Curtis Pozniak

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/11997791/publications.pdf

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25 papers	5,664 citations	430874 18 h-index	580821 25 g-index
28 all docs	28 docs citations	28 times ranked	4735 citing authors

#	Article	IF	Citations
1	Genomic Predictions for Common Bunt, FHB, Stripe Rust, Leaf Rust, and Leaf Spotting Resistance in Spring Wheat. Genes, 2022, 13, 565.	2.4	13
2	Comparison of single-trait and multi-trait genomic predictions on agronomic and disease resistance traits in spring wheat. Theoretical and Applied Genetics, 2022, 135, 2747-2767.	3.6	4
3	Physical Mapping of QTL in Four Spring Wheat Populations under Conventional and Organic Management Systems. I. Earliness. Plants, 2021, 10, 853.	3.5	13
4	Physical mapping of QTL associated with agronomic and end-use quality traits in spring wheat under conventional and organic management systems. Theoretical and Applied Genetics, 2021, 134, 3699-3719.	3.6	23
5	Genome-based prediction of agronomic traits in spring wheat under conventional and organic management systems. Theoretical and Applied Genetics, 2021, 135, 537.	3.6	10
6	Genetic diversity and selective sweeps in historical and modern Canadian spring wheat cultivars using the 90K SNP array. Scientific Reports, 2021, 11, 23773.	3.3	10
7	Grain protein content and thousand kernel weight QTLs identified in a durumâ€‰Ã—â€‰wild emmer wheat mapping population tested in five environments. Theoretical and Applied Genetics, 2020, 133, 119-131.	3.6	47
8	A haplotype-led approach to increase the precision of wheat breeding. Communications Biology, 2020, 3, 712.	4.4	68
9	The Global Durum Wheat Panel (GDP): An International Platform to Identify and Exchange Beneficial Alleles. Frontiers in Plant Science, 2020, 11, 569905.	3.6	44
10	Three previously characterized resistances to yellow rust are encoded by a single locus Wtk1. Journal of Experimental Botany, 2020, 71, 2561-2572.	4.8	23
11	Exome sequencing highlights the role of wild-relative introgression in shaping the adaptive landscape of the wheat genome. Nature Genetics, 2019, 51, 896-904.	21.4	225
12	Genome Based Meta-QTL Analysis of Grain Weight in Tetraploid Wheat Identifies Rare Alleles of GRF4 Associated with Larger Grains. Genes, 2018, 9, 636.	2.4	37
13	Genomeâ€wide Association Study of Agronomic Traits in a Springâ€Planted North American Elite Hard Red Spring Wheat Panel. Crop Science, 2018, 58, 1838-1852.	1.8	29
14	High Density Single Nucleotide Polymorphism (SNP) Mapping and Quantitative Trait Loci (QTL) Analysis in a Biparental Spring Triticale Population Localized Major and Minor Effect Fusarium Head Blight Resistance and Associated Traits QTL. Genes, 2018, 9, 19.	2.4	32
15	Shifting the limits in wheat research and breeding using a fully annotated reference genome. Science, 2018, 361, .	12.6	2,424
16	Mapping QTLs Controlling Agronomic Traits in the â€˜Attilaâ€™ Ã— â€˜CDC Goâ€™ Spring Wheat Population under Organic Management using 90K SNP Array. Crop Science, 2017, 57, 365-377.	1.8	30
17	Allelic variation and effects of 16 candidate genes on disease resistance in western Canadian spring wheat cultivars. Molecular Breeding, 2017, 37, 1.	2.1	11
18	Genome-wide association mapping of genomic regions associated with phenotypic traits in Canadian western spring wheat. Molecular Breeding, 2017, 37, 1.	2.1	30

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19	Population Structure and Genomewide Association Analysis of Resistance to Disease and Insensitivity to Ptr Toxins in Canadian Spring Wheat Using 90K SNP Array. Crop Science, 2017, 57, 1522-1539.	1.8	24
20	QTLs associated with agronomic traits in the Attila Ã— CDC Go spring wheat population evaluated under conventional management. PLoS ONE, 2017, 12, e0171528.	2.5	68
21	QTLs Associated with Agronomic Traits in the Cutler Ã— AC Barrie Spring Wheat Mapping Population Using Single Nucleotide Polymorphic Markers. PLoS ONE, 2016, 11, e0160623.	2.5	36
22	A haplotype map of allohexaploid wheat reveals distinct patterns of selection on homoeologous genomes. Genome Biology, 2015, 16, 48.	8.8	216
23	A highâ€density, <scp>SNP</scp>â€based consensus map of tetraploid wheat as a bridge to integrate durum and bread wheat genomics and breeding. Plant Biotechnology Journal, 2015, 13, 648-663.	8.3	386
24	Characterization of polyploid wheat genomic diversity using a highâ€density 90Â000 single nucleotide polymorphism array. Plant Biotechnology Journal, 2014, 12, 787-796.	8.3	1,828
25	Durum wheat genomics comes of age. Molecular Breeding, 2014, 34, 1527-1530.	2.1	23