

# CandidaDB: a genome database for *Candida albicans* pathogenomics.

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[Details](#)



## Abstract

CandidaDB is a database dedicated to the genome of the most prevalent systemic fungal pathogen of humans, *Candida albicans*. CandidaDB is based on an annotation of the Stanford Genome Technology Center *C.albicans* genome sequence data by the European Galar Fungal Consortium. CandidaDB Release 2.0 (June 2004) contains information pertaining to Assembly 19 of the genome of *C.albicans* strain SC5314. The current release contains 6244 annotated entries corresponding to 130 tRNA genes and 5917 protein-coding genes. For these, it provides tentative functional assignments along with numerous pre-run analyses that can assist the researcher in the evaluation of gene function for the purpose of specific or large-scale analysis. CandidaDB is based on GenoList, a generic relational data schema and a World Wide Web interface that has been adapted to the handling of eukaryotic genomes. The interface allows users to browse easily through genome data and retrieve information. CandidaDB also provides more elaborate tools,

such as pattern searching, that are tightly connected to the overall browsing system. As the *C.albicans* genome is diploid and still incompletely assembled, CandidaDB provides tools to browse the genome by individual supercontigs and to examine information about allelic sequences obtained from complementary contigs. CandidaDB is accessible at <http://genolist.pasteur.fr/CandidaDB>.

## Beteiligte Forschungseinheiten

[Mikrobielle Pathogenitätsmechanismen](#) [Bernhard Hube](#) [Mehr erfahren](#)

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