

? ?? ??? ??? ??

??? Quota? ??

AWS 的 的 的 HealthOmics 的 Quota 的 . 的 的 的 的 的 . (的 的 的 的)

- 的 的 : <https://docs.aws.amazon.com/general/latest/gr/healthomics-quotas.html>
- Quota: <https://docs.aws.amazon.com/omics/latest/dev/quotas.html>

HealthOmics Etag ? ??? ??

HealthOmics 的 Etag 的 的 的 Hash 的 . 的 的 的 的 的 的 的 .

Etag 的 的 的 的 的 的 的 的 . 的 的 bitwise identity 的 semantic identity 的 , 的 的 的 的 的 的 的 的 的 的 . 的 的 的 的 的 的 的 的 的 的 的 的 .

HealthOmics 的 的 Read sets 的 的 的 的 的 的 / 的 的 的 的 的 的 . 的 的 的 的 的 的 的 的 .

的 的 的 的 的 .




























<https://docs.aws.amazon.com/omics/latest/dev/etags-and-provenance.html>

??? ?????? ?? ??????

HealthOmics Transfer Manager 的 的 的 的 . 的 的 的 的 的 的 .

<https://docs.aws.amazon.com/omics/latest/dev/synchronous-uploads.html>

??? ???? ?? ???? ?? 3rd party?? ??
 ????

- Integrative Genomics Viewer (IGV)  UCSC Genome Browser 
- CWL, WDL  Nextflow      Amazon S3   
-     Amazon S3 URIs  presigned Amazon S3 URIs   
- Mountpoint  CloudFront   Amazon S3     

<https://docs.aws.amazon.com/omics/latest/dev/s3-access.html>

?? ?? ??

HealthOmics             

ACTIVE  .30  ARCHIVE

```

    if ( ! active ) {
        ReadSet = new ReadSet(
            AmazonS3GlacierInstantRetrievalStorageClass
        )
    }

```

2023년 10월 10일 10:10 1Gbase 3 110Gbase 2 45

<https://docs.aws.amazon.com/omics/latest/dev/activating-read-sets.html>

?? ?? ??

AWS Lake Formation █████ Amazon Athena █████ AMaozn EMR █████ █████ █████ █████ █████ █████

██████.

2024年9月26日，HealthOmics ID

1. The first step is to create a new Amazon ECR repository.
 2. Next, you need to build a Docker image for the linter.

3. Then, you can push the image to the repository.
 4. Finally, you can use the image to lint your workflows.

Why? Why? Why? Why? Why?

The reason for this is that the current linter is not able to handle certain types of workflows.
 This is a known issue and we are working on a fix.

WDL is a workflow description language. HealthOmics is a workflow engine.
 The linter is a tool that checks workflows for errors.
 The CLI is a command-line interface.
 The get-Workflow command is used to retrieve workflow information.
 The StatusMessage command is used to get the status of a workflow.
 The ID is the identifier for the workflow.

- **WDL** – A public Amazon ECR image to run a [WDL linter](#).
- **Nextflow** – A public Amazon ECR image to run [Linter rules for Nextflow](#). You can access the source code for this linter from [GitHub](#).
- **CWL** – not available

<https://docs.aws.amazon.com/omics/latest/dev/workflows-linter.html>

Why? Why? Why? Why? Why?

HealthOmics is a workflow engine. The linter is a tool that checks workflows for errors.
 The CLI is a command-line interface. The get-Workflow command is used to retrieve workflow information.
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<https://docs.aws.amazon.com/omics/latest/dev/workflows-call-caching.html>

HealthOmics? ?? ??

- HealthOmics variant stores, HealthOmics annotation stores, Private workflows

<https://docs.aws.amazon.com/omics/latest/dev/resource-sharing.html>

HealthOmics? ?? ?? (EventBridge ??)

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

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