

# Resource Summary Report

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## Introduction to read mapping

DOI:10.17504/protocols.io.piadkae

Type: Protocol

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### Proper Citation

Frank Aylward 2018. Introduction to read mapping. protocols.io  
[dx.doi.org/10.17504/protocols.io.piadkae](https://dx.doi.org/10.17504/protocols.io.piadkae)

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### Protocol Information

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

**Authors:** Frank Aylward

**Summary:** This is an example of a simple read mapping workflow. It is designed to be performed via the command line on an Ubuntu 16.06 OS. After completing this tutorial you should:1) Have a practical understanding of how read mapping analyses are performed in the command line.2) Understand the basics of how to process SAM and BAM files.3) Be able to calculate depth of coverage of a contig/scaffold/chromosome in a query read dataset.

**Affiliations:** Virginia Tech

**Version:** 2

**Publication Date:** 2018

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### Data and Source Information

**Source:**