021**, 11, | 3 |
| 990 | Identification of anthracnose (Colletotrichum lentis) race 1 resistance loci in lentil by integrating linkage mapping and a genome-wide association study. | 1 |
| 989 | QTL Analysis of Adult Plant Resistance to Stripe Rust in a Winter Wheat Recombinant Inbred Population. **2021**, 10, | 1 |
| 988 | Identification of SNP markers associated with soybean fatty acids contents by genome-wide association analyses. **2021**, 41, 1 | 2 |
| 987 | Genome-wide association study and identification of candidate genes for seed oil content in Brassica napus. **2021**, 217, 1 | 2 |
| 986 | First genomic prediction and genome-wide association for complex growth-related traits in Rock Bream ().. **2022**, 15, 523-536 | 3 |
| 985 | Uncovering genomic regions controlling plant architectural traits in hexaploid wheat using different GWAS models. **2021**, 11, 6767 | 7 |
| 984 | Genome-wide association study to identify chromosomal regions related to panicle architecture in rice (Oryza sativa). **2021**, 68, 2849-2865 | 0 |
| 983 | Genome-wide association mapping identifies novel loci underlying fire blight resistance in apple. **2021**, 14, e20087 | 2 |
| 982 | Candidate Rlm6 resistance genes against Leptosphaeria. maculans identified through a genome-wide association study in Brassica juncea (L.) Czern. **2021**, 134, 2035-2050 | 4 |
| 981 | Interdisciplinary strategies to enable data-driven plant breeding in a changing climate. **2021**, 4, 372-383 | 3 |
| 980 | Genome wide association mapping for heat tolerance in sub-tropical maize. **2021**, 22, 154 | 9 |
| 979 | rMVP: A Memory-efficient, Visualization-enhanced, and Parallel-accelerated tool for Genome-Wide Association Study. **2021**, | 78 |
| 978 | NAC Candidate Gene Marker for and Interaction With QTL for Resistance to in Common Bean. **2021**, 12, 628443 | 3 |
| 977 | Genome-Wide Association Studies of Mineral Content in Common Bean. **2021**, 12, 636484 | 10 |
| 976 | Dissecting the genetic basis of grain morphology traits in Chinese wheat by genome wide association study. **2021**, 217, 1 | 4 |

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| 975 | Genome-wide association analysis of bean fly resistance and agro-morphological traits in common bean. **2021**, 16, e0250729 | 1 |
| 974 | Genomic Basis of Striking Fin Shapes and Colors in the Fighting Fish. **2021**, 38, 3383-3396 | 13 |
| 973 | Genome-wide association analysis for response of Senegalese sorghum accessions to Texas isolates of anthracnose. **2021**, 14, e20097 | 1 |
| 972 | Genome-wide association study reveals candidate genes for flowering time in cowpea (Vigna unguiculata [L.] Walp). | |
| 971 | Population structure and genome-wide association studies in bread wheat for phosphorus efficiency traits using 35´K Wheat Breeder's Affymetrix array. **2021**, 11, 7601 | 3 |
| 970 | GWAS of pod morphological and color characters in common bean. **2021**, 21, 184 | 3 |
| 969 | Mapping of seed quality traits in the C genome of Brassica napus by using a population carrying genome content of B. oleracea and their effect on other traits. **2021**, 14, e20078 | 1 |
| 968 | Crop breeding for a changing climate: integrating phenomics and genomics with bioinformatics. **2021**, 134, 1677-1690 | 10 |
| 967 | Genome-Wide Association Studies and Genomic Selection for Grain Protein Content Stability in a Nested Association Mapping Population of Spring Wheat. | 4 |
| 966 | Enriched-GWAS and Transcriptome Analysis to Refine and Characterize a Major QTL for Anaerobic Germination Tolerance in Rice. **2021**, 22, | 1 |
| 965 | Genomic prediction for growth using a low-density SNP panel in dromedary camels. **2021**, 11, 7675 | 3 |
| 964 | Meta-GWAS for quantitative trait loci identification in soybean. **2021**, | 6 |
| 963 | Genome-Wide Association Mapping of Seedling Biomass and Root Traits Under Different Water Conditions in Wheat. **2021**, 12, 663557 | 0 |
| 962 | A genomics resource for genetics, physiology, and breeding of West African sorghum. **2021**, 14, e20075 | 6 |
| 961 | TWAS results are complementary to and less affected by linkage disequilibrium than GWAS. **2021**, 186, 1800-1811 | 5 |
| 960 | Classical phenotyping and deep learning concur on genetic control of stomatal density and area in sorghum. **2021**, 186, 1562-1579 | 4 |
| 959 | Genome-wide identification of loci modifying spike-branching in tetraploid wheat. **2021**, 134, 1925-1943 | 3 |
| 958 | GmST1, which encodes a sulfotransferase, confers resistance to soybean mosaic virus strains G2 and G3. **2021**, 44, 2777-2792 | 5 |

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| 957 | GWAS analysis reveals distinct pathogenicity profiles of Australian Parastagonospora nodorum isolates and identification of marker-trait-associations to septoria nodorum blotch. **2021**, 11, 10085 | 3 |
| 956 | Genome-wide association study suggests an independent genetic basis of zinc and cadmium concentrations in fresh sweet corn kernels. **2021**, 11, | 2 |
| 955 | Genome-wide association mapping reveals race-specific SNP markers associated with anthracnose resistance in carioca common beans. **2021**, 16, e0251745 | 1 |
| 954 | Predicting Moisture Content During Maize Nixtamalization Using Machine Learning with NIR Spectroscopy. | |
| 953 | Specific adaptation for early maturity and height stability in Icelandic spring barley. **2021**, 61, 2306-2323 | 1 |
| 952 | Identification of Novel Marker-Trait Associations for Lint Yield Contributing Traits in Upland Cotton ( L.) Using SSRs. **2021**, 12, 653270 | 1 |
| 951 | Identification of candidate SNPs and genes associated with anti-RGNNV using GWAS in the red-spotted grouper, Epinephelus akaara. **2021**, 112, 31-37 | 1 |
| 950 | Genetic dissection of soybean partial resistance to sclerotinia stem rot through genome wide association study and high throughout single nucleotide polymorphisms. **2021**, 113, 1262-1271 | 3 |
| 949 | Unoccupied aerial systems discovered overlooked loci capturing the variation of entire growing period in maize. **2021**, 14, e20102 | 3 |
| 948 | QTL mapping and candidate gene identification of lint percentage based on a recombinant inbred line population of upland cotton. **2021**, 217, 1 | |
| 947 | Genome-wide association studies for agronomical traits in winter rice accessions of Assam. **2021**, 113, 1037-1047 | 6 |
| 946 | Novel Genes and Genetic Loci Associated With Root Morphological Traits, Phosphorus-Acquisition Efficiency and Phosphorus-Use Efficiency in Chickpea. **2021**, 12, 636973 | 4 |
| 945 | Genome-wide association mapping of the 'super-soft' kernel texture in white winter wheat. **2021**, 134, 2547-2559 | 5 |
| 944 | Genome-wide association study of myrtle rust (Austropuccinia psidii) resistance in Eucalyptus obliqua (subgenus Eucalyptus). **2021**, 17, 1 | 1 |
| 943 | Gene-based mapping of trehalose biosynthetic pathway genes reveals association with source- and sink-related yield traits in a spring wheat panel. **2021**, 10, e292 | 3 |
| 942 | Genome-Wide Association Analysis and Genomic Prediction for Adult-Plant Resistance to Septoria Tritici Blotch and Powdery Mildew in Winter Wheat. **2021**, 12, 661742 | 5 |
| 941 | Genome-wide association mapping identifies yellow rust resistance loci in Ethiopian durum wheat germplasm. **2021**, 16, e0243675 | 2 |
| 940 | Genome-Wide Association Study Uncover the Genetic Architecture of Salt Tolerance-Related Traits in Common Wheat ( L.). **2021**, 12, 663941 | 5 |

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| 939 | Genome-Wide Association Study for Ultraviolet-B Resistance in Soybean ( L.). **2021**, 10, | 4 |
| 938 | Genome-Wide Association Study and Genomic Prediction for Soybean Cyst Nematode Resistance in USDA Common Bean () Core Collection. **2021**, 12, 624156 | 5 |
| 937 | Quantitative and population genomics suggest a broad role of staygreen loci in the drought adaptation of sorghum. | |
| 936 | Genetic and Morphological Approach for Western Corn Rootworm Resistance Management. **2021**, 11, 585 | 1 |
| 935 | Machine Learning based Genome-Wide Association Studies for Uncovering QTL Underlying Soybean Yield and its Components. | 2 |
| 934 | Genome Wide Association Study of Rice (Oryza sativa L.) during Heading Stage under a High Temperature. **2021**, 9, 104-111 | 0 |
| 933 | Toward identification of a putative candidate gene for nutrient mineral accumulation in wheat grains for human nutrition purposes. **2021**, 72, 6305-6318 | 5 |
| 932 | Genome-wide association analysis of drought adaptive traits in common bean. **2021**, 61, 3232-3253 | 2 |
| 931 | Robustification of GWAS to explore effective SNPs addressing the challenges of hidden population stratification and polygenic effects. **2021**, 11, 13060 | 0 |
| 930 | Genome-wide association study and its applications in the non-model crop Sesamum indicum. **2021**, 21, 283 | 6 |
| 929 | Genome-wide association study and transcriptome analysis discover new genes for bacterial leaf blight resistance in rice (Oryza sativa L.). **2021**, 21, 255 | 3 |
| 928 | Genome-Wide Association Study Reveals Candidate Genes for Flowering Time in Cowpea ( [L.] Walp.). **2021**, 12, 667038 | 3 |
| 927 | Genetic dissection of natural variation in oilseed traits of camelina by whole-genome resequencing and QTL mapping. **2021**, 14, e20110 | 7 |
| 926 | Genome-wide association mapping of seedling and adult plant response to stem rust in a durum wheat panel. **2021**, 14, e20105 | 2 |
| 925 | Genome-wide approaches delineate the additive, epistatic, and pleiotropic nature of variants controlling fatty acid composition in peanut (Arachis hypogaea L.). | |
| 924 | Sorghum Pan-Genome Explores the Functional Utility for Genomic-Assisted Breeding to Accelerate the Genetic Gain. **2021**, 12, 666342 | 7 |
| 923 | Genome-Wide SNP Markers for Genotypic and Phenotypic Differentiation of Melon ( L.) Varieties Using Genotyping-by-Sequencing. **2021**, 22, | 1 |
| 922 | Simulation study evaluating the ability of two statistical approaches to identify variance quantitative trait loci Arabidopsis and maize. | |

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| 921 | Genome-Wide Association Mapping of and Reveals Candidate Genes and New Adjustments to the Host-Pathogen Interaction for Resistance to in Common Bean. **2021**, 12, 699569 | 2 |
| 920 | Deterministic and stochastic modelling of impacts from genomic selection and phenomics on genetic gain for perennial ryegrass dry matter yield. **2021**, 11, 13265 | 0 |
| 919 | Genome-wide association study uncovers new genetic loci and candidate genes underlying seed chilling-germination in maize. **2021**, 9, e11707 | 4 |
| 918 | Resequencing of 672 Native Rice Accessions to Explore Genetic Diversity and Trait Associations in Vietnam. **2021**, 14, 52 | 5 |
| 917 | High-resolution genome-wide association study and genomic prediction for disease resistance and cold tolerance in wheat. **2021**, 134, 2857-2873 | 5 |
| 916 | Reduced expression of lipoxygenase genes improves flour processing quality in soft wheat. **2021**, 72, 6247-6259 | 0 |
| 915 | Novel insights into genome-wide associations in reveal genetic linkages between fertility and growth. **2021**, 1-17 | 2 |
| 914 | Identification of Gene Associated with Sweetness in Corn ( L.) by Genome-Wide Association Study (GWAS) and Development of a Functional SNP Marker for Predicting Sweet Corn. **2021**, 10, | 1 |
| 913 | Genome-Wide Association Mapping for Yield and Related Traits Under Drought Stressed and Non-stressed Environments in Wheat. **2021**, 12, 649988 | 2 |
| 912 | GmRAV confers ecological adaptation through photoperiod control of flowering time and maturity in soybean. **2021**, 187, 361-377 | 5 |
| 911 | Fine Mapping and Candidate Gene Identification for the Locus Controlling Fruit Orientation in Pepper ( spp.). **2021**, 12, 675474 | 2 |
| 910 | Genome wide association study of agronomic and seed traits in a world collection of proso millet (Panicum miliaceum L.). **2021**, 21, 330 | 6 |
| 909 | Multi-Allelic Haplotype-Based Association Analysis Identifies Genomic Regions Controlling Domestication Traits in Intermediate Wheatgrass. **2021**, 11, 667 | 1 |
| 908 | Rapid Identification of QTL for Mesocotyl Length in Rice Through Combining QTL-seq and Genome-Wide Association Analysis. **2021**, 12, 713446 | 2 |
| 907 | Association mapping of sponge cake volume in U.S. Pacific Northwest elite soft white wheat (Triticum aestivum L.). **2021**, 100, 103250 | 1 |
| 906 | Genetic basis and network underlying synergistic roots and shoots biomass accumulation revealed by genome-wide association studies in rice. **2021**, 11, 13769 | 0 |
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| 904 | Genome‐wide association study of grain morphology in wheat. **2021**, 217, 1 | 0 |

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| 903 | Single-trait, multi-locus and multi-trait GWAS using four different models for yield traits in bread wheat. **2021**, 41, 1 | 2 |
| 902 | Insight into the genetic contribution of maximum yield potential, spikelet development and abortion in barley. | 2 |
| 901 | Using chlorate as an analogue to nitrate to identify candidate genes for nitrogen use efficiency in barley. **2021**, 41, 1 | 1 |
| 900 | Genetic control of kernel compositional variation in a maize diversity panel. **2021**, 14, e20115 | 2 |
| 899 | Genetic Dissection of Quantitative Resistance to Common Rust () in Tropical Maize ( L.) by Combined Genome-Wide Association Study, Linkage Mapping, and Genomic Prediction. **2021**, 12, 692205 | 2 |
| 898 | Genetic Dissection of Grain Yield of Maize and Yield-Related Traits Through Association Mapping and Genomic Prediction. **2021**, 12, 690059 | 0 |
| 897 | Genetic analysis of grain protein content and dough quality traits in elite spring bread wheat (Triticum aestivum) lines through association study. **2021**, 100, 103214 | 2 |
| 896 | GWAS and WGCNA uncover hub genes controlling salt tolerance in maize (Zea mays L.) seedlings. **2021**, 134, 3305-3318 | 10 |
| 895 | The DNA Replication, Repair, and Recombination Pathway Genes Modulating Yield and Stress Tolerance Traits in Chickpea. 1 | 1 |
| 894 | Identification of Genomic Regions Influencing N-Metabolism and N-Excretion in Lactating Holstein-Friesians. **2021**, 12, 699550 | 1 |
| 893 | Insights into the effect of human civilization on Malus evolution and domestication. **2021**, 19, 2206-2220 | 6 |
| 892 | GWAS identified candidate variants and genes associated with acute heat tolerance of large yellow croaker. **2021**, 540, 736696 | 6 |
| 891 | Predicting moisture content during maize nixtamalization using machine learning with NIR spectroscopy. **2021**, 134, 3743-3757 | 1 |
| 890 | Multiomics approach reveals a role of translational machinery in shaping maize kernel amino acid composition. **2021**, | 1 |
| 889 | GWAS provides biological insights into mechanisms of the parasitic plant (Striga) resistance in sorghum. **2021**, 21, 392 | 3 |
| 888 | DArT-based evaluation of soybean germplasm from Polish Gene Bank. **2021**, 14, 343 | 2 |
| 887 | Multi-locus genome-wide association mapping for spike-related traits in bread wheat (Triticum aestivum L.). **2021**, 22, 597 | 2 |
| 886 | Evaluation and GWAS of radicle gravitropic response in a core rice germplasm population. **2021**, 468, 211 | |

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| 885 | Genome-Wide Association Mapping for Stomata and Yield Indices in Bread Wheat under Water Limited Conditions. **2021**, 11, 1646 | 4 |
| 884 | Genome-Wide Association Study Reveals Key Genes for Differential Lead Accumulation and Tolerance in Natural Accessions. **2021**, 12, 689316 | 0 |
| 883 | Genetic Diversity Relationship Between Grain Quality and Appearance in Rice. **2021**, 12, 708996 | 2 |
| 882 | Genomic signatures of vegetable and oilseed allopolyploid Brassica juncea and genetic loci controlling the accumulation of glucosinolates. **2021**, 19, 2619-2628 | 4 |
| 881 | Identification and Fine-Mapping of Quantitative Trait Loci Controlling Plant Height in Central European Winter Triticale (□Wittmack). **2021**, 10, | 2 |
| 880 | Genetic associations uncover candidate SNP markers and genes associated with salt tolerance during seedling developmental phase in barley. **2021**, 188, 104499 | 9 |
| 879 | Genome-level diversification of eight ancient tea populations in the Guizhou and Yunnan regions identifies candidate genes for core agronomic traits. **2021**, 8, 190 | 1 |
| 878 | A gene regulatory network for tiller development mediated by Tin8 in maize. **2021**, | |
| 877 | Pyramiding of scald resistance genes in four spring barley MAGIC populations. **2021**, 134, 3829-3843 | 3 |
| 876 | Linkage and association mapping and Kompetitive allele-specific PCR marker development for improving grain protein content in wheat. **2021**, 134, 3563-3575 | 2 |
| 875 | Genome-Wide Association Mapping of Mixed Linkage (1,3;1,4)-□Glucan and Starch Contents in Rice Whole Grain. **2021**, 12, 665745 | 0 |
| 874 | Characterizing Winter Wheat Germplasm for Fusarium Head Blight Resistance Under Accelerated Growth Conditions. **2021**, 12, 705006 | 0 |
| 873 | Genome-wide analysis reveals demographic and life-history patterns associated with habitat modification in landlocked, deep-spawning sockeye salmon (). **2021**, 11, 13186-13205 | 0 |
| 872 | Genomic Scan of Male Fertility Restoration Genes in a 'G□zow' Type Hybrid Breeding System of Rye ( L.). **2021**, 22, | 2 |
| 871 | Genetic Dissection of Phosphorus Use Efficiency in a Maize Association Population under Two P Levels in the Field. **2021**, 22, | 2 |
| 870 | Genome-wide association study identifies QTL for eight fruit traits in cultivated tomato (Solanum lycopersicum L.). **2021**, 8, 203 | 1 |
| 869 | Genome wide association and prediction studies of agronomic and quality traits in spring beard wheat (Triticum aestivum L.) under rain-fed environment with terminal moisture stress. **2021**, 101, 103278 | 0 |
| 868 | Genome-Wide Association Study Reveals Novel Genetic Loci for Quantitative Resistance to Septoria Tritici Blotch in Wheat ( L.). **2021**, 12, 671323 | 0 |

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| 867 | Transcriptome-wide association and prediction for carotenoids and tocochromanols in fresh sweet corn kernels. | |
| 866 | Polyphenol oxidase genes as integral part of the evolutionary history of domesticated tetraploid wheat. **2021**, 113, 2989-3001 | 2 |
| 865 | Genome-wide association study for candidate genes controlling seed yield and its components in rapeseed (). **2021**, 27, 1933-1951 | 1 |
| 864 | GWAS identifies an ortholog of the rice D11 gene as a candidate gene for grain size in an international collection of hexaploid wheat. **2021**, 11, 19483 | 1 |
| 863 | Genome-Wide Association Study to Map Genomic Regions Related to the Initiation Time of Four Growth Stage Traits in Soybean. **2021**, 12, 715529 | 0 |
| 862 | Time series barley germination is predictable using functional principal component analysis or logistic regression and associated with known seed dormancy loci. | 0 |
| 861 | Advances and trends on the utilization of multi-parent advanced generation intercross (MAGIC) for crop improvement. **2021**, 217, 1 | 3 |
| 860 | Genomic region associated with run timing has similar haplotypes and phenotypic effects across three lineages of Chinook salmon. **2021**, 14, 2273-2285 | 1 |
| 859 | Exploring natural diversity reveals alleles to enhance antioxidant system in barley under salt stress. **2021**, 166, 789-798 | 5 |
| 858 | Genetic control and allele variation among soybean maturity groups 000 through IX. **2021**, 14, e20146 | |
| 857 | Identification of anthracnose race 1 resistance loci in lentil by integrating linkage mapping and genome-wide association study. **2021**, 14, e20131 | 0 |
| 856 | Identification of genetic loci associated with major agronomic traits of wheat (Triticum aestivum L.) based on genome-wide association analysis. **2021**, 21, 418 | 2 |
| 855 | Dissection of the genetic basis of genotype-by-environment interactions for grain yield and main agronomic traits in Iranian bread wheat landraces and cultivars. **2021**, 11, 17742 | 1 |
| 854 | Resistance of Corynespora cassiicola from soybean to QoI and MBC fungicides in Brazil. | 0 |
| 853 | GAPIT Version 3: Boosting Power and Accuracy for Genomic Association and Prediction. **2021**, | 36 |
| 852 | Genetic dissection of grain architecture-related traits in a winter wheat population. **2021**, 21, 417 | 5 |
| 851 | Genome wide association mapping through 90K SNP array against Leaf rust pathogen in bread wheat genotypes under field conditions. **2021**, 101628 | 1 |
| 850 | Linkage and association study discovered loci and candidate genes for glycinin and Ɛconglycinin in soybean (Glycine max L. Merr.). **2021**, 134, 1201-1215 | 3 |

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| 849 | Genome-wide association analysis of fiber fineness and yield in ramie (Boehmeria nivea) using SLAF-seq. **2021**, 217, 1 | 0 |
| 848 | Linking anthocyanin diversity, hue, and genetics in purple corn. **2021**, 11, | 3 |
| 847 | Genome-wide association study reveals the genetic complexity of fructan accumulation patterns in barley grain. **2021**, 72, 2383-2402 | 5 |
| 846 | Genome-wide association study of yield and related traits in common wheat under salt-stress conditions. **2021**, 21, 27 | 14 |
| 845 | Genome-wide association study for resistance to the Meloidogyne javanica causing root-knot nematode in soybean. **2021**, 134, 777-792 | 3 |
| 844 | Uncovering the genetic mechanisms regulating panicle architecture in rice with GPWAS and GWAS. **2021**, 22, 86 | 6 |
| 843 | Building pan-genome infrastructures for crop plants and their use in association genetics. **2021**, 28, | 22 |
| 842 | Genome-wide association among soybean accessions for the genetic basis of salinity-alkalinity tolerance during germination. **2021**, 72, 255 | 0 |
| 841 | Genomic Analyses of Phenotypic Differences Between Native and Invasive Populations of Diffuse Knapweed (Centaurea diffusa). **2021**, 8, | 0 |
| 840 | Natural variation in GmRAV confers ecological adaptation through photoperiod control of flowering time and maturity in soybean. | |
| 839 | Genome-wide association study in diverse Iranian wheat germplasms detected several putative genomic regions associated with stem rust resistance. **2021**, 9, 1357-1374 | 1 |
| 838 | Sensitivity of Cercospora spp. from soybean to quinone outside inhibitors and methyl benzimidazole carbamate fungicides in Brazil. **2021**, 46, 69-80 | 1 |
| 837 | Status and prospects of genome-wide association studies in plants. **2021**, 14, e20077 | 43 |
| 836 | Multiparental Population in Crops: Methods of Development and Dissection of Genetic Traits. **2021** , 2264, 13-32 | 1 |
| 835 | Association Mapping in Plants. **2021**, 2264, 105-117 | 3 |
| 834 | Linkage Mapping. **2015**, 47-70 | 7 |
| 833 | Association Mapping of Genetic Resources: Achievements and Future Perspectives. **2014**, 207-235 | 21 |
| 832 | Efficient weighting methods for genomic best linear-unbiased prediction (BLUP) adapted to the genetic architectures of quantitative traits. **2021**, 126, 320-334 | 3 |

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| 831 | Population structure and genetic diversity in red clover (Trifolium pratense L.) germplasm. **2020**, 10, 8364 | 5 |
| 830 | Natural variation in DNA methylation homeostasis and the emergence of epialleles. **2020**, 117, 4874-4884 | 24 |
| 829 | Non-Mendelian inheritance of SNP markers reveals extensive chromosomal translocations in dioecious hops (Humulus lupulus L.). | 2 |
| 828 | Genome-Wide Association Study of Ionomic Traits on Diverse Soybean Populations from Germplasm Collections. | 1 |
| 827 | Genome wide association study pinpoints key agronomic QTLs in African rice Oryza glaberrima. | 3 |
| 826 | Genome Wide Association Study of Resistance to PstS2 and Warrior Races of Stripe (Yellow) Rust in Bread Wheat Landraces. | 1 |
| 825 | mrMLM v4.0: An R Platform for Multi-locus Genome-wide Association Studies. | 4 |
| 824 | The Genetic Architecture of Leaf Stable Carbon Isotope Composition in Zea mays and the Effect of Transpiration Efficiency on Elemental Accumulation. | 1 |
| 823 | A Combinatorial Approach of Biparental QTL Mapping and Genome-Wide Association Analysis Identifies Candidate Genes for Phytophthora Blight Resistance in Sesame. | 1 |
| 822 | Population genetics of sugar kelp in the Northwest Atlantic region using genome-wide markers. | 1 |
| 821 | Gwas and Genomic Selection For Increased Anthocyanin Content in Purple Corn. | 1 |
| 820 | Temporal dynamics of QTL effects on vegetative growth inArabidopsis thaliana. | 1 |
| 819 | GWAS reveals the genetic complexity of fructan accumulation patterns in barley grain. | 1 |
| 818 | Gene-based mapping of trehalose biosynthetic pathway genes reveals association with source- and sink-related yield traits in a spring wheat panel. | 2 |
| 817 | Eleven biosynthetic genes explain the majority of natural variation for carotenoid levels in maize grain. | 2 |
| 816 | rMVP: A Memory-efficient, Visualization-enhanced, and Parallel-accelerated tool for Genome-Wide Association Study. | 16 |
| 815 | GAPIT Version 3: Boosting Power and Accuracy for Genomic Association and Prediction. | 21 |
| 814 | The p-coumaroyl arabinoxylan transferase HvAT10 underlies natural variation in whole-grain cell wall phenolic acids in cultivated barley. | 2 |

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| 4 | Genome-wide association study of grain iron and zinc concentration in common bean ( Phaseolus vulgaris ). | 0 |

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