

Resource Summary Report

Generated by [dkNET](#) on Jul 30, 2026

Protochlamydia amoebophila UWE25

RRID:SCR_008222

Type: Tool

Proper Citation

Protochlamydia amoebophila UWE25 (RRID:SCR_008222)

Resource Information

URL: <http://mips.gsf.de/services/genomes/uwe25/>

Proper Citation: Protochlamydia amoebophila UWE25 (RRID:SCR_008222)

Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented on July 15, 2013. This is the official database of the environmental chlamydia genome project. This resource provides access to finished sequence for Parachlamydia-related symbiont UWE25 and to a wide range of manual annotations, automatical analyses and derived datasets. Functional classification and description has been manually annotated according to the Annotation guidelines. Chlamydiae are the major cause of preventable blindness and sexually transmitted disease. Genome analysis of a chlamydia-related symbiont of free-living amoebae revealed that it is twice as large as any of the pathogenic chlamydiae and had few signs of recent lateral gene acquisition. We showed that about 700 million years ago the last common ancestor of pathogenic and symbiotic chlamydiae was already adapted to intracellular survival in early eukaryotes and contained many virulence factors found in modern pathogenic chlamydiae, including a type III secretion system. Ancient chlamydiae appear to be the originators of mechanisms for the exploitation of eukaryotic cells. Environmental chlamydiae have recently been recognized as obligate endosymbionts of free-living amoebae and have been implicated as potential human pathogens. Environmental chlamydiae form a deep branching evolutionary lineage within the medically important order Chlamydiales. Despite their high diversity and ubiquitous distribution in clinical and environmental samples only limited information about genetics and ecology of these microorganisms is available. The Parachlamydia-related Acanthamoeba symbiont UWE25 was therefore selected as representative environmental chlamydia strain for whole genome sequencing. Comparative genome analysis was performed using PEDANT and simap. Sponsors: The environmental chlamydia genome project was funded by the bmb+f (German Federal Ministry of Education and Research) and is part of the Competence Network PathoGenoMiK.

Synonyms: Protochlamydia amoebophila UWE25

Resource Type: data or information resource, database

Keywords: ecology, endosymbiont, environmental, eukaryote, eukaryotic, evolutionary, functional, gene, genetic, acanthamoeba, amoebae, blindness, cell, chlamydia, classification, clinical, genome, human, intracellular, lateral, lineage, mechanism, microorganism, obligate, parachlamydia, pathogen, pathogenic, sequence, sexually, strain, survival, symbiont, transmitted disease, uwe25, virulence

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Protochlamydia amoebophila UWE25

Resource ID: SCR_008222

Alternate IDs: nif-0000-21310

Record Creation Time: 20220129T080246+0000

Record Last Update: 20260729T044205+0000

Ratings and Alerts

No rating or validation information has been found for Protochlamydia amoebophila UWE25.

No alerts have been found for Protochlamydia amoebophila UWE25.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.