Resource Summary Report

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Sequencing of Candida Albicans

RRID:SCR_013437
Type: Tool

Proper Citation

Sequencing of Candida Albicans (RRID:SCR_013437)

Resource Information

URL: http://www-sequence.stanford.edu/group/candida/

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Description: The Stanford Genome Technology Center began a whole genome shotgun sequencing of strain SC5314 of Candida albicans. After reaching its original goal of 1.5X mean coverage of the haploid genome (16Mb) in summer, 1998, Stanford was awarded a supplemental grant to continue sequencing up to a coverage of 10X, performing as much assembly of the sequence as possible, using recognizable genes as nucleation points. Candida albicans is one of the most commonly encountered human pathogens, causing a wide variety of infections ranging from mucosal infections in generally healthy persons to life-threatening systemic infections in individuals with impaired immunity. Oral and esophogeal Candida infections are frequently seen in AIDS patients. Few classes of drugs are effective against these fungal infections, and all of them have limitations with regard to efficacy and side-effects.

Synonyms: Candida Albicans

Resource Type: data or information resource, topical portal, portal

Keywords: stanford, genome, technology, shotgun, sequencing, strain, haploid, gene, nucleation, health, life, aids, drug, patient

Funding: Burroughs Wellcome Fund ;
NIDCR DE12302-02S2;
NIAID RO1AI16567;
NIAID RO1AI46351;
NIAID NO1AI05406;
NIDCR R01DE12940;
NIDCR P01DE07946

Resource Name: Sequencing of Candida Albicans

Resource ID: SCR_013437

Alternate IDs: nif-0000-30294

Record Creation Time: 20220129T080316+0000

Record Last Update: 20260729T044329+0000

Ratings and Alerts

No rating or validation information has been found for Sequencing of Candida Albicans.

No alerts have been found for Sequencing of Candida Albicans.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 21 mentions in open access literature.

Listed below are recent publications. The full list is available at nidm-terms .

de Souza PC, et al. (2023) Production of IgY against iron permease Ftr1 from Candida albicans and evaluation of its antifungal activity using Galleria mellonella as a model of systemic infection. Microbial pathogenesis, 181, 106166.

Todd RT, et al. (2020) Expandable and reversible copy number amplification drives rapid adaptation to antifungal drugs. eLife, 9.

Todd RT, et al. (2019) Genome plasticity in Candida albicans is driven by long repeat sequences. eLife, 8.

Chavez-Dozal AA, et al. (2015) The Candida albicans Exocyst Subunit Sec6 Contributes to Cell Wall Integrity and Is a Determinant of Hyphal Branching. Eukaryotic cell, 14(7), 684.

Liang RM, et al. (2010) Transcriptional response of Candida albicans biofilms following exposure to 2-amino-nonyl-6-methoxyl-tetralin muriate. Acta pharmacologica Sinica, 31(5), 616.

Chua PR, et al. (2007) Effective killing of the human pathogen Candida albicans by a specific inhibitor of non-essential mitotic kinesin Kip1p. Molecular microbiology, 65(2), 347.

Doyle TC, et al. (2006) Expression of firefly luciferase in Candida albicans and its use in the selection of stable transformants. Microbial pathogenesis, 40(2), 69.

Wang Y, et al. (2006) Cap1p is involved in multiple pathways of oxidative stress response in Candida albicans. Free radical biology & medicine, 40(7), 1201.

Clark RM, et al. (2006) Expansion of GAA trinucleotide repeats in mammals. Genomics, 87(1), 57.

Barker D, et al. (2005) Predicting functional gene links from phylogenetic-statistical analyses of whole genomes. PLoS computational biology, 1(1), e3.

Lee KH, et al. (2005) Candida albicans protein analysis during hyphal differentiation using an integrative HA-tagging method. Biochemical and biophysical research communications, 337(3), 784.

Wightman R, et al. (2004) In Candida albicans, the Nim1 kinases Gin4 and Hsl1 negatively regulate pseudohypha formation and Gin4 also controls septin organization. The Journal of cell biology, 164(4), 581.

Bennett RJ, et al. (2003) Completion of a parasexual cycle in Candida albicans by induced chromosome loss in tetraploid strains. The EMBO journal, 22(10), 2505.

Sengupta M, et al. (2003) Two membrane proteins located in the Nag regulon of Candida albicans confer multidrug resistance. Biochemical and biophysical research communications, 301(4), 1099.

Tsong AE, et al. (2003) Evolution of a combinatorial transcriptional circuit: a case study in yeasts. Cell, 115(4), 389.

Uhl MA, et al. (2003) Haploinsufficiency-based large-scale forward genetic analysis of filamentous growth in the diploid human fungal pathogen C.albicans. The EMBO journal, 22(11), 2668.

Westermann S, et al. (2003) Architecture of the budding yeast kinetochore reveals a conserved molecular core. The Journal of cell biology, 163(2), 215.

Wendland J, et al. (2003) Analysis of the landmark protein Bud3 of Ashbya gossypii reveals a novel role in septum construction. EMBO reports, 4(2), 200.

Tripathi G, et al. (2002) Gcn4 co-ordinates morphogenetic and metabolic responses to amino acid starvation in Candida albicans. The EMBO journal, 21(20), 5448.

Murad AM, et al. (2001) NRG1 represses yeast-hypha morphogenesis and hypha-specific gene expression in Candida albicans. The EMBO journal, 20(17), 4742.