

***De Novo* Whole-Genome Sequence and Genome Annotation of *Lichtheimia ramosa*.**

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Abstract

We report the annotated draft genome sequence of *Lichtheimia ramosa* (JMRC FSU:6197). It has been reported to be a causative organism of mucormycosis, a rare but rapidly progressive infection in immunocompromised humans. The functionally annotated genomic sequence consists of 74 scaffolds with a total number of 11,510 genes.

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