Resource Summary Report

Generated by dkNET on Apr 27, 2025

Ashbya Genome Database

RRID:SCR_007548
Type: Tool

Proper Citation

Ashbya Genome Database (RRID:SCR_007548)

Resource Information

URL: http://agd.vital-it.ch/index.html

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Description: AGD is a genome/transcriptome database containing gene annotation and high-density oligonucleotide microarray expression data for protein-coding genes from Ashbya gossypii and the model organism Saccharomyces cerevisiae. It also provides access to comparative genomics data from those two fungi as well as Schizosaccharomyces pombe and Neurospora crassa. Comparative DNA and protein-level data is available, including synteny information in fungi. Additionally, AGD now displays microarray expression data from A.gossypii and S.cerevisiae.

Abbreviations: AGD

Synonyms: AGD: the Ashbya Genome Database

Resource Type: data or information resource, database

Defining Citation: PMID:17212814

Keywords: n. crassa, s. pombe, s. cerevisiae, a. gossypii

Funding:

Resource Name: Ashbya Genome Database

Resource ID: SCR_007548

Alternate IDs: nif-0000-02538

Record Creation Time: 20220129T080242+0000

Record Last Update: 20250426T055939+0000

Ratings and Alerts

No rating or validation information has been found for Ashbya Genome Database.

No alerts have been found for Ashbya Genome Database.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 11 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Averianova LA, et al. (2020) Production of Vitamin B2 (Riboflavin) by Microorganisms: An Overview. Frontiers in bioengineering and biotechnology, 8, 570828.

Aguiar TQ, et al. (2014) Investigation of protein secretion and secretion stress in Ashbya gossypii. BMC genomics, 15(1), 1137.

Perez-Nadales E, et al. (2014) Fungal model systems and the elucidation of pathogenicity determinants. Fungal genetics and biology : FG & B, 70(100), 42.

Wendland J, et al. (2014) Chromosome number reduction in Eremothecium coryli by two telomere-to-telomere fusions. Genome biology and evolution, 6(5), 1186.

Kabran P, et al. (2012) Alternative splicing regulates targeting of malate dehydrogenase in Yarrowia lipolytica. DNA research : an international journal for rapid publication of reports on genes and genomes, 19(3), 231.

Wendland J, et al. (2011) Genome evolution in the eremothecium clade of the Saccharomyces complex revealed by comparative genomics. G3 (Bethesda, Md.), 1(7), 539.

Nieduszynski CA, et al. (2011) From sequence to function: Insights from natural variation in budding yeasts. Biochimica et biophysica acta, 1810(10), 959.

Lang C, et al. (2010) Structural mutants of the spindle pole body cause distinct alteration of cytoplasmic microtubules and nuclear dynamics in multinucleated hyphae. Molecular biology of the cell, 21(5), 753.

González-Fernández R, et al. (2010) Proteomics of plant pathogenic fungi. Journal of biomedicine & biotechnology, 2010, 932527.

Nikolaou E, et al. (2009) Phylogenetic diversity of stress signalling pathways in fungi. BMC evolutionary biology, 9, 44.

Jiménez A, et al. (2008) Phosphoribosyl pyrophosphate synthetase activity affects growth and riboflavin production in Ashbya gossypii. BMC biotechnology, 8, 67.