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MIPS sequences: a promising molecular consideration in angiosperm phylogeny and systematics

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Abstract

The diversity among myo inositol 1-phosphate synthase (MIPS) complete protein sequences, the essential inositol synthesis regulatory enzyme, reported for almost 38 species representing 19 plant families (from Dicotyledons and Monocotyledons), undoubtedly endorses its applicability in molecular systematics. The sequences retrieved from GenBank and their potential application to angiosperm systematics has been emphasized here. Site-specific amino acid residue signatures and their variation among angiosperm genera have been studied. Multiple sequence alignment using Multiple Sequence Comparison by Log-Expectation (MUSCLE) and further manual analysis exposed a major part of ±510 aa residues that have been found to be highly conserved. Moreover, variations of MIPS sequences are very informative in systematics and the phylogeny of angiosperm. The MIPS sequences aligned based on the Maximum Likelihood method and the generated phylogenetic tree strongly support the modern taxonomic hierarchy, especially the Angiosperm Phylogeny Group-IV (APG-IV, 2016) scheme.

Key words: angiosperm phylogeny, APG IV, cladogram, MIPS, multiple sequence alignment

Supplementary Fig. 1. Complete multiple sequence alignment performed using MUSCLE among MIPS amino acid sequences and visualized with the help of Boxshade server

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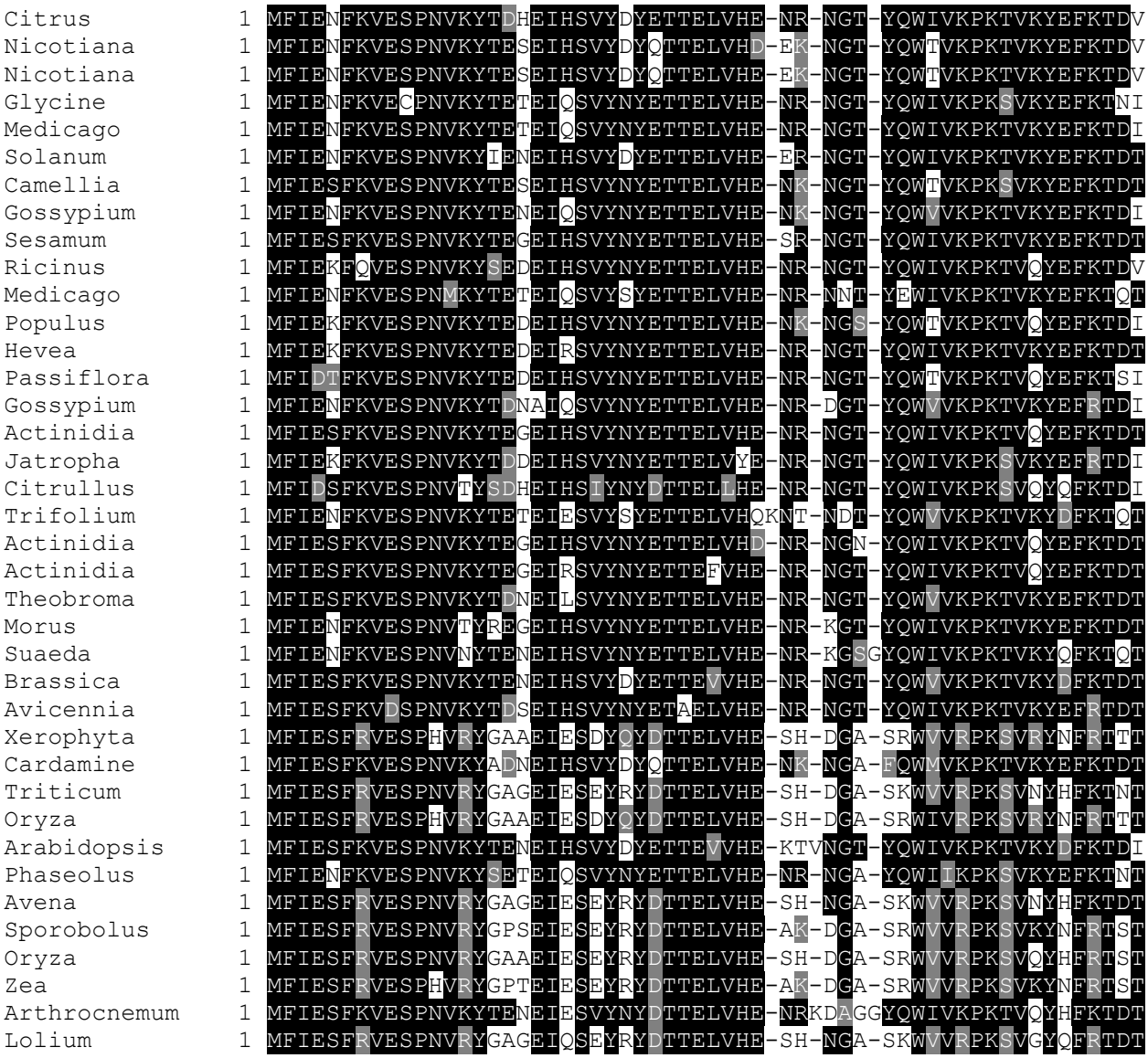
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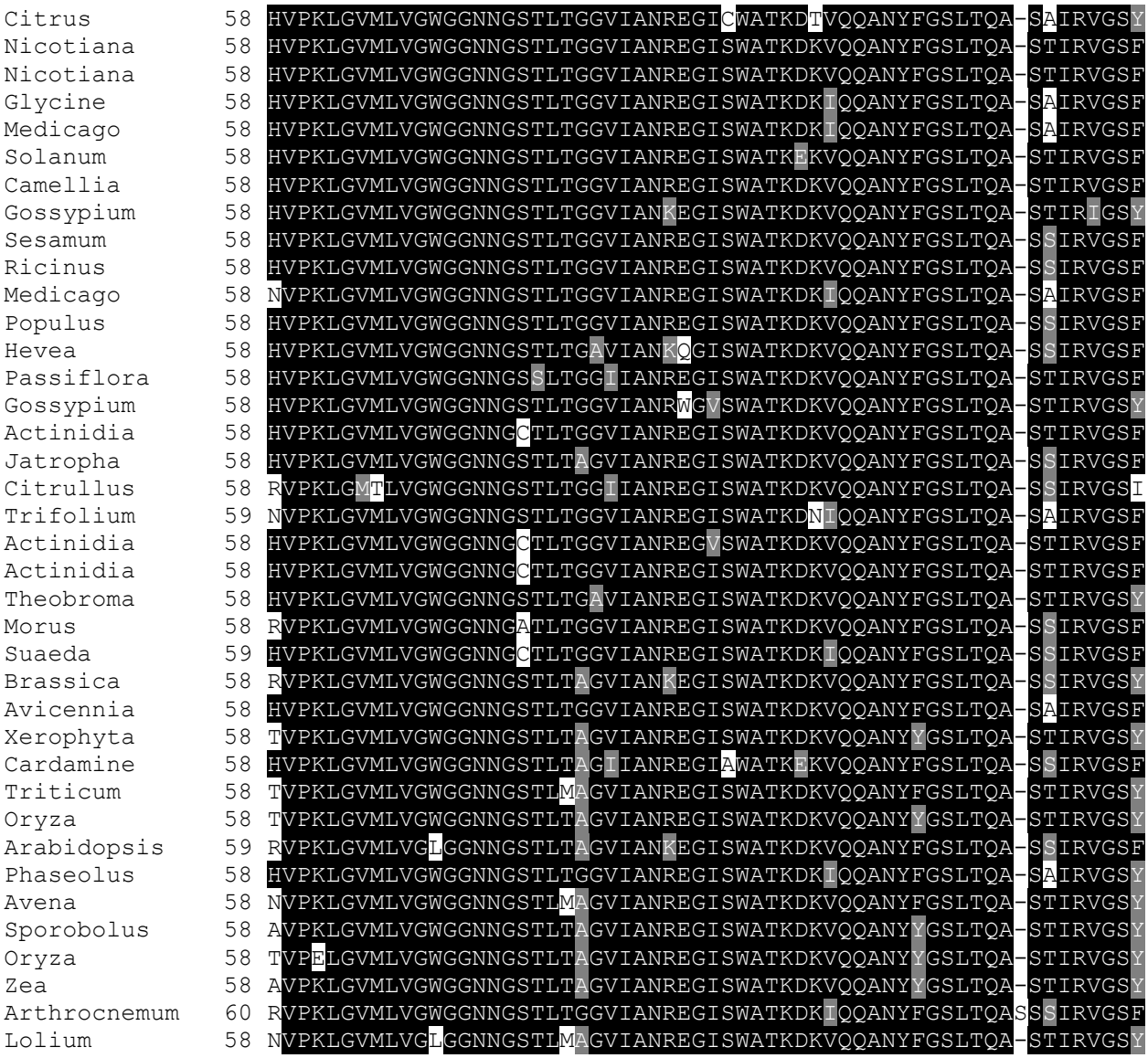
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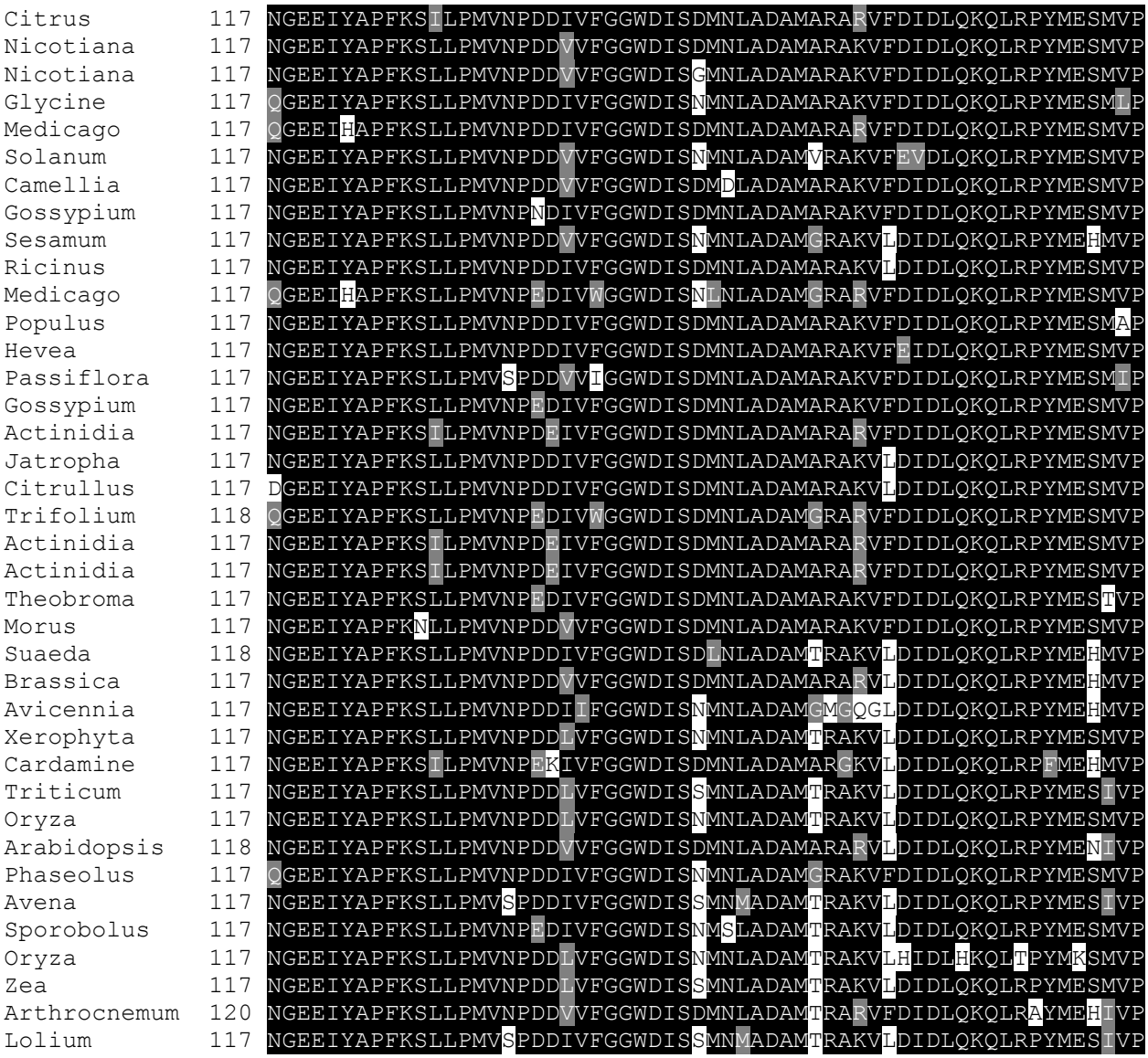
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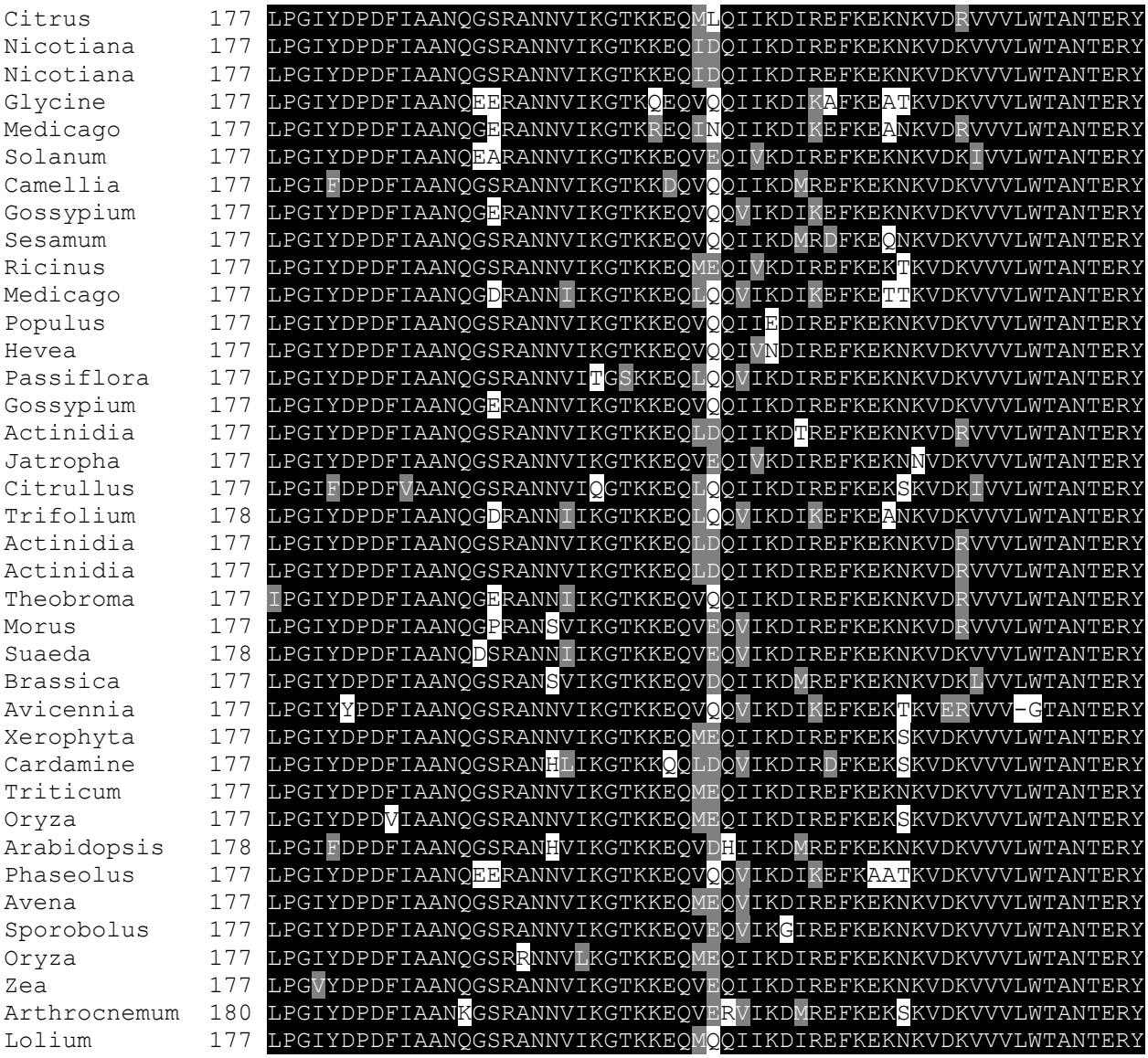
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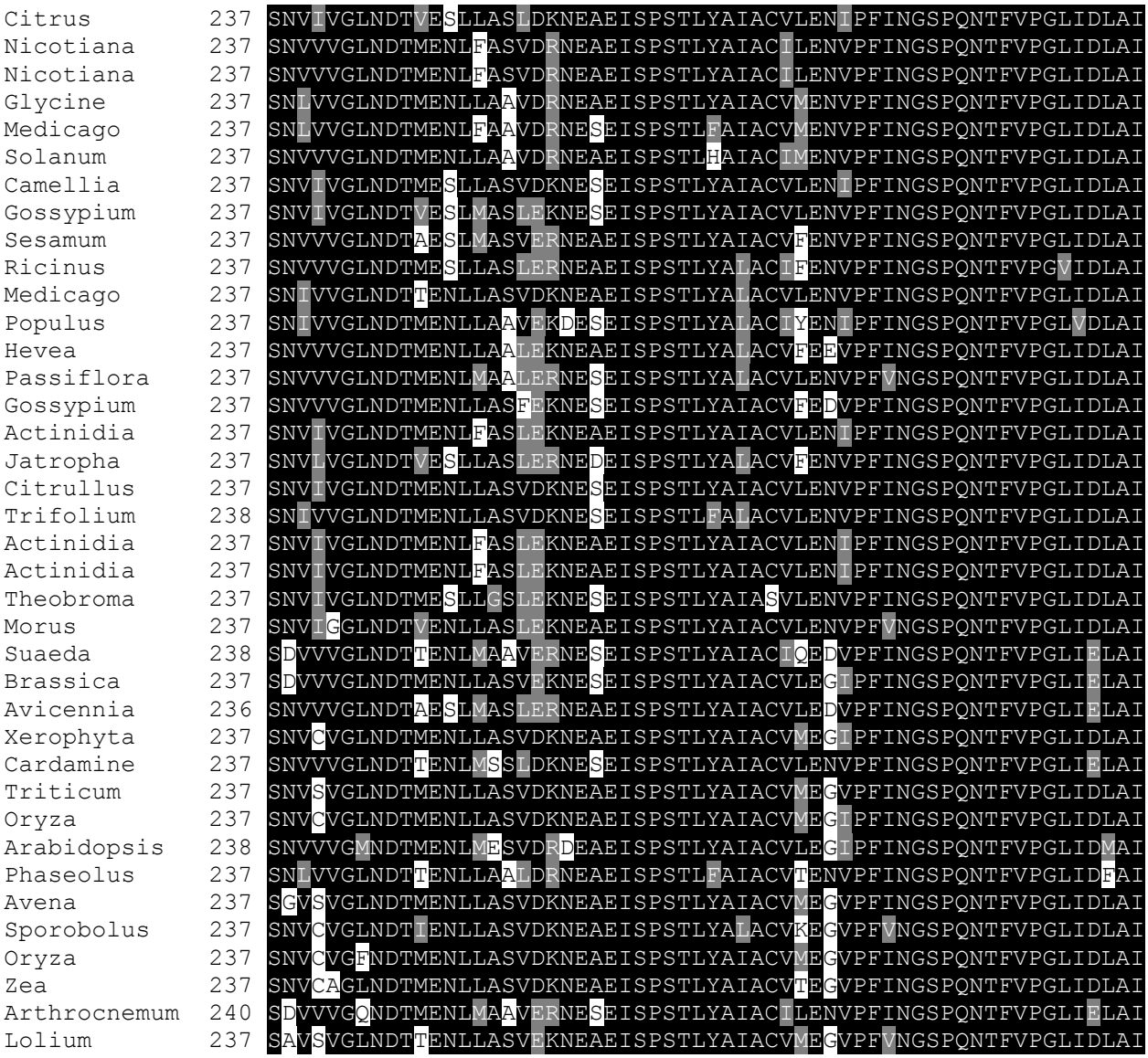
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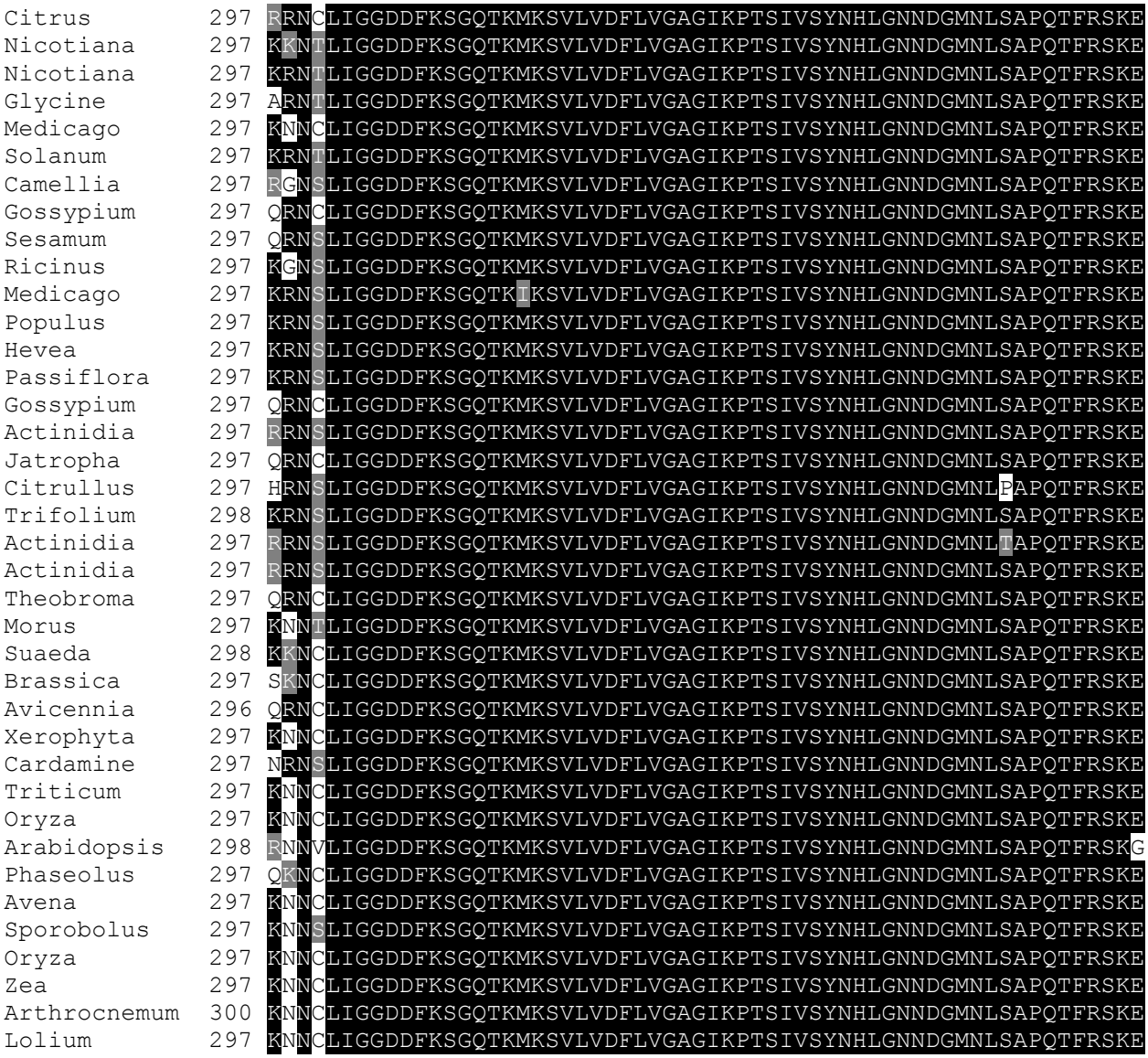
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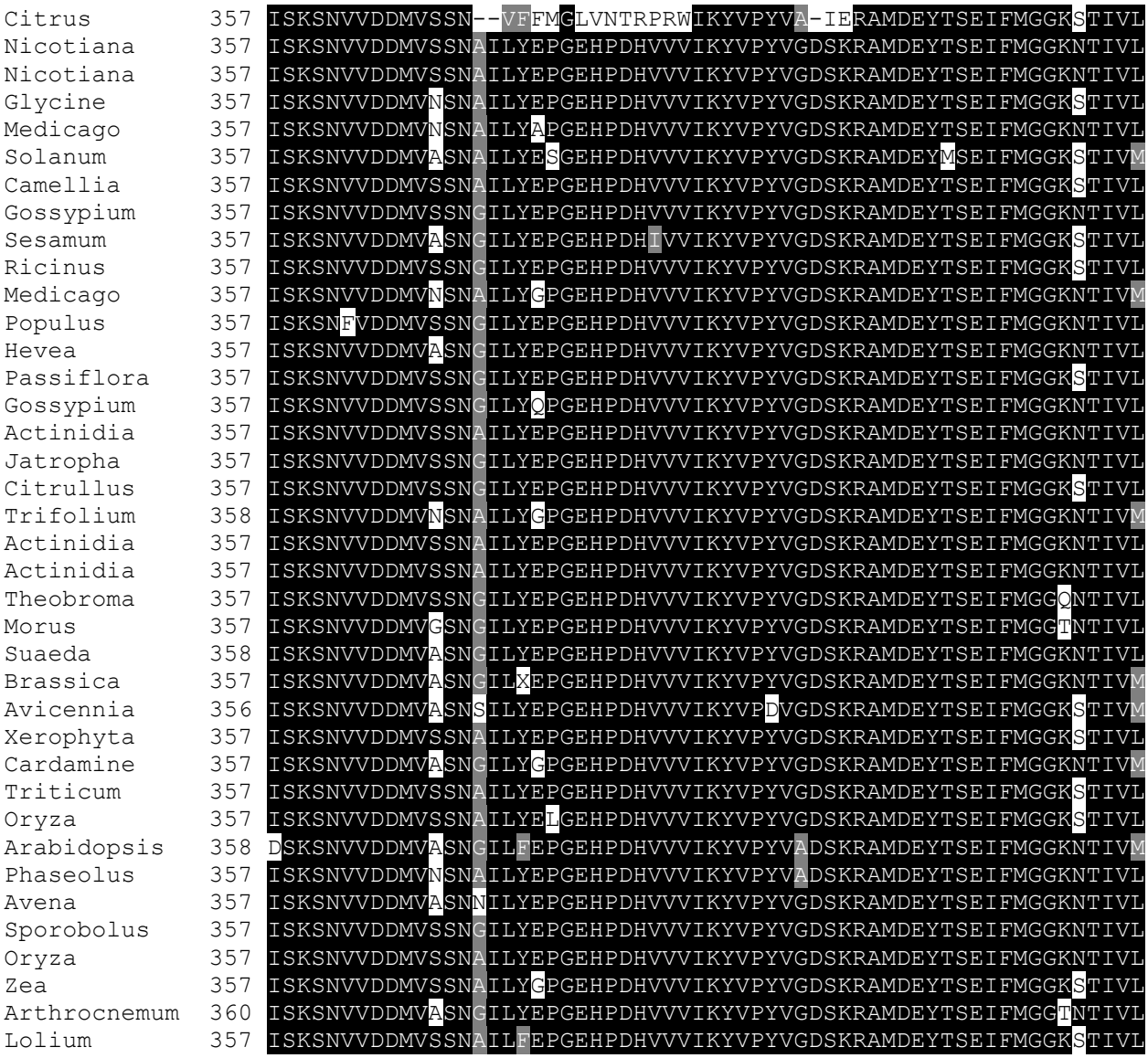
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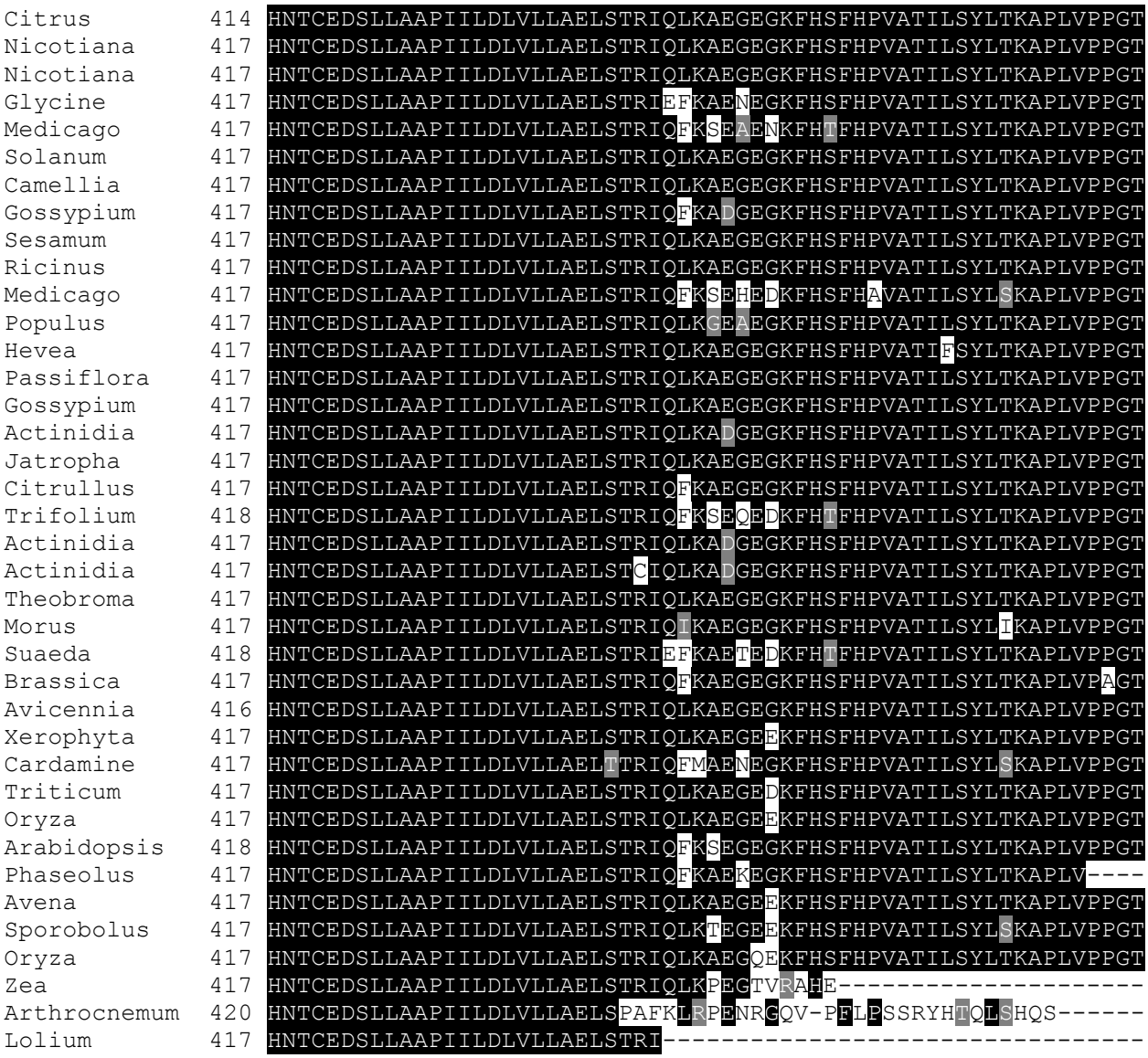
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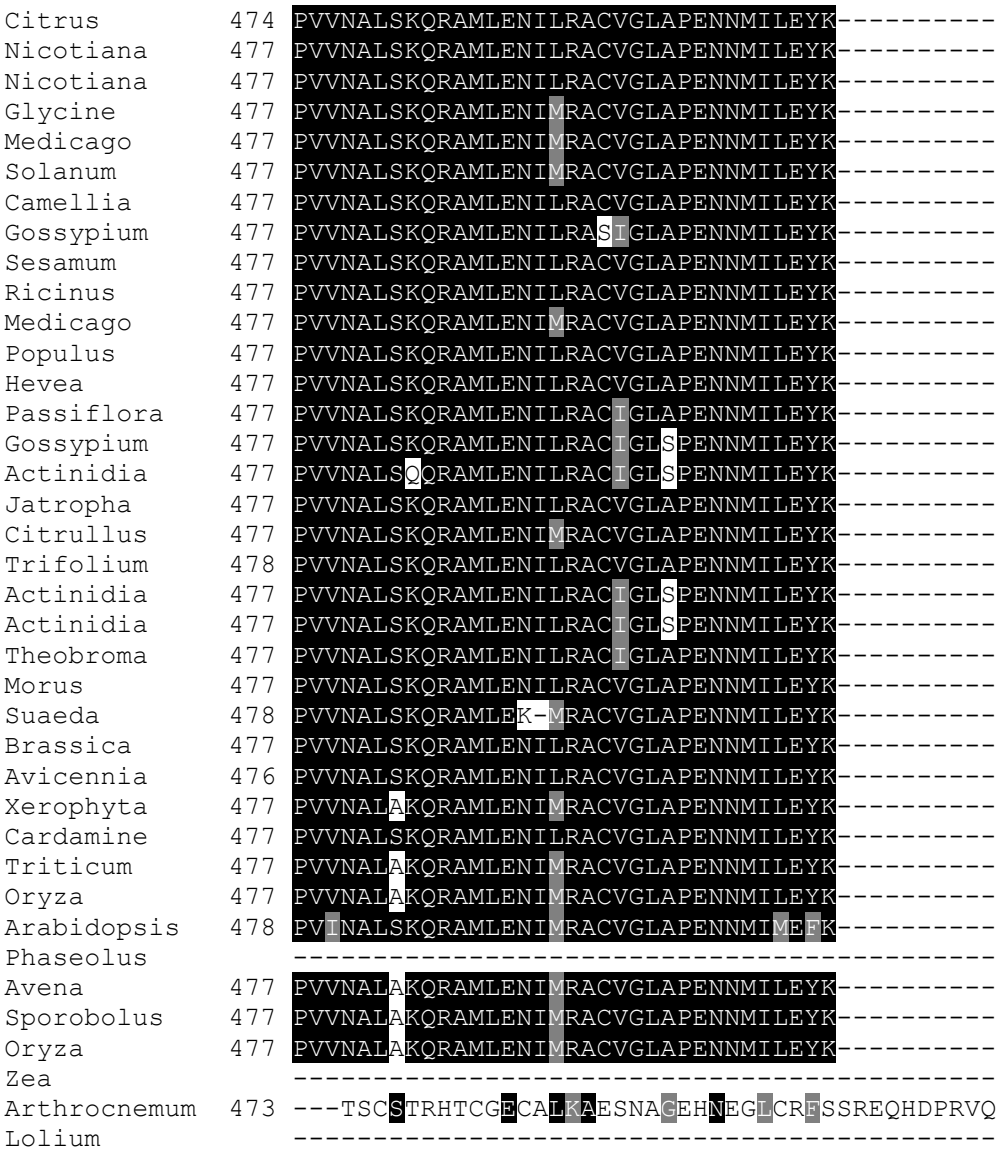
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