

AWS HealthOmics - Troubleshooting

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<https://docs.aws.amazon.com/omics/latest/dev/troubleshooting.html>

ECR_PERMISSION_ERROR

Unable to access image URI: {account_id}.dkr.ecr.us-east-1.amazonaws.com/quay/quay.io/biocontainers/bioconductor-dropletutils:1.18.0--r42hf17093f_1. Ensure the ECR private repository exists and has granted access for the omics service principle to access the repository.

{account_id}.dkr.ecr.us-east-1.amazonaws.com/quay/biocontainers/python:3.9--1
{account_id}.dkr.ecr.us-east-1.amazonaws.com/quay/nf-core/seurat:4.3.0
{account_id}.dkr.ecr.us-east-1.amazonaws.com/quay/biocontainers/fastqc:0.12.1--hdfd78af_0

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```
process FASTQC {
  tag "$meta.id"
  label 'process_medium'

  conda "${moduleDir}/environment.yml"
  container "${ workflow.containerEngine == 'singularity' && !task.ext.singularity_pull_docker_container ?
    'https://depot.galaxyproject.org/singularity/fastqc:0.12.1--hdfd78af_0' :
    'biocontainers/fastqc:0.12.1--hdfd78af_0' }"
```

{account_id}.dkr.ecr.us-east-1.amazonaws.com/**quay/quay.io**/biocontainers/bioconductor-dropletutils:1.18.0--r42hf17093f_1

```

process EMPTYDROPS_CELL_CALLING {
  tag "$meta.id"
  label 'process_medium'

  conda "bioconda::bioconductor-dropletutils"
  container "${ workflow.containerEngine == 'singularity' && !task.ext.singularity_pull_docker_container ?
    'https://depot.galaxyproject.org/singularity/bioconductor-dropletutils:1.18.0--r42hf17093f_1' :
    'quay.io/biocontainers/bioconductor-dropletutils:1.18.0--r42hf17093f_1' }"

```

scrnaseq/conf/omics.config

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```

process {
  withName: '.*' { conda = null }
  withName: '(.+)?ALEVINQC' { container = 'quay/biocontainers/bioconductor-alevinqc:1.12.1--r41h9f5acd7_0' }
  withName: '(.+)?CONCAT_H5AD' { container = 'quay/biocontainers/scanpy:1.7.2--pyhdfd78af_0' }
  withName: '(.+)?EMPTYDROPS_CELL_CALLING' { container = 'quay/quay.io/biocontainers/bioconductor-dropletutils:1.18.0--r42hf17093f_1' }
  withName: '(.+)?GFFREAD_TRANSCRIPTOME' { container = 'quay/biocontainers/gffread:0.12.7--hd03093a_1' }
  withName: '(.+)?GTF2_GTF5_FILTER' { container = 'quay/biocontainers/htseq:0.11.1--r41h9f5acd7_0' }
}

```

to

```

process {
  withName: '.*' { conda = null }
  withName: '(.+)?ALEVINQC' { container = 'quay/biocontainers/bioconductor-alevinqc:1.12.1--r41h9f5acd7_0' }
  withName: '(.+)?CONCAT_H5AD' { container = 'quay/biocontainers/scanpy:1.7.2--pyhdfd78af_0' }
  withName: '(.+)?EMPTYDROPS_CELL_CALLING' { container = 'quay/biocontainers/bioconductor-dropletutils:1.18.0--r42hf17093f_1' }
  withName: '(.+)?GFFREAD_TRANSCRIPTOME' { container = 'quay/biocontainers/gffread:0.12.7--hd03093a_1' }
}

```