Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 20, 2025

NON-RED

RRID:SCR_006225
Type: Tool

Proper Citation

NON-RED (RRID:SCR_006225)

Resource Information

URL: http://athina.biol.uoa.gr/bioinformatics/NON-RED/index.html

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Description: A web tool to select biological sequences from a given set, with similarity / homology less than a user-defined level. This web-based application takes as input a set of N sequences and outputs a set of sequences of user-determined redundancy. Initially, the algorithm runs an all-against-all BLAST alignment on the input data set and creates an NxN matrix of pairwise distances defined by the similarity percentages. In the next step, the algorithm removes the sequence with the largest number of neighbors, causing that sequence not to be counted as a neighbor of any other sequence during the next iterations. It then reassesses the number of neighbors of each sequence and repeats the previous step until the sequences left over have no more neighbors. The user can specify the similarity (%) threshold and the minimum coverage length of the alignments. Sequences with a similarity below the threshold or a smaller coverage than the minimum length are not considered to be neighbors.

Abbreviations: NON-RED

Synonyms: NON-RED

Resource Type: data analysis service, production service resource, analysis service resource, service resource

Keywords: protein sequence, nucleotide, blast, algorithm, alignment, similarity, homology, sequence

Funding:

Resource Name: NON-RED

Resource ID: SCR_006225

Alternate IDs: nlx_151778

Record Creation Time: 20220129T080235+0000

Record Last Update: 20250420T015532+0000

Ratings and Alerts

No rating or validation information has been found for NON-RED.

No alerts have been found for NON-RED.

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 FDI Lab - SciCrunch.org.

Li Z, et al. (2020) Deep learning from "passive feeding" to "selective eating" of real-world data. NPJ digital medicine, 3, 143.