Resource Summary Report

Generated by dkNET on Apr 16, 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: 20250410T064656+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 dkNET.

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