

RefSeqMash 0.0.2 Version 2

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Abstract

RefSeqMash uses the MinHash (<http://genomebiology.biomedcentral.com/articles/10.1186/s13059-016-0997-x>) algorithm to characterize the genera/species/strains present in metagenomic samples by comparing the reads to ~11K known RefSeq genomes.

Citation: Ken Youens-Clark RefSeqMash 0.0.2. **protocols.io**

[dx.doi.org/10.17504/protocols.io.fy7bpzn](https://doi.org/10.17504/protocols.io.fy7bpzn)

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Protocol

Step 1.

Upload your into the [Cyverse/iPlant Discovery Environment](#) either by logging in and choosing to upload or by using iRODS to 'iput' your FASTA files.

Step 2.

Open the "Apps" by clicking on the button on the left. Search for "refseq" to find the RefSeqMash-0.0.2 app.

Step 3.

Indicate a FASTA file or a directory of FASTA files for the "query." Click on "Run Analysis."