Resource Summary Report

Generated by NIF on Apr 25, 2025

cpnDB: A Chaperonin Database

RRID:SCR_002263
Type: Tool

Proper Citation

cpnDB: A Chaperonin Database (RRID:SCR_002263)

Resource Information

URL: http://www.cpndb.ca/cpnDB/home.php

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Description: A curated collection of chaperonin sequence data collected from public databases or generated by a network of collaborators exploiting the cpn60 target in clinical, phylogenetic and microbial ecology studies. The database contains all available sequences for both group I and group II chaperonins. Users can search the database by Chaperonin type, group (I or II), BLAST, or other options, and can also enter and analyze FASTA sequences.

Abbreviations: cpnDB

Resource Type: analysis service resource, data analysis service, data or information resource, production service resource, database, service resource

Defining Citation: PMID:15289485

Keywords: chaperonin sequence, microbial ecology, phylogenetics, chaperonin, plastid, mitochondria, cytoplasm, sequence, blast, fasta, bio.tools

Funding: Canadian Biotechnology Strategy ;
National Research Council Genomics and Health Initiative

Resource Name: cpnDB: A Chaperonin Database

Resource ID: SCR_002263

Alternate IDs: biotools:cpndb, OMICS_01511, nif-0000-02694

Alternate URLs: https://bio.tools/cpndb

Old URLs: http://cpndb.cbr.nrc.ca/

Record Creation Time: 20220129T080212+0000

Record Last Update: 20250425T055252+0000

Ratings and Alerts

No rating or validation information has been found for cpnDB: A Chaperonin Database.

No alerts have been found for cpnDB: A Chaperonin Database.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Pasternak JA, et al. (2015) Claudin-4 undergoes age-dependent change in cellular localization on pig jejunal villous epithelial cells, independent of bacterial colonization. Mediators of inflammation, 2015, 263629.

Das Roy R, et al. (2014) How do eubacterial organisms manage aggregation-prone proteome? F1000Research, 3, 137.

Baffoni L, et al. (2013) Identification of species belonging to the Bifidobacterium genus by PCR-RFLP analysis of a hsp60 gene fragment. BMC microbiology, 13, 149.