



Identify

BagIt

Completeness



RO-Crate

Describe and Relate



BioCompute  
Objects

Explain

results/

Exemplify

Execute

nextflow

- bwa/mergedLibrary
- fastqc
- genome
- igv/broadPeak
- multiqc/broadPeak
- pipeline\_info
- trim\_galore



Access



GitHub  
LFS

Attribution

ORCID



License



docker

BIOCONDA

Software Packages