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To Enable Effective and Affordable Healthcare Solutions for All

MegaBOLT Bioinformatics Analysis Accelerator

User Manual | ZLIMS

Research Use Only

MGI Tech Co., Ltd.

Edition 1.0

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About the user manual

This user manual is applicable to MegaBOLT Bioinformatics Analysis Accelerator (MegaBOLT_scheduler). The edition is 1.0 and the software version is V2.1.0.

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Release date: November 30, 2019

Manufacturer information

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Revision history

Revision	Date
1.0	November 30, 2019

Contents

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1

Introduction

MegaBOLT bioinformatics analysis accelerator (hereinafter called MegaBOLT) is an MGI self-developed and NGS-concentrated hardware (FPGA, Field-Programmable Gate Array) accelerating system and multi-task scheduling system for bioinformatics analysis. MegaBOLT supports the analysis of Whole Genome Sequencing (WGS), Whole Exome Sequencing (WES), and Panel Sequencing on Germline or Somatic data, fulfilling from FASTQ input of sequencing data to BAM output of alignment result and VCF/gVCF output of variant calling result. And it is 20 times faster than the traditional GATK approach.

The MegaBOLT Rack Server mode is a rack server equipped with the MegaBOLT analysis system for large-scale data analysis scenarios in a cluster environment. It is flexible because it supports a variety of analysis processes, and it is suitable for users with background of bioinformatics analysis.

The MegaBOLT Workstation mode is a workstation equipped with the MegaBOLT analysis system for small to medium data analysis scenarios. It provides one-stop services from sequencing to WGS/WES analysis. It provides an interactive web interface and analysis report, which is easy to operate and suitable for most users with non-biological information analysis backgrounds.

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Configuration requirements

Item	Minimum configuration	Recommended configuration
CPU	2 × Intel Xeon E5-26XX Series	2 × Intel Xeon Gold 62XX Series
Memory	96 GB	128 GB
Storage	1 TB HDD	>2 TB SSD
OS	CentOS 7.3-7.5	CentOS 7.3-7.5
Network card	1 Gbps	>10 Gbps

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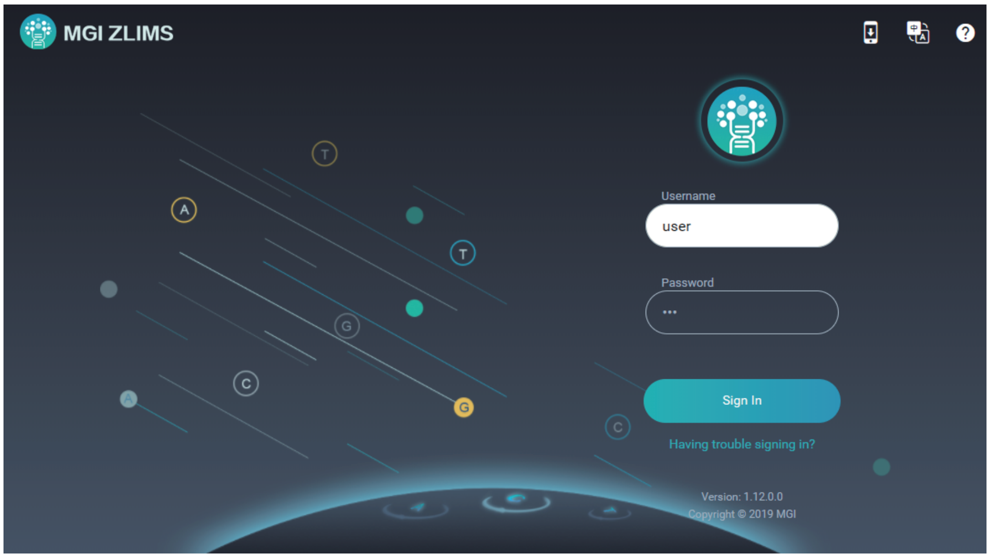
Procedure

To use MegaBOLT in ZLIMS system, perform the following steps:

1. Access ZLIMS through the approaches below:
    1) Launch Google Chrome browser, enter *127.0.0.1* in the address bar, and press Enter.
    2) Double-click the ZLIMS shortcut on the desktop.
2. Input the user name “user” and password “123” to log into the ZLIMS system.



Username
user

Password
•••

Version: 1.12.0.0
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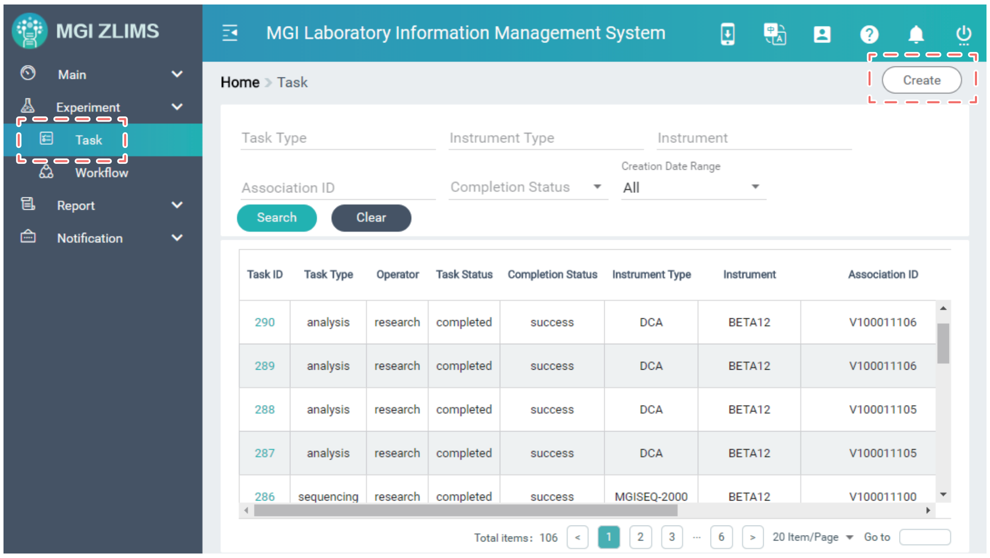
Figure 1 Logging into ZLIMS

3. Select **Experiment** > **Task** to enter the task page, and click **Create**.

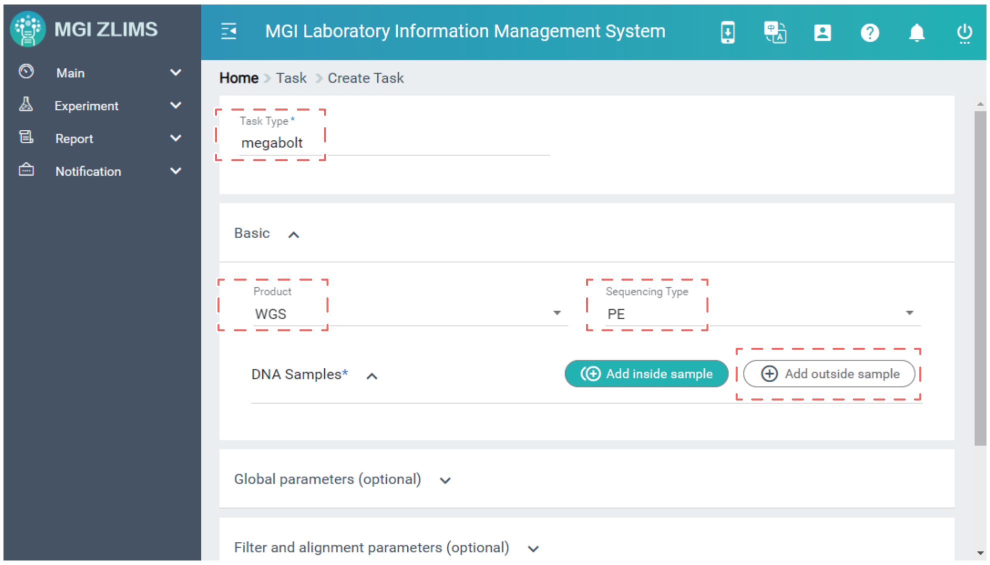


Creation Date Range: All

Task ID	Task Type	Operator	Task Status	Completion Status	Instrument Type	Instrument	Association ID
290	analysis	research	completed	success	DCA	BETA12	V100011106
289	analysis	research	completed	success	DCA	BETA12	V100011106
288	analysis	research	completed	success	DCA	BETA12	V100011105
287	analysis	research	completed	success	DCA	BETA12	V100011105
286	sequencing	research	completed	success	MGISEQ-2000	BETA12	V100011100

Figure 2 Creating a task

4. Set **Task Type** to **megabolt**, set **Product** to **WGS** or **WES**, and set **Sequencing Type** to **PE**.



Task Type*: megabolt

Product: WGS

Sequencing Type: PE

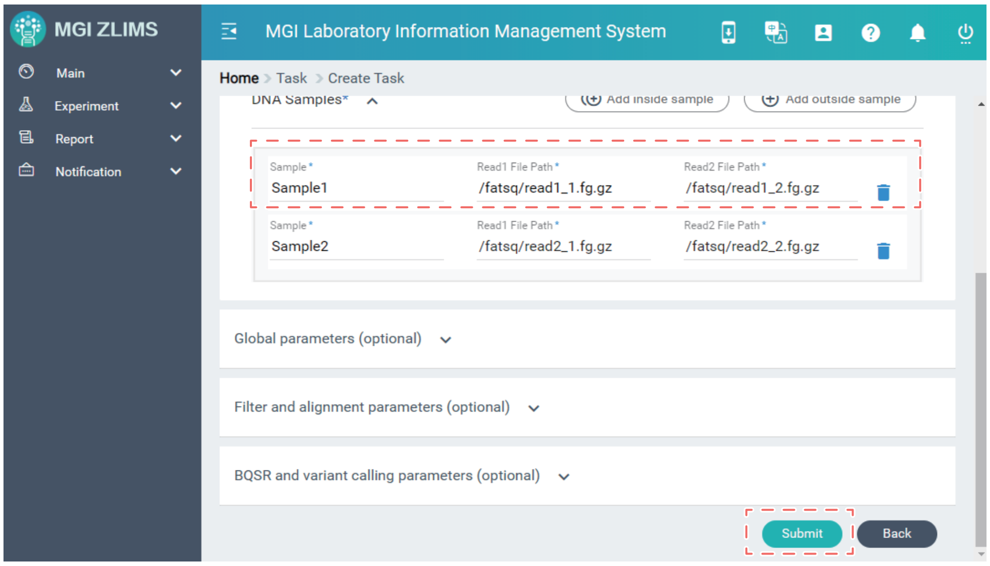
Figure 3 Adding sample information

5. Click **Add outside sample** to add sample information and click **Submit**.

NOTE

- Items marked with "*" are required.
- Multiple lines of sample information can be added.
- More optional parameters could be specified in **Global parameters**, **Filter and alignment parameters**, and **BQSR and variant calling parameters**. For details about commandline parameters, refer to *MegaBOLT_user_manual*.

You will be prompted when the submission succeeds and the newly added task will be listed in the task page for analysis.



Sample *	Read1 File Path *	Read2 File Path *
Sample1	/fatsq/read1_1.fg.gz	/fatsq/read1_2.fg.gz
Sample2	/fatsq/read2_1.fg.gz	/fatsq/read2_2.fg.gz

Figure 4 Submitting a task

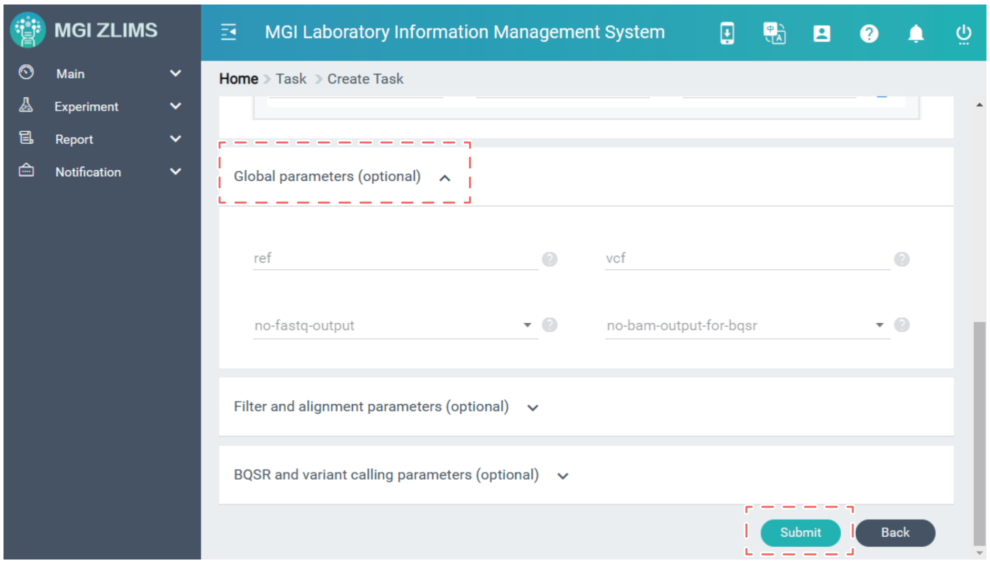
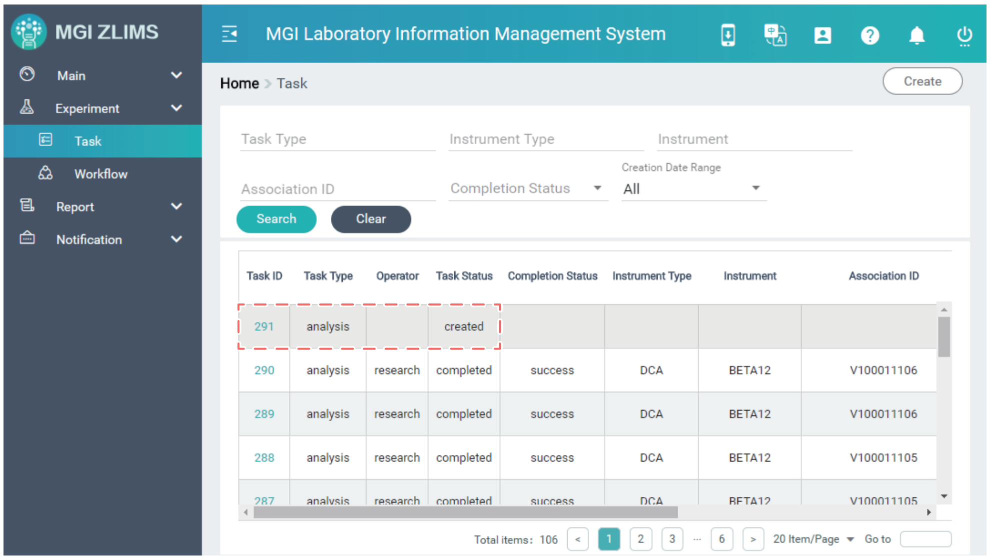


Figure 5 Specifying optional parameters

6. Wait till the analysis completes.

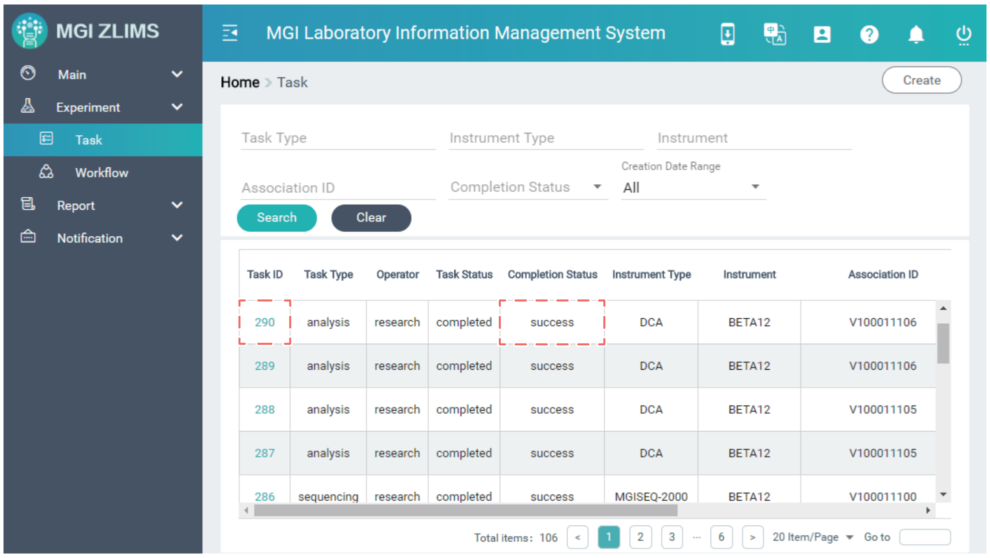
You can check the status of the submitted task in the **Task Status** column on the task page.



Task ID	Task Type	Operator	Task Status	Completion Status	Instrument Type	Instrument	Association ID
291	analysis		created				
290	analysis	research	completed	success	DCA	BETA12	V100011106
289	analysis	research	completed	success	DCA	BETA12	V100011106
288	analysis	research	completed	success	DCA	BETA12	V100011105
287	analysis	research	completed	success	DCA	BETA12	V100011105

Figure 6 Checking task creation status

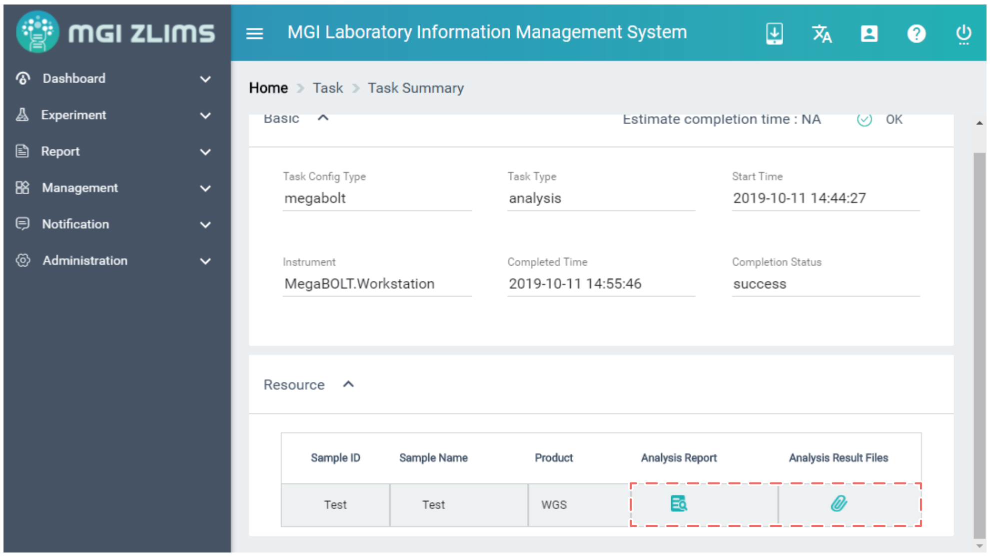
7. After the **Completion Status** of the task turns to **success**, click the task ID to enter the **Task Summary** page.



Task ID	Task Type	Operator	Task Status	Completion Status	Instrument Type	Instrument	Association ID
290	analysis	research	completed	success	DCA	BETA12	V100011106
289	analysis	research	completed	success	DCA	BETA12	V100011106
288	analysis	research	completed	success	DCA	BETA12	V100011105
287	analysis	research	completed	success	DCA	BETA12	V100011105
286	sequencing	research	completed	success	MGISEQ-2000	BETA12	V100011100

Figure 7 Checking task completion status

8. On the **Task Summary** page, you can click the icons in the **Analysis Report** or **Result Files** column to view the results.



Estimate completion time : NA ✓ OK

Task Config Type: megabolt
Task Type: analysis
Start Time: 2019-10-11 14:44:27
Instrument: MegaBOLT.Workstation
Completed Time: 2019-10-11 14:55:46
Completion Status: success

Sample ID	Sample Name	Product	Analysis Report	Analysis Result Files
Test	Test	WGS		

Figure 8 Viewing analysis report and results

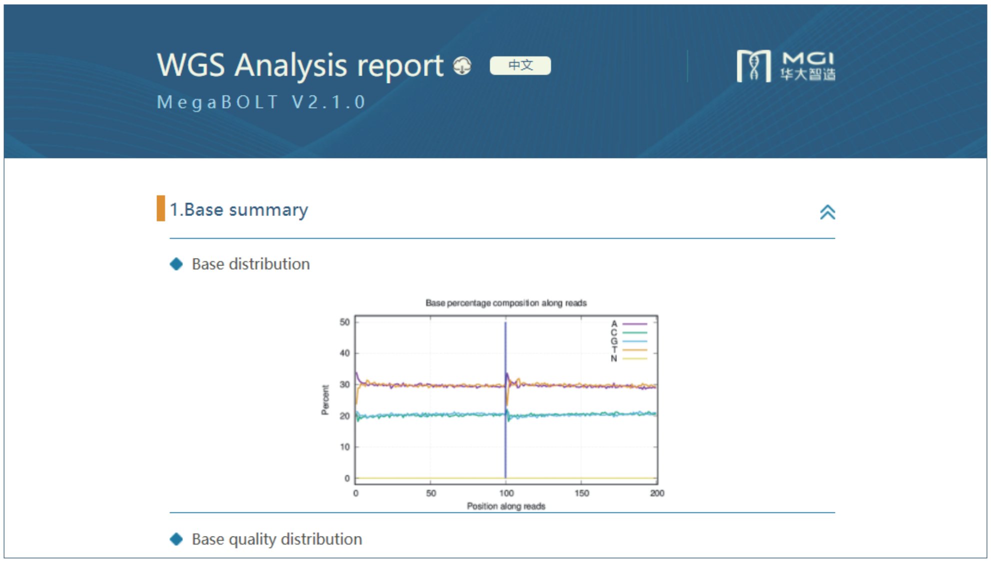


Figure 9 Exemplary analysis report

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