

Resource Summary Report

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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

Resource Name: Ashbya Genome Database

Resource ID: SCR_007548

Alternate IDs: nif-0000-02538

Record Creation Time: 20220129T080242+0000

Record Last Update: 20260905T133140+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 [Kravitz](#) .

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.