

QIAcuity Software Suite API 3.5.0.0 (build 120.0.0.621)

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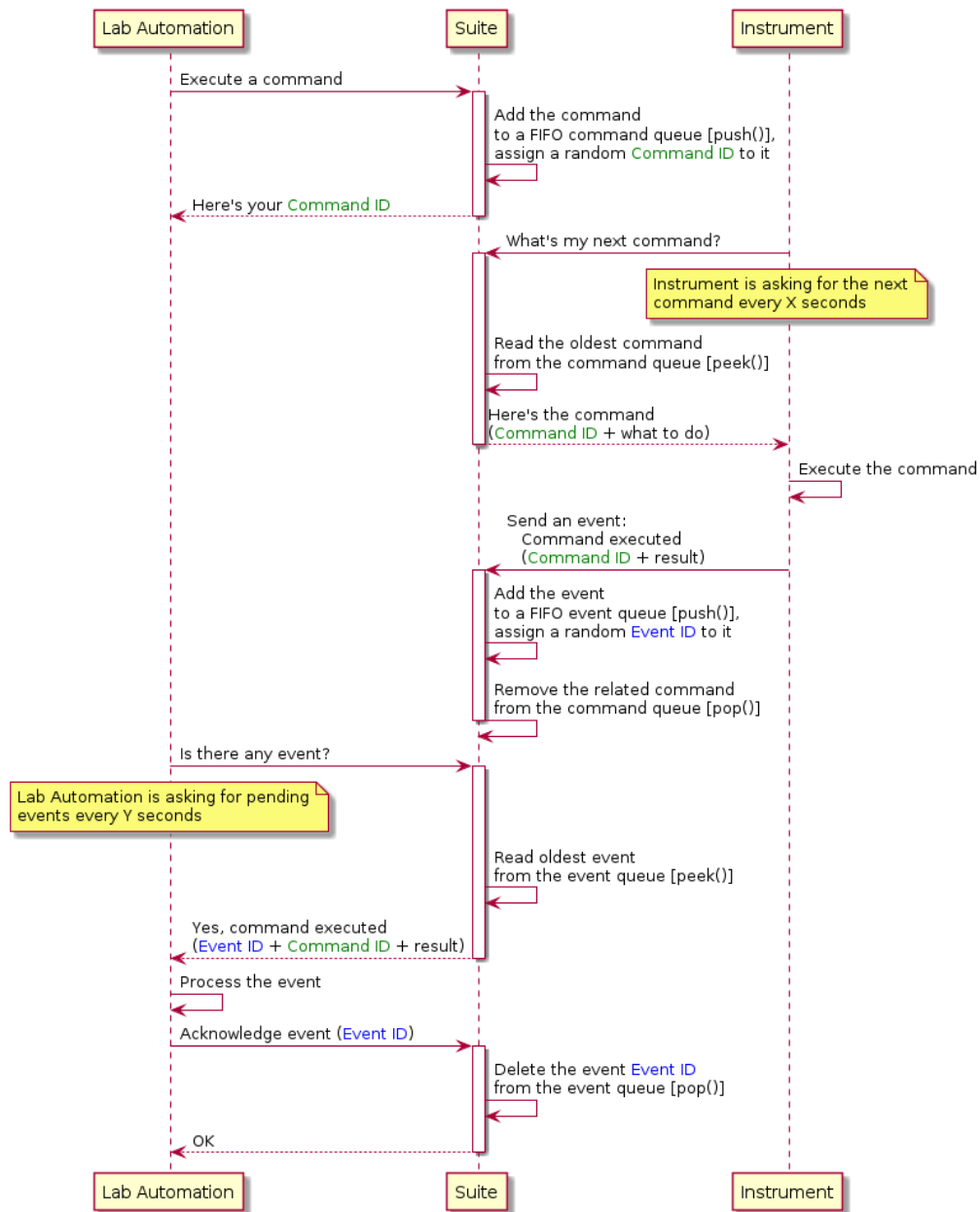
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1 Usage

When controlling the instruments, the Lab Automation Service uses a concept of command and event queues. Both queues are working in a “first in, first out” fashion which means the oldest element in the queue will be retrieved (processed) first.

Commands tell the QIAcuity instrument what to do. Events tell what the instrument or Software Suite has done. The Lab Automation API provides endpoints for adding and retrieving commands and events.



2 Identifying instruments, drawers and plate slots in the API

There are three models of the QIAcuity instrument: QIAcuity One, QIAcuity Four and QIAcuity Eight.

The models differ by the number of drawers and the number of slots for plates in the drawers.

Whenever the API requires to provide the model of the instrument or identifiers of drawers and slots, the following values must be used:

Note: slots are counted from the left when standing in front of the instrument

Instrument model	Model type code	Identifiers of drawers and slots
QIAcuity One	P1	- Drawer0 , slot 0
QIAcuity Four	P4	- Drawer0 , slots 0, 1, 2, 3
QIAcuity Eight	P8	- upper drawer: Drawer0 , slots 0, 1, 2, 3 - lower drawer: Drawer1 , slots 0, 1, 2, 3

3 Channels in imaging

Imaging channels are defined by the colors of the excitation and emission filters. Some of the filter combinations require the High-Multiplexing-Reference Channel to be enabled in the imaging step.

The following filter combinations are supported:

Excitation	Emission	High Multiplexing Reference Channel required?
GREEN	GREEN	No
YELLOW	YELLOW	No
ORANGE	ORANGE	No
RED	RED	No
CRIMSON	CRIMSON	No
FARRED	FARRED	Yes
GREEN	YELLOW	Yes
YELLOW	ORANGE	Yes
ORANGE	RED	Yes
RED	CRIMSON	Yes
CRIMSON	FARRED	Yes

4 Commands

Each of the following commands has a corresponding API endpoint with the same name. The parameters are specified in the description of the particular endpoint.

4.1 BookDrawer

Books particular drawers for exclusive robot use.

In order to prevent a human to open the drawer while the Lab Automation commands the robot to insert/remove plate(s) to/from the instrument, the Lab Automation must book a drawer for exclusive use. Afterwards, manual operation of the drawer via a physical button or a button on the Instrument's UI is disabled. In order to enable it again, ReleaseDrawerBooking endpoint must be called.

4.2 ReleaseDrawerBooking

Releases the exclusive booking of the drawers specified in the command.

Afterwards, manual operation of the drawer via a physical button or a button on the Instrument's UI is enabled.

Tip: in fully-automated use scenarios, there is no need to release the booking at all. Releasing the booking is only required if a human needs to interact with the drawer.

4.3 OpenDrawer

Opens the drawer specified in the command. The drawer must be booked beforehand.

4.4 CloseDrawer

Closes the drawer specified in the command. The drawer must be booked beforehand.

4.5 RunExperiment

Links a physical plate to an experiment definition in Software Suite, then starts the experiment. The drawer must be booked beforehand.

5 Events

Events can be received in the `/lab-automation/v1/events` endpoint.

Events are available in two forms:

- command-related - results of executing a command;
- unsolicited - side-effects of actions happening in the background of Software Suite.

Events may contain payloads. To make it possible to change the schema of the payloads and recognize changed schema by the consumers of the API, the payloads are versioned by a `payloadSchemaVersion` property.

Example of a response from the `/lab-automation/v1/events` endpoint.

```
{
  "id": "21ebe258-ec80-4f73-aafc-4faa863d8a22",
  "commandId": "21ebe258-ec80-4f73-aafc-4faa863d8a22",
  "instrumentId": "instrument1234",
  "type": "DRAWER_BOOKED",
  "payloadSchemaVersion": 1,
  "payload": {
    "freeSlotsInDrawers": {
      "Drawer0": [0,1,2,3],
      "Drawer1": [0,1,2,3]
    }
  }
}
```

In case of unsolicited events, the `commandId` property is `null`.

5.1 DRAWER_BOOKED

Event for the `BookDrawer` command:

- When drawer was successfully booked
- When drawer was already booked and Lab Automation asked for it once again

Payload example:

```
{
  "freeSlotsInDrawers": {
    "Drawer0": [0, 1, 2, 3],
    "Drawer1": [0, 1, 2, 3]
  }
}
```

Schema version: 1

5.2 DRAWER_OPENED

Event for the `OpenDrawer` command:

- When booking for the requested drawer is active and the drawer was successfully opened
- When booking for the requested drawer is active and the drawer was already open

Payload example:

```
{
  "drawerName": "Drawer1",
  "freeSlotsInDrawers": {
    "Drawer0": [0, 1, 2, 3],
    "Drawer1": [0, 1, 2, 3]
  }
}
```

Schema version: 1

5.3 DRAWER_NOT_OPENED

Event for the `OpenDrawer` command:

- When Lab Automation Software does not have an active booking for the requested drawer

Payload example:

```
{
  "drawerName": "Drawer1",
  "reason": "NO_ACTIVE_BOOKING"
}
```

`reason` is one of:

- UNKNOWN_ISSUE
- INVALID_MODULE_ID (drawer with specified name does not exist)
- NO_ACTIVE_BOOKING (drawer is not booked by Lab Automation Software)
- OTHER_DRAWER_OPENED_BY_COMMAND (for instruments with more than one drawer: if another drawer is already open)

Schema version: 1

5.4 DRAWER_OPENED_MANUALLY

Unsolicited event occurring when a human opened a drawer manually.

Payload example:

```
{
  "drawerName": "Drawer1"
}
```

Schema version: 1

5.5 DRAWER_CLOSED

Event for the `CloseDrawer` endpoint:

- When booking for the requested drawer is active, the drawer was successfully closed and plates on the drawer were identified
- When booking for the requested drawer is active and the drawer was already closed

Payload example:

```
{
  "drawerName": "Drawer1"
}
```

Schema version: 1

5.6 DRAWER_NOT_CLOSED

Event for the `CloseDrawer` endpoint:

- When Lab Automation Software does not have an active booking for the requested drawer

Payload example:

```
{
  "drawerName": "Drawer1",
  "reason": "NO_ACTIVE_BOOKING"
}
```

`reason` is one of:

- UNKNOWN_ISSUE
- INVALID_MODULE_ID (drawer with specified name does not exist)
- NO_ACTIVE_BOOKING (drawer is not booked by Lab Automation Software)
- OTHER_DRAWER_OPENED_BY_COMMAND (for instruments with more than one drawer: if another drawer is already open)

Schema version: 1

5.7 DRAWER_CLOSED_MANUALLY

Unsolicited event occurring when a human closed a drawer manually.

Payload example:

```
{  
  "drawerName": "Drawer1"  
}
```

Schema version: 1

5.8 DRAWER_BOOKING_RELEASED

Event for the `ReleaseDrawerBooking` command when any of the following happens:

- booking was released
- Lab Automation Software asked for releasing more bookings than it owned
- there was nothing to release (no bookings were active)

Payload example:

```
{  
  "drawerName": "Drawer1"  
}
```

Schema version: 1

5.9 DRAWER_BOOKING_NOT_RELEASED

Event for the `ReleaseDrawerBooking` command when Lab Automation owns a booking for the requested drawer and the drawer is open

Payload is `null`.

Schema version: 1

5.10 EXPERIMENT_PROCESSING_STARTED

Event for the `RunExperiment` command when instrument started the experiment.

Payload is `null`.

Schema version: 1

5.11 EXPERIMENT_READY

Unsolicited event created when for all configured imaging steps in the experiment:

- all wells are analyzed by Suite (including analysis template) in all defined imaging steps OR
- instrument notified that image transfer is finished for a particular imaging step and all the wells for which pictures were received were analyzed by Suite (including analysis template) in all defined imaging steps

Payload:

```
{
  "plateId": "7da11fca-31e9-4bdd-9ed4-2a47eacefcf0",
  "imagingStepIndexes": [3],
  "allImagingStepIndexes": [3, 4],
  "allImagingStepsReady": false
}
```

The `allImagingStepsReady` flag will be `true` if `imagingStepIndexes` contains all elements from `allImagingStepIndexes`.

If new imaging steps are added and performed in an experiment, then this event will be sent once again after all the added imaging steps are completed and analysis is performed.

Schema version: 3

5.12 EXPERIMENT_PROGRESS

Unsolicited event created when the instrument notifies Suite about the current step of the experiment.

Payload example:

```
{
  "plateId": "7da11fca-31e9-4bdd-9ed4-2a47eacefcf0",
  "runStepIndex": 2,
  "experimentStatus": "IMAGING_STARTED"
}
```

`experimentStatus` is one of:

- RUN_STARTED
- PRIMING_STARTED
- PRIMING_COMPLETED
- CYCLING_STARTED
- CYCLING_COMPLETED
- IMAGING_STARTED

- IMAGE_TRANSFER_STARTED
- IMAGE_TRANSFER_COMPLETED
- IMAGING_COMPLETED
- RUN_FAILED
- RUN_STOPPED
- RUN_COMPLETED

Schema version: 1

5.13 EXPERIMENT_ABORTED

Event for the `RunExperiment` command when the instrument cannot start the experiment due to the reason specified in the Payload.

Payload example:

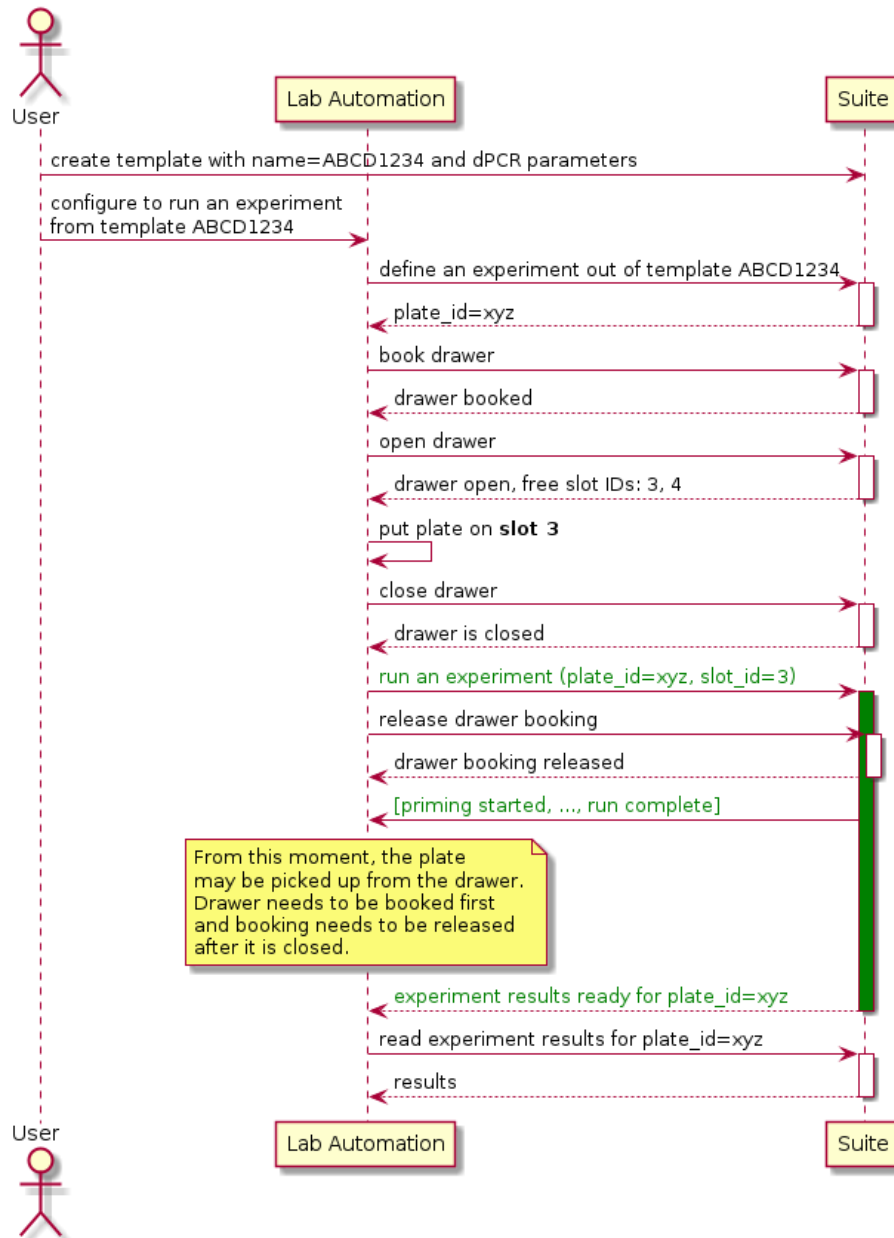
```
{
  "reason": "PLATE_INVALID_STATE"
}
```

`reason` is one of:

- ISSUE_WITH_LINKING_PLATE (could not link a plate from the drawer to a plate in Software Suite, contact QIAGEN support)
- UNKNOWN_ISSUE
- INVALID_MODULE_ID (drawer with specified name does not exist)
- NO_ACTIVE_BOOKING (drawer is not booked by Lab Automation Software)
- NO_PLATE (the plate does not have a barcode)
- PLATE_INVALID_STATE (attempting to run an experiment on a plate which has already been aborted during priming)
- NO_MATCHING_BARCODES (the barcode of the provided plate does not match the barcode specified for this plate in Software Suite)
- NO_ENOUGH_DISK_SPACE (there is not enough disk space on the instrument to run the experiment)

Schema version: 1

6 Sequence to run an experiment



7 Authentication

The API is secured by an API key. The key can be obtained in QIAcuity Software Suite. Please refer to the User Manual for instructions.

The key must be included in every request to the API in the **Authorization** header with an **ApiKey** prefix. Example: **Authorization: ApiKey <your_api_key>**.

This authentication method is later referred to as *Lab Automation API Key Authorization*.

8 Monitoring

Lab Automation API provides two endpoints to monitor the state of the system:

- **GetInstruments** to enumerate the instruments registered in Suite, see their online status and state of their drawers
- **HealthCheck** to see how many events are in the command and event queues per instrument

9 Setting thresholds via analysis templates

Please refer to QIAcuity user manual for details.

10 Changelog

10.1 3.1.1.0

- the **EXPERIMENT_READY** event got an extension of its schema, it now indicates if all imaging steps of an experiment are ready;
- the **DRAWER_CLOSED** event will now be triggered after the instrument finishes identification the plates on the drawer(s). Only then the instrument will proceed with the next command in the queue. Previously, in case **RunExperiment** was the next command in the queue, it could be processed too soon, before the plates were identified and it could result in a **NO_PLATE** error.
- the **OpenDrawer** command will wait until the internal robot stops moving before opening the drawer. Previously, this command would result in an error if it was requested while the internal robot was still moving.

10.2 3.2.0.0

- new endpoint added: **GetRfuDetails**
- **AddParametersToExperiment** endpoint:
 - sample ID may now be provided. This allows to create samples with the same name but different IDs. The use case here is setting up different dilution and conversion factors for the same sample (same as in having the same name).
- **AssignAnalysisTemplate** endpoint:
 - allows to set up automatic amplitude multiplexing thresholds;

- allows to set up “quality assurance” validation rules and dynamic thresholds based on controls or NTCs.
- **GetExperimentResults** endpoint:
 - provides values of the automatic threshold(s) and an **isAutoThreshold** flag which indicates if the current threshold is automatic;
 - provides the **lambda** value in the concentration results;
 - provides a new field **qualityAssuranceValidationRules**. If a validation rule was set up for a well in **AssignAnalysisTemplate**, then this field specifies the type of the rule and whether the validation has passed or not;
 - provides new types of automation rules in **thresholdSource** field; for details, see the documentation chapter for assigning analysis templates.
 - in previous API version, if an automation rule set a threshold to the automatic threshold, then **thresholdSource** field would have a value of { "type": "Auto" }. Now, in such case, **thresholdSource** will have a value of { "type": "AutomationRule", "name": "name of the rule" }. To easily recognize that auto threshold is set, an additional flag **isAutoThreshold** is present.
- (bugfix) **GetInstrumentStatus** endpoint presents drawer names in the correct letter case. In the previous API version the drawer names were always stated in lowercase. If such drawer name was used in a command, instrument would not recognize it and - as an example - would not open a drawer.

10.3 3.5.0.0

- **DefineExperiment** endpoint:
 - field **owners** requires at least one element, cannot be sent empty
- New endpoints added: **GetExperimentDetails**, **GetExperimentDetailsByBarcode**, **GetMultipleOccupancyResult**, **RemoveAnalysisTemplate**
- **GetExperimentResults** endpoint:
 - V1 is now deprecated in favor of **GetExperimentResultsV2**; V1 still works but will fail with an HTTP 400 error if the experiment contains any analysis rules;
 - V2 provides new fields in the response to support the new features of analysis templates;
- **AssignAnalysisTemplate** endpoint:
 - V1 is now deprecated in favor of **AssignAnalysisTemplateV2**; calling V1 will result in a 400 HTTP error;
 - V2 has a new payload schema to allow using the new features of analysis rules;
- Endpoint **AddExperimentParameters**:
 - provides new fields in **controls** and **nonTemplateControls**: **volumeOfTemplate**, **concentrationFactor**, **conversionFactor**, **conversionUnit**
- **EXPERIMENT_READY** event:
 - will be sent only once per experiment instead of per completed imaging step;
 - it will not be sent again when reanalysis is performed in cases where analysis template is changed;

11 Running an experiment – an end-to-end scenario example with real API calls

Prerequisites:

- Lab Automation Service is enabled
- An instrument is registered in Suite (refer to the QIAcuity Software Suite User Manual for instructions)

11.1 Define an experiment

11.1.1 Option A – define an experiment based on an existing template

Create a template of a plate in Software Suite (refer to the QIAcuity Software Suite User Manual for instructions):

```
curl -X 'POST' \
  'https://localhost:8687/lab-automation/v1/experiment/define/template' \
  -H 'accept: application/json' \
  -H 'Authorization: ApiKey some_api_key' \
  -H 'Content-Type: application/json' \
  -d '{
    "barcode": "00031234567891113151719212",
    "plateName": "example_plate_name",
    "templateName": "example_template_name",
    "owners": [ "admin" ]
  }'
```

Response:

```
2a7e25f7-c2c2-469e-8edb-3b3b9430d83a
```

11.1.2 Option B – define an experiment from scratch

First, load dictionaries with plate type IDs:

```
curl -X 'GET' \
  'https://localhost:8687/lab-automation/v1/experiment/plate-types' \
  -H 'accept: application/json' \
  -H 'Authorization: ApiKey some_api_key'
```

Response:

```
{
  "bb52fd68-effd-4168-a2a3-8b3e6dfdb597": "Nanoplate 26K 8-well",
  "d27fb9bb-bc7f-4502-9b51-b5fd552b8837": "Nanoplate 26K 24-well"
}
```

Then, request for velocity profiles for a particular type of plate:

```
curl -X 'GET' \
  'https://localhost:8687/lab-automation/v1/experiment/velocity-profiles?plateTypeId=d27fb9bb-bc7f-4502-9b51-b5fd552b8837' \
  -H 'accept: application/json' \
  -H 'Authorization: ApiKey some_api_key'
```

Response:

```
{
  "d2844690-b50f-4563-b764-fd32ed95e76b": "QIAGEN Priming Profile Probe (RT-) PCR",
  "97a3e10f-2484-4f88-bf13-ac1911e4423b": "QIAGEN Priming Profile EvaGreen (RT-) PCR"
}
```

Now, define an experiment:

```
curl -X 'POST' \
  'https://localhost:8687/lab-automation/v1/experiment/define' \
  -H 'accept: application/json' \
  -H 'Authorization: ApiKey some_api_key' \
  -H 'Content-Type: application/json' \
  -d '{
    "barcode": "00011234567891113151719212",
    "plateName": "example_plate_name",
    "plateTypeId": "d27fb9bb-bc7f-4502-9b51-b5fd552b8837",
    "dpcrRunSteps": {
      "primingDPCRStep": {
        "velocityProfile": "d2844690-b50f-4563-b764-fd32ed95e76b"
      },
      "cyclingDPCRSteps": [
        {
          "index": 1,
          "cycles": [
            {
              "count": 1,
              "position": 0,
              "steps": [
                {
                  "temperature": 55,
                  "duration": 55
                }
              ]
            }
          ]
        }
      ],
      "imagingDPCRSteps": [
```



```
{
  "index": 2,
  "referenceChannel": "REF2",
  "imagingProfiles": [
    {
      "channel": {
        "excitation": "GREEN",
        "emission": "GREEN"
      },
      "durationOfExposure": 4000,
      "gain": 40
    }
  ]
},
"owners": [
  "admin"
]
}'
```

Note: the request contains the barcode of the plate. This is optional. If it is provided, the instrument will do a sanity check to recognize if the correct plate was put into a particular slot on the drawer. If it is not provided, the instrument will automatically read the barcode and assign it to the plate once the experiment is run.

Response:

```
2a7e25f7-c2c2-469e-8edb-3b3b9430d83a
```

This is the ID of the plate created in Software Suite.

11.2 Put the plate into the instrument

To operate a particular drawer, a booking needs to be made for it on a particular instrument. To get the list of instruments:

```
curl -X 'GET' \
  'https://localhost:8687/lab-automation/v1/instruments' \
  -H 'accept: application/json'
  -H 'Authorization: ApiKey some_api_key'
```

Response:

```
[
  {
    "instrumentId": "instrument123",
    "deviceName": "Instrument in Lab A",
    "type": "P4",
    "isOnline": true,
    "drawers": {
      "Drawer0": {
        "isBooked": false,
        "platesInSlots": {
          "0": "3fa85f64-5717-4562-b3fc-2c963f66afa6"
        }
      }
    }
  }
]
```

The response tells that this is an instrument with one drawer “Drawer1” and that “slot 0” is occupied by a plate. The drawer is not booked, so the booking can be made:

```
curl -X 'POST' \
  'https://localhost:8687/lab-automation/v1/command/drawer/book' \
  -H 'accept: application/json' \
  -H 'Authorization: ApiKey some_api_key' \
  -H 'Content-Type: application/json' \
  -d '{
    "instrumentId": "instrument123",
    "drawerName": "Drawer0"
  }'
```

Response:

```
"a392f741-3015-4a6a-883f-42d64cb5159a"
```

This is the command ID. The event telling that the booking is active will be soon available via this endpoint:

```
curl -X 'GET' \
  'https://localhost:8687/lab-automation/v1/event' \
  -H 'accept: application/json' \
  -H 'Authorization: ApiKey some_api_key'
```

This endpoint needs to be polled until the event appears in the response:

```
{
  "id": "21ebe258-ec80-4f73-aafc-4faa863d8a22",
  "commandId": "a392f741-3015-4a6a-883f-42d64cb5159a",
  "instrumentId": "instrument123",
  "type": "DRAWER_BOOKED",
  "event": "{\"freeSlotsInDrawers\":{\"Drawer0\":[1,2,3]}}",
  "payloadSchemaVersion": 1
}
```

The event must be acknowledged to be able to see the events that follow.

```
curl -X 'DELETE' \
  'https://localhost:8687/lab-automation/v1/event?eventId=21ebe258-ec80-4f73-aafc-4faa863d8a22' \
  -H 'accept: application/json' \
  -H 'Authorization: ApiKey some_api_key'
```

Note: different commands will result in different event types and payloads. However, all events need to be acknowledged.

When the booking is done, the drawer can be opened:

```
curl -X 'POST' \
  'https://localhost:8687/lab-automation/v1/command/drawer/open' \
  -H 'accept: application/json' \
  -H 'Authorization: ApiKey some_api_key' \
  -H 'Content-Type: application/json' \
  -d '{
    "instrumentId": "instrument123",
    "drawerName": "Drawer0"
  }'
```

Wait for the confirmation event and acknowledge it. Then, the plate may be placed on a free slot and the drawer may be closed:

```
curl -X 'POST' \
  'https://localhost:8687/lab-automation/v1/command/drawer/close' \
  -H 'accept: application/json' \
  -H 'Authorization: ApiKey some_api_key' \
  -H 'Content-Type: application/json' \
  -d '{
    "instrumentId": "instrument123",
    "drawerName": "Drawer0"
  }'
```

11.3 Run the experiment

```
curl -X 'POST' \
  'https://localhost:8687/lab-automation/v1/command/experiment/run' \
  -H 'accept: application/json' \
  -H 'Authorization: ApiKey some_api_key' \
  -H 'Content-Type: application/json' \
  -d '{
    "instrumentId": "instrument123",
    "plateId": "2a7e25f7-c2c2-469e-8edb-3b3b9430d83a",
    "drawerName": "Drawer0",
    "slotId": 1
  }'
```

Await the event of type EXPERIMENT_PROCESSING_STARTED.

11.4 [Optionally] Release the booking

Now, you can optionally release the booking of the drawer if you wish to enable human interaction with the instrument. If you have a fully-automated use scenario, you don't need to release the booking at all.

```
curl -X 'POST' \
  'https://localhost:8687/lab-automation/v1/command/drawer/release-booking' \
  -H 'accept: application/json' \
  -H 'Authorization: ApiKey some_api_key' \
  -H 'Content-Type: application/json' \
  -d '{
    "instrumentId": "instrument123",
    "drawerName": "Drawer0"
  }'
```

11.5 Wait for the results to be ready

Await the event of type EXPERIMENT_READY. Before it happens, multiple events of type EXPERIMENT_PROGRESS will be sent to inform about the progress of the experiment like the current dPCR step.

Please note that EXPERIMENT_PROGRESS event with a status of RUN_COMPLETED does not mean the results are ready. Until EXPERIMENT_READY is sent, the results are still being processed by the Software Suite.

11.6 Download the results

```
curl -X 'GET' \
  'https://localhost:8687/lab-automation/v1/experiment/2a7e25f7-c2c2-469e-8edb-3b3b9430d83a/result' \
  -H 'accept: application/json' \
  -H 'Authorization: ApiKey some_api_key'
```

12 Endpoints

Interactive API specification (Swagger UI) can be accessed via the browser at https://<URL_TO_SOFTWARE_SUITE>:8687/swagger-ui/index.html. It can also be accessed in form of an OpenAPI specification at https://<URL_TO_SOFTWARE_SUITE>:8687/api-docs/lab-automation-api.

When trying out interactive examples in Swagger, the `Authorization` header value must be specified as `ApiKey {api_key_here}`.

12.1 AddExperimentParameters

PUT /lab-automation/v1/experiment/{plateId}/add-parameters

To perform this operation, you must be authenticated by means of one of the following methods: Lab Automation API Key Authorization.

Adds reactions, samples and wells configuration to an existing experiment. The provided parameters will overwrite the already existing parameters from scratch, so the request body must contain all desired experiment parameters even if only a single detail (e.g. reaction mix name) is to be changed. Exception: reaction mixes that share the same name as an already existing reaction mix will be updated rather than replaced, preserving their configured analysis rules and crosstalk matrix.

12.1.1 Request body example

```
{
  "reactions": [
    {
      "name": "Reaction1",
      "totalReactionVolume": 30.5,
      "targets": [
        {
          "channel": {
            "excitation": "GREEN",
            "emission": "GREEN",
            "thresholdMode": "ST"
          },
          "name": "Target1",
```

```

        "internalControl": false,
        "dyeId": "1ef3cc8a-8a5e-4709-8101-e8293fd63e2d"
    }
}
],
"sampleControl": {
    "samples": [
        {
            "name": "Sample1",
            "sampleId": 1,
            "volumeOfTemplate": 15,
            "concentrationFactor": 15,
            "conversionFactor": 15,
            "conversionUnit": "lm/kg",
            "description": "Description1",
            "labels": [
                "string"
            ]
        }
    ],
    "controls": [
        {
            "name": "Control1",
            "volumeOfTemplate": 15,
            "concentrationFactor": 15,
            "conversionFactor": 15,
            "conversionUnit": "lm/kg"
        }
    ],
    "nonTemplateControls": [
        {
            "name": "NonTemplateControl1",
            "volumeOfTemplate": 15,
            "concentrationFactor": 15,
            "conversionFactor": 15,
            "conversionUnit": "lm/kg"
        }
    ]
}
]

```

```

},
"wells": [
  {
    "wellRow": "A",
    "column": 1,
    "blank": false,
    "reactionName": "Reaction1",
    "sample": {
      "name": "Sample1",
      "sampleId": 1,
      "type": "SAMPLE"
    },
  },
  "controlTypes": [
    {
      "channel": {
        "excitation": "GREEN",
        "emission": "GREEN",
        "thresholdMode": "ST"
      },
      "positive": true
    }
  ]
}
]
}

```

12.1.1.2 Request body properties

Name	In	Type	Required	Description
plateId	path	string(uuid)	true	ID of the experiment for which parameters should be updated
body	body	AddParametersToExperimentRequest	true	Replaces existing parameters with requested ones
» reactions	body	[AddParametersToExperimentRequest.Reaction]	false	List of defined reaction mixes with assigned targets

Name	In	Type	Required	Description
» » name	body	string	true	Reaction name
» » totalReactionVolume	body	number(double)	false	Total reaction volume
» » targets	body	[AddParametersToExperimentRequest.Reaction.Target]	true	List of assigned targets
» » » channel	body	ChannelSliceDefinition	true	none
» » » » excitation	body	string	true	Excitation filter color
» » » » emission	body	string	true	Emission filter color
» » » » thresholdMode	body	string	true	Channel threshold mode
» » » name	body	string	true	Target name
» » » internalControl	body	boolean	false	Indication whether target is an internal control
» » » dyeId	body	string(uuid)	false	Assigned dye ID. Available dyes can be listed via the /experiment/dyes endpoint.
» sampleControl	body	AddParametersToExperimentRequest.SampleControl	false	none
» » samples	body	[AddParametersToExperimentRequest.SampleControl.Sample]	false	List of sample definitions
» » » name	body	string	true	Sample name
» » » sampleId	body	integer(int32)	false	Unique sample id, used for distinction between two samples with same names. Software is using the following algorithm to assign sample IDs:
» » » volumeOfTemplate	body	number(double)	false	Volume of template
» » » concentrationFactor	body	number(double)	false	Concentration factor
» » » conversionFactor	body	number	false	Conversion factor
» » » conversionUnit	body	string	false	Conversion unit
» » » description	body	string	false	Sample description
» » » labels	body	[string]	false	List of sample labels

Name	In	Type	Required	Description
»» controls	body	[AddParametersToExperimentRequest.SampleControl.Control]	false	List of control definitions
»»» name	body	string	true	Control name
»»» volumeOfTemplate	body	number(double)	false	Volume of template
»»» concentrationFactor	body	number(double)	false	Concentration factor
»»» conversionFactor	body	number	false	Conversion factor
»»» conversionUnit	body	string	false	Conversion unit
»» nonTemplateControls	body	[AddParametersToExperimentRequest.SampleControl.NonTemplateControl]	false	List of non template control definitions
»»» name	body	string	true	Non template control name
»»» volumeOfTemplate	body	number(double)	false	Volume of template
»»» concentrationFactor	body	number(double)	false	Concentration factor
»»» conversionFactor	body	number	false	Conversion factor
»»» conversionUnit	body	string	false	Conversion unit
» wells	body	[AddParametersToExperimentRequest.Well]	false	Collection of well definitions
»» wellRow	body	string	true	Well row
»» column	body	integer(int32)	false	Well column
»» blank	body	boolean	true	If a well is blank, it explicitly states that it does not have a reaction mix or sample assigned. This is optional.
»» reactionName	body	string	false	Assigned reaction name
»» sample	body	AddParametersToExperimentRequest.Well.Sample	false	none
»»» name	body	string	true	Sample, control or non template control name

Name	In	Type	Required	Description
»»» sampleId	body	integer(int32)	false	Unique sample id, used for distinction between two samples with same names. Needs to be provided if the sample name is not unique within samples defined in plate.
»»» type	body	string	true	Sample type
»» controlTypes	body	[AddParametersToExperimentRequest.Well.ControlType]	false	List of control types. Only needs to be provided if a control is assigned to the well.
»»» channel	body	ChannelSliceDefinition	true	none
»»» positive	body	boolean	false	Indication whether control type is positive

12.1.2.1 Detailed descriptions »»» **sampleId**: Unique sample id, used for distinction between two samples with same names. Software is using the following algorithm to assign sample IDs: * if sample id is not provided and provided sample names are unique, the software will generate an unique id, starting from 1 and incrementing by 1 for each new sample without an id, omitting ids provided in the request * if sample id is provided, the software will use it as an unique id for the sample

12.1.2.2 Enumerated Values

Parameter	Value
»»»» excitation	GREEN
»»»» excitation	YELLOW
»»»» excitation	ORANGE
»»»» excitation	RED
»»»» excitation	CRIMSON
»»»» excitation	FARRED
»»»» emission	GREEN
»»»» emission	YELLOW
»»»» emission	ORANGE
»»»» emission	RED
»»»» emission	CRIMSON

Parameter	Value
»»»» emission	FARRED
»»»» thresholdMode	ST
»»»» thresholdMode	AM_LOW
»»»» thresholdMode	AM_HIGH
»»» type	SAMPLE
»»» type	CONTROL
»»» type	NON_TEMPLATE_CONTROL

12.1.3 Example responses

12.1.3.1 200 Response

"497f6eca-6276-4993-bfeb-53cbbbba6f08"

12.1.4 Responses

Status	Meaning	Description	Schema
200	OK	Returns ID of updated plate	string
400	Bad Request	Missing or invalid requested params	ErrorResponse
401	Unauthorized	Unauthorized	None
403	Forbidden	Access denied	None
404	Not Found	Requested plate not found	ErrorResponse
405	Method Not Allowed	HTTP method is not supported	None
500	Internal Server Error	Unexpected error	ErrorResponse

12.2 AddDpcrSteps

PUT /lab-automation/v1/experiment/{plateId}/add-dpcr-steps

To perform this operation, you must be authenticated by means of one of the following methods: Lab Automation API Key Authorization.

Adds cycling and imaging steps to an existing experiment.

The steps must follow these rules:

- a cycling must be followed by an imaging
- imaging step may be followed by another imaging step

Steps may only be added after the already existing steps and they must continue the indexing. There must not be a gap in the indexes.

Example:

An experiment already contains three dPCR steps:

- priming at index 0
- cycling at index 1
- imaging at index 2

The next step must have an index of 3, the next one must have an index of 4 and so on.

12.2.1 Request body example

```
{
  "cyclingDPCRSteps": [
    {
      "index": 3,
      "cycles": [
        {
          "count": 1,
          "position": 0,
          "steps": [
            {
              "temperature": 35,
              "duration": 0,
              "position": 0
            }
          ]
        }
      ]
    }
  ],
  "imagingDPCRSteps": [
    {
      "index": 4,
      "enableHighMultiplexingReferenceChannel": true,
      "imagingProfiles": [
        {
          "channel": {
            "excitation": "GREEN",
```

```

        "emission": "GREEN"
    },
    "durationOfExposure": 1,
    "gain": 40
}
]
}
]
}

```

12.2.2 Request body properties

Name	In	Type	Required	Description
plateId	path	string(uuid)	true	ID of the experiment to which dPCR steps should be added
body	body	AddDPCRStepsToExperimentRequest	true	Adds requested dPCR steps to existing ones
» cyclingDPCRSteps	body	[AddDPCRStepsToExperimentRequest.Cycling]	false	List of defined cycling steps
» » index	body	integer(int32)	false	Cycling step index
» » cycles	body	[AddDPCRStepsToExperimentRequest.Cycling.Cycle]	false	Defined cycles
» » » count	body	integer(int32)	false	Number of cycles
» » » position	body	integer(int32)	true	Cycle position in order
» » » steps	body	[AddDPCRStepsToExperimentRequest.Cycling.Cycle.CycleStep]	false	List of steps within the cycle
» » » » temperature	body	number(double)	true	Step temperature
» » » » duration	body	integer(int32)	true	Step duration in seconds
» » » » position	body	integer(int32)	true	Step position. For all cycle steps within a cycle, each cycle step must have a unique position from 1 to N (where N is the number of cycle steps in the cycle).

Name	In	Type	Required	Description
» imagingDPCRSteps	body	[AddDPCRStepsToExperimentRequest.Imaging]	true	List of defined cycling steps
»» index	body	integer(int32)	false	Imaging step index
»» enableHighMultiplexingReferenceChannel	body	boolean	true	Enabling High-Multiplexing Reference channel will make additional channels and amplitude multiplexing “mode” available. Please note that this will require usage of the QIAcuity High Multiplex Kit.
»» imagingProfiles	body	[AddDPCRStepsToExperimentRequest.Imaging.ImagingProfile]	false	Imaging profiles
»»» channel	body	ChannelDefinition	true	none
»»»» excitation	body	string	true	Excitation filter color
»»»» emission	body	string	true	Emission filter color
»»» durationOfExposure	body	integer(int64)	false	Duration of exposure value
»»» gain	body	integer(int32)	false	Gain value

12.2.2.1 Enumerated Values

Parameter	Value
»»»» excitation	GREEN
»»»» excitation	YELLOW
»»»» excitation	ORANGE
»»»» excitation	RED
»»»» excitation	CRIMSON
»»»» excitation	FARRED
»»»» emission	GREEN
»»»» emission	YELLOW
»»»» emission	ORANGE

Parameter	Value
»»»» emission	RED
»»»» emission	CRIMSON
»»»» emission	FARRED

12.2.3 Example responses

12.2.3.1 200 Response

"497f6eca-6276-4993-bfeb-53cbbbba6f08"

12.2.4 Responses

Status	Meaning	Description	Schema
200	OK	Returns ID of updated plate	string
400	Bad Request	Missing or invalid requested params	ErrorResponse
401	Unauthorized	Unauthorized	None
403	Forbidden	Access denied	None
404	Not Found	Requested plate not found	ErrorResponse
405	Method Not Allowed	HTTP method is not supported	None
500	Internal Server Error	Unexpected error	ErrorResponse

12.3 AssignAnalysisTemplateV2

POST /lab-automation/v2/experiment/{plateId}/analysis-template

To perform this operation, you must be authenticated by means of one of the following methods: Lab Automation API Key Authorization.

Assigns an analysis template to the requested experiment and triggers the analysis process if applicable

12.3.1 Request body example

```
{
  "reactionMixAutomationRules": {
    "ReactionMix A": {
      "thresholdingMethods": [
        {
```

```

    "channel": {
      "excitation": "GREEN",
      "emission": "GREEN"
    },
    "amplitudeMultiplexing": false,
    "thresholdingPropagationConfig": {
      "type": "WITH_PROPAGATION",
      "thresholdingConfig": {
        "type": "POSITIVE_CONTROL",
        "thresholdingMethod": {
          "type": "AUTO_WITH_OFFSET",
          "offset": 5
        }
      }
    }
  }
},
],
"ReactionMix B": {
  "thresholdingMethods": [
    {
      "channel": {
        "excitation": "YELLOW",
        "emission": "YELLOW"
      },
      "amplitudeMultiplexing": false,
      "thresholdingPropagationConfig": {
        "type": "WITH_PROPAGATION",
        "thresholdingConfig": {
          "type": "POSITIVE_CONTROL",
          "thresholdingMethod": {
            "type": "AUTO_WITH_OFFSET",
            "offset": 4
          }
        }
      }
    }
  ]
},
],
"qualityControlValidationRules": {

```



```

"strategy": "INVALIDATE_WELL",
"perChannel": [
  {
    "channel": {
      "excitation": "GREEN",
      "emission": "GREEN"
    },
    "samples": {
      "minimumValidPartitionsPercentage": 30
    },
    "controls": {
      "minimumValidPartitionsPercentage": 50,
      "negativeControlMaxPartitions": 6400,
      "positiveControlExpectedConcentration": {
        "min": 5,
        "max": 5000
      }
    }
  },
  {
    "channel": {
      "excitation": "YELLOW",
      "emission": "YELLOW"
    },
    "samples": {
      "minimumValidPartitionsPercentage": 40
    },
    "controls": {
      "minimumValidPartitionsPercentage": 60,
      "negativeControlMaxPartitions": 3500
    }
  }
]
}
}
}
}
}

```

12.3.2 Requeset body properties

Name	In	Type	Required	Description
plateId	path	string(uuid)	true	ID of the experiment
body	body	AssignAnalysisTemplateV2Request	true	none
» reactionMixAutomationRules	body	object	true	A dictionary with keys representing names of reaction mixes and values representing analysis rules for these reaction mixes
» » additionalProperties	body	AssignAnalysisTemplateV2Request.ReactionMixAnalysisRules	false	Contains a list of rules for automated analysis
» » » thresholdingMethods	body	[AssignAnalysisTemplateV2Request.ThresholdingMethodPerChannel]	true	[Thresholding method configuration per channel]
» » » » channel	body	ChannelDefinition	true	none
» » » » » excitation	body	string	true	Excitation filter color
» » » » » emission	body	string	true	Emission filter color
» » » » » amplitudeMultiplexing	body	boolean	false	Indicates whether amplitude multiplexing is enabled for this channel
» » » » » thresholdingPropagationConfig	body	any	true	none
» » » » » » <i>anonymous</i>	body	object	false	none
» » » » » » » <i>anonymous</i>	body	object	false	Thresholding propagation configuration
» » » » » » » type	body	string	true	none
» » » » » » » <i>anonymous</i>	body	object	false	none
» » » » » » » type	body	string	false	none
» » » » » » » thresholdingConfig	body	any	false	none
» » » » » » » » <i>anonymous</i>	body	AssignAnalysisTemplateV2Request.ThresholdingConfig.NegativeControl	false	none
» » » » » » » » » type	body	string	false	none

Name	In	Type	Required	Description
» » » » » » » » thresholdingMethod	body	any	true	none
» » » » » » » » <i>anonymous</i>	body	any	false	none
» » » » » » » » <i>anonymous</i>	body	object	false	Thresholding method specification
» » » » » » » » type	body	string	true	none
» » » » » » » » <i>anonymous</i>	body	object	false	none
» » » » » » » » type	body	string	false	none
» » » » » » » » <i>anonymous</i>	body	any	false	none
» » » » » » » » <i>anonymous</i>	body	object	false	Thresholding method specification
» » » » » » » » <i>anonymous</i>	body	object	false	none
» » » » » » » » type	body	string	false	none
» » » » » » » » offset	body	number(double)	false	none
» » » » » » » » <i>anonymous</i>	body	any	false	none
» » » » » » » » <i>anonymous</i>	body	object	false	Thresholding method specification
» » » » » » » » <i>anonymous</i>	body	object	false	none
» » » » » » » » type	body	string	false	none
» » » » » » » »	body	number(double)	false	none
fallbackAvgNegativeBand				
» » » » » » » »	body	number(double)	false	none
fallbackAvgPositiveBand				
» » » » » » » » ratio	body	number(double)	false	none
» » » » » » » » <i>anonymous</i>	body	any	false	none
» » » » » » » » <i>anonymous</i>	body	object	false	Thresholding method specification
» » » » » » » » <i>anonymous</i>	body	object	false	none
» » » » » » » » type	body	string	false	none
» » » » » » » »	body	number(double)	false	none
fallbackMin				
» » » » » » » »	body	number(double)	false	none
fallbackMax				

Name	In	Type	Required	Description
» » » » » » » » » » ratio	body	number(double)	false	none
» » » » » » » » » » <i>anonymous</i>	body	any	false	none
» » » » » » » » » »	body	object	false	Thresholding method specification
<i>anonymous</i>				
» » » » » » » » » »	body	object	false	none
<i>anonymous</i>				
» » » » » » » » » » type	body	string	false	none
» » » » » » » » » » offset	body	number(double)	false	none
» » » » » » » » » » <i>anonymous</i>	body	any	false	none
» » » » » » » » » »	body	object	false	Thresholding method specification
<i>anonymous</i>				
» » » » » » » » » »	body	object	false	none
<i>anonymous</i>				
» » » » » » » » » » type	body	string	false	none
» » » » » » » » » » threshold	body	number(double)	false	none
» » » » » » » » » » <i>anonymous</i>	body	any	false	none
» » » » » » » » » »	body	object	false	Thresholding method specification
<i>anonymous</i>				
» » » » » » » » » »	body	object	false	none
<i>anonymous</i>				
» » » » » » » » » » type	body	string	false	none
» » » » » » » » » »	body	number(double)	false	none
lowThreshold				
» » » » » » » » » »	body	number(double)	false	none
highThreshold				
» » » » » » » » » »	body	number(double)	false	none
doublePositiveThreshold				
» » » » » » » » » » <i>anonymous</i>	body	any	false	none
» » » » » » » » » »	body	object	false	Thresholding method specification
<i>anonymous</i>				
» » » » » » » » » »	body	object	false	none
<i>anonymous</i>				
» » » » » » » » » » type	body	string	false	none
» » » » » » » » » » offset	body	number(double)	false	none

Name	In	Type	Required	Description
» » » » » » » » <i>anonymous</i>	body	AssignAnalysisTem- plateV2Request.Thresh- oldingConfig.NonTem- plateControl	false	none
» » » » » » » » type	body	string	false	none
» » » » » » » » thresholdingMethod	body	any	true	none
» » » » » » » » <i>anonymous</i>	body	any	false	none
» » » » » » » » <i>anonymous</i>	body	any	false	none
» » » » » » » » <i>anonymous</i>	body	any	false	none
» » » » » » » » <i>anonymous</i>	body	any	false	none
» » » » » » » » <i>anonymous</i>	body	any	false	none
» » » » » » » » <i>anonymous</i>	body	any	false	none
» » » » » » » » <i>anonymous</i>	body	any	false	none
» » » » » » » » <i>anonymous</i>	body	AssignAnalysisTem- plateV2Request.Thresh- oldingConfig.PositiveCon- trol	false	none
» » » » » » » » type	body	string	false	none
» » » » » » » » thresholdingMethod	body	any	true	none
» » » » » » » » <i>anonymous</i>	body	any	false	none
» » » » » » » » <i>anonymous</i>	body	any	false	none
» » » » » » » » <i>anonymous</i>	body	any	false	none
» » » » » » » » <i>anonymous</i>	body	any	false	none
» » » » » » » » <i>anonymous</i>	body	any	false	none
» » » » » » » » <i>anonymous</i>	body	any	false	none
» » » » » » » » <i>anonymous</i>	body	any	false	none
» » » » » <i>anonymous</i>	body	any	false	none
» » » » » <i>anonymous</i>	body	object	false	Thresholding propagation configuration
» » » » » <i>anonymous</i>	body	object	false	none
» » » » » type	body	string	false	none

Name	In	Type	Required	Description
»»»»»» thresholding- ConfigForSample	body	AssignAnalysisTem- plateV2Request.Thresh- oldingConfig.Unknown- Samples	false	none
»»»»»» type	body	string	false	none
»»»»»» thresholdingMethod	body	any	true	none
»»»»»» <i>anonymous</i>	body	any	false	none
»»»»»» <i>anonymous</i>	body	any	false	none
»»»»»» <i>anonymous</i>	body	any	false	none
»»»»»» <i>anonymous</i>	body	any	false	none
»»»»»» <i>anonymous</i>	body	any	false	none
»»»»»» <i>anonymous</i>	body	any	false	none
»»»»»» <i>anonymous</i>	body	any	false	none
»»»»»» thresholding- ConfigForPositiveControl	body	AssignAnalysisTem- plateV2Request.Thresh- oldingConfig.PositiveCon- trol	false	none
»»»»»» thresholdingConfig- ForNegativeControl	body	AssignAnalysisTem- plateV2Request.Thresh- oldingConfig.Negative- Control	false	none
»»»»»» thresholdingConfigForNtc	body	AssignAnalysisTem- plateV2Request.Thresh- oldingConfig.NonTem- plateControl	false	none
»»» qualityControlValida- tionRules	body	AssignAnalysisTem- plateV2Request.Quality- ControlValidationRules	false	Validation rules for specific Reaction Mix
»»» strategy	body	string	true	Quality control validation strategy
»»» perChannel	body	[AssignAnalysisTem- plateV2Request.Quality- ControlValidationRules- PerChannel]	false	[Quality control validation rules per channel]
»»» channel	body	ChannelDefinition	true	none

Name	In	Type	Required	Description
»»»»» samples	body	AssignAnalysisTemplateV2Request.SampleQualityControlRules	false	Quality control rules for sample
»»»»»» minimumValidPartitionsPercentage	body	integer(int32)	false	Minimum valid partitions percentage
»»»»» controls	body	AssignAnalysisTemplateV2Request.ControlQualityControlRules	false	Quality control rules for control
»»»»»» minimumValidPartitionsPercentage	body	integer(int32)	false	Minimum valid partitions percentage
»»»»»» negativeControlMaxPartitions	body	integer(int32)	false	none
»»»»»» positiveControlExpectedConcentration	body	PositiveControlExpectedConcentration	false	none
»»»»»»» min	body	number(double)	false	none
»»»»»»» max	body	number(double)	false	none

12.3.2.1 Enumerated Values

Parameter	Value
»»»»» excitation	GREEN
»»»»» excitation	YELLOW
»»»»» excitation	ORANGE
»»»»» excitation	RED
»»»»» excitation	CRIMSON
»»»»» excitation	FARRED
»»»»» emission	GREEN
»»»»» emission	YELLOW
»»»»» emission	ORANGE
»»»»» emission	RED
»»»»» emission	CRIMSON
»»»»» emission	FARRED
»»»»» strategy	WARNING_CHANNEL
»»»»» strategy	WARNING_WELL
»»»»» strategy	INVALIDATE_CHANNEL
»»»»» strategy	INVALIDATE_WELL

12.3.3 Example responses

12.3.3.1 400 Response

```
{
  "message": "string",
  "code": "string",
  "uuid": "095be615-a8ad-4c33-8e9c-c7612fbf6c9f",
  "validationErrors": {
    "property1": [
      {
        "code": "string",
        "arguments": [
          "string"
        ]
      }
    ],
    "property2": [
      {
        "code": "string",
        "arguments": [
          "string"
        ]
      }
    ]
  }
}
```

12.3.4 Responses

Status	Meaning	Description	Schema
200	OK	Analysis template assigned	None
400	Bad Request	Request validation failed. Possible validation error codes:	

- **WRONG_POSITIVE_CONTROLS_CONCENTRATION_PRECISION** – The provided values for ‘Expected concentration for Positive Controls in dPCR reaction (Min/Range/Max, cp/μL)’ do not meet the required precision. Please refer to the Robot API User Manual for the allowed precision limits.
- **MIN_RANGE_HIGHER_THAN_MAX** – Min range value must be less than max range value.

- **MIN_MUST_BE_LESS_OR_EQUAL_TO_MAX** – Min must be less than max.
- **AMPLITUDE_MULTIPLEXING_WITH_PROPAGATION** – NumericAmplitudeMultiplexing thresholding method is not supported with propagation enabled.
- **AUTO_THRESHOLD_OFFSET_WITH_AM** – When Amplitude Multiplexing is enabled in ‘No propagation’ mode with AUTO_WITH_OFFSET, offset cannot be defined and must be null.
- **AM_CHANNEL_WITH_PROPAGATION** – When Amplitude Multiplexing is enabled for a channel, propagation mode must be ‘No propagation’.
- **NUMERIC_AM_METHOD_FOR_ST_CHANNEL** – NumericAmplitudeMultiplexing thresholding method is not supported when Amplitude Multiplexing is disabled; use Numeric instead.
- **NUMERIC_ST_METHOD_FOR_AM_CHANNEL** – Numeric thresholding method is not supported when Amplitude Multiplexing is enabled; use NumericAmplitudeMultiplexing instead.
- **INVALID_THRESHOLDING_METHOD_CONFIGURATION** – Invalid thresholding method configuration.
- **MISSING_REACTION_FOR_ANALYSIS_TEMPLATE_RULE** – Analysis rules reference a reaction mix that does not exist on the plate.
- **INVALID_CHANNELS_IN_ANALYSIS_TEMPLATE_RULE** – Analysis rules contain invalid or unrecognized channel definitions.
- **DUPLICATED_CHANNELS_IN_ANALYSIS_TEMPLATE_RULE** – Analysis rules contain duplicated channel entries for the same reaction mix.
- **TOO_MANY_CHANNELS_IN_ANALYSIS_TEMPLATE_RULE** – Analysis rules exceed the maximum number of channels allowed per reaction mix (limit: 8).
- **CHANNEL_DOES_NOT_EXIST_IN_REACTION_MIX** – Analysis rules reference a channel that is not configured for the given reaction mix.
- **MISSING_THRESHOLDING_METHOD_FOR_CHANNEL** – Thresholding methods do not cover all channels configured in the reaction mix.
- **AMPLITUDE_MULTIPLEXING_MUST_BE_ENABLED_FOR_AM_MODE_CHANNEL** – Amplitude Multiplexing must be enabled for channels that use AM thresholding mode.
|ErrorResponse| |401|Unauthorized|Unauthorized|None| |403|Forbidden|Access denied|None| |404|Not Found|Requested plate not found|ErrorResponse| |405|Method Not Allowed|HTTP method is not supported|None| |500|Internal Server Error|Unexpected error|ErrorResponse|

12.4 GetRfuDetails

POST /lab-automation/v1/experiment/{plateId}/rfu

To perform this operation, you must be authenticated by means of one of the following methods: **Lab Automation API Key Authorization**.

Provides RFU values for the requested portion of data of an experiment.

12.4.1 Request body example

```
{
  "dpcrRunStepIndex": 2,
  "wellPositions": [
    1,
    2,
    4
  ],
  "channels": [
    {
      "excitation": "GREEN",
      "emission": "GREEN"
    }
  ],
  "sortType": "VERTICAL"
}
```

12.4.2 Request body properties

Name	In	Type	Required	Description
plateId	path	string(uuid)	true	ID of the experiment
body	body	RfuRequest	true	none
» dpcrRunStepIndex	body	integer(int32)	true	DPCR run step index
» wellPositions	body	[integer]	false	Selected wells
» channels	body	[ChannelDefinition]	true	Selected channels
»» excitation	body	string	true	Excitation filter color
»» emission	body	string	true	Emission filter color
» sortType	body	string	false	Vertical or Horizontal result sorting

12.4.2.1 Enumerated Values

Parameter	Value
»» excitation	GREEN
»» excitation	YELLOW
»» excitation	ORANGE
»» excitation	RED

Parameter	Value
»» excitation	CRIMSON
»» excitation	FARRED
»» emission	GREEN
»» emission	YELLOW
»» emission	ORANGE
»» emission	RED
»» emission	CRIMSON
»» emission	FARRED
» sortType	VERTICAL
» sortType	HORIZONTAL

12.4.3 Example responses

12.4.3.1 200 Response

```
{
  "plate": {
    "id": "dd9a347c-68ce-47e5-a4e0-d88e0f9e113f",
    "name": "Example RFU data",
    "plateTypeName": "Nanoplate 26K 8-well"
  },
  "dpcrRunStepIndex": 2,
  "rfuRefResults": [
    {
      "wellLabel": "A1",
      "sampleId": 1,
      "sampleName": "sample1",
      "cycledVolume": 1,
      "thresholdHigh": 24,
      "thresholdLow": 3,
      "ref": "Std-Ref",
      "rfuValues": [
        {
          "n": 1,
          "i": "3,C",
          "r": 1
        }
      ]
    }
  ],
}
```

```

    {
      "n": 2,
      "i": "0",
      "r": 10
    }
  ]
},
"rfuPerChannelSlice": [
  {
    "channelSlice": "GREEN_GREEN (ST)",
    "signalRfuData": [
      {
        "wellLabel": "A1",
        "sampleId": 1,
        "sampleName": "sample1",
        "cycledVolume": 2,
        "threshold": 3,
        "ref": "Std-Ref",
        "rfuValues": [
          {
            "n": 1,
            "i": "1",
            "p": 1,
            "r": 10
          },
          {
            "n": 2,
            "i": "0",
            "p": 0,
            "r": 1
          }
        ]
      }
    ]
  }
]
}

```

12.4.3.2 400 Response

```
{
  "message": "string",
  "code": "string",
  "uuid": "095be615-a8ad-4c33-8e9c-c7612fbf6c9f",
  "validationErrors": {
    "property1": [
      {
        "code": "string",
        "arguments": [
          "string"
        ]
      }
    ],
    "property2": [
      {
        "code": "string",
        "arguments": [
          "string"
        ]
      }
    ]
  }
}
```

12.4.4 Responses

Status	Meaning	Description	Schema
200	OK	Get RFU details	None
400	Bad Request	Missing or invalid requested params	ErrorResponse
401	Unauthorized	Unauthorized	None
403	Forbidden	Access denied	None
404	Not Found	Requested plate not found	ErrorResponse
405	Method Not Allowed	HTTP method is not supported	None
500	Internal Server Error	Unexpected error	ErrorResponse

12.5 GetMultipleOccupancyResult

POST /lab-automation/v1/experiment/{plateId}/multiple-occupancy

To perform this operation, you must be authenticated by means of one of the following methods: Lab Automation API Key Authorization.

Retrieves Multiple Occupancy analysis results for the specified experiment based on the provided channel configuration

12.5.1 Request body example

```
{
  "dpcrRunStepIndex": 2,
  "wellPositions": [
    1,
    2,
    4
  ],
  "channels": [
    {
      "excitation": "GREEN",
      "emission": "GREEN"
    }
  ],
  "sortType": "VERTICAL",
  "showMeanValuesForReplicates": true,
  "positivesChannels": [
    0
  ]
}
```

12.5.2 Request body properties

Name	In	Type	Required	Description
plateId	path	string(uuid)	true	ID of the experiment
body	body	MultipleOccupancyFor-ChannelRequest	true	none
» dpcrRunStepIndex	body	integer(int32)	true	DPCR run step index
» wellPositions	body	[integer]	false	Selected wells
» channels	body	[ChannelDefinition]	true	Selected channels

Name	In	Type	Required	Description
»» excitation	body	string	true	Excitation filter color
»» emission	body	string	true	Emission filter color
» sortType	body	string	false	Vertical or Horizontal result sorting
» showMeanValuesFor-Replicates	body	boolean	false	Was option show Mean Values for Replicates was checked
» positivesChannels	body	[integer]	false	Presentation of positive channels

12.5.2.1 Enumerated Values

Parameter	Value
»» excitation	GREEN
»» excitation	YELLOW
»» excitation	ORANGE
»» excitation	RED
»» excitation	CRIMSON
»» excitation	FARRED
»» emission	GREEN
»» emission	YELLOW
»» emission	ORANGE
»» emission	RED
»» emission	CRIMSON
»» emission	FARRED
» sortType	VERTICAL
» sortType	HORIZONTAL

12.5.3 Example responses

12.5.3.1 200 Response

null

12.5.4 Responses

Status	Meaning	Description	Schema
200	OK	Get MO details	StreamingResponseBody
400	Bad Request	Missing or invalid requested params	ErrorResponse
401	Unauthorized	Unauthorized	None
403	Forbidden	Access denied	None
404	Not Found	Requested plate not found	ErrorResponse
405	Method Not Allowed	HTTP method is not supported	None
500	Internal Server Error	Unexpected error	ErrorResponse

12.6 AssignAnalysisTemplate

POST /lab-automation/v1/experiment/{plateId}/analysis-template

To perform this operation, you must be authenticated by means of one of the following methods: **Lab Automation API Key Authorization**.

DEPRECATED: please switch to AssignAnalysisTemplateV2. Assigns an analysis template to the requested experiment and triggers the analysis process if applicable

12.6.1 Request body example

```
{}
```

12.6.2 Request body properties

Name	In	Type	Required	Description
plateId	path	string(uuid)	true	ID of the experiment
body	body	object	true	none

12.6.3 Example responses

12.6.3.1 400 Response

```
{
  "message": "string",
  "code": "string",
  "uuid": "095be615-a8ad-4c33-8e9c-c7612fbf6c9f",
  "validationErrors": {
```



```

    "property1": [
      {
        "code": "string",
        "arguments": [
          "string"
        ]
      }
    ],
    "property2": [
      {
        "code": "string",
        "arguments": [
          "string"
        ]
      }
    ]
  }
}

```

12.6.4 Responses

Status	Meaning	Description	Schema
400	Bad Request	Missing or invalid requested params	ErrorResponse
401	Unauthorized	Unauthorized	None
403	Forbidden	Access denied	None
405	Method Not Allowed	HTTP method is not supported	None
500	Internal Server Error	Unexpected error	ErrorResponse

12.7 RemoveAnalysisTemplate

DELETE /lab-automation/v1/experiment/{plateId}/analysis-template

To perform this operation, you must be authenticated by means of one of the following methods: Lab Automation API Key Authorization.

Removes analysis rules from all reaction mixes of the requested experiment

12.7.1 Requeset body properties

Name	In	Type	Required	Description
plateId	path	string(uuid)	true	ID of the experiment

12.7.2 Example responses

12.7.2.1 400 Response

```
{
  "message": "string",
  "code": "string",
  "uuid": "095be615-a8ad-4c33-8e9c-c7612fbf6c9f",
  "validationErrors": {
    "property1": [
      {
        "code": "string",
        "arguments": [
          "string"
        ]
      }
    ],
    "property2": [
      {
        "code": "string",
        "arguments": [
          "string"
        ]
      }
    ]
  }
}
```

12.7.3 Responses

Status	Meaning	Description	Schema
200	OK	Analysis rules removed	None
400	Bad Request	Missing or invalid requested params	ErrorResponse
401	Unauthorized	Unauthorized	None
403	Forbidden	Access denied	None

Status	Meaning	Description	Schema
404	Not Found	Requested plate not found	ErrorResponse
405	Method Not Allowed	HTTP method is not supported	None
500	Internal Server Error	Unexpected error	ErrorResponse

12.8 DefineExperiment

POST /lab-automation/v1/experiment/define

To perform this operation, you must be authenticated by means of one of the following methods: Lab Automation API Key Authorization.

Defines an experiment based on provided parameters

12.8.1 Request body example

```
{
  "barcode": "00031234567891113151719212",
  "plateName": "example_plate_name",
  "plateTypeId": "67e02b72-768c-4bde-a4ec-d4c70c1c777a",
  "dpcrRunSteps": {
    "primingDPCRStep": {
      "velocityProfile": "0282a51b-422f-491a-8e66-cebc06cb8990"
    },
    "cyclingDPCRSteps": [
      {
        "index": 1,
        "cycles": [
          {
            "count": 1,
            "position": 0,
            "steps": [
              {
                "temperature": 40,
                "duration": 180,
                "position": 0
              }
            ]
          }
        ]
      }
    ]
  }
}
```

```

    ]
  }
],
"imagingDPCRSteps": [
  {
    "index": 2,
    "enableHighMultiplexingReferenceChannel": true,
    "imagingProfiles": [
      {
        "channel": {
          "excitation": "GREEN",
          "emission": "GREEN"
        },
        "durationOfExposure": 1,
        "gain": 40
      }
    ]
  }
]
},
"owners": [
  "admin",
  "carl"
]
}

```

12.8.2 Requet body properties

Name	In	Type	Required	Description
body	body	DefineExperimentRe- quest	true	none
» barcode	body	string	false	Plate barcode. Used to make a sanity check if the plate in the slot is the one that is defined. Optional
» plateName	body	string	true	Plate name

Name	In	Type	Required	Description
» plateTypeId	body	string(uuid)	true	Plate type ID. Available plate types can be listed via the /experiment/plate-types endpoint.
» dpcrRunSteps	body	DefineExperimentRequest.DPCRRunSteps	true	none
»» primingDPCRStep	body	DefineExperimentRequest.DPCRRunSteps.Priming	true	none
»»» velocityProfile	body	string(uuid)	true	ID of velocity profile used in priming. Available velocity profiles for a particular plate type can be listed via the /experiment/velocity-profiles endpoint.
»» cyclingDPCRSteps	body	[DefineExperimentRequest.DPCRRunSteps.Cycling]	true	List of defined cycling steps
»»» index	body	integer(int32)	false	Cycling step index
»»» cycles	body	[DefineExperimentRequest.DPCRRunSteps.Cycling.Cycle]	false	Defined cycles
»»»» count	body	integer(int32)	false	Number of cycles
»»»» position	body	integer(int32)	true	Cycle position in order
»»»» steps	body	[DefineExperimentRequest.DPCRRunSteps.Cycling.Cycle.CycleStep]	false	List of steps within the cycle
»»»»» temperature	body	number(double)	false	Step temperature
»»»»» duration	body	integer(int32)	true	Step duration in seconds
»»»»» position	body	integer(int32)	true	Step position in order
»» imagingDPCRSteps	body	[DefineExperimentRequest.DPCRRunSteps.Imaging]	true	List of defined cycling steps

Name	In	Type	Required	Description
»»» index	body	integer(int32)	false	Imaging step index
»»» enableHighMultiplexingReferenceChannel	body	boolean	true	Enabling High-Multiplexing Reference channel will make additional channels and amplitude multiplexing “mode” available. Please note that this will require usage of the QIAcuity High Multiplex Kit.
»»» imagingProfiles	body	[DefineExperimentRequest.DPCRRunSteps.Imaging.ImagingProfile]	false	Imaging profiles
»»»» channel	body	ChannelDefinition	true	none
»»»»» excitation	body	string	true	Excitation filter color
»»»»» emission	body	string	true	Emission filter color
»»»» durationOfExposure	body	integer(int64)	false	Duration of exposure value
»»»» gain	body	integer(int32)	false	Gain value
» owners	body	[string]	true	Username of plate owners. The owners must exist in the current system.

12.8.2.1 Enumerated Values

Parameter	Value
»»»»» excitation	GREEN
»»»»» excitation	YELLOW
»»»»» excitation	ORANGE
»»»»» excitation	RED
»»»»» excitation	CRIMSON
»»»»» excitation	FARRED
»»»»» emission	GREEN

Parameter	Value
»»»»» emission	YELLOW
»»»»» emission	ORANGE
»»»»» emission	RED
»»»»» emission	CRIMSON
»»»»» emission	FARRED

12.8.3 Example responses

12.8.3.1 200 Response

"497f6eca-6276-4993-bfeb-53cbbbba6f08"

12.8.4 Responses

Status	Meaning	Description	Schema
200	OK	Returns ID of created experiment	string
400	Bad Request	Missing or invalid requested params	ErrorResponse
401	Unauthorized	Unauthorized	None
403	Forbidden	Access denied	None
405	Method Not Allowed	HTTP method is not supported	None
500	Internal Server Error	Unexpected error	ErrorResponse

12.9 DefineExperimentFromTemplate

POST /lab-automation/v1/experiment/define/template

To perform this operation, you must be authenticated by means of one of the following methods: Lab Automation API Key Authorization.

Defines an experiment based on existing template

12.9.1 Request body example

```
{
  "barcode": "00031234567891113151719212",
  "plateName": "example_plate_name",
  "templateName": "example_template_name",
```

```

"owners": [
  "admin",
  "carl"
]
}

```

12.9.2 Request body properties

Name	In	Type	Required	Description
body	body	DefineExperiment-FromTemplateRequest	true	none
» barcode	body	string	false	Plate barcode. Used to make a sanity check if the plate in the slot is the one that is defined. Optional
» plateName	body	string	false	Plate name. Needs to be provided if given template does not specify plate's name. Optional
» templateName	body	string	true	Name of the template which will be used to create a plate
» owners	body	[string]	false	List of plate owners existing in the current system

12.9.3 Example responses

12.9.3.1 200 Response

"497f6eca-6276-4993-bfeb-53cbbbba6f08"

12.9.4 Responses

Status	Meaning	Description	Schema
200	OK	Returns ID of created experiment	string
400	Bad Request	Missing or invalid requested params	ErrorResponse

Status	Meaning	Description	Schema
401	Unauthorized	Unauthorized	None
403	Forbidden	Access denied	None
404	Not Found	Requested plate template not found	ErrorResponse
405	Method Not Allowed	HTTP method is not supported	None
500	Internal Server Error	Unexpected error	ErrorResponse

12.10 RunExperiment

POST /lab-automation/v1/command/experiment/run

To perform this operation, you must be authenticated by means of one of the following methods: **Lab Automation API Key Authorization**.

Adds command that runs a previously defined plate experiment, returns queued command's ID

12.10.1 Request body example

```
{
  "instrumentId": "instrument123",
  "plateId": "21ebe258-ec80-4f73-aafc-4faa863d8a22",
  "drawerName": "Drawer1",
  "slotId": 2
}
```

12.10.2 Request body properties

Name	In	Type	Required	Description
body	body	RunExperimentRequest	true	none
» instrumentId	body	string	true	ID of the instrument on which the command is to be executed.
» plateId	body	string(uuid)	true	ID of the plate which should be run by the instrument
» drawerName	body	string	false	Name of the drawer in which the requested plate is placed

Name	In	Type	Required	Description
» slotId	body	integer(int32)	false	ID of the slot within the drawer in which the requested plate is placed

12.10.3 Example responses

12.10.3.1 201 Response

"497f6eca-6276-4993-bfeb-53cbbbba6f08"

12.10.4 Responses

Status	Meaning	Description	Schema
201	Created	Command successfully added to the queue. Returns queued command's ID	string
400	Bad Request	Missing or invalid requested params	ErrorResponse
401	Unauthorized	Unauthorized	None
403	Forbidden	Access denied	None
405	Method Not Allowed	HTTP method is not supported	None
500	Internal Server Error	Unexpected error	ErrorResponse

12.11 ReleaseDrawerBooking

POST /lab-automation/v1/command/drawer/release-booking

To perform this operation, you must be authenticated by means of one of the following methods: Lab Automation API Key Authorization.

Adds command that releases drawers from exclusive robot use to queue, returns queued command's ID

12.11.1 Request body example

```
{
  "instrumentId": "instrument123",
```

```
"drawerName": "Drawer1"
}
```

12.11.2 Requeset body properties

Name	In	Type	Required	Description
body	body	ReleaseDrawerBook- ingRequest	true	none
» instrumentId	body	string	true	ID of the instrument on which the command is to be executed.
» drawerName	body	string	true	Name of drawer to be released from exclusive robot use

12.11.3 Example responses

12.11.3.1 201 Response

```
"497f6eca-6276-4993-bfeb-53cbbbba6f08"
```

12.11.4 Responses

Status	Meaning	Description	Schema
201	Created	Command successfully added to the queue. Returns queued command's ID	string
400	Bad Request	Missing or invalid requested params	ErrorResponse
401	Unauthorized	Unauthorized	None
403	Forbidden	Access denied	None
405	Method Not Allowed	HTTP method is not supported	None
500	Internal Server Error	Unexpected error	ErrorResponse

12.12 OpenDrawer

POST /lab-automation/v1/command/drawer/open

To perform this operation, you must be authenticated by means of one of the following methods: Lab Automation API Key Authorization.

Adds command that opens a specific drawer which was previously booked, returns queued command's ID

12.12.1 Request body example

```
{  
  "instrumentId": "instrument123",  
  "drawerName": "Drawer1"  
}
```

12.12.2 Request body properties

Name	In	Type	Required	Description
body	body	OpenDrawerRequest	true	none
» instrumentId	body	string	true	ID of the instrument on which the command is to be executed.
» drawerName	body	string	true	Name of the drawer to be opened

12.12.3 Example responses

12.12.3.1 201 Response

"497f6eca-6276-4993-bfeb-53cbbbba6f08"

12.12.4 Responses

Status	Meaning	Description	Schema
201	Created	Command successfully added to the queue. Returns queued command's ID	string
400	Bad Request	Missing or invalid requested params	ErrorResponse
401	Unauthorized	Unauthorized	None
403	Forbidden	Access denied	None

Status	Meaning	Description	Schema
405	Method Not Allowed	HTTP method is not supported	None
500	Internal Server Error	Unexpected error	ErrorResponse

12.13 CloseDrawer

POST /lab-automation/v1/command/drawer/close

To perform this operation, you must be authenticated by means of one of the following methods: Lab Automation API Key Authorization.

Adds command that closes a specific drawer which was previously booked, returns queued command's ID

12.13.1 Request body example

```
{
  "instrumentId": "instrument123",
  "drawerName": "Drawer1"
}
```

12.13.2 Request body properties

Name	In	Type	Required	Description
body	body	CloseDrawerRequest	true	none
» instrumentId	body	string	true	ID of the instrument on which the command is to be executed.
» drawerName	body	string	true	Name of the drawer to be opened

12.13.3 Example responses

12.13.3.1 201 Response

"497f6eca-6276-4993-bfeb-53cbbbba6f08"

12.13.4 Responses

Status	Meaning	Description	Schema
201	Created	Command successfully added to the queue. Returns queued command's ID	string
400	Bad Request	Missing or invalid requested params	ErrorResponse
401	Unauthorized	Unauthorized	None
403	Forbidden	Access denied	None
405	Method Not Allowed	HTTP method is not supported	None
500	Internal Server Error	Unexpected error	ErrorResponse

12.14 BookDrawer

POST /lab-automation/v1/command/drawer/book

To perform this operation, you must be authenticated by means of one of the following methods: Lab Automation API Key Authorization.

Adds command that books a drawer for exclusive robot use to queue, returns queued command's ID

12.14.1 Request body example

```
{
  "instrumentId": "instrument123",
  "drawerName": "Drawer1"
}
```

12.14.2 Request body properties

Name	In	Type	Required	Description
body	body	BookDrawerRequest	true	none
» instrumentId	body	string	true	ID of the instrument on which the command is to be executed.
» drawerName	body	string	true	Name of drawer to be booked for exclusive robot use

12.14.3 Example responses

12.14.3.1 201 Response

"497f6eca-6276-4993-bfeb-53cbbbba6f08"

12.14.4 Responses

Status	Meaning	Description	Schema
201	Created	Command successfully added to the queue. Returns queued command's ID	string
400	Bad Request	Missing or invalid requested params	ErrorResponse
401	Unauthorized	Unauthorized	None
403	Forbidden	Access denied	None
405	Method Not Allowed	HTTP method is not supported	None
500	Internal Server Error	Unexpected error	ErrorResponse

12.15 GetExperimentResultsV2

GET /lab-automation/v2/experiment/{plateId}/result

To perform this operation, you must be authenticated by means of one of the following methods: Lab Automation API Key Authorization.

Fetches results for requested experiment

12.15.1 Request body properties

Name	In	Type	Required	Description
plateId	path	string(uuid)	true	ID of the experiment which results should be fetched

12.15.2 Example responses

12.15.2.1 200 Response

```

[
  {
    "dpcrRunStepIndex": 2,
    "results": [
      {
        "wellDetails": {
          "wellPosition": 5,
          "rowLetter": "A",
          "columnNumber": 1,
          "replicateWellPositions": [
            5,
            8
          ],
          "cycledVolume": 2.57
        },
        "sample": {
          "name": "S1",
          "uniqueId": 1,
          "volumeOfTemplate": 2,
          "concentrationFactor": 20,
          "type": "SAMPLE",
          "conversionFactor": 10.999999999,
          "conversionUnit": "cp/ml"
        },
        "reaction": {
          "name": "corona_g",
          "totalReactionVolume": 2
        },
        "concentrations": [
          {
            "channel": {
              "excitation": "GREEN",
              "emission": "GREEN",
              "thresholdMode": "ST"
            },
            "target": {
              "id": "95f6cb04-fc4d-4c03-bd22-30ef11300e8c",
              "name": "COVID-19_G2",
              "controlType": "NONE",

```



```

    "isInternalControl": false
  },
  "concentration": {
    "value": 10.484819643300222,
    "concentrationOfOriginalSample": 10.484819643300222,
    "concentrationWithCustomUnitOfDpcrReaction": 0,
    "concentrationWithCustomUnitOfUndilutedSample": 0,
    "dilutedCi": 0,
    "undilutedCi": 0,
    "dilutedConvCi": 0,
    "undilutedConvCi": 0,
    "errorCode": "SATURATION_ERROR",
    "lambda": 5.9643300222
  },
  "validsCount": {
    "count": 24000,
    "qualityControlRuleResult": {
      "settings": {
        "minimumConcentration": 75,
        "maximumConcentration": 15000
      },
      "passed": true
    }
  },
  "positivesCount": {
    "count": 24000,
    "qualityControlRuleResult": {
      "settings": {
        "minimumConcentration": 75,
        "maximumConcentration": 15000
      },
      "passed": true
    }
  },
  "negativesCount": 23703,
  "ci": 1.4353845944578065,
  "relativeCi": 0.1369012194096266,
  "meanConcentration": {
    "value": 10.484819643300222,

```

```

    "concentrationOfOriginalSample": 10.484819643300222,
    "concentrationWithCustomUnitOfDpcrReaction": 0,
    "concentrationWithCustomUnitOfUndilutedSample": 0,
    "dilutedCi": 0,
    "undilutedCi": 0,
    "dilutedConvCi": 0,
    "undilutedConvCi": 0,
    "errorCode": "SATURATION_ERROR",
    "lambda": 5.9643300222
  },
  "meanRelativeCi": 0.03922849550198258,
  "meanCi": 2.4208812652882585,
  "threshold": [
    7.24,
    8.34,
    9.85
  ],
  "autoThreshold": [
    7.24,
    8.34,
    9.85
  ],
  "thresholdStrategy": "AUTO_THRESHOLD, LASSO, ANALYSIS_RULES_AUTO_THRESHOLD, ANALYSIS_RULES_DBA, FALLBACK_FROM_ANALYSIS_RULES",
  "dispersionMeasure": {
    "stdDevOfUndilutedSample": 299.3133873057806,
    "stdDevInDpcrReaction": 299.3133873057806,
    "stdDevForConcentrationWithCustomUnitOfUndilutedSample": 299.3133873057806,
    "stdDevForConcentrationWithCustomUnitInDpcrReaction": 299.3133873057806,
    "cv": 154.91933384829665
  },
  "qualityControlStatus": {
    "strategy": "INVALIDATE_WELL",
    "failedValidationRules": [
      {
        "type": "MINIMUM_VALID_PARTITIONS_PERCENTAGE_FOR_SAMPLE",
        "channels": [
          {
            "excitation": "GREEN",
            "emission": "GREEN",

```

12.15.3 Responses

12.15.4 Response Schema

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Name	Type	Required	Restrictions	Description
<i>anonymous</i>	[ExperimentResultsV2Response]	false	none	none
» dpcrRunStepIndex	integer(int32)	false	none	dPCR run step index
» results	[AbsoluteQuantification-ResultV2]	false	none	List of absolute quantification results for requested plate, run step, channels and wells
» » wellDetails	AbsoluteQuantification-ResultV2.Well	false	none	none
» » » wellPosition	integer(int32)	true	none	Well position
» » » rowLetter	string	false	none	Row letter
» » » columnNumber	integer(int32)	false	none	Column number
» » » replicateWellPositions	[integer]	false	none	Well positions of replicate wells
» » » cycledVolume	number(double)	false	none	Cycled volume of this well
» » sample	AbsoluteQuantification-ResultV2.Sample	false	none	none
» » » name	string	false	none	Name of the sample
» » » uniqueId	integer(int32)	false	none	Unique id of the sample
» » » volumeOfTemplate	number(double)	false	none	Dilution Factor: volume of template value
» » » concentrationFactor	number(double)	false	none	Dilution Factor: concentration factor value
» » » type	string	false	none	Sample type - SAMPLE, CONTROL or NON_TEM-PLATE_CONTROL
» » » conversionFactor	number	false	none	Conversion Factor
» » » conversionUnit	string	false	none	Unit for conversion factor value
» » reaction	AbsoluteQuantification-ResultV2.Reaction	false	none	none
» » » name	string	false	none	Reaction mix name
» » » totalReactionVolume	number(double)	false	none	Dilution Factor: total reaction volume value

Name	Type	Required	Restrictions	Description
»» concentrations	[AbsoluteQuantification-ResultV2.ConcentrationPerChannelWith-Mean]	false	none	Concentrations per channel with mean data for single well
»»» channel	ChannelSliceDefinition	false	none	none
»»»» excitation	string	true	none	Excitation filter color
»»»» emission	string	true	none	Emission filter color
»»»» thresholdMode	string	true	none	Channel threshold mode
»»» target	AbsoluteQuantification-ResultV2.ConcentrationPerChannelWith-Mean.Target	false	none	none
»»»» id	string(uuid)	false	none	Target ID
»»»» name	string	false	none	Target name
»»»» controlType	string	false	none	Control type (positive, negative or none)
»»»» isInternalControl	boolean	false	none	Internal control indicator
»»» concentration	AbsoluteQuantification-ResultV2.ConcentrationWithErrorCode	false	none	none
»»»» value	number(double)	false	none	Concentration of diluted sample
»»»» concentrationOfOriginalSample	number(double)	false	none	Concentration of sample before dilution
»»»» concentrationWithCustomUnitOfDpcrReaction	number	false	none	Conversion Factor multiplied by concentration of dcpr reaction result
»»»» concentrationWithCustomUnitOfUndilutedSample	number	false	none	Conversion Factor multiplied by concentration of undiluted Sample result
»»»» dilutedCi	number	false	none	Diluted CI value
»»»» undilutedCi	number	false	none	Undiluted CI value

Name	Type	Required	Restrictions	Description
»»»» dilutedConvCi	number	false	none	Diluted CI value for concentration with custom unit of dpcr reaction
»»»» undilutedConvCi	number	false	none	Undiluted CI value for concentration with custom unit of undiluted sample
»»»» errorCode	string	false	none	Error code
»»»» lambda	number(double)	false	none	Lambda
»»» validsCount	PartitionsWithQuality-ControlRuleResult	false	none	none
»»»» count	integer(int32)	false	none	Count of partitions
»»»» qualityControlRuleResult	any	false	none	Quality control rule result

oneOf

Name	Type	Required	Restrictions	Description
»»»»» <i>anonymous</i>	any	false	none	none

allOf - discriminator: type

Name	Type	Required	Restrictions	Description
»»»»»» <i>anonymous</i>	object	false	none	none
»»»»»» type	string	true	none	none

and

Name	Type	Required	Restrictions	Description
»»»»»» <i>anonymous</i>	object	false	none	none
»»»»»» settings	Settings	false	none	none

Name	Type	Required	Restrictions	Description
» » » » » » » » minimumConcentration	number(double)	false	none	Minimum concentration
» » » » » » » » maximumConcentration	number(double)	false	none	Maximum concentration
» » » » » » » » passed	boolean	false	none	Indicates if the validation rule passed

xor

Name	Type	Required	Restrictions	Description
» » » » » <i>anonymous</i>	any	false	none	none

allOf - discriminator: type

Name	Type	Required	Restrictions	Description
» » » » » » <i>anonymous</i>	object	false	none	none

and

Name	Type	Required	Restrictions	Description
» » » » » » <i>anonymous</i>	object	false	none	none
» » » » » » settings	Settings	false	none	none
» » » » » » passed	boolean	false	none	Indicates if the validation rule passed

xor

Name	Type	Required	Restrictions	Description
» » » » » <i>anonymous</i>	any	false	none	none

allOf - discriminator: type

Name	Type	Required	Restrictions	Description
» » » » » <i>anonymous</i>	object	false	none	none

and

Name	Type	Required	Restrictions	Description
» » » » » <i>anonymous</i>	object	false	none	none
» » » » » <i>settings</i>	Settings	false	none	none
» » » » » <i>passed</i>	boolean	false	none	Indicates if the validation rule passed

xor

Name	Type	Required	Restrictions	Description
» » » » » <i>anonymous</i>	any	false	none	none

allOf - discriminator: type

Name	Type	Required	Restrictions	Description
» » » » » <i>anonymous</i>	object	false	none	none

and

Name	Type	Required	Restrictions	Description
» » » » » <i>anonymous</i>	object	false	none	none
» » » » » <i>settings</i>	Settings	false	none	none
» » » » » <i>passed</i>	boolean	false	none	Indicates if the validation rule passed

continued

Name	Type	Required	Restrictions	Description
»»» positivesCount	PartitionsWithQuality-ControlRuleResult	false	none	none
»»» negativesCount	integer(int32)	false	none	Number of negative partitions
»»» ci	number(double)	false	none	Confidence interval
»»» relativeCi	number(double)	false	none	Relative confidence interval
»»» meanConcentration	AbsoluteQuantification-ResultV2.ConcentrationWithErrorCode	false	none	none
»»» meanRelativeCi	number(double)	false	none	Mean confidence interval, if the well has replicates or is a part of hyperwell
»»» meanCi	number(double)	false	none	Mean relative confidence interval, if the well has replicates or is a part of hyperwell
»»» threshold	any	false	none	Thresholds values, for AM [low, high, doublePositives], for SingleThreshold[lower]

oneOf

Name	Type	Required	Restrictions	Description
»»»» <i>anonymous</i>	any	false	none	Amplitude multiplexing threshold

allOf - discriminator: type

Name	Type	Required	Restrictions	Description
»»»»» <i>anonymous</i>	object	false	none	Signal threshold
»»»»» type	string	true	none	none

and

Name	Type	Required	Restrictions	Description
»»»»» <i>anonymous</i>	object	false	none	none
»»»»» low	number(double)	false	none	none
»»»»» high	number(double)	false	none	none
»»»»» doublePositives	number(double)	false	none	none
»»»»» warnings	[string]	false	none	none

xor

Name	Type	Required	Restrictions	Description
»»»» <i>anonymous</i>	any	false	none	Single threshold value

allOf - discriminator: type

Name	Type	Required	Restrictions	Description
»»»»» <i>anonymous</i>	object	false	none	Signal threshold

and

Name	Type	Required	Restrictions	Description
»»»»» <i>anonymous</i>	object	false	none	none
»»»»» value	number(double)	false	none	none
»»»»» warnings	[string]	false	none	none

continued

Name	Type	Required	Restrictions	Description
»»» autoThreshold	any	false	none	Auto Thresholds values, for AM [low, high, doublePositives], for Signal[lower]

oneOf

Name	Type	Required	Restrictions	Description
»»»» <i>anonymous</i>	any	false	none	Amplitude multiplexing threshold

xor

Name	Type	Required	Restrictions	Description
»»»» <i>anonymous</i>	any	false	none	Single threshold value

continued

Name	Type	Required	Restrictions	Description
»»» thresholdStrategy	string	false	none	Threshold strategy name
»»» dispersionMeasure	DispersionMeasureResponse	false	none	none
»»»» stdDevOfUndilutedSample	number(double)	false	none	Standard deviation calculated with Dilution Factor values
»»»» stdDevInDpcrReaction	number(double)	false	none	Standard deviation calculated in dpcr reaction
»»»» stdDevForConcentrationWithCustomUnitOfUndilutedSample	number	false	none	Standard deviation calculated with custom unit values
»»»» stdDevForConcentrationWithCustomUnitInDpcrReaction	number	false	none	Standard deviation calculated with custom unit in dpcr reaction

Name	Type	Required	Restrictions	Description
»»»» cv	number(double)	false	none	Coefficient of Variation
»»» qualityControlStatus	AbsoluteQuantification- ResultV2.Concentra- tionPerChannelWith- Mean.QualityControlSta- tus	false	none	none
»»»» strategy	string	false	none	Quality control validation strategy
»»»» failedValidationRules	[FailedValidationRule]	false	none	List of validation rules
»»»»» type	string	false	none	none
»»»»» channels	[SignalChannel]	false	none	none
»»»»»» excitation	string	false	none	none
»»»»»» emission	string	false	none	none
»»»»»» referenceChannel	boolean	false	none	none
»»»»»» mixed	boolean	false	none	none
»»»»» passed	boolean	false	none	none
»»»»» propagatedValida- tionRules	[PropagatedQualityCon- trolRuleFailure]	false	none	List of propagated validation rules
»»»»» qualityControlVali- dationRuleType	string	false	none	none
»»»»» propagationSource	string	false	none	none

12.15.4.2 Enumerated Values

Property	Value
type	SAMPLE
type	CONTROL
type	NON_TEMPLATE_CONTROL
excitation	GREEN
excitation	YELLOW
excitation	ORANGE
excitation	RED
excitation	CRIMSON
excitation	FARRED
emission	GREEN

Property	Value
emission	YELLOW
emission	ORANGE
emission	RED
emission	CRIMSON
emission	FARRED
thresholdMode	ST
thresholdMode	AM_LOW
thresholdMode	AM_HIGH
controlType	POSITIVE
controlType	NEGATIVE
controlType	NONE
errorCode	SATURATION_ERROR
errorCode	IMAGE_BLUR
errorCode	MISSING_CHANNEL_IN_CXTM
errorCode	WELL_OFF_CENTER
strategy	WARNING_CHANNEL
strategy	WARNING_WELL
strategy	INVALIDATE_CHANNEL
strategy	INVALIDATE_WELL
type	MINIMUM_VALID_PARTITIONS_PERCENTAGE_FOR_SAMPLE
type	MINIMUM_VALID_PARTITIONS_PERCENTAGE_FOR_CONTROL
type	MAXIMUM_POSITIVE_PARTITIONS_NUMBER_FOR_NEGATIVE_CONTROL
type	CONCENTRATION_RANGE_FOR_POSITIVE_CONTROL
excitation	GREEN
excitation	YELLOW
excitation	ORANGE
excitation	RED
excitation	CRIMSON
excitation	FARRED
emission	GREEN
emission	YELLOW
emission	ORANGE
emission	RED
emission	CRIMSON

Property	Value
emission	FARRED
qualityControlValidationRuleType	MINIMUM_VALID_PARTITIONS_PERCENTAGE_FOR_SAMPLE
qualityControlValidationRuleType	MINIMUM_VALID_PARTITIONS_PERCENTAGE_FOR_CONTROL
qualityControlValidationRuleType	MAXIMUM_POSITIVE_PARTITIONS_NUMBER_FOR_NEGATIVE_CONTROL
qualityControlValidationRuleType	CONCENTRATION_RANGE_FOR_POSITIVE_CONTROL
propagationSource	REPLICATE
propagationSource	CONTROL

12.16 GetInstruments

GET /lab-automation/v1/instruments

To perform this operation, you must be authenticated by means of one of the following methods: Lab Automation API Key Authorization.

Returns the state of the instruments registered in Suite.

12.16.1 Example responses

12.16.1.1 200 Response

```
[
  {
    "instrumentId": "instrument123",
    "deviceName": "Instrument in Lab A",
    "type": "P4",
    "isOnline": true,
    "drawers": {
      "Drawer0": {
        "isBooked": true,
        "platesInSlots": {}
      },
      "Drawer1": {
        "isBooked": false,
        "platesInSlots": {
          "0": "3fa85f64-5717-4562-b3fc-2c963f66afa6"
        }
      }
    }
  }
]
```

```

    }
  }
}
]

```

12.16.2 Responses

Status	Meaning	Description	Schema
200	OK	Successfully retrieved the instruments.	Inline
400	Bad Request	Missing or invalid requested params	ErrorResponse
401	Unauthorized	Unauthorized	None
403	Forbidden	Access denied	None
405	Method Not Allowed	HTTP method is not supported	None
500	Internal Server Error	Unexpected error	ErrorResponse

12.16.3 Response Schema

12.16.3.1 Status Code 200

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	[InstrumentStateResponse]	false	none	none
» instrumentId	string	false	none	ID of the instrument
» deviceName	string	false	none	Name of the instrument
» type	string	false	none	Type of the instrument
» isOnline	boolean	false	none	Whether an instrument has sent a heartbeat in the last PT5S (ISO8601 notation).
» drawers	object	false	none	Drawer state per drawer name
»» <dictionary>	InstrumentStateResponse.DrawerState	false	none	Drawer state per drawer name
»»» isBooked	boolean	false	none	Whether the drawer is currently booked or not
»»» platesInSlots	object	false	none	ID of plate per slot ID.

Name	Type	Required	Restrictions	Description
»»»» <dictionary>	string(uuid)	false	none	ID of plate per slot ID.

12.17 HealthCheck

GET /lab-automation/v1/health-check

To perform this operation, you must be authenticated by means of one of the following methods: Lab Automation API Key Authorization.

Check number of tasks in robot queues per instrument

12.17.1 Example responses

12.17.1.1 200 Response

```
{
  "instrumentA": {
    "commandQueueTasks": 4,
    "eventQueueTasks": 2
  },
  "instrumentB": {
    "commandQueueTasks": 1,
    "eventQueueTasks": 0
  }
}
```

12.17.2 Responses

Status	Meaning	Description	Schema
200	OK	Returns number of tasks in robot queues per instrument	Inline
400	Bad Request	Missing or invalid requested params	ErrorResponse
401	Unauthorized	Unauthorized	None
403	Forbidden	Access denied	None
405	Method Not Allowed	HTTP method is not supported	None
500	Internal Server Error	Unexpected error	ErrorResponse

12.17.3 Response Schema

12.17.3.1 Status Code 200

Name	Type	Required	Restrictions	Description
» <dictionary>	HealthCheck	false	none	none
»» commandQueueTasks	integer(int32)	false	none	Number of tasks in command queue
»» eventQueueTasks	integer(int32)	false	none	Number of tasks in event queue

12.18 GetExperimentDetails

GET /lab-automation/v1/experiment/{plateId}

To perform this operation, you must be authenticated by means of one of the following methods: **Lab Automation API Key Authorization**.

Fetches details for requested experiment

12.18.1 Request body properties

Name	In	Type	Required	Description
plateId	path	string(uuid)	true	ID of the experiment which details should be fetched

12.18.2 Example responses

12.18.2.1 200 Response

```
{
  "plateId": "3fa85f64-5717-4562-b3fc-2c963f66afa6",
  "name": "3fa85f64-5717-4562-b3fc-2c963f66afa6",
  "barcode": "00031234567891113151719212",
  "plateTypeId": "67e02b72-768c-4bde-a4ec-d4c70c1c777a",
  "dpcrRunSteps": {
    "primingDPCRStep": {
      "velocityProfile": "0282a51b-422f-491a-8e66-cebc06cb8990"
```

```

},
"cycliningDPCRSteps": [
  {
    "index": 0,
    "cycles": [
      {
        "count": 1,
        "position": 0,
        "steps": [
          {
            "temperature": 40,
            "duration": 180,
            "position": 0
          }
        ]
      }
    ]
  }
],
"imagingDPCRSteps": [
  {
    "index": 0,
    "enableHighMultiplexingReferenceChannel": true,
    "imagingProfiles": [
      {
        "channel": {
          "excitation": "GREEN",
          "emission": "GREEN"
        },
        "durationOfExposure": 0,
        "gain": 0
      }
    ]
  }
],
"reactions": [
  {
    "name": "Reaction1",

```

```

    "totalReactionVolume": 30.5,
    "targets": [
      {
        "channel": {
          "excitation": "GREEN",
          "emission": "GREEN",
          "thresholdMode": "ST"
        },
        "name": "Target1",
        "internalControl": false,
        "dyeId": "1ef3cc8a-8a5e-4709-8101-e8293fd63e2d"
      }
    ]
  },
  "sampleControl": {
    "samples": [
      {
        "name": "Sample1",
        "sampleId": 1,
        "volumeOfTemplate": 15,
        "concentrationFactor": 15,
        "conversionFactor": 15,
        "conversionUnit": "lm/kg",
        "description": "Description1",
        "labels": [
          "string"
        ]
      }
    ]
  },
  "controls": [
    {
      "name": "Control1",
      "volumeOfTemplate": 15,
      "concentrationFactor": 15,
      "conversionFactor": 15,
      "conversionUnit": "lm/kg"
    }
  ],

```

```

    "nonTemplateControls": [
      {
        "name": "NonTemplateControl1",
        "volumeOfTemplate": 15,
        "concentrationFactor": 15,
        "conversionFactor": 15,
        "conversionUnit": "lm/kg"
      }
    ],
    "wells": [
      {
        "wellPosition": 5,
        "wellRow": "A",
        "column": 1,
        "blank": false,
        "reactionName": "Reaction1",
        "sample": {
          "name": "Control1"
        },
        "controlTypes": [
          {
            "channel": {
              "excitation": "GREEN",
              "emission": "GREEN",
              "thresholdMode": "ST"
            },
            "positive": true
          }
        ]
      }
    ]
  }
}

```

12.18.3 Responses

Status	Meaning	Description	Schema
200	OK	Returns experiment details	ExperimentDetailsResponse

Status	Meaning	Description	Schema
400	Bad Request	Missing or invalid requested params	ErrorResponse
401	Unauthorized	Unauthorized	None
403	Forbidden	Access denied	None
404	Not Found	Requested plate not found	ErrorResponse
405	Method Not Allowed	HTTP method is not supported	None
500	Internal Server Error	Unexpected error	ErrorResponse

12.19 DeleteExperiment

DELETE /lab-automation/v1/experiment/{plateId}

To perform this operation, you must be authenticated by means of one of the following methods: Lab Automation API Key Authorization.

Deletes an existing experiment

12.19.1 Request body properties

Name	In	Type	Required	Description
plateId	path	string(uuid)	true	ID of the experiment which should be deleted

12.19.2 Example responses

12.19.2.1 200 Response

"497f6eca-6276-4993-bfeb-53cbbbba6f08"

12.19.3 Responses

Status	Meaning	Description	Schema
200	OK	Returns ID of deleted experiment	string
400	Bad Request	Missing or invalid requested params	ErrorResponse
401	Unauthorized	Unauthorized	None
403	Forbidden	Access denied	None
404	Not Found	Requested plate not found	ErrorResponse
405	Method Not Allowed	HTTP method is not supported	None

Status	Meaning	Description	Schema
500	Internal Server Error	Unexpected error	ErrorResponse

12.20 GetExperimentStatus

GET /lab-automation/v1/experiment/{plateId}/status

To perform this operation, you must be authenticated by means of one of the following methods: Lab Automation API Key Authorization.

Fetches status of the most recent run of the requested experiment

12.20.1 Request body properties

Name	In	Type	Required	Description
plateId	path	string(uuid)	true	ID of the experiment

12.20.2 Example responses

12.20.2.1 200 Response

```
{
  "status": "IDLE",
  "estimatedTimeTillEndOfExperiment": 300
}
```

12.20.3 Responses

Status	Meaning	Description	Schema
200	OK	Returns the status of the most recent run of the experiment	ExperimentStatusResponse
400	Bad Request	Missing or invalid requested params	ErrorResponse
401	Unauthorized	Unauthorized	None
403	Forbidden	Access denied	None
404	Not Found	Requested plate not found	ErrorResponse
405	Method Not Allowed	HTTP method is not supported	None

Status	Meaning	Description	Schema
500	Internal Server Error	Unexpected error	ErrorResponse

12.21 GetExperimentResults

GET /lab-automation/v1/experiment/{plateId}/result

To perform this operation, you must be authenticated by means of one of the following methods: **Lab Automation API Key Authorization**.

DEPRECATED: this endpoint will still provide results but only if analysis rules were not configured in any reaction mix in the experiment. It is scheduled for removal in future releases of the software. Please switch to GetExperimentResultsV2. Fetches results for requested experiment

12.21.1 Request body properties

Name	In	Type	Required	Description
plateId	path	string(uuid)	true	ID of the experiment which results should be fetched

12.21.2 Example responses

12.21.2.1 200 Response

```
[
  {
    "dpcrRunStepIndex": 2,
    "results": [
      {
        "wellDetails": {
          "wellPosition": 5,
          "rowLetter": "A",
          "columnNumber": 1,
          "replicateWellPositions": [
            5,
            8
          ],
          "cycledVolume": 2.57
        }
      }
    ]
  }
]
```

```

},
"sample": {
  "name": "S1",
  "uniqueId": 1,
  "volumeOfTemplate": 2,
  "concentrationFactor": 20,
  "type": "SAMPLE",
  "conversionFactor": 10.999999999,
  "conversionUnit": "cp/ml"
},
"reaction": {
  "name": "corona_g",
  "totalReactionVolume": 2
},
"concentrations": [
  {
    "channel": {
      "excitation": "GREEN",
      "emission": "GREEN",
      "thresholdMode": "ST"
    },
    "target": {
      "id": "95f6cb04-fc4d-4c03-bd22-30ef11300e8c",
      "name": "COVID-19_G2",
      "controlType": "NONE",
      "isInternalControl": false
    },
    "concentration": {
      "value": 10.484819643300222,
      "concentrationOfOriginalSample": 10.484819643300222,
      "concentrationWithCustomUnitOfDpcrReaction": 0,
      "concentrationWithCustomUnitOfUndilutedSample": 0,
      "dilutedCi": 0,
      "undilutedCi": 0,
      "dilutedConvCi": 0,
      "undilutedConvCi": 0,
      "errorCode": "SATURATION_ERROR",
      "lambda": 5.9643300222
    }
  },

```



```

    "validsCount": 23908,
    "positivesCount": 205,
    "negativesCount": 23703,
    "ci": 1.4353845944578065,
    "relativeCi": 0.1369012194096266,
    "meanConcentration": {
      "value": 10.484819643300222,
      "concentrationOfOriginalSample": 10.484819643300222,
      "concentrationWithCustomUnitOfDpcrReaction": 0,
      "concentrationWithCustomUnitOfUndilutedSample": 0,
      "dilutedCi": 0,
      "undilutedCi": 0,
      "dilutedConvCi": 0,
      "undilutedConvCi": 0,
      "errorCode": "SATURATION_ERROR",
      "lambda": 5.9643300222
    },
    "meanRelativeCi": 0.03922849550198258,
    "meanCi": 2.4208812652882585,
    "threshold": [
      7.24,
      8.34,
      9.85
    ],
    "autoThreshold": [
      7.24,
      8.34,
      9.85
    ],
    "isAutoThreshold": true,
    "thresholdSource": {},
    "dispersionMeasure": {
      "stdDevOfUndilutedSample": 299.3133873057806,
      "stdDevInDpcrReaction": 299.3133873057806,
      "stdDevForConcentrationWithCustomUnitOfUndilutedSample": 299.3133873057806,
      "stdDevForConcentrationWithCustomUnitInDpcrReaction": 299.3133873057806,
      "cv": 154.91933384829665
    }
  }
}

```

```

    ],
    "qualityAssuranceValidationRules": [
      {
        "channel": {
          "excitation": "GREEN",
          "emission": "GREEN"
        },
        "settings": 80,
        "passed": true,
        "strategy": "INVALIDATE_WELL"
      }
    ]
  }
}
]

```

12.21.3 Responses

Status	Meaning	Description	Schema
200	OK	Returns full experiment results	Inline
400	Bad Request	Missing or invalid requested params	ErrorResponse
401	Unauthorized	Unauthorized	None
403	Forbidden	Access denied	None
404	Not Found	Requested plate not found	ErrorResponse
405	Method Not Allowed	HTTP method is not supported	None
500	Internal Server Error	Unexpected error	ErrorResponse

12.21.4 Response Schema

12.21.4.1 Status Code 200

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	[ExperimentResultsResponse]	false	none	none
» dpcrRunStepIndex	integer(int32)	false	none	dPCR run step index

Name	Type	Required	Restrictions	Description
» results	[AbsoluteQuantification-Result]	false	none	List of absolute quantification results for requested plate, run step, channels and wells
»» wellDetails	AbsoluteQuantification-Result.Well	false	none	none
»»» wellPosition	integer(int32)	false	none	Well position
»»» rowLetter	string	false	none	Row letter
»»» columnNumber	integer(int32)	false	none	Column number
»»» replicateWellPositions	[integer]	false	none	Well positions of replicate wells
»»» cycledVolume	number(double)	false	none	Cycled volume of this well
»» sample	AbsoluteQuantification-Result.Sample	false	none	none
»»» name	string	false	none	Name of the sample
»»» uniqueId	integer(int32)	false	none	Unique id of the sample
»»» volumeOfTemplate	number(double)	false	none	Dilution Factor: volume of template value
»»» concentrationFactor	number(double)	false	none	Dilution Factor: concentration factor value
»»» type	string	false	none	Sample type - SAMPLE, CONTROL or NON_TEM-PLATE_CONTROL
»»» conversionFactor	number	false	none	Conversion Factor
»»» conversionUnit	string	false	none	Unit for conversion factor value
»» reaction	AbsoluteQuantification-Result.Reaction	false	none	none
»»» name	string	false	none	Reaction mix name
»»» totalReactionVolume	number(double)	false	none	Dilution Factor: total reaction volume value
»» concentrations	[AbsoluteQuantification-Result.ConcentrationPer-ChannelWithMean]	false	none	Concentrations per channel with mean data for single well

Name	Type	Required	Restrictions	Description
»»» channel	ChannelSliceDefinition	false	none	none
»»»» excitation	string	true	none	Excitation filter color
»»»» emission	string	true	none	Emission filter color
»»»» thresholdMode	string	true	none	Channel threshold mode
»»» target	AbsoluteQuantification- Result.ConcentrationPer- ChannelWithMean.Tar- get	false	none	none
»»»» id	string(uuid)	false	none	Target ID
»»»» name	string	false	none	Target name
»»»» controlType	string	false	none	Control type (positive, negative or none)
»»»» isInternalControl	boolean	false	none	Internal control indicator
»»» concentration	AbsoluteQuantification- Result.Concentra- tionWithErrorCode	false	none	none
»»»» value	number(double)	false	none	Concentration of diluted sample
»»»» concentrationOfO- riginalSample	number(double)	false	none	Concentration of sample before dilution
»»»» concentrationWithCusto- mUnitOfDpcrReaction	number	false	none	Conversion Factor multiplied by concentration of dpcr reaction result
»»»» concentrationWith- CustomUnitOfUndiluted- Sample	number	false	none	Conversion Factor multiplied by concentration of undiluted Sample result
»»»» dilutedCi	number	false	none	Diluted CI value
»»»» undilutedCi	number	false	none	Undiluted CI value
»»»» dilutedConvCi	number	false	none	Diluted CI value for concentration with custom unit of dpcr reaction

Name	Type	Required	Restrictions	Description
»»»» undilutedConvCi	number	false	none	Undiluted CI value for concentration with custom unit of undiluted sample
»»»» errorCode	string	false	none	Error code
»»»» lambda	number(double)	false	none	Lambda
»»» validsCount	integer(int32)	false	none	Number of valid partitions
»»» positivesCount	integer(int32)	false	none	Number of positive partitions
»»» negativesCount	integer(int32)	false	none	Number of negative partitions
»»» ci	number(double)	false	none	Confidence interval
»»» relativeCi	number(double)	false	none	Relative confidence interval
»»» meanConcentration	AbsoluteQuantification-Result.ConcentrationWithErrorCode	false	none	none
»»» meanRelativeCi	number(double)	false	none	Mean confidence interval, if the well has replicates or is a part of hyperwell
»»» meanCi	number(double)	false	none	Mean relative confidence interval, if the well has replicates or is a part of hyperwell
»»» threshold	any	false	none	Thresholds values, for AM [low, high, doublePositives], for SingleThreshold[lower]

oneOf

Name	Type	Required	Restrictions	Description
»»»» <i>anonymous</i>	any	false	none	Amplitude multiplexing threshold

allOf - discriminator: type

Name	Type	Required	Restrictions	Description
»»»»» <i>anonymous</i>	object	false	none	Signal threshold
»»»»» type	string	true	none	none

and

Name	Type	Required	Restrictions	Description
»»»»» <i>anonymous</i>	object	false	none	none
»»»»» low	number(double)	false	none	none
»»»»» high	number(double)	false	none	none
»»»»» doublePositives	number(double)	false	none	none
»»»»» warnings	[string]	false	none	none

xor

Name	Type	Required	Restrictions	Description
»»»»» <i>anonymous</i>	any	false	none	Single threshold value

allOf - discriminator: type

Name	Type	Required	Restrictions	Description
»»»»» <i>anonymous</i>	object	false	none	Signal threshold

and

Name	Type	Required	Restrictions	Description
»»»»» <i>anonymous</i>	object	false	none	none
»»»»» value	number(double)	false	none	none
»»»»» warnings	[string]	false	none	none

continued

Name	Type	Required	Restrictions	Description
»»» autoThreshold	any	false	none	Auto Thresholds values, for AM [low, high, doublePositives], for Signal[lower]

oneOf

Name	Type	Required	Restrictions	Description
»»»» <i>anonymous</i>	any	false	none	Amplitude multiplexing threshold

xor

Name	Type	Required	Restrictions	Description
»»»» <i>anonymous</i>	any	false	none	Single threshold value

continued

Name	Type	Required	Restrictions	Description
»»» isAutoThreshold	boolean	false	none	Is auto or manual threshold
»»» thresholdSource	any	false	none	Where this threshold comes from

oneOf - discriminator: type

Name	Type	Required	Restrictions	Description
»»»» <i>anonymous</i>	object	false	none	Automatic threshold
»»»»» type	string	true	none	none

xor

Name	Type	Required	Restrictions	Description
»»»» <i>anonymous</i>	any	false	none	Threshold set by analysis automation rule

allOf - discriminator: type

Name	Type	Required	Restrictions	Description
»»»»» <i>anonymous</i>	object	false	none	Where this threshold comes from
»»»»» type	string	true	none	none

and

Name	Type	Required	Restrictions	Description
»»»»» <i>anonymous</i>	object	false	none	none
»»»»» ruleName	string	false	none	none

xor - discriminator: type

Name	Type	Required	Restrictions	Description
»»»» <i>anonymous</i>	object	false	none	Lasso threshold
»»»» type	string	true	none	none

xor - discriminator: type

Name	Type	Required	Restrictions	Description
»»»» <i>anonymous</i>	object	false	none	Manually set threshold
»»»» type	string	true	none	none

continued

Name	Type	Required	Restrictions	Description
»»» dispersionMeasure	DispersionMeasureResponse	false	none	none
»»»» stdDevOfUndilutedSample	number(double)	false	none	Standard deviation calculated with Dilution Factor values
»»»» stdDevInDpcrReaction	number(double)	false	none	Standard deviation calculated in dpcr reaction
»»»» stdDevForConcentrationWithCustomUnitOfUndilutedSample	number	false	none	Standard deviation calculated with custom unit values
»»»» stdDevForConcentrationWithCustomUnitInDpcrReaction	number	false	none	Standard deviation calculated with custom unit in dpcr reaction
»»»» cv	number(double)	false	none	Coefficient of Variation
»» qualityAssuranceValidationRules	[oneOf]	false	none	Quality assurance validation results

allOf - discriminator: type

Name	Type	Required	Restrictions	Description
»»» <i>anonymous</i>	object	false	none	none
»»»» type	string	true	none	none

and

Name	Type	Required	Restrictions	Description
»»» <i>anonymous</i>	object	false	none	none
»»»» channel	ChannelDefinition	false	none	none
»»»»» excitation	string	true	none	Excitation filter color
»»»»» emission	string	true	none	Emission filter color
»»»» settings	integer(int32)	false	none	Settings for the validation rule
»»»» passed	boolean	false	none	Indicates if the validation rule passed
»»»» strategy	string	false	none	Validation rule strategy

12.21.4.2 Enumerated Values

Property	Value
type	SAMPLE
type	CONTROL
type	NON_TEMPLATE_CONTROL
excitation	GREEN
excitation	YELLOW
excitation	ORANGE
excitation	RED
excitation	CRIMSON
excitation	FARRED
emission	GREEN
emission	YELLOW
emission	ORANGE
emission	RED
emission	CRIMSON
emission	FARRED
thresholdMode	ST
thresholdMode	AM_LOW
thresholdMode	AM_HIGH
controlType	POSITIVE
controlType	NEGATIVE
controlType	NONE
errorCode	SATURATION_ERROR
errorCode	IMAGE_BLUR
errorCode	MISSING_CHANNEL_IN_CXTM
errorCode	WELL_OFF_CENTER
excitation	GREEN
excitation	YELLOW
excitation	ORANGE
excitation	RED
excitation	CRIMSON
excitation	FARRED
emission	GREEN
emission	YELLOW
emission	ORANGE
emission	RED
emission	CRIMSON

Property	Value
emission	FARRED
strategy	WARNING_CHANNEL
strategy	WARNING_WELL
strategy	INVALIDATE_CHANNEL
strategy	INVALIDATE_WELL

12.22 GetPrimingProfiles

GET /lab-automation/v1/experiment/velocity-profiles

To perform this operation, you must be authenticated by means of one of the following methods: **Lab Automation API Key Authorization**.

Gets a dictionary of available priming (velocity) profiles with its ID for requested plate type

12.22.1 Request body properties

Name	In	Type	Required	Description
plateTypeId	query	string(uuid)	true	Plate type ID for which velocity profiles dictionary should be provided

12.22.2 Example responses

12.22.2.1 200 Response

```
{
  "d2844690-b50f-4563-b764-fd32ed95e76b": "QIAGEN Priming Profile Probe (RT-) PCR",
  "97a3e10f-2484-4f88-bf13-ac1911e4423b": "QIAGEN Priming Profile EvaGreen (RT-) PCR"
}
```

12.22.3 Responses

Status	Meaning	Description	Schema
200	OK	Provides a dictionary of velocity profile names by their IDs	Inline

Status	Meaning	Description	Schema
400	Bad Request	Missing or invalid requested params	ErrorResponse
401	Unauthorized	Unauthorized	None
403	Forbidden	Access denied	None
405	Method Not Allowed	HTTP method is not supported	None
500	Internal Server Error	Unexpected error	ErrorResponse

12.22.4 Response Schema

12.22.4.1 Status Code 200 *Keys are velocity profile IDs, values are names*

Name	Type	Required	Restrictions	Description
» <dictionary>	string	false	none	none

12.23 GetPlateTypes

GET /lab-automation/v1/experiment/plate-types

To perform this operation, you must be authenticated by means of one of the following methods: Lab Automation API Key Authorization.

Provides a dictionary of plate type names by their IDs

12.23.1 Example responses

12.23.1.1 200 Response

```
{
  "bb52fd68-effd-4168-a2a3-8b3e6dfdb597": "Nanoplate 26K 8-well",
  "d27fb9bb-bc7f-4502-9b51-b5fd552b8837": "Nanoplate 26K 24-well"
}
```

12.23.2 Responses

Status	Meaning	Description	Schema
200	OK	Returns plate types dictionary	Inline
400	Bad Request	Missing or invalid requested params	ErrorResponse
401	Unauthorized	Unauthorized	None

Status	Meaning	Description	Schema
403	Forbidden	Access denied	None
405	Method Not Allowed	HTTP method is not supported	None
500	Internal Server Error	Unexpected error	ErrorResponse

12.23.3 Response Schema

12.23.3.1 Status Code 200 *Keys are plate type IDs, values are names*

Name	Type	Required	Restrictions	Description
» <dictionary>	string	false	none	none

12.24 GetDyes

GET /lab-automation/v1/experiment/dyes

To perform this operation, you must be authenticated by means of one of the following methods: Lab Automation API Key Authorization.

Gets a dictionary of available dyes with its ID

12.24.1 Example responses

12.24.1.1 200 Response

```
{
  "97ca742b-259c-48c9-8e49-e3c9588281f5": "VIC",
  "53c43d01-6eee-43ea-bb63-d74dd5e39115": "SYBR Green",
  "68b8965e-6bbc-46a7-b16b-2f496151fa05": "FAM",
  "2be8adbe-5875-45da-9702-2144c2c20ed6": "HEX"
}
```

12.24.2 Responses

Status	Meaning	Description	Schema
200	OK	Provides a dictionary of dye names by their IDs	Inline
400	Bad Request	Missing or invalid requested params	ErrorResponse
401	Unauthorized	Unauthorized	None

Status	Meaning	Description	Schema
403	Forbidden	Access denied	None
405	Method Not Allowed	HTTP method is not supported	None
500	Internal Server Error	Unexpected error	ErrorResponse

12.24.3 Response Schema

12.24.3.1 Status Code 200

Name	Type	Required	Restrictions	Description
» <dictionary>	string	false	none	none

12.25 GetExperimentDetailsByBarcode

GET /lab-automation/v1/experiment/by-barcode/{barcode}

To perform this operation, you must be authenticated by means of one of the following methods: **Lab Automation API Key Authorization**.

Fetches details of requested experiment by barcode

12.25.1 Request body properties

Name	In	Type	Required	Description
barcode	path	string	true	Barcode of the experiments plate which details should be fetched

12.25.2 Example responses

12.25.2.1 200 Response

```
{
  "plateId": "3fa85f64-5717-4562-b3fc-2c963f66afa6",
  "name": "3fa85f64-5717-4562-b3fc-2c963f66afa6",
  "barcode": "00031234567891113151719212",
  "plateTypeId": "67e02b72-768c-4bde-a4ec-d4c70c1c777a",
```

```

"dpcrRunSteps": {
  "primingDPCRStep": {
    "velocityProfile": "0282a51b-422f-491a-8e66-cebc06cb8990"
  },
  "cyclingDPCRSteps": [
    {
      "index": 0,
      "cycles": [
        {
          "count": 1,
          "position": 0,
          "steps": [
            {
              "temperature": 40,
              "duration": 180,
              "position": 0
            }
          ]
        }
      ]
    }
  ],
  "imagingDPCRSteps": [
    {
      "index": 0,
      "enableHighMultiplexingReferenceChannel": true,
      "imagingProfiles": [
        {
          "channel": {
            "excitation": "GREEN",
            "emission": "GREEN"
          },
          "durationOfExposure": 0,
          "gain": 0
        }
      ]
    }
  ]
},

```

```

"reactions": [
  {
    "name": "Reaction1",
    "totalReactionVolume": 30.5,
    "targets": [
      {
        "channel": {
          "excitation": "GREEN",
          "emission": "GREEN",
          "thresholdMode": "ST"
        },
        "name": "Target1",
        "internalControl": false,
        "dyeId": "1ef3cc8a-8a5e-4709-8101-e8293fd63e2d"
      }
    ]
  }
],
"sampleControl": {
  "samples": [
    {
      "name": "Sample1",
      "sampleId": 1,
      "volumeOfTemplate": 15,
      "concentrationFactor": 15,
      "conversionFactor": 15,
      "conversionUnit": "lm/kg",
      "description": "Description1",
      "labels": [
        "string"
      ]
    }
  ]
},
"controls": [
  {
    "name": "Control1",
    "volumeOfTemplate": 15,
    "concentrationFactor": 15,
    "conversionFactor": 15,

```



```

        "conversionUnit": "lm/kg"
    }
],
"nonTemplateControls": [
    {
        "name": "NonTemplateControl1",
        "volumeOfTemplate": 15,
        "concentrationFactor": 15,
        "conversionFactor": 15,
        "conversionUnit": "lm/kg"
    }
]
},
"wells": [
    {
        "wellPosition": 5,
        "wellRow": "A",
        "column": 1,
        "blank": false,
        "reactionName": "Reaction1",
        "sample": {
            "name": "Control1"
        },
        "controlTypes": [
            {
                "channel": {
                    "excitation": "GREEN",
                    "emission": "GREEN",
                    "thresholdMode": "ST"
                },
                "positive": true
            }
        ]
    }
]
}

```

12.25.3 Responses

Status	Meaning	Description	Schema
200	OK	Returns experiment details list	ExperimentDetailsResponse
400	Bad Request	Missing or invalid requested params	ErrorResponse
401	Unauthorized	Unauthorized	None
403	Forbidden	Access denied	None
405	Method Not Allowed	HTTP method is not supported	None
500	Internal Server Error	Unexpected error	ErrorResponse

12.26 GetEvent

GET /lab-automation/v1/event

To perform this operation, you must be authenticated by means of one of the following methods: Lab Automation API Key Authorization.

Returns the event that occurred as a result of the executed command. Shows the oldest event from the queue. To remove an event from the queue, it must be acknowledged using the DELETE /event endpoint.

12.26.1 Example responses

12.26.1.1 200 Response

```
{
  "id": "21ebe258-ec80-4f73-aa8c-4faa863d8a22",
  "commandId": "21ebe258-ec80-4f73-aa8c-4faa863d8a22",
  "instrumentId": "instrument1234",
  "type": "DRAWER_BOOKED",
  "payloadSchemaVersion": 1,
  "payload": null
}
```

12.26.2 Responses

Status	Meaning	Description	Schema
200	OK	Returns event with its ID, ID of command from which it resulted and event body.	EventResponse
400	Bad Request	Missing or invalid requested params	ErrorResponse

Status	Meaning	Description	Schema
401	Unauthorized	Unauthorized	None
403	Forbidden	Access denied	None
404	Not Found	No items found in event queue	ErrorResponse
405	Method Not Allowed	HTTP method is not supported	None
500	Internal Server Error	Unexpected error	ErrorResponse

12.27 AcknowledgeEvent

DELETE /lab-automation/v1/event

To perform this operation, you must be authenticated by means of one of the following methods: Lab Automation API Key Authorization.

Acknowledge the event, so it can be deleted from the event queue.

12.27.1 Request body properties

Name	In	Type	Required	Description
eventId	query	string(uuid)	true	UUID of an event to be deleted from the queue

12.27.2 Example responses

12.27.2.1 400 Response

```
{
  "message": "string",
  "code": "string",
  "uuid": "095be615-a8ad-4c33-8e9c-c7612fbf6c9f",
  "validationErrors": {
    "property1": [
      {
        "code": "string",
        "arguments": [
          "string"
        ]
      }
    ]
  }
}
```

```

],
"property2": [
  {
    "code": "string",
    "arguments": [
      "string"
    ]
  }
]
}
}
}

```

12.27.3 Responses

Status	Meaning	Description	Schema
200	OK	Event successfully removed from the event queue.	None
400	Bad Request	Missing or invalid requested params	ErrorResponse
401	Unauthorized	Unauthorized	None
403	Forbidden	Access denied	None
405	Method Not Allowed	HTTP method is not supported	None
500	Internal Server Error	Unexpected error	ErrorResponse

13 Endpoint schemas

13.1 AddParametersToExperimentRequest

```

{
  "reactions": [
    {
      "name": "Reaction1",
      "totalReactionVolume": 30.5,
      "targets": [
        {
          "channel": {
            "excitation": "GREEN",
            "emission": "GREEN",
            "thresholdMode": "ST"
          }
        }
      ]
    }
  ]
}

```

```

    },
    "name": "Target1",
    "internalControl": false,
    "dyeId": "1ef3cc8a-8a5e-4709-8101-e8293fd63e2d"
  }
]
},
"sampleControl": {
  "samples": [
    {
      "name": "Sample1",
      "sampleId": 1,
      "volumeOfTemplate": 15,
      "concentrationFactor": 15,
      "conversionFactor": 15,
      "conversionUnit": "lm/kg",
      "description": "Description1",
      "labels": [
        "string"
      ]
    }
  ],
  "controls": [
    {
      "name": "Control1",
      "volumeOfTemplate": 15,
      "concentrationFactor": 15,
      "conversionFactor": 15,
      "conversionUnit": "lm/kg"
    }
  ],
  "nonTemplateControls": [
    {
      "name": "NonTemplateControl1",
      "volumeOfTemplate": 15,
      "concentrationFactor": 15,
      "conversionFactor": 15,
      "conversionUnit": "lm/kg"
    }
  ]
}

```

```

    }
  ]
},
"wells": [
  {
    "wellRow": "A",
    "column": 1,
    "blank": false,
    "reactionName": "Reaction1",
    "sample": {
      "name": "Sample1",
      "sampleId": 1,
      "type": "SAMPLE"
    },
    "controlTypes": [
      {
        "channel": {
          "excitation": "GREEN",
          "emission": "GREEN",
          "thresholdMode": "ST"
        },
        "positive": true
      }
    ]
  }
]
}

```

Name	Type	Required	Restrictions	Description
reactions	[AddParametersToExperimentRequest.Reaction]	false	none	List of defined reaction mixes with assigned targets
sampleControl	AddParametersToExperimentRequest.SampleControl	false	none	Collection of samples, controls and non template controls definitions
wells	[AddParametersToExperimentRequest.Well]	false	none	Collection of well definitions

13.2 AddParametersToExperimentRequest.Reaction

```
{
  "name": "Reaction1",
  "totalReactionVolume": 30.5,
  "targets": [
    {
      "channel": {
        "excitation": "GREEN",
        "emission": "GREEN",
        "thresholdMode": "ST"
      },
      "name": "Target1",
      "internalControl": false,
      "dyeId": "1ef3cc8a-8a5e-4709-8101-e8293fd63e2d"
    }
  ]
}
```

Name	Type	Required	Restrictions	Description
name	string	true	none	Reaction name
totalReactionVolume	number(double)	false	none	Total reaction volume
targets	[AddParametersToExperimentRequest.Reaction.Target]	true	none	List of assigned targets

13.3 AddParametersToExperimentRequest.Reaction.Target

```
{
  "channel": {
    "excitation": "GREEN",
    "emission": "GREEN",
    "thresholdMode": "ST"
  },
  "name": "Target1",
  "internalControl": false,
  "dyeId": "1ef3cc8a-8a5e-4709-8101-e8293fd63e2d"
}
```

Name	Type	Required	Restrictions	Description
channel	ChannelSliceDefinition	true	none	Target channel
name	string	true	none	Target name
internalControl	boolean	false	none	Indication whether target is an internal control
dyeId	string(uuid)	false	none	Assigned dye ID. Available dyes can be listed via the /experiment/dyes endpoint.

13.4 AddParametersToExperimentRequest.SampleControl

```
{
  "samples": [
    {
      "name": "Sample1",
      "sampleId": 1,
      "volumeOfTemplate": 15,
      "concentrationFactor": 15,
      "conversionFactor": 15,
      "conversionUnit": "lm/kg",
      "description": "Description1",
      "labels": [
        "string"
      ]
    }
  ],
  "controls": [
    {
      "name": "Control1",
      "volumeOfTemplate": 15,
      "concentrationFactor": 15,
      "conversionFactor": 15,
      "conversionUnit": "lm/kg"
    }
  ],
  "nonTemplateControls": [
```



```

{
  "name": "NonTemplateControl1",
  "volumeOfTemplate": 15,
  "concentrationFactor": 15,
  "conversionFactor": 15,
  "conversionUnit": "lm/kg"
}
]
}

```

Name	Type	Required	Restrictions	Description
samples	[AddParametersToExperimentRequest.SampleControl.Sample]	false	none	List of sample definitions
controls	[AddParametersToExperimentRequest.SampleControl.Control]	false	none	List of control definitions
nonTemplateControls	[AddParametersToExperimentRequest.SampleControl.NonTemplateControl]	false	none	List of non template control definitions

13.5 AddParametersToExperimentRequest.SampleControl.Control

```

{
  "name": "Control1",
  "volumeOfTemplate": 15,
  "concentrationFactor": 15,
  "conversionFactor": 15,
  "conversionUnit": "lm/kg"
}

```

Name	Type	Required	Restrictions	Description
name	string	true	none	Control name
volumeOfTemplate	number(double)	false	none	Volume of template
concentrationFactor	number(double)	false	none	Concentration factor
conversionFactor	number	false	none	Conversion factor

Name	Type	Required	Restrictions	Description
conversionUnit	string	false	none	Conversion unit

13.6 AddParametersToExperimentRequest.SampleControl.NonTemplateControl

```
{
  "name": "NonTemplateControl1",
  "volumeOfTemplate": 15,
  "concentrationFactor": 15,
  "conversionFactor": 15,
  "conversionUnit": "lm/kg"
}
```

Name	Type	Required	Restrictions	Description
name	string	true	none	Non template control name
volumeOfTemplate	number(double)	false	none	Volume of template
concentrationFactor	number(double)	false	none	Concentration factor
conversionFactor	number	false	none	Conversion factor
conversionUnit	string	false	none	Conversion unit

13.7 AddParametersToExperimentRequest.SampleControl.Sample

```
{
  "name": "Sample1",
  "sampleId": 1,
  "volumeOfTemplate": 15,
  "concentrationFactor": 15,
  "conversionFactor": 15,
  "conversionUnit": "lm/kg",
  "description": "Description1",
  "labels": [
    "string"
  ]
}
```

Name	Type	Required	Restrictions	Description
name	string	true	none	Sample name
sampleId	integer(int32)	false	none	Unique sample id, used for distinction between two samples with same names. Software is using the following algorithm to assign sample IDs:* if sample id is not provided and provided sample names are unique, the software will generate an unique id, starting from 1 and incrementing by 1 for each new sample without an id, omitting ids provided in the request* if sample id is provided, the software will use it as an unique id for the sample
volumeOfTemplate	number(double)	false	none	Volume of template
concentrationFactor	number(double)	false	none	Concentration factor
conversionFactor	number	false	none	Conversion factor
conversionUnit	string	false	none	Conversion unit
description	string	false	none	Sample description
labels	[string]	false	none	List of sample labels

13.8 AddParametersToExperimentRequest.Well

```
{
  "wellRow": "A",
  "column": 1,
  "blank": false,
  "reactionName": "Reaction1",
  "sample": {
    "name": "Sample1",
    "sampleId": 1,
  }
}
```

```

    "type": "SAMPLE"
  },
  "controlTypes": [
    {
      "channel": {
        "excitation": "GREEN",
        "emission": "GREEN",
        "thresholdMode": "ST"
      },
      "positive": true
    }
  ]
}

```

Name	Type	Required	Restrictions	Description
wellRow	string	true	none	Well row
column	integer(int32)	false	none	Well column
blank	boolean	true	none	If a well is blank, it explicitly states that it does not have a reaction mix or sample assigned. This is optional.
reactionName	string	false	none	Assigned reaction name

Name	Type	Required	Restrictions	Description
sample	AddParametersToExperimentRequest.Well.Sample	false	none	Specifies the sample or control type assigned to the well. Depending on the type of the sample, the software looks it up in the <code>sampleControl</code> array provided in the request:* for type <code>SAMPLE</code> , it'll look for <code>sampleControl.samples</code> with the specified name* for type <code>CONTROL</code> , it'll look for <code>sampleControl.controls</code> with the specified name* for type <code>NON_TEMPLATE_CONTROL</code> , it'll look for <code>sampleControl.nonTemplateControls</code> with the specified name
controlTypes	[AddParametersToExperimentRequest.Well.ControlType]	false	none	List of control types. Only needs to be provided if a control is assigned to the well.

13.9 AddParametersToExperimentRequest.Well.ControlType

```

{
  "channel": {
    "excitation": "GREEN",
    "emission": "GREEN",
    "thresholdMode": "ST"
  },
  "positive": true
}

```

Name	Type	Required	Restrictions	Description
channel	ChannelSliceDefinition	true	none	Control type channel
positive	boolean	false	none	Indication whether control type is positive

13.10 AddParametersToExperimentRequest.Well.Sample

```
{
  "name": "Sample1",
  "sampleId": 1,
  "type": "SAMPLE"
}
```

Name	Type	Required	Restrictions	Description
name	string	true	none	Sample, control or non template control name
sampleId	integer(int32)	false	none	Unique sample id, used for distinction between two samples with same names. Needs to be provided if the sample name is not unique within samples defined in plate.
type	string	true	none	Sample type

13.10.0.1 Enumerated Values

Property	Value
type	SAMPLE
type	CONTROL
type	NON_TEMPLATE_CONTROL

13.11 ChannelSliceDefinition

```
{  
  "excitation": "GREEN",  
  "emission": "GREEN",  
  "thresholdMode": "ST"  
}
```

Name	Type	Required	Restrictions	Description
excitation	string	true	none	Excitation filter color
emission	string	true	none	Emission filter color
thresholdMode	string	true	none	Channel threshold mode

13.11.0.1 Enumerated Values

Property	Value
excitation	GREEN
excitation	YELLOW
excitation	ORANGE
excitation	RED
excitation	CRIMSON
excitation	FARRED
emission	GREEN
emission	YELLOW
emission	ORANGE
emission	RED
emission	CRIMSON
emission	FARRED
thresholdMode	ST
thresholdMode	AM_LOW
thresholdMode	AM_HIGH

13.12 ErrorResponse

```
{  
  "message": "string",  
  "code": "string",  
}
```

```

"uuid": "095be615-a8ad-4c33-8e9c-c7612fbf6c9f",
"validationErrors": {
  "property1": [
    {
      "code": "string",
      "arguments": [
        "string"
      ]
    }
  ],
  "property2": [
    {
      "code": "string",
      "arguments": [
        "string"
      ]
    }
  ]
}
}

```

Name	Type	Required	Restrictions	Description
message	string	false	none	none
code	string	false	none	none
uuid	string(uuid)	false	none	none
validationErrors	object	false	none	none
» <dictionary>	[ValidationErrorResponse]	false	none	none

13.13 ValidationErrorResponse

```

{
  "code": "string",
  "arguments": [
    "string"
  ]
}

```


Name	Type	Required	Restrictions	Description
code	string	false	none	none
arguments	[string]	false	none	none

13.14 AddDPCRStepsToExperimentRequest

```
{
  "cyclingDPCRSteps": [
    {
      "index": 3,
      "cycles": [
        {
          "count": 1,
          "position": 0,
          "steps": [
            {
              "temperature": 35,
              "duration": 0,
              "position": 0
            }
          ]
        }
      ]
    }
  ],
  "imagingDPCRSteps": [
    {
      "index": 4,
      "enableHighMultiplexingReferenceChannel": true,
      "imagingProfiles": [
        {
          "channel": {
            "excitation": "GREEN",
            "emission": "GREEN"
          },
          "durationOfExposure": 1,
          "gain": 40
        }
      ]
    }
  ]
}
```

```

    ]
  }
]
}

```

Name	Type	Required	Restrictions	Description
cyclingDPCRSteps	[AddDPCRStepsToExperimentRequest.Cycling]	false	none	List of defined cycling steps
imagingDPCRSteps	[AddDPCRStepsToExperimentRequest.Imaging]	true	none	List of defined cycling steps

13.15 AddDPCRStepsToExperimentRequest.Cycling

```

{
  "index": 3,
  "cycles": [
    {
      "count": 1,
      "position": 0,
      "steps": [
        {
          "temperature": 35,
          "duration": 0,
          "position": 0
        }
      ]
    }
  ]
}

```

Name	Type	Required	Restrictions	Description
index	integer(int32)	false	none	Cycling step index
cycles	[AddDPCRStepsToExperimentRequest.Cycling.Cycle]	false	none	Defined cycles

13.16 AddDPCRStepsToExperimentRequest.Cycling.Cycle

```
{
  "count": 1,
  "position": 0,
  "steps": [
    {
      "temperature": 35,
      "duration": 0,
      "position": 0
    }
  ]
}
```

Name	Type	Required	Restrictions	Description
count	integer(int32)	false	none	Number of cycles
position	integer(int32)	true	none	Cycle position in order
steps	[AddDPCRStepsToExperimentRequest.Cycling.Cycle.CycleStep]	false	none	List of steps within the cycle

13.17 AddDPCRStepsToExperimentRequest.Cycling.Cycle.CycleStep

```
{
  "temperature": 35,
  "duration": 0,
  "position": 0
}
```

Name	Type	Required	Restrictions	Description
temperature	number(double)	true	none	Step temperature
duration	integer(int32)	true	none	Step duration in seconds

Name	Type	Required	Restrictions	Description
position	integer(int32)	true	none	Step position. For all cycle steps within a cycle, each cycle step must have a unique position from 1 to N (where N is the number of cycle steps in the cycle).

13.18 AddDPCRStepsToExperimentRequest.Imaging

```
{
  "index": 4,
  "enableHighMultiplexingReferenceChannel": true,
  "imagingProfiles": [
    {
      "channel": {
        "excitation": "GREEN",
        "emission": "GREEN"
      },
      "durationOfExposure": 1,
      "gain": 40
    }
  ]
}
```

Name	Type	Required	Restrictions	Description
index	integer(int32)	false	none	Imaging step index
enableHighMultiplexingReferenceChannel	boolean	true	none	Enabling High-Multiplexing Reference channel will make additional channels and amplitude multiplexing “mode” available. Please note that this will require usage of the QIAcuity High Multiplex Kit.

Name	Type	Required	Restrictions	Description
imagingProfiles	[AddDPCRStepsToExperimentRequest.Imaging.ImagingProfile]	false	none	Imaging profiles

13.19 AddDPCRStepsToExperimentRequest.Imaging.ImagingProfile

```
{
  "channel": {
    "excitation": "GREEN",
    "emission": "GREEN"
  },
  "durationOfExposure": 1,
  "gain": 40
}
```

Name	Type	Required	Restrictions	Description
channel	ChannelDefinition	true	none	Channel name
durationOfExposure	integer(int64)	false	none	Duration of exposure value
gain	integer(int32)	false	none	Gain value

13.20 ChannelDefinition

```
{
  "excitation": "GREEN",
  "emission": "GREEN"
}
```

Name	Type	Required	Restrictions	Description
excitation	string	true	none	Excitation filter color
emission	string	true	none	Emission filter color

13.20.0.1 Enumerated Values

Property	Value
excitation	GREEN
excitation	YELLOW
excitation	ORANGE
excitation	RED
excitation	CRIMSON
excitation	FARRED
emission	GREEN
emission	YELLOW
emission	ORANGE
emission	RED
emission	CRIMSON
emission	FARRED

13.21 AssignAnalysisTemplateV2Request

```
{
  "reactionMixAutomationRules": {
    "ReactionMix A": {
      "thresholdingMethods": [
        {
          "channel": {
            "excitation": "GREEN",
            "emission": "GREEN"
          },
          "amplitudeMultiplexing": false,
          "thresholdingPropagationConfig": {
            "type": "WITH_PROPAGATION",
            "thresholdingConfig": {
              "type": "POSITIVE_CONTROL",
              "thresholdingMethod": {
                "type": "AUTO_WITH_OFFSET",
                "offset": 5
              }
            }
          }
        }
      ]
    }
  }
}
```

```

},
"ReactionMix B": {
  "thresholdingMethods": [
    {
      "channel": {
        "excitation": "YELLOW",
        "emission": "YELLOW"
      },
      "amplitudeMultiplexing": false,
      "thresholdingPropagationConfig": {
        "type": "WITH_PROPAGATION",
        "thresholdingConfig": {
          "type": "POSITIVE_CONTROL",
          "thresholdingMethod": {
            "type": "AUTO_WITH_OFFSET",
            "offset": 4
          }
        }
      }
    }
  ],
  "qualityControlValidationRules": {
    "strategy": "INVALIDATE_WELL",
    "perChannel": [
      {
        "channel": {
          "excitation": "GREEN",
          "emission": "GREEN"
        },
        "samples": {
          "minimumValidPartitionsPercentage": 30
        },
        "controls": {
          "minimumValidPartitionsPercentage": 50,
          "negativeControlMaxPartitions": 6400,
          "positiveControlExpectedConcentration": {
            "min": 5,
            "max": 5000
          }
        }
      }
    ]
  }
}

```

```

    }
  },
  {
    "channel": {
      "excitation": "YELLOW",
      "emission": "YELLOW"
    },
    "samples": {
      "minimumValidPartitionsPercentage": 40
    },
    "controls": {
      "minimumValidPartitionsPercentage": 60,
      "negativeControlMaxPartitions": 3500
    }
  }
]
}
}
}
}
}

```

Name	Type	Required	Restrictions	Description
reactionMixAutomation-Rules	object	true	none	A dictionary with keys representing names of reaction mixes and values representing analysis rules for these reaction mixes
» <dictionary>	AssignAnalysisTemplateV2Request.Reaction-MixAnalysisRules	false	none	Contains a list of rules for automated analysis

13.22 AssignAnalysisTemplateV2Request.ControlQualityControlRules

```

{
  "minimumValidPartitionsPercentage": 50,
  "negativeControlMaxPartitions": 1,
  "positiveControlExpectedConcentration": {

```



```

    "min": 0.5,
    "max": 0.5
  }
}

```

Quality control rules for control

Name	Type	Required	Restrictions	Description
minimumValidPartitionsPercentage	integer(int32)	false	none	Minimum valid partitions percentage
negativeControlMaxPartitions	integer(int32)	false	none	none
positiveControlExpectedConcentration	PositiveControlExpectedConcentration	false	none	none

13.23 AssignAnalysisTemplateV2Request.QualityControlValidationRules

```

{
  "strategy": "INVALIDATE_WELL",
  "perChannel": [
    {
      "channel": {
        "excitation": "GREEN",
        "emission": "GREEN"
      },
      "samples": {
        "minimumValidPartitionsPercentage": 30
      },
      "controls": {
        "minimumValidPartitionsPercentage": 50,
        "negativeControlMaxPartitions": 1,
        "positiveControlExpectedConcentration": {
          "min": 0.5,
          "max": 0.5
        }
      }
    }
  ]
}

```

```
}
```

Validation rules for specific Reaction Mix

Name	Type	Required	Restrictions	Description
strategy	string	true	none	Quality control validation strategy
perChannel	[AssignAnalysisTemplateV2Request.QualityControlValidationRulesPerChannel]	false	none	[Quality control validation rules per channel]

13.23.0.1 Enumerated Values

Property	Value
strategy	WARNING_CHANNEL
strategy	WARNING_WELL
strategy	INVALIDATE_CHANNEL
strategy	INVALIDATE_WELL

13.24 AssignAnalysisTemplateV2Request.QualityControlValidationRulesPerChannel

```
{
  "channel": {
    "excitation": "GREEN",
    "emission": "GREEN"
  },
  "samples": {
    "minimumValidPartitionsPercentage": 30
  },
  "controls": {
    "minimumValidPartitionsPercentage": 50,
    "negativeControlMaxPartitions": 1,
    "positiveControlExpectedConcentration": {
      "min": 0.5,
      "max": 0.5
    }
  }
}
```

```

    }
  }
}

```

Quality control validation rules per channel

Name	Type	Required	Restrictions	Description
channel	ChannelDefinition	true	none	none
samples	AssignAnalysisTemplateV2Request.SampleQualityControlRules	false	none	Quality control rules for sample
controls	AssignAnalysisTemplateV2Request.ControlQualityControlRules	false	none	Quality control rules for control

13.25 AssignAnalysisTemplateV2Request.ReactionMixAnalysisRules

```

{
  "thresholdingMethods": [
    {
      "channel": {
        "excitation": "GREEN",
        "emission": "GREEN"
      },
      "amplitudeMultiplexing": true,
      "thresholdingPropagationConfig": {
        "type": "WITH_PROPAGATION",
        "thresholdingConfig": {
          "type": "NEGATIVE_CONTROL",
          "thresholdingMethod": {
            "type": "AUTO_THRESHOLD"
          }
        }
      }
    }
  ],
  "qualityControlValidationRules": {
    "strategy": "INVALIDATE_WELL",
    "perChannel": [

```

```

{
  "channel": {
    "excitation": "GREEN",
    "emission": "GREEN"
  },
  "samples": {
    "minimumValidPartitionsPercentage": 30
  },
  "controls": {
    "minimumValidPartitionsPercentage": 50,
    "negativeControlMaxPartitions": 1,
    "positiveControlExpectedConcentration": {
      "min": 0.5,
      "max": 0.5
    }
  }
}
]
}
}

```

Contains a list of rules for automated analysis

Name	Type	Required	Restrictions	Description
thresholdingMethods	[AssignAnalysisTemplateV2Request.ThresholdingMethodPerChannel]	true	none	[Thresholding method configuration per channel]
qualityControlValidationRules	AssignAnalysisTemplateV2Request.QualityControlValidationRules	false	none	Validation rules for specific Reaction Mix

13.26 AssignAnalysisTemplateV2Request.SampleQualityControlRules

```

{
  "minimumValidPartitionsPercentage": 30
}

```

Quality control rules for sample

Name	Type	Required	Restrictions	Description
minimumValidPartitionsPercentage	integer(int32)	false	none	Minimum valid partitions percentage

13.27 AssignAnalysisTemplateV2Request.ThresholdingConfig.NegativeControl

```
{
  "type": "NEGATIVE_CONTROL",
  "thresholdingMethod": {
    "type": "AUTO_THRESHOLD"
  }
}
```

Name	Type	Required	Restrictions	Description
type	string	false	write-only	none
thresholdingMethod	any	true	none	none

oneOf

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingMethod.Auto	false	none	none

xor

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingMethod.AutoWithOffset	false	none	none

xor

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingMethod.Dba	false	none	none

xor

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingMethod.Dmm	false	none	none

xor

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingMethod.Nct	false	none	none

xor

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingMethod.Numeric	false	none	none

xor

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingMethod.NumericAmplitudeMultiplexing	false	none	none

xor

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingMethod.Pct	false	none	none

13.28 AssignAnalysisTemplateV2Request.ThresholdingConfig.NonTemplateControl

```
{
  "type": "NON_TEMPLATE_CONTROL",
  "thresholdingMethod": {
    "type": "AUTO_THRESHOLD"
  }
}
```

Name	Type	Required	Restrictions	Description
type	string	false	write-only	none
thresholdingMethod	any	true	none	none

oneOf

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingMethod.Auto	false	none	none

xor

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingMethod.AutoWithOffset	false	none	none

xor

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingMethod.Dba	false	none	none

xor

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingMethod.Dmm	false	none	none

xor

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingMethod.Nct	false	none	none

xor

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingMethod.Numeric	false	none	none

xor

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingMethod.NumericAmplitudeMultiplexing	false	none	none

xor

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingMethod.Pct	false	none	none

13.29 AssignAnalysisTemplateV2Request.ThresholdingConfig.PositiveControl

```
{
  "type": "POSITIVE_CONTROL",
  "thresholdingMethod": {
    "type": "AUTO_THRESHOLD"
  }
}
```

Name	Type	Required	Restrictions	Description
type	string	false	write-only	none
thresholdingMethod	any	true	none	none

oneOf

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingMethod.Auto	false	none	none

xor

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingMethod.AutoWithOffset	false	none	none

xor

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingMethod.Dba	false	none	none

xor

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingMethod.Dmm	false	none	none

xor

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingMethod.Nct	false	none	none

xor

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingMethod.Numeric	false	none	none

xor

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingMethod.NumericAmplitudeMultiplexing	false	none	none

xor

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingMethod.Pct	false	none	none

13.30 AssignAnalysisTemplateV2Request.ThresholdingConfig.UnknownSamples

```
{
  "type": "UNKNOWN_SAMPLES",
  "thresholdingMethod": {
    "type": "AUTO_THRESHOLD"
```

```

    }
}

```

Name	Type	Required	Restrictions	Description
type	string	false	write-only	none
thresholdingMethod	any	true	none	none

oneOf

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingMethod.Auto	false	none	none

xor

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingMethod.AutoWithOffset	false	none	none

xor

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingMethod.Dba	false	none	none

xor

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingMethod.Dmm	false	none	none

xor

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingMethod.Nct	false	none	none

xor

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingMethod.Numeric	false	none	none

xor

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingMethod.NumericAmplitudeMultiplexing	false	none	none

xor

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingMethod.Pct	false	none	none

13.31 AssignAnalysisTemplateV2Request.ThresholdingMethod

```
{
  "type": "string"
}
```

Thresholding method specification

Name	Type	Required	Restrictions	Description
type	string	true	none	none

13.32 AssignAnalysisTemplateV2Request.ThresholdingMethod.Auto

```
{
  "type": "AUTO_THRESHOLD"
}
```

allOf - discriminator: AssignAnalysisTemplateV2Request.ThresholdingMethod.type

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingMethod	false	none	Thresholding method specification

and

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	object	false	none	none
» type	string	false	write-only	none

13.33 AssignAnalysisTemplateV2Request.ThresholdingMethod.AutoWithOffset

```
{  
  "type": "AUTO_WITH_OFFSET",  
  "offset": -255  
}
```

allOf - discriminator: AssignAnalysisTemplateV2Request.ThresholdingMethod.type

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingMethod	false	none	Thresholding method specification

and

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	object	false	none	none
» type	string	false	write-only	none
» offset	number(double)	false	none	none

13.34 AssignAnalysisTemplateV2Request.ThresholdingMethod.Dba

```
{  
  "type": "DBA",  
  "fallbackAvgNegativeBand": 255,  
  "fallbackAvgPositiveBand": 255,  
  "ratio": 100  
}
```

allOf - discriminator: AssignAnalysisTemplateV2Request.ThresholdingMethod.type

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingMethod	false	none	Thresholding method specification

and

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	object	false	none	none
» type	string	false	write-only	none
» fallbackAvgNegativeBand	number(double)	false	none	none
» fallbackAvgPositiveBand	number(double)	false	none	none
» ratio	number(double)	false	none	none

13.35 AssignAnalysisTemplateV2Request.ThresholdingMethod.Dmm

```
{  
  "type": "DMM",  
  "fallbackMin": 255,  
  "fallbackMax": 255,  
  "ratio": 100  
}
```

allOf - discriminator: AssignAnalysisTemplateV2Request.ThresholdingMethod.type

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingMethod	false	none	Thresholding method specification

and

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	object	false	none	none
» type	string	false	write-only	none
» fallbackMin	number(double)	false	none	none
» fallbackMax	number(double)	false	none	none
» ratio	number(double)	false	none	none

13.36 AssignAnalysisTemplateV2Request.ThresholdingMethod.Nct

```
{  
  "type": "NCT",  
  "offset": -255  
}
```

allOf - discriminator: AssignAnalysisTemplateV2Request.ThresholdingMethod.type

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingMethod	false	none	Thresholding method specification

and

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	object	false	none	none
» type	string	false	write-only	none
» offset	number(double)	false	none	none

13.37 AssignAnalysisTemplateV2Request.ThresholdingMethod.Numeric

```
{  
  "type": "NUMERIC",  
  "threshold": 255  
}
```

allOf - discriminator: AssignAnalysisTemplateV2Request.ThresholdingMethod.type

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingMethod	false	none	Thresholding method specification

and

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	object	false	none	none
» type	string	false	write-only	none
» threshold	number(double)	false	none	none

13.38 AssignAnalysisTemplateV2Request.ThresholdingMethod.NumericAmplitudeMultiplexing

```
{
  "type": "NUMERIC_AMPLITUDE_MULTIPLEXING",
  "lowThreshold": 255,
  "highThreshold": 255,
  "doublePositiveThreshold": 255
}
```

allOf - discriminator: AssignAnalysisTemplateV2Request.ThresholdingMethod.type

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingMethod	false	none	Thresholding method specification

and

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	object	false	none	none
» type	string	false	write-only	none
» lowThreshold	number(double)	false	none	none
» highThreshold	number(double)	false	none	none
» doublePositiveThreshold	number(double)	false	none	none

13.39 AssignAnalysisTemplateV2Request.ThresholdingMethod.Pct

```
{
  "type": "PCT",
  "offset": -255
}
```

allOf - discriminator: AssignAnalysisTemplateV2Request.ThresholdingMethod.type

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingMethod	false	none	Thresholding method specification

and

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	object	false	none	none
» type	string	false	write-only	none
» offset	number(double)	false	none	none

13.40 AssignAnalysisTemplateV2Request.ThresholdingMethodPerChannel

```
{
  "channel": {
    "excitation": "GREEN",
    "emission": "GREEN"
  },
  "amplitudeMultiplexing": true,
  "thresholdingPropagationConfig": {
    "type": "WITH_PROPAGATION",
    "thresholdingConfig": {
      "type": "NEGATIVE_CONTROL",
      "thresholdingMethod": {
        "type": "AUTO_THRESHOLD"
      }
    }
  }
}
```

Thresholding method configuration per channel

Name	Type	Required	Restrictions	Description
channel	ChannelDefinition	true	none	none
amplitudeMultiplexing	boolean	false	none	Indicates whether amplitude multiplexing is enabled for this channel
thresholdingPropagationConfig	any	true	none	none

oneOf

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingPropagationConfig.WithPropagation	false	none	none

xor

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingPropagationConfig.WithoutPropagation	false	none	none

13.41 AssignAnalysisTemplateV2Request.ThresholdingPropagationConfig

```
{
  "type": "string"
}
```

Thresholding propagation configuration

Name	Type	Required	Restrictions	Description
type	string	true	none	none

13.42 AssignAnalysisTemplateV2Request.ThresholdingPropagationConfig.WithPropagation

```
{
  "type": "WITH_PROPAGATION",
  "thresholdingConfig": {
    "type": "NEGATIVE_CONTROL",
    "thresholdingMethod": {
      "type": "AUTO_THRESHOLD"
    }
  }
}
```

allOf - discriminator: AssignAnalysisTemplateV2Request.ThresholdingPropagationConfig.type

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingPropagationConfig	false	none	Thresholding propagation configuration

and

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	object	false	none	none
» type	string	false	write-only	none
» thresholdingConfig	any	false	none	none

oneOf

Name	Type	Required	Restrictions	Description
»» <i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingConfig.NegativeControl	false	none	none

xor

Name	Type	Required	Restrictions	Description
»» <i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingConfig.NonTemplateControl	false	none	none

xor

Name	Type	Required	Restrictions	Description
»» <i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingConfig.PositiveControl	false	none	none

13.43 AssignAnalysisTemplateV2Request.ThresholdingPropagationConfig.WithoutPropagation

```
{
  "type": "WITHOUT_PROPAGATION",
  "thresholdingConfigForSample": {
    "type": "UNKNOWN_SAMPLES",
    "thresholdingMethod": {
      "type": "AUTO_THRESHOLD"
    }
  },
  "thresholdingConfigForPositiveControl": {
    "type": "POSITIVE_CONTROL",
    "thresholdingMethod": {
      "type": "AUTO_THRESHOLD"
    }
  },
  "thresholdingConfigForNegativeControl": {
    "type": "NEGATIVE_CONTROL",
    "thresholdingMethod": {
      "type": "AUTO_THRESHOLD"
    }
  }
},
```

```

"thresholdingConfigForNtc": {
  "type": "NON_TEMPLATE_CONTROL",
  "thresholdingMethod": {
    "type": "AUTO_THRESHOLD"
  }
}
}
}

```

allOf - discriminator: AssignAnalysisTemplateV2Request.ThresholdingPropagationConfig.type

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	AssignAnalysisTemplateV2Request.ThresholdingPropagationConfig	false	none	Thresholding propagation configuration

and

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	object	false	none	none
» type	string	false	write-only	none
» thresholdingConfigForSample	AssignAnalysisTemplateV2Request.ThresholdingConfig.UnknownSamples	false	none	none
» thresholdingConfigForPositiveControl	AssignAnalysisTemplateV2Request.ThresholdingConfig.PositiveControl	false	none	none
» thresholdingConfigForNegativeControl	AssignAnalysisTemplateV2Request.ThresholdingConfig.NegativeControl	false	none	none
» thresholdingConfigForNtc	AssignAnalysisTemplateV2Request.ThresholdingConfig.NonTemplateControl	false	none	none

13.44 PositiveControlExpectedConcentration

```
{
  "min": 0.5,
  "max": 0.5
}
```

Name	Type	Required	Restrictions	Description
min	number(double)	false	none	none
max	number(double)	false	none	none

13.45 RfuRequest

```
{
  "dpcrRunStepIndex": 2,
  "wellPositions": [
    1,
    2,
    4
  ],
  "channels": [
    {
      "excitation": "GREEN",
      "emission": "GREEN"
    }
  ],
  "sortType": "VERTICAL"
}
```

Name	Type	Required	Restrictions	Description
dpcrRunStepIndex	integer(int32)	true	none	DPCR run step index
wellPositions	[integer]	false	none	Selected wells
channels	[ChannelDefinition]	true	none	Selected channels
sortType	string	false	none	Vertical or Horizontal result sorting

13.45.0.1 Enumerated Values

Property	Value
sortType	VERTICAL
sortType	HORIZONTAL

13.46 MultipleOccupancyForChannelRequest

```
{
  "dpcrRunStepIndex": 2,
  "wellPositions": [
    1,
    2,
    4
  ],
  "channels": [
    {
      "excitation": "GREEN",
      "emission": "GREEN"
    }
  ],
  "sortType": "VERTICAL",
  "showMeanValuesForReplicates": true,
  "positivesChannels": [
    0
  ]
}
```

Name	Type	Required	Restrictions	Description
dpcrRunStepIndex	integer(int32)	true	none	DPCR run step index
wellPositions	[integer]	false	none	Selected wells
channels	[ChannelDefinition]	true	none	Selected channels
sortType	string	false	none	Vertical or Horizontal result sorting
showMeanValuesForReplicates	boolean	false	none	Was option show Mean Values for Replicates was checked
positivesChannels	[integer]	false	none	Presentation of positive channels

13.46.0.1 Enumerated Values

Property	Value
sortType	VERTICAL
sortType	HORIZONTAL

13.47 StreamingResponseBody

null

None

13.48 DefineExperimentRequest

```
{
  "barcode": "00031234567891113151719212",
  "plateName": "example_plate_name",
  "plateTypeId": "67e02b72-768c-4bde-a4ec-d4c70c1c777a",
  "dpcrRunSteps": {
    "primingDPCRStep": {
      "velocityProfile": "0282a51b-422f-491a-8e66-cebc06cb8990"
    },
    "cyclingDPCRSteps": [
      {
        "index": 1,
        "cycles": [
          {
            "count": 1,
            "position": 0,
            "steps": [
              {
                "temperature": 40,
                "duration": 180,
                "position": 0
              }
            ]
          }
        ]
      }
    ]
  }
}
```

```

],
"imagingDPCRSteps": [
  {
    "index": 2,
    "enableHighMultiplexingReferenceChannel": true,
    "imagingProfiles": [
      {
        "channel": {
          "excitation": "GREEN",
          "emission": "GREEN"
        },
        "durationOfExposure": 1,
        "gain": 40
      }
    ]
  }
]
},
"owners": [
  "admin",
  "carl"
]
}

```

Name	Type	Required	Restrictions	Description
barcode	string	false	none	Plate barcode. Used to make a sanity check if the plate in the slot is the one that is defined.
plateName	string	true	none	Optional Plate name
plateTypeId	string(uuid)	true	none	Plate type ID. Available plate types can be listed via the /experiment/plate-types endpoint.
dpcrRunSteps	DefineExperimentRequest.DPCRRunSteps	true	none	dPCR run steps including Priming, Cycling or Imaging.

Name	Type	Required	Restrictions	Description
owners	[string]	true	none	Username of plate owners. The owners must exist in the current system.

13.49 DefineExperimentRequest.DPCRRunSteps

```
{
  "primingDPCRStep": {
    "velocityProfile": "0282a51b-422f-491a-8e66-cebc06cb8990"
  },
  "cyclingDPCRSteps": [
    {
      "index": 1,
      "cycles": [
        {
          "count": 1,
          "position": 0,
          "steps": [
            {
              "temperature": 40,
              "duration": 180,
              "position": 0
            }
          ]
        }
      ]
    }
  ],
  "imagingDPCRSteps": [
    {
      "index": 2,
      "enableHighMultiplexingReferenceChannel": true,
      "imagingProfiles": [
        {
          "channel": {
            "excitation": "GREEN",
```

```

        "emission": "GREEN"
    },
    "durationOfExposure": 1,
    "gain": 40
}
]
}
]
}

```

Name	Type	Required	Restrictions	Description
primingDPCRStep	DefineExperimentRequest.DPCRRunSteps.Priming	true	none	Priming step definition
cyclingDPCRSteps	[DefineExperimentRequest.DPCRRunSteps.Cycling]	true	none	List of defined cycling steps
imagingDPCRSteps	[DefineExperimentRequest.DPCRRunSteps.Imaging]	true	none	List of defined cycling steps

13.50 DefineExperimentRequest.DPCRRunSteps.Cycling

```

{
  "index": 1,
  "cycles": [
    {
      "count": 1,
      "position": 0,
      "steps": [
        {
          "temperature": 40,
          "duration": 180,
          "position": 0
        }
      ]
    }
  ]
}
]

```

```
}
```

Name	Type	Required	Restrictions	Description
index	integer(int32)	false	none	Cycling step index
cycles	[DefineExperimentRequest.DPCRRunSteps.Cycling.Cycle]	false	none	Defined cycles

13.51 DefineExperimentRequest.DPCRRunSteps.Cycling.Cycle

```
{  
  "count": 1,  
  "position": 0,  
  "steps": [  
    {  
      "temperature": 40,  
      "duration": 180,  
      "position": 0  
    }  
  ]  
}
```

Name	Type	Required	Restrictions	Description
count	integer(int32)	false	none	Number of cycles
position	integer(int32)	true	none	Cycle position in order
steps	[DefineExperimentRequest.DPCRRunSteps.Cycling.Cycle.CycleStep]	false	none	List of steps within the cycle

13.52 DefineExperimentRequest.DPCRRunSteps.Cycling.Cycle.CycleStep

```
{  
  "temperature": 40,  
  "duration": 180,  
  "position": 0  
}
```

Name	Type	Required	Restrictions	Description
temperature	number(double)	false	none	Step temperature
duration	integer(int32)	true	none	Step duration in seconds
position	integer(int32)	true	none	Step position in order

13.53 DefineExperimentRequest.DPCRRunSteps.Imaging

```
{
  "index": 2,
  "enableHighMultiplexingReferenceChannel": true,
  "imagingProfiles": [
    {
      "channel": {
        "excitation": "GREEN",
        "emission": "GREEN"
      },
      "durationOfExposure": 1,
      "gain": 40
    }
  ]
}
```

Name	Type	Required	Restrictions	Description
index	integer(int32)	false	none	Imaging step index
enableHighMultiplexingReferenceChannel	boolean	true	none	Enabling High-Multiplexing Reference channel will make additional channels and amplitude multiplexing “mode” available. Please note that this will require usage of the QIAcuity High Multiplex Kit.

Name	Type	Required	Restrictions	Description
imagingProfiles	[DefineExperimentRequest.DPCRRunSteps.Imaging.ImagingProfile]	false	none	Imaging profiles

13.54 DefineExperimentRequest.DPCRRunSteps.Imaging.ImagingProfile

```
{
  "channel": {
    "excitation": "GREEN",
    "emission": "GREEN"
  },
  "durationOfExposure": 1,
  "gain": 40
}
```

Name	Type	Required	Restrictions	Description
channel	ChannelDefinition	true	none	Channel name
durationOfExposure	integer(int64)	false	none	Duration of exposure value
gain	integer(int32)	false	none	Gain value

13.55 DefineExperimentRequest.DPCRRunSteps.Priming

```
{
  "velocityProfile": "0282a51b-422f-491a-8e66-cebc06cb8990"
}
```


Name	Type	Required	Restrictions	Description
velocityProfile	string(uuid)	true	none	ID of velocity profile used in priming. Available velocity profiles for a particular plate type can be listed via the /experiment/velocity-profiles endpoint.

13.56 DefineExperimentFromTemplateRequest

```
{
  "barcode": "00031234567891113151719212",
  "plateName": "example_plate_name",
  "templateName": "example_template_name",
  "owners": [
    "admin",
    "carl"
  ]
}
```

Name	Type	Required	Restrictions	Description
barcode	string	false	none	Plate barcode. Used to make a sanity check if the plate in the slot is the one that is defined. Optional
plateName	string	false	none	Plate name. Needs to be provided if given template does not specify plate's name. Optional
templateName	string	true	none	Name of the template which will be used to create a plate

Name	Type	Required	Restrictions	Description
owners	[string]	false	none	List of plate owners existing in the current system

13.57 RunExperimentRequest

```
{
  "instrumentId": "instrument123",
  "plateId": "21ebe258-ec80-4f73-aa8c-4faa863d8a22",
  "drawerName": "Drawer1",
  "slotId": 2
}
```

Name	Type	Required	Restrictions	Description
instrumentId	string	true	none	ID of the instrument on which the command is to be executed.
plateId	string(uuid)	true	none	ID of the plate which should be run by the instrument
drawerName	string	false	none	Name of the drawer in which the requested plate is placed
slotId	integer(int32)	false	none	ID of the slot within the drawer in which the requested plate is placed

13.58 ReleaseDrawerBookingRequest

```
{
  "instrumentId": "instrument123",
  "drawerName": "Drawer1"
}
```

Name	Type	Required	Restrictions	Description
instrumentId	string	true	none	ID of the instrument on which the command is to be executed.
drawerName	string	true	none	Name of drawer to be released from exclusive robot use

13.59 OpenDrawerRequest

```
{
  "instrumentId": "instrument123",
  "drawerName": "Drawer1"
}
```

Name	Type	Required	Restrictions	Description
instrumentId	string	true	none	ID of the instrument on which the command is to be executed.
drawerName	string	true	none	Name of the drawer to be opened

13.60 CloseDrawerRequest

```
{
  "instrumentId": "instrument123",
  "drawerName": "Drawer1"
}
```

Name	Type	Required	Restrictions	Description
instrumentId	string	true	none	ID of the instrument on which the command is to be executed.
drawerName	string	true	none	Name of the drawer to be opened

13.61 BookDrawerRequest

```
{  
  "instrumentId": "instrument123",  
  "drawerName": "Drawer1"  
}
```

Name	Type	Required	Restrictions	Description
instrumentId	string	true	none	ID of the instrument on which the command is to be executed.
drawerName	string	true	none	Name of drawer to be booked for exclusive robot use

13.62 AbsoluteQuantificationResult.ConcentrationPerChannelWithMean.QualityControlValidationResults.ConcentrationRangeForPositiveControl

```
{  
  "settings": {  
    "minimumConcentration": 75,  
    "maximumConcentration": 15000  
  },  
  "passed": true  
}
```

allOf - discriminator: AbsoluteQuantificationResultV2.ConcentrationPerChannelWithMean.QualityControlValidationResults.type

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	AbsoluteQuantificationResultV2.ConcentrationPerChannelWithMean.QualityControlValidationResults	false	none	none

and

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	object	false	none	none
» settings	Settings	false	none	Settings for the validation rule
» passed	boolean	false	none	Indicates if the validation rule passed

13.63 AbsoluteQuantificationResult.ConcentrationPerChannelWithMean.QualityControlValidationResults.MaximumPositivePartitionsNumberForNegativeControl

```
{
  "settings": {
    "minimumConcentration": 75,
    "maximumConcentration": 15000
  },
  "passed": true
}
```

allOf - discriminator: AbsoluteQuantificationResultV2.ConcentrationPerChannelWithMean.QualityControlValidationResults.type

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	AbsoluteQuantification- ResultV2.Concentra- tionPerChannelWith- Mean.QualityControlVali- dationResults	false	none	none

and

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	object	false	none	none
» settings	Settings	false	none	Settings for the validation rule
» passed	boolean	false	none	Indicates if the validation rule passed

13.64 AbsoluteQuantificationResult.ConcentrationPerChannelWithMean.QualityControlValidationResults.MinimumValidPartitionsForControl

```
{
  "settings": {
    "minimumConcentration": 75,
    "maximumConcentration": 15000
  },
  "passed": true
}
```

allOf - discriminator: AbsoluteQuantificationResultV2.ConcentrationPerChannelWithMean.QualityControlValidationResults.type

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	AbsoluteQuantification- ResultV2.Concentra- tionPerChannelWith- Mean.QualityControlVali- dationResults	false	none	none

and

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	object	false	none	none
» settings	Settings	false	none	Settings for the validation rule
» passed	boolean	false	none	Indicates if the validation rule passed

13.65 AbsoluteQuantificationResult.ConcentrationPerChannelWithMean.QualityControlValidationResults.MinimumValidPartitionsForSample

```
{
  "settings": {
    "minimumConcentration": 75,
    "maximumConcentration": 15000
  },
  "passed": true
}
```

allOf - discriminator: AbsoluteQuantificationResultV2.ConcentrationPerChannelWithMean.QualityControlValidationResults.type

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	AbsoluteQuantification- ResultV2.Concentra- tionPerChannelWith- Mean.QualityControlVali- dationResults	false	none	none

and

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	object	false	none	none
» settings	Settings	false	none	Settings for the validation rule
» passed	boolean	false	none	Indicates if the validation rule passed

13.66 AbsoluteQuantificationResultV2

```
{
  "wellDetails": {
    "wellPosition": 5,
    "rowLetter": "A",
    "columnNumber": 1,
    "replicateWellPositions": [
      5,
      8
    ],
    "cycledVolume": 2.57
  },
  "sample": {
    "name": "S1",
    "uniqueId": 1,
    "volumeOfTemplate": 2,
    "concentrationFactor": 20,
    "type": "SAMPLE",
    "conversionFactor": 10.999999999,
```

```

    "conversionUnit": "cp/ml"
  },
  "reaction": {
    "name": "corona_g",
    "totalReactionVolume": 2
  },
  "concentrations": [
    {
      "channel": {
        "excitation": "GREEN",
        "emission": "GREEN",
        "thresholdMode": "ST"
      },
      "target": {
        "id": "95f6cb04-fc4d-4c03-bd22-30ef11300e8c",
        "name": "COVID-19_G2",
        "controlType": "NONE",
        "isInternalControl": false
      },
      "concentration": {
        "value": 10.484819643300222,
        "concentrationOfOriginalSample": 10.484819643300222,
        "concentrationWithCustomUnitOfDpcrReaction": 0,
        "concentrationWithCustomUnitOfUndilutedSample": 0,
        "dilutedCi": 0,
        "undilutedCi": 0,
        "dilutedConvCi": 0,
        "undilutedConvCi": 0,
        "errorCode": "SATURATION_ERROR",
        "lambda": 5.9643300222
      },
      "validsCount": {
        "count": 24000,
        "qualityControlRuleResult": {
          "settings": {
            "minimumConcentration": 75,
            "maximumConcentration": 15000
          },
          "passed": true
        }
      }
    }
  ]
}

```



```

    }
  },
  "positivesCount": {
    "count": 24000,
    "qualityControlRuleResult": {
      "settings": {
        "minimumConcentration": 75,
        "maximumConcentration": 15000
      },
      "passed": true
    }
  },
  "negativesCount": 23703,
  "ci": 1.4353845944578065,
  "relativeCi": 0.1369012194096266,
  "meanConcentration": {
    "value": 10.484819643300222,
    "concentrationOfOriginalSample": 10.484819643300222,
    "concentrationWithCustomUnitOfDpcrReaction": 0,
    "concentrationWithCustomUnitOfUndilutedSample": 0,
    "dilutedCi": 0,
    "undilutedCi": 0,
    "dilutedConvCi": 0,
    "undilutedConvCi": 0,
    "errorCode": "SATURATION_ERROR",
    "lambda": 5.9643300222
  },
  "meanRelativeCi": 0.03922849550198258,
  "meanCi": 2.4208812652882585,
  "threshold": [
    7.24,
    8.34,
    9.85
  ],
  "autoThreshold": [
    7.24,
    8.34,
    9.85
  ],

```

```

"thresholdStrategy": "AUTO_THRESHOLD, LASSO, ANALYSIS_RULES_AUTO_THRESHOLD, ANALYSIS_RULES_DBA, FALLBACK_FROM_ANALYSIS_RULES",
"dispersionMeasure": {
  "stdDevOfUndilutedSample": 299.3133873057806,
  "stdDevInDpcrReaction": 299.3133873057806,
  "stdDevForConcentrationWithCustomUnitOfUndilutedSample": 299.3133873057806,
  "stdDevForConcentrationWithCustomUnitInDpcrReaction": 299.3133873057806,
  "cv": 154.91933384829665
},
"qualityControlStatus": {
  "strategy": "INVALIDATE_WELL",
  "failedValidationRules": [
    {
      "type": "MINIMUM_VALID_PARTITIONS_PERCENTAGE_FOR_SAMPLE",
      "channels": [
        {
          "excitation": "GREEN",
          "emission": "GREEN",
          "referenceChannel": true,
          "mixed": true
        }
      ],
      "passed": true
    }
  ],
  "propagatedValidationRules": [
    {
      "qualityControlValidationRuleType": "MINIMUM_VALID_PARTITIONS_PERCENTAGE_FOR_SAMPLE",
      "propagationSource": "REPLICATE"
    }
  ]
}
]
}
}

```

Name	Type	Required	Restrictions	Description
wellDetails	AbsoluteQuantification- ResultV2.Well	false	none	Well

Name	Type	Required	Restrictions	Description
sample	AbsoluteQuantification-ResultV2.Sample	false	none	Sample
reaction	AbsoluteQuantification-ResultV2.Reaction	false	none	Reaction mix
concentrations	[AbsoluteQuantification-ResultV2.ConcentrationPerChannelWithMean]	false	none	Concentrations per channel with mean data for single well

13.67 AbsoluteQuantificationResultV2.ConcentrationPerChannelWithMean

```
{
  "channel": {
    "excitation": "GREEN",
    "emission": "GREEN",
    "thresholdMode": "ST"
  },
  "target": {
    "id": "95f6cb04-fc4d-4c03-bd22-30ef11300e8c",
    "name": "COVID-19_G2",
    "controlType": "NONE",
    "isInternalControl": false
  },
  "concentration": {
    "value": 10.484819643300222,
    "concentrationOfOriginalSample": 10.484819643300222,
    "concentrationWithCustomUnitOfDpcrReaction": 0,
    "concentrationWithCustomUnitOfUndilutedSample": 0,
    "dilutedCi": 0,
    "undilutedCi": 0,
    "dilutedConvCi": 0,
    "undilutedConvCi": 0,
    "errorCode": "SATURATION_ERROR",
    "lambda": 5.9643300222
  },
  "validsCount": {
    "count": 24000,

```

```

    "qualityControlRuleResult": {
      "settings": {
        "minimumConcentration": 75,
        "maximumConcentration": 15000
      },
      "passed": true
    }
  },
  "positivesCount": {
    "count": 24000,
    "qualityControlRuleResult": {
      "settings": {
        "minimumConcentration": 75,
        "maximumConcentration": 15000
      },
      "passed": true
    }
  },
  "negativesCount": 23703,
  "ci": 1.4353845944578065,
  "relativeCi": 0.1369012194096266,
  "meanConcentration": {
    "value": 10.484819643300222,
    "concentrationOfOriginalSample": 10.484819643300222,
    "concentrationWithCustomUnitOfDpcrReaction": 0,
    "concentrationWithCustomUnitOfUndilutedSample": 0,
    "dilutedCi": 0,
    "undilutedCi": 0,
    "dilutedConvCi": 0,
    "undilutedConvCi": 0,
    "errorCode": "SATURATION_ERROR",
    "lambda": 5.9643300222
  },
  "meanRelativeCi": 0.03922849550198258,
  "meanCi": 2.4208812652882585,
  "threshold": [
    7.24,
    8.34,
    9.85
  ]

```

```

],
"autoThreshold": [
  7.24,
  8.34,
  9.85
],
"thresholdStrategy": "AUTO_THRESHOLD, LASSO, ANALYSIS_RULES_AUTO_THRESHOLD, ANALYSIS_RULES_DBA, FALLBACK_FROM_ANALYSIS_RULES",
"dispersionMeasure": {
  "stdDevOfUndilutedSample": 299.3133873057806,
  "stdDevInDpcrReaction": 299.3133873057806,
  "stdDevForConcentrationWithCustomUnitOfUndilutedSample": 299.3133873057806,
  "stdDevForConcentrationWithCustomUnitInDpcrReaction": 299.3133873057806,
  "cv": 154.91933384829665
},
"qualityControlStatus": {
  "strategy": "INVALIDATE_WELL",
  "failedValidationRules": [
    {
      "type": "MINIMUM_VALID_PARTITIONS_PERCENTAGE_FOR_SAMPLE",
      "channels": [
        {
          "excitation": "GREEN",
          "emission": "GREEN",
          "referenceChannel": true,
          "mixed": true
        }
      ]
    }
  ],
  "passed": true
}
],
"propagatedValidationRules": [
  {
    "qualityControlValidationRuleType": "MINIMUM_VALID_PARTITIONS_PERCENTAGE_FOR_SAMPLE",
    "propagationSource": "REPLICATE"
  }
]
}
}

```

Name	Type	Required	Restrictions	Description
channel	ChannelSliceDefinition	false	none	Imaging channel
target	AbsoluteQuantification-ResultV2.ConcentrationPerChannelWithMean.Target	false	none	Specific gene sequence to be detected by a dPCR process
concentration	AbsoluteQuantification-ResultV2.ConcentrationWithErrorCode	false	none	Concentration of diluted sample and before dilution, with analysis error
validsCount	PartitionsWithQuality-ControlRuleResult	false	none	Valid partitions with quality control result
positivesCount	PartitionsWithQuality-ControlRuleResult	false	none	Positive partitions with quality control result
negativesCount	integer(int32)	false	none	Number of negative partitions
ci	number(double)	false	none	Confidence interval
relativeCi	number(double)	false	none	Relative confidence interval
meanConcentration	AbsoluteQuantification-ResultV2.ConcentrationWithErrorCode	false	none	Mean concentration, if the well has replicates or is a part of hyperwell, with mean error code
meanRelativeCi	number(double)	false	none	Mean confidence interval, if the well has replicates or is a part of hyperwell
meanCi	number(double)	false	none	Mean relative confidence interval, if the well has replicates or is a part of hyperwell
threshold	any	false	none	Thresholds values, for AM [low, high, doublePositives], for SingleThreshold[lower]

oneOf

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	SignalThreshold.AmplitudeMultiplexingThreshold	false	none	Amplitude multiplexing threshold

xor

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	SignalThreshold.SingleThreshold	false	none	Single threshold value

continued

Name	Type	Required	Restrictions	Description
autoThreshold	any	false	none	Auto Thresholds values, for AM [low, high, doublePositives], for Signal[lower]

oneOf

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	SignalThreshold.AmplitudeMultiplexingThreshold	false	none	Amplitude multiplexing threshold

xor

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	SignalThreshold.SingleThreshold	false	none	Single threshold value

continued

Name	Type	Required	Restrictions	Description
thresholdStrategy	string	false	none	Threshold strategy name
dispersionMeasure	DispersionMeasureResponse	false	none	Dispersion measure details
qualityControlStatus	AbsoluteQuantificationResultV2.ConcentrationPerChannelWithMean.QualityControlStatus	false	none	Quality Control status

13.68 AbsoluteQuantificationResultV2.ConcentrationPerChannelWithMean.QualityControlStatus

```
{
  "strategy": "INVALIDATE_WELL",
  "failedValidationRules": [
    {
      "type": "MINIMUM_VALID_PARTITIONS_PERCENTAGE_FOR_SAMPLE",
      "channels": [
        {
          "excitation": "GREEN",
          "emission": "GREEN",
          "referenceChannel": true,
          "mixed": true
        }
      ],
      "passed": true
    }
  ],
  "propagatedValidationRules": [
    {
      "qualityControlValidationRuleType": "MINIMUM_VALID_PARTITIONS_PERCENTAGE_FOR_SAMPLE",
      "propagationSource": "REPLICATE"
    }
  ]
}
```


Name	Type	Required	Restrictions	Description
strategy	string	false	none	Quality control validation strategy
failedValidationRules	[FailedValidationRule]	false	none	List of validation rules
propagatedValidationRules	[PropagatedQualityControlRuleFailure]	false	none	List of propagated validation rules

13.68.0.1 Enumerated Values

Property	Value
strategy	WARNING_CHANNEL
strategy	WARNING_WELL
strategy	INVALIDATE_CHANNEL
strategy	INVALIDATE_WELL

13.69 AbsoluteQuantificationResultV2.ConcentrationPerChannelWithMean.QualityControlValidationResults

```
{
  "type": "string"
}
```

Name	Type	Required	Restrictions	Description
type	string	true	none	none

13.70 AbsoluteQuantificationResultV2.ConcentrationPerChannelWithMean.Target

```
{
  "id": "95f6cb04-fc4d-4c03-bd22-30ef11300e8c",
  "name": "COVID-19_G2",
  "controlType": "NONE",
  "isInternalControl": false
}
```

Name	Type	Required	Restrictions	Description
id	string(uuid)	false	none	Target ID
name	string	false	none	Target name
controlType	string	false	none	Control type (positive, negative or none)
isInternalControl	boolean	false	none	Internal control indicator

13.70.0.1 Enumerated Values

Property	Value
controlType	POSITIVE
controlType	NEGATIVE
controlType	NONE

13.71 AbsoluteQuantificationResultV2.ConcentrationWithErrorCode

```
{
  "value": 10.484819643300222,
  "concentrationOfOriginalSample": 10.484819643300222,
  "concentrationWithCustomUnitOfDpcrReaction": 0,
  "concentrationWithCustomUnitOfUndilutedSample": 0,
  "dilutedCi": 0,
  "undilutedCi": 0,
  "dilutedConvCi": 0,
  "undilutedConvCi": 0,
  "errorCode": "SATURATION_ERROR",
  "lambda": 5.9643300222
}
```

Name	Type	Required	Restrictions	Description
value	number(double)	false	none	Concentration of diluted sample
concentrationOfOriginal-Sample	number(double)	false	none	Concentration of sample before dilution

Name	Type	Required	Restrictions	Description
concentrationWithCustomUnitOfDpcrReaction	number	false	none	Conversion Factor multiplied by concentration of dpcr reaction result
concentrationWithCustomUnitOfUndilutedSample	number	false	none	Conversion Factor multiplied by concentration of undiluted Sample result
dilutedCi	number	false	none	Diluted CI value
undilutedCi	number	false	none	Undiluted CI value
dilutedConvCi	number	false	none	Diluted CI value for concentration with custom unit of dpcr reaction
undilutedConvCi	number	false	none	Undiluted CI value for concentration with custom unit of undiluted sample
errorCode	string	false	none	Error code
lambda	number(double)	false	none	Lambda

13.71.0.1 Enumerated Values

Property	Value
errorCode	SATURATION_ERROR
errorCode	IMAGE_BLUR
errorCode	MISSING_CHANNEL_IN_CXTM
errorCode	WELL_OFF_CENTER

13.72 AbsoluteQuantificationResultV2.Reaction

```
{
  "name": "corona_g",
  "totalReactionVolume": 2
}
```

Name	Type	Required	Restrictions	Description
name	string	false	none	Reaction mix name
totalReactionVolume	number(double)	false	none	Dilution Factor: total reaction volume value

13.73 AbsoluteQuantificationResultV2.Sample

```
{
  "name": "S1",
  "uniqueId": 1,
  "volumeOfTemplate": 2,
  "concentrationFactor": 20,
  "type": "SAMPLE",
  "conversionFactor": 10.999999999,
  "conversionUnit": "cp/ml"
}
```

Name	Type	Required	Restrictions	Description
name	string	false	none	Name of the sample
uniqueId	integer(int32)	false	none	Unique id of the sample
volumeOfTemplate	number(double)	false	none	Dilution Factor: volume of template value
concentrationFactor	number(double)	false	none	Dilution Factor: concentration factor value
type	string	false	none	Sample type - SAMPLE, CONTROL or NON_TEMPLATE_CONTROL
conversionFactor	number	false	none	Conversion Factor
conversionUnit	string	false	none	Unit for conversion factor value

13.73.0.1 Enumerated Values

Property	Value
type	SAMPLE
type	CONTROL
type	NON_TEMPLATE_CONTROL

13.74 AbsoluteQuantificationResultV2.Well

```
{
  "wellPosition": 5,
  "rowLetter": "A",
  "columnNumber": 1,
  "replicateWellPositions": [
    5,
    8
  ],
  "cycledVolume": 2.57
}
```

Name	Type	Required	Restrictions	Description
wellPosition	integer(int32)	true	none	Well position
rowLetter	string	false	none	Row letter
columnNumber	integer(int32)	false	none	Column number
replicateWellPositions	[integer]	false	none	Well positions of replicate wells
cycledVolume	number(double)	false	none	Cycled volume of this well

13.75 DispersionMeasureResponse

```
{
  "stdDevOfUndilutedSample": 299.3133873057806,
  "stdDevInDpcrReaction": 299.3133873057806,
  "stdDevForConcentrationWithCustomUnitOfUndilutedSample": 299.3133873057806,
  "stdDevForConcentrationWithCustomUnitInDpcrReaction": 299.3133873057806,
  "cv": 154.91933384829665
}
```

Name	Type	Required	Restrictions	Description
stdDevOfUndilutedSample	number(double)	false	none	Standard deviation calculated with Dilution Factor values
stdDevInDpcrReaction	number(double)	false	none	Standard deviation calculated in dpcr reaction
stdDevForConcentrationWithCustomUnitOfUndilutedSample	number	false	none	Standard deviation calculated with custom unit values
stdDevForConcentrationWithCustomUnitInDpcrReaction	number	false	none	Standard deviation calculated with custom unit in dpcr reaction
cv	number(double)	false	none	Coefficient of Variation

13.76 ExperimentResultsV2Response

```
{
  "dpcrRunStepIndex": 2,
  "results": [
    {
      "wellDetails": {
        "wellPosition": 5,
        "rowLetter": "A",
        "columnNumber": 1,
        "replicateWellPositions": [
          5,
          8
        ],
        "cycledVolume": 2.57
      },
      "sample": {
        "name": "S1",
        "uniqueId": 1,
        "volumeOfTemplate": 2,
        "concentrationFactor": 20,
        "type": "SAMPLE",
        "conversionFactor": 10.999999999,

```

```

    "conversionUnit": "cp/ml"
  },
  "reaction": {
    "name": "corona_g",
    "totalReactionVolume": 2
  },
  "concentrations": [
    {
      "channel": {
        "excitation": "GREEN",
        "emission": "GREEN",
        "thresholdMode": "ST"
      },
      "target": {
        "id": "95f6cb04-fc4d-4c03-bd22-30ef11300e8c",
        "name": "COVID-19_G2",
        "controlType": "NONE",
        "isInternalControl": false
      },
      "concentration": {
        "value": 10.484819643300222,
        "concentrationOfOriginalSample": 10.484819643300222,
        "concentrationWithCustomUnitOfDpcrReaction": 0,
        "concentrationWithCustomUnitOfUndilutedSample": 0,
        "dilutedCi": 0,
        "undilutedCi": 0,
        "dilutedConvCi": 0,
        "undilutedConvCi": 0,
        "errorCode": "SATURATION_ERROR",
        "lambda": 5.9643300222
      },
      "validsCount": {
        "count": 24000,
        "qualityControlRuleResult": {
          "settings": {
            "minimumConcentration": 75,
            "maximumConcentration": 15000
          },
          "passed": true
        }
      }
    }
  ]
}

```

```

    }
  },
  "positivesCount": {
    "count": 24000,
    "qualityControlRuleResult": {
      "settings": {
        "minimumConcentration": 75,
        "maximumConcentration": 15000
      },
      "passed": true
    }
  },
  "negativesCount": 23703,
  "ci": 1.4353845944578065,
  "relativeCi": 0.1369012194096266,
  "meanConcentration": {
    "value": 10.484819643300222,
    "concentrationOfOriginalSample": 10.484819643300222,
    "concentrationWithCustomUnitOfDpcrReaction": 0,
    "concentrationWithCustomUnitOfUndilutedSample": 0,
    "dilutedCi": 0,
    "undilutedCi": 0,
    "dilutedConvCi": 0,
    "undilutedConvCi": 0,
    "errorCode": "SATURATION_ERROR",
    "lambda": 5.9643300222
  },
  "meanRelativeCi": 0.03922849550198258,
  "meanCi": 2.4208812652882585,
  "threshold": [
    7.24,
    8.34,
    9.85
  ],
  "autoThreshold": [
    7.24,
    8.34,
    9.85
  ],

```



```

"thresholdStrategy": "AUTO_THRESHOLD, LASSO, ANALYSIS_RULES_AUTO_THRESHOLD, ANALYSIS_RULES_DBA, FALLBACK_FROM_ANALYSIS_RULES",
"dispersionMeasure": {
  "stdDevOfUndilutedSample": 299.3133873057806,
  "stdDevInDpcrReaction": 299.3133873057806,
  "stdDevForConcentrationWithCustomUnitOfUndilutedSample": 299.3133873057806,
  "stdDevForConcentrationWithCustomUnitInDpcrReaction": 299.3133873057806,
  "cv": 154.91933384829665
},
"qualityControlStatus": {
  "strategy": "INVALIDATE_WELL",
  "failedValidationRules": [
    {
      "type": "MINIMUM_VALID_PARTITIONS_PERCENTAGE_FOR_SAMPLE",
      "channels": [
        {
          "excitation": "GREEN",
          "emission": "GREEN",
          "referenceChannel": true,
          "mixed": true
        }
      ],
      "passed": true
    }
  ],
  "propagatedValidationRules": [
    {
      "qualityControlValidationRuleType": "MINIMUM_VALID_PARTITIONS_PERCENTAGE_FOR_SAMPLE",
      "propagationSource": "REPLICATE"
    }
  ]
}
]
}
]
}
]
}
}

```

Name	Type	Required	Restrictions	Description
dpcrRunStepIndex	integer(int32)	false	none	dPCR run step index
results	[AbsoluteQuantification-ResultV2]	false	none	List of absolute quantification results for requested plate, run step, channels and wells

13.77 FailedValidationRule

```
{
  "type": "MINIMUM_VALID_PARTITIONS_PERCENTAGE_FOR_SAMPLE",
  "channels": [
    {
      "excitation": "GREEN",
      "emission": "GREEN",
      "referenceChannel": true,
      "mixed": true
    }
  ],
  "passed": true
}
```

Name	Type	Required	Restrictions	Description
type	string	false	none	none
channels	[SignalChannel]	false	none	none
passed	boolean	false	none	none

13.77.0.1 Enumerated Values

Property	Value
type	MINIMUM_VALID_PARTITIONS_PERCENTAGE_FOR_SAMPLE
type	MINIMUM_VALID_PARTITIONS_PERCENTAGE_FOR_CONTROL
type	MAXIMUM_POSITIVE_PARTITIONS_NUMBER_FOR_NEGATIVE_CONTROL
type	CONCENTRATION_RANGE_FOR_POSITIVE_CONTROL

13.78 PartitionsWithQualityControlRuleResult

```
{
  "count": 24000,
  "qualityControlRuleResult": {
    "settings": {
      "minimumConcentration": 75,
      "maximumConcentration": 15000
    },
    "passed": true
  }
}
```

Name	Type	Required	Restrictions	Description
count	integer(int32)	false	none	Count of partitions
qualityControlRuleResult	any	false	none	Quality control rule result

oneOf

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	AbsoluteQuantification- Result.ConcentrationPer- ChannelWithMean.Quali- tyControlValidationRe- sults.Concentra- tionRangeForPositive- Control	false	none	none

xor

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	AbsoluteQuantification-Result.ConcentrationPer-ChannelWithMean.QualityControlValidationResults.MaximumPositivePartitionsNumberForNegativeControl	false	none	none

xor

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	AbsoluteQuantification-Result.ConcentrationPer-ChannelWithMean.QualityControlValidationResults.MinimumValidPartitionsForControl	false	none	none

xor

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	AbsoluteQuantification-Result.ConcentrationPer-ChannelWithMean.QualityControlValidationResults.MinimumValidPartitionsForSample	false	none	none

13.79 PropagatedQualityControlRuleFailure

```
{
  "qualityControlValidationRuleType": "MINIMUM_VALID_PARTITIONS_PERCENTAGE_FOR_SAMPLE",
  "propagationSource": "REPLICATE"
}
```

Name	Type	Required	Restrictions	Description
qualityControlValidationRuleType	string	false	none	none
propagationSource	string	false	none	none

13.79.0.1 Enumerated Values

Property	Value
qualityControlValidationRuleType	MINIMUM_VALID_PARTITIONS_PERCENTAGE_FOR_SAMPLE
qualityControlValidationRuleType	MINIMUM_VALID_PARTITIONS_PERCENTAGE_FOR_CONTROL
qualityControlValidationRuleType	MAXIMUM_POSITIVE_PARTITIONS_NUMBER_FOR_NEGATIVE_CONTROL
qualityControlValidationRuleType	CONCENTRATION_RANGE_FOR_POSITIVE_CONTROL
propagationSource	REPLICATE
propagationSource	CONTROL

13.80 Settings

```
{
  "minimumConcentration": 75,
  "maximumConcentration": 15000
}
```

Name	Type	Required	Restrictions	Description
minimumConcentration	number(double)	false	none	Minimum concentration
maximumConcentration	number(double)	false	none	Maximum concentration

13.81 SignalChannel

```
{
  "excitation": "GREEN",
  "emission": "GREEN",
  "referenceChannel": true,
  "mixed": true
}
```

```
}
```

Name	Type	Required	Restrictions	Description
excitation	string	false	none	none
emission	string	false	none	none
referenceChannel	boolean	false	none	none
mixed	boolean	false	none	none

13.81.0.1 Enumerated Values

Property	Value
excitation	GREEN
excitation	YELLOW
excitation	ORANGE
excitation	RED
excitation	CRIMSON
excitation	FARRED
emission	GREEN
emission	YELLOW
emission	ORANGE
emission	RED
emission	CRIMSON
emission	FARRED

13.82 SignalThreshold

```
{
  "type": "string"
}
```

Signal threshold

Name	Type	Required	Restrictions	Description
type	string	true	none	none

13.83 SignalThreshold.AmplitudeMultiplexingThreshold

```
{
  "low": 0.1,
  "high": 0.1,
  "doublePositives": 0.1,
  "warnings": [
    "SATURATION"
  ]
}
```

SignalThreshold.AmplitudeMultiplexingThreshold

Name	Type	Required	Restrictions	Description
SignalThreshold.AmplitudeMultiplexingThreshold	any	false	none	Amplitude multiplexing threshold

allOf - discriminator: SignalThreshold.type

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	SignalThreshold	false	none	Signal threshold

and

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	object	false	none	none
» low	number(double)	false	none	none
» high	number(double)	false	none	none
» doublePositives	number(double)	false	none	none
» warnings	[string]	false	none	none

13.84 SignalThreshold.SingleThreshold

```
{
  "value": 0.1,
```

```

    "warnings": [
      "SATURATION"
    ]
  }

```

SignalThreshold.SingleThreshold

Name	Type	Required	Restrictions	Description
SignalThreshold.SingleThreshold	any	false	none	Single threshold value

allOf - discriminator: SignalThreshold.type

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	SignalThreshold	false	none	Signal threshold

and

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	object	false	none	none
» value	number(double)	false	none	none
» warnings	[string]	false	none	none

13.85 InstrumentStateResponse

```

{
  "instrumentId": "instrument123",
  "deviceName": "Instrument in Lab A",
  "type": "P4",
  "isOnline": true,
  "drawers": {
    "Drawer0": {
      "isBooked": true,
      "platesInSlots": {}
    },
    "Drawer1": {

```



```

    "isBooked": false,
    "platesInSlots": {
      "0": "3fa85f64-5717-4562-b3fc-2c963f66afa6"
    }
  }
}
}

```

Name	Type	Required	Restrictions	Description
instrumentId	string	false	none	ID of the instrument
deviceName	string	false	none	Name of the instrument
type	string	false	none	Type of the instrument
isOnline	boolean	false	none	Whether an instrument has sent a heartbeat in the last PT5S (ISO8601 notation).
drawers	object	false	none	Drawer state per drawer name
» <dictionary>	InstrumentStateResponse.DrawerState	false	none	Drawer state per drawer name

13.86 InstrumentStateResponse.DrawerState

```

{
  "Drawer0": {
    "isBooked": true,
    "platesInSlots": {}
  },
  "Drawer1": {
    "isBooked": false,
    "platesInSlots": {
      "0": "3fa85f64-5717-4562-b3fc-2c963f66afa6"
    }
  }
}

```

Drawer state per drawer name

Name	Type	Required	Restrictions	Description
isBooked	boolean	false	none	Whether the drawer is currently booked or not
platesInSlots	object	false	none	ID of plate per slot ID.
» <dictionary>	string(uuid)	false	none	ID of plate per slot ID.

13.87 HealthCheck

```
{
  "commandQueueTasks": 4,
  "eventQueueTasks": 2
}
```

Name	Type	Required	Restrictions	Description
commandQueueTasks	integer(int32)	false	none	Number of tasks in command queue
eventQueueTasks	integer(int32)	false	none	Number of tasks in event queue

13.88 CycleStep

```
{
  "type": "string"
}
```

Name	Type	Required	Restrictions	Description
type	string	true	none	none

13.89 ExperimentDetailsResponse

```
{
  "plateId": "3fa85f64-5717-4562-b3fc-2c963f66afa6",
  "name": "3fa85f64-5717-4562-b3fc-2c963f66afa6",
  "barcode": "00031234567891113151719212",
  "plateTypeId": "67e02b72-768c-4bde-a4ec-d4c70c1c777a",
  "dpcrRunSteps": {
    "primingDPCRStep": {
      "velocityProfile": "0282a51b-422f-491a-8e66-cebc06cb8990"
    }
  }
}
```

```

},
"cycliningDPCRSteps": [
  {
    "index": 0,
    "cycles": [
      {
        "count": 1,
        "position": 0,
        "steps": [
          {
            "temperature": 40,
            "duration": 180,
            "position": 0
          }
        ]
      }
    ]
  }
],
"imagingDPCRSteps": [
  {
    "index": 0,
    "enableHighMultiplexingReferenceChannel": true,
    "imagingProfiles": [
      {
        "channel": {
          "excitation": "GREEN",
          "emission": "GREEN"
        },
        "durationOfExposure": 0,
        "gain": 0
      }
    ]
  }
],
"reactions": [
  {
    "name": "Reaction1",

```

```

    "totalReactionVolume": 30.5,
    "targets": [
      {
        "channel": {
          "excitation": "GREEN",
          "emission": "GREEN",
          "thresholdMode": "ST"
        },
        "name": "Target1",
        "internalControl": false,
        "dyeId": "1ef3cc8a-8a5e-4709-8101-e8293fd63e2d"
      }
    ]
  },
  "sampleControl": {
    "samples": [
      {
        "name": "Sample1",
        "sampleId": 1,
        "volumeOfTemplate": 15,
        "concentrationFactor": 15,
        "conversionFactor": 15,
        "conversionUnit": "lm/kg",
        "description": "Description1",
        "labels": [
          "string"
        ]
      }
    ]
  },
  "controls": [
    {
      "name": "Control1",
      "volumeOfTemplate": 15,
      "concentrationFactor": 15,
      "conversionFactor": 15,
      "conversionUnit": "lm/kg"
    }
  ],

```

```

    "nonTemplateControls": [
      {
        "name": "NonTemplateControl1",
        "volumeOfTemplate": 15,
        "concentrationFactor": 15,
        "conversionFactor": 15,
        "conversionUnit": "lm/kg"
      }
    ],
    "wells": [
      {
        "wellPosition": 5,
        "wellRow": "A",
        "column": 1,
        "blank": false,
        "reactionName": "Reaction1",
        "sample": {
          "name": "Control1"
        },
        "controlTypes": [
          {
            "channel": {
              "excitation": "GREEN",
              "emission": "GREEN",
              "thresholdMode": "ST"
            },
            "positive": true
          }
        ]
      }
    ]
  }
}

```

Name	Type	Required	Restrictions	Description
plateId	string(uuid)	false	none	Plate ID
name	string	false	none	Plate name
barcode	string	false	none	Plate barcode

Name	Type	Required	Restrictions	Description
plateTypeId	string(uuid)	false	none	Plate type ID. Available plate types can be listed via the <code>/experiment/plate-types</code> endpoint.
dpcrRunSteps	ExperimentDetailsResponse.DPCRRunSteps	false	none	dPCR run steps including Priming, Cycling or Imaging.
reactions	[ExperimentDetailsResponse.Reaction]	false	none	List of defined reaction mixes with assigned targets
sampleControl	ExperimentDetailsResponse.SampleControl	false	none	Collection of samples, controls and non template controls definitions
wells	[ExperimentDetailsResponse.Well]	false	none	Collection of well definitions

13.90 ExperimentDetailsResponse.DPCRRunSteps

```
{
  "primingDPCRStep": {
    "velocityProfile": "0282a51b-422f-491a-8e66-cebc06cb8990"
  },
  "cyclingDPCRSteps": [
    {
      "index": 0,
      "cycles": [
        {
          "count": 1,
          "position": 0,
          "steps": [
            {
              "temperature": 40,
              "duration": 180,
              "position": 0
            }
          ]
        }
      ]
    }
  ]
}
```

```

    ]
  }
]
},
"imagingDPCRSteps": [
{
  "index": 0,
  "enableHighMultiplexingReferenceChannel": true,
  "imagingProfiles": [
    {
      "channel": {
        "excitation": "GREEN",
        "emission": "GREEN"
      },
      "durationOfExposure": 0,
      "gain": 0
    }
  ]
}
]
}

```

Name	Type	Required	Restrictions	Description
primingDPCRStep	ExperimentDetailsResponse.DPCRRunSteps.Priming	false	none	Priming step definition
cyclingDPCRSteps	[ExperimentDetailsResponse.DPCRRunSteps.Cycling]	false	none	List of defined cycling steps
imagingDPCRSteps	[ExperimentDetailsResponse.DPCRRunSteps.Imaging]	false	none	List of defined cycling steps

13.91 ExperimentDetailsResponse.DPCRRunSteps.Cycling

```

{
  "index": 0,

```

```

"cycles": [
  {
    "count": 1,
    "position": 0,
    "steps": [
      {
        "temperature": 40,
        "duration": 180,
        "position": 0
      }
    ]
  }
]
}

```

Name	Type	Required	Restrictions	Description
index	integer(int32)	false	none	Cycling step index
cycles	[ExperimentDetailsResponse.DPCRRunSteps.Cycling.Cycle]	false	none	Defined cycles

13.92 ExperimentDetailsResponse.DPCRRunSteps.Cycling.Cycle

```

{
  "count": 1,
  "position": 0,
  "steps": [
    {
      "temperature": 40,
      "duration": 180,
      "position": 0
    }
  ]
}

```

Name	Type	Required	Restrictions	Description
count	integer(int32)	false	none	Number of cycles
position	integer(int32)	false	none	Cycle position in order

Name	Type	Required	Restrictions	Description
steps	[oneOf]	false	none	List of steps within the cycle

oneOf

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	ExperimentDetailsResponse.DPCRRunSteps.Cycling.Cycle.SingleTemperatureStep	false	none	none

xor

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	ExperimentDetailsResponse.DPCRRunSteps.Cycling.Cycle.TemperatureGradientStep	false	none	none

13.93 ExperimentDetailsResponse.DPCRRunSteps.Cycling.Cycle.SingleTemperatureStep

```
{
  "temperature": 40,
  "duration": 180,
  "position": 0
}
```

allOf - discriminator: CycleStep.type

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	CycleStep	false	none	none

and

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	object	false	none	none
» temperature	number(double)	false	none	Step temperature
» duration	number(double)	false	none	Step duration in seconds
» position	integer(int32)	false	none	Step position in order

13.94 ExperimentDetailsResponse.DPCRRunSteps.Cycling.Cycle.TemperatureGradientStep

```
{
  "minTemperature": 40,
  "maxTemperature": 60,
  "duration": 180,
  "position": 0
}
```

allOf - discriminator: CycleStep.type

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	CycleStep	false	none	none

and

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	object	false	none	none
» minTemperature	number(double)	false	none	Lower range of temperature gradient
» maxTemperature	number(double)	false	none	Upper range of temperature gradient
» duration	number(double)	false	none	Step duration in seconds
» position	integer(int32)	false	none	Step position in order

13.95 ExperimentDetailsResponse.DPCRRunSteps.Imaging

```
{
  "index": 0,
  "enableHighMultiplexingReferenceChannel": true,
}
```

```

"imagingProfiles": [
  {
    "channel": {
      "excitation": "GREEN",
      "emission": "GREEN"
    },
    "durationOfExposure": 0,
    "gain": 0
  }
]
}

```

Name	Type	Required	Restrictions	Description
index	integer(int32)	false	none	Imaging step index
enableHighMultiplexingReferenceChannel	boolean	false	none	Enabling High-Multiplexing Reference channel makes additional channels and amplitude multiplexing “mode” available. Please note that this requires usage of the QIAcuity High Multiplex Kit.
imagingProfiles	[ExperimentDetailsResponse.DPCRRunSteps.Imaging.ImagingProfile]	false	none	Imaging profiles

13.96 ExperimentDetailsResponse.DPCRRunSteps.Imaging.ImagingProfile

```

{
  "channel": {
    "excitation": "GREEN",
    "emission": "GREEN"
  },
  "durationOfExposure": 0,
  "gain": 0
}

```

Name	Type	Required	Restrictions	Description
channel	ChannelDefinition	false	none	Channel name
durationOfExposure	integer(int64)	false	none	Duration of exposure value
gain	integer(int32)	false	none	Gain value

13.97 ExperimentDetailsResponse.DPCRRunSteps.Priming

```
{
  "velocityProfile": "0282a51b-422f-491a-8e66-cebc06cb8990"
}
```

Name	Type	Required	Restrictions	Description
velocityProfile	string(uuid)	false	none	ID of velocity profile used in priming. Available velocity profiles for a particular plate type can be listed via the /experiment/velocity-profiles endpoint.

13.98 ExperimentDetailsResponse.Reaction

```
{
  "name": "Reaction1",
  "totalReactionVolume": 30.5,
  "targets": [
    {
      "channel": {
        "excitation": "GREEN",
        "emission": "GREEN",
        "thresholdMode": "ST"
      },
      "name": "Target1",
      "internalControl": false,
      "dyeId": "1ef3cc8a-8a5e-4709-8101-e8293fd63e2d"
    }
  ]
}
```

```
]
}
```

Name	Type	Required	Restrictions	Description
name	string	false	none	Reaction name
totalReactionVolume	number(double)	false	none	Total reaction volume
targets	[ExperimentDetailsResponse.Reaction.Target]	false	none	List of assigned targets

13.99 ExperimentDetailsResponse.Reaction.Target

```
{
  "channel": {
    "excitation": "GREEN",
    "emission": "GREEN",
    "thresholdMode": "ST"
  },
  "name": "Target1",
  "internalControl": false,
  "dyeId": "1ef3cc8a-8a5e-4709-8101-e8293fd63e2d"
}
```

Name	Type	Required	Restrictions	Description
channel	ChannelSliceDefinition	false	none	Target channel
name	string	false	none	Target name
internalControl	boolean	false	none	Indication whether target is an internal control
dyeId	string(uuid)	false	none	Assigned dye ID. Available dyes can be listed via the /experiment/dyes endpoint.

13.100 ExperimentDetailsResponse.SampleControl

```
{
  "samples": [
```

```

{
  "name": "Sample1",
  "sampleId": 1,
  "volumeOfTemplate": 15,
  "concentrationFactor": 15,
  "conversionFactor": 15,
  "conversionUnit": "lm/kg",
  "description": "Description1",
  "labels": [
    "string"
  ]
}
],
"controls": [
  {
    "name": "Control1",
    "volumeOfTemplate": 15,
    "concentrationFactor": 15,
    "conversionFactor": 15,
    "conversionUnit": "lm/kg"
  }
],
"nonTemplateControls": [
  {
    "name": "NonTemplateControl1",
    "volumeOfTemplate": 15,
    "concentrationFactor": 15,
    "conversionFactor": 15,
    "conversionUnit": "lm/kg"
  }
]
}

```

Name	Type	Required	Restrictions	Description
samples	[ExperimentDetailsResponse.SampleControl.Sample]	false	none	List of sample definitions

Name	Type	Required	Restrictions	Description
controls	[ExperimentDetailsResponse.SampleControl.Control]	false	none	List of control definitions
nonTemplateControls	[ExperimentDetailsResponse.SampleControl.NonTemplateControl]	false	none	List of non template control definitions

13.101 ExperimentDetailsResponse.SampleControl.Control

```
{
  "name": "Control1",
  "volumeOfTemplate": 15,
  "concentrationFactor": 15,
  "conversionFactor": 15,
  "conversionUnit": "lm/kg"
}
```

Name	Type	Required	Restrictions	Description
name	string	false	none	Control name
volumeOfTemplate	number(double)	false	none	Volume of template
concentrationFactor	number(double)	false	none	Concentration factor
conversionFactor	number	false	none	Conversion factor
conversionUnit	string	false	none	Conversion unit

13.102 ExperimentDetailsResponse.SampleControl.NonTemplateControl

```
{
  "name": "NonTemplateControl1",
  "volumeOfTemplate": 15,
  "concentrationFactor": 15,
  "conversionFactor": 15,
  "conversionUnit": "lm/kg"
}
```

Name	Type	Required	Restrictions	Description
name	string	false	none	Non template control name
volumeOfTemplate	number(double)	false	none	Volume of template
concentrationFactor	number(double)	false	none	Concentration factor
conversionFactor	number	false	none	Conversion factor
conversionUnit	string	false	none	Conversion unit

13.103 ExperimentDetailsResponse.SampleControl.Sample

```
{
  "name": "Sample1",
  "sampleId": 1,
  "volumeOfTemplate": 15,
  "concentrationFactor": 15,
  "conversionFactor": 15,
  "conversionUnit": "lm/kg",
  "description": "Description1",
  "labels": [
    "string"
  ]
}
```

Name	Type	Required	Restrictions	Description
name	string	false	none	Sample name
sampleId	integer(int32)	false	none	Unique sample id, used for distinction between two samples with same names.
volumeOfTemplate	number(double)	false	none	Volume of template
concentrationFactor	number(double)	false	none	Concentration factor
conversionFactor	number	false	none	Conversion factor
conversionUnit	string	false	none	Conversion unit
description	string	false	none	Sample description
labels	[string]	false	none	List of sample labels

13.104 ExperimentDetailsResponse.Well

```
{
  "wellPosition": 5,
  "wellRow": "A",
  "column": 1,
  "blank": false,
  "reactionName": "Reaction1",
  "sample": {
    "name": "Control1"
  },
  "controlTypes": [
    {
      "channel": {
        "excitation": "GREEN",
        "emission": "GREEN",
        "thresholdMode": "ST"
      },
      "positive": true
    }
  ]
}
```

Name	Type	Required	Restrictions	Description
wellPosition	integer(int32)	false	none	Well position
wellRow	string	false	none	Well row
column	integer(int32)	false	none	Well column
blank	boolean	false	none	If a well is blank, it explicitly states that it does not have a reaction mix or sample assigned.
reactionName	string	false	none	Assigned reaction name
sample	any	false	none	Specifies the sample or control type assigned to the well.

oneOf

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	ExperimentDetailsResponse.Well.SampleControlOrNTC.Control	false	none	none

xor

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	ExperimentDetailsResponse.Well.SampleControlOrNTC.NonTemplateControl	false	none	none

xor

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	ExperimentDetailsResponse.Well.SampleControlOrNTC.Sample	false	none	none

continued

Name	Type	Required	Restrictions	Description
controlTypes	[ExperimentDetailsResponse.Well.ControlType]	false	none	List of control types.

13.105 ExperimentDetailsResponse.Well.ControlType

```
{
  "channel": {
    "excitation": "GREEN",
    "emission": "GREEN",
    "thresholdMode": "ST"
  },
}
```

```

    "positive": true
}

```

Name	Type	Required	Restrictions	Description
channel	ChannelSliceDefinition	false	none	Control type channel
positive	boolean	false	none	Indication whether control type is positive

13.106 ExperimentDetailsResponse.Well.SampleControlOrNTC.Control

```

{
  "name": "Control1"
}

```

allOf - discriminator: Sample OR control OR NTC.type

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	Sample OR control OR NTC	false	none	Assigned sample or control or NTC

and

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	object	false	none	none
» name	string	false	none	Control name

13.107 ExperimentDetailsResponse.Well.SampleControlOrNTC.NonTemplateControl

```

{
  "name": "NonTemplateControl1"
}

```

allOf - discriminator: Sample OR control OR NTC.type

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	Sample OR control OR NTC	false	none	Assigned sample or control or NTC

and

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	object	false	none	none
» name	string	false	none	Non template control name

13.108 ExperimentDetailsResponse.Well.SampleControlOrNTC.Sample

```
{
  "name": "Sample1",
  "sampleId": 1
}
```

allOf - discriminator: Sample OR control OR NTC.type

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	Sample OR control OR NTC	false	none	Assigned sample or control or NTC

and

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	object	false	none	none
» name	string	false	none	Sample name
» sampleId	integer(int32)	false	none	Unique sample id, used for distinction between two samples with same names.

13.109 Sample OR control OR NTC

```
{  
  "type": "string"  
}
```

Assigned sample or control or NTC

Name	Type	Required	Restrictions	Description
type	string	true	none	none

13.110 ExperimentStatusResponse

```
{  
  "status": "IDLE",  
  "estimatedTimeTillEndOfExperiment": 300  
}
```

Name	Type	Required	Restrictions	Description
status	string	false	none	Status of the experiment
estimatedTimeTillEndOfExperiment	integer(int32)	false	none	Estimated time till end of experiment in seconds. Null if status is IDLE

13.110.0.1 Enumerated Values

Property	Value
status	IDLE
status	RUNNING
status	RUN_STOPPED
status	RUN_COMPLETED
status	RUN_FAILED

13.111 AbsoluteQuantificationResult

```
{
  "wellDetails": {
    "wellPosition": 5,
    "rowLetter": "A",
    "columnNumber": 1,
    "replicateWellPositions": [
      5,
      8
    ],
    "cycledVolume": 2.57
  },
  "sample": {
    "name": "S1",
    "uniqueId": 1,
    "volumeOfTemplate": 2,
    "concentrationFactor": 20,
    "type": "SAMPLE",
    "conversionFactor": 10.999999999,
    "conversionUnit": "cp/ml"
  },
  "reaction": {
    "name": "corona_g",
    "totalReactionVolume": 2
  },
  "concentrations": [
    {
      "channel": {
        "excitation": "GREEN",
        "emission": "GREEN",
        "thresholdMode": "ST"
      },
      "target": {
        "id": "95f6cb04-fc4d-4c03-bd22-30ef11300e8c",
        "name": "COVID-19_G2",
        "controlType": "NONE",
        "isInternalControl": false
      }
    }
  ],
}
```

```

"concentration": {
  "value": 10.484819643300222,
  "concentrationOfOriginalSample": 10.484819643300222,
  "concentrationWithCustomUnitOfDpcrReaction": 0,
  "concentrationWithCustomUnitOfUndilutedSample": 0,
  "dilutedCi": 0,
  "undilutedCi": 0,
  "dilutedConvCi": 0,
  "undilutedConvCi": 0,
  "errorCode": "SATURATION_ERROR",
  "lambda": 5.9643300222
},
"validsCount": 23908,
"positivesCount": 205,
"negativesCount": 23703,
"ci": 1.4353845944578065,
"relativeCi": 0.1369012194096266,
"meanConcentration": {
  "value": 10.484819643300222,
  "concentrationOfOriginalSample": 10.484819643300222,
  "concentrationWithCustomUnitOfDpcrReaction": 0,
  "concentrationWithCustomUnitOfUndilutedSample": 0,
  "dilutedCi": 0,
  "undilutedCi": 0,
  "dilutedConvCi": 0,
  "undilutedConvCi": 0,
  "errorCode": "SATURATION_ERROR",
  "lambda": 5.9643300222
},
"meanRelativeCi": 0.03922849550198258,
"meanCi": 2.4208812652882585,
"threshold": [
  7.24,
  8.34,
  9.85
],
"autoThreshold": [
  7.24,
  8.34,

```

```

    9.85
  ],
  "isAutoThreshold": true,
  "thresholdSource": {},
  "dispersionMeasure": {
    "stdDevOfUndilutedSample": 299.3133873057806,
    "stdDevInDpcrReaction": 299.3133873057806,
    "stdDevForConcentrationWithCustomUnitOfUndilutedSample": 299.3133873057806,
    "stdDevForConcentrationWithCustomUnitInDpcrReaction": 299.3133873057806,
    "cv": 154.91933384829665
  }
}
],
"qualityAssuranceValidationRules": [
{
  "channel": {
    "excitation": "GREEN",
    "emission": "GREEN"
  },
  "settings": 80,
  "passed": true,
  "strategy": "INVALIDATE_WELL"
}
]
}

```

Name	Type	Required	Restrictions	Description
wellDetails	AbsoluteQuantification-Result.Well	false	none	Well
sample	AbsoluteQuantification-Result.Sample	false	none	Sample
reaction	AbsoluteQuantification-Result.Reaction	false	none	Reaction mix
concentrations	[AbsoluteQuantification-Result.ConcentrationPer-ChannelWithMean]	false	none	Concentrations per channel with mean data for single well
qualityAssuranceValidationRules	[oneOf]	false	none	Quality assurance validation results

13.112 AbsoluteQuantificationResult.ConcentrationPerChannelWithMean

```
{
  "channel": {
    "excitation": "GREEN",
    "emission": "GREEN",
    "thresholdMode": "ST"
  },
  "target": {
    "id": "95f6cb04-fc4d-4c03-bd22-30ef11300e8c",
    "name": "COVID-19_G2",
    "controlType": "NONE",
    "isInternalControl": false
  },
  "concentration": {
    "value": 10.484819643300222,
    "concentrationOfOriginalSample": 10.484819643300222,
    "concentrationWithCustomUnitOfDpcrReaction": 0,
    "concentrationWithCustomUnitOfUndilutedSample": 0,
    "dilutedCi": 0,
    "undilutedCi": 0,
    "dilutedConvCi": 0,
    "undilutedConvCi": 0,
    "errorCode": "SATURATION_ERROR",
    "lambda": 5.9643300222
  },
  "validsCount": 23908,
  "positivesCount": 205,
  "negativesCount": 23703,
  "ci": 1.4353845944578065,
  "relativeCi": 0.1369012194096266,
  "meanConcentration": {
    "value": 10.484819643300222,
    "concentrationOfOriginalSample": 10.484819643300222,
    "concentrationWithCustomUnitOfDpcrReaction": 0,
    "concentrationWithCustomUnitOfUndilutedSample": 0,
    "dilutedCi": 0,
    "undilutedCi": 0,
    "dilutedConvCi": 0,
  }
}
```

```

    "undilutedConvCi": 0,
    "errorCode": "SATURATION_ERROR",
    "lambda": 5.9643300222
  },
  "meanRelativeCi": 0.03922849550198258,
  "meanCi": 2.4208812652882585,
  "threshold": [
    7.24,
    8.34,
    9.85
  ],
  "autoThreshold": [
    7.24,
    8.34,
    9.85
  ],
  "isAutoThreshold": true,
  "thresholdSource": {},
  "dispersionMeasure": {
    "stdDevOfUndilutedSample": 299.3133873057806,
    "stdDevInDpcrReaction": 299.3133873057806,
    "stdDevForConcentrationWithCustomUnitOfUndilutedSample": 299.3133873057806,
    "stdDevForConcentrationWithCustomUnitInDpcrReaction": 299.3133873057806,
    "cv": 154.91933384829665
  }
}

```

Name	Type	Required	Restrictions	Description
channel	ChannelSliceDefinition	false	none	Imaging channel
target	AbsoluteQuantification- Result.ConcentrationPer- ChannelWithMean.Tar- get	false	none	Specific gene sequence to be detected by a dPCR process
concentration	AbsoluteQuantification- Result.Concentra- tionWithErrorCode	false	none	Concentration of diluted sample and before dilution, with analysis error
validsCount	integer(int32)	false	none	Number of valid partitions

Name	Type	Required	Restrictions	Description
positivesCount	integer(int32)	false	none	Number of positive partitions
negativesCount	integer(int32)	false	none	Number of negative partitions
ci	number(double)	false	none	Confidence interval
relativeCi	number(double)	false	none	Relative confidence interval
meanConcentration	AbsoluteQuantification-Result.ConcentrationWithErrorCode	false	none	Mean concentration, if the well has replicates or is a part of hyperwell, with mean error code
meanRelativeCi	number(double)	false	none	Mean confidence interval, if the well has replicates or is a part of hyperwell
meanCi	number(double)	false	none	Mean relative confidence interval, if the well has replicates or is a part of hyperwell
threshold	any	false	none	Thresholds values, for AM [low, high, doublePositives], for SingleThreshold[lower]

oneOf

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	SignalThreshold.AmplitudeMultiplexingThreshold	false	none	Amplitude multiplexing threshold

xor

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	SignalThreshold.SingleThreshold	false	none	Single threshold value

continued

Name	Type	Required	Restrictions	Description
autoThreshold	any	false	none	Auto Thresholds values, for AM [low, high, doublePositives], for Signal[lower]

oneOf

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	SignalThreshold.AmplitudeMultiplexingThreshold	false	none	Amplitude multiplexing threshold

xor

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	SignalThreshold.SingleThreshold	false	none	Single threshold value

continued

Name	Type	Required	Restrictions	Description
isAutoThreshold	boolean	false	none	Is auto or manual threshold
thresholdSource	any	false	none	Where this threshold comes from

oneOf

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	ThresholdSource.Auto	false	none	Automatic threshold

xor

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	ThresholdSource.AutomationRule	false	none	Threshold set by analysis automation rule

xor

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	ThresholdSource.Lasso	false	none	Lasso threshold

xor

Name	Type	Required	Restrictions	Description
» <i>anonymous</i>	ThresholdSource.Manual	false	none	Manually set threshold

continued

Name	Type	Required	Restrictions	Description
dispersionMeasure	DispersionMeasureResponse	false	none	Dispersion measure details

13.113 AbsoluteQuantificationResult.ConcentrationPerChannelWithMean.Target

```
{
  "id": "95f6cb04-fc4d-4c03-bd22-30ef11300e8c",
  "name": "COVID-19_G2",
  "controlType": "NONE",
  "isInternalControl": false
}
```

```
}
```

Name	Type	Required	Restrictions	Description
id	string(uuid)	false	none	Target ID
name	string	false	none	Target name
controlType	string	false	none	Control type (positive, negative or none)
isInternalControl	boolean	false	none	Internal control indicator

13.113.0.1 Enumerated Values

Property	Value
controlType	POSITIVE
controlType	NEGATIVE
controlType	NONE

13.114 AbsoluteQuantificationResult.ConcentrationWithErrorCode

```
{
  "value": 10.484819643300222,
  "concentrationOfOriginalSample": 10.484819643300222,
  "concentrationWithCustomUnitOfDpcrReaction": 0,
  "concentrationWithCustomUnitOfUndilutedSample": 0,
  "dilutedCi": 0,
  "undilutedCi": 0,
  "dilutedConvCi": 0,
  "undilutedConvCi": 0,
  "errorCode": "SATURATION_ERROR",
  "lambda": 5.9643300222
}
```

Name	Type	Required	Restrictions	Description
value	number(double)	false	none	Concentration of diluted sample
concentrationOfOriginal-Sample	number(double)	false	none	Concentration of sample before dilution

Name	Type	Required	Restrictions	Description
concentrationWithCustomUnitOfDpcrReaction	number	false	none	Conversion Factor multiplied by concentration of dpcr reaction result
concentrationWithCustomUnitOfUndilutedSample	number	false	none	Conversion Factor multiplied by concentration of undiluted Sample result
dilutedCi	number	false	none	Diluted CI value
undilutedCi	number	false	none	Undiluted CI value
dilutedConvCi	number	false	none	Diluted CI value for concentration with custom unit of dpcr reaction
undilutedConvCi	number	false	none	Undiluted CI value for concentration with custom unit of undiluted sample
errorCode	string	false	none	Error code
lambda	number(double)	false	none	Lambda

13.114.0.1 Enumerated Values

Property	Value
errorCode	SATURATION_ERROR
errorCode	IMAGE_BLUR
errorCode	MISSING_CHANNEL_IN_CXTM
errorCode	WELL_OFF_CENTER

13.115 AbsoluteQuantificationResult.QualityAssuranceValidationRuleResults

```
{
  "type": "string"
}
```

Name	Type	Required	Restrictions	Description
type	string	true	none	none

13.116 AbsoluteQuantificationResult.QualityAssuranceValidationRuleResults.MinimumValidPartitions

```
{
  "channel": {
    "excitation": "GREEN",
    "emission": "GREEN"
  },
  "settings": 80,
  "passed": true,
  "strategy": "INVALIDATE_WELL"
}
```

allOf - discriminator: AbsoluteQuantificationResult.QualityAssuranceValidationRuleResults.type

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	AbsoluteQuantification- Result.QualityAssurance- ValidationRuleResults	false	none	none

and

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	object	false	none	none
» channel	ChannelDefinition	false	none	Channel
» settings	integer(int32)	false	none	Settings for the validation rule
» passed	boolean	false	none	Indicates if the validation rule passed
» strategy	string	false	none	Validation rule strategy

13.116.0.1 Enumerated Values

Property	Value
strategy	WARNING_CHANNEL
strategy	WARNING_WELL
strategy	INVALIDATE_CHANNEL
strategy	INVALIDATE_WELL

13.117 AbsoluteQuantificationResult.Reaction

```
{
  "name": "corona_g",
  "totalReactionVolume": 2
}
```

Name	Type	Required	Restrictions	Description
name	string	false	none	Reaction mix name
totalReactionVolume	number(double)	false	none	Dilution Factor: total reaction volume value

13.118 AbsoluteQuantificationResult.Sample

```
{
  "name": "S1",
  "uniqueId": 1,
  "volumeOfTemplate": 2,
  "concentrationFactor": 20,
  "type": "SAMPLE",
  "conversionFactor": 10.999999999,
  "conversionUnit": "cp/ml"
}
```

Name	Type	Required	Restrictions	Description
name	string	false	none	Name of the sample
uniqueId	integer(int32)	false	none	Unique id of the sample
volumeOfTemplate	number(double)	false	none	Dilution Factor: volume of template value

Name	Type	Required	Restrictions	Description
concentrationFactor	number(double)	false	none	Dilution Factor: concentration factor value
type	string	false	none	Sample type - SAMPLE, CONTROL or NON_TEM- PLATE_CONTROL
conversionFactor	number	false	none	Conversion Factor
conversionUnit	string	false	none	Unit for conversion factor value

13.118.0.1 Enumerated Values

Property	Value
type	SAMPLE
type	CONTROL
type	NON_TEMPLATE_CONTROL

13.119 AbsoluteQuantificationResult.Well

```
{
  "wellPosition": 5,
  "rowLetter": "A",
  "columnNumber": 1,
  "replicateWellPositions": [
    5,
    8
  ],
  "cycledVolume": 2.57
}
```

Name	Type	Required	Restrictions	Description
wellPosition	integer(int32)	false	none	Well position
rowLetter	string	false	none	Row letter
columnNumber	integer(int32)	false	none	Column number

Name	Type	Required	Restrictions	Description
replicateWellPositions	[integer]	false	none	Well positions of replicate wells
cycledVolume	number(double)	false	none	Cycled volume of this well

13.120 ExperimentResultsResponse

```
{
  "dpcrRunStepIndex": 2,
  "results": [
    {
      "wellDetails": {
        "wellPosition": 5,
        "rowLetter": "A",
        "columnNumber": 1,
        "replicateWellPositions": [
          5,
          8
        ],
        "cycledVolume": 2.57
      },
      "sample": {
        "name": "S1",
        "uniqueId": 1,
        "volumeOfTemplate": 2,
        "concentrationFactor": 20,
        "type": "SAMPLE",
        "conversionFactor": 10.999999999,
        "conversionUnit": "cp/ml"
      },
      "reaction": {
        "name": "corona_g",
        "totalReactionVolume": 2
      },
      "concentrations": [
        {
          "channel": {
```

```

    "excitation": "GREEN",
    "emission": "GREEN",
    "thresholdMode": "ST"
  },
  "target": {
    "id": "95f6cb04-fc4d-4c03-bd22-30ef11300e8c",
    "name": "COVID-19_G2",
    "controlType": "NONE",
    "isInternalControl": false
  },
  "concentration": {
    "value": 10.484819643300222,
    "concentrationOfOriginalSample": 10.484819643300222,
    "concentrationWithCustomUnitOfDpcrReaction": 0,
    "concentrationWithCustomUnitOfUndilutedSample": 0,
    "dilutedCi": 0,
    "undilutedCi": 0,
    "dilutedConvCi": 0,
    "undilutedConvCi": 0,
    "errorCode": "SATURATION_ERROR",
    "lambda": 5.9643300222
  },
  "validsCount": 23908,
  "positivesCount": 205,
  "negativesCount": 23703,
  "ci": 1.4353845944578065,
  "relativeCi": 0.1369012194096266,
  "meanConcentration": {
    "value": 10.484819643300222,
    "concentrationOfOriginalSample": 10.484819643300222,
    "concentrationWithCustomUnitOfDpcrReaction": 0,
    "concentrationWithCustomUnitOfUndilutedSample": 0,
    "dilutedCi": 0,
    "undilutedCi": 0,
    "dilutedConvCi": 0,
    "undilutedConvCi": 0,
    "errorCode": "SATURATION_ERROR",
    "lambda": 5.9643300222
  },

```

```

    "meanRelativeCi": 0.03922849550198258,
    "meanCi": 2.4208812652882585,
    "threshold": [
      7.24,
      8.34,
      9.85
    ],
    "autoThreshold": [
      7.24,
      8.34,
      9.85
    ],
    "isAutoThreshold": true,
    "thresholdSource": {},
    "dispersionMeasure": {
      "stdDevOfUndilutedSample": 299.3133873057806,
      "stdDevInDpcrReaction": 299.3133873057806,
      "stdDevForConcentrationWithCustomUnitOfUndilutedSample": 299.3133873057806,
      "stdDevForConcentrationWithCustomUnitInDpcrReaction": 299.3133873057806,
      "cv": 154.91933384829665
    }
  }
},
"qualityAssuranceValidationRules": [
  {
    "channel": {
      "excitation": "GREEN",
      "emission": "GREEN"
    },
    "settings": 80,
    "passed": true,
    "strategy": "INVALIDATE_WELL"
  }
]
}

```

Name	Type	Required	Restrictions	Description
dpcrRunStepIndex	integer(int32)	false	none	dPCR run step index
results	[AbsoluteQuantification-Result]	false	none	List of absolute quantification results for requested plate, run step, channels and wells

13.121 ThresholdSource

```
{
  "type": "string"
}
```

Where this threshold comes from

Name	Type	Required	Restrictions	Description
type	string	true	none	none

13.122 ThresholdSource.Auto

null

Automatic threshold

None

13.123 ThresholdSource.AutomationRule

```
{
  "ruleName": "string"
}
```

Threshold set by analysis automation rule

allOf - discriminator: ThresholdSource.type

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	ThresholdSource	false	none	Where this threshold comes from

and

Name	Type	Required	Restrictions	Description
<i>anonymous</i>	object	false	none	none
» ruleName	string	false	none	none

13.124 ThresholdSource.Lasso

null

Lasso threshold

None

13.125 ThresholdSource.Manual

null

Manually set threshold

None

13.126 EventResponse

```
{
  "id": "21ebe258-ec80-4f73-aa8c-4faa863d8a22",
  "commandId": "21ebe258-ec80-4f73-aa8c-4faa863d8a22",
  "instrumentId": "instrument1234",
  "type": "DRAWER_BOOKED",
  "payloadSchemaVersion": 1,
  "payload": null
}
```

Name	Type	Required	Restrictions	Description
id	string(uuid)	false	none	ID of the event
commandId	string(uuid)	false	none	ID of the command [optional]
instrumentId	string	false	none	ID of the instrument from which the event originated

Name	Type	Required	Restrictions	Description
type	string	false	none	Event type, used to properly decode the payload
payloadSchemaVersion	integer(int32)	false	none	Payload schema version, used for backward compatibility
payload	JsonNode	false	none	Specifics of the event resulting in command execution by the instrument

13.126.0.1 Enumerated Values

Property	Value
type	DRAWER_BOOKED
type	DRAWER_OPENED
type	DRAWER_NOT_OPENED
type	DRAWER_OPENED_MANUALLY
type	DRAWER_CLOSED
type	DRAWER_NOT_CLOSED
type	DRAWER_CLOSED_MANUALLY
type	DRAWER_BOOKING_RELEASED
type	DRAWER_BOOKING_NOT_RELEASED
type	EXPERIMENT_PROCESSING_STARTED
type	EXPERIMENT_READY
type	EXPERIMENT_PROGRESS
type	EXPERIMENT_ABORTED

13.127 JsonNode

null

None