

Resource Summary Report

Generated by SPARC SAWG on Sep 17, 2026

ASPGD

RRID:SCR_002047

Type: Tool

Proper Citation

ASPGD (RRID:SCR_002047)

Resource Information

URL: <http://www.aspgd.org/>

Proper Citation: ASPGD (RRID:SCR_002047)

Description: Database of genetic and molecular biological information about the filamentous fungi of the genus *Aspergillus* including information about genes and proteins of *Aspergillus nidulans* and *Aspergillus fumigatus*; descriptions and classifications of their biological roles, molecular functions, and subcellular localizations; gene, protein, and chromosome sequence information; tools for analysis and comparison of sequences; and links to literature information; as well as a multispecies comparative genomics browser tool (Sybil) for exploration of orthology and synteny across multiple sequenced *Sgenus* species. Also available are Gene Ontology (GO) and community resources. Based on the Candida Genome Database, the *Aspergillus* Genome Database is a resource for genomic sequence data and gene and protein information for *Aspergilli*. Among its many species, the genus contains an excellent model organism (*A. nidulans*, or its teleomorph *Emericella nidulans*), an important pathogen of the immunocompromised (*A. fumigatus*), an agriculturally important toxin producer (*A. flavus*), and two species used in industrial processes (*A. niger* and *A. oryzae*). Search options allow you to: *Search AspGD database using keywords. *Find chromosomal features that match specific properties or annotations. *Find AspGD web pages using keywords located on the page. *Find information on one gene from many databases. *Search for keywords related to a phenotype (e.g., conidiation), an allele (such as *veA1*), or an experimental condition (e.g., light). Analysis and Tools allow you to: *Find similarities between a sequence of interest and *Aspergillus* DNA or protein sequences. *Display and analyze an *Aspergillus* sequence (or other sequence) in many ways. *Navigate the chromosomes set. View nucleotide and protein sequence. *Find short DNA/protein sequence matches in *Aspergillus*. *Design sequencing and PCR primers for *Aspergillus* or other input sequences. *Display the restriction map for a *Aspergillus* or other input sequence. *Find similarities between a sequence of interest and fungal nucleotide or protein sequences. AspGD welcomes data submissions.

Abbreviations: ASPGD, ASPGD LOCUS, ASPGD REF

Synonyms: Aspergillus Genome Database, ASPGD REF, ASPGD LOCUS

Resource Type: data or information resource, data repository, database, service resource, storage service resource

Defining Citation: [PMID:19773420](#)

Keywords: function, gene, gene name, annotation, aspergillus, aspergillus nidulans, chromosome, community, dna, genome, genomic, localization, orthology, phenotype, protein, protein-coding genes, s. cerevisiae, sequence, allele, data analysis service, bio.tools, FASEB list

Funding: NIAID R01 AI077599

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: ASPGD

Resource ID: SCR_002047

Alternate IDs: nif-0000-12244, biotools:aspgd

Alternate URLs: <http://www.aspergillusgenome.org/>, <https://bio.tools/aspgd>

Record Creation Time: 20220129T080211+0000

Record Last Update: 20260912T195536+0000

Ratings and Alerts

No rating or validation information has been found for ASPGD.

No alerts have been found for ASPGD.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 218 mentions in open access literature.

Listed below are recent publications. The full list is available at [SPARC SAWG](#) .

Schubert S, et al. (2026) FungiNetDB: a uniform (pre-)processing platform for fungal expression data. *microLife*, 7, uqag012.

Strohdiek A, et al. (2025) The *Aspergillus nidulans* velvet domain containing transcription factor VeA is shuttled from cytoplasm into nucleus during vegetative growth and stays there for sexual development, but has to return into cytoplasm for asexual development. *PLoS genetics*, 21(6), e1011687.

Jorge JMP, et al. (2024) NmrB (AN9181) expression is activated under oxidative stress conditions acting as a metabolic repressor of *Aspergillus nidulans*. *Frontiers in microbiology*, 15, 1373469.

Baroncelli R, et al. (2024) Genome evolution and transcriptome plasticity is associated with adaptation to monocot and dicot plants in *Colletotrichum* fungi. *GigaScience*, 13.

Bitencourt T, et al. (2024) Integrated multi-omics identifies pathways governing interspecies interaction between *A. fumigatus* and *K. pneumoniae*. *Communications biology*, 7(1), 1496.

Cleere MM, et al. (2024) New colours for old in the blue-cheese fungus *Penicillium roqueforti*. *NPJ science of food*, 8(1), 3.

Portaels J, et al. (2024) *Aspergillus Fumigatus* Spore Proteases Alter the Respiratory Mucosa Architecture and Facilitate Equine Herpesvirus 1 Infection. *Viruses*, 16(8).

He X, et al. (2024) Genomic diversity of the pathogenic fungus *Aspergillus fumigatus* in Japan reveals the complex genomic basis of azole resistance. *Communications biology*, 7(1), 274.

Mamun MAA, et al. (2023) Fungal transglutaminase domain-containing proteins are involved in hyphal protection at the septal pore against wounding. *Molecular biology of the cell*, 34(13), ar127.

Choi YH, et al. (2023) Functional Characterization of the GNAT Family Histone Acetyltransferase Elp3 and GcnE in *Aspergillus fumigatus*. *International journal of molecular sciences*, 24(3).

Chang PK, et al. (2023) Kojic Acid Gene Clusters and the Transcriptional Activation Mechanism of *Aspergillus flavus* KojR on Expression of Clustered Genes. *Journal of fungi* (Basel, Switzerland), 9(2).

Gawlik J, et al. (2022) Nuclear Functions of KaeA, a Subunit of the KEOPS Complex in *Aspergillus nidulans*. *International journal of molecular sciences*, 23(19).

Cano R, et al. (2022) Gene Regulatory Network Inference and Gene Module Regulating Virulence in *Fusarium oxysporum*. *Frontiers in microbiology*, 13, 861528.

Wang G, et al. (2022) Fungal-fungal cocultivation leads to widespread secondary metabolite alteration requiring the partial loss-of-function VeA1 protein. *Science advances*, 8(17), eabo6094.

Colabardini AC, et al. (2022) Chromatin profiling reveals heterogeneity in clinical isolates of the human pathogen *Aspergillus fumigatus*. *PLoS genetics*, 18(1), e1010001.

Gila BC, et al. (2022) Strategies Shaping the Transcription of Carbohydrate-Active Enzyme Genes in *Aspergillus nidulans*. *Journal of fungi* (Basel, Switzerland), 8(1).

Padilla-Garfias F, et al. (2022) DhDIT2 Encodes a *Debaryomyces hansenii* Cytochrome P450 Involved in Benzo(a)pyrene Degradation-A Proposal for Mycoremediation. *Journal of fungi* (Basel, Switzerland), 8(11).

Son SH, et al. (2021) HbxB Is a Key Regulator for Stress Response and α -Glucan Biogenesis in *Aspergillus nidulans*. *Microorganisms*, 9(1).

Hage H, et al. (2021) Distribution of methionine sulfoxide reductases in fungi and conservation of the free-methionine-R-sulfoxide reductase in multicellular eukaryotes. *Free radical biology & medicine*, 169, 187.

Steyer JT, et al. (2021) Duplication and Functional Divergence of Branched-Chain Amino Acid Biosynthesis Genes in *Aspergillus nidulans*. *mBio*, 12(3), e0076821.