Resource Summary Report

Archaeal and Bacterial ABC Transporter Database

RRID:SCR_001692
Type: Tool

Proper Citation

Archaeal and Bacterial ABC Transporter Database (RRID:SCR_001692)

Resource Information

URL: http://www-abcdb.biotoul.fr

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Description: ABCdb is a public resource devoted to the ATP-binding Cassette (ABC) transporters encoded by completely sequenced prokaryotic genomes. In order to establish, in a complete genome, the repertory of ABC systems, we have to: i) identify the different partners, ii) assemble the partners in putative systems, and iii) classify the system into the correct functional subfamily (Quentin et al., 2002). The main pitfalls were the identification of loosely conserved domains and the assembly of partners encoded by genes dispersed over the chromosome. In order to face the avalanche of newly sequenced genomes, we decided to also feed into the database the raw prediction issued by this automatic procedure, before time consuming review by an expert occurs. Therefore, the database comprises two sections: CleanDb, for data checked by an expert and AutoDb for raw data. The ABC proteins are involved in a wide variety of physiological processes in Archaea, Bacteria and Eucaryota where they are encoded by large families of paralogous genes. The majority of ABC domains energize the transport of compounds across membranes. In bacteria, ABC transporters are involved in the uptake of a wide variety of molecules, as well as in mechanisms of virulence and antibiotic resistance. In eukaryotes, most of them are involved in drug resistance and in human cell, many are associated with diseases. Sequence analysis reveals that members of the ABC superfamily can be organized into sub-families, and suggests that they have diverged from common ancestral forms. A typical ABC transporter system is composed of an assembly of protein domains that serve different functions: i) two Nucleotide Binding Domains (NBD) that energize transport via ATP hydrolysis, ii) two Membrane Spanning Domains (MSD) that act as a membrane channel for the substrate, and iii) for the importer, a Solute Binding Protein (SBP) that confers substrates specificity on the transporter. The different partners of an ABC system are generally encoded by neighboring genes. The database includes information on: * ABC transporters * Protein partners * Protein domains (NBD, MSD and SBP) * Classification of ABC transporters and their protein

partners * Taxonomy of the species Each model Protein includes a link to the Peptide sequence, general information extracted from EMBL files, and specific tags to store results of predictions. The results of the annotation procedure are reachable through the class Prediction. The origin of the proteins is modeled as a path through the classes Chromosome, Strain, Species, and Taxon. Assembly and protein compilation tables are also provided for each of the chromosomes (Assembly and Protein).

Abbreviations: ABCdb,

Synonyms: Archaeal and Bacterial ABC Systems database

Resource Type: data or information resource, database

Defining Citation: PMID:16499625

Keywords: abc transporters, archaea, bacteria, prokaryotic genomes, genome, complete genome

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ACI-IMPbio

Resource Name: Archaeal and Bacterial ABC Transporter Database

Resource ID: SCR_001692

Alternate IDs: nif-0000-02530

Record Creation Time: 20220129T080209+0000

Record Last Update: 20250426T055455+0000

Ratings and Alerts

No rating or validation information has been found for Archaeal and Bacterial ABC Transporter Database.

No alerts have been found for Archaeal and Bacterial ABC Transporter Database.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Badalato N, et al. (2017) Whole Proteome Analyses on Ruminiclostridium cellulolyticum Show a Modulation of the Cellulolysis Machinery in Response to Cellulosic Materials with Subtle Differences in Chemical and Structural Properties. PloS one, 12(1), e0170524.

Schellenberg JJ, et al. (2014) Enhanced whole genome sequence and annotation of Clostridium stercorarium DSM8532T using RNA-seq transcriptomics and high-throughput proteomics. BMC genomics, 15(1), 567.

Siddaramappa S, et al. (2012) A comparative genomics perspective on the genetic content of the alkaliphilic haloarchaeon Natrialba magadii ATCC 43099T. BMC genomics, 13, 165.

Zijnge V, et al. (2012) Proteomics of protein secretion by Aggregatibacter actinomycetemcomitans. PloS one, 7(7), e41662.

Anderson CM, et al. (2010) GATMD: ?-aminobutyric acid transporter mutagenesis database. Database : the journal of biological databases and curation, 2010, baq028.