

Tencent HealthCare Omics Platform

FAQs

Product Documentation



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FAQs

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How to Log in to the Tencent Healthcare Omics Platform?

This platform consists of [Console > Tencent HealthCare Omics Platform Module](#) and [Tencent HealthCare Omics Platform Website](#). The administrator can use the Tencent Cloud account to log in to the Tencent Cloud console and enter [Console > Tencent HealthCare Omics Platform Module](#) to create an environment and multiple user accounts. For related operations, see [Environment Management](#) and [User Management](#). After the administrator completes the creation of the environment and user accounts, platform users can go to [Tencent HealthCare Omics Platform Website](#), log in with the user account created by the administrator, and use the platform to start the analysis task.

Where Are the Data Files Stored?

The data storage of this platform depends on [Tencent Cloud COS](#) to provide file management services to users. Data is stored in COS buckets. Upload and download operations of data files must be completed in COS. The file management page of the platform mainly provides the feature of viewing file directories.

How to Upload a File?

There are three ways to upload files to COS: console upload, command line upload, and data migration.

Console upload: See [COS Documentation: Uploading Objects](#).

Command line upload: See [COS Documentation: Upload, Download, or Copy Files](#).

Data migration: See [COS Documentation: Migrating Local Data to COS](#).

How to Download a File?

Console download: See [COS Documentation: Downloading Objects](#).

Command line download: See [COS Documentation: COSCLI Introduction - Upload, Download, or Copy Files](#).

Are Other Workflow Languages Supported Besides WDL?

The Tencent HealthCare Omics Platform currently only supports WDL language editing of bioinformatics applications. We plan to support more workflow languages (Nextflow, Snakemake, etc.) in the next stage, and related functional modules are under development. If you have more workflow language requirements, contact us to give your feedback.

How to View the Job execution environment and Resource Usage?

1. If you want to view the execution environment and resource usage of a job, you can click **Details** of the job you want to view on the run details page.

The screenshot displays the 'Run Details' page for a Nextflow job. The top navigation bar shows the job's progress through stages: Analyzing, Initializing, Computing, Completed, Failed, and Terminated. The main content area is divided into two sections: job metadata and a list of jobs.

Job Metadata:

- Name: nfscrnaseq私有应用类型cos1
- ID: run-damp-silver-piranha-676102
- Application type: Private Application
- AccessMode: Private Application
- Description: Private Application
- Environment: Private Application
- Environment ID: menv-rr6el746
- Profile: test
- Config: View
- manifest: View
- Nextflow Version: 23.10.1
- Application File Path: /vol-05lihgiw/env/menv-rr6el746/nextflow/nfpath/https/e.coding.net/biotech/nf-core/scrnaseq.git/branch/master
- Volume: vol-05lihgiw
- Volume ID: vol-05lihgiw
- Mount path: /vol-05lihgiw
- workdir: /vol-05lihgiw/env/menv-rr6el746
- Startup path: /vol-05lihgiw/env/menv-rr6el746
- Cache Duration: Clean up immediately

List of Jobs:

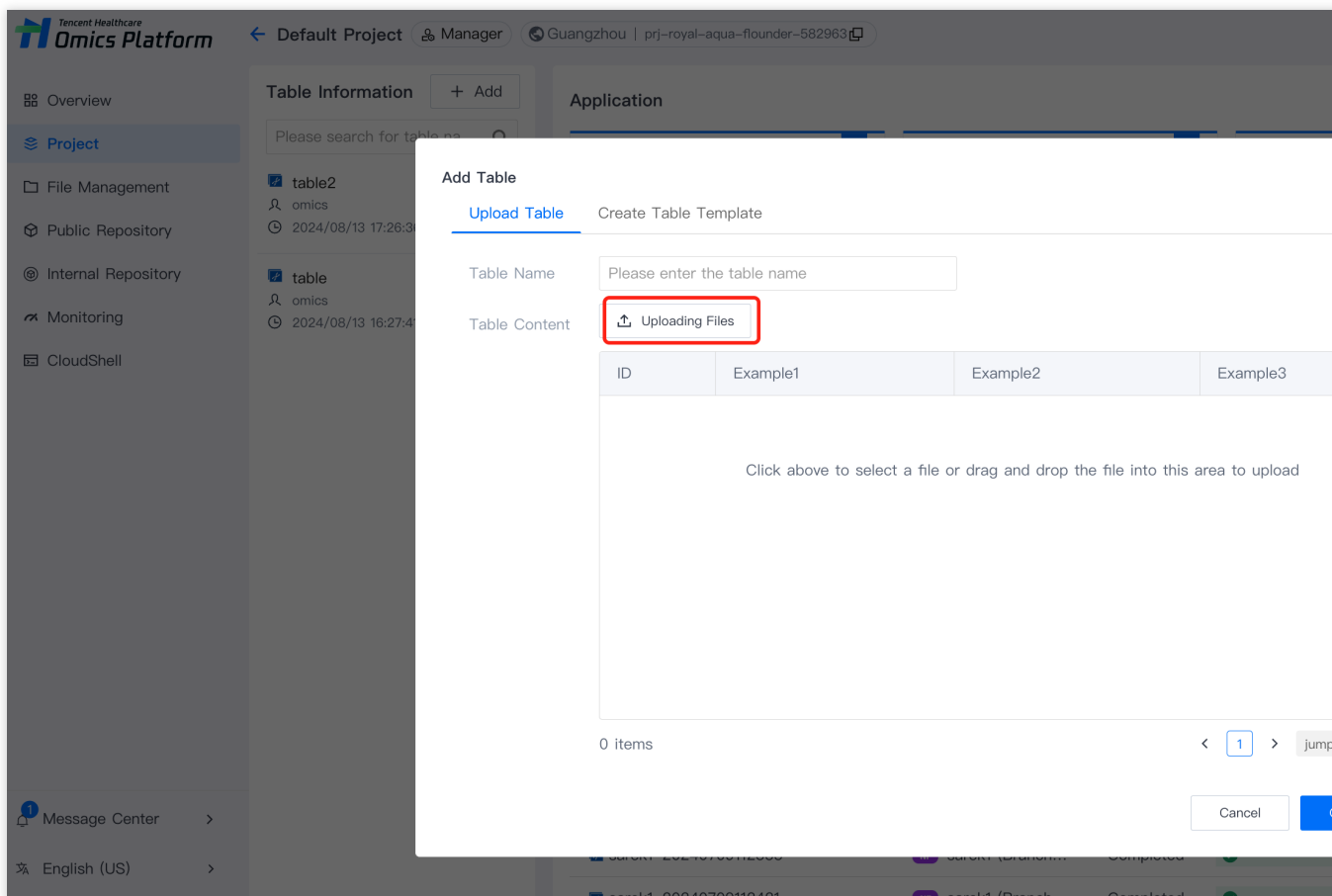
Job name	Status	Start Time	Duration
NFCORE_SCRNASEQ:SCRNASEQ:INPUT_CHECK:SAMPLESHEET_CHECK (sampleshe...	Completed	2024/03/26 18:25:13	39s
NFCORE_SCRNASEQ:SCRNASEQ:MTX_CONVERSION:MTX_TO_H5AD (Sample_X)	Completed	2024/03/26 18:32:59	42s
NFCORE_SCRNASEQ:SCRNASEQ:MTX_CONVERSION:MTX_TO_SEURAT (Sample_X)	Completed	2024/03/26 18:33:00	48s
NFCORE_SCRNASEQ:SCRNASEQ:CUSTOM_DUMPSOFTWAREVERSIONS (1)	Completed	2024/03/26 18:32:59	46s
NFCORE_SCRNASEQ:SCRNASEQ:MTX_CONVERSION:CONCAT_H5AD	Completed	2024/03/26 18:33:42	41s
NFCORE_SCRNASEQ:SCRNASEQ:MULTIQC	Completed	2024/03/26 18:33:46	1m13s
NFCORE_SCRNASEQ:SCRNASEQ:GTF_GENE_FILTER (GRCm38.p6.genome.chr19.fa)	Completed	2024/03/26 18:25:13	41s
NFCORE_SCRNASEQ:SCRNASEQ:FASTQC_CHECK:FASTQC (Sample_X)	Completed	2024/03/26 18:25:54	36s
NFCORE_SCRNASEQ:SCRNASEQ:FASTQC_CHECK:FASTQC (Sample_Y)	Completed	2024/03/26 18:25:53	48s
NFCORE_SCRNASEQ:SCRNASEQ:STARSOLO:STAR_GENOMEGENERATE (GRCm38.p...	Completed	2024/03/26 18:25:55	1m57s
NFCORE_SCRNASEQ:SCRNASEQ:STARSOLO:STAR_ALIGN (Sample_X)	Completed	2024/03/26 18:27:53	5m5s
NFCORE_SCRNASEQ:SCRNASEQ:STARSOLO:STAR_ALIGN (Sample_Y)	Completed	2024/03/26 18:27:53	4m35s

2. The job details page will display the job's execution environment (such as the number of CPU cores, memory specifications, and docker image address) and resource monitoring charts (such as CPU utilization and memory utilization).

The screenshot displays the Tencent HealthCare Omics Platform interface. On the left is a navigation sidebar with options like Overview, Project, File Management, Public Repository, Internal Repository, Monitoring, and CloudShell. The main area is titled 'Failed' and shows a progress bar with stages: Analyzing, Initializing, Preprocessing, Computing, and Archiving. Below this, job details are listed, including Name, ID, Application type, AccessMode, Description, Environment, Environment ID, Options, Failure Mode, and Directory. On the right, 'ExomeGermlineSingleSample.CollectHsMetrics Job Details' are shown, including Job ID and tabs for Details and Event. Below this is the 'Execution Environment' section with parameters for Custom Runtime CPU, Custom Runtime, Memory, disks, and docker. At the bottom right, 'Monitoring Details' includes a line graph for CPU Usage, CPU Utilization, Memory Usage, and Memory Utilization over time.

How to Upload a Sample Containing Multiple Fastq Files for Analysis?

1. Create a table template. You can refer to the following format settings for a sample table. Each sample_id corresponds to multiple fastq file addresses, set the type to Array[File]. For operations related to creating a table, see [Table Management](#).



2. Upload the table.

3. In the WDL file, define the input file data type as `Array[File]` and select the corresponding column on the running settings page. For related operations on running settings, see [Application Management](#).

Default Project ap-guangzhou | gatk-WES-germline-snps/indels / Run Configuration

Table: **table2** [Select data] All selected

Options: Use Call-Caching feature Use relative directory output

* Failure Mode: NoNewCalls

* Cache Retention Period: 24 hours 3 days 7 days 30 days Indefinite

* Environment: test2 (menv-8x529447)

* Select Volume: volume1 (menv-8x529447) (vol-3do6m9y6)

* Output Directory: please enter Add run group name

* Result Notification: Internal Message Internal Message + Email

Run Parameter Settings

Input Settings [inputs_ap-guar]

Variable Name	Type
ExomeGermlineSingleSample.BamToGvcf.ref_str	File
*ExomeGermlineSingleSample.BamToGvcf.make_gvcf	Boolean
*ExomeGermlineSingleSample.BamToGvcf.make_bamout	Boolean
*ExomeGermlineSingleSample.BamToGvcf.use_gatk3_haplotype_caller	Boolean
*ExomeGermlineSingleSample.BamToGvcf.skip_reblocking	Boolean
*ExomeGermlineSingleSample.BamToGvcf.use_dragen_hard_filtering	Boolean
*ExomeGermlineSingleSample.BamToGvcf.DragstrAutoCalibration.do...	abc String

4. Start analysis.

How to Use the Enterprise Tencent Container Registry in the Omics Computing Environment?

If you want to use the Tencent Container Registry Enterprise in the omics computing environment, you need to **ensure that you have selected the corresponding image access credential and ensure network integration between the Omics Computing Environment and TCR.**

Ensure That You Have Selected the Corresponding Tencent Container Registry Enterprise Credential

Container images are private by default, so when creating an environment, you need to issue the corresponding credential to the environment. For specific operations, see [Operation Guide > Console > Environment Management](#).

Ensure that the environment is reachable to the Tencent Container Registry Enterprise.

There is no network connection between the omics computing environment and the Tencent Container Registry Enterprise by default, so a network unreachable error will be reported when you pull images from the enterprise image repository.

Solutions

There are two solutions. For specific operations, see corresponding documentation instructions in the following table:

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Solutions	Description	Documentation
Solution 1: Private Network Access	On TCR console, create a private network linkage in the same VPC as the Omics Environment and config private network DNS. Then the Omics Environment can access TCR instance through private network.	Image Repository Related
Solution 2: Public Network Access	On TCR console, open internet access entry. Then, create a NAT instance in the same VPC as the Omics Environment to allow public network access.	