# **Resource Summary Report**

Generated by NIF on Apr 25, 2025

## Sequedex

RRID:SCR\_001233

Type: Tool

### **Proper Citation**

Sequedex (RRID:SCR\_001233)

#### **Resource Information**

URL: http://sequedex.lanl.gov/

**Proper Citation:** Sequedex (RRID:SCR\_001233)

**Description:** Software to classify the function and phylogeny of reads as short as 30 bp. It is flexible, which can utilize multiple data modules and downstream analysis scripts. It is fast, reading in signature lists of 5-500 million peptide signatures in 1-15 minutes, and subsequently processes genomic fragments at the rate of 6 Gbp/hr. It parallelizes without significant increase in memory requirements until I/O bound on multiple input files; parallelization works well on 64 processors.

**Abbreviations:** Sequedex

Resource Type: software resource

**Defining Citation: PMID:22925230** 

**Keywords:** phylogenetic, function, profile, metagenomics, synthetic, dna sequence,

classification, java, linux, mac os, genomic analysis, bio.tools

**Funding:** 

Availability: Demo license, License required

**Resource Name:** Sequedex

Resource ID: SCR\_001233

Alternate IDs: OMICS\_02110, biotools:sequedex

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

**Record Creation Time:** 20220129T080206+0000

Record Last Update: 20250420T014023+0000

## **Ratings and Alerts**

No rating or validation information has been found for Sequedex.

No alerts have been found for Sequedex.

### **Data and Source Information**

Source: SciCrunch Registry

## **Usage and Citation Metrics**

We found 1 mentions in open access literature.

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

Jacobs L, et al. (2019) California condor microbiomes: Bacterial variety and functional properties in captive-bred individuals. PloS one, 14(12), e0225858.