The Ribosomal Database Project II

http://rdp.cme.msu.edu/

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Introduction

The Ribosomal Database Project (RDP) provides data programs and services related to the ribosome. The RDP is a value-added database available to the research community through the RDP website. The RDP provides information about a sequence in a several phylogenetic scheme along with system information and other identifying information about the source organism.

Growth of the Database

The RDP database has grown to include 16,277 aligned prokaryotic sequences, 2055 aligned eukaryotic sequences, and 26,790 associated environmental clone sequences. The RDP was initially developed at Michigan State University (MSU) in 1998.

The growth of the RDP database has been substantial, with over 16,000 prokaryotic sequences and 2,000 eukaryotic sequences added since the initial release in 1998. The RDP has become a valuable resource for researchers studying the diversity and evolution of the ribosome.

Figure 1

Introduction to the RDP database. The RDP is a database of ribosomal RNA sequences that has been developed to help researchers understand the diversity and evolution of the ribosome. The RDP database contains over 16,000 aligned prokaryotic sequences and 2,000 eukaryotic sequences, and it is widely used in microbial ecology, molecular phylogeny, and evolutionary biology.

Figure 2

Breakdown of RDP users by primary field of study. This figure shows the distribution of RDP users across various fields of study, including general microbiology, medical microbiology, and other fields. The majority of users are from general microbiology, followed by medical microbiology and other fields.

Figure 3

Breakdown of RDP releases by source organism. This figure shows the distribution of releases across various types of organisms, including prokaryotes, eukaryotes, and other organisms. The majority of releases are for prokaryotes, followed by eukaryotes and other organisms.

Figure 4

A new way to view the phylogenetic diversity of the RDP II database is shown in Figure 4 (right). The phylogenetic tree was generated using the software package PHYLIP, and it includes over 16,000 prokaryotic sequences. The tree provides a comprehensive view of the diversity of the ribosome across various lineages.

Figure 5

The RDP provides information about where a sequence fits in an overall phylogenetic scheme, along with up-to-date data. It is not solely a collection of rRNA sequences extracted from the public nucleotide databases. The RDP provides a comprehensive view of the diversity of the ribosome across various lineages.

Figure 6

The RDP-II is widely used in microbial ecology, molecular phylogeny, and evolutionary biology, organism identification, characterization of microbial populations, and studies of biodiversity.