

Resource Summary Report

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Demultiplexing Nanopore reads with LAST

DOI:10.17504/protocols.io.xj3fkqn

Type: Protocol

Proper Citation

David Eccles 2019. Demultiplexing Nanopore reads with LAST. protocols.io
[dx.doi.org/10.17504/protocols.io.xj3fkqn](https://doi.org/10.17504/protocols.io.xj3fkqn)

Protocol Information

URL: <https://dx.doi.org/10.17504/protocols.io.xj3fkqn>

Authors: David Eccles

Group: High molecular weight DNA extraction from all kingdoms

Summary: This protocol is for a semi-manual method for read demultiplexing, as used after my presentation Sequencing DNA with Linux Cores and Nanopores to work out the number of reads captured by different barcodes. Input: reads as a FASTQ file, barcode sequences as a FASTA file Output: reads split into single FASTQ files per target [barcode] Note: barcode / adapter sequences are not trimmed by this protocol

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External URL: <https://doi.org/10.5281/zenodo.2535894>

Version: 1

Publication Date: 2019

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Record Creation Time: 20210329T220523+0000

Record Last Update: 20210329T220858+0000

Data and Source Information

Source: