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K-mer counting and curated libraries drive efficient annotation of repeats in plant genomes

DOI: 10.1002/tpg2.20143 Plant Genome, 2021, 14, e20143.

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3	Ensembl Genomes 2022: an expanding genome resource for non-vertebrates. <i>Nucleic Acids Research</i> , 2021 ,	20.1	12
2	A multiple alignment workflow shows the effect of repeat masking and parameter tuning on alignment in plants <i>Plant Genome</i> , 2022 , e20204	4.4	0
1	Graph-based pan-genome: increased opportunities in plant genomics.		O