
Catia V5r21 X64 Full Professional Iso Activator

Category:Fiber-optic communications Category:Optical fiber Category:Network performanceGENOME ANNOUNCEMENT {#h0.0} ===== *Saccharomyces cerevisiae* strain RN1 (RN1, \[@B1\]) was isolated from apiary waste in Tunisia (2002). It exhibits phenotypic properties that differentiate it from other *Saccharomyces* yeasts: (i) resistance to H~2~O~2~, a d-tyrosine-containing molecule that is a major cause of damage in honey; (ii) susceptibility to an enzymatic browning activity; (iii) osmotolerance, which was identified by its ability to grow in YPD medium with 0.2 M NaCl; and (iv) thermotolerance, which was demonstrated by its resistance to a 42°C treatment. This strain is able to produce ethanol and to accumulate a high amount of proteins, lipids, and carbohydrates when subjected to nutritional stress. In addition, RN1 is able to produce citric acid, which is an important organic acid for both the food and cosmetics industries. Based on the morphological and biochemical analysis, RN1 was identified as *S. cerevisiae* strain RN1 (RN1), and its genome was sequenced by using the Illumina Genome Analyzer at the McGill University and Genome Québec Innovation Center (Montreal, Quebec, Canada). Paired-end libraries with insert sizes of ~250 bp were constructed using the Nextera XT DNA sample preparation kit (Illumina, San Diego, CA). The resulting sequences were assembled with the Trinity assembler (version 2013-02-25) using default parameters and a k-mer length of 31. The short-read sequences obtained from the *S. cerevisiae* RN1 strain genome are included in the GenBank assembly under the accession no. AYWC00000000.1. The raw reads from the *S. cerevisiae* RN1 are available under the accession no. SRX727535. Nucleotide sequence accession numbers. {#s1 } ----- This whole-genome shotgun project has been deposited in DDBJ/EMBL/GenBank under the accession no. AYWC00000000.1. The version described in this paper is the first version,

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