



Identify

BagIt

Completeness



Access



RO-Crate

Describe and Relate



BioCompute
Objects

Explain

Exemplify

results/

- folder bwa/mergedLibrary
- folder fastqc
- folder genome
- folder igv/broadPeak
- folder multiqc/broadPeak
- folder pipeline_info
- folder trim_galore

Execute

nextflow

Attribution

ORCID



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docker

BIOCONDA®

Software Packages

GitHub
LFS