Torrent SDK Documentation

Release 5.10

Ion Torrent

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Plugin Framework

Release v5.10.

This document reviews all the points of interest for programmatically interfacing with Torrent Suite™ Software.

CHAPTER 1

Torrent Suite™ Software Plugin System

This section describes the plugin framework and explains how to create plugins using all the available features. To understand this section, we recommend that you have at a minimum a working knowledge of python, object-oriented programming and HTML/javascript.

Getting Started with Plugins

The plugin framework is primarily an extension of the analysis pipeline and executes custom python modules (plugins) at different points in the pipeline process. There are three reasons for writing a plugin:

1. Data Management: The transfer or backup of data to a secondary file server or remote site.
2. Quality Assurance/Quality Control: These plugins check the quality of the data and give you access to some of the larger and transient data used in signal processing, which are eventually deleted.
3. Application Analysis: This is broadest and most useful category which bridges the gap between general pipeline workflow and application-specific analysis and reporting.

There is nothing strict about these categories. They have no technical bearing on the functioning of the plugins other than a conceptual framework for deciding whether to use a plugin or not.

Quick Start

Enter the following python code into a file called *MyPlugin.py* inside a new directory called *MyPlugin*.

```
import subprocess
from ion.plugin import *


class MyPlugin(IonPlugin):
    version = "1.0.0.0"

    def launch(self, data=None):
```

```
        output = subprocess.check_output(['ls', '-l'])
        with open("status_block.html", "w") as html_fp:
            html_fp.write("<html><body><pre>")
            html_fp.write(output)
            html_fp.write("</pre></body></html>")


if __name__ == "__main__":
    PluginCLI()
```

Compress the *MyPlugin* directory (ZIP file format). See *Packaging & Installation* for help. Click *Install or Upgrade Plugin* to upload the archive on the Torrent Suite™ Software plugins page. Navigate to an existing Torrent Suite™ Software run report, click *Select Plugins to Run*, then select *MyPlugin*. The plugin code executes and the output displays in an iframe on the report.

Pipeline Overview

Plugins are fundamentally an ability to extend the functionality of the analysis pipeline. At certain stages of the pipeline execution, each of these stages is represented as a "Run Level".

Configuration

Occasionally, you need to configure plugins before their execution. To do this, the Plugin Framework offers three different caches for storing the configurations for the two different workflows for executing a plugin.

Automated Pipeline Workflow

- **1st Priority**: Plan Configuration
- **2nd Priority**: Global Configuration

Manual Plugin Execution

- **1st Priority**: Instance Configuration
- **2nd Priority**: Global Configuration

Run Levels

One of the key attributes of any given plugin is the run level that directs the pipeline to execute the plugin at each of these stages specified in the module. It is important to remember that the same method is called in the plugin no matter what run level is currently being executed. So if you are going to use more than one run level, write the plugin code so it is conditionally based on the *Run Levels*.

When employing run levels, use one of the two following strategies. The conventional workflow covers almost all situations; therefore, it is the default approach.

Block Levels

When you use block-based run levels, we recommend that you use a combination of the three following run levels:

- PRE: This stage occurs before any significant processing happens, and is sufficient for preparation.
- BLOCK: Plugins are triggered once per block on the chip. This run level is never executed for runs that do not have block-level processing.
- POST: This stage occurs after the analysis pipeline is completely executed. When executed, the plugin results output directory is a child directory of the normal plugin output directory named "post".

Conventional Workflow

This strategy is the default for non-block-level specific run levels and is used in a more conventional workflow.

- DEFAULT: Plugins are triggered at the end of pipeline processing after the four usual steps (see pipeline documentation for details).
- LAST: Plugins are executed after all other plugins that are not "LAST" have been executed. If there is more than one, all "LAST" run level plugins run concurrently.

Internal Use Only

- SEPARATOR: Do not use.

Run Types

Run Types define which type of data the plugin is capable of running on. This controls whether the plugin is executed on a specific report type when it is selected during planning. If no run types are defined, the plugin will be launched for thumbnail and Ion PGM™ System reports only. In order to auto-run on Ion GeneStudio™ S5 System/Ion Proton™ System reports, the plugin must include COMPOSITE in its runtypes specification.

- COMPOSITE: Plugin will run on Ion GeneStudio™ S5 System/Ion Proton™ System report.
- THUMB: Plugin will run on Ion GeneStudio™ S5 System/Ion Proton™ System thumbnail report.
- FULLCHIP: Plugin will run on Ion PGM™ System report.

Dependencies

The term "dependency" is not quite accurate. This attribute ensures that when a plugin with a "dependency" is set to run at a run level, it is scheduled to run after the declared dependency that also shares that run level. If the declared dependency is not scheduled to run at the same run level, then the plugin runs without any special scheduling.

OIA Integration

Currently, the "On Instrument Analysis" (OIA) is responsible for the first two portions of the pipeline execution. The OIA does not normally interfere with plugin execution. However, if you select the PRE run level, any OIA-based workflows are executed after the signal processing step. A pure Torrent Suite™ Software implementation's PRE step is executed before the signal processing step.

Plugin Code

You must write the code for all plugins in python, therefore a basic understanding of both python and object oriented programming is required.

In order for the plugin to function, it must inherit from the base class IonPlugin contained in the module at ion.plugin. At a minimum, the version attribute and launch method need to be overridden.

Legacy Note

Legacy plugins that use a bash script called "launch.sh" are obsolete and should not be replicated.

Naming Your Plugin

It is important to include the name of your plugin in the following:

- The directory containing the python plugin file
- The name of the python plugin file (not including the required .py file extension)
- The name of the class declared within the python plugin file that derives the IonPlugin base class

  NOTE: All are case-sensitive.

Plugin Version

The version of the plugin must be a string that has the standard four-number formatting as follows:

<Major>.<Minor>.<Revision>.<Build>

Launch Method

The one required override method to implement in the plugin class is the launch method, which has only the self argument, and an unused "Data" argument with the "None" default. This method performs all the required actions to achieve the goal of the plugin as well as to produce all the results files.

Packaging & Installation

There are two supported methods for packaging and installing plugins into the system: the debian packaging system and a simple zip archive method. This section describes only the zip archive method. The debian packaging system is described elsewhere because it is more advanced.

When you create a zip package, the contents must use a file structure with a root folder that has the same name as the plugin. All other contents are a child of this root folder:

Linux Bash Shell: 'zip -r –exclude=*.git* PluginName.zip PluginDirectory'

After you create the archive, go to http://TS_hostname/configure/plugins/ on the Torrent Suite™ Software, then click "Install or Upgrade Plugin" to submit your new archive.

Plugin Reference

Plugin Files

- **Plugin Python File**: The primary file for implementing the logic contained in the plugin. The name of this file must be <PluginName>.py and be contained in the top level directory, which also has the same name as the plugin. Names are case-sensitive.
- **Configuration Interfaces**: There are three different configuration interfaces, all of which are optional. If your plugin does not require any configuration to execute, you do not need to implement all of the following:
  - instance.html: If present, this page appears when a plugin is run from the Manual Launch button on the Run Report page.
  - plan.html: When you create a plan in the Plugin chevron, you have the option of launching a configuration interface for that plan. If not present, you can still select the plugin to run, but there will be no configuration data.

  - config.html: This interface is presented in the plugin configuration interface and sets up the default configuration, which is used if neither of the other two configuration caches are present.

- **Static Files**: HTML files included in or generated by a plugin may need to load static assets (JS/CSS/Images). Include these files in a directory called **pluginMedia** in the root plugin directory. Reference the static files using the following URL pattern: /pluginMedia/<PluginName>/example.css
- **Documentation**:
  - about.html: If present, this information is accessible from the plugins manage menu on the plugin page.

Base Class

All plugins must create one and only one class that inherits from the IonPlugin base class. The IonPlugin base class requires that the following attributes and methods be overridden, although some are optional.

Attributes & Properties

Attribute Name	Required	Type	Default	Description
name	No	string	Empty	Stores the name of the plugin in addition to the name of the class itself for logging.
version	Yes	string	Empty	The four number version number for the plugin.
runtypes	No	list(string)	Empty	Indicates if this plugin is used for wholechip and/or thumbnails.
features	No	list(string)	Empty	Holds a list of current features enabled for this plugin.
runlevels	Yes	list(string)	Empty	Holds a list for each run level that this plugin executes during the pipeline execution.
depends	No	list(string)	Empty	Lists all plugins which are executed before this one, if present.
major_block	No	boolean	False	If true, indicates that this plugin's output is presented as part of the run report.
requires	No	list(string)	['BAM']	Currently unused.
output	No	dictionary	Empty	Currently unused.
results	No	dictionary	Empty	Currently unused.
exit_status	No	int	Empty	Currently unused.
context	No	dictionary	Empty	Currently unused.
blockcount	No	int	0	Currently unused.
plugin	No	Plugin	None	Currently unused.
analysis	No	Result	None	Currently unused.
pluginresult	No	PluginResult	None	Currently unused.
startplugin	No	dictionary	None	This returns "an" in the memory dictionary of the startplugin.json.

Methods

Method Name	Required	Return Type	Description
launch_wrapper	No	None	Do not use.
generate_output	No	None	Currently unused.
pre_block	No	None	Currently unused.
post_block	No	None	Currently unused.
pre_launch	No	boolean	Run prior to launch. Return False if you do not want the plugin to execute.
post_launch	No	None	Currently unused.
launch	Yes	boolean	If true, this indicates that this plugin's output is presented as part of the run report.
getUserInput	No	None	Currently unused.
barcodetable_columns	No	list	This method returns a list of columns to be used to generate the plugin barcodes table ui.
barcodetable_data	No	dictionary	This returns a dictionary to populate the contents of the plugin barcodes table ui.
get_restobj	No	dictionary	This method returns a dictionary based on a REST API function call.

Enums

Import the enumerations from the ion.plugin.constants module. Since enumerations are not supported in python 2, you implement them by creating a type with static members according to the following scheme.

- **Feature**
  - EXPORT: Used to indicate that this plugin is run last because it exports data.
- ***Run Types***
  - COMPOSITE: Block based chip runs.
  - THUMB: A thumbnail result.
  - FULLCHIP: Ion PGM™ System Full chip results.
- ***Run Levels***
  - PRE
  - DEFAULT
  - BLOCK
  - POST
  - SEPARATOR
  - LAST

Execution Environment

When you execute plugins, they are controlled with a script which is written to the results output directory call ion_plugin_*<Plugin Name>*_launch.sh. The plugin framework creates this file and directs the Grid Engine to execute this as the entry point for the plugin execution. The file handles the following:

- Updating the status in the database to be reflected in the run results page

- Setting up environmental variables (these are used in legacy plugins)
- Setting the umask to 0000
- Preventing core files from being written from core dumps
- Implementing the use of the output.json to create output (currently incomplete)

Run Levels

To use the run levels, you must assign them to your plugin class. If none are assigned the plugin will use DEFAULT runlevel. The run levels, block and conventional, are described in the Getting Started section. While it is technically possible, we do not recommend that you assign run levels from both groups concurrently.

Clusters

To accommplish clustering, the execution of the plugins is queued through a grid engine which, for single servers, is executed on the same computer as the one hosting the web site. In a cluster, the plugins are run only on the computer nodes and never on the head node. Consider the following when writing a plugin:

- The plugin is not run on the head node, so any references to "localhost" are incorrect. For example, if you are making a REST call and you have hard-coded the domain name of the url to be localhost, this attempts to call the REST API from the compute node, which results in an error. Instead, ensure that any REST API calls use the protocol and domain name in the *startplugin.json* contents *runinfo->net_location*.
- To distribute the executable code to the compute nodes, the system piggy-backs on the commonly shared NFS mount "/results" by creating a child folder at "/results/plugins/". This means that the stability of the plugin framework is going to be intimately tied to the stability of the network. Ensure that the connection to the results folder is as stable and redundant as reasonably possible.

Dependencies

Due to the method of distribution of plugin logic over NFS mounts, there are very few libraries on the compute nodes during run time. To work around this, package all dependencies (beyond the standard python libraries) into the install file with the core logic so they are also installed into the /results/plugins/<Plugin Name> directory on the NFS mount to be redistributed out to the compute nodes.

REST API Extensions

The plugin framework currently gives you an option of extending the REST API with custom endpoints by implementing a python file in the root of the plugin folder, which must have the name "extend.py". By implementing a method in this module with a single dictionary argument named "bucket", which is described below, the extension is exposed through the REST API for execution using the following url:

http(s)://{HOSTNAME}/rundb/api/v1/plugin/{PLUGIN}/extend/{METHOD_NAME}

```
bucket["request_get"] = request.GET
# assume json
if request.method == "POST":
    bucket["request_post"] = json.loads(request.body)
bucket["user"] = request.user
bucket["request_method"] = request.method
bucket["name"] = plugin.name
bucket["version"] = plugin.version
```

```
# not sure if we want this or not, keep it for now
bucket["config"] = plugin.config
```

Configuration

In many situations for plugins, there needs to be some sort of configuration declared before the plugin run time. This means that the plugin needs to implement an interface to allow users to configure it. Users can select from three configuration options in Torrent Suite™ Software: global, plan, and manual. The HTML pages can reference static assets, see *Plugin Files*.

Global Configuration

Include an HTML file named *config.html* in your root plugin directory to enable global configuration. This HTML window appears in an iframe on the global plugin configuration page at */configure/plugins/*. Click the  (Settings) next to a plugin, then select "Configure".

Reading Configuration

Read from the plugin api endpoint. "/rundb/api/v1/plugin/" + TB_plugin.pk + "/" Or Read the window.TB_plugin js variable.

Writing Configuration

Write to the plugin api endpoint with a PUT request. "/rundb/api/v1/plugin/" + TB_plugin.pk + "/"

Plan Configuration

Include an HTML file named *plan.html* in your root plugin directory to enable plan configuration. This HTML window appears in an iframe on the planning screen plugin configuration page at */plan/page_plan_plugins/*. Click the checkbox next to a plugin, then select "Configure".

Reading Configuration

Read the window.TB_plugin js variable, then wait for window.restoreForm to be called with the last data passed to serializeForm.

Writing Configuration

window.serializeForm is called by the parent frame to gather the current configuration when users click "Save" in the parent frame.

Manual Configuration

Include an HTML file named *instance.html* in your root plugin directory to enable manual configuration. The HTML window appears in an iframe on the report page at */report/<ID>/*. Click "Select Plugins To Run", then select a plugin.

Reading Configuration

Read the window. TB_plugin js variable.

Writing Configuration

Write to the results endpoint with a POST request. "/rundb/api/v1/results/" + TB_result + "/plugin/" Then call the following to close the iframe. window.parent.$.colorbox.close()

Barcode Table UI

Plugin Barcode Table UI is an optional service provided by the plugin framework. It allows plugins to generate a simple GUI that can be used to select which barcodes to process and specify per-barcode parameters. The table is similar to the barcode sample table in plan screen with one row per barcode and columns specified by the plugin. This UI is provided for manual plugin launch only and is an opt-in service for plugins to use if desired.

Defining table columns

```
def barcodetable_columns(self):
    # plugin class method to specify which columns to display
    # inputs: none
    # outputs: list of columns and options to show
    columns_list = [
        {
            "field": "selected",
            "editable": True
        },
        {
            "field": "barcode_name",
            "editable": False
        },
        {
            "field": "sample",
            "editable": False
        },
        ...
    ]
    return columns_list
```

List of available columns can be retrieved from framework by executing the following command line:

```
python /results/plugins/<myPlugin>/<myPlugin>.py --bctable-columns
```

Providing default table contents (optional)

Plugin barcode table will be populated on page load from existing samples information entered during run planning. Additionally, the plugin can modify or augment this initial data if it specifies the following function:

```
def barcodetable_data(self, data, planconfig={}, globalconfig={}):
    # plugin class method to specify default table contents
    # inputs:
    #    data - same structure as in barcodes.json
    #    planconfig - plugin configuration from planning (plan.html)
    #    globalconfig - plugin global configuration (config.html)
    # outputs:
    #    data, modified as needed
    return data
```

Changing instance.html

The plugin's instance.html must add the contents of barcodes table to the plugin data before POSTing it to the results API. This data will be written to startplugin.json file at plugin runtime under "pluginconfig" section.

Helper TB_plugin_functions js variable is available to interact with the barcode table UI:

- **TB_plugin_functions.get_plugin_barcodetable()** returns table data as json object
- **TB_plugin_functions.update_plugin_barcodetable(data)** can be used to update the table with data json object

- **TB_plugin_functions.plugin_barcodetable_div** barcode table DIV element

Input Files

The plugin framework creates two different files for general plugin consumption as its inputs. The variables, which are communicated to the plugin from the framework, are spread across two separate JSON files.

barcodes.json

This file has all the references required for iterating through all of the barcodes for a particular run.

Developer Option

By default all the barcodes where the filtered key is true are not included in the barcodes.json file. You can overwrite this behavior by adding "PLUGINS_INCLUDE_FILTERED_BARCODES = True" to the local_settings.py and restarting the ionPlugin service.

```
nonbarcoded: {
    aligned <bool>: Flags if the reads in bam_file are aligned to the reference␣
↪genome.
    bam_file <string>: Name of reads file. (May or may not be be aligned to the␣
↪reference.)
    bam_filepath <string>: Full file path to bam_file on the local torrent server.␣
↪(File may not exist if read_count is 0.)
    control_sequence_type <string>: Currently either ERCC Mix 1 or ERCC Mix 2 and␣
↪only defined in plan screen for RNA Sequencing. (Purpose unspecified.)
    filtered <bool>: Flags if the barcode passed the |TS| analysis pipeline filtering␣
↪criteria.
    hotspot_filepath <string>: Full file path to HotSpot target regions (BED) file on␣
↪the local torrent server. ("" if not used.)
    genome_urlpath <string>: URL path used to specify the genome for applications␣
↪like IGV. Typically the path to the FASTA file on the local torrent server.
    nucleotide_type <string>: Currently either DNA or RNA depending on application.␣
↪Primarily used to distinguish barcodes with AmpliSeq DNA+RNA runs.
    read_count <int>: Total number of barcode-assigned reads in bam_file (prior to␣
↪alignment).
    reference <string>: Common (short) name of the reference genome used in the␣
↪pipeline for this barcode, e.g. hg19
    reference_fullpath <string>: Full file path to the to the reference sequences in␣
↪FASTA format on the local torrent server. (May be "" for unaligned reads.)
    sample <string>: Name of the sample associated with this barcode. (May be␣
↪associated with multiple barcodes.)
    sample_id <string>: Sample identification code associated with sample.
    target_region_filepath <string>: Full file path to target regions (BED) file on␣
↪the local torrent server. ("" if not used.)
}
barcode_name: {
    aligned <bool>: Flags if the reads in bam_file are aligned to the reference␣
↪genome.
    bam_file <string>: Name of reads file. (May or may not be be aligned to the␣
↪reference.)
    bam_filepath <string>: Full file path to bam_file on the local torrent server.
    barcode_adapter <string>: DNA adapter sequence used to separate barcode_sequence␣
↪from sequenced read.
    barcode_annotation <string>: User-specified annotation for this barcode.
    barcode_description <string>: Description text associated with this barcode.
    barcode_index <int>: Index of barcode in the barcode set, starting at 1.
```

```
    barcode_name <string>: Name of the barcode in the barcode set (barcode_name).
    barcode_sequence <string>: DNA sequence used to identify this barcode.
    barcode_type <string>: User-specified type for this barcode.
    control_sequence_type <string>: Currently either ERCC Mix 1 or ERCC Mix 2 and␣
↪only defined in plan screen for RNA Sequencing. (Purpose unspecified.)
    filtered <bool>: Flags if the barcode passed the |TS| analysis pipeline filtering␣
↪criteria.
    hotspot_filepath <string>: Full file path to HotSpot target regions (BED) file on␣
↪the local torrent server. ("" if not used.)
    genome_urlpath <string>: URL path used to specify the genome for applications␣
↪like IGV. Typically the path to the FASTA file on the local torrent server.
    nucleotide_type <string>: Currently either DNA or RNA depending on application.␣
↪Primarily used to distinguish barcodes with AmpliSeq DNA+RNA runs.
    read_count <int>: Total number of barcode-assigned reads in bam_file (prior to␣
↪alignment).
    reference <string>: Common (short) name of the reference genome used in the␣
↪pipeline for this barcode, e.g. hg19
    reference_fullpath <string>: Full file path to the to the reference sequences in␣
↪FASTA format on the local torrent server. (May be "" for unaligned reads.)
    sample <string>: Name of the sample associated with this barcode. (May be␣
↪associated with multiple barcodes.)
    sample_id <string>: Sample identification code associated with sample.
    target_region_filepath <string>: Full file path to target regions (BED) file on␣
↪the local torrent server. ("" if not used.)
}

Example barcodes.json for a barcoded run (TSS v5.0.3)
{
   "IonXpress_001":{
      "aligned":true,
      "bam_file":"IonXpress_001_rawlib.bam",
      "bam_filepath":"/results/analysis/output/Local/with_many_samples_017/IonXpress_
↪001_rawlib.bam",
      "barcode_adapter":"GAT",
      "barcode_annotation":"",
      "barcode_description":"",
      "barcode_index":1,
      "barcode_name":"IonXpress_001",
      "barcode_sequence":"CTAAGGTAAC",
      "barcode_type":"",
      "control_sequence_type":"",
      "filtered":false,
      "genome_urlpath":"/auth/output/tmap-f3/hg19/hg19.fasta",
      "hotspot_filepath":"",
      "nucleotide_type":"DNA",
      "read_count":20,
      "reference":"hg19",
      "reference_fullpath":"/results/referenceLibrary/tmap-f3/hg19/hg19.fasta",
      "sample":"First Sample name",
      "sample_id":"",
      "target_region_filepath":""
   },
   "IonXpress_033":{
      "aligned":true,
      "bam_file":"IonXpress_033_rawlib.bam",
      "bam_filepath":"/results/analysis/output/Local/with_many_samples_017/IonXpress_
↪033_rawlib.bam",
      "barcode_adapter":"GAT",
```

```
      "barcode_annotation":"",
      "barcode_description":"",
      "barcode_index":33,
      "barcode_name":"IonXpress_033",
      "barcode_sequence":"TTCTCATTGAAC",
      "barcode_type":"",
      "control_sequence_type":"",
      "filtered":false,
      "genome_urlpath":"/auth/output/tmap-f3/hg19/hg19.fasta",
      "hotspot_filepath":"",
      "nucleotide_type":"DNA",
      "read_count":231321,
      "reference":"hg19",
      "reference_fullpath":"/results/referenceLibrary/tmap-f3/hg19/hg19.fasta",
      "sample":"Second Sample Name",
      "sample_id":"",
      "target_region_filepath":""
   },
   "IonXpress_034":{
      "aligned":true,
      "bam_file":"IonXpress_034_rawlib.bam",
      "bam_filepath":"/results/analysis/output/Local/with_many_samples_017/IonXpress_
↪034_rawlib.bam",
      "barcode_adapter":"GAT",
      "barcode_annotation":"",
      "barcode_description":"",
      "barcode_index":34,
      "barcode_name":"IonXpress_034",
      "barcode_sequence":"TCGCATCGTTC",
      "barcode_type":"",
      "control_sequence_type":"",
      "filtered":false,
      "genome_urlpath":"/auth/output/tmap-f3/hg19/hg19.fasta",
      "hotspot_filepath":"",
      "nucleotide_type":"",
      "read_count":267041,
      "reference":"hg19",
      "reference_fullpath":"/results/referenceLibrary/tmap-f3/hg19/hg19.fasta",
      "sample":"",
      "sample_id":"",
      "target_region_filepath":""
   }
}
```


Usage Notes

1. For consistency, we recommend that you iterate and present barcodes in order of increasing barcode_index value.
2. For default plugin configurations, barcodes with filtered == true are not output. (A plugin option to include these may become available soon.)
3. Barcodes with a sample name provided (i.e. not "") are represented with filtered == false, regardless of read_count value.
4. The bam_filepath value is set to the expected location of the bam_file on the Torrent Server. Barcodes with read_count == 0 may not have a bam_file saved, so you can expect a failure to find the bam_file at bam_filepath. If read_count > 0 then a missing bam_file should be treated as an unexpected error. (This would most likely be a result of automated deletion of old files to make space on the server.)

5. Although control_sequence_type and nucleotide_type appear to be general attributes, at 5.0.3 these are only defined for barcodes that were specified (associated with samples) in the plan. For nonbarcoded elements or barcodes with no sample data that had sufficient reads. these attributes have the value “”.

startplugin.json

This is the primary file to get all of the information regarding the file.

```
{
    chefSummaary <dictionary> : This optional section will convey information␣
↪regarding the chef parameters used. {
    }
    datamanagement <dictionary>: Holds information regarding the data management␣
↪state of the run. {
        Basecalling Input <bool>: This will indicate if the basecalling information␣
↪is available for use.
        Intermediate Files <bool>: This will indicate if the intermediate files are␣
↪available for use.
        Output Files <bool>: This will indicate if the output files are available for␣
↪use.
        Signal Processing Input <bool>: This will indicate if the signal processing␣
↪information is available for use.
    }
    expmeta <dictionary>: This is an aggregate of data contained in the expMeta.dat␣
↪file and the ion_params_00.json file. {
        analysis_date <date>: Gets the time of results analysis based on the last␣
↪modified time stamp on the ion_params_00.json file.
        barcodeId <string>: The barcode kit name from the experiment analysis␣
↪settings.
        chipBarcode <string>: The barcode of the chip derived from the ion_params_00.
↪json->exp_json->chipBarcode... mostly.
        chiptype <string>: This is the chip which was used to do the run.
        flowOrder <string>: The flow order used to sequence the run.
        instrument <string>: The name (not type) of the instrument which was used to␣
↪do the sequencing.
        notes <string>: Any notes which may have been included in the experiment.
        project <string>: A list of all of the projects which this result may belong␣
↪to.
        results_name <string>: The name of the results that will be processed.
        run_date <datetime>: The date/time stamp of the experiment.
        run_flows <int>: The number of flows used in the run.
        run_name <string>: The name of the run as opposed to the name of the result.
        runid <string>: A short identifies for each id.
        sample <string>: This is the name of the first sample which is associated␣
↪with this run.
        output_file_name_stem <string>: This is a merger of the experiment name and␣
↪the results name.
    }
    globalconfig <dictionary>: This section is for the global environment of the␣
↪result. {
        MEM_MAX <string>: Hardcoded to always read "15G".
        debug <int>: Hardcoded to always read 0.
    }
    plan <dictionary>: This section is where all of the elements of the experiment␣
↪plan are stored. {
        barcodeId <string>: The barcode kit name from the experiment analysis␣
↪settings.
```

```
        barcodedSamples <dictionary>: This is a dictionary of all of the samples␣
↪information and the barcodes they are associated with. {
            -Sample Name- <dictionary>: The name of the sample {
                barcodeSampleInfo <dictionary>: Contains the information for the␣
↪barcodes. {
                    -Barcode ID- <dictionary>: {
                        controlSequenceType <string>: The name of the kit used for␣
↪the controls for specific per Sample applications.
                        controlType <string>: The experimental control used for this␣
↪sample. eg (No Template Control)
                        description <string>: Free form description field.
                        externalId <string>: Free form id from any external sources
                        hotSpotRegionBedFile <string>: The name of the hotspot data␣
↪used for this sample.
                        nucleotideType <string>: This will be the nucleotideType used␣
↪for this barcode (DNA/RNA/Fusions).
                        reference <string>: The name of the reference
                        sseBedFile <string>: The SSE Bed file reference.
                        targetRegionBedFile <string>: The name of the target region␣
↪data used for this sample.
                    }
                }
                barcodes <list>: A list of strings which should only have one entry␣
↪equal to the single dictionary key for barcodeSampleInfo.
            }
        }
        bedfile <string>: The name of a bed file used in this plan.
        controlSequencekitname <string, nullable>: The name of the kit used for the␣
↪controls.
        librarykitname <string>: The name of the library kit used in the plan.
        planName <string>: The name of the plan used in the run.
        regionfile <string>: The file to define regions for this plan.
        reverse_primer <string>: The reverse primer used in the plan.
        runMode <string>: The run mode value of 'SingleRead', 'PairedEnd' or
↪'Undefined'
        runType <string>: The type of sequencing for this plan, for example "GENS"
        runTypeDescription <string> : A plain english description of the run type,␣
↪for example "Generic Sequencing".
        sampleGrouping <dictionary>: A representation of the sample group.
        samplePrepKitName <string>: The name of the sample prep kit.
        sampleSet_name <string>: The name of the sample set.
        sampleSet_planIndex <int>: deprecated
        sampleSet_planTotal <int>: deprecated
        sampleSet_uid <string>: deprecated
        sampleTubeLabel <string>: The barcode sample prep label on the sample tube.
        sequencekitname <string>: The name of the kit used for sequencing.
        templatingKitName <string>: The name of the kit used for templating.
        threePrimeAdapter <string>: The sequence of the three prime adapter being␣
↪used.
        username <string>: The name of the user who created the plan.
    }
    runinfo <dictionary>: Information regarding the sequencing run. {
        alignment_dir <string>: The path of the directory with the alignment data.
        analysis_dir <string>: The path of the directory using the Analysis data.
        api_key <string>: The api key which can be used to access the
        api_url <string>: The base directory url for *most* of the rest api calls.
        barcodeId <string>: The identifier for the barcoding kit.
        basecaller_dir <string>: The path to the directory with the basecaller␣
↪information.
```

```
        chipDescription <string>: The description of the chip used for sequencing.
        chipType <string>: The type of the chip used for sequencing.
        library <string>: The reference library used.
        library_key <string>: The key sequence to the library.
        net_location <string>: The url to the master node used for the run.
        pk <int>: The primary key for this run in the database.
        platform <string>: The type of sequencer being used.
        plugin <dictionary>: This section describes the run parameters for this␣
↪plugin in this run. {
            depends <list>: The list of dependency plugins for this run.
            features <list>: The list of features for this plugin.
            hold_jid <list>: A list of SGE job id's which this process was asked to␣
↪hold on.
            id <int>: The database pk for the id of the plugin.
            name <string>: The name of this plugin.
            path <string>: The path to the plugin executable directory.
            pluginconfig <dictionary>: This is a freeform dictionary which contains␣
↪the global configuration used for this plugin run.
            pluginresult <int>:  The database primary key for the plugin results␣
↪entry.
            results_dir <string>: The directory path to the plugin result output.
            runlevel <list>: The list of run levels this plugin has been asked to run␣
↪at.
            runtype <list>: This list of run types that this plugin can be run on.
            userInput <dictionary>: This is a freeform dictionary which contains the␣
↪run configuration used for this plugin run.
            version <string>: The version of the plugin running.
        }
        plugin_dir <string>: The path to the plugin executable directory.
        plugin_name <string>: The name of this plugin.
        pluginresult <int>: The database primary key for the plugin results entry.
        raw_data_dir <string>: The path to the directory which contains the raw␣
↪observational data.
        report_root_dir <string>: The path to the directory of the report.
        results_dir <string>: The path to the directory of the plugin results.
        sigproc_dir <string>: The path to the directory of the signal processing data.
        systemType <string>: The type of sequencer being used.
        testfrag_key <string>: The sequence key to the test fragments.
        tmap_version <string>: The version of the tmap program being used.
        url_root <string>: The file path to the directory of the results data. (not a␣
↪url)
        username <string>: The user who is performing the run.
    {
    runplugin <dictionary>: The exact parameters used for this plugin run. {
        blockId <string>: The id for the block currently being processed.  Blank if␣
↪not a block process.
        block_dirs <list>: A list of all of the directories of all of the block data.
        numBlocks <int>: The total number of blocks processed.
        run_mode <string>: The run mode that this is being processed in, either
↪'pipeline' or 'manual'.
        run_type <string>: The type of the run.  Thumbnail, wholechip or composite.
        runlevel <string>: The current run level being run.
    }
    sampleinfo <dictionary>: A dictionary of information used to convey information␣
↪regarding the samples. {
        SampleName <dictionary>: The name of the sample. {
            attributes <dictionary>: Any attributes {
            }
```

```
            description <????>: A free form description of the sample.
            displayedName <string>: The name of the sample.
            externalId <string>: Any remote identifier used for the sample.
            name <string>: The name of the sample without whitespace.
        }
    pluginconfig <dictionary>: This is a freeform dictionary which contains the run␣
↪configuration used for this plugin run. {
    }
}

Example
{
    "datamanagement": {
        "Basecalling Input": true,
        "Intermediate Files": true,
        "Output Files": true,
        "Signal Processing Input": true
    },
    "expmeta": {
        "analysis_date": "2015-09-02",
        "barcodeId": "",
        "chipBarcode": "AA0026665",
        "chiptype": "\"314R\"",
        "flowOrder": "TACGTACGTCTGAGCATCGATCGATGTACAGC",
        "instrument": "PGM_test",
        "notes": "",
        "project": "SampleData",
        "results_name": "Auto_user_CB1-42-r9723-314wfa-tl_36",
        "run_date": "2011-04-07T12:44:38Z",
        "run_flows": 260,
        "run_name": "R_2011_04_07_12_44_38_user_CB1-42-r9723-314wfa-tl",
        "runid": "ZN2MB",
        "sample": "e5272-wfa-1165"
    },
    "globalconfig": {
        "MEM_MAX": "15G",
        "debug": 0
    },
    "plan": {
        "barcodeId": "",
        "barcodedSamples": {},
        "bedfile": "",
        "controlSequencekitname": null,
        "librarykitname": "Ion Xpress Plus Fragment Library Kit",
        "planName": "CopyOfSystemDefault_R_2011_04_07_12_44_38_user_CB1-42-r9723-
↪314wfa-tl",
        "regionfile": "",
        "reverse_primer": null,
        "runMode": "single",
        "runType": "GENS",
        "runTypeDescription": "",
        "sampleGrouping": null,
        "samplePrepKitName": null,
        "sampleSet_name": null,
        "sampleSet_planIndex": 0,
        "sampleSet_planTotal": 0,
        "sampleSet_uid": null,
        "sampleTubeLabel": null,
```

```
        "sequencekitname": "IonPGM200Kit-v2",
        "templatingKitName": "Ion PGM Template OT2 200 Kit",
        "threePrimeAdapter": "ATCACCGACTGCCCATAGAGAGGCTGAGAC",
        "username": string
    },
    "pluginconfig": {},
    "runinfo": {
        "alignment_dir": "/results/analysis/output/Disabled/Auto_user_CB1-42-r9723-
↪314wfa-tl_36_001",
        "analysis_dir": "/results/analysis/output/Disabled/Auto_user_CB1-42-r9723-
↪314wfa-tl_36_001",
        "api_key": "9516e00c170496012b6df5810431aca7ac558163",
        "api_url": "http://ion-ts-vm/rundb/api",
        "barcodeId": "",
        "basecaller_dir": "/results/analysis/output/Disabled/Auto_user_CB1-42-r9723-
↪314wfa-tl_36_001/basecaller_results",
        "chipDescription": "",
        "chipType": "\"314R\"",
        "library": "e_coli_dh10b",
        "library_key": "TCAG",
        "net_location": "http://ion-ts-vm",
        "pk": 1,
        "platform": "pgm",
        "plugin": {
            "depends": [],
            "features": [],
            "hold_jid": [],
            "id": 11,
            "name": "FilterDuplicates",
            "path": "/results/plugins/FilterDuplicates",
            "pluginconfig": {},
            "pluginresult": 5,
            "results_dir": "/results/analysis/output/Disabled/Auto_user_CB1-42-r9723-
↪314wfa-tl_36_001/plugin_out/FilterDuplicates_out.5",
            "runlevel": [],
            "runtype": [
                "composite",
                "wholechip",
                "thumbnail"
            ],
            "userInput": "",
            "version": "5.0.0.0"
        },
        "plugin_dir": "/results/plugins/FilterDuplicates",
        "plugin_name": "FilterDuplicates",
        "pluginresult": 5,
        "raw_data_dir": "/results/PGM_test/cropped_CB1-42",
        "report_root_dir": "/results/analysis/output/Disabled/Auto_user_CB1-42-r9723-
↪314wfa-tl_36_001",
        "results_dir": "/results/analysis/output/Disabled/Auto_user_CB1-42-r9723-
↪314wfa-tl_36_001/plugin_out/FilterDuplicates_out.5",
        "sigproc_dir": "/results/analysis/output/Disabled/Auto_user_CB1-42-r9723-
↪314wfa-tl_36_001/sigproc_results",
        "systemType": "pgm",
        "testfrag_key": "ATCG",
        "tmap_version": "tmap-f3",
        "url_root": "/output/Disabled/Auto_user_CB1-42-r9723-314wfa-tl_36_001",
        "username": "ionadmin"
```

```
    },
    "runplugin": {
        "blockId": "",
        "block_dirs": [
            "."
        ],
        "numBlocks": 1,
        "run_mode": "manual",
        "run_type": "wholechip",
        "runlevel": "default"
    },
    "sampleinfo": {
        "e5272-wfa-l165": {
            "attributes": {},
            "description": null,
            "displayedName": "e5272-wfa-l165",
            "externalId": "",
            "name": "e5272-wfa-l165"
        }
    }
}
```


Seq Files (BAMs)

The actual sequence information is a critical portion of all of the plugins running information. When you attempt to access them, refer to the barcodes.json file for references to their path in the "bam_filepath" key.

Output Files

The primary output of all of the plugins is the report HTML file, which is produced by the plugin. Name this file *_block.html or *_block.php. There can be any number of them, and they are all displayed in separate iFrames. If plugin output doesn't contain a _block.html or _block.php file then all HTML/PHP files in the plugin result folder will be shown as links in the plugin section.

Additionally, the SGE produces a log file for recording the standard output of the plugin execution, which is called drmaa_stdout.txt. This contains all the information printed from the controlling script, including the standard output of the plugin itself, and is a primary source of information for debugging.

See *Rendering Templates* for an example using HTML templates. This usually results in cleaner code than assembling large strings or multiple-file writes.

File Permissions

The SGE executes all of the plugins as the user 'ionian' to perform the execution. All files produced have both the owner and group of ionian and full read/write access to the plugin result directory. This also includes the ability to create new directories. The plugins have only read access to all other files, most notably the file in the run results directory.

Upgrades

When upgrading the plugins, after all of the changes have been made to the logic of plugin, all you need to do is to increment the version of the plugin and repackage the plugin for deployment.

Plugin Examples

This section has a very basic example plugin and its code.

Basic Plugin

This plugin goes through the explog and presents a few entries in the plugin output. It produces an HTML output but does not take any parameters.

```
#!/usr/bin/python
# Copyright (C) 2018 Thermo Fisher Scientific, Inc. All Rights Reserved

#
# Samples: LogParser
# plugin demonstrating simple log parsing ability
#

import json
import os
from django.utils.functional import cached_property
from ion.plugin import *


class LogParser(IonPlugin):
    # The version number for this plugin
    version = "5.4.0.0"

    # this plugin can run on fullchip runs, thumbnail runs, and composite (merged via␣
↪project page) runs
    # when this plugin is manually launched, only the 'launch' method is called
    runtypes = [RunType.FULLCHIP, RunType.THUMB, RunType.COMPOSITE]

    # specify when the plugin is called.  For log parsing, stay simple and just get␣
↪called when the run completes.
    # the plugin can also be called before the run starts, at the block level, or␣
↪after all other default plugins run
    runlevels = [RunLevel.DEFAULT]

    # a simple cached version of the start plugin property
    @cached_property
    def startplugin_json(self):
        return self.startplugin

    def read_explog(self):
        """This method reads and outputs an array of colon-delimited key/value pairs␣
↪from the explog_final.txt"""

        path = os.path.join(self.startplugin_json['runinfo']['raw_data_dir'], "explog_
↪final.txt")
        if not os.path.exists(path):
            raise Exception("explog_final.txt missing")

        # parse the log file for all of the values in a colon-delimited parameter
        data = dict()
        for line in open(path):
            # accommodates formatting issues in explog
```

```
            datum = line.split(":", 1)
            if len(datum) == 2:
                key, value = datum
                data[key.strip()] = value.strip()

        return data

    def launch(self, data=None):
        """This is the primary launch method for the plugin."""

        na = '<strong>NA</strong>'
        # creates a results object that is written out later.  This holds data that
↪can be scrapped by a LIMS system,
                    and will be part of the |TS| database
        exp_log_data = self.read_explog()
        results_json = {
            'Project': exp_log_data.get('Project', None) or na,
            'Sample': exp_log_data.get('Sample', None) or na,
            'Library': exp_log_data.get('Library', None) or na,
        }

        # open up an HTML file to dump interesting log file findings to
        with open(self.startplugin_json['runinfo']['results_dir'] + '/LogParser_block.
↪html', 'w') as html_handle:
            html_handle.write('<html><body>')
            html_handle.write("Project is: %s<br \>" % results_json['Project'])
            html_handle.write("Sample is: %s<br \>" % results_json['Sample'])
            html_handle.write("Library is: %s<br \>" % results_json['Library'])
            html_handle.write('</body></hmtl>')

        # write out our results json object
        with open(self.startplugin_json['runinfo']['results_dir'] + '/results.json',
↪'w') as results_handle:
            json.dump(results_json, results_handle, indent=4)

        return True

# Devel use - running directly
if __name__ == "__main__":
    PluginCLI()
```

Plugin which uses a subprocess

```
#!/usr/bin/python
# Copyright (C) 2018 Thermo Fisher Scientific, Inc. All Rights Reserved

#
# Samples: LogParser
# plugin demonstrating simple log parsing ability
#

import json
import os
from django.utils.functional import cached_property
from ion.plugin import *
from subprocess import check_output
```

```
class CallSubprocessExample(IonPlugin):
    # The version number for this plugin
    version = "5.4.0.0"

    # this plugin can run on fullchip runs, thumbnail runs, and composite (merged via␣
↪project page) runs
    # note that when the plugin is manually launched, only the 'launch' method will␣
↪be called
    runtypes = [RunType.FULLCHIP, RunType.THUMB, RunType.COMPOSITE]

    # specify when the plugin is called.  For log parsing, stay simple and just get␣
↪called when the run completes.
    # but can also be called before the run starts, at the block level, or after all␣
↪other default plugins run
    runlevels = [RunLevel.DEFAULT]

    # a simple cached version of the start plugin property
    @cached_property
    def startplugin_json(self):
        return self.startplugin

    def launch(self, data=None):
        """This is the primary launch method for the plugin."""

        path_to_executable = "MyExecutable"
        arg1 = 'First Argument'
        arg2 = 'Second Argument'
        results = check_output([path_to_executable, arg1, arg2], cwd=self.startplugin_
↪json['runinfo']['plugin']['path'])

        return True

# Devel use - running directly
if __name__ == "__main__":
    PluginCLI()
```

Accessing Barcode Data

```
#!/usr/bin/python
# Copyright (C) 2018 Thermo Fisher Scientific, Inc. All Rights Reserved

#
# Samples: LogParser
# plugin demonstrating simple log parsing ability
#

import json
import os
from django.utils.functional import cached_property
from ion.plugin import *
from subprocess import check_output


class BarcodesExample(IonPlugin):
```

```
    # The version number for this plugin
    version = "5.4.0.0"

    # this plugin can run on fullchip runs, thumbnail runs, and composite (merged via␣
↪project page) runs
    # note that when the plugin is manually launched, only the 'launch' method will␣
↪be called
    runtypes = [RunType.FULLCHIP, RunType.THUMB, RunType.COMPOSITE]

    # specify when the plugin is called.  For log parsing, stay simple and just get␣
↪called when the run completes.
    # but can also be called before the run starts, at the block level, or after all␣
↪other default plugins run
    runlevels = [RunLevel.DEFAULT]

    # a simple cached version of the start plugin property
    @cached_property
    def startplugin_json(self):
        return self.startplugin

    @cached_property
    def barcodes_json:
        with open('barcodes.json', 'r') as barcodes_handle:
            return json.load(barcodes_handle)

    def launch(self, data=None):
        """This is the primary launch method for the plugin."""

        for barcode_name, barcode_values in self.barcodes_json.iteritems():
            # do you work per barcode here!
            print("Barcode Name: " + barcode_name)
            print("Bam File: " + barcode_values['bam_file']

        return True

# Devel use - running directly
if __name__ == "__main__":
    PluginCLI()
```

Using the REST API

```
import json
import requests
api_response = requests.get('http://HOSTNAME/APPNAME/api/v1/APIENDPOINT/?ARG1=VAL1&
↪pluginresult=self.startplugin['runinfo']['pluginresult']&api_key=' + self.
↪startplugin['runinfo']['api_key'])
api_response.raise_for_status()
api_json_response = json.loads(api_response.content)
```

Note: api-key is tied to the specific plugin run so the system must also get which "pluginresult" is sending the API request.

Example 1: How to get the installed annotation files during the plugin execution?

```
#!/usr/bin/env python
# -*- coding: utf-8 -*-
```

```
# Copyright (C) 2018 Thermo Fisher Scientific, Inc. All Rights Reserved

import os
import sys
import requests
import json

from ion.plugin import RunType, PluginCLI, IonPlugin

API_VER = '/v1'

class PluginApiTest(IonPlugin):
    """
       This will make REST api call to get the installed annotation files
       with 'api_key' corresponding to the specific plugin run
    """

    version = "1.0"
    runtypes = [RunType.THUMB, RunType.FULLCHIP]

    def launch(self):
        sp_json_fpath = os.path.join(
            os.environ.get('RESULTS_DIR', ''),
            'startplugin.json'
        )

        with open(sp_json_fpath, 'r') as sp_fh:
            sp_json = json.load(sp_fh)

        endpoint = '/content'
        auth_params = {
            'api_key': sp_json['runinfo']['api_key'],
            'pluginresult': sp_json['runinfo']['pluginresult'],
        }
        query_params = {
            'type': 'Annotation'
        }
        request_params = {}
        request_params.update(auth_params)
        request_params.update(query_params)

        url = sp_json['runinfo']['api_url'] + API_VER + endpoint
        resp = requests.get(url, params=request_params)
        if resp:
            print(resp.url)
            print(resp.json())
            sys.exit(0)
        else:
            print(resp.status_code)
            sys.exit(1)


if __name__ == "__main__":
    PluginCLI()
```

Example 2: Use the below query_params to list all the files of mm10 auxiliary references for RNASeqAnalysis. Please note the type of camelcase, AuxiliaryReference.

```
...
query_params = {
    'application_tags__icontains' : 'RNA',
    'extra':'mm10',
    'type' :'AuxiliaryReference'
}
...
```

Displaying Progress

When displaying progress, this needs to be manually updated by re-writing the *_block.html file intermittently during the process. Here is a simple example of how to construct a method to do this.

```
...
def update_progress(self, current_progress, max_progress)
    with open(self.startplugin['runinfo']['results_dir'] + '/progress_block.html', 'w
↪') as html_handle:
            html_handle.write('<html><body>')
            html_handle.write("The current progress is %d of %d" %(current_progress,␣
↪max_progress))
            html_handle.write('</body></hmtl>')
...
```

Rendering Templates

When outputting HTML files, using templates can be cleaner than assembling long strings. Below is an example of using Django templates. This example uses an HTML template named *progress_block_template.html* inside a *templates* directory inside the plugins root directory.

```
from django.conf import settings
from django.template.loader import render_to_string

settings.configure(TEMPLATE_DIR=self.startplugin["runinfo"]["plugin"]["path"] + '/
↪templates')

with open(self.startplugin['runinfo']['results_dir'] + '/progress_block.html', 'w')␣
↪as html_handle:
    html_handle.write(render_to_string("progress_block_template.html", {"current_
↪progress": 54}))
```

CHAPTER 2

Torrent Suite™ Software REST API

This section describes all of the REST API end points that Torrent Suite™ Software makes available and the ways in which you access them.

Getting Started with the API

API Overview

Our API is RESTful and HTTP based. All resources use HTTP standard verbs return JSON data.

The main API endpoint for Torrent Suite™ Software is `/rundb/api/v1/`. This endpoint returns a JSON object containing information for each resource available from the API. To see each resource's list endpoint, go to `/rundb/api/v1/resource-name/` . To see each resource's schema, go to `/rundb/api/v1/resource-name/schema/`.

Authentication

To use the API you need to authenticate as an existing Torrent Suite™ Software user. To see API keys for each Torrent Suite™ Software user, go to `/admin/tastypie/apikey/` . You must include an API key with every API request. There are two methods:

As a header. Format is `Authorization: ApiKey <username>:<api_key> Authorization: ApiKey daniel:204db7bcfafb2deb7506b89eb3b9b715b09905c8`

As GET params `http://127.0.0.1:8000/api/v1/entries/?username=daniel&api_key=204db7bcfafb2deb75`

Pagination

The meta section of the list endpoint's response contains pagination details. Use the following GET params to control pagination.

`limit` The maximum number of resources the objects list will contain.
`next` A URL pointing to the next page of results.
`offset` The object number the current list of objects starts at.
`previous` A URL pointing to the previous page of results.
`total_count` The total number of objects remaining after filtering.

Modify `limit` and `offset` with URL parameters.

Sorting

Use the `order_by` GET param to specify a field to sort returned objects. Add a - character in front of the field name to switch the sort direction from ascending order (the default) to descending order. You can use most fields of an object to sort.

Filtering

Perform basic filtering by using a GET param with the same name as an object field. Using `name=alexander` only returns objects with a name field of "alexander".

Use more advanced filters by appending the correct suffix to the GET param. The suffix consists of __ plus one of the filters that follow. Using `name__startswith=alex` only returns objects with a name field starting with "alex".

Filter	Description
exact	Exact match.
iexact	Case-insensitive exact match.
contains	Case-sensitive containment test.
icontains	Case-insensitive containment test.
in	In a given list. Comma delimited.
gt	Greater than.
gte	Greater than or equal to.
lt	Less than.
lte	Less than or equal to.
startswith	Case-sensitive starts-with.
istartswith	Case-insensitive starts-with.
endswith	Case-sensitive ends-with.
iendswith	Case-insensitive ends-with.
range	Range test (inclusive).
year	Exact year match (date fields).
month	Exact month number match (date fields).
day	Exact day number match (date fields).
week_day	Exact week day number match. 1-7. Sunday=1 (date fields).
hour	Exact hour match. 0-23. (date fields).
minute	Exact minute match. 0-59. (date fields).
second	Exact second match. 0-59. (date fields).
isnull	Null check. True or False.
regex	Case-sensitive regular expression match.
iregex	Case-insensitive regular expression match.

API Reference

This section has automatically generated reference pages for each endpoint the REST API provides.

Active Ion Chef Library Prep Kit Info Resource

Resource URL
`http://mytorrentserver/rundb/api/v1/activeioncheflibraryprepkitinfo/`
Schema URL
`http://mytorrentserver/rundb/api/v1/activeioncheflibraryprepkitinfo/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
isActive	Boolean data. Ex: True	true	false	false	true	false	boolean
samplePrep_instrumentType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
kitType	Unicode string data. Ex: "Hello World"	n/a	false	false	false	false	string
description	Unicode string data. Ex: "Hello World"		false	false	true	false	string
nucleotideType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
defaultCartridgeUsageCount	Integer data. Ex: 2673	n/a	true	false	false	false	integer
instrumentType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
chipTypes	Unicode string data. Ex: "Hello World"		false	false	true	false	string
runMode	Unicode string data. Ex: "Hello World"		false	false	true	false	string
parts	Many related resources. Can be either a list of URIs or list of individually nested resource data.	n/a	false	false	false	false	related
flowCount	Integer data. Ex: 2673	n/a	false	false	false	false	integer
applicationType	Unicode string data. Ex: "Hello World"		true	false	false	false	string
cartridgeExpirationDayLimit	Integer data. Ex: 2673	n/a	true	false	false	false	integer
libraryReadLength	Integer data. Ex: 2673	0	false	false	false	false	integer
cartridgeBetweenUsageAbsoluteMaxDayLimit	Integer data. Ex: 2673	n/a	true	false	false	false	integer
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string
uid	Unicode string data. Ex: "Hello World"	n/a	false	false	false	true	string
id	Integer data. Ex: 2673		false	false	true	true	integer
categories	Unicode string data. Ex: "Hello World"		true	false	false	false	string
name	Unicode string data. Ex: "Hello World"	n/a	false	false	false	true	string

Example Response

```
{
    "meta": {
        "previous": null,
        "total_count": 2,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/activeioncheflibraryprepkitinfo/?offset=1&limit=1&
↪format=json"
    },
    "objects": [
```

```
        {
            "isActive": true,
            "samplePrep_instrumentType": "IC",
            "kitType": "LibraryPrepKit",
            "description": "Precision ID Chef DL8",
            "nucleotideType": "",
            "defaultCartridgeUsageCount": null,
            "instrumentType": "",
            "chipTypes": "",
            "runMode": "",
            "parts": [
                {
                    "barcode": "A32926C",
                    "id": 20245,
                    "resource_uri": "/rundb/api/v1/kitpart/20245/",
                    "kit": "/rundb/api/v1/kitinfo/20105/"
                },
                {
                    "barcode": "A33212",
                    "id": 20261,
                    "resource_uri": "/rundb/api/v1/kitpart/20261/",
                    "kit": "/rundb/api/v1/kitinfo/20105/"
                }
            ],
            "flowCount": 0,
            "applicationType": "AMPS",
            "cartridgeExpirationDayLimit": null,
            "libraryReadLength": 0,
            "cartridgeBetweenUsageAbsoluteMaxDayLimit": null,
            "resource_uri": "/rundb/api/v1/activeioncheflibraryprepkitinfo/20105/",
            "uid": "LPREP0003",
            "id": 20105,
            "categories": "filter_s5HidKit",
            "name": "Ion Chef HID Library V2"
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT

- DELETE
- PATCH

Active Ion Chef Prep Kit Info Resource

Resource URL `http://mytorrentserver/rundb/api/v1/activeionchefprepkitinfo/`
Schema URL `http://mytorrentserver/rundb/api/v1/activeionchefprepkitinfo/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	kunique	type
isActive	Boolean data. Ex: True	true	false	false	true	false	boolean
samplePrep_instrumentType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
kitType	Unicode string data. Ex: "Hello World"	n/a	false	false	false	false	string
description	Unicode string data. Ex: "Hello World"		false	false	true	false	string
nucleotideType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
defaultCartridgeUsageCount	Integer data. Ex: 2673	n/a	true	false	false	false	integer
instrumentType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
chipTypes	Unicode string data. Ex: "Hello World"		false	false	true	false	string
runMode	Unicode string data. Ex: "Hello World"		false	false	true	false	string
parts	Many related resources. Can be either a list of URIs or list of individually nested resource data.	n/a	false	false	false	false	related
flowCount	Integer data. Ex: 2673	n/a	false	false	false	false	integer
applicationType	Unicode string data. Ex: "Hello World"		true	false	false	false	string
cartridgeExpirationDayLimit	Integer data. Ex: 2673	n/a	true	false	false	false	integer
libraryReadLength	Integer data. Ex: 2673	0	false	false	false	false	integer
cartridgeBetweenUsageAbsoluteMaxDayLimit	Integer data. Ex: 2673	n/a	true	false	false	false	integer
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string
uid	Unicode string data. Ex: "Hello World"	n/a	false	false	false	true	string
id	Integer data. Ex: 2673		false	false	true	true	integer
categories	Unicode string data. Ex: "Hello World"		true	false	false	false	string
name	Unicode string data. Ex: "Hello World"	n/a	false	false	false	true	string

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 9,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/activeionchefprepkitinfo/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "isActive": true,
            "samplePrep_instrumentType": "IC",
            "kitType": "IonChefPrepKit",
            "description": "Precision ID Chef Reagents",
            "nucleotideType": "",
            "defaultCartridgeUsageCount": null,
            "instrumentType": "S5",
            "chipTypes": "510;520;530",
            "runMode": "",
            "parts": [
                {
                    "barcode": "A32882C",
                    "id": 20246,
                    "resource_uri": "/rundb/api/v1/kitpart/20246/",
                    "kit": "/rundb/api/v1/kitinfo/20106/"
                }
            ],
            "flowCount": 0,
            "applicationType": "AMPS",
            "cartridgeExpirationDayLimit": null,
            "libraryReadLength": 0,
            "cartridgeBetweenUsageAbsoluteMaxDayLimit": null,
            "resource_uri": "/rundb/api/v1/activeionchefprepkitinfo/20106/",
            "uid": "ICPREP0011",
            "id": 20106,
            "categories": "filter_s5HidKit;samplePrepProtocol;s5hidSamplePrep",
            "name": "Ion Chef HID S530 V2"
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Active Library Kit Info Resource

Resource URL `http://mytorrentserver/rundb/api/v1/activelibrarykitinfo/`
Schema URL `http://mytorrentserver/rundb/api/v1/activelibrarykitinfo/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
isActive	Boolean data. Ex: True	true	false	false	true	false	boolean
samplePrep_instrumentType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
kitType	Unicode string data. Ex: "Hello World"	n/a	false	false	false	false	string
description	Unicode string data. Ex: "Hello World"		false	false	true	false	string
nucleotideType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
defaultCartridgeUsageCount	Integer data. Ex: 2673	n/a	true	false	false	false	integer
instrumentType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
chipTypes	Unicode string data. Ex: "Hello World"		false	false	true	false	string
runMode	Unicode string data. Ex: "Hello World"		false	false	true	false	string
parts	Many related resources. Can be either a list of URIs or list of individually nested resource data.	n/a	false	false	false	false	related
flowCount	Integer data. Ex: 2673	n/a	false	false	false	false	integer
applicationType	Unicode string data. Ex: "Hello World"		true	false	false	false	string
cartridgeExpirationDayLimit	Integer data. Ex: 2673	n/a	true	false	false	false	integer
libraryReadLength	Integer data. Ex: 2673	0	false	false	false	false	integer
cartridgeBetweenUsageAbsoluteMaxDayLimit	Integer data. Ex: 2673	n/a	true	false	false	false	integer
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string
uid	Unicode string data. Ex: "Hello World"	n/a	false	false	false	true	string
id	Integer data. Ex: 2673		false	false	true	true	integer
categories	Unicode string data. Ex: "Hello World"		true	false	false	false	string
name	Unicode string data. Ex: "Hello World"	n/a	false	false	false	true	string

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 21,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/activelibrarykitinfo/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
```

```
            "isActive": true,
            "samplePrep_instrumentType": "",
            "kitType": "LibraryKit",
            "description": "MuSeek Library Preparation Kit",
            "nucleotideType": "dna",
            "defaultCartridgeUsageCount": null,
            "instrumentType": "",
            "chipTypes": "",
            "runMode": "",
            "parts": [],
            "flowCount": 0,
            "applicationType": "GENS",
            "cartridgeExpirationDayLimit": null,
            "libraryReadLength": 0,
            "cartridgeBetweenUsageAbsoluteMaxDayLimit": null,
            "resource_uri": "/rundb/api/v1/activelibrarykitinfo/20025/",
            "uid": "LIB0012",
            "id": 20025,
            "categories": "filter_muSeek",
            "name": "MuSeek(tm) Library Preparation Kit"
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Active Pgm Library Kit Info Resource

Resource URL `http://mytorrentserver/rundb/api/v1/activepgmlibrarykitinfo/`
Schema URL `http://mytorrentserver/rundb/api/v1/activepgmlibrarykitinfo/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
isActive	Boolean data. Ex: True	true	false	false	true	false	boolean
samplePrep_instrumentType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
kitType	Unicode string data. Ex: "Hello World"	n/a	false	false	false	false	string
description	Unicode string data. Ex: "Hello World"		false	false	true	false	string
nucleotideType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
defaultCartridgeUsageCount	Integer data. Ex: 2673	n/a	true	false	false	false	integer
instrumentType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
chipTypes	Unicode string data. Ex: "Hello World"		false	false	true	false	string
runMode	Unicode string data. Ex: "Hello World"		false	false	true	false	string
parts	Many related resources. Can be either a list of URIs or list of individually nested resource data.	n/a	false	false	false	false	related
flowCount	Integer data. Ex: 2673	n/a	false	false	false	false	integer
applicationType	Unicode string data. Ex: "Hello World"		true	false	false	false	string
cartridgeExpirationDayLimit	Integer data. Ex: 2673	n/a	true	false	false	false	integer
libraryReadLength	Integer data. Ex: 2673	0	false	false	false	false	integer
cartridgeBetweenUsageAbsoluteMaxDayLimit	Integer data. Ex: 2673	n/a	true	false	false	false	integer
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string
uid	Unicode string data. Ex: "Hello World"	n/a	false	false	false	true	string
id	Integer data. Ex: 2673		false	false	true	true	integer
categories	Unicode string data. Ex: "Hello World"		true	false	false	false	string
name	Unicode string data. Ex: "Hello World"	n/a	false	false	false	true	string

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 18,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/activepgmlibrarykitinfo/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
```

```
            "isActive": true,
            "samplePrep_instrumentType": "",
            "kitType": "LibraryKit",
            "description": "MuSeek Library Preparation Kit",
            "nucleotideType": "dna",
            "defaultCartridgeUsageCount": null,
            "instrumentType": "",
            "chipTypes": "",
            "runMode": "",
            "parts": [],
            "flowCount": 0,
            "applicationType": "GENS",
            "cartridgeExpirationDayLimit": null,
            "libraryReadLength": 0,
            "cartridgeBetweenUsageAbsoluteMaxDayLimit": null,
            "resource_uri": "/rundb/api/v1/activepgmlibrarykitinfo/20025/",
            "uid": "LIB0012",
            "id": 20025,
            "categories": "filter_muSeek",
            "name": "MuSeek(tm) Library Preparation Kit"
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Active Pgm Sequencing Kit Info Resource

Resource URL `http://mytorrentserver/rundb/api/v1/activepgmsequencingkitinfo/`
Schema URL
`http://mytorrentserver/rundb/api/v1/activepgmsequencingkitinfo/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
isActive	Boolean data. Ex: True	true	false	false	true	false	boolean
samplePrep_instrumentType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
kitType	Unicode string data. Ex: "Hello World"	n/a	false	false	false	false	string
defaultFlowOrder	A single related resource. Can be either a URI or set of nested resource data.	n/a	true	false	false	false	related
name	Unicode string data. Ex: "Hello World"	n/a	false	false	false	true	string
nucleotideType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
defaultCartridgeUsageCount	Integer data. Ex: 2673	n/a	true	false	false	false	integer
instrumentType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
chipTypes	Unicode string data. Ex: "Hello World"		false	false	true	false	string
runMode	Unicode string data. Ex: "Hello World"		false	false	true	false	string
parts	Many related resources. Can be either a list of URIs or list of individually nested resource data.	n/a	false	false	false	false	related
flowCount	Integer data. Ex: 2673	n/a	false	false	false	false	integer
applicationType	Unicode string data. Ex: "Hello World"		true	false	false	false	string
cartridgeExpirationDayLimit	Integer data. Ex: 2673	n/a	true	false	false	false	integer
libraryReadLength	Integer data. Ex: 2673	0	false	false	false	false	integer
cartridgeBetweenUsageAbsoluteMaxDayLimit	Integer data. Ex: 2673	n/a	true	false	false	false	integer
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string
uid	Unicode string data. Ex: "Hello World"	n/a	false	false	false	true	string
id	Integer data. Ex: 2673		false	false	true	true	integer
categories	Unicode string data. Ex: "Hello World"		true	false	false	false	string
description	Unicode string data. Ex: "Hello World"		false	false	true	false	string

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 4,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/activepgmsequencingkitinfo/?offset=1&limit=1&
↪format=json"
```

```
    },
    "objects": [
        {
            "isActive": true,
            "samplePrep_instrumentType": "OT_IC",
            "kitType": "SequencingKit",
            "defaultFlowOrder": null,
            "name": "IonPGMInstallKit",
            "nucleotideType": "",
            "defaultCartridgeUsageCount": null,
            "instrumentType": "pgm",
            "chipTypes": "",
            "runMode": "",
            "parts": [
                {
                    "barcode": "4480217",
                    "id": 20019,
                    "resource_uri": "/rundb/api/v1/kitpart/20019/",
                    "kit": "/rundb/api/v1/kitinfo/20020/"
                },
                {
                    "barcode": "4480282",
                    "id": 20020,
                    "resource_uri": "/rundb/api/v1/kitpart/20020/",
                    "kit": "/rundb/api/v1/kitinfo/20020/"
                },
                {
                    "barcode": "4480284",
                    "id": 20021,
                    "resource_uri": "/rundb/api/v1/kitpart/20021/",
                    "kit": "/rundb/api/v1/kitinfo/20020/"
                }
            ],
            "flowCount": 100,
            "applicationType": "",
            "cartridgeExpirationDayLimit": null,
            "libraryReadLength": 0,
            "cartridgeBetweenUsageAbsoluteMaxDayLimit": null,
            "resource_uri": "/rundb/api/v1/activepgmsequencingkitinfo/20020/",
            "uid": "SEQ0006",
            "id": 20020,
            "categories": "readLengthDerivableFromFlows;",
            "description": "Ion PGM Install Kit"
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Active Proton Library Kit Info Resource

Resource URL `http://mytorrentserver/rundb/api/v1/activeprotonlibrarykitinfo/`
Schema URL
`http://mytorrentserver/rundb/api/v1/activeprotonlibrarykitinfo/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
isActive	Boolean data. Ex: True	true	false	false	true	false	boolean
samplePrep_instrumentType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
kitType	Unicode string data. Ex: "Hello World"	n/a	false	false	false	false	string
description	Unicode string data. Ex: "Hello World"		false	false	true	false	string
nucleotideType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
defaultCartridgeUsageCount	Integer data. Ex: 2673	n/a	true	false	false	false	integer
instrumentType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
chipTypes	Unicode string data. Ex: "Hello World"		false	false	true	false	string
runMode	Unicode string data. Ex: "Hello World"		false	false	true	false	string
parts	Many related resources. Can be either a list of URIs or list of individually nested resource data.	n/a	false	false	false	false	related
flowCount	Integer data. Ex: 2673	n/a	false	false	false	false	integer
applicationType	Unicode string data. Ex: "Hello World"		true	false	false	false	string
cartridgeExpirationDayLimit	Integer data. Ex: 2673	n/a	true	false	false	false	integer
libraryReadLength	Integer data. Ex: 2673	0	false	false	false	false	integer
cartridgeBetweenUsageAbsoluteMaxDayLimit	Integer data. Ex: 2673	n/a	true	false	false	false	integer
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string
uid	Unicode string data. Ex: "Hello World"	n/a	false	false	false	true	string
id	Integer data. Ex: 2673		false	false	true	true	integer
categories	Unicode string data. Ex: "Hello World"		true	false	false	false	string
name	Unicode string data. Ex: "Hello World"	n/a	false	false	false	true	string

Example Response

```
{
    "meta": {
        "previous": null,
        "total_count": 19,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/activeprotonlibrarykitinfo/?offset=1&limit=1&
↪format=json"
    },
    "objects": [
```

```
        {
            "isActive": true,
            "samplePrep_instrumentType": "",
            "kitType": "LibraryKit",
            "description": "MuSeek Library Preparation Kit",
            "nucleotideType": "dna",
            "defaultCartridgeUsageCount": null,
            "instrumentType": "",
            "chipTypes": "",
            "runMode": "",
            "parts": [],
            "flowCount": 0,
            "applicationType": "GENS",
            "cartridgeExpirationDayLimit": null,
            "libraryReadLength": 0,
            "cartridgeBetweenUsageAbsoluteMaxDayLimit": null,
            "resource_uri": "/rundb/api/v1/activeprotonlibrarykitinfo/20025/",
            "uid": "LIB0012",
            "id": 20025,
            "categories": "filter_muSeek",
            "name": "MuSeek(tm) Library Preparation Kit"
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Active Proton Sequencing Kit Info Resource

Resource URL `http://mytorrentserver/rundb/api/v1/activeprotonsequencingkitinfo/`
Schema URL
`http://mytorrentserver/rundb/api/v1/activeprotonsequencingkitinfo/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
isActive	Boolean data. Ex: True	true	false	false	true	false	boolean
samplePrep_instrumentType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
kitType	Unicode string data. Ex: "Hello World"	n/a	false	false	false	false	string
defaultFlowOrder	A single related resource. Can be either a URI or set of nested resource data.	n/a	true	false	false	false	related
name	Unicode string data. Ex: "Hello World"	n/a	false	false	false	true	string
nucleotideType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
defaultCartridgeUsageCount	Integer data. Ex: 2673	n/a	true	false	false	false	integer
instrumentType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
chipTypes	Unicode string data. Ex: "Hello World"		false	false	true	false	string
runMode	Unicode string data. Ex: "Hello World"		false	false	true	false	string
parts	Many related resources. Can be either a list of URIs or list of individually nested resource data.	n/a	false	false	false	false	related
flowCount	Integer data. Ex: 2673	n/a	false	false	false	false	integer
applicationType	Unicode string data. Ex: "Hello World"		true	false	false	false	string
cartridgeExpirationDayLimit	Integer data. Ex: 2673	n/a	true	false	false	false	integer
libraryReadLength	Integer data. Ex: 2673	0	false	false	false	false	integer
cartridgeBetweenUsageAbsoluteMaxDayLimit	Integer data. Ex: 2673	n/a	true	false	false	false	integer
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string
uid	Unicode string data. Ex: "Hello World"	n/a	false	false	false	true	string
id	Integer data. Ex: 2673		false	false	true	true	integer
categories	Unicode string data. Ex: "Hello World"		true	false	false	false	string
description	Unicode string data. Ex: "Hello World"		false	false	true	false	string

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 5,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/activeprotonsequencingkitinfo/?offset=1&limit=1&
↪format=json"
```

```
    },
    "objects": [
        {
            "isActive": true,
            "samplePrep_instrumentType": "",
            "kitType": "SequencingKit",
            "defaultFlowOrder": null,
            "name": "ProtonI200Kit-v2",
            "nucleotideType": "",
            "defaultCartridgeUsageCount": null,
            "instrumentType": "proton",
            "chipTypes": "900;P1.0.19;P1.0.20;P1.1.17;P1.1.541;P1.2.18;P2.0.1;P2.1.1;
↪P2.3.1",
            "runMode": "",
            "parts": [
                {
                    "barcode": "4485149",
                    "id": 20094,
                    "resource_uri": "/rundb/api/v1/kitpart/20094/",
                    "kit": "/rundb/api/v1/kitinfo/20044/"
                },
                {
                    "barcode": "4485521",
                    "id": 20095,
                    "resource_uri": "/rundb/api/v1/kitpart/20095/",
                    "kit": "/rundb/api/v1/kitinfo/20044/"
                },
                {
                    "barcode": "4484082",
                    "id": 20096,
                    "resource_uri": "/rundb/api/v1/kitpart/20096/",
                    "kit": "/rundb/api/v1/kitinfo/20044/"
                },
                {
                    "barcode": "4482282",
                    "id": 20078,
                    "resource_uri": "/rundb/api/v1/kitpart/20078/",
                    "kit": "/rundb/api/v1/kitinfo/20044/"
                },
                {
                    "barcode": "4482284",
                    "id": 20079,
                    "resource_uri": "/rundb/api/v1/kitpart/20079/",
                    "kit": "/rundb/api/v1/kitinfo/20044/"
                }
            ],
            "flowCount": 500,
            "applicationType": "",
            "cartridgeExpirationDayLimit": null,
            "libraryReadLength": 0,
            "cartridgeBetweenUsageAbsoluteMaxDayLimit": null,
            "resource_uri": "/rundb/api/v1/activeprotonsequencingkitinfo/20044/",
            "uid": "SEQ0012",
            "id": 20044,
            "categories": "readLengthDerivableFromFlows;",
            "description": "Ion PI Sequencing 200 Kit v2"
        }
    ]
```

```
}
```

Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Active Sequencing Kit Info Resource

Resource URL `http://mytorrentserver/rundb/api/v1/activesequencingkitinfo/`
Schema URL `http://mytorrentserver/rundb/api/v1/activesequencingkitinfo/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
isActive	Boolean data. Ex: True	true	false	false	true	false	boolean
samplePrep_instrumentType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
kitType	Unicode string data. Ex: "Hello World"	n/a	false	false	false	false	string
defaultFlowOrder	A single related resource. Can be either a URI or set of nested resource data.	n/a	true	false	false	false	related
name	Unicode string data. Ex: "Hello World"	n/a	false	false	false	true	string
nucleotideType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
defaultCartridgeUsageCount	Integer data. Ex: 2673	n/a	true	false	false	false	integer
instrumentType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
chipTypes	Unicode string data. Ex: "Hello World"		false	false	true	false	string
runMode	Unicode string data. Ex: "Hello World"		false	false	true	false	string
parts	Many related resources. Can be either a list of URIs or list of individually nested resource data.	n/a	false	false	false	false	related
flowCount	Integer data. Ex: 2673	n/a	false	false	false	false	integer
applicationType	Unicode string data. Ex: "Hello World"		true	false	false	false	string
cartridgeExpirationDayLimit	Integer data. Ex: 2673	n/a	true	false	false	false	integer
libraryReadLength	Integer data. Ex: 2673	0	false	false	false	false	integer
cartridgeBetweenUsageAbsoluteMaxDayLimit	Integer data. Ex: 2673	n/a	true	false	false	false	integer
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string
uid	Unicode string data. Ex: "Hello World"	n/a	false	false	false	true	string
id	Integer data. Ex: 2673		false	false	true	true	integer
categories	Unicode string data. Ex: "Hello World"		true	false	false	false	string
description	Unicode string data. Ex: "Hello World"		false	false	true	false	string

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 13,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/activesequencingkitinfo/?offset=1&limit=1&format=json"
    },
```

```
    "objects": [
        {
            "isActive": true,
            "samplePrep_instrumentType": "OT_IC",
            "kitType": "SequencingKit",
            "defaultFlowOrder": null,
            "name": "IonPGMInstallKit",
            "nucleotideType": "",
            "defaultCartridgeUsageCount": null,
            "instrumentType": "pgm",
            "chipTypes": "",
            "runMode": "",
            "parts": [
                {
                    "barcode": "4480217",
                    "id": 20019,
                    "resource_uri": "/rundb/api/v1/kitpart/20019/",
                    "kit": "/rundb/api/v1/kitinfo/20020/"
                },
                {
                    "barcode": "4480282",
                    "id": 20020,
                    "resource_uri": "/rundb/api/v1/kitpart/20020/",
                    "kit": "/rundb/api/v1/kitinfo/20020/"
                },
                {
                    "barcode": "4480284",
                    "id": 20021,
                    "resource_uri": "/rundb/api/v1/kitpart/20021/",
                    "kit": "/rundb/api/v1/kitinfo/20020/"
                }
            ],
            "flowCount": 100,
            "applicationType": "",
            "cartridgeExpirationDayLimit": null,
            "libraryReadLength": 0,
            "cartridgeBetweenUsageAbsoluteMaxDayLimit": null,
            "resource_uri": "/rundb/api/v1/activesequencingkitinfo/20020/",
            "uid": "SEQ0006",
            "id": 20020,
            "categories": "readLengthDerivableFromFlows;",
            "description": "Ion PGM Install Kit"
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Analysis Args Resource

Resource URL `http://mytorrentserver/rundb/api/v1/analysisargs/`
Schema URL `http://mytorrentserver/rundb/api/v1/analysisargs/schema/`

Resource Fields

field	help text	default	nullable
ionstatsargs	Unicode string data. Ex: “Hello World”		false
chipType	Unicode string data. Ex: “Hello World”		false
creator	A single related resource. Can be either a URI or set of nested resource data.	n/a	true
thumbnailionstatsargs	Unicode string data. Ex: “Hello World”		false
thumbnailalignmentargs	Unicode string data. Ex: “Hello World”		false
thumbnailanalysisargs	Unicode string data. Ex: “Hello World”		false
samplePrepKitName	Unicode string data. Ex: “Hello World”		false
id	Integer data. Ex: 2673		false
creationDate	A date & time as a string. Ex: “2010-11-10T03:07:43”	true	true
sequenceKitName	Unicode string data. Ex: “Hello World”		false
analysisargs	Unicode string data. Ex: “Hello World”		false
thumbnailcalibrateargs	Unicode string data. Ex: “Hello World”		false
applGroup	A single related resource. Can be either a URI or set of nested resource data.	n/a	true
chip_default	Boolean data. Ex: True	false	false
lastModifiedDate	A date & time as a string. Ex: “2010-11-10T03:07:43”	true	true
beadfindargs	Unicode string data. Ex: “Hello World”		false
templateKitName	Unicode string data. Ex: “Hello World”		false
prebasecallerargs	Unicode string data. Ex: “Hello World”		false
description	Unicode string data. Ex: “Hello World”	n/a	true
prethumbnailbasecallerargs	Unicode string data. Ex: “Hello World”		false
applType	A single related resource. Can be either a URI or set of nested resource data.	n/a	true
alignmentargs	Unicode string data. Ex: “Hello World”		false
thumbnailbasecallerargs	Unicode string data. Ex: “Hello World”		false
active	Boolean data. Ex: True	true	false
isSystem	Boolean data. Ex: True	false	false
thumbnailbeadfindargs	Unicode string data. Ex: “Hello World”		false
calibrateargs	Unicode string data. Ex: “Hello World”		false
libraryKitName	Unicode string data. Ex: “Hello World”		false
name	Unicode string data. Ex: “Hello World”	n/a	false
basecallerargs	Unicode string data. Ex: “Hello World”		false

Table 2.1 – continued from previous page

field	help text	default	nullable
lastModifiedUser	A single related resource. Can be either a URI or set of nested resource data.	n/a	true
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 129,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/analysisargs/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "ionstatsargs": "ionstats alignment",
            "chipType": "314",
            "creator": null,
            "thumbnailionstatsargs": "",
            "thumbnailalignmentargs": "",
            "thumbnailanalysisargs": "",
            "samplePrepKitName": "",
            "id": 1,
            "creationDate": "2018-06-08T06:20:39.000036+00:00",
            "sequenceKitName": "",
            "analysisargs": "Analysis --args-json /opt/ion/config/args_314_analysis.
↪json",
            "thumbnailcalibrateargs": "",
            "applGroup": null,
            "chip_default": true,
            "lastModifiedDate": "2018-06-08T06:20:39.000036+00:00",
            "beadfindargs": "justBeadFind --args-json /opt/ion/config/args_314_
↪beadfind.json",
            "templateKitName": "",
            "prebasecallerargs": "BaseCaller --barcode-filter-minreads 20",
            "description": "Ion 314 chip v2 analysis arguments",
            "prethumbnailbasecallerargs": "",
            "applType": null,
            "alignmentargs": "tmap mapall ... stage1 map4",
            "thumbnailbasecallerargs": "",
            "active": true,
            "isSystem": true,
            "thumbnailbeadfindargs": "",
            "calibrateargs": "Calibration",
            "libraryKitName": "",
            "name": "ion_default_314",
            "basecallerargs": "BaseCaller --barcode-filter-minreads 20",
            "lastModifiedUser": null,
            "resource_uri": "/rundb/api/v1/analysisargs/1/"
        }
    ]
}
```

Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Analysis Metrics Resource

Resource URL `http://mytorrentserver/rundb/api/v1/analysismetrics/`
Schema URL `http://mytorrentserver/rundb/api/v1/analysismetrics/schema/`

Resource Fields

field	help text	default	nullable	rea
libLive	Integer data. Ex: 2673	n/a	false	fals
ignored	Integer data. Ex: 2673	n/a	false	fals
washout_ambiguous	Integer data. Ex: 2673	n/a	false	fals
tfLive	Integer data. Ex: 2673	n/a	false	fals
sysIE	Floating point numeric data. Ex: 26.73	n/a	false	fals
bead	Integer data. Ex: 2673	n/a	false	fals
tfKp	Integer data. Ex: 2673	n/a	false	fals
washout_live	Integer data. Ex: 2673	n/a	false	fals
id	Integer data. Ex: 2673		false	fals
libFinal	Integer data. Ex: 2673	n/a	false	fals
loading	Floating point numeric data. Ex: 26.73	0	false	fals
lib	Integer data. Ex: 2673	n/a	false	fals
keypass_all_beads	Integer data. Ex: 2673	n/a	false	fals
dud	Integer data. Ex: 2673	n/a	false	fals
sysCF	Floating point numeric data. Ex: 26.73	n/a	false	fals
pinned	Integer data. Ex: 2673	n/a	false	fals
live	Integer data. Ex: 2673	n/a	false	fals
excluded	Integer data. Ex: 2673	n/a	false	fals
tf	Integer data. Ex: 2673	n/a	false	fals

Table 2.2 – continued from previous page

field	help text	default	nullable	rea
empty	Integer data. Ex: 2673	n/a	false	fals
tfFinal	Integer data. Ex: 2673	n/a	false	fals
amb	Integer data. Ex: 2673	n/a	false	fals
lib_pass_basecaller	Integer data. Ex: 2673	n/a	false	fals
lib_pass_cafie	Integer data. Ex: 2673	n/a	false	fals
washout_dud	Integer data. Ex: 2673	n/a	false	fals
libMix	Integer data. Ex: 2673	n/a	false	fals
report	A single related resource. Can be either a URI or set of nested resource data.	n/a	false	fals
libKp	Integer data. Ex: 2673	n/a	false	fals
adjusted_addressable	Integer data. Ex: 2673	0	false	fals
sysDR	Floating point numeric data. Ex: 26.73	n/a	false	fals
total	Integer data. Ex: 2673	0	false	fals
washout_test_fragment	Integer data. Ex: 2673	n/a	false	fals
washout_library	Integer data. Ex: 2673	n/a	false	fals
washout	Integer data. Ex: 2673	n/a	false	fals
tfMix	Integer data. Ex: 2673	n/a	false	fals
resource_uri	Unicode string data. Ex: “Hello World”	n/a	false	true

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 6,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/analysismetrics/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "libLive": 0,
            "ignored": 1042801,
            "washout_ambiguous": 0,
            "tfLive": 0,
            "sysIE": 0.465626595541835,
            "bead": 140400602,
            "tfKp": 0,
            "washout_live": 0,
            "id": 1,
            "libFinal": 93974105,
            "loading": 94.7655552064634,
            "lib": 139085639,
            "keypass_all_beads": 0,
            "dud": 60690,
            "sysCF": 0.603865925222635,
            "pinned": 2329,
            "live": 140339912,
            "excluded": 16543404,
            "tf": 1254273,
            "empty": 6710000,
            "tfFinal": 1198552,
            "amb": 0,
            "lib_pass_basecaller": 0,
```

```
            "lib_pass_cafie": 0,
            "washout_dud": 0,
            "libMix": 0,
            "report": "/rundb/api/v1/results/3/",
            "libKp": 0,
            "adjusted_addressable": 148155732,
            "sysDR": 0.168037705589086,
            "total": 164699136,
            "washout_test_fragment": 0,
            "washout_library": 0,
            "washout": 0,
            "tfMix": 0,
            "resource_uri": "/rundb/api/v1/analysismetrics/1/"
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Application Group Resource

Resource URL `http://mytorrentserver/rundb/api/v1/applicationgroup/`
Schema URL `http://mytorrentserver/rundb/api/v1/applicationgroup/schema/`

Resource Fields

field	help text	default	nullable	readonly	blank	unique	type
name	Unicode string data. Ex: “Hello World”	n/a	false	false	false	false	string
description	Unicode string data. Ex: “Hello World”	n/a	true	false	false	false	string
applications	Many related resources. Can be either a list of URIs or list of individually nested resource data.	n/a	true	false	false	false	related
uid	Unicode string data. Ex: “Hello World”	n/a	false	false	false	true	string
id	Integer data. Ex: 2673		false	false	true	true	integer
isActive	Boolean data. Ex: True	true	false	false	true	false	boolean
resource_uri	Unicode string data. Ex: “Hello World”	n/a	false	true	false	false	string

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 12,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/applicationgroup/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "name": "DNA",
            "description": "DNA",
            "applications": [
                {
                    "applicationGroups": [
                        "/rundb/api/v1/applicationgroup/1/",
                        "/rundb/api/v1/applicationgroup/3/",
                        "/rundb/api/v1/applicationgroup/4/"
                    ],
                    "description": "Generic Sequencing",
                    "nucleotideType": "dna",
                    "barcode": "",
                    "meta": {},
                    "alternate_name": "Other",
                    "runType": "GENS",
                    "id": 1,
                    "isActive": true,
                    "resource_uri": "/rundb/api/v1/runtype/1/"
                },
                {
                    "applicationGroups": [
                        "/rundb/api/v1/applicationgroup/1/",
                        "/rundb/api/v1/applicationgroup/6/",
                        "/rundb/api/v1/applicationgroup/8/",
                        "/rundb/api/v1/applicationgroup/10/"
```

```
            ],
            "description": "AmpliSeq DNA",
            "nucleotideType": "dna",
            "barcode": "",
            "meta": {},
            "alternate_name": "AmpliSeq DNA",
            "runType": "AMPS",
            "id": 2,
            "isActive": true,
            "resource_uri": "/rundb/api/v1/runtype/2/"
        },
        {
            "applicationGroups": [
                "/rundb/api/v1/applicationgroup/1/"
            ],
            "description": "TargetSeq",
            "nucleotideType": "dna",
            "barcode": "",
            "meta": {},
            "alternate_name": "TargetSeq",
            "runType": "TARS",
            "id": 3,
            "isActive": true,
            "resource_uri": "/rundb/api/v1/runtype/3/"
        },
        {
            "applicationGroups": [
                "/rundb/api/v1/applicationgroup/1/",
                "/rundb/api/v1/applicationgroup/4/"
            ],
            "description": "Whole Genome",
            "nucleotideType": "dna",
            "barcode": "",
            "meta": {},
            "alternate_name": "Whole Genome",
            "runType": "WGNM",
            "id": 4,
            "isActive": true,
            "resource_uri": "/rundb/api/v1/runtype/4/"
        },
        {
            "applicationGroups": [
                "/rundb/api/v1/applicationgroup/1/"
            ],
            "description": "AmpliSeq Exome",
            "nucleotideType": "dna",
            "barcode": "",
            "meta": {},
            "alternate_name": "AmpliSeq Exome",
            "runType": "AMPS_EXOME",
            "id": 7,
            "isActive": true,
            "resource_uri": "/rundb/api/v1/runtype/7/"
        },
        {
            "applicationGroups": [
                "/rundb/api/v1/applicationgroup/1/"
            ],
```

```
                    "description": "AmpliSeq HD - DNA",
                    "nucleotideType": "dna",
                    "barcode": "",
                    "meta": {},
                    "alternate_name": "AmpliSeq HD - DNA",
                    "runType": "AMPS_HD_DNA",
                    "id": 12,
                    "isActive": true,
                    "resource_uri": "/rundb/api/v1/runtype/12/"
                }
            ],
            "uid": "APPLGROUP_0001",
            "id": 1,
            "isActive": true,
            "resource_uri": "/rundb/api/v1/applicationgroup/1/"
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Appl Product Resource

Resource URL `http://mytorrentserver/rundb/api/v1/applproduct/`
Schema URL `http://mytorrentserver/rundb/api/v1/applproduct/schema/`

Resource Fields

field	help text
isDualNucleotideTypeBySampleSupported	Boolean data. Ex: True

Table 2.3 – continued from previous page

field	help text
defaultHotSpotRegionBedFileName	Unicode string data. Ex: “Hello World”
isTargetRegionBEDFileSupported	Boolean data. Ex: True
isSamplePrepKitSupported	Boolean data. Ex: True
defaultSeqKit	A single related resource. Can be either a URI or set of nested resour
isControlSeqTypeBySampleSupported	Boolean data. Ex: True
defaultBarcodeKitName	Unicode string data. Ex: “Hello World”
isHotSpotBEDFileBySampleSupported	Boolean data. Ex: True
id	Integer data. Ex: 2673
isTargetRegionBEDFileBySampleSupported	Boolean data. Ex: True
isReferenceSelectionSupported	Boolean data. Ex: True
productCode	Unicode string data. Ex: “Hello World”
applicationGroup	A single related resource. Can be either a URI or set of nested resour
dualBarcodingRule	Unicode string data. Ex: “Hello World”
defaultChipType	Unicode string data. Ex: “Hello World”
appl	A single related resource. Can be either a URI or set of nested resour
categories	Unicode string data. Ex: “Hello World”
instrumentType	Unicode string data. Ex: “Hello World”
isDefault	Boolean data. Ex: True
isTargetTechniqueSelectionSupported	Boolean data. Ex: True
description	Unicode string data. Ex: “Hello World”
isHotspotRegionBEDFileSuppported	Boolean data. Ex: True
isVisible	Boolean data. Ex: True
productName	Unicode string data. Ex: “Hello World”
isBarcodeKitSelectionRequired	Boolean data. Ex: True
isDefaultBarcoded	Boolean data. Ex: True
isTargetRegionBEDFileSelectionRequiredForRefSelection	Boolean data. Ex: True
isDualBarcodingBySampleSupported	Boolean data. Ex: True
defaultTargetRegionBedFileName	Unicode string data. Ex: “Hello World”
isActive	Boolean data. Ex: True
isReferenceBySampleSupported	Boolean data. Ex: True
defaultFlowCount	Integer data. Ex: 2673
defaultLibKit	A single related resource. Can be either a URI or set of nested resour
barcodeKitSelectableType	Unicode string data. Ex: “Hello World”
isDefaultForInstrumentType	Boolean data. Ex: True
defaultGenomeRefName	Unicode string data. Ex: “Hello World”
defaultSamplePrepKit	A single related resource. Can be either a URI or set of nested resour
defaultControlSeqKit	A single related resource. Can be either a URI or set of nested resour
defaultIonChefPrepKit	A single related resource. Can be either a URI or set of nested resour
resource_uri	Unicode string data. Ex: “Hello World”
defaultIonChefSequencingKit	A single related resource. Can be either a URI or set of nested resour
defaultTemplateKit	A single related resource. Can be either a URI or set of nested resour

Example Response

```
{
    "meta": {
        "previous": null,
        "total_count": 59,
        "offset": 0,
        "limit": 1,
```

```
        "next": "/rundb/api/v1/applproduct/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "isDualNucleotideTypeBySampleSupported": false,
            "defaultHotSpotRegionBedFileName": "",
            "isTargetRegionBEDFileSupported": true,
            "isSamplePrepKitSupported": true,
            "defaultSeqKit": {
                "isActive": true,
                "samplePrep_instrumentType": "OT_IC_IA",
                "kitType": "SequencingKit",
                "defaultFlowOrder": null,
                "name": "IonPGMHiQView",
                "nucleotideType": "",
                "defaultCartridgeUsageCount": null,
                "instrumentType": "pgm",
                "chipTypes": "",
                "runMode": "",
                "parts": [
                    {
                        "barcode": "A30044",
                        "id": 20203,
                        "resource_uri": "/rundb/api/v1/kitpart/20203/",
                        "kit": "/rundb/api/v1/kitinfo/20090/"
                    },
                    {
                        "barcode": "A30043",
                        "id": 20204,
                        "resource_uri": "/rundb/api/v1/kitpart/20204/",
                        "kit": "/rundb/api/v1/kitinfo/20090/"
                    },
                    {
                        "barcode": "A30275",
                        "id": 20205,
                        "resource_uri": "/rundb/api/v1/kitpart/20205/",
                        "kit": "/rundb/api/v1/kitinfo/20090/"
                    },
                    {
                        "barcode": "A25590",
                        "id": 20206,
                        "resource_uri": "/rundb/api/v1/kitpart/20206/",
                        "kit": "/rundb/api/v1/kitinfo/20090/"
                    }
                ],
                "flowCount": 500,
                "applicationType": "",
                "cartridgeExpirationDayLimit": null,
                "libraryReadLength": 0,
                "cartridgeBetweenUsageAbsoluteMaxDayLimit": null,
                "resource_uri": "/rundb/api/v1/kitinfo/20090/",
                "uid": "SEQ0024",
                "id": 20090,
                "categories": "flowOverridable;readLengthDerivableFromFlows;",
                "description": "Ion PGM Hi-Q View Sequencing Kit"
            },
            "isControlSeqTypeBySampleSupported": false,
            "defaultBarcodeKitName": null,
```

```
            "isHotSpotBEDFileBySampleSupported": true,
            "id": 20001,
            "isTargetRegionBEDFileBySampleSupported": true,
            "isReferenceSelectionSupported": true,
            "productCode": "AMPS_0",
            "applicationGroup": {
                "name": "DNA",
                "description": "DNA",
                "applications": [
                    {
                        "applicationGroups": [
                            "/rundb/api/v1/applicationgroup/1/",
                            "/rundb/api/v1/applicationgroup/3/",
                            "/rundb/api/v1/applicationgroup/4/"
                        ],
                        "description": "Generic Sequencing",
                        "nucleotideType": "dna",
                        "barcode": "",
                        "meta": {},
                        "alternate_name": "Other",
                        "runType": "GENS",
                        "id": 1,
                        "isActive": true,
                        "resource_uri": "/rundb/api/v1/runtype/1/"
                    },
                    {
                        "applicationGroups": [
                            "/rundb/api/v1/applicationgroup/1/",
                            "/rundb/api/v1/applicationgroup/6/",
                            "/rundb/api/v1/applicationgroup/8/",
                            "/rundb/api/v1/applicationgroup/10/"
                        ],
                        "description": "AmpliSeq DNA",
                        "nucleotideType": "dna",
                        "barcode": "",
                        "meta": {},
                        "alternate_name": "AmpliSeq DNA",
                        "runType": "AMPS",
                        "id": 2,
                        "isActive": true,
                        "resource_uri": "/rundb/api/v1/runtype/2/"
                    },
                    {
                        "applicationGroups": [
                            "/rundb/api/v1/applicationgroup/1/"
                        ],
                        "description": "TargetSeq",
                        "nucleotideType": "dna",
                        "barcode": "",
                        "meta": {},
                        "alternate_name": "TargetSeq",
                        "runType": "TARS",
                        "id": 3,
                        "isActive": true,
                        "resource_uri": "/rundb/api/v1/runtype/3/"
                    },
                    {
                        "applicationGroups": [
```

```
                        "/rundb/api/v1/applicationgroup/1/",
                        "/rundb/api/v1/applicationgroup/4/"
                    ],
                    "description": "Whole Genome",
                    "nucleotideType": "dna",
                    "barcode": "",
                    "meta": {},
                    "alternate_name": "Whole Genome",
                    "runType": "WGNM",
                    "id": 4,
                    "isActive": true,
                    "resource_uri": "/rundb/api/v1/runtype/4/"
                },
                {
                    "applicationGroups": [
                        "/rundb/api/v1/applicationgroup/1/"
                    ],
                    "description": "AmpliSeq Exome",
                    "nucleotideType": "dna",
                    "barcode": "",
                    "meta": {},
                    "alternate_name": "AmpliSeq Exome",
                    "runType": "AMPS_EXOME",
                    "id": 7,
                    "isActive": true,
                    "resource_uri": "/rundb/api/v1/runtype/7/"
                },
                {
                    "applicationGroups": [
                        "/rundb/api/v1/applicationgroup/1/"
                    ],
                    "description": "AmpliSeq HD - DNA",
                    "nucleotideType": "dna",
                    "barcode": "",
                    "meta": {},
                    "alternate_name": "AmpliSeq HD - DNA",
                    "runType": "AMPS_HD_DNA",
                    "id": 12,
                    "isActive": true,
                    "resource_uri": "/rundb/api/v1/runtype/12/"
                }
            ],
            "uid": "APPLGROUP_0001",
            "id": 1,
            "isActive": true,
            "resource_uri": "/rundb/api/v1/applicationgroup/1/"
        },
        "dualBarcodingRule": "",
        "defaultChipType": "318",
        "appl": {
            "applicationGroups": [
                "/rundb/api/v1/applicationgroup/1/",
                "/rundb/api/v1/applicationgroup/6/",
                "/rundb/api/v1/applicationgroup/8/",
                "/rundb/api/v1/applicationgroup/10/"
            ],
            "description": "AmpliSeq DNA",
            "nucleotideType": "dna",
```

```
            "barcode": "",
            "meta": {},
            "alternate_name": "AmpliSeq DNA",
            "runType": "AMPS",
            "id": 2,
            "isActive": true,
            "resource_uri": "/rundb/api/v1/runtype/2/"
        },
        "categories": "",
        "instrumentType": "pgm",
        "isDefault": true,
        "isTargetTechniqueSelectionSupported": true,
        "description": "",
        "isHotspotRegionBEDFileSuppported": true,
        "isVisible": true,
        "productName": "AMPS_default",
        "isBarcodeKitSelectionRequired": false,
        "isDefaultBarcoded": false,
        "isTargetRegionBEDFileSelectionRequiredForRefSelection": true,
        "isDualBarcodingBySampleSupported": false,
        "defaultTargetRegionBedFileName": "",
        "isActive": true,
        "isReferenceBySampleSupported": true,
        "defaultFlowCount": 500,
        "defaultLibKit": {
            "isActive": true,
            "samplePrep_instrumentType": "",
            "kitType": "LibraryKit",
            "defaultFlowOrder": null,
            "name": "Ion AmpliSeq 2.0 Library Kit",
            "nucleotideType": "dna",
            "defaultCartridgeUsageCount": null,
            "instrumentType": "",
            "chipTypes": "",
            "runMode": "",
            "parts": [
                {
                    "barcode": "4475345",
                    "id": 20034,
                    "resource_uri": "/rundb/api/v1/kitpart/20034/",
                    "kit": "/rundb/api/v1/kitinfo/20012/"
                }
            ],
            "flowCount": 0,
            "applicationType": "AMPS_ANY",
            "cartridgeExpirationDayLimit": null,
            "libraryReadLength": 0,
            "cartridgeBetweenUsageAbsoluteMaxDayLimit": null,
            "resource_uri": "/rundb/api/v1/kitinfo/20012/",
            "uid": "LIB0008",
            "id": 20012,
            "categories": "",
            "description": "Ion AmpliSeq 2.0 Library Kit"
        },
        "barcodeKitSelectableType": "all",
        "isDefaultForInstrumentType": true,
        "defaultGenomeRefName": "hg19",
        "defaultSamplePrepKit": null,
```

```
            "defaultControlSeqKit": null,
            "defaultIonChefPrepKit": "/rundb/api/v1/kitinfo/20093/",
            "resource_uri": "/rundb/api/v1/applproduct/20001/",
            "defaultIonChefSequencingKit": "/rundb/api/v1/kitinfo/20090/",
            "defaultTemplateKit": "/rundb/api/v1/kitinfo/20091/"
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Available Ion Chef Planned Experiment Resource

Resource URL
`http://mytorrentserver/rundb/api/v1/availableionchefplannedexperiment/`
Schema URL
`http://mytorrentserver/rundb/api/v1/availableionchefplannedexperiment/schema/`

Resource Fields

field	help text	default	nullal
origin	Unicode string data. Ex: “Hello World”		true
isReverseRun	Boolean data. Ex: True	false	false
planDisplayedName	Unicode string data. Ex: “Hello World”	n/a	true
storage_options	Unicode string data. Ex: “Hello World”	A	false
preAnalysis	Boolean data. Ex: True	true	false
chipType	Unicode string data. Ex: “Hello World”	n/a	true
planShortID	Unicode string data. Ex: “Hello World”	n/a	true
planStatus	Unicode string data. Ex: “Hello World”		false

Table 2.4 – continued from previous page

field	help text	default	nullal
runMode	Unicode string data. Ex: “Hello World”		false
isCustom_kitSettings	Boolean data. Ex: True	false	false
sampleTubeLabel	Unicode string data. Ex: “Hello World”	n/a	true
planExecutedDate	A date & time as a string. Ex: “2010-11-10T03:07:43”	n/a	true
samplePrepKitName	Unicode string data. Ex: “Hello World”	n/a	true
reverse_primer	Unicode string data. Ex: “Hello World”	n/a	true
seqKitBarcode	Unicode string data. Ex: “Hello World”	n/a	true
id	Integer data. Ex: 2673		false
metaData	Unicode string data. Ex: “Hello World”	{}	false
isFavorite	Boolean data. Ex: True	false	false
samplePrepProtocol	Unicode string data. Ex: “Hello World”		true
isPlanGroup	Boolean data. Ex: True	false	false
experiment	A single related resource. Can be either a URI or set of nested resource data.	n/a	true
templatingKitName	Unicode string data. Ex: “Hello World”	n/a	true
runType	Unicode string data. Ex: “Hello World”	GENS	false
templatingKitBarcode	Unicode string data. Ex: “Hello World”	n/a	true
planPGM	Unicode string data. Ex: “Hello World”	n/a	true
isSystemDefault	Boolean data. Ex: True	false	false
autoName	Unicode string data. Ex: “Hello World”	n/a	true
isReusable	Boolean data. Ex: True	false	false
controlSequencekitname	Unicode string data. Ex: “Hello World”	n/a	true
date	A date & time as a string. Ex: “2010-11-10T03:07:43”	n/a	true
isSystem	Boolean data. Ex: True	false	false
libkit	Unicode string data. Ex: “Hello World”	n/a	true
categories	Unicode string data. Ex: “Hello World”		true
planName	Unicode string data. Ex: “Hello World”	n/a	true
pairedEndLibraryAdapterName	Unicode string data. Ex: “Hello World”	n/a	true
adapter	Unicode string data. Ex: “Hello World”	n/a	true
irworkflow	Unicode string data. Ex: “Hello World”		false
planExecuted	Boolean data. Ex: True	false	false
username	Unicode string data. Ex: “Hello World”	n/a	true
usePostBeadfind	Boolean data. Ex: True	true	false
storageHost	Unicode string data. Ex: “Hello World”	n/a	true
expName	Unicode string data. Ex: “Hello World”		false
libraryReadLength	Integer data. Ex: 2673	0	false
runname	Unicode string data. Ex: “Hello World”	n/a	true
usePreBeadfind	Boolean data. Ex: True	true	false
planGUID	Unicode string data. Ex: “Hello World”	n/a	true
cycles	Integer data. Ex: 2673	n/a	true
resource_uri	Unicode string data. Ex: “Hello World”	n/a	false

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 2,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/availableionchefplannedexperiment/?offset=1&limit=1&
↪format=json"
```

```
    },
    "objects": [
        {
            "planName": "Ion_AmpliSeq_HD_for_Tumor_-_DNA",
            "isReverseRun": false,
            "chipType": "540",
            "planShortID": "SP1XE",
            "username": "ionadmin",
            "samplePrepProtocol": "",
            "isPlanGroup": false,
            "planStatus": "pending",
            "samplePrepProtocolName": "",
            "experiment": "/rundb/api/v1/experiment/136/",
            "sampleTubeLabel": "",
            "date": "2018-04-13T22:17:13.000108+00:00",
            "id": 143,
            "templatingKitName": "Ion Chef S540 V1"
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Available Ion Chef Planned Experiment Summary Resource

Resource URL
`http://mytorrentserver/rundb/api/v1/availableionchefplannedexperimentsummary/`
Schema URL `http://mytorrentserver/rundb/api/v1/availableionchefplannedexperimentsummary/schema/`

Resource Fields

field	help text	default	nullal
origin	Unicode string data. Ex: “Hello World”		true
isReverseRun	Boolean data. Ex: True	false	false
planDisplayedName	Unicode string data. Ex: “Hello World”	n/a	true
storage_options	Unicode string data. Ex: “Hello World”	A	false
preAnalysis	Boolean data. Ex: True	true	false
planShortID	Unicode string data. Ex: “Hello World”	n/a	true
planStatus	Unicode string data. Ex: “Hello World”		false
runMode	Unicode string data. Ex: “Hello World”		false
isCustom_kitSettings	Boolean data. Ex: True	false	false
sampleTubeLabel	Unicode string data. Ex: “Hello World”	n/a	true
planExecutedDate	A date & time as a string. Ex: “2010-11-10T03:07:43”	n/a	true
samplePrepKitName	Unicode string data. Ex: “Hello World”	n/a	true
reverse_primer	Unicode string data. Ex: “Hello World”	n/a	true
seqKitBarcode	Unicode string data. Ex: “Hello World”	n/a	true
id	Integer data. Ex: 2673		false
metaData	Unicode string data. Ex: “Hello World”	{}	false
isFavorite	Boolean data. Ex: True	false	false
samplePrepProtocol	Unicode string data. Ex: “Hello World”		true
isPlanGroup	Boolean data. Ex: True	false	false
experiment	A single related resource. Can be either a URI or set of nested resource data.	n/a	true
templatingKitName	Unicode string data. Ex: “Hello World”	n/a	true
runType	Unicode string data. Ex: “Hello World”	GENS	false
templatingKitBarcode	Unicode string data. Ex: “Hello World”	n/a	true
planPGM	Unicode string data. Ex: “Hello World”	n/a	true
isSystemDefault	Boolean data. Ex: True	false	false
autoName	Unicode string data. Ex: “Hello World”	n/a	true
isReusable	Boolean data. Ex: True	false	false
controlSequencekitname	Unicode string data. Ex: “Hello World”	n/a	true
date	A date & time as a string. Ex: “2010-11-10T03:07:43”	n/a	true
isSystem	Boolean data. Ex: True	false	false
libkit	Unicode string data. Ex: “Hello World”	n/a	true
categories	Unicode string data. Ex: “Hello World”		true
planName	Unicode string data. Ex: “Hello World”	n/a	true
pairedEndLibraryAdapterName	Unicode string data. Ex: “Hello World”	n/a	true
adapter	Unicode string data. Ex: “Hello World”	n/a	true
irworkflow	Unicode string data. Ex: “Hello World”		false
planExecuted	Boolean data. Ex: True	false	false
username	Unicode string data. Ex: “Hello World”	n/a	true
usePostBeadfind	Boolean data. Ex: True	true	false
storageHost	Unicode string data. Ex: “Hello World”	n/a	true
expName	Unicode string data. Ex: “Hello World”		false
libraryReadLength	Integer data. Ex: 2673	0	false
runname	Unicode string data. Ex: “Hello World”	n/a	true
usePreBeadfind	Boolean data. Ex: True	true	false
planGUID	Unicode string data. Ex: “Hello World”	n/a	true
cycles	Integer data. Ex: 2673	n/a	true
resource_uri	Unicode string data. Ex: “Hello World”	n/a	false

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 2,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/availableionchefplannedexperimentsummary/?offset=1&
↪limit=1&format=json"
    },
    "objects": [
        {
            "planName": "Ion_AmpliSeq_HD_for_Tumor_-_DNA",
            "isReverseRun": false,
            "planShortID": "SP1XE",
            "samplePrepProtocol": "",
            "isPlanGroup": false,
            "planStatus": "pending",
            "username": "ionadmin",
            "experiment": "/rundb/api/v1/experiment/136/",
            "sampleTubeLabel": "",
            "date": "2018-04-13T22:17:13.000108+00:00",
            "id": 143,
            "templatingKitName": "Ion Chef S540 V1"
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Available Onetouch Planned Experiment Resource

Resource URL
`http://mytorrentserver/rundb/api/v1/availableonetouchplannedexperiment/`

Schema URL
`http://mytorrentserver/rundb/api/v1/availableonetouchplannedexperiment/schema/`

Resource Fields

field	help text
planDisplayedName	Unicode string data. Ex: “Hello World”
autoAnalyze	Boolean data. Ex: True
endBarcodeKitName	Unicode string data. Ex: “Hello World”
templatingKitBarcode	Unicode string data. Ex: “Hello World”
preAnalysis	Boolean data. Ex: True
applicationGroup	A single related resource. Can be either a URI or set of nested resource data.
mixedTypeRNA_hotSpotRegionBedFile	Unicode string data. Ex: “Hello World”
mixedTypeRNA_targetRegionBedFile	Unicode string data. Ex: “Hello World”
platform	Unicode string data. Ex: “Hello World”
categories	Unicode string data. Ex: “Hello World”
planPGM	Unicode string data. Ex: “Hello World”
libkit	Unicode string data. Ex: “Hello World”
projects	Many related resources. Can be either a list of URIs or list of individually nested resourc
notes	Unicode string data. Ex: “Hello World”
sequencekitname	Unicode string data. Ex: “Hello World”
base_recalibration_mode	Unicode string data. Ex: “Hello World”
storageHost	Unicode string data. Ex: “Hello World”
expName	Unicode string data. Ex: “Hello World”
cycles	Integer data. Ex: 2673
isReverseRun	Boolean data. Ex: True
storage_options	Unicode string data. Ex: “Hello World”
chipType	Unicode string data. Ex: “Hello World”
library	Unicode string data. Ex: “Hello World”
reverselibrarykey	Unicode string data. Ex: “Hello World”
sampleTubeLabel	Unicode string data. Ex: “Hello World”
seqKitBarcode	Unicode string data. Ex: “Hello World”
barcodeId	Unicode string data. Ex: “Hello World”
isPlanGroup	Boolean data. Ex: True
realign	Boolean data. Ex: True
sampleGroupingName	Unicode string data. Ex: “Hello World”
experiment	A single related resource. Can be either a URI or set of nested resource data.
bedfile	Unicode string data. Ex: “Hello World”
applicationCategoryDisplayedName	Unicode string data. Ex: “Hello World”
isReusable	Boolean data. Ex: True
isDuplicateReads	Boolean data. Ex: True
sampleSets	Many related resources. Can be either a list of URIs or list of individually nested resourc
librarykitname	Unicode string data. Ex: “Hello World”
sseBedFile	Unicode string data. Ex: “Hello World”
adapter	Unicode string data. Ex: “Hello World”
earlyDatFileDeletion	Boolean data. Ex: True
parentPlan	Unicode string data. Ex: “Hello World”
origin	Unicode string data. Ex: “Hello World”
forward3primeadapter	Unicode string data. Ex: “Hello World”

Table 2.6 – continued from previous page

field	help text
isCustom_kitSettings	Boolean data. Ex: True
samplePrepKitName	Unicode string data. Ex: “Hello World”
applicationGroupDisplayedName	Unicode string data. Ex: “Hello World”
metaData	Unicode string data. Ex: “Hello World”
isFavorite	Boolean data. Ex: True
qcValues	Many related resources. Can be either a list of URIs or list of individually nested resourc
planStatus	Unicode string data. Ex: “Hello World”
templatingKitName	Unicode string data. Ex: “Hello World”
runType	Unicode string data. Ex: “Hello World”
username	Unicode string data. Ex: “Hello World”
planName	Unicode string data. Ex: “Hello World”
sampleDisplayedName	Unicode string data. Ex: “Hello World”
controlSequencekitname	Unicode string data. Ex: “Hello World”
tfKey	Unicode string data. Ex: “Hello World”
mixedTypeRNA_reference	Unicode string data. Ex: “Hello World”
childPlans	A list of data. Ex: [’abc’, 26.73, 8]
pairedEndLibraryAdapterName	Unicode string data. Ex: “Hello World”
runMode	Unicode string data. Ex: “Hello World”
irworkflow	Unicode string data. Ex: “Hello World”
planExecuted	Boolean data. Ex: True
project	Unicode string data. Ex: “Hello World”
usePostBeadfind	Boolean data. Ex: True
libraryReadLength	Integer data. Ex: 2673
runname	Unicode string data. Ex: “Hello World”
chefInfo	A dictionary of data. Ex: {‘price’: 26.73, ‘name’: ‘Daniel’}
planGUID	Unicode string data. Ex: “Hello World”
samplePrepProtocol	Unicode string data. Ex: “Hello World”
planShortID	Unicode string data. Ex: “Hello World”
sample	Unicode string data. Ex: “Hello World”
planExecutedDate	A date & time as a string. Ex: “2010-11-10T03:07:43”
reverse_primer	Unicode string data. Ex: “Hello World”
id	Integer data. Ex: 2673
barcodedSamples	Unicode string data. Ex: “Hello World”
regionfile	Unicode string data. Ex: “Hello World”
selectedPlugins	Unicode string data. Ex: “Hello World”
isSystemDefault	Boolean data. Ex: True
autoName	Unicode string data. Ex: “Hello World”
libraryKey	Unicode string data. Ex: “Hello World”
flows	Integer data. Ex: 2673
date	A date & time as a string. Ex: “2010-11-10T03:07:43”
isSystem	Boolean data. Ex: True
variantfrequency	Unicode string data. Ex: “Hello World”
sampleSetDisplayedName	Unicode string data. Ex: “Hello World”
flowsInOrder	Unicode string data. Ex: “Hello World”
libraryPrepType	Unicode string data. Ex: “Hello World”
sampleGrouping	A single related resource. Can be either a URI or set of nested resource data.
chipBarcode	Unicode string data. Ex: “Hello World”
usePreBeadfind	Boolean data. Ex: True
resource_uri	Unicode string data. Ex: “Hello World”

Table 2.6 – continued from previous page

field	help text
libraryPrepTypeDisplayedName	Unicode string data. Ex: “Hello World”
reverse3primeadapter	Unicode string data. Ex: “Hello World”

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 1,
        "offset": 0,
        "limit": 1,
        "next": null
    },
    "objects": [
        {
            "planDisplayedName": "Ion ReproSeq Aneuploidy - Ion PGM System",
            "autoAnalyze": true,
            "endBarcodeKitName": "",
            "templatingKitBarcode": null,
            "preAnalysis": true,
            "thumbnailanalysisargs": "",
            "applicationGroup": "/rundb/api/v1/applicationgroup/1/",
            "mixedTypeRNA_hotSpotRegionBedFile": "",
            "mixedTypeRNA_targetRegionBedFile": "",
            "platform": "",
            "categories": "repro",
            "planPGM": null,
            "prebasecallerargs": "BaseCaller --barcode-filter 0.01 --barcode-filter-
↪minreads 20 --extra-trim-left 30",
            "alignmentargs": "tmap mapall ... stage1 map4",
            "thumbnailbasecallerargs": "",
            "libkit": null,
            "projects": [],
            "notes": "",
            "sequencekitname": "IonPGMHiQ",
            "base_recalibration_mode": "standard_recal",
            "storageHost": null,
            "expName": "",
            "thumbnailionstatsargs": "",
            "cycles": null,
            "isReverseRun": false,
            "storage_options": "A",
            "thumbnailalignmentargs": "",
            "chipType": "318",
            "library": "hg19",
            "runMode": "single",
            "sampleTubeLabel": "",
            "seqKitBarcode": null,
            "barcodeId": "Ion SingleSeq Barcode set 1-24",
            "isPlanGroup": false,
            "realign": false,
            "sampleGroupingName": "Self",
            "experiment": "/rundb/api/v1/experiment/123/",
            "bedfile": "",
            "applicationCategoryDisplayedName": "Reproductive",
```

```
            "isReusable": false,
            "isDuplicateReads": false,
            "sampleSets": [],
            "thumbnailbeadfindargs": "",
            "librarykitname": "IonPicoPlex",
            "sseBedFile": "",
            "adapter": null,
            "basecallerargs": "BaseCaller  --barcode-filter 0.01 --barcode-filter-
↪minreads 20 --extra-trim-left 30",
            "earlyDatFileDeletion": false,
            "parentPlan": null,
            "origin": "gui|5.8.0",
            "forward3primeadapter": "ATCACCGACTGCCCATAGAGAGGAAAGCGG",
            "planStatus": "planned",
            "isCustom_kitSettings": false,
            "samplePrepKitName": null,
            "applicationGroupDisplayedName": "DNA",
            "metaData": {
                "fromTemplate": "Ion_ReproSeq_Aneuploidy_-_Ion_PGM_System",
                "fromTemplateSource": "ION"
            },
            "isFavorite": false,
            "qcValues": [
                {
                    "threshold": 30,
                    "plannedExperiment": "/rundb/api/v1/plannedexperiment/131/",
                    "id": 370,
                    "qcType": {
                        "description": "",
                        "minThreshold": 0,
                        "maxThreshold": 100,
                        "defaultThreshold": 30,
                        "qcName": "Bead Loading (%)",
                        "id": 1,
                        "resource_uri": "/rundb/api/v1/qctype/1/"
                    },
                    "resource_uri": "/rundb/api/v1/plannedexperimentqc/370/"
                },
                {
                    "threshold": 30,
                    "plannedExperiment": "/rundb/api/v1/plannedexperiment/131/",
                    "id": 371,
                    "qcType": {
                        "description": "",
                        "minThreshold": 1,
                        "maxThreshold": 100,
                        "defaultThreshold": 30,
                        "qcName": "Key Signal (1-100)",
                        "id": 2,
                        "resource_uri": "/rundb/api/v1/qctype/2/"
                    },
                    "resource_uri": "/rundb/api/v1/plannedexperimentqc/371/"
                },
                {
                    "threshold": 30,
                    "plannedExperiment": "/rundb/api/v1/plannedexperiment/131/",
                    "id": 372,
                    "qcType": {
```

```
                        "description": "",
                        "minThreshold": 0,
                        "maxThreshold": 100,
                        "defaultThreshold": 30,
                        "qcName": "Usable Sequence (%)",
                        "id": 3,
                        "resource_uri": "/rundb/api/v1/qctype/3/"
                    },
                    "resource_uri": "/rundb/api/v1/plannedexperimentqc/372/"
                }
            ],
            "analysisargs": "Analysis --args-json /opt/ion/config/args_318_analysis.
↪json --mixed-first-flow 51 --mixed-last-flow 111",
            "thumbnailcalibrateargs": "",
            "templatingKitName": "Ion PGM Template IA Tech Access Kit",
            "runType": "WGNM",
            "username": "ionadmin",
            "planShortID": "6TGIO",
            "sampleDisplayedName": "",
            "prethumbnailbasecallerargs": "",
            "controlSequencekitname": null,
            "tfKey": "ATCG",
            "mixedTypeRNA_reference": "",
            "childPlans": [],
            "pairedEndLibraryAdapterName": "",
            "reverselibrarykey": "",
            "irworkflow": "",
            "planExecuted": false,
            "project": "",
            "usePostBeadfind": true,
            "libraryReadLength": 0,
            "runname": null,
            "chefInfo": {},
            "planGUID": "d1ed9718-b6f4-4dfd-8de5-bbd150092997",
            "ionstatsargs": "ionstats alignment",
            "samplePrepProtocol": "",
            "sample": "",
            "planExecutedDate": null,
            "reverse_primer": null,
            "id": 131,
            "barcodedSamples": {
                "Sample 6": {
                    "dualBarcodes": [],
                    "barcodeSampleInfo": {
                        "SingleSeq_006": {
                            "description": "",
                            "reference": "hg19",
                            "targetRegionBedFile": "",
                            "hotSpotRegionBedFile": "",
                            "nucleotideType": "DNA",
                            "controlSequenceType": "",
                            "externalId": "",
                            "endBarcode": "",
                            "controlType": "",
                            "sseBedFile": ""
                        }
                    },
                    "barcodes": [
```

```
                    "SingleSeq_006"
                ]
            },
            "Sample 7": {
                "dualBarcodes": [],
                "barcodeSampleInfo": {
                    "SingleSeq_007": {
                        "description": "",
                        "reference": "hg19",
                        "targetRegionBedFile": "",
                        "hotSpotRegionBedFile": "",
                        "nucleotideType": "DNA",
                        "controlSequenceType": "",
                        "externalId": "",
                        "endBarcode": "",
                        "controlType": "",
                        "sseBedFile": ""
                    }
                },
                "barcodes": [
                    "SingleSeq_007"
                ]
            },
            "Sample 4": {
                "dualBarcodes": [],
                "barcodeSampleInfo": {
                    "SingleSeq_004": {
                        "description": "",
                        "reference": "hg19",
                        "targetRegionBedFile": "",
                        "hotSpotRegionBedFile": "",
                        "nucleotideType": "DNA",
                        "controlSequenceType": "",
                        "externalId": "",
                        "endBarcode": "",
                        "controlType": "",
                        "sseBedFile": ""
                    }
                },
                "barcodes": [
                    "SingleSeq_004"
                ]
            },
            "Sample 5": {
                "dualBarcodes": [],
                "barcodeSampleInfo": {
                    "SingleSeq_005": {
                        "description": "",
                        "reference": "hg19",
                        "targetRegionBedFile": "",
                        "hotSpotRegionBedFile": "",
                        "nucleotideType": "DNA",
                        "controlSequenceType": "",
                        "externalId": "",
                        "endBarcode": "",
                        "controlType": "",
                        "sseBedFile": ""
                    }
```

```
            },
            "barcodes": [
                "SingleSeq_005"
            ]
        },
        "Sample 2": {
            "dualBarcodes": [],
            "barcodeSampleInfo": {
                "SingleSeq_002": {
                    "description": "",
                    "reference": "hg19",
                    "targetRegionBedFile": "",
                    "hotSpotRegionBedFile": "",
                    "nucleotideType": "DNA",
                    "controlSequenceType": "",
                    "externalId": "",
                    "endBarcode": "",
                    "controlType": "",
                    "sseBedFile": ""
                }
            },
            "barcodes": [
                "SingleSeq_002"
            ]
        },
        "Sample 3": {
            "dualBarcodes": [],
            "barcodeSampleInfo": {
                "SingleSeq_003": {
                    "description": "",
                    "reference": "hg19",
                    "targetRegionBedFile": "",
                    "hotSpotRegionBedFile": "",
                    "nucleotideType": "DNA",
                    "controlSequenceType": "",
                    "externalId": "",
                    "endBarcode": "",
                    "controlType": "",
                    "sseBedFile": ""
                }
            },
            "barcodes": [
                "SingleSeq_003"
            ]
        },
        "Sample 1": {
            "dualBarcodes": [],
            "barcodeSampleInfo": {
                "SingleSeq_001": {
                    "description": "",
                    "reference": "hg19",
                    "targetRegionBedFile": "",
                    "hotSpotRegionBedFile": "",
                    "nucleotideType": "DNA",
                    "controlSequenceType": "",
                    "externalId": "",
                    "endBarcode": "",
                    "controlType": "",
```

```
                            "sseBedFile": ""
                        }
                    },
                    "barcodes": [
                        "SingleSeq_001"
                    ]
                }
            },
            "custom_args": false,
            "regionfile": "",
            "selectedPlugins": {
                "FilterDuplicates": {
                    "userInput": "",
                    "version": "5.8.0.0",
                    "features": [],
                    "name": "FilterDuplicates",
                    "id": 34
                }
            },
            "beadfindargs": "justBeadFind --args-json /opt/ion/config/args_318_
↪beadfind.json",
            "isSystemDefault": false,
            "autoName": null,
            "libraryKey": "TCAG",
            "flows": 250,
            "date": "2018-02-26T17:28:33.000588+00:00",
            "isSystem": false,
            "variantfrequency": "",
            "planName": "Ion_ReproSeq_Aneuploidy_-_Ion_PGM_System",
            "calibrateargs": "Calibration",
            "flowsInOrder": "",
            "libraryPrepType": "",
            "sampleGrouping": "/rundb/api/v1/samplegrouptype_cv/2/",
            "chipBarcode": "",
            "sampleSetDisplayedName": "",
            "usePreBeadfind": true,
            "resource_uri": "/rundb/api/v1/availableonetouchplannedexperiment/131/",
            "libraryPrepTypeDisplayedName": "",
            "reverse3primeadapter": ""
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Available Onetouch Planned Experiment Summary Resource

Resource URL
`http://mytorrentserver/rundb/api/v1/availableonetouchplannedexperimentsummary/`
Schema URL `http://mytorrentserver/rundb/api/v1/availableonetouchplannedexperimentsummary/schema/`

Resource Fields

field	help text	default	nullable	readonly	bla
origin	Unicode string data. Ex: “Hello World”		true	false	fals
isReverseRun	Boolean data. Ex: True	false	false	false	tru
planDisplayedName	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
storage_options	Unicode string data. Ex: “Hello World”	A	false	false	fals
preAnalysis	Boolean data. Ex: True	true	false	false	tru
planShortID	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
planStatus	Unicode string data. Ex: “Hello World”		false	false	tru
runMode	Unicode string data. Ex: “Hello World”		false	false	tru
isCustom_kitSettings	Boolean data. Ex: True	false	false	false	tru
sampleTubeLabel	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
planExecutedDate	A date & time as a string. Ex: “2010-11-10T03:07:43”	n/a	true	false	fals
samplePrepKitName	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
reverse_primer	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
seqKitBarcode	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
id	Integer data. Ex: 2673		false	false	tru
metaData	Unicode string data. Ex: “Hello World”	{}	false	false	tru
isFavorite	Boolean data. Ex: True	false	false	false	tru
samplePrepProtocol	Unicode string data. Ex: “Hello World”		true	false	fals
isPlanGroup	Boolean data. Ex: True	false	false	false	tru
templatingKitName	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
runType	Unicode string data. Ex: “Hello World”	GENS	false	false	fals
templatingKitBarcode	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
planPGM	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
isSystemDefault	Boolean data. Ex: True	false	false	false	tru
autoName	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
isReusable	Boolean data. Ex: True	false	false	false	tru
controlSequencekitname	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
date	A date & time as a string. Ex: “2010-11-10T03:07:43”	n/a	true	false	fals

Table 2.7 – continued from previous page

field	help text	default	nullable	readonly	bla
isSystem	Boolean data. Ex: True	false	false	false	tru
libkit	Unicode string data. Ex: “Hello World”	n/a	true	false	fal
categories	Unicode string data. Ex: “Hello World”		true	false	fal
planName	Unicode string data. Ex: “Hello World”	n/a	true	false	fal
pairedEndLibraryAdapterName	Unicode string data. Ex: “Hello World”	n/a	true	false	fal
adapter	Unicode string data. Ex: “Hello World”	n/a	true	false	fal
irworkflow	Unicode string data. Ex: “Hello World”		false	false	tru
planExecuted	Boolean data. Ex: True	false	false	false	tru
username	Unicode string data. Ex: “Hello World”	n/a	true	false	fal
usePostBeadfind	Boolean data. Ex: True	true	false	false	tru
storageHost	Unicode string data. Ex: “Hello World”	n/a	true	false	fal
expName	Unicode string data. Ex: “Hello World”		false	false	tru
libraryReadLength	Integer data. Ex: 2673	0	false	false	fal
runname	Unicode string data. Ex: “Hello World”	n/a	true	false	fal
usePreBeadfind	Boolean data. Ex: True	true	false	false	tru
planGUID	Unicode string data. Ex: “Hello World”	n/a	true	false	fal
cycles	Integer data. Ex: 2673	n/a	true	false	fal
resource_uri	Unicode string data. Ex: “Hello World”	n/a	false	true	fal

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 1,
        "offset": 0,
        "limit": 1,
        "next": null
    },
    "objects": [
        {
            "origin": "gui|5.8.0",
            "isReverseRun": false,
            "planDisplayedName": "Ion ReproSeq Aneuploidy - Ion PGM System",
            "storage_options": "A",
            "preAnalysis": true,
            "planShortID": "6TGIO",
            "planStatus": "planned",
            "runMode": "single",
            "isCustom_kitSettings": false,
            "sampleTubeLabel": "",
            "planExecutedDate": null,
            "samplePrepKitName": null,
            "reverse_primer": null,
            "seqKitBarcode": null,
            "id": 131,
            "metaData": {
                "fromTemplate": "Ion_ReproSeq_Aneuploidy_-_Ion_PGM_System",
                "fromTemplateSource": "ION"
            },
            "isFavorite": false,
            "samplePrepProtocol": "",
            "isPlanGroup": false,
```

```
            "templatingKitName": "Ion PGM Template IA Tech Access Kit",
            "runType": "WGNM",
            "templatingKitBarcode": null,
            "planPGM": null,
            "isSystemDefault": false,
            "autoName": null,
            "isReusable": false,
            "controlSequencekitname": null,
            "date": "2018-02-26T17:28:33.000588+00:00",
            "isSystem": false,
            "libkit": null,
            "categories": "repro",
            "planName": "Ion_ReproSeq_Aneuploidy_-_Ion_PGM_System",
            "pairedEndLibraryAdapterName": "",
            "adapter": null,
            "irworkflow": "",
            "planExecuted": false,
            "username": "ionadmin",
            "usePostBeadfind": true,
            "storageHost": null,
            "expName": "",
            "libraryReadLength": 0,
            "runname": null,
            "usePreBeadfind": true,
            "planGUID": "d1ed9718-b6f4-4dfd-8de5-bbd150092997",
            "cycles": null,
            "resource_uri": "/rundb/api/v1/availableonetouchplannedexperimentsummary/
↪131/"
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Available Planned Experiment Summary Resource

Resource URL
`http://mytorrentserver/rundb/api/v1/availableplannedexperimentsummary/`
Schema URL
`http://mytorrentserver/rundb/api/v1/availableplannedexperimentsummary/schema/`

Resource Fields

field	help text
planDisplayedName	Unicode string data. Ex: “Hello World”
autoAnalyze	Boolean data. Ex: True
endBarcodeKitName	Unicode string data. Ex: “Hello World”
templatingKitBarcode	Unicode string data. Ex: “Hello World”
preAnalysis	Boolean data. Ex: True
applicationGroup	A single related resource. Can be either a URI or set of nested resource data.
mixedTypeRNA_hotSpotRegionBedFile	Unicode string data. Ex: “Hello World”
mixedTypeRNA_targetRegionBedFile	Unicode string data. Ex: “Hello World”
platform	Unicode string data. Ex: “Hello World”
categories	Unicode string data. Ex: “Hello World”
planPGM	Unicode string data. Ex: “Hello World”
libkit	Unicode string data. Ex: “Hello World”
projects	Many related resources. Can be either a list of URIs or list of individually nested resourc
notes	Unicode string data. Ex: “Hello World”
sequencekitname	Unicode string data. Ex: “Hello World”
base_recalibration_mode	Unicode string data. Ex: “Hello World”
storageHost	Unicode string data. Ex: “Hello World”
expName	Unicode string data. Ex: “Hello World”
cycles	Integer data. Ex: 2673
isReverseRun	Boolean data. Ex: True
storage_options	Unicode string data. Ex: “Hello World”
chipType	Unicode string data. Ex: “Hello World”
library	Unicode string data. Ex: “Hello World”
reverselibrarykey	Unicode string data. Ex: “Hello World”
sampleTubeLabel	Unicode string data. Ex: “Hello World”
seqKitBarcode	Unicode string data. Ex: “Hello World”
barcodeId	Unicode string data. Ex: “Hello World”
isPlanGroup	Boolean data. Ex: True
realign	Boolean data. Ex: True
sampleGroupingName	Unicode string data. Ex: “Hello World”
experiment	A single related resource. Can be either a URI or set of nested resource data.
bedfile	Unicode string data. Ex: “Hello World”
applicationCategoryDisplayedName	Unicode string data. Ex: “Hello World”
isReusable	Boolean data. Ex: True
isDuplicateReads	Boolean data. Ex: True
sampleSets	Many related resources. Can be either a list of URIs or list of individually nested resourc
librarykitname	Unicode string data. Ex: “Hello World”
sseBedFile	Unicode string data. Ex: “Hello World”
adapter	Unicode string data. Ex: “Hello World”

Table 2.8 – continued from previous page

field	help text
earlyDatFileDeletion	Boolean data. Ex: True
parentPlan	Unicode string data. Ex: “Hello World”
origin	Unicode string data. Ex: “Hello World”
forward3primeadapter	Unicode string data. Ex: “Hello World”
isCustom_kitSettings	Boolean data. Ex: True
samplePrepKitName	Unicode string data. Ex: “Hello World”
applicationGroupDisplayedName	Unicode string data. Ex: “Hello World”
metaData	Unicode string data. Ex: “Hello World”
isFavorite	Boolean data. Ex: True
qcValues	Many related resources. Can be either a list of URIs or list of individually nested resourc
planStatus	Unicode string data. Ex: “Hello World”
templatingKitName	Unicode string data. Ex: “Hello World”
runType	Unicode string data. Ex: “Hello World”
username	Unicode string data. Ex: “Hello World”
planName	Unicode string data. Ex: “Hello World”
sampleDisplayedName	Unicode string data. Ex: “Hello World”
controlSequencekitname	Unicode string data. Ex: “Hello World”
tfKey	Unicode string data. Ex: “Hello World”
mixedTypeRNA_reference	Unicode string data. Ex: “Hello World”
childPlans	A list of data. Ex: [’abc’, 26.73, 8]
pairedEndLibraryAdapterName	Unicode string data. Ex: “Hello World”
runMode	Unicode string data. Ex: “Hello World”
irworkflow	Unicode string data. Ex: “Hello World”
planExecuted	Boolean data. Ex: True
project	Unicode string data. Ex: “Hello World”
usePostBeadfind	Boolean data. Ex: True
libraryReadLength	Integer data. Ex: 2673
runname	Unicode string data. Ex: “Hello World”
chefInfo	A dictionary of data. Ex: {‘price’: 26.73, ‘name’: ‘Daniel’}
planGUID	Unicode string data. Ex: “Hello World”
samplePrepProtocol	Unicode string data. Ex: “Hello World”
planShortID	Unicode string data. Ex: “Hello World”
sample	Unicode string data. Ex: “Hello World”
planExecutedDate	A date & time as a string. Ex: “2010-11-10T03:07:43”
reverse_primer	Unicode string data. Ex: “Hello World”
id	Integer data. Ex: 2673
barcodedSamples	Unicode string data. Ex: “Hello World”
regionfile	Unicode string data. Ex: “Hello World”
selectedPlugins	Unicode string data. Ex: “Hello World”
isSystemDefault	Boolean data. Ex: True
autoName	Unicode string data. Ex: “Hello World”
libraryKey	Unicode string data. Ex: “Hello World”
flows	Integer data. Ex: 2673
date	A date & time as a string. Ex: “2010-11-10T03:07:43”
isSystem	Boolean data. Ex: True
variantfrequency	Unicode string data. Ex: “Hello World”
sampleSetDisplayedName	Unicode string data. Ex: “Hello World”
flowsInOrder	Unicode string data. Ex: “Hello World”
libraryPrepType	Unicode string data. Ex: “Hello World”

Table 2.8 – continued from previous page

field	help text
sampleGrouping	A single related resource. Can be either a URI or set of nested resource data.
chipBarcode	Unicode string data. Ex: “Hello World”
usePreBeadfind	Boolean data. Ex: True
resource_uri	Unicode string data. Ex: “Hello World”
libraryPrepTypeDisplayedName	Unicode string data. Ex: “Hello World”
reverse3primeadapter	Unicode string data. Ex: “Hello World”

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 1,
        "offset": 0,
        "limit": 1,
        "next": null
    },
    "objects": [
        {
            "planDisplayedName": "Ion ReproSeq Aneuploidy - Ion PGM System",
            "autoAnalyze": true,
            "endBarcodeKitName": "",
            "templatingKitBarcode": null,
            "preAnalysis": true,
            "thumbnailanalysisargs": "",
            "applicationGroup": "/rundb/api/v1/applicationgroup/1/",
            "mixedTypeRNA_hotSpotRegionBedFile": "",
            "mixedTypeRNA_targetRegionBedFile": "",
            "platform": "",
            "categories": "repro",
            "planPGM": null,
            "prebasecallerargs": "BaseCaller --barcode-filter 0.01 --barcode-filter-
↪minreads 20 --extra-trim-left 30",
            "alignmentargs": "tmap mapall ... stage1 map4",
            "thumbnailbasecallerargs": "",
            "libkit": null,
            "projects": [],
            "notes": "",
            "sequencekitname": "IonPGMHiQ",
            "base_recalibration_mode": "standard_recal",
            "storageHost": null,
            "expName": "",
            "thumbnailionstatsargs": "",
            "cycles": null,
            "isReverseRun": false,
            "storage_options": "A",
            "thumbnailalignmentargs": "",
            "chipType": "318",
            "library": "hg19",
            "runMode": "single",
            "sampleTubeLabel": "",
            "seqKitBarcode": null,
            "barcodeId": "Ion SingleSeq Barcode set 1-24",
            "isPlanGroup": false,
```

```
            "realign": false,
            "sampleGroupingName": "Self",
            "experiment": "/rundb/api/v1/experiment/123/",
            "bedfile": "",
            "applicationCategoryDisplayedName": "Reproductive",
            "isReusable": false,
            "isDuplicateReads": false,
            "sampleSets": [],
            "thumbnailbeadfindargs": "",
            "librarykitname": "IonPicoPlex",
            "sseBedFile": "",
            "adapter": null,
            "basecallerargs": "BaseCaller  --barcode-filter 0.01 --barcode-filter-
↪minreads 20 --extra-trim-left 30",
            "earlyDatFileDeletion": false,
            "parentPlan": null,
            "origin": "gui|5.8.0",
            "forward3primeadapter": "ATCACCGACTGCCCATAGAGAGGAAAGCGG",
            "planStatus": "planned",
            "isCustom_kitSettings": false,
            "samplePrepKitName": null,
            "applicationGroupDisplayedName": "DNA",
            "metaData": {
                "fromTemplate": "Ion_ReproSeq_Aneuploidy_-_Ion_PGM_System",
                "fromTemplateSource": "ION"
            },
            "isFavorite": false,
            "qcValues": [
                {
                    "threshold": 30,
                    "plannedExperiment": "/rundb/api/v1/plannedexperiment/131/",
                    "id": 370,
                    "qcType": {
                        "description": "",
                        "minThreshold": 0,
                        "maxThreshold": 100,
                        "defaultThreshold": 30,
                        "qcName": "Bead Loading (%)",
                        "id": 1,
                        "resource_uri": "/rundb/api/v1/qctype/1/"
                    },
                    "resource_uri": "/rundb/api/v1/plannedexperimentqc/370/"
                },
                {
                    "threshold": 30,
                    "plannedExperiment": "/rundb/api/v1/plannedexperiment/131/",
                    "id": 371,
                    "qcType": {
                        "description": "",
                        "minThreshold": 1,
                        "maxThreshold": 100,
                        "defaultThreshold": 30,
                        "qcName": "Key Signal (1-100)",
                        "id": 2,
                        "resource_uri": "/rundb/api/v1/qctype/2/"
                    },
                    "resource_uri": "/rundb/api/v1/plannedexperimentqc/371/"
                },
```

```
                {
                    "threshold": 30,
                    "plannedExperiment": "/rundb/api/v1/plannedexperiment/131/",
                    "id": 372,
                    "qcType": {
                        "description": "",
                        "minThreshold": 0,
                        "maxThreshold": 100,
                        "defaultThreshold": 30,
                        "qcName": "Usable Sequence (%)",
                        "id": 3,
                        "resource_uri": "/rundb/api/v1/qctype/3/"
                    },
                    "resource_uri": "/rundb/api/v1/plannedexperimentqc/372/"
                }
            ],
            "analysisargs": "Analysis --args-json /opt/ion/config/args_318_analysis.
↪json --mixed-first-flow 51 --mixed-last-flow 111",
            "thumbnailcalibrateargs": "",
            "templatingKitName": "Ion PGM Template IA Tech Access Kit",
            "runType": "WGNM",
            "username": "ionadmin",
            "planShortID": "6TGIO",
            "sampleDisplayedName": "",
            "prethumbnailbasecallerargs": "",
            "controlSequencekitname": null,
            "tfKey": "ATCG",
            "mixedTypeRNA_reference": "",
            "childPlans": [],
            "pairedEndLibraryAdapterName": "",
            "reverselibrarykey": "",
            "irworkflow": "",
            "planExecuted": false,
            "project": "",
            "usePostBeadfind": true,
            "libraryReadLength": 0,
            "runname": null,
            "chefInfo": {},
            "planGUID": "d1ed9718-b6f4-4dfd-8de5-bbd150092997",
            "ionstatsargs": "ionstats alignment",
            "samplePrepProtocol": "",
            "sample": "",
            "planExecutedDate": null,
            "reverse_primer": null,
            "id": 131,
            "barcodedSamples": {
                "Sample 6": {
                    "dualBarcodes": [],
                    "barcodeSampleInfo": {
                        "SingleSeq_006": {
                            "description": "",
                            "reference": "hg19",
                            "targetRegionBedFile": "",
                            "hotSpotRegionBedFile": "",
                            "nucleotideType": "DNA",
                            "controlSequenceType": "",
                            "externalId": "",
                            "endBarcode": "",
```

```
                    "controlType": "",
                    "sseBedFile": ""
                }
            },
            "barcodes": [
                "SingleSeq_006"
            ]
        },
        "Sample 7": {
            "dualBarcodes": [],
            "barcodeSampleInfo": {
                "SingleSeq_007": {
                    "description": "",
                    "reference": "hg19",
                    "targetRegionBedFile": "",
                    "hotSpotRegionBedFile": "",
                    "nucleotideType": "DNA",
                    "controlSequenceType": "",
                    "externalId": "",
                    "endBarcode": "",
                    "controlType": "",
                    "sseBedFile": ""
                }
            },
            "barcodes": [
                "SingleSeq_007"
            ]
        },
        "Sample 4": {
            "dualBarcodes": [],
            "barcodeSampleInfo": {
                "SingleSeq_004": {
                    "description": "",
                    "reference": "hg19",
                    "targetRegionBedFile": "",
                    "hotSpotRegionBedFile": "",
                    "nucleotideType": "DNA",
                    "controlSequenceType": "",
                    "externalId": "",
                    "endBarcode": "",
                    "controlType": "",
                    "sseBedFile": ""
                }
            },
            "barcodes": [
                "SingleSeq_004"
            ]
        },
        "Sample 5": {
            "dualBarcodes": [],
            "barcodeSampleInfo": {
                "SingleSeq_005": {
                    "description": "",
                    "reference": "hg19",
                    "targetRegionBedFile": "",
                    "hotSpotRegionBedFile": "",
                    "nucleotideType": "DNA",
                    "controlSequenceType": "",
```

```
                        "externalId": "",
                        "endBarcode": "",
                        "controlType": "",
                        "sseBedFile": ""
                    }
                },
                "barcodes": [
                    "SingleSeq_005"
                ]
            },
            "Sample 2": {
                "dualBarcodes": [],
                "barcodeSampleInfo": {
                    "SingleSeq_002": {
                        "description": "",
                        "reference": "hg19",
                        "targetRegionBedFile": "",
                        "hotSpotRegionBedFile": "",
                        "nucleotideType": "DNA",
                        "controlSequenceType": "",
                        "externalId": "",
                        "endBarcode": "",
                        "controlType": "",
                        "sseBedFile": ""
                    }
                },
                "barcodes": [
                    "SingleSeq_002"
                ]
            },
            "Sample 3": {
                "dualBarcodes": [],
                "barcodeSampleInfo": {
                    "SingleSeq_003": {
                        "description": "",
                        "reference": "hg19",
                        "targetRegionBedFile": "",
                        "hotSpotRegionBedFile": "",
                        "nucleotideType": "DNA",
                        "controlSequenceType": "",
                        "externalId": "",
                        "endBarcode": "",
                        "controlType": "",
                        "sseBedFile": ""
                    }
                },
                "barcodes": [
                    "SingleSeq_003"
                ]
            },
            "Sample 1": {
                "dualBarcodes": [],
                "barcodeSampleInfo": {
                    "SingleSeq_001": {
                        "description": "",
                        "reference": "hg19",
                        "targetRegionBedFile": "",
                        "hotSpotRegionBedFile": "",
```

```
                            "nucleotideType": "DNA",
                            "controlSequenceType": "",
                            "externalId": "",
                            "endBarcode": "",
                            "controlType": "",
                            "sseBedFile": ""
                        }
                    },
                    "barcodes": [
                        "SingleSeq_001"
                    ]
                }
            },
            "custom_args": false,
            "regionfile": "",
            "selectedPlugins": {
                "FilterDuplicates": {
                    "userInput": "",
                    "version": "5.8.0.0",
                    "features": [],
                    "name": "FilterDuplicates",
                    "id": 34
                }
            },
            "beadfindargs": "justBeadFind --args-json /opt/ion/config/args_318_
↪beadfind.json",
            "isSystemDefault": false,
            "autoName": null,
            "libraryKey": "TCAG",
            "flows": 250,
            "date": "2018-02-26T17:28:33.000588+00:00",
            "isSystem": false,
            "variantfrequency": "",
            "planName": "Ion_ReproSeq_Aneuploidy_-_Ion_PGM_System",
            "calibrateargs": "Calibration",
            "flowsInOrder": "",
            "libraryPrepType": "",
            "sampleGrouping": "/rundb/api/v1/samplegrouptype_cv/2/",
            "chipBarcode": "",
            "sampleSetDisplayedName": "",
            "usePreBeadfind": true,
            "resource_uri": "/rundb/api/v1/availableplannedexperimentsummary/131/",
            "libraryPrepTypeDisplayedName": "",
            "reverse3primeadapter": ""
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE

- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Chip Resource

Resource URL `http://mytorrentserver/rundb/api/v1/chip/`
Schema URL `http://mytorrentserver/rundb/api/v1/chip/schema/`

Resource Fields

field	help text	default	nullable	readonly	blank	unique	type
name	Unicode string data. Ex: "Hello World"	n/a	false	false	false	false	string
id	Integer data. Ex: 2673		false	false	true	true	integer
earlyDatFileDeletion	Unicode string data. Ex: "Hello World"		false	false	true	false	string
slots	Integer data. Ex: 2673	n/a	false	false	false	false	integer
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string
instrumentType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
isActive	Boolean data. Ex: True	true	false	false	true	false	boolean
description	Unicode string data. Ex: "Hello World"		false	false	false	false	string

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 28,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/chip/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
```

```
            "ionstatsargs": "ionstats alignment",
            "thumbnailionstatsargs": "",
            "thumbnailalignmentargs": "",
            "thumbnailanalysisargs": "",
            "slots": 1,
            "id": 1,
            "analysisargs": "Analysis --args-json /opt/ion/config/args_314_analysis.
↪json",
            "thumbnailcalibrateargs": "",
            "beadfindargs": "justBeadFind --args-json /opt/ion/config/args_314_
↪beadfind.json",
            "instrumentType": "pgm",
            "prebasecallerargs": "BaseCaller --barcode-filter-minreads 20",
            "description": "314v2",
            "prethumbnailbasecallerargs": "",
            "alignmentargs": "tmap mapall ... stage1 map4",
            "thumbnailbasecallerargs": "",
            "isActive": true,
            "thumbnailbeadfindargs": "",
            "calibrateargs": "Calibration",
            "name": "314",
            "basecallerargs": "BaseCaller --barcode-filter-minreads 20",
            "earlyDatFileDeletion": "",
            "resource_uri": "/rundb/api/v1/chip/1/"
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Cluster Info History Resource

Resource URL `http://mytorrentserver/rundb/api/v1/clusterinfohistory/`
Schema URL `http://mytorrentserver/rundb/api/v1/clusterinfohistory/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
username	Unicode string data. Ex: “Hello World”	ION	false	false	true	false	string
name	Unicode string data. Ex: “Hello World”	n/a	true	true	false	false	string
created	A date & time as a string. Ex: “2010-11-10T03:07:43”	true	false	false	true	false	date-time
text	Unicode string data. Ex: “Hello World”		false	false	false	false	string
object_pk	Integer data. Ex: 2673	n/a	false	false	false	false	integer
id	Integer data. Ex: 2673		false	false	true	true	integer
resource_uri	Unicode string data. Ex: “Hello World”	n/a	false	true	false	false	string

Example Response

```
{
    "meta": {
        "previous": null,
        "total_count": 0,
        "offset": 0,
        "limit": 1,
        "next": null
    },
    "objects": []
}
```

Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Common Cv Resource

Resource URL `http://mytorrentserver/rundb/api/v1/common_cv/`
Schema URL `http://mytorrentserver/rundb/api/v1/common_cv/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
displayedValue	Unicode string data. Ex: "Hello World"	n/a	false	false	false	true	string
sequencing_instrumentType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
description	Unicode string data. Ex: "Hello World"	n/a	true	false	false	false	string
categories	Unicode string data. Ex: "Hello World"		true	false	false	false	string
value	Unicode string data. Ex: "Hello World"	n/a	false	false	false	false	string
samplePrep_instrumentType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
cv_type	Unicode string data. Ex: "Hello World"	n/a	false	false	false	false	string
isVisible	Boolean data. Ex: True	true	false	false	true	false	boolean
uid	Unicode string data. Ex: "Hello World"	n/a	false	false	false	true	string
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string
id	Integer data. Ex: 2673		false	false	true	true	integer
isActive	Boolean data. Ex: True	true	false	false	true	false	boolean
isDefault	Boolean data. Ex: True	true	false	false	true	false	boolean

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 13,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/common_cv/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "displayedValue": "Ion PGM Hi-Q Chef for STR",
            "sequencing_instrumentType": "pgm",
            "description": "Use Ion Chef script protocol optimized for HID STR on PGM
↪",
            "categories": "hidSamplePrep",
            "value": "anneal62no10xab",
```

```
            "samplePrep_instrumentType": "IC",
            "cv_type": "samplePrepProtocol",
            "isVisible": true,
            "uid": "CV0001",
            "resource_uri": "/rundb/api/v1/common_cv/1/",
            "id": 1,
            "isActive": true,
            "isDefault": false
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Composite Data Management Resource

Resource URL `http://mytorrentserver/rundb/api/v1/compositedatamanagement/`
Schema URL `http://mytorrentserver/rundb/api/v1/compositedatamanagement/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
basecall_state	Unicode string data. Ex: "Hello World"	Unknown	false	true	false	false	string
in_process	Boolean data. Ex: True	false	false	false	false	false	boolean
misc_state	Unicode string data. Ex: "Hello World"	Unknown	false	true	false	false	string
timeStamp	A date & time as a string. Ex: "2010-11-10T03:07:43"	true	false	false	true	false	datetime
basecall_keep	Unicode string data. Ex: "Hello World"	n/a	true	true	false	false	string
misc_keep	Unicode string data. Ex: "Hello World"	n/a	true	true	false	false	string
output_keep	Unicode string data. Ex: "Hello World"	n/a	true	true	false	false	string
expName	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string
resultsName	Unicode string data. Ex: "Hello World"	n/a	false	false	false	false	string
output_state	Unicode string data. Ex: "Hello World"	Unknown	false	true	false	false	string
sigproc_state	Unicode string data. Ex: "Hello World"	Unknown	false	true	false	false	string
sigproc_keep	Unicode string data. Ex: "Hello World"	n/a	true	true	false	false	string
diskusage	Integer data. Ex: 2673	n/a	true	false	false	false	integer
expDir	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string
id	Integer data. Ex: 2673		false	false	true	true	integer
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 6,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/compositedatamanagement/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "misc_diskspace": 0,
            "expName": "S5-540_WholeTranscriptomeRNA",
            "basecall_state": "Local",
            "in_process": false,
            "misc_state": "Deleted",
            "timeStamp": "2017-07-22T13:15:56.000197+00:00",
            "basecall_keep": false,
            "misc_keep": null,
```

```
            "output_keep": false,
            "basecall_diskspace": 175694.536458969,
            "resultsName": "Auto_S5-540_WholeTranscriptomeRNA_91",
            "output_state": "Error",
            "sigproc_state": "Local",
            "sigproc_keep": false,
            "sigproc_diskspace": 0.0160617828369141,
            "diskusage": 229301,
            "resource_uri": "/rundb/api/v1/compositedatamanagement/3/",
            "expDir": "/results/S5_DemoData/S5-540_WholeTranscriptomeRNA",
            "id": 3,
            "output_diskspace": 53607.1456193924
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Composite Experiment Resource

Resource URL `http://mytorrentserver/rundb/api/mesh/v1/compositeexperiment/`
Schema URL `http://mytorrentserver/rundb/api/mesh/v1/compositeexperiment/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
storage_options	Unicode string data. Ex: “Hello World”	A	false	false	false	false	string
chipType	Unicode string data. Ex: “Hello World”	n/a	false	false	false	false	string
results	Many related resources. Can be either a list of URIs or list of individually nested resource data.	n/a	false	false	false	false	related
runMode	Unicode string data. Ex: “Hello World”		false	false	true	false	string
chefStartTime	A date & time as a string. Ex: “2010-11-10T03:07:43”	n/a	true	false	false	false	datetime
_host	Host this resource is located on.	n/a	false	true	false	false	string
id	Integer data. Ex: 2673		false	false	true	true	integer
chefSolutionsSerialNum	Unicode string data. Ex: “Hello World”		false	false	true	false	string
platform	Unicode string data. Ex: “Hello World”		false	false	true	false	string
status	Unicode string data. Ex: “Hello World”		false	false	true	false	string
star	Boolean data. Ex: True	false	false	false	true	false	boolean
resultDate	A date & time as a string. Ex: “2010-11-10T03:07:43”	true	true	false	false	false	datetime
flows	Integer data. Ex: 2673	n/a	false	false	false	false	integer
plan	A single related resource. Can be either a URI or set of nested resource data.	n/a	true	false	true	false	related
date	A date & time as a string. Ex: “2010-11-10T03:07:43”	n/a	false	false	false	false	datetime
ftpStatus	Unicode string data. Ex: “Hello World”		false	false	true	false	string
displayName	Unicode string data. Ex: “Hello World”		false	false	false	false	string
notes	Unicode string data. Ex: “Hello World”	n/a	true	false	false	false	string
pgmName	Unicode string data. Ex: “Hello World”	n/a	false	false	false	false	string
repResult	A single related resource. Can be either a URI or set of nested resource data.	n/a	true	false	true	false	related
expName	Unicode string data. Ex: “Hello World”	n/a	false	false	false	false	string
chefReagentsSerialNum	Unicode string data. Ex: “Hello World”		false	false	true	false	string
resource_uri	Unicode string data. Ex: “Hello World”	n/a	false	true	false	false	string

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 8,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/mesh/v1/compositeexperiment/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
```

```
            "chipDescription": "540",
            "chipType": "540",
            "results": [
                {
                    "status": "Completed",
                    "processedflows": 0,
                    "libmetrics": {
                        "i100Q20_reads": 0,
                        "aveKeyCounts": 88,
                        "id": 1,
                        "resource_uri": "",
                        "q20_mean_alignment_length": 0
                    },
                    "representative": false,
                    "analysis_metrics": {
                        "ignored": 1042801,
                        "lib": 139085639,
                        "total_wells": 164699136,
                        "pinned": 2329,
                        "live": 140339912,
                        "excluded": 16543404,
                        "bead": 140400602,
                        "resource_uri": "",
                        "id": 1,
                        "empty": 6710000,
                        "libFinal": 93974105
                    },
                    "timeStamp": "2017-07-22T13:15:56.000197+00:00",
                    "analysismetrics": {
                        "ignored": 1042801,
                        "lib": 139085639,
                        "total_wells": 164699136,
                        "pinned": 2329,
                        "live": 140339912,
                        "excluded": 16543404,
                        "bead": 140400602,
                        "resource_uri": "",
                        "id": 1,
                        "empty": 6710000,
                        "libFinal": 93974105
                    },
                    "reportLink": "/output/Home/Auto_S5-540_WholeTranscriptomeRNA_91_
↪003/",
                    "reportStatus": "Nothing",
                    "quality_metrics": {
                        "q0_mean_read_length": 149.579903660696,
                        "q0_reads": 93969124,
                        "q0_bases": "14055892515",
                        "q20_reads": 93969124,
                        "q20_bases": "11916010889",
                        "q20_mean_read_length": 149,
                        "id": 1,
                        "resource_uri": ""
                    },
                    "resultsName": "Auto_S5-540_WholeTranscriptomeRNA_91",
                    "projects": [
                        {
                            "resource_uri": "",
```

```
                        "id": 1,
                        "name": "demo",
                        "modified": "2018-02-28T17:32:01.000703+00:00"
                    }
                ],
                "status_display": "Completed",
                "qualitymetrics": {
                    "q0_mean_read_length": 149.579903660696,
                    "q0_reads": 93969124,
                    "q0_bases": "14055892515",
                    "q20_reads": 93969124,
                    "q20_bases": "11916010889",
                    "q20_mean_read_length": 149,
                    "id": 1,
                    "resource_uri": ""
                },
                "eas": {
                    "chipType": "540",
                    "reference": "",
                    "isPQ": false,
                    "references": "",
                    "barcodeKitName": "IonXpressRNA",
                    "resource_uri": ""
                },
                "resource_uri": "/rundb/api/v1/compositeresult/3/",
                "id": 3,
                "autoExempt": false,
                "isShowAllMetrics": true
            }
        ],
        "library": "",
        "sample": "",
        "runMode": "single",
        "storage_options": "A",
        "references": "",
        "chefStartTime": null,
        "repResult": "/rundb/api/v1/compositeresult/3/",
        "id": 91,
        "barcodedSamples": {},
        "chefSolutionsSerialNum": "",
        "barcodeId": "IonXpressRNA",
        "sampleSetName": "",
        "platform": "S5",
        "status": "run",
        "applicationCategoryDisplayedName": "RNA Sequencing",
        "star": false,
        "sampleDisplayedName": "",
        "resultDate": "2017-07-22T13:15:56.000197+00:00",
        "flows": 500,
        "plan": {
            "runType": "RNA",
            "sampleTubeLabel": null,
            "id": 99,
            "resource_uri": ""
        },
        "date": "2017-02-21T12:59:23+00:00",
        "ftpStatus": "0",
        "displayName": "S5-540 WholeTranscriptomeRNA",
```

```
            "notes": "",
            "chipInstrumentType": "S5",
            "pgmName": "S16",
            "keep": false,
            "expName": "S5-540_WholeTranscriptomeRNA",
            "chefReagentsSerialNum": "",
            "resource_uri": "/rundb/api/mesh/v1/compositeexperiment/91/"
        }
    ],
    "warnings": []
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Composite Result Resource

Resource URL `http://mytorrentserver/rundb/api/v1/compositeresult/`
Schema URL `http://mytorrentserver/rundb/api/v1/compositeresult/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
status	Unicode string data. Ex: "Hello World"	n/a	false	false	false	false	string
processedflows	Integer data. Ex: 2673	n/a	false	false	false	false	integer
timeStamp	A date & time as a string. Ex: "2010-11-10T03:07:43"	true	false	false	true	false	datetime
analysismetrics	A single related resource. Can be either a URI or set of nested resource data.	n/a	true	false	false	false	related
reportLink	Unicode string data. Ex: "Hello World"	n/a	false	false	false	false	string
id	Integer data. Ex: 2673		false	false	true	true	integer
reportStatus	Unicode string data. Ex: "Hello World"	Nothing	true	false	false	false	string
resultsName	Unicode string data. Ex: "Hello World"	n/a	false	false	false	false	string
projects	Many related resources. Can be either a list of URIs or list of individually nested resource data.	n/a	false	false	false	false	related
qualitymetrics	A single related resource. Can be either a URI or set of nested resource data.	n/a	true	false	false	false	related
eas	A single related resource. Can be either a URI or set of nested resource data.	n/a	false	false	false	false	related
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string
libmetrics	A single related resource. Can be either a URI or set of nested resource data.	n/a	true	false	false	false	related
autoExempt	Boolean data. Ex: True	false	false	false	true	false	boolean
representative	Boolean data. Ex: True	false	false	false	true	false	boolean

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 7,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/compositeresult/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "status": "Completed",
            "processedflows": 0,
            "libmetrics": {
                "i100Q20_reads": 0,
                "aveKeyCounts": 88,
                "id": 1,
```

```
            "resource_uri": "",
            "q20_mean_alignment_length": 0
        },
        "representative": false,
        "analysis_metrics": {
            "ignored": 1042801,
            "lib": 139085639,
            "total_wells": 164699136,
            "pinned": 2329,
            "live": 140339912,
            "excluded": 16543404,
            "bead": 140400602,
            "resource_uri": "",
            "id": 1,
            "empty": 6710000,
            "libFinal": 93974105
        },
        "timeStamp": "2017-07-22T13:15:56.000197+00:00",
        "analysismetrics": {
            "ignored": 1042801,
            "lib": 139085639,
            "total_wells": 164699136,
            "pinned": 2329,
            "live": 140339912,
            "excluded": 16543404,
            "bead": 140400602,
            "resource_uri": "",
            "id": 1,
            "empty": 6710000,
            "libFinal": 93974105
        },
        "reportLink": "/output/Home/Auto_S5-540_WholeTranscriptomeRNA_91_003/",
        "reportStatus": "Nothing",
        "quality_metrics": {
            "q0_mean_read_length": 149.579903660696,
            "q0_reads": 93969124,
            "q0_bases": "14055892515",
            "q20_reads": 93969124,
            "q20_bases": "11916010889",
            "q20_mean_read_length": 149,
            "id": 1,
            "resource_uri": ""
        },
        "resultsName": "Auto_S5-540_WholeTranscriptomeRNA_91",
        "projects": [
            {
                "resource_uri": "",
                "id": 1,
                "name": "demo",
                "modified": "2018-02-28T17:32:01.000703+00:00"
            }
        ],
        "qualitymetrics": {
            "q0_mean_read_length": 149.579903660696,
            "q0_reads": 93969124,
            "q0_bases": "14055892515",
            "q20_reads": 93969124,
            "q20_bases": "11916010889",
```

```
                "q20_mean_read_length": 149,
                "id": 1,
                "resource_uri": ""
            },
            "eas": {
                "chipType": "540",
                "reference": "",
                "isPQ": false,
                "references": "",
                "barcodeKitName": "IonXpressRNA",
                "resource_uri": ""
            },
            "resource_uri": "/rundb/api/v1/compositeresult/3/",
            "id": 3,
            "autoExempt": false,
            "isShowAllMetrics": true
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Content Resource

Resource URL `http://mytorrentserver/rundb/api/v1/content/`
Schema URL `http://mytorrentserver/rundb/api/v1/content/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
publisher	A single related resource. Can be either a URI or set of nested resource data.	n/a	false	false	false	false	related
description	Unicode string data. Ex: "Hello World"		false	false	true	false	string
extra	Unicode string data. Ex: "Hello World"		false	false	true	false	string
contentupload	A single related resource. Can be either a URI or set of nested resource data.	n/a	false	false	false	false	related
notes	Unicode string data. Ex: "Hello World"		false	false	true	false	string
enabled	Boolean data. Ex: True	true	false	false	true	false	boolean
upload_date	A date & time as a string. Ex: "2010-11-10T03:07:43"	n/a	false	true	false	false	datetime
application_tags	Unicode string data. Ex: "Hello World"		false	false	true	false	string
meta	Unicode string data. Ex: "Hello World"	{}	false	false	true	false	string
upload_id	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string
file	Unicode string data. Ex: "Hello World"	n/a	false	false	false	false	string
path	Unicode string data. Ex: "Hello World"	n/a	false	false	false	false	string
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string
type	Unicode string data. Ex: "Hello World"		false	false	true	false	string
id	Integer data. Ex: 2673		false	false	true	true	integer
name	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 31,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/content/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "publisher": "/rundb/api/v1/publisher/BED/",
            "description": "Noonan Panel",
            "extra": "hg19",
            "contentupload": "/rundb/api/v1/contentupload/1/",
            "notes": "",
            "enabled": true,
            "upload_date": "2018-01-16T18:30:05+00:00",
            "application_tags": "",
            "meta": {
                "upload_date": "2018-01-16T18:30:05",
                "description": "Noonan Panel",
                "reference": "hg19",
                "is_ampliseq": true,
                "hotspot": false,
```

```
                "choice": "pgm",
                "num_targets": 268,
                "num_genes": 14,
                "design": {
                    "number_of_amplicon_pools": 2,
                    "design_name": "Noonan Panel",
                    "configuration_choices": [],
                    "solution_name": null,
                    "id": 60011570,
                    "number_of_amplicons": 268,
                    "genome_reference": null,
                    "target_size": 26992,
                    "genome": "hg19",
                    "type": "COMMUNITY_PANEL",
                    "status": "ORDERABLE",
                    "min_number_amplicons_per_pool": 132,
                    "description": "<table class=\"design-template-info-wrapper-table\
↪">\r\n    <tr>\r\n        <td colspan=\"3\">\r\n        <br>\r\n            <p>
↪Noonan syndrome is a relatively common autosomal dominant congenital disorder with␣
↪a high phenotypic variability. It is a clinically and genetically heterogeneous␣
↪disorder that belongs to the group of Rasopathy diseases, caused by mutations in␣
↪genes dysregulating the RAS/MAPK pathway.\r\nThe Noonan  Research Gene Panel has␣
↪been developed in collaboration with an European consortia composed by  Marco␣
↪Tartaglia(1), Jose Luis Costa (2), Kornelia Neveling and Marcel Nelen (3) . 1)␣
↪Istituto Superiore di Sanit\u00e0, Rome, Italy, 2) Ipatimup, Porto 3) Human␣
↪Genetics, Radboud UMC Nijmegen .\r\nThe panel assesses 14 genes known to be related␣
↪with this disorder. <i>A2ML1</i>, <i>BRAF</i>, <i>CBL</i>, <i>HRAS</i>, <i>KRAS</i>,
↪ <i>MAP2K1</i>, <i>MAP2K2</i>, <i>NRAS</i>, <i>PTPN11</i>, <i>RAF1</i>, <i>RIT1</i>,
↪ <i>SHOC2</i>, <i>SOS1</i>, <i>SPRED1</i>. In a first study of 60 archived samples␣
↪we showed that very high sensitivity and specificity are achievable. For further␣
↪details see ASHG 2014 poster \u201cDevelopment and verification of a Noonan genes␣
↪Ion AmpliSeq\u2122 panel\u201d M. Nelen et al.\r\n</p>\r\n        </td>\r\n    </tr>
↪\r\n    <tr class=\"design-template-statistics\">\r\n        <td><strong>Design Date
↪</strong></td>\r\n        <td colspan=\"2\" style=\"text-align: left\">\r\n
↪    <b>Publication:</b> ASHG 2014 Poster \"Development and verification of a Noonan␣
↪genes Ion AmpliSeq\u2122 panel\"<br/>\r\n            <b>Author:</b> Marcel Nelen (
↪<a href='Marcel.Nelen@radboudumc.nl'>Marcel.Nelen@radboudumc.nl</a>)<br/>\r\n
↪     <b>Affiliation:</b> Dept. of Human Genetics, Radboud university medical center,
↪ Nijmegen, The Netherlands<br/>\r\n        </td>\r\n    </tr>\r\n    <tr class=\
↪"design-template-statistics\">\r\n        <td>\r\n            <strong>Recommended␣
↪Application</strong>\r\n            Germ line mutation detection\r\n        </td>
↪\r\n        <td>\r\n            <strong>Recommended Configuration</strong>\r\n
↪      Sample per Chip: 8 per 318 chip<br/>\r\n            Minimum coverage: 684␣
↪\r\n        </td>\r\n        <td>\r\n            <strong>Sample Type</strong>\r\n
↪         High molecular weight DNA\r\n        </td>\r\n    </tr>\r\n    <tr class=\
↪"design-template-statistics\">\r\n        <td>\r\n            <strong>Number of␣
↪sample in Publication</strong>\r\n            60 samples \r\n        </td>\r\n
↪  <td>\r\n            <strong>Observed Performance</strong>\r\n            Panel␣
↪uniformity: 93.05%<br/>\r\n            Reads on-targets: 98.42% \r\n        </td>
↪\r\n        <td>\r\n            <strong>Input DNA required </strong>\r\n
↪2 pool<br/>\r\n            20 ng total\r\n        </td>\r\n    </tr>\r\n    <tr>
↪\r\n        <td colspan=\"3\">\r\n            <b>Disease Research Area</b>:␣
↪Developmental Disorders\r\n        </td>\r\n    </tr>\r\n</table>",
                    "results_uri": "/ws/tmpldesign/60011570/download/results",
                    "plan": {
                        "missed_bed": "WG_noonan.20150501.missed.bed",
                        "hotspot_bed": null,
                        "coverage_summary": "WG_noonan.20150501.results_coverage_
↪summary.csv",
```

```
                        "designed_bed": "WG_noonan.20150501.designed.bed",
                        "target_mutations": null,
                        "primer_bed": null,
                        "runType": "AMPS",
                        "selectedPlugins": {},
                        "inputDna": "20 ng",
                        "coverage_detail": "WG_noonan.20150501.results_coverage_
↪details.csv",
                        "primer_sequences": null,
                        "displayedPanelSize": "26.99 kb",
                        "submitted_bed": "WG_noonan.20150501.submitted.bed",
                        "well_plate_data": "WG_noonan.20150501.384WellPlateDataSheet.
↪csv"
                    },
                    "design_id": "Noonan",
                    "pipeline": "DNA",
                    "request_id_and_solution_ordering_id": "Noonan",
                    "pipeline_version": null,
                    "created_date": "2015-05-22T20:52:38.703+0000",
                    "order_number": 0,
                    "amplicons_coverage_summary": 100
                },
                "pre_process_files": [
                    "WG_noonan.20150501.designed.bed",
                    "WG_noonan.20150501.missed.bed",
                    "WG_noonan.20150501.submitted.bed",
                    "WG_noonan.20150501.results_coverage_details.csv",
                    "WG_noonan.20150501.ampliconDataSheet.csv",
                    "WG_noonan.20150501.384WellPlateDataSheet.csv",
                    "WG_noonan.20150501.concentration.tab",
                    "WG_noonan.20150501.results_coverage_summary.csv",
                    "plan.json"
                ],
                "num_bases": 47724
            },
            "upload_id": "1",
            "file": "/results/uploads/BED/1/hg19/unmerged/plain/WG_noonan.20150501.
↪designed.bed",
            "path": "/hg19/unmerged/plain/WG_noonan.20150501.designed.bed",
            "resource_uri": "/rundb/api/v1/content/1/",
            "type": "target",
            "id": 1,
            "name": "WG_noonan.20150501.designed.bed"
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Content Upload Resource

Resource URL `http://mytorrentserver/rundb/api/v1/contentupload/`
Schema URL `http://mytorrentserver/rundb/api/v1/contentupload/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
status	Unicode string data. Ex: "Hello World"		false	false	true	false	string
upload_date	A date & time as a string. Ex: "2010-11-10T03:07:43"	true	true	false	false	false	datetime
name	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string
pub	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string
id	Integer data. Ex: 2673		false	false	true	true	integer
username	Unicode string data. Ex: "Hello World"		false	false	true	false	string
source	Unicode string data. Ex: "Hello World"		false	false	true	false	string
meta	Unicode string data. Ex: "Hello World"	{}	false	false	true	false	string
upload_type	Unicode string data. Ex: "Hello World"		false	false	true	false	string
file_path	Unicode string data. Ex: "Hello World"	n/a	false	false	false	false	string
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 20,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/contentupload/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "status": "Successfully Completed",
            "upload_date": "2018-04-13T18:54:45.000418+00:00",
            "name": "gencode.v19.annotation_and_tRNAs.gtf",
```

```
            "pub": "refAnnot",
            "id": 21,
            "username": "ionadmin",
            "source": "http://updates.itw/internal_reference_downloads/hg19/gencode.
↪v19.annotation_and_tRNAs.gtf",
            "meta": {
                "username": "ionadmin",
                "upload_date": "2018-04-13T18:54:45",
                "description": "hg19 and tRNA gene annotation file for smallRNA",
                "reference": "hg19",
                "url": "http://updates.itw/internal_reference_downloads/hg19/gencode.
↪v19.annotation_and_tRNAs.gtf",
                "upload_type": "Annotation",
                "identity_hash": "c47c7d854a9767400224e119246494ec",
                "application_tags": "smallRNA",
                "updateversion": "1.0",
                "filesize": "1109491",
                "short_description": "hg19 and tRNA GTF annotation",
                "publication_date": "2018-02-14",
                "annot_type": "GTF"
            },
            "upload_type": "Annotation",
            "file_path": "/results/uploads/refAnnot/21/gencode.v19.annotation_and_
↪tRNAs.gtf",
            "resource_uri": "/rundb/api/v1/contentupload/21/"
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Data Management History Resource

Resource URL `http://mytorrentserver/rundb/api/v1/datamanagementhistory/`
Schema URL `http://mytorrentserver/rundb/api/v1/datamanagementhistory/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
username	Unicode string data. Ex: "Hello World"	ION	false	false	true	false	string
created	A date & time as a string. Ex: "2010-11-10T03:07:43"	true	false	false	true	false	date-time
text	Unicode string data. Ex: "Hello World"		false	false	false	false	string
object_pk	Integer data. Ex: 2673	n/a	false	false	false	false	integer
resultsName	Unicode string data. Ex: "Hello World"	n/a	true	true	false	false	string
id	Integer data. Ex: 2673		false	false	true	true	integer
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 36,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/datamanagementhistory/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "username": "ionadmin",
            "created": "2017-07-22T06:59:07.000501+00:00",
            "text": "Started from Local Basecalling Input /results/S5_DemoData/S5-530_
↪cfDNA.",
            "object_pk": 1,
            "resultsName": "Auto_S5-530_cfDNA_89",
            "id": 8,
            "resource_uri": "/rundb/api/v1/datamanagementhistory/8/"
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Dna Barcode Resource

Resource URL `http://mytorrentserver/rundb/api/v1/dnabarcode/`
Schema URL `http://mytorrentserver/rundb/api/v1/dnabarcode/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
index	Integer data. Ex: 2673	n/a	false	false	false	false	integer
end_adapter	Unicode string data. Ex: “Hello World”		false	false	true	false	string
name	Unicode string data. Ex: “Hello World”	n/a	false	false	false	false	string
score_cutoff	Floating point numeric data. Ex: 26.73	0	false	false	false	false	float
sequence	Unicode string data. Ex: “Hello World”	n/a	false	false	false	false	string
is_end_barcode	Boolean data. Ex: True	false	false	false	true	false	boolean
adapter	Unicode string data. Ex: “Hello World”		false	false	true	false	string
system	Boolean data. Ex: True	false	false	false	true	false	boolean
id	Integer data. Ex: 2673		false	false	true	true	integer
length	Integer data. Ex: 2673	0	false	false	true	false	integer
id_str	Unicode string data. Ex: “Hello World”	n/a	false	false	false	false	string
active	Boolean data. Ex: True	true	false	false	true	false	boolean
end_sequence	Unicode string data. Ex: “Hello World”		false	false	true	false	string
score_mode	Integer data. Ex: 2673	0	false	false	true	false	integer
type	Unicode string data. Ex: “Hello World”		false	false	true	false	string
annotation	Unicode string data. Ex: “Hello World”		false	false	true	false	string
resource_uri	Unicode string data. Ex: “Hello World”	n/a	false	true	false	false	string

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 2090,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/dnabarcode/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "index": 1,
            "end_adapter": "",
            "name": "MuSeek_5prime_tag",
            "score_cutoff": 2,
            "sequence": "TTCA",
            "is_end_barcode": false,
            "adapter": "",
            "system": false,
            "id": 1,
            "length": 4,
            "id_str": "MuSeek_5prime_tag_001",
            "active": true,
            "end_sequence": "",
            "score_mode": 1,
            "type": "none",
            "annotation": "",
            "resource_uri": "/rundb/api/v1/dnabarcode/1/"
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Email Address Resource

Resource URL `http://mytorrentserver/rundb/api/v1/emailaddress/`
Schema URL `http://mytorrentserver/rundb/api/v1/emailaddress/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
selected	Boolean data. Ex: True		false	false	true	false	boolean
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string
email	Unicode string data. Ex: "Hello World"		false	false	true	false	string
id	Integer data. Ex: 2673		false	false	true	true	integer

Example Response

```
{
    "meta": {
        "previous": null,
        "total_count": 0,
        "offset": 0,
        "limit": 1,
        "next": null
    },
    "objects": []
}
```

Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Event Log Resource

Resource URL `http://mytorrentserver/rundb/api/v1/eventlog/`
Schema URL `http://mytorrentserver/rundb/api/v1/eventlog/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
username	Unicode string data. Ex: "Hello World"	ION	false	false	true	false	string
created	A date & time as a string. Ex: "2010-11-10T03:07:43"	true	false	false	true	false	datetime
text	Unicode string data. Ex: "Hello World"		false	false	false	false	string
object_pk	Integer data. Ex: 2673	n/a	false	false	false	false	integer
id	Integer data. Ex: 2673		false	false	true	true	integer
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 56,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/eventlog/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "username": "ionadmin",
            "created": "2018-02-26T17:28:33.000742+00:00",
            "text": "Created Planned Run: Ion_ReproSeq_Aneuploidy_-_Ion_PGM_System␣
↪(131)",
            "object_pk": 131,
            "id": 51,
            "resource_uri": "/rundb/api/v1/eventlog/51/"
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE

- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Experiment Resource

Resource URL `http://mytorrentserver/rundb/api/v1/experiment/`
Schema URL `http://mytorrentserver/rundb/api/v1/experiment/schema/`

Resource Fields

field	help text	de
isReverseRun	Boolean data. Ex: True	fal
chefLotNumber	Unicode string data. Ex: “Hello World”	
chipType	Unicode string data. Ex: “Hello World”	n/a
chefProtocolDeviationName	Unicode string data. Ex: “Hello World”	n/a
chefReagentID	Unicode string data. Ex: “Hello World”	
results	Many related resources. Can be either a list of URIs or list of individually nested resource data.	n/a
chefSolutionsPart	Unicode string data. Ex: “Hello World”	
runtype	Unicode string data. Ex: “Hello World”	n/a
chefLastUpdate	A date & time as a string. Ex: “2010-11-10T03:07:43”	n/a
storage_options	Unicode string data. Ex: “Hello World”	A
chefChipExpiration1	Unicode string data. Ex: “Hello World”	
chefChipExpiration2	Unicode string data. Ex: “Hello World”	
diskusage	Integer data. Ex: 2673	n/a
chefStatus	Unicode string data. Ex: “Hello World”	
reverse_primer	Unicode string data. Ex: “Hello World”	n/a
seqKitBarcode	Unicode string data. Ex: “Hello World”	
id	Integer data. Ex: 2673	
chefReagentsPart	Unicode string data. Ex: “Hello World”	
metaData	Unicode string data. Ex: “Hello World”	{}
chefInstrumentName	Unicode string data. Ex: “Hello World”	
chefSolutionsSerialNum	Unicode string data. Ex: “Hello World”	
sample	Unicode string data. Ex: “Hello World”	n/a
log	Unicode string data. Ex: “Hello World”	{}
sequencekitbarcode	Unicode string data. Ex: “Hello World”	n/a
resource_uri	Unicode string data. Ex: “Hello World”	n/a
eas_set	Many related resources. Can be either a list of URIs or list of individually nested resource data.	n/a
chefLogPath	Unicode string data. Ex: “Hello World”	n/a

Table 2.9 – continued from previous page

field	help text	de
chefFlexibleWorkflow	Unicode string data. Ex: “Hello World”	
platform	Unicode string data. Ex: “Hello World”	
chefScriptVersion	Unicode string data. Ex: “Hello World”	
samples	Many related resources. Can be either a list of URIs or list of individually nested resource data.	n/a
chefOperationMode	Unicode string data. Ex: “Hello World”	
chefManufactureDate	Unicode string data. Ex: “Hello World”	
chefSamplePos	Unicode string data. Ex: “Hello World”	
pinnedRepResult	Boolean data. Ex: True	fal
chefReagentsExpiration	Unicode string data. Ex: “Hello World”	
chefSolutionsLot	Unicode string data. Ex: “Hello World”	
reagentBarcode	Unicode string data. Ex: “Hello World”	
chefProgress	Floating point numeric data. Ex: 26.73	0
chefKitType	Unicode string data. Ex: “Hello World”	
star	Boolean data. Ex: True	fal
chefPackageVer	Unicode string data. Ex: “Hello World”	
usePreBeadfind	Boolean data. Ex: True	tru
isProton	Unicode string data. Ex: “Hello World”	n/a
expCompInfo	Unicode string data. Ex: “Hello World”	
flowsInOrder	Unicode string data. Ex: “Hello World”	
flows	Integer data. Ex: 2673	n/a
resultDate	A date & time as a string. Ex: “2010-11-10T03:07:43”	tru
chefTipRackBarcode	Unicode string data. Ex: “Hello World”	
chefRemainingSeconds	Integer data. Ex: 2673	n/a
plan	A single related resource. Can be either a URI or set of nested resource data.	n/a
date	A date & time as a string. Ex: “2010-11-10T03:07:43”	n/a
chefExtraInfo_1	Unicode string data. Ex: “Hello World”	
chefExtraInfo_2	Unicode string data. Ex: “Hello World”	
unique	Unicode string data. Ex: “Hello World”	n/a
expDir	Unicode string data. Ex: “Hello World”	n/a
autoAnalyze	Boolean data. Ex: True	tru
ftpStatus	Unicode string data. Ex: “Hello World”	
chefMessage	Unicode string data. Ex: “Hello World”	
chefEndTime	A date & time as a string. Ex: “2010-11-10T03:07:43”	n/a
displayName	Unicode string data. Ex: “Hello World”	
pgmName	Unicode string data. Ex: “Hello World”	n/a
runMode	Unicode string data. Ex: “Hello World”	
notes	Unicode string data. Ex: “Hello World”	n/a
sequencekitname	Unicode string data. Ex: “Hello World”	n/a
chipBarcode	Unicode string data. Ex: “Hello World”	
chefStartTime	A date & time as a string. Ex: “2010-11-10T03:07:43”	n/a
chefSolutionsExpiration	Unicode string data. Ex: “Hello World”	
chefReagentsLot	Unicode string data. Ex: “Hello World”	
storageHost	Unicode string data. Ex: “Hello World”	n/a
expName	Unicode string data. Ex: “Hello World”	n/a
status	Unicode string data. Ex: “Hello World”	
chefReagentsSerialNum	Unicode string data. Ex: “Hello World”	
cycles	Integer data. Ex: 2673	n/a
chefChipType2	Unicode string data. Ex: “Hello World”	
chefChipType1	Unicode string data. Ex: “Hello World”	

Table 2.9 – continued from previous page

field	help text	de
baselineRun	Boolean data. Ex: True	fal
user_ack	Unicode string data. Ex: “Hello World”	U
rawdatastyle	Unicode string data. Ex: “Hello World”	sir

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 112,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/experiment/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "isReverseRun": false,
            "chefLotNumber": "",
            "chipType": "P1.1.17",
            "chefProtocolDeviationName": null,
            "chefReagentID": "",
            "results": [],
            "chefSolutionsPart": "",
            "runtype": "GENS",
            "chefLastUpdate": null,
            "storage_options": "A",
            "chefChipExpiration1": "",
            "chefChipExpiration2": "",
            "diskusage": null,
            "chefStatus": "",
            "reverse_primer": null,
            "seqKitBarcode": "",
            "id": 5,
            "chefReagentsPart": "",
            "metaData": {},
            "chefInstrumentName": "",
            "chefSolutionsSerialNum": "",
            "sample": "",
            "log": {},
            "sequencekitbarcode": "",
            "resource_uri": "/rundb/api/v1/experiment/5/",
            "eas_set": [
                {
                    "ionstatsargs": "",
                    "isEditable": true,
                    "endBarcodeKitName": "",
                    "hotSpotRegionBedFile": "",
                    "results": [],
                    "mixedTypeRNA_reference": null,
                    "mixedTypeRNA_targetRegionBedFile": null,
                    "targetRegionBedFile": "",
                    "thumbnailalignmentargs": "",
                    "thumbnailanalysisargs": "",
                    "id": 5,
                    "barcodedSamples": {},
```

```
                "base_recalibration_mode": "standard_recal",
                "reference": "",
                "isOneTimeOverride": false,
                "mixedTypeRNA_hotSpotRegionBedFile": null,
                "analysisargs": "",
                "thumbnailcalibrateargs": "",
                "realign": false,
                "selectedPlugins": {
                    "RNASeqAnalysis": {
                        "userInput": {},
                        "version": "5.8.0.0",
                        "features": [],
                        "name": "RNASeqAnalysis",
                        "id": 29
                    },
                    "PartekFlowUploader": {
                        "userInput": {},
                        "version": "1.0",
                        "features": [],
                        "name": "PartekFlowUploader",
                        "id": 9999
                    }
                },
                "experiment": "/rundb/api/v1/experiment/5/",
                "barcodeKitName": "IonXpressRNA",
                "beadfindargs": "",
                "threePrimeAdapter": "ATCACCGACTGCCCATAGAGAGGCTGAGAC",
                "thumbnailbasecallerargs": "",
                "status": "planned",
                "prebasecallerargs": "",
                "thumbnailionstatsargs": "",
                "prethumbnailbasecallerargs": "",
                "alignmentargs": "",
                "isDuplicateReads": false,
                "libraryKey": "TCAG",
                "date": "2018-01-12T19:38:34.000886+00:00",
                "libraryKitName": "Ion Total RNA Seq Kit v2",
                "thumbnailbeadfindargs": "",
                "calibrateargs": "",
                "tfKey": "ATCG",
                "libraryKitBarcode": null,
                "sseBedFile": "",
                "basecallerargs": "",
                "custom_args": false,
                "resource_uri": "/rundb/api/v1/experimentanalysissettings/5/"
            }
        ],
        "chefLogPath": null,
        "chefFlexibleWorkflow": "",
        "platform": "PROTON",
        "chefScriptVersion": "",
        "samples": [],
        "chefOperationMode": "",
        "chefManufactureDate": "",
        "chefSamplePos": "",
        "pinnedRepResult": false,
        "chefReagentsExpiration": "",
        "chefSolutionsLot": "",
```

```
            "reagentBarcode": "",
            "chefProgress": 0,
            "chefKitType": "",
            "star": false,
            "chefPackageVer": "",
            "usePreBeadfind": false,
            "isProton": "True",
            "expCompInfo": "",
            "flowsInOrder": "",
            "flows": 500,
            "resultDate": "2017-07-22T06:41:42.000088+00:00",
            "chefTipRackBarcode": "",
            "chefRemainingSeconds": null,
            "plan": "/rundb/api/v1/plannedexperiment/20/",
            "date": "2017-07-22T06:41:42.000087+00:00",
            "chefExtraInfo_1": "",
            "chefExtraInfo_2": "",
            "unique": "39ef1391-032b-44d8-a7a1-d11dbb6028e2",
            "expDir": "",
            "autoAnalyze": true,
            "ftpStatus": "Complete",
            "chefMessage": "",
            "chefEndTime": null,
            "displayName": "NN4E0",
            "pgmName": "",
            "runMode": "single",
            "notes": "",
            "sequencekitname": "ProtonI200Kit-v3",
            "chipBarcode": "",
            "chefStartTime": null,
            "chefSolutionsExpiration": "",
            "chefReagentsLot": "",
            "storageHost": "",
            "expName": "39ef1391-032b-44d8-a7a1-d11dbb6028e2",
            "status": "planned",
            "chefReagentsSerialNum": "",
            "cycles": 0,
            "chefChipType2": "",
            "chefChipType1": "",
            "baselineRun": false,
            "user_ack": "U",
            "rawdatastyle": "single"
        }
    ]
}
```


Allowed list HTTP methods

- GET
- PATCH
- PUT
- DELETE

Allowed detail HTTP methods

- GET
- PATCH
- PUT
- DELETE

Experiment Analysis Settings Resource

Resource URL `http://mytorrentserver/rundb/api/v1/experimentanalysissettings/`
Schema URL
`http://mytorrentserver/rundb/api/v1/experimentanalysissettings/schema/`

Resource Fields

field	help text
ionstatsargs	Unicode string data. Ex: “Hello World”
isEditable	Boolean data. Ex: True
endBarcodeKitName	Unicode string data. Ex: “Hello World”
hotSpotRegionBedFile	Unicode string data. Ex: “Hello World”
results	Many related resources. Can be either a list of URIs or list of individually nested resourc
mixedTypeRNA_reference	Unicode string data. Ex: “Hello World”
mixedTypeRNA_targetRegionBedFile	Unicode string data. Ex: “Hello World”
targetRegionBedFile	Unicode string data. Ex: “Hello World”
thumbnailalignmentargs	Unicode string data. Ex: “Hello World”
thumbnailanalysisargs	Unicode string data. Ex: “Hello World”
id	Integer data. Ex: 2673
barcodedSamples	Unicode string data. Ex: “Hello World”
base_recalibration_mode	Unicode string data. Ex: “Hello World”
reference	Unicode string data. Ex: “Hello World”
isOneTimeOverride	Boolean data. Ex: True
mixedTypeRNA_hotSpotRegionBedFile	Unicode string data. Ex: “Hello World”
analysisargs	Unicode string data. Ex: “Hello World”
thumbnailcalibrateargs	Unicode string data. Ex: “Hello World”
realign	Boolean data. Ex: True
selectedPlugins	Unicode string data. Ex: “Hello World”
experiment	A single related resource. Can be either a URI or set of nested resource data.
barcodeKitName	Unicode string data. Ex: “Hello World”
beadfindargs	Unicode string data. Ex: “Hello World”
threePrimeAdapter	Unicode string data. Ex: “Hello World”
thumbnailbasecallerargs	Unicode string data. Ex: “Hello World”
status	Unicode string data. Ex: “Hello World”
prebasecallerargs	Unicode string data. Ex: “Hello World”
thumbnailionstatsargs	Unicode string data. Ex: “Hello World”
prethumbnailbasecallerargs	Unicode string data. Ex: “Hello World”
alignmentargs	Unicode string data. Ex: “Hello World”

Table 2.10 – continued from previous page

field	help text
isDuplicateReads	Boolean data. Ex: True
libraryKey	Unicode string data. Ex: “Hello World”
date	A date & time as a string. Ex: “2010-11-10T03:07:43”
libraryKitName	Unicode string data. Ex: “Hello World”
thumbnailbeadfindargs	Unicode string data. Ex: “Hello World”
calibrateargs	Unicode string data. Ex: “Hello World”
tfKey	Unicode string data. Ex: “Hello World”
libraryKitBarcode	Unicode string data. Ex: “Hello World”
sseBedFile	Unicode string data. Ex: “Hello World”
basecallerargs	Unicode string data. Ex: “Hello World”
custom_args	Boolean data. Ex: True
resource_uri	Unicode string data. Ex: “Hello World”

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 112,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/experimentanalysissettings/?offset=1&limit=1&
↪format=json"
    },
    "objects": [
        {
            "ionstatsargs": "",
            "isEditable": true,
            "endBarcodeKitName": "",
            "hotSpotRegionBedFile": "",
            "results": [],
            "mixedTypeRNA_reference": null,
            "mixedTypeRNA_targetRegionBedFile": null,
            "targetRegionBedFile": "",
            "thumbnailalignmentargs": "",
            "thumbnailanalysisargs": "",
            "id": 2,
            "barcodedSamples": {},
            "base_recalibration_mode": "standard_recal",
            "reference": "",
            "isOneTimeOverride": false,
            "mixedTypeRNA_hotSpotRegionBedFile": null,
            "analysisargs": "",
            "thumbnailcalibrateargs": "",
            "realign": false,
            "selectedPlugins": {},
            "experiment": "/rundb/api/v1/experiment/2/",
            "barcodeKitName": "",
            "beadfindargs": "",
            "threePrimeAdapter": "ATCACCGACTGCCCATAGAGAGGCTGAGAC",
            "thumbnailbasecallerargs": "",
            "status": "planned",
            "prebasecallerargs": "",
```

```
            "thumbnailionstatsargs": "",
            "prethumbnailbasecallerargs": "",
            "alignmentargs": "",
            "isDuplicateReads": false,
            "libraryKey": "TCAG",
            "date": "2017-07-22T06:43:55.000629+00:00",
            "libraryKitName": "Ion Xpress Plus Fragment Library Kit",
            "thumbnailbeadfindargs": "",
            "calibrateargs": "",
            "tfKey": "ATCG",
            "libraryKitBarcode": null,
            "sseBedFile": "",
            "basecallerargs": "",
            "custom_args": false,
            "resource_uri": "/rundb/api/v1/experimentanalysissettings/2/"
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

File Monitor Resource

Resource URL `http://mytorrentserver/rundb/api/v1/filemonitor/`
Schema URL `http://mytorrentserver/rundb/api/v1/filemonitor/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
status	Unicode string data. Ex: "Hello World"		false	false	false	false	string
updated	A date & time as a string. Ex: "2010-11-10T03:07:43"	true	false	false	true	false	date-time
name	Unicode string data. Ex: "Hello World"		false	false	false	false	string
created	A date & time as a string. Ex: "2010-11-10T03:07:43"	true	false	false	true	false	date-time
url	Unicode string data. Ex: "Hello World"	n/a	false	false	false	false	string
md5sum	Unicode string data. Ex: "Hello World"	None	true	false	false	false	string
celery_task_id	Unicode string data. Ex: "Hello World"		false	false	true	false	string
local_dir	Unicode string data. Ex: "Hello World"		false	false	false	false	string
progress	Unicode string data. Ex: "Hello World"	0	false	false	false	false	string
size	Unicode string data. Ex: "Hello World"	None	true	false	false	false	string
id	Integer data. Ex: 2673		false	false	true	true	integer
tags	Unicode string data. Ex: "Hello World"		false	false	false	false	string
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 9,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/filemonitor/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "status": "Complete",
            "updated": "2018-04-13T18:54:39.000796+00:00",
            "name": "gene.gtf",
            "created": "2018-04-13T18:54:08.000422+00:00",
            "url": "http://updates.itw/internal_reference_downloads/hg19/gene.gtf",
            "md5sum": "72fbd490a4d3be60e53e642d4401c944",
            "celery_task_id": "7db1de03-b295-4b62-9cdc-9cbb4c6065b0",
            "local_dir": "/tmp/tmppTeNvf",
            "progress": "1111970946",
            "size": "1111970946",
            "id": 7,
            "tags": "annotation",
            "resource_uri": "/rundb/api/v1/filemonitor/7/"
        }
    ]
}
```

Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

File Server Resource

Resource URL `http://mytorrentserver/rundb/api/v1/fileserver/`
Schema URL `http://mytorrentserver/rundb/api/v1/fileserver/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
percentfull	Floating point numeric data. Ex: 26.73	0	true	false	false	false	float
name	Unicode string data. Ex: “Hello World”	n/a	false	false	false	false	string
filesPrefix	Unicode string data. Ex: “Hello World”	n/a	false	false	false	false	string
comments	Unicode string data. Ex: “Hello World”		false	false	true	false	string
id	Integer data. Ex: 2673		false	false	true	true	integer
resource_uri	Unicode string data. Ex: “Hello World”	n/a	false	true	false	false	string

Example Response

```
{
    "meta": {
        "previous": null,
        "total_count": 1,
```

```
        "offset": 0,
        "limit": 1,
        "next": null
    },
    "objects": [
        {
            "percentfull": 39.0445528646121,
            "name": "Home",
            "filesPrefix": "/results/",
            "comments": "",
            "id": 1,
            "resource_uri": "/rundb/api/v1/fileserver/1/"
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Flow Order Resource

Resource URL `http://mytorrentserver/rundb/api/v1/floworder/`
Schema URL `http://mytorrentserver/rundb/api/v1/floworder/schema/`

Resource Fields

field	help text	de-fault	nul-lable	read-only	blank	unique	type
description	Unicode string data. Ex: "Hello World"		false	false	true	false	string
re-source_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string
flowOrder	Unicode string data. Ex: "Hello World"		false	false	true	false	string
isActive	Boolean data. Ex: True	true	false	false	true	false	boolean
isSystem	Boolean data. Ex: True	false	false	false	true	false	boolean
id	Integer data. Ex: 2673		false	false	true	true	integer
isDefault	Boolean data. Ex: True	false	false	false	true	false	boolean
name	Unicode string data. Ex: "Hello World"	n/a	false	false	false	true	string

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 7,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/floworder/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "description": "Ion contradanzon flow order",
            "resource_uri": "/rundb/api/v1/floworder/3/",
            "flowOrder":
↪"TACGTACGTAGCTTGACGTACGTCATGCATCGATCAGCTAAGCTGACGTAGCTAGCATCGATCCAGTCATGACTGACGTAGCTGACTGGATCAGTCA
↪",
            "isActive": false,
            "isSystem": true,
            "id": 3,
            "isDefault": false,
            "name": "Ion contradanzon"
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Get Chef Cartridgeusage Resource

Resource URL `http://mytorrentserver/rundb/api/v1/getchefcartridgeusage/`
Schema URL `http://mytorrentserver/rundb/api/v1/getchefcartridgeusage/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
hoursSinceSolutionFirstUse	Integer number of hours between (oldest associated experiment using Solution) and (chefCurrentTime). Rounded down to the nearest hour is OK. Ex: 24	n/a	true	true	true	false	Integer
numberSolutionSerialUsage	Integer number. No of Solution cartridge Usage Ex: 2	n/a	true	true	true	false	Integer
errorCodes	A lists of data. Ex: [”E200”] or [”W100”, “W200”]	n/a	true	true	true	false	List Object
allowRunToContinue	Boolean string data. Ex: “true or false”	n/a	true	true	true	false	boolean
detailMessages	A dictionary of data. Ex: {‘E300’: ‘No. of reagent and solution usage do not match’}	n/a	true	true	true	false	dict
numberReagentSerialUsage	Integer number. No of Reagent cartridge Usage Ex: 2	n/a	true	true	true	false	Integer
hoursSinceReagentFirstUse	Integer number of hours between (oldest associated experiment using Reagent) and (chefCurrentTime). Rounded down to the nearest hour is OK. Ex: 48	n/a	true	true	true	false	Integer

Example Response

```
{
    "hoursSinceSolutionFirstUse": "",
    "numberSolutionSerialUsage": 0,
    "errorCodes": [
        "E305"
```

```
    ],
    "allowRunToContinue": false,
    "detailMessages": {
        "E305": "Missing chef inputs filter option ['chefReagentsSerialNum',
↪'chefSolutionsSerialNum', 'kitName']"
    },
    "numberReagentSerialUsage": 0,
    "hoursSinceReagentFirstUse": ""
}
```


Allowed list HTTP methods

- GET

Allowed detail HTTP methods

None

Get Chef Script Info Resource

Resource URL `http://mytorrentserver/rundb/api/v1/getchefscriptinfo/`
Schema URL `http://mytorrentserver/rundb/api/v1/getchefscriptinfo/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
availableversion	A dictionary of data. Ex: {'Compatible_Chef_release': ['IC.5.4.0'], 'IS_scripts': '00515'}	n/a	true	true	true	false	dict

Example Response


```
{
    "object": {
        "availableversion": {
            "IS_scripts": "000803",
            "Compatible_Chef_release": [
                "IC.5.10.0"
            ]
        }
    }
}
```


Allowed list HTTP methods

- GET

Allowed detail HTTP methods

None

Global Config Resource

Resource URL `http://mytorrentserver/rundb/api/v1/globalconfig/`
Schema URL `http://mytorrentserver/rundb/api/v1/globalconfig/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
enable_version_lock	Boolean data. Ex: True	false	false	false	true	false	boolean
site_name	Unicode string data. Ex: "Hello World"		false	false	true	false	string
enable_support_upload	Boolean data. Ex: True	false	false	false	true	false	boolean
plugin_output_folder	Unicode string data. Ex: "Hello World"		false	false	true	false	string
auto_archive_ack	Boolean data. Ex: True	false	false	false	true	false	boolean
enable_compendia_OCP	Boolean data. Ex: True	false	false	false	true	false	boolean
id	Integer data. Ex: 2673		false	false	true	true	integer
base_recalibration_mode	Unicode string data. Ex: "Hello World"	standard_recalD	false	false	false	false	string
default_storage_options	Unicode string data. Ex: "Hello World"		false	false	true	false	string
selected	Boolean data. Ex: True		false	false	true	false	boolean
check_news_posts	Boolean data. Ex: True	true	false	false	true	false	boolean
realign	Boolean data. Ex: True	false	false	false	true	false	boolean
ts_update_status	Unicode string data. Ex: "Hello World"		false	false	true	false	string
mark_duplicates	Boolean data. Ex: True	false	false	false	true	false	boolean
auto_archive_enable	Boolean data. Ex: True	false	false	false	true	false	boolean
enable_auto_security	Boolean data. Ex: True	true	false	false	true	false	boolean
enable_nightly_email	Boolean data. Ex: True	true	false	false	true	false	boolean
sec_update_status	Unicode string data. Ex: "Hello World"		false	false	true	false	string
default_flow_order	Unicode string data. Ex: "Hello World"		false	false	true	false	string
name	Unicode string data. Ex: "Hello World"	n/a	false	false	false	false	string
records_to_display	Integer data. Ex: 2673	20	false	false	true	false	integer
telemetry_enabled	Boolean data. Ex: True	true	false	false	true	false	boolean
default_library_key	Unicode string data. Ex: "Hello World"		false	false	true	false	string
cluster_auto_disable	Boolean data. Ex: True	true	false	false	true	false	boolean
web_root	Unicode string data. Ex: "Hello World"		false	false	true	false	string
default_test_fragment_key	Unicode string data. Ex: "Hello World"		false	false	true	false	string
enable_auto_pkg_dl	Boolean data. Ex: True	true	false	false	true	false	boolean
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 1,
        "offset": 0,
        "limit": 1,
        "next": null
    },
    "objects": [
        {
            "enable_version_lock": false,
            "site_name": "Torrent Server",
            "enable_support_upload": false,
            "plugin_output_folder": "plugin_out",
            "auto_archive_ack": true,
            "enable_compendia_OCP": true,
            "id": 1,
            "base_recalibration_mode": "standard_recal",
            "default_storage_options": "A",
            "selected": false,
            "check_news_posts": true,
            "realign": false,
            "ts_update_status": "Ready to install",
            "mark_duplicates": false,
            "auto_archive_enable": true,
            "enable_auto_security": true,
            "enable_nightly_email": true,
            "sec_update_status": "",
            "default_flow_order": "TACG",
            "name": "Config",
            "records_to_display": 20,
            "telemetry_enabled": true,
            "default_library_key": "TCAG",
            "cluster_auto_disable": true,
            "web_root": "",
            "default_test_fragment_key": "ATCG",
            "enable_auto_pkg_dl": true,
            "resource_uri": "/rundb/api/v1/globalconfig/1/"
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Ion Chef Plan Template Resource

Resource URL `http://mytorrentserver/rundb/api/v1/ionchefplantemplate/`
Schema URL `http://mytorrentserver/rundb/api/v1/ionchefplantemplate/schema/`

Resource Fields

field	help text
planDisplayedName	Unicode string data. Ex: “Hello World”
autoAnalyze	Boolean data. Ex: True
endBarcodeKitName	Unicode string data. Ex: “Hello World”
templatingKitBarcode	Unicode string data. Ex: “Hello World”
preAnalysis	Boolean data. Ex: True
applicationGroup	A single related resource. Can be either a URI or set of nested resource data.
mixedTypeRNA_hotSpotRegionBedFile	Unicode string data. Ex: “Hello World”
mixedTypeRNA_targetRegionBedFile	Unicode string data. Ex: “Hello World”
platform	Unicode string data. Ex: “Hello World”
categories	Unicode string data. Ex: “Hello World”
planPGM	Unicode string data. Ex: “Hello World”
libkit	Unicode string data. Ex: “Hello World”
projects	Many related resources. Can be either a list of URIs or list of individually nested resourc
notes	Unicode string data. Ex: “Hello World”
sequencekitname	Unicode string data. Ex: “Hello World”
base_recalibration_mode	Unicode string data. Ex: “Hello World”
storageHost	Unicode string data. Ex: “Hello World”
expName	Unicode string data. Ex: “Hello World”
cycles	Integer data. Ex: 2673
isReverseRun	Boolean data. Ex: True
storage_options	Unicode string data. Ex: “Hello World”
chipType	Unicode string data. Ex: “Hello World”
library	Unicode string data. Ex: “Hello World”
reverselibrarykey	Unicode string data. Ex: “Hello World”
sampleTubeLabel	Unicode string data. Ex: “Hello World”
seqKitBarcode	Unicode string data. Ex: “Hello World”
barcodeId	Unicode string data. Ex: “Hello World”
isPlanGroup	Boolean data. Ex: True
realign	Boolean data. Ex: True
sampleGroupingName	Unicode string data. Ex: “Hello World”

Table 2.11 – continued from previous page

field	help text
experiment	A single related resource. Can be either a URI or set of nested resource data.
bedfile	Unicode string data. Ex: “Hello World”
applicationCategoryDisplayedName	Unicode string data. Ex: “Hello World”
isReusable	Boolean data. Ex: True
isDuplicateReads	Boolean data. Ex: True
sampleSets	Many related resources. Can be either a list of URIs or list of individually nested resourc
librarykitname	Unicode string data. Ex: “Hello World”
sseBedFile	Unicode string data. Ex: “Hello World”
adapter	Unicode string data. Ex: “Hello World”
earlyDatFileDeletion	Boolean data. Ex: True
parentPlan	Unicode string data. Ex: “Hello World”
origin	Unicode string data. Ex: “Hello World”
forward3primeadapter	Unicode string data. Ex: “Hello World”
isCustom_kitSettings	Boolean data. Ex: True
samplePrepKitName	Unicode string data. Ex: “Hello World”
applicationGroupDisplayedName	Unicode string data. Ex: “Hello World”
metaData	Unicode string data. Ex: “Hello World”
isFavorite	Boolean data. Ex: True
qcValues	Many related resources. Can be either a list of URIs or list of individually nested resourc
planStatus	Unicode string data. Ex: “Hello World”
templatingKitName	Unicode string data. Ex: “Hello World”
runType	Unicode string data. Ex: “Hello World”
username	Unicode string data. Ex: “Hello World”
planName	Unicode string data. Ex: “Hello World”
sampleDisplayedName	Unicode string data. Ex: “Hello World”
controlSequencekitname	Unicode string data. Ex: “Hello World”
tfKey	Unicode string data. Ex: “Hello World”
mixedTypeRNA_reference	Unicode string data. Ex: “Hello World”
childPlans	A list of data. Ex: [’abc’, 26.73, 8]
pairedEndLibraryAdapterName	Unicode string data. Ex: “Hello World”
runMode	Unicode string data. Ex: “Hello World”
irworkflow	Unicode string data. Ex: “Hello World”
planExecuted	Boolean data. Ex: True
project	Unicode string data. Ex: “Hello World”
usePostBeadfind	Boolean data. Ex: True
libraryReadLength	Integer data. Ex: 2673
runname	Unicode string data. Ex: “Hello World”
chefInfo	A dictionary of data. Ex: {‘price’: 26.73, ‘name’: ‘Daniel’}
planGUID	Unicode string data. Ex: “Hello World”
samplePrepProtocol	Unicode string data. Ex: “Hello World”
planShortID	Unicode string data. Ex: “Hello World”
sample	Unicode string data. Ex: “Hello World”
planExecutedDate	A date & time as a string. Ex: “2010-11-10T03:07:43”
reverse_primer	Unicode string data. Ex: “Hello World”
id	Integer data. Ex: 2673
barcodedSamples	Unicode string data. Ex: “Hello World”
regionfile	Unicode string data. Ex: “Hello World”
selectedPlugins	Unicode string data. Ex: “Hello World”
isSystemDefault	Boolean data. Ex: True

Table 2.11 – continued from previous page

field	help text
autoName	Unicode string data. Ex: “Hello World”
libraryKey	Unicode string data. Ex: “Hello World”
flows	Integer data. Ex: 2673
date	A date & time as a string. Ex: “2010-11-10T03:07:43”
isSystem	Boolean data. Ex: True
variantfrequency	Unicode string data. Ex: “Hello World”
sampleSetDisplayedName	Unicode string data. Ex: “Hello World”
flowsInOrder	Unicode string data. Ex: “Hello World”
libraryPrepType	Unicode string data. Ex: “Hello World”
sampleGrouping	A single related resource. Can be either a URI or set of nested resource data.
chipBarcode	Unicode string data. Ex: “Hello World”
usePreBeadfind	Boolean data. Ex: True
resource_uri	Unicode string data. Ex: “Hello World”
libraryPrepTypeDisplayedName	Unicode string data. Ex: “Hello World”
reverse3primeadapter	Unicode string data. Ex: “Hello World”

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 66,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/ionchefplantemplate/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "planDisplayedName": "Ion AmpliSeq HD for Tumor - DNA and Fusions -␣
↪Separate Libraries",
            "autoAnalyze": true,
            "endBarcodeKitName": "",
            "templatingKitBarcode": null,
            "preAnalysis": true,
            "thumbnailanalysisargs": "",
            "applicationGroup": "/rundb/api/v1/applicationgroup/5/",
            "mixedTypeRNA_hotSpotRegionBedFile": null,
            "mixedTypeRNA_targetRegionBedFile": null,
            "platform": "S5",
            "categories": "onco_solidTumor;onco_heme;",
            "planPGM": "",
            "prebasecallerargs": "",
            "alignmentargs": "",
            "thumbnailbasecallerargs": "",
            "libkit": null,
            "projects": [],
            "notes": "",
            "sequencekitname": "Ion S5 Sequencing Kit",
            "base_recalibration_mode": "standard_recal",
            "storageHost": null,
            "expName": "",
            "thumbnailionstatsargs": "",
            "cycles": null,
```

```
            "isReverseRun": false,
            "storage_options": "A",
            "thumbnailalignmentargs": "",
            "chipType": "540",
            "library": "hg19",
            "runMode": "single",
            "sampleTubeLabel": null,
            "seqKitBarcode": null,
            "barcodeId": "Ion AmpliSeq HD Dual Barcode Kit 1-24",
            "isPlanGroup": false,
            "realign": false,
            "sampleGroupingName": "DNA and Fusions",
            "experiment": "/rundb/api/v1/experiment/134/",
            "bedfile": "",
            "applicationCategoryDisplayedName": "Oncology - Solid Tumor | Oncology -␣
↪HemeOnc",
            "isReusable": true,
            "isDuplicateReads": false,
            "sampleSets": [],
            "thumbnailbeadfindargs": "",
            "librarykitname": "Ion AmpliSeq HD Library Kit",
            "sseBedFile": "",
            "adapter": null,
            "basecallerargs": "",
            "earlyDatFileDeletion": false,
            "parentPlan": null,
            "origin": "|5.10.0.RC4",
            "forward3primeadapter": "ATCACCGACTGCCCATAGAGAGGCTGAGAC",
            "planStatus": "planned",
            "isCustom_kitSettings": false,
            "samplePrepKitName": null,
            "applicationGroupDisplayedName": "DNA and Fusions (Separate Libraries)",
            "metaData": {},
            "isFavorite": false,
            "qcValues": [
                {
                    "threshold": 30,
                    "plannedExperiment": "/rundb/api/v1/plannedexperiment/141/",
                    "id": 400,
                    "qcType": {
                        "description": "",
                        "minThreshold": 0,
                        "maxThreshold": 100,
                        "defaultThreshold": 30,
                        "qcName": "Bead Loading (%)",
                        "id": 1,
                        "resource_uri": "/rundb/api/v1/qctype/1/"
                    },
                    "resource_uri": "/rundb/api/v1/plannedexperimentqc/400/"
                },
                {
                    "threshold": 30,
                    "plannedExperiment": "/rundb/api/v1/plannedexperiment/141/",
                    "id": 401,
                    "qcType": {
                        "description": "",
                        "minThreshold": 1,
                        "maxThreshold": 100,
```

```
                    "defaultThreshold": 30,
                    "qcName": "Key Signal (1-100)",
                    "id": 2,
                    "resource_uri": "/rundb/api/v1/qctype/2/"
                },
                "resource_uri": "/rundb/api/v1/plannedexperimentqc/401/"
            },
            {
                "threshold": 30,
                "plannedExperiment": "/rundb/api/v1/plannedexperiment/141/",
                "id": 402,
                "qcType": {
                    "description": "",
                    "minThreshold": 0,
                    "maxThreshold": 100,
                    "defaultThreshold": 30,
                    "qcName": "Usable Sequence (%)",
                    "id": 3,
                    "resource_uri": "/rundb/api/v1/qctype/3/"
                },
                "resource_uri": "/rundb/api/v1/plannedexperimentqc/402/"
            }
        ],
        "analysisargs": "",
        "thumbnailcalibrateargs": "",
        "templatingKitName": "Ion Chef S540 V1",
        "runType": "AMPS_HD_DNA_RNA",
        "username": null,
        "planShortID": "A628Z",
        "sampleDisplayedName": "",
        "prethumbnailbasecallerargs": "",
        "controlSequencekitname": null,
        "tfKey": "ATCG",
        "mixedTypeRNA_reference": null,
        "childPlans": [],
        "pairedEndLibraryAdapterName": null,
        "reverselibrarykey": "",
        "irworkflow": "",
        "planExecuted": false,
        "project": "",
        "usePostBeadfind": false,
        "libraryReadLength": 200,
        "runname": null,
        "chefInfo": {},
        "planGUID": "e52fac66-4086-433e-b8e7-ad1d1403946f",
        "ionstatsargs": "",
        "samplePrepProtocol": "",
        "sample": "",
        "planExecutedDate": null,
        "reverse_primer": null,
        "id": 141,
        "barcodedSamples": {},
        "custom_args": false,
        "regionfile": "",
        "selectedPlugins": {
            "coverageAnalysis": {
                "userInput": {},
                "version": "5.8.0.8",
```

```
                    "features": [],
                    "name": "coverageAnalysis",
                    "id": 41
                },
                "variantCaller": {
                    "userInput": {
                        "meta": {
                            "configuration": "ampliseq_hd_ffpe"
                        }
                    },
                    "version": "5.8.0.19",
                    "features": [],
                    "name": "variantCaller",
                    "id": 36
                }
            },
            "beadfindargs": "",
            "isSystemDefault": false,
            "autoName": null,
            "libraryKey": "TCAG",
            "flows": 500,
            "date": "2018-04-12T05:54:10.000222+00:00",
            "isSystem": true,
            "variantfrequency": "",
            "planName": "Ion_AmpliSeq_HD_for_Tumor_-_DNA_and_Fusions_-_Separate_
↪Libraries",
            "calibrateargs": "",
            "flowsInOrder": "",
            "libraryPrepType": "",
            "sampleGrouping": "/rundb/api/v1/samplegrouptype_cv/6/",
            "chipBarcode": "",
            "sampleSetDisplayedName": "",
            "usePreBeadfind": true,
            "resource_uri": "/rundb/api/v1/ionchefplantemplate/141/",
            "libraryPrepTypeDisplayedName": "",
            "reverse3primeadapter": ""
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST

- PUT
- DELETE
- PATCH

Ion Chef Plan Template Summary Resource

Resource URL `http://mytorrentserver/rundb/api/v1/ionchefplantemplatesummary/`
Schema URL
`http://mytorrentserver/rundb/api/v1/ionchefplantemplatesummary/schema/`

Resource Fields

field	help text	default	nullable	readonly	bla
origin	Unicode string data. Ex: “Hello World”		true	false	fals
isReverseRun	Boolean data. Ex: True	false	false	false	tru
planDisplayedName	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
storage_options	Unicode string data. Ex: “Hello World”	A	false	false	fals
preAnalysis	Boolean data. Ex: True	true	false	false	tru
planShortID	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
planStatus	Unicode string data. Ex: “Hello World”		false	false	tru
runMode	Unicode string data. Ex: “Hello World”		false	false	tru
isCustom_kitSettings	Boolean data. Ex: True	false	false	false	tru
sampleTubeLabel	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
planExecutedDate	A date & time as a string. Ex: “2010-11-10T03:07:43”	n/a	true	false	fals
samplePrepKitName	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
reverse_primer	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
seqKitBarcode	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
id	Integer data. Ex: 2673		false	false	tru
metaData	Unicode string data. Ex: “Hello World”	{}	false	false	tru
isFavorite	Boolean data. Ex: True	false	false	false	tru
samplePrepProtocol	Unicode string data. Ex: “Hello World”		true	false	fals
isPlanGroup	Boolean data. Ex: True	false	false	false	tru
templatingKitName	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
runType	Unicode string data. Ex: “Hello World”	GENS	false	false	fals
templatingKitBarcode	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
planPGM	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
isSystemDefault	Boolean data. Ex: True	false	false	false	tru
autoName	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
isReusable	Boolean data. Ex: True	false	false	false	tru
controlSequencekitname	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
date	A date & time as a string. Ex: “2010-11-10T03:07:43”	n/a	true	false	fals
isSystem	Boolean data. Ex: True	false	false	false	tru
libkit	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
categories	Unicode string data. Ex: “Hello World”		true	false	fals
planName	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
pairedEndLibraryAdapterName	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
adapter	Unicode string data. Ex: “Hello World”	n/a	true	false	fals

Table 2.12 – continued from previous page

field	help text	default	nullable	readonly	bla
irworkflow	Unicode string data. Ex: “Hello World”		false	false	tru
planExecuted	Boolean data. Ex: True	false	false	false	tru
username	Unicode string data. Ex: “Hello World”	n/a	true	false	fal
usePostBeadfind	Boolean data. Ex: True	true	false	false	tru
storageHost	Unicode string data. Ex: “Hello World”	n/a	true	false	fal
expName	Unicode string data. Ex: “Hello World”		false	false	tru
libraryReadLength	Integer data. Ex: 2673	0	false	false	fal
runname	Unicode string data. Ex: “Hello World”	n/a	true	false	fal
usePreBeadfind	Boolean data. Ex: True	true	false	false	tru
planGUID	Unicode string data. Ex: “Hello World”	n/a	true	false	fal
cycles	Integer data. Ex: 2673	n/a	true	false	fal
resource_uri	Unicode string data. Ex: “Hello World”	n/a	false	true	fal

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 66,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/ionchefplantemplatesummary/?offset=1&limit=1&
↪format=json"
    },
    "objects": [
        {
            "origin": "|5.10.0.RC4",
            "isReverseRun": false,
            "planDisplayedName": "Ion AmpliSeq HD for Tumor - DNA and Fusions -␣
↪Separate Libraries",
            "storage_options": "A",
            "preAnalysis": true,
            "planShortID": "A628Z",
            "planStatus": "planned",
            "runMode": "single",
            "isCustom_kitSettings": false,
            "sampleTubeLabel": null,
            "planExecutedDate": null,
            "samplePrepKitName": null,
            "reverse_primer": null,
            "seqKitBarcode": null,
            "id": 141,
            "metaData": {},
            "isFavorite": false,
            "samplePrepProtocol": "",
            "isPlanGroup": false,
            "templatingKitName": "Ion Chef S540 V1",
            "runType": "AMPS_HD_DNA_RNA",
            "templatingKitBarcode": null,
            "planPGM": "",
            "isSystemDefault": false,
            "autoName": null,
            "isReusable": true,
```

```
            "controlSequencekitname": null,
            "date": "2018-04-12T05:54:10.000222+00:00",
            "isSystem": true,
            "libkit": null,
            "categories": "onco_solidTumor;onco_heme;",
            "planName": "Ion_AmpliSeq_HD_for_Tumor_-_DNA_and_Fusions_-_Separate_
↪Libraries",
            "pairedEndLibraryAdapterName": null,
            "adapter": null,
            "irworkflow": "",
            "planExecuted": false,
            "username": null,
            "usePostBeadfind": false,
            "storageHost": null,
            "expName": "",
            "libraryReadLength": 200,
            "runname": null,
            "usePreBeadfind": true,
            "planGUID": "e52fac66-4086-433e-b8e7-ad1d1403946f",
            "cycles": null,
            "resource_uri": "/rundb/api/v1/ionchefplantemplatesummary/141/"
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Ion Chef Prep Kit Info Resource

Resource URL `http://mytorrentserver/rundb/api/v1/ionchefprepkitinfo/`
Schema URL `http://mytorrentserver/rundb/api/v1/ionchefprepkitinfo/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
isActive	Boolean data. Ex: True	true	false	false	true	false	boolean
samplePrep_instrumentType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
kitType	Unicode string data. Ex: "Hello World"	n/a	false	false	false	false	string
description	Unicode string data. Ex: "Hello World"		false	false	true	false	string
nucleotideType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
defaultCartridgeUsageCount	Integer data. Ex: 2673	n/a	true	false	false	false	integer
instrumentType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
chipTypes	Unicode string data. Ex: "Hello World"		false	false	true	false	string
runMode	Unicode string data. Ex: "Hello World"		false	false	true	false	string
parts	Many related resources. Can be either a list of URIs or list of individually nested resource data.	n/a	false	false	false	false	related
flowCount	Integer data. Ex: 2673	n/a	false	false	false	false	integer
applicationType	Unicode string data. Ex: "Hello World"		true	false	false	false	string
cartridgeExpirationDayLimit	Integer data. Ex: 2673	n/a	true	false	false	false	integer
libraryReadLength	Integer data. Ex: 2673	0	false	false	false	false	integer
cartridgeBetweenUsageAbsoluteMaxDayLimit	Integer data. Ex: 2673	n/a	true	false	false	false	integer
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string
uid	Unicode string data. Ex: "Hello World"	n/a	false	false	false	true	string
id	Integer data. Ex: 2673		false	false	true	true	integer
categories	Unicode string data. Ex: "Hello World"		true	false	false	false	string
name	Unicode string data. Ex: "Hello World"	n/a	false	false	false	true	string

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 14,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/ionchefprepkitinfo/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
```

```
            "isActive": true,
            "samplePrep_instrumentType": "IC",
            "kitType": "IonChefPrepKit",
            "description": "Precision ID Chef Reagents",
            "nucleotideType": "",
            "defaultCartridgeUsageCount": null,
            "instrumentType": "S5",
            "chipTypes": "510;520;530",
            "runMode": "",
            "parts": [
                {
                    "barcode": "A32882C",
                    "id": 20246,
                    "resource_uri": "/rundb/api/v1/kitpart/20246/",
                    "kit": "/rundb/api/v1/kitinfo/20106/"
                }
            ],
            "flowCount": 0,
            "applicationType": "AMPS",
            "cartridgeExpirationDayLimit": null,
            "libraryReadLength": 0,
            "cartridgeBetweenUsageAbsoluteMaxDayLimit": null,
            "resource_uri": "/rundb/api/v1/ionchefprepkitinfo/20106/",
            "uid": "ICPREP0011",
            "id": 20106,
            "categories": "filter_s5HidKit;samplePrepProtocol;s5hidSamplePrep",
            "name": "Ion Chef HID S530 V2"
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Ion Mesh Node Resource

Resource URL `http://mytorrentserver/rundb/api/v1/ionmeshnode/`
Schema URL `http://mytorrentserver/rundb/api/v1/ionmeshnode/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
apikey_local	Unicode string data. Ex: "Hello World"	n/a	true	false	false	false	string
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string
hostname	Unicode string data. Ex: "Hello World"	n/a	false	false	false	true	string
system_id	Unicode string data. Ex: "Hello World"	n/a	false	false	false	true	string
active	Boolean data. Ex: True	true	false	false	true	false	boolean
apikey_remote	Unicode string data. Ex: "Hello World"	n/a	true	false	false	false	string
id	Integer data. Ex: 2673		false	false	true	true	integer
name	Unicode string data. Ex: "Hello World"	n/a	true	false	false	true	string

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 1,
        "offset": 0,
        "limit": 1,
        "next": null
    },
    "objects": [
        {
            "apikey_local": "2ef92cb0069d1d1b156fa081ec1717807c1cd105",
            "resource_uri": "/rundb/api/v1/ionmeshnode/4/",
            "hostname": "tsvm.itw",
            "system_id": "tsvm",
            "active": true,
            "apikey_remote": "f45e8c2251095469140a12bf47349d72c68422e9",
            "id": 4,
            "name": ""
        }
    ]
}
```

Allowed list HTTP methods

- PATCH
- GET
- DELETE

Allowed detail HTTP methods

- PATCH
- GET
- DELETE

Kit Info Resource

Resource URL `http://mytorrentserver/rundb/api/v1/kitinfo/`
Schema URL `http://mytorrentserver/rundb/api/v1/kitinfo/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
isActive	Boolean data. Ex: True	true	false	false	true	false	boolean
samplePrep_instrumentType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
kitType	Unicode string data. Ex: "Hello World"	n/a	false	false	false	false	string
defaultFlowOrder	A single related resource. Can be either a URI or set of nested resource data.	n/a	true	false	false	false	related
name	Unicode string data. Ex: "Hello World"	n/a	false	false	false	true	string
nucleotideType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
defaultCartridgeUsageCount	Integer data. Ex: 2673	n/a	true	false	false	false	integer
instrumentType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
chipTypes	Unicode string data. Ex: "Hello World"		false	false	true	false	string
runMode	Unicode string data. Ex: "Hello World"		false	false	true	false	string
parts	Many related resources. Can be either a list of URIs or list of individually nested resource data.	n/a	false	false	false	false	related
flowCount	Integer data. Ex: 2673	n/a	false	false	false	false	integer
applicationType	Unicode string data. Ex: "Hello World"		true	false	false	false	string
cartridgeExpirationDayLimit	Integer data. Ex: 2673	n/a	true	false	false	false	integer
libraryReadLength	Integer data. Ex: 2673	0	false	false	false	false	integer
cartridgeBetweenUsageAbsoluteMaxDayLimit	Integer data. Ex: 2673	n/a	true	false	false	false	integer
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string
uid	Unicode string data. Ex: "Hello World"	n/a	false	false	false	true	string
id	Integer data. Ex: 2673		false	false	true	true	integer
categories	Unicode string data. Ex: "Hello World"		true	false	false	false	string
description	Unicode string data. Ex: "Hello World"		false	false	true	false	string

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 114,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/kitinfo/?offset=1&limit=1&format=json"
    },
```

```
    "objects": [
        {
            "isActive": false,
            "samplePrep_instrumentType": "",
            "kitType": "ControlSequenceKit",
            "defaultFlowOrder": null,
            "name": "Ion PGM Controls Kit v2",
            "nucleotideType": "",
            "defaultCartridgeUsageCount": null,
            "instrumentType": "pgm",
            "chipTypes": "",
            "runMode": "",
            "parts": [
                {
                    "barcode": "4482010",
                    "id": 20072,
                    "resource_uri": "/rundb/api/v1/kitpart/20072/",
                    "kit": "/rundb/api/v1/kitinfo/20037/"
                },
                {
                    "barcode": "4482011",
                    "id": 20073,
                    "resource_uri": "/rundb/api/v1/kitpart/20073/",
                    "kit": "/rundb/api/v1/kitinfo/20037/"
                }
            ],
            "flowCount": 0,
            "applicationType": "",
            "cartridgeExpirationDayLimit": null,
            "libraryReadLength": 0,
            "cartridgeBetweenUsageAbsoluteMaxDayLimit": null,
            "resource_uri": "/rundb/api/v1/kitinfo/20037/",
            "uid": "CONSEQ0003",
            "id": 20037,
            "categories": "",
            "description": "Ion PGM Controls Kit v2"
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST

- PUT
- DELETE
- PATCH

Kit Part Resource

Resource URL `http://mytorrentserver/rundb/api/v1/kitpart/`
Schema URL `http://mytorrentserver/rundb/api/v1/kitpart/schema/`

Resource Fields

field	help text	default	nullable	readonly	blank	unique	type
barcode	Unicode string data. Ex: "Hello World"	n/a	false	false	false	true	string
id	Integer data. Ex: 2673		false	false	true	true	integer
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string
kit	A single related resource. Can be either a URI or set of nested resource data.	n/a	false	false	false	false	related

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 263,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/kitpart/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "barcode": "100020580",
            "id": 20086,
            "resource_uri": "/rundb/api/v1/kitpart/20086/",
            "kit": "/rundb/api/v1/kitinfo/20042/"
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE

- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Lib Metrics Resource

Resource URL `http://mytorrentserver/rundb/api/v1/libmetrics/`
Schema URL `http://mytorrentserver/rundb/api/v1/libmetrics/schema/`

Resource Fields

field	help text	default	nullable
i350Q17_reads	Integer data. Ex: 2673	n/a	false
i150Q47_reads	Integer data. Ex: 2673	n/a	false
i300Q47_reads	Integer data. Ex: 2673	n/a	false
i600Q20_reads	Integer data. Ex: 2673	n/a	false
i300Q20_reads	Integer data. Ex: 2673	n/a	false
i250Q17_reads	Integer data. Ex: 2673	n/a	false
q10_longest_alignment	Integer data. Ex: 2673	n/a	false
i50Q10_reads	Integer data. Ex: 2673	n/a	false
aveKeyCounts	Floating point numeric data. Ex: 26.73	n/a	false
i50Q17_reads	Integer data. Ex: 2673	n/a	false
total_mapped_target_bases	Unicode string data. Ex: “Hello World”	n/a	false
i200Q7_reads	Integer data. Ex: 2673	n/a	false
i100Q47_reads	Integer data. Ex: 2673	n/a	false
i50Q20_reads	Integer data. Ex: 2673	n/a	false
i450Q7_reads	Integer data. Ex: 2673	n/a	false
genomesize	Unicode string data. Ex: “Hello World”	n/a	false
i550Q20_reads	Integer data. Ex: 2673	n/a	false
report	A single related resource. Can be either a URI or set of nested resource data.	n/a	false
i450Q47_reads	Integer data. Ex: 2673	n/a	false
dr	Floating point numeric data. Ex: 26.73	n/a	false
i150Q17_reads	Integer data. Ex: 2673	n/a	false
q7_mapped_bases	Unicode string data. Ex: “Hello World”	n/a	false
i350Q7_reads	Integer data. Ex: 2673	n/a	false
i500Q20_reads	Integer data. Ex: 2673	n/a	false
q20_mapped_bases	Unicode string data. Ex: “Hello World”	n/a	false
i250Q47_reads	Integer data. Ex: 2673	n/a	false
q47_longest_alignment	Integer data. Ex: 2673	n/a	false

Table 2.13 – continued from previous page

field	help text	default	nullable
i550Q17_reads	Integer data. Ex: 2673	n/a	false
i50Q47_reads	Integer data. Ex: 2673	n/a	false
i200Q17_reads	Integer data. Ex: 2673	n/a	false
i250Q20_reads	Integer data. Ex: 2673	n/a	false
q47_alignments	Integer data. Ex: 2673	n/a	false
align_sample	Integer data. Ex: 2673	n/a	false
i100Q10_reads	Integer data. Ex: 2673	n/a	false
i350Q20_reads	Integer data. Ex: 2673	n/a	false
i100Q7_reads	Integer data. Ex: 2673	n/a	false
i400Q17_reads	Integer data. Ex: 2673	n/a	false
i500Q47_reads	Integer data. Ex: 2673	n/a	false
i450Q20_reads	Integer data. Ex: 2673	n/a	false
q7_mean_alignment_length	Integer data. Ex: 2673	n/a	false
q7_alignments	Integer data. Ex: 2673	n/a	false
total_mapped_reads	Unicode string data. Ex: “Hello World”	n/a	false
i600Q10_reads	Integer data. Ex: 2673	n/a	false
i250Q10_reads	Integer data. Ex: 2673	n/a	false
cf	Floating point numeric data. Ex: 26.73	n/a	false
i500Q7_reads	Integer data. Ex: 2673	n/a	false
q10_mapped_bases	Unicode string data. Ex: “Hello World”	n/a	false
i550Q7_reads	Integer data. Ex: 2673	n/a	false
duplicate_reads	Integer data. Ex: 2673	n/a	true
i350Q47_reads	Integer data. Ex: 2673	n/a	false
totalNumReads	Integer data. Ex: 2673	n/a	false
resource_uri	Unicode string data. Ex: “Hello World”	n/a	false
i350Q10_reads	Integer data. Ex: 2673	n/a	false
i300Q10_reads	Integer data. Ex: 2673	n/a	false
q20_mean_alignment_length	Integer data. Ex: 2673	n/a	false
i250Q7_reads	Integer data. Ex: 2673	n/a	false
i200Q10_reads	Integer data. Ex: 2673	n/a	false
i400Q7_reads	Integer data. Ex: 2673	n/a	false
i200Q47_reads	Integer data. Ex: 2673	n/a	false
q7_longest_alignment	Integer data. Ex: 2673	n/a	false
i500Q10_reads	Integer data. Ex: 2673	n/a	false
Genome_Version	Unicode string data. Ex: “Hello World”	n/a	false
i400Q20_reads	Integer data. Ex: 2673	n/a	false
q10_alignments	Integer data. Ex: 2673	n/a	false
i450Q17_reads	Integer data. Ex: 2673	n/a	false
i100Q20_reads	Integer data. Ex: 2673	n/a	false
i550Q10_reads	Integer data. Ex: 2673	n/a	false
i450Q10_reads	Integer data. Ex: 2673	n/a	false
i400Q47_reads	Integer data. Ex: 2673	n/a	false
q17_longest_alignment	Integer data. Ex: 2673	n/a	false
i150Q7_reads	Integer data. Ex: 2673	n/a	false
i400Q10_reads	Integer data. Ex: 2673	n/a	false
q10_mean_alignment_length	Integer data. Ex: 2673	n/a	false
raw_accuracy	Floating point numeric data. Ex: 26.73	n/a	false
sysSNR	Floating point numeric data. Ex: 26.73	n/a	false
q17_mapped_bases	Unicode string data. Ex: “Hello World”	n/a	false

Table 2.13 – continued from previous page

field	help text	default	nullable
Index_Version	Unicode string data. Ex: “Hello World”	n/a	false
i300Q17_reads	Integer data. Ex: 2673	n/a	false
q17_mean_alignment_length	Integer data. Ex: 2673	n/a	false
ie	Floating point numeric data. Ex: 26.73	n/a	false
id	Integer data. Ex: 2673		false
q20_alignments	Integer data. Ex: 2673	n/a	false
q47_mapped_bases	Unicode string data. Ex: “Hello World”	n/a	false
genome	Unicode string data. Ex: “Hello World”	n/a	false
i300Q7_reads	Integer data. Ex: 2673	n/a	false
i150Q20_reads	Integer data. Ex: 2673	n/a	false
i550Q47_reads	Integer data. Ex: 2673	n/a	false
i600Q47_reads	Integer data. Ex: 2673	n/a	false
i100Q17_reads	Integer data. Ex: 2673	n/a	false
q47_mean_alignment_length	Integer data. Ex: 2673	n/a	false
i50Q7_reads	Integer data. Ex: 2673	n/a	false
i600Q7_reads	Integer data. Ex: 2673	n/a	false
i600Q17_reads	Integer data. Ex: 2673	n/a	false
q17_alignments	Integer data. Ex: 2673	n/a	false
i500Q17_reads	Integer data. Ex: 2673	n/a	false
i150Q10_reads	Integer data. Ex: 2673	n/a	false
q20_longest_alignment	Integer data. Ex: 2673	n/a	false
i200Q20_reads	Integer data. Ex: 2673	n/a	false

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 6,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/libmetrics/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "i350Q17_reads": 0,
            "i150Q47_reads": 0,
            "i300Q47_reads": 0,
            "i600Q20_reads": 0,
            "i300Q20_reads": 0,
            "i250Q17_reads": 0,
            "q10_longest_alignment": 0,
            "i50Q10_reads": 0,
            "aveKeyCounts": 88,
            "i50Q17_reads": 0,
            "total_mapped_target_bases": "0",
            "i200Q7_reads": 0,
            "i100Q47_reads": 0,
            "i50Q20_reads": 0,
            "i450Q7_reads": 0,
            "genomesize": "0",
            "i550Q20_reads": 0,
```

```
            "report": "/rundb/api/v1/results/3/",
            "i450Q47_reads": 0,
            "dr": 0.168037705589086,
            "i150Q17_reads": 0,
            "q7_mapped_bases": "0",
            "i350Q7_reads": 0,
            "i500Q20_reads": 0,
            "q20_mapped_bases": "0",
            "i250Q47_reads": 0,
            "q47_longest_alignment": 0,
            "i550Q17_reads": 0,
            "i50Q47_reads": 0,
            "i200Q17_reads": 0,
            "i250Q20_reads": 0,
            "q47_alignments": 0,
            "align_sample": -1,
            "i100Q10_reads": 0,
            "i350Q20_reads": 0,
            "i100Q7_reads": 0,
            "i400Q17_reads": 0,
            "i500Q47_reads": 0,
            "i450Q20_reads": 0,
            "q7_mean_alignment_length": 0,
            "q7_alignments": 0,
            "total_mapped_reads": "0",
            "i600Q10_reads": 0,
            "i250Q10_reads": 0,
            "cf": 0.603865925222635,
            "i500Q7_reads": 0,
            "q10_mapped_bases": "0",
            "i550Q7_reads": 0,
            "duplicate_reads": null,
            "i350Q47_reads": 0,
            "totalNumReads": 93969124,
            "resource_uri": "/rundb/api/v1/libmetrics/1/",
            "i350Q10_reads": 0,
            "i300Q10_reads": 0,
            "q20_mean_alignment_length": 0,
            "i250Q7_reads": 0,
            "i200Q10_reads": 0,
            "i400Q7_reads": 0,
            "i200Q47_reads": 0,
            "q7_longest_alignment": 0,
            "i500Q10_reads": 0,
            "Genome_Version": "None",
            "i400Q20_reads": 0,
            "q10_alignments": 0,
            "i450Q17_reads": 0,
            "i100Q20_reads": 0,
            "i550Q10_reads": 0,
            "i450Q10_reads": 0,
            "i400Q47_reads": 0,
            "q17_longest_alignment": 0,
            "i150Q7_reads": 0,
            "i400Q10_reads": 0,
            "q10_mean_alignment_length": 0,
            "raw_accuracy": 0,
            "sysSNR": 0.103568483421323,
```

```
            "q17_mapped_bases": "0",
            "Index_Version": "None",
            "i300Q17_reads": 0,
            "q17_mean_alignment_length": 0,
            "ie": 0.465626595541835,
            "id": 1,
            "q20_alignments": 0,
            "q47_mapped_bases": "0",
            "genome": "None",
            "i300Q7_reads": 0,
            "i150Q20_reads": 0,
            "i550Q47_reads": 0,
            "i600Q47_reads": 0,
            "i100Q17_reads": 0,
            "q47_mean_alignment_length": 0,
            "i50Q7_reads": 0,
            "i600Q7_reads": 0,
            "i600Q17_reads": 0,
            "q17_alignments": 0,
            "i500Q17_reads": 0,
            "i150Q10_reads": 0,
            "q20_longest_alignment": 0,
            "i200Q20_reads": 0
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Library Key Resource

Resource URL `http://mytorrentserver/rundb/api/v1/librarykey/`
Schema URL `http://mytorrentserver/rundb/api/v1/librarykey/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
direction	Unicode string data. Ex: "Hello World"	Forward	false	false	false	false	string
name	Unicode string data. Ex: "Hello World"	n/a	false	false	false	true	string
sequence	Unicode string data. Ex: "Hello World"	n/a	false	false	false	false	string
description	Unicode string data. Ex: "Hello World"		false	false	true	false	string
runMode	Unicode string data. Ex: "Hello World"	single	false	false	true	false	string
id	Integer data. Ex: 2673		false	false	true	true	integer
isDefault	Boolean data. Ex: True	false	false	false	true	false	boolean
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 3,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/librarykey/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "direction": "Forward",
            "name": "Ion TCAG",
            "sequence": "TCAG",
            "description": "Default forward library key",
            "runMode": "single",
            "id": 1,
            "isDefault": true,
            "resource_uri": "/rundb/api/v1/librarykey/1/"
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Library Kit Info Resource

Resource URL `http://mytorrentserver/rundb/api/v1/librarykitinfo/`
Schema URL `http://mytorrentserver/rundb/api/v1/librarykitinfo/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
isActive	Boolean data. Ex: True	true	false	false	true	false	boolean
samplePrep_instrumentType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
kitType	Unicode string data. Ex: "Hello World"	n/a	false	false	false	false	string
description	Unicode string data. Ex: "Hello World"		false	false	true	false	string
nucleotideType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
defaultCartridgeUsageCount	Integer data. Ex: 2673	n/a	true	false	false	false	integer
instrumentType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
chipTypes	Unicode string data. Ex: "Hello World"		false	false	true	false	string
runMode	Unicode string data. Ex: "Hello World"		false	false	true	false	string
parts	Many related resources. Can be either a list of URIs or list of individually nested resource data.	n/a	false	false	false	false	related
flowCount	Integer data. Ex: 2673	n/a	false	false	false	false	integer
applicationType	Unicode string data. Ex: "Hello World"		true	false	false	false	string
cartridgeExpirationDayLimit	Integer data. Ex: 2673	n/a	true	false	false	false	integer
libraryReadLength	Integer data. Ex: 2673	0	false	false	false	false	integer
cartridgeBetweenUsageAbsoluteMaxDayLimit	Integer data. Ex: 2673	n/a	true	false	false	false	integer
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string
uid	Unicode string data. Ex: "Hello World"	n/a	false	false	false	true	string
id	Integer data. Ex: 2673		false	false	true	true	integer
categories	Unicode string data. Ex: "Hello World"		true	false	false	false	string
name	Unicode string data. Ex: "Hello World"	n/a	false	false	false	true	string

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 27,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/librarykitinfo/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
```

```
            "isActive": true,
            "samplePrep_instrumentType": "",
            "kitType": "LibraryKit",
            "description": "MuSeek Library Preparation Kit",
            "nucleotideType": "dna",
            "defaultCartridgeUsageCount": null,
            "instrumentType": "",
            "chipTypes": "",
            "runMode": "",
            "parts": [],
            "flowCount": 0,
            "applicationType": "GENS",
            "cartridgeExpirationDayLimit": null,
            "libraryReadLength": 0,
            "cartridgeBetweenUsageAbsoluteMaxDayLimit": null,
            "resource_uri": "/rundb/api/v1/librarykitinfo/20025/",
            "uid": "LIB0012",
            "id": 20025,
            "categories": "filter_muSeek",
            "name": "MuSeek(tm) Library Preparation Kit"
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Library Kit Part Resource

Resource URL `http://mytorrentserver/rundb/api/v1/librarykitpart/`
Schema URL `http://mytorrentserver/rundb/api/v1/librarykitpart/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
barcode	Unicode string data. Ex: “Hello World”	n/a	false	false	false	true	string
id	Integer data. Ex: 2673		false	false	true	true	integer
resource_uri	Unicode string data. Ex: “Hello World”	n/a	false	true	false	false	string
kit	A single related resource. Can be either a URI or set of nested resource data.	n/a	false	false	false	false	related

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 35,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/librarykitpart/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "barcode": "A31204",
            "id": 20243,
            "resource_uri": "/rundb/api/v1/librarykitpart/20243/",
            "kit": "/rundb/api/v1/kitinfo/20103/"
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Location Resource

Resource URL `http://mytorrentserver/rundb/api/v1/location/`
Schema URL `http://mytorrentserver/rundb/api/v1/location/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
name	Unicode string data. Ex: "Hello World"	n/a	false	false	false	false	string
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string
defaultlocation	Only one location can be the default	false	false	false	true	false	boolean
comments	Unicode string data. Ex: "Hello World"		false	false	true	false	string
id	Integer data. Ex: 2673		false	false	true	true	integer

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 2,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/location/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "name": "Disabled",
            "resource_uri": "/rundb/api/v1/location/2/",
            "defaultlocation": false,
            "comments": "A location which will not be assigned to any File Servers so␣
↪that Rigs assigned to this location will not be treated as valid Rigs when␣
↪ionCrawler attempts to find new raw data directories. This is so that we do not␣
↪have to delete a Rig from the Rigs table but still want to prevent new Experiments␣
↪from appearing associated with the Rig.",
            "id": 2
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT

- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Log Resource

Resource URL `http://mytorrentserver/rundb/api/v1/log/`
Schema URL `http://mytorrentserver/rundb/api/v1/log/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
text	Unicode string data. Ex: "Hello World"		false	false	true	false	string
timeStamp	A date & time as a string. Ex: "2010-11-10T03:07:43"	true	false	false	true	false	datetime
upload	A single related resource. Can be either a URI or set of nested resource data.	n/a	false	false	false	false	related
id	Integer data. Ex: 2673		false	false	true	true	integer
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string

Example Response

```
{
    "meta": {
        "previous": null,
        "total_count": 0,
        "offset": 0,
        "limit": 1,
        "next": null
    },
    "objects": []
}
```

Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Message Resource

Resource URL `http://mytorrentserver/rundb/api/v1/message/`
Schema URL `http://mytorrentserver/rundb/api/v1/message/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
body	Unicode string data. Ex: "Hello World"		false	false	true	false	string
status	Unicode string data. Ex: "Hello World"	unread	false	false	true	false	string
level	Integer data. Ex: 2673	20	false	false	false	false	integer
route	Unicode string data. Ex: "Hello World"		false	false	true	false	string
expires	Unicode string data. Ex: "Hello World"	read	false	false	true	false	string
time	A date & time as a string. Ex: "2010-11-10T03:07:43"	true	false	false	true	false	datetime
id	Integer data. Ex: 2673		false	false	true	true	integer
tags	Unicode string data. Ex: "Hello World"		false	false	true	false	string
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string

Example Response

```
{
    "meta": {
        "previous": null,
        "total_count": 1,
        "offset": 0,
        "limit": 1,
        "next": null
    },
    "objects": [
        {
            "body": "There is an update available for your Torrent Server. <a class=\
↪"btn btn-success\" href=\"/admin/update\">Update Now</a>",
            "status": "unread",
            "level": 20,
            "route": "_StaffOnly",
            "expires": "read",
            "time": "2018-06-15T18:51:37.000649+00:00",
            "id": 40,
            "tags": "new-upgrade",
            "resource_uri": "/rundb/api/v1/message/40/"
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Monitor Data Resource

Resource URL `http://mytorrentserver/rundb/api/v1/monitordata/`
Schema URL `http://mytorrentserver/rundb/api/v1/monitordata/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string
treeDat	Unicode string data. Ex: "Hello World"	{}	false	false	true	false	string
id	Integer data. Ex: 2673		false	false	true	true	integer
name	Unicode string data. Ex: "Hello World"		false	false	false	false	string

Example Response

```
{
    "meta": {
        "previous": null,
        "total_count": 0,
        "offset": 0,
        "limit": 1,
        "next": null
    },
    "objects": []
}
```

Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Monitor Result Resource

Resource URL `http://mytorrentserver/rundb/api/v1/monitorresult/`
Schema URL `http://mytorrentserver/rundb/api/v1/monitorresult/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
status	Unicode string data. Ex: “Hello World”	n/a	false	false	false	false	string
processedflows	Integer data. Ex: 2673	n/a	false	false	false	false	integer
libmetrics	A single related resource. Can be either a URI or set of nested resource data.	n/a	true	false	false	false	related
timeStamp	A date & time as a string. Ex: “2010-11-10T03:07:43”	true	false	false	true	false	datetime
analysismetrics	A single related resource. Can be either a URI or set of nested resource data.	n/a	true	false	false	false	related
reportLink	Unicode string data. Ex: “Hello World”	n/a	false	false	false	false	string
library	Unicode string data. Ex: “Hello World”	n/a	true	true	false	false	string
id	Integer data. Ex: 2673		false	false	true	true	integer
reportStatus	Unicode string data. Ex: “Hello World”	Nothing	true	false	false	false	string
experiment	A single related resource. Can be either a URI or set of nested resource data.	n/a	false	false	false	false	related
resultsName	Unicode string data. Ex: “Hello World”	n/a	false	false	false	false	string
projects	Many related resources. Can be either a list of URIs or list of individually nested resource data.	n/a	false	false	false	false	related
qualitymetrics	A single related resource. Can be either a URI or set of nested resource data.	n/a	true	false	false	false	related
eas	A single related resource. Can be either a URI or set of nested resource data.	n/a	false	false	false	false	related
resource_uri	Unicode string data. Ex: “Hello World”	n/a	false	true	false	false	string
barcodeId	Unicode string data. Ex: “Hello World”	n/a	true	true	false	false	string
autoExempt	Boolean data. Ex: True	false	false	false	true	false	boolean
representative	Boolean data. Ex: True	false	false	false	true	false	boolean

Example Response

```
{
    "meta": {
        "previous": null,
        "total_count": 0,
        "offset": 0,
        "limit": 1,
        "next": null
```

```
    },
    "objects": []
}
```

Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Network Resource

Resource URL `http://mytorrentserver/rundb/api/v1/network/`
Schema URL `http://mytorrentserver/rundb/api/v1/network/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
eth_device	Unicode string data. Ex: "Hello World"	n/a	true	true	true	false	boolean
external_ip	Unicode string data. Ex: "Hello World"	n/a	true	true	true	false	string
internal_ip	Unicode string data. Ex: "Hello World"	n/a	true	true	true	false	string
route	Unicode string data. Ex: "Hello World"	n/a	true	true	true	false	boolean

Example Response

```
{
    "eth_device": true,
    "external_ip": "12.27.71.34",
    "internal_ip": "10.45.2.119",
    "route": true
}
```


Allowed list HTTP methods

- GET

Allowed detail HTTP methods

None

Onetouch Plan Template Resource

Resource URL `http://mytorrentserver/rundb/api/v1/onetouchplantemplate/`
Schema URL `http://mytorrentserver/rundb/api/v1/onetouchplantemplate/schema/`

Resource Fields

field	help text
planDisplayedName	Unicode string data. Ex: “Hello World”
autoAnalyze	Boolean data. Ex: True
endBarcodeKitName	Unicode string data. Ex: “Hello World”
templatingKitBarcode	Unicode string data. Ex: “Hello World”
preAnalysis	Boolean data. Ex: True
applicationGroup	A single related resource. Can be either a URI or set of nested resource data.
mixedTypeRNA_hotSpotRegionBedFile	Unicode string data. Ex: “Hello World”
mixedTypeRNA_targetRegionBedFile	Unicode string data. Ex: “Hello World”
platform	Unicode string data. Ex: “Hello World”
categories	Unicode string data. Ex: “Hello World”
planPGM	Unicode string data. Ex: “Hello World”
libkit	Unicode string data. Ex: “Hello World”
projects	Many related resources. Can be either a list of URIs or list of individually nested resourc
notes	Unicode string data. Ex: “Hello World”
sequencekitname	Unicode string data. Ex: “Hello World”
base_recalibration_mode	Unicode string data. Ex: “Hello World”
storageHost	Unicode string data. Ex: “Hello World”
expName	Unicode string data. Ex: “Hello World”
cycles	Integer data. Ex: 2673
isReverseRun	Boolean data. Ex: True
storage_options	Unicode string data. Ex: “Hello World”
chipType	Unicode string data. Ex: “Hello World”
library	Unicode string data. Ex: “Hello World”

Table 2.14 – continued from previous page

field	help text
reverselibrarykey	Unicode string data. Ex: “Hello World”
sampleTubeLabel	Unicode string data. Ex: “Hello World”
seqKitBarcode	Unicode string data. Ex: “Hello World”
barcodeId	Unicode string data. Ex: “Hello World”
isPlanGroup	Boolean data. Ex: True
realign	Boolean data. Ex: True
sampleGroupingName	Unicode string data. Ex: “Hello World”
experiment	A single related resource. Can be either a URI or set of nested resource data.
bedfile	Unicode string data. Ex: “Hello World”
applicationCategoryDisplayedName	Unicode string data. Ex: “Hello World”
isReusable	Boolean data. Ex: True
isDuplicateReads	Boolean data. Ex: True
sampleSets	Many related resources. Can be either a list of URIs or list of individually nested resourc
librarykitname	Unicode string data. Ex: “Hello World”
sseBedFile	Unicode string data. Ex: “Hello World”
adapter	Unicode string data. Ex: “Hello World”
earlyDatFileDeletion	Boolean data. Ex: True
parentPlan	Unicode string data. Ex: “Hello World”
origin	Unicode string data. Ex: “Hello World”
forward3primeadapter	Unicode string data. Ex: “Hello World”
isCustom_kitSettings	Boolean data. Ex: True
samplePrepKitName	Unicode string data. Ex: “Hello World”
applicationGroupDisplayedName	Unicode string data. Ex: “Hello World”
metaData	Unicode string data. Ex: “Hello World”
isFavorite	Boolean data. Ex: True
qcValues	Many related resources. Can be either a list of URIs or list of individually nested resourc
planStatus	Unicode string data. Ex: “Hello World”
templatingKitName	Unicode string data. Ex: “Hello World”
runType	Unicode string data. Ex: “Hello World”
username	Unicode string data. Ex: “Hello World”
planName	Unicode string data. Ex: “Hello World”
sampleDisplayedName	Unicode string data. Ex: “Hello World”
controlSequencekitname	Unicode string data. Ex: “Hello World”
tfKey	Unicode string data. Ex: “Hello World”
mixedTypeRNA_reference	Unicode string data. Ex: “Hello World”
childPlans	A list of data. Ex: [’abc’, 26.73, 8]
pairedEndLibraryAdapterName	Unicode string data. Ex: “Hello World”
runMode	Unicode string data. Ex: “Hello World”
irworkflow	Unicode string data. Ex: “Hello World”
planExecuted	Boolean data. Ex: True
project	Unicode string data. Ex: “Hello World”
usePostBeadfind	Boolean data. Ex: True
libraryReadLength	Integer data. Ex: 2673
runname	Unicode string data. Ex: “Hello World”
chefInfo	A dictionary of data. Ex: {‘price’: 26.73, ‘name’: ‘Daniel’}
planGUID	Unicode string data. Ex: “Hello World”
samplePrepProtocol	Unicode string data. Ex: “Hello World”
planShortID	Unicode string data. Ex: “Hello World”
sample	Unicode string data. Ex: “Hello World”

Table 2.14 – continued from previous page

field	help text
planExecutedDate	A date & time as a string. Ex: “2010-11-10T03:07:43”
reverse_primer	Unicode string data. Ex: “Hello World”
id	Integer data. Ex: 2673
barcodedSamples	Unicode string data. Ex: “Hello World”
regionfile	Unicode string data. Ex: “Hello World”
selectedPlugins	Unicode string data. Ex: “Hello World”
isSystemDefault	Boolean data. Ex: True
autoName	Unicode string data. Ex: “Hello World”
libraryKey	Unicode string data. Ex: “Hello World”
flows	Integer data. Ex: 2673
date	A date & time as a string. Ex: “2010-11-10T03:07:43”
isSystem	Boolean data. Ex: True
variantfrequency	Unicode string data. Ex: “Hello World”
sampleSetDisplayedName	Unicode string data. Ex: “Hello World”
flowsInOrder	Unicode string data. Ex: “Hello World”
libraryPrepType	Unicode string data. Ex: “Hello World”
sampleGrouping	A single related resource. Can be either a URI or set of nested resource data.
chipBarcode	Unicode string data. Ex: “Hello World”
usePreBeadfind	Boolean data. Ex: True
resource_uri	Unicode string data. Ex: “Hello World”
libraryPrepTypeDisplayedName	Unicode string data. Ex: “Hello World”
reverse3primeadapter	Unicode string data. Ex: “Hello World”

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 37,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/onetouchplantemplate/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "planDisplayedName": "PGx Research Panel",
            "autoAnalyze": true,
            "endBarcodeKitName": "",
            "templatingKitBarcode": null,
            "preAnalysis": true,
            "thumbnailanalysisargs": "",
            "applicationGroup": "/rundb/api/v1/applicationgroup/6/",
            "mixedTypeRNA_hotSpotRegionBedFile": null,
            "mixedTypeRNA_targetRegionBedFile": null,
            "platform": "PGM",
            "categories": "",
            "planPGM": null,
            "prebasecallerargs": "",
            "alignmentargs": "",
            "thumbnailbasecallerargs": "",
            "libkit": null,
            "projects": [],
```

```
            "notes": "",
            "sequencekitname": "IonPGMHiQ",
            "base_recalibration_mode": "standard_recal",
            "storageHost": null,
            "expName": "",
            "thumbnailionstatsargs": "",
            "cycles": null,
            "isReverseRun": false,
            "storage_options": "A",
            "thumbnailalignmentargs": "",
            "chipType": "",
            "library": "hg19",
            "runMode": "",
            "sampleTubeLabel": null,
            "seqKitBarcode": null,
            "barcodeId": "IonXpress",
            "isPlanGroup": false,
            "realign": false,
            "sampleGroupingName": "",
            "experiment": "/rundb/api/v1/experiment/122/",
            "bedfile": "/results/uploads/BED/5/hg19/unmerged/detail/PGx.20150728.
↪designed.bed",
            "applicationCategoryDisplayedName": "",
            "isReusable": true,
            "isDuplicateReads": false,
            "sampleSets": [],
            "thumbnailbeadfindargs": "",
            "librarykitname": "Ion AmpliSeq 2.0 Library Kit",
            "sseBedFile": "",
            "adapter": null,
            "basecallerargs": "",
            "earlyDatFileDeletion": false,
            "parentPlan": null,
            "origin": "ampliseq.com|5.8.0",
            "forward3primeadapter": "ATCACCGACTGCCCATAGAGAGGCTGAGAC",
            "planStatus": "planned",
            "isCustom_kitSettings": false,
            "samplePrepKitName": null,
            "applicationGroupDisplayedName": "Pharmacogenomics",
            "metaData": {},
            "isFavorite": false,
            "qcValues": [],
            "analysisargs": "",
            "thumbnailcalibrateargs": "",
            "templatingKitName": "Ion PGM Hi-Q OT2 Kit - 200",
            "runType": "AMPS",
            "username": "ionuser",
            "planShortID": "OO9C5",
            "sampleDisplayedName": "",
            "prethumbnailbasecallerargs": "",
            "controlSequencekitname": "",
            "tfKey": "ATCG",
            "mixedTypeRNA_reference": null,
            "childPlans": [],
            "pairedEndLibraryAdapterName": "",
            "reverselibrarykey": "",
            "irworkflow": "",
            "planExecuted": false,
```

```
            "project": "",
            "usePostBeadfind": true,
            "libraryReadLength": 0,
            "runname": null,
            "chefInfo": {},
            "planGUID": "7489c32d-d3ed-4cc1-a7a2-e59b819ea395",
            "ionstatsargs": "",
            "samplePrepProtocol": "",
            "sample": "",
            "planExecutedDate": null,
            "reverse_primer": null,
            "id": 130,
            "barcodedSamples": {},
            "custom_args": false,
            "regionfile": "/results/uploads/BED/15/hg19/unmerged/detail/PGx.20180131.
↪hotspots.bed",
            "selectedPlugins": {
                "variantCaller": {
                    "features": [],
                    "ampliSeqVariantCallerConfig": {
                        "torrent_variant_caller": {
                            "snp_min_allele_freq": "0.1",
                            "snp_strand_bias": "0.95",
                            "hotspot_min_coverage": 6,
                            "hotspot_min_cov_each_strand": 3,
                            "position_bias": "0.75",
                            "hotspot_min_allele_freq": "0.1",
                            "snp_min_variant_score": 10,
                            "mnp_min_variant_score": 10,
                            "hotspot_strand_bias": "0.98",
                            "hp_max_length": 10,
                            "filter_insertion_predictions": "0.4",
                            "indel_min_variant_score": 10,
                            "indel_min_coverage": 15,
                            "heavy_tailed": 3,
                            "outlier_probability": "0.01",
                            "position_bias_ref_fraction": "0.05",
                            "indel_strand_bias_pval": 1,
                            "data_quality_stringency": "6.5",
                            "snp_min_cov_each_strand": 0,
                            "indel_as_hpindel": 0,
                            "snp_strand_bias_pval": 1,
                            "mnp_strand_bias": "0.95",
                            "mnp_strand_bias_pval": 1,
                            "process_input_positions_only": 1,
                            "hotspot_strand_bias_pval": "0.01",
                            "hotspot_min_variant_score": 4,
                            "do_mnp_realignment": 1,
                            "indel_strand_bias": "0.85",
                            "downsample_to_coverage": 4000,
                            "filter_unusual_predictions": "0.7",
                            "indel_min_allele_freq": "0.1",
                            "mnp_min_allele_freq": "0.1",
                            "mnp_min_coverage": 6,
                            "do_snp_realignment": 1,
                            "mnp_min_cov_each_strand": 0,
                            "snp_min_coverage": 6,
                            "prediction_precision": 1,
```

```
                "indel_min_cov_each_strand": 5,
                "filter_deletion_predictions": "0.2",
                "realignment_threshold": 1,
                "suppress_recalibration": 0,
                "position_bias_pval": "0.05",
                "use_position_bias": 0
            },
            "meta": {
                "repository_id": "",
                "ts_version": "5.0",
                "name": "PGx - Germ Line - Customized parameters",
                "user_selections": {
                    "chip": "pgm",
                    "frequency": "germline",
                    "library": "ampliseq",
                    "panel": "/rundb/api/v1/contentupload/15/"
                },
                "tooltip": "Panel-optimized parameters from AmpliSeq.com",
                "tvcargs": "tvc --use-input-allele-only",
                "built_in": true,
                "configuration": "PGx_germline_low_stringency",
                "compatibility": {
                    "panel": "/rundb/api/v1/contentupload/15/"
                }
            },
            "long_indel_assembler": {
                "min_indel_size": 4,
                "short_suffix_match": 5,
                "output_mnv": 0,
                "min_var_count": 5,
                "min_var_freq": "0.15",
                "kmer_len": 19,
                "max_hp_length": 8,
                "relative_strand_bias": "0.8"
            },
            "freebayes": {
                "gen_min_coverage": 10,
                "allow_mnps": 1,
                "allow_complex": 0,
                "read_snp_limit": 10,
                "read_max_mismatch_fraction": 1,
                "allow_indels": 1,
                "min_mapping_qv": 4,
                "gen_min_alt_allele_freq": "0.15",
                "allow_snps": 1,
                "gen_min_indel_alt_allele_freq": "0.15"
            }
        },
        "userInput": {
            "torrent_variant_caller": {
                "snp_min_allele_freq": "0.1",
                "snp_strand_bias": "0.95",
                "hotspot_min_coverage": 6,
                "hotspot_min_cov_each_strand": 3,
                "position_bias": "0.75",
                "hotspot_min_allele_freq": "0.1",
                "snp_min_variant_score": 10,
                "mnp_min_variant_score": 10,
```

```
            "hotspot_strand_bias": "0.98",
            "hp_max_length": 10,
            "filter_insertion_predictions": "0.4",
            "indel_min_variant_score": 10,
            "indel_min_coverage": 15,
            "heavy_tailed": 3,
            "outlier_probability": "0.01",
            "position_bias_ref_fraction": "0.05",
            "indel_strand_bias_pval": 1,
            "data_quality_stringency": "6.5",
            "snp_min_cov_each_strand": 0,
            "indel_as_hpindel": 0,
            "snp_strand_bias_pval": 1,
            "mnp_strand_bias": "0.95",
            "mnp_strand_bias_pval": 1,
            "process_input_positions_only": 1,
            "hotspot_strand_bias_pval": "0.01",
            "hotspot_min_variant_score": 4,
            "do_mnp_realignment": 1,
            "indel_strand_bias": "0.85",
            "downsample_to_coverage": 4000,
            "filter_unusual_predictions": "0.7",
            "indel_min_allele_freq": "0.1",
            "mnp_min_allele_freq": "0.1",
            "mnp_min_coverage": 6,
            "do_snp_realignment": 1,
            "mnp_min_cov_each_strand": 0,
            "snp_min_coverage": 6,
            "prediction_precision": 1,
            "indel_min_cov_each_strand": 5,
            "filter_deletion_predictions": "0.2",
            "realignment_threshold": 1,
            "suppress_recalibration": 0,
            "position_bias_pval": "0.05",
            "use_position_bias": 0
        },
        "meta": {
            "repository_id": "",
            "ts_version": "5.0",
            "name": "PGx - Germ Line - Customized parameters",
            "user_selections": {
                "chip": "pgm",
                "frequency": "germline",
                "library": "ampliseq",
                "panel": "/rundb/api/v1/contentupload/15/"
            },
            "tooltip": "Panel-optimized parameters from AmpliSeq.com",
            "tvcargs": "tvc --use-input-allele-only",
            "built_in": true,
            "configuration": "PGx_germline_low_stringency",
            "compatibility": {
                "panel": "/rundb/api/v1/contentupload/15/"
            }
        },
        "long_indel_assembler": {
            "min_indel_size": 4,
            "short_suffix_match": 5,
            "output_mnv": 0,
```

```
                            "min_var_count": 5,
                            "min_var_freq": "0.15",
                            "kmer_len": 19,
                            "max_hp_length": 8,
                            "relative_strand_bias": "0.8"
                        },
                        "freebayes": {
                            "gen_min_coverage": 10,
                            "allow_mnps": 1,
                            "allow_complex": 0,
                            "read_snp_limit": 10,
                            "read_max_mismatch_fraction": 1,
                            "allow_indels": 1,
                            "min_mapping_qv": 4,
                            "gen_min_alt_allele_freq": "0.15",
                            "allow_snps": 1,
                            "gen_min_indel_alt_allele_freq": "0.15"
                        }
                    },
                    "version": "5.8.0.19",
                    "id": 36,
                    "name": "variantCaller"
                }
            },
            "beadfindargs": "",
            "isSystemDefault": false,
            "autoName": null,
            "libraryKey": "TCAG",
            "flows": 500,
            "date": "2018-02-08T19:41:44.000698+00:00",
            "isSystem": false,
            "variantfrequency": "",
            "planName": "PGx_Research_Panel",
            "calibrateargs": "",
            "flowsInOrder": "",
            "libraryPrepType": "",
            "sampleGrouping": null,
            "chipBarcode": "",
            "sampleSetDisplayedName": "",
            "usePreBeadfind": true,
            "resource_uri": "/rundb/api/v1/onetouchplantemplate/130/",
            "libraryPrepTypeDisplayedName": "",
            "reverse3primeadapter": ""
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Onetouch Plan Template Summary Resource

Resource URL `http://mytorrentserver/rundb/api/v1/onetouchplantemplatesummary/`
Schema URL
`http://mytorrentserver/rundb/api/v1/onetouchplantemplatesummary/schema/`

Resource Fields

field	help text	default	nullable	readonly	bla
origin	Unicode string data. Ex: “Hello World”		true	false	fals
isReverseRun	Boolean data. Ex: True	false	false	false	tru
planDisplayedName	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
storage_options	Unicode string data. Ex: “Hello World”	A	false	false	fals
preAnalysis	Boolean data. Ex: True	true	false	false	tru
planShortID	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
planStatus	Unicode string data. Ex: “Hello World”		false	false	tru
runMode	Unicode string data. Ex: “Hello World”		false	false	tru
isCustom_kitSettings	Boolean data. Ex: True	false	false	false	tru
sampleTubeLabel	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
planExecutedDate	A date & time as a string. Ex: “2010-11-10T03:07:43”	n/a	true	false	fals
samplePrepKitName	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
reverse_primer	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
seqKitBarcode	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
id	Integer data. Ex: 2673		false	false	tru
metaData	Unicode string data. Ex: “Hello World”	{}	false	false	tru
isFavorite	Boolean data. Ex: True	false	false	false	tru
samplePrepProtocol	Unicode string data. Ex: “Hello World”		true	false	fals
isPlanGroup	Boolean data. Ex: True	false	false	false	tru
templatingKitName	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
runType	Unicode string data. Ex: “Hello World”	GENS	false	false	fals
templatingKitBarcode	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
planPGM	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
isSystemDefault	Boolean data. Ex: True	false	false	false	tru
autoName	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
isReusable	Boolean data. Ex: True	false	false	false	tru
controlSequencekitname	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
date	A date & time as a string. Ex: “2010-11-10T03:07:43”	n/a	true	false	fals
isSystem	Boolean data. Ex: True	false	false	false	tru

Table 2.15 – continued from previous page

field	help text	default	nullable	readonly	bla
libkit	Unicode string data. Ex: "Hello World"	n/a	true	false	fal
categories	Unicode string data. Ex: "Hello World"		true	false	fal
planName	Unicode string data. Ex: "Hello World"	n/a	true	false	fal
pairedEndLibraryAdapterName	Unicode string data. Ex: "Hello World"	n/a	true	false	fal
adapter	Unicode string data. Ex: "Hello World"	n/a	true	false	fal
irworkflow	Unicode string data. Ex: "Hello World"		false	false	tru
planExecuted	Boolean data. Ex: True	false	false	false	tru
username	Unicode string data. Ex: "Hello World"	n/a	true	false	fal
usePostBeadfind	Boolean data. Ex: True	true	false	false	tru
storageHost	Unicode string data. Ex: "Hello World"	n/a	true	false	fal
expName	Unicode string data. Ex: "Hello World"		false	false	tru
libraryReadLength	Integer data. Ex: 2673	0	false	false	fal
runname	Unicode string data. Ex: "Hello World"	n/a	true	false	fal
usePreBeadfind	Boolean data. Ex: True	true	false	false	tru
planGUID	Unicode string data. Ex: "Hello World"	n/a	true	false	fal
cycles	Integer data. Ex: 2673	n/a	true	false	fal
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	fal

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 37,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/onetouchplantemplatesummary/?offset=1&limit=1&
↪format=json"
    },
    "objects": [
        {
            "origin": "ampliseq.com|5.8.0",
            "isReverseRun": false,
            "planDisplayedName": "PGx Research Panel",
            "storage_options": "A",
            "preAnalysis": true,
            "planShortID": "OO9C5",
            "planStatus": "planned",
            "runMode": "",
            "isCustom_kitSettings": false,
            "sampleTubeLabel": null,
            "planExecutedDate": null,
            "samplePrepKitName": null,
            "reverse_primer": null,
            "seqKitBarcode": null,
            "id": 130,
            "metaData": {},
            "isFavorite": false,
            "samplePrepProtocol": "",
            "isPlanGroup": false,
            "templatingKitName": "Ion PGM Hi-Q OT2 Kit - 200",
            "runType": "AMPS",
            "templatingKitBarcode": null,
```

```
            "planPGM": null,
            "isSystemDefault": false,
            "autoName": null,
            "isReusable": true,
            "controlSequencekitname": "",
            "date": "2018-02-08T19:41:44.000698+00:00",
            "isSystem": false,
            "libkit": null,
            "categories": "",
            "planName": "PGx_Research_Panel",
            "pairedEndLibraryAdapterName": "",
            "adapter": null,
            "irworkflow": "",
            "planExecuted": false,
            "username": "ionuser",
            "usePostBeadfind": true,
            "storageHost": null,
            "expName": "",
            "libraryReadLength": 0,
            "runname": null,
            "usePreBeadfind": true,
            "planGUID": "7489c32d-d3ed-4cc1-a7a2-e59b819ea395",
            "cycles": null,
            "resource_uri": "/rundb/api/v1/onetouchplantemplatesummary/130/"
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Planned Experiment Resource

Resource URL `http://mytorrentserver/rundb/api/v1/plannedexperiment/`
Schema URL `http://mytorrentserver/rundb/api/v1/plannedexperiment/schema/`

Resource Fields

field	help text
planDisplayedName	Unicode string data. Ex: “Hello World”
autoAnalyze	Boolean data. Ex: True
endBarcodeKitName	Unicode string data. Ex: “Hello World”
templatingKitBarcode	Unicode string data. Ex: “Hello World”
preAnalysis	Boolean data. Ex: True
applicationGroup	A single related resource. Can be either a URI or set of nested resource data.
mixedTypeRNA_hotSpotRegionBedFile	Unicode string data. Ex: “Hello World”
mixedTypeRNA_targetRegionBedFile	Unicode string data. Ex: “Hello World”
platform	Unicode string data. Ex: “Hello World”
categories	Unicode string data. Ex: “Hello World”
planPGM	Unicode string data. Ex: “Hello World”
libkit	Unicode string data. Ex: “Hello World”
projects	Many related resources. Can be either a list of URIs or list of individually nested resourc
notes	Unicode string data. Ex: “Hello World”
sequencekitname	Unicode string data. Ex: “Hello World”
base_recalibration_mode	Unicode string data. Ex: “Hello World”
storageHost	Unicode string data. Ex: “Hello World”
expName	Unicode string data. Ex: “Hello World”
cycles	Integer data. Ex: 2673
isReverseRun	Boolean data. Ex: True
storage_options	Unicode string data. Ex: “Hello World”
chipType	Unicode string data. Ex: “Hello World”
library	Unicode string data. Ex: “Hello World”
reverselibrarykey	Unicode string data. Ex: “Hello World”
sampleTubeLabel	Unicode string data. Ex: “Hello World”
seqKitBarcode	Unicode string data. Ex: “Hello World”
barcodeId	Unicode string data. Ex: “Hello World”
isPlanGroup	Boolean data. Ex: True
realign	Boolean data. Ex: True
sampleGroupingName	Unicode string data. Ex: “Hello World”
experiment	A single related resource. Can be either a URI or set of nested resource data.
bedfile	Unicode string data. Ex: “Hello World”
applicationCategoryDisplayedName	Unicode string data. Ex: “Hello World”
isReusable	Boolean data. Ex: True
isDuplicateReads	Boolean data. Ex: True
sampleSets	Many related resources. Can be either a list of URIs or list of individually nested resourc
librarykitname	Unicode string data. Ex: “Hello World”
sseBedFile	Unicode string data. Ex: “Hello World”
adapter	Unicode string data. Ex: “Hello World”
earlyDatFileDeletion	Boolean data. Ex: True
parentPlan	Unicode string data. Ex: “Hello World”
origin	Unicode string data. Ex: “Hello World”
forward3primeadapter	Unicode string data. Ex: “Hello World”
isCustom_kitSettings	Boolean data. Ex: True
samplePrepKitName	Unicode string data. Ex: “Hello World”
applicationGroupDisplayedName	Unicode string data. Ex: “Hello World”
metaData	Unicode string data. Ex: “Hello World”
isFavorite	Boolean data. Ex: True

Table 2.16 – continued from previous page

field	help text
qcValues	Many related resources. Can be either a list of URIs or list of individually nested resourc
planStatus	Unicode string data. Ex: “Hello World”
templatingKitName	Unicode string data. Ex: “Hello World”
runType	Unicode string data. Ex: “Hello World”
username	Unicode string data. Ex: “Hello World”
planName	Unicode string data. Ex: “Hello World”
sampleDisplayedName	Unicode string data. Ex: “Hello World”
controlSequencekitname	Unicode string data. Ex: “Hello World”
tfKey	Unicode string data. Ex: “Hello World”
mixedTypeRNA_reference	Unicode string data. Ex: “Hello World”
childPlans	A list of data. Ex: [’abc’, 26.73, 8]
pairedEndLibraryAdapterName	Unicode string data. Ex: “Hello World”
runMode	Unicode string data. Ex: “Hello World”
irworkflow	Unicode string data. Ex: “Hello World”
planExecuted	Boolean data. Ex: True
project	Unicode string data. Ex: “Hello World”
usePostBeadfind	Boolean data. Ex: True
libraryReadLength	Integer data. Ex: 2673
runname	Unicode string data. Ex: “Hello World”
chefInfo	A dictionary of data. Ex: {‘price’: 26.73, ‘name’: ‘Daniel’}
planGUID	Unicode string data. Ex: “Hello World”
samplePrepProtocol	Unicode string data. Ex: “Hello World”
planShortID	Unicode string data. Ex: “Hello World”
sample	Unicode string data. Ex: “Hello World”
planExecutedDate	A date & time as a string. Ex: “2010-11-10T03:07:43”
reverse_primer	Unicode string data. Ex: “Hello World”
id	Integer data. Ex: 2673
barcodedSamples	Unicode string data. Ex: “Hello World”
regionfile	Unicode string data. Ex: “Hello World”
selectedPlugins	Unicode string data. Ex: “Hello World”
isSystemDefault	Boolean data. Ex: True
autoName	Unicode string data. Ex: “Hello World”
libraryKey	Unicode string data. Ex: “Hello World”
flows	Integer data. Ex: 2673
date	A date & time as a string. Ex: “2010-11-10T03:07:43”
isSystem	Boolean data. Ex: True
variantfrequency	Unicode string data. Ex: “Hello World”
sampleSetDisplayedName	Unicode string data. Ex: “Hello World”
flowsInOrder	Unicode string data. Ex: “Hello World”
libraryPrepType	Unicode string data. Ex: “Hello World”
sampleGrouping	A single related resource. Can be either a URI or set of nested resource data.
chipBarcode	Unicode string data. Ex: “Hello World”
usePreBeadfind	Boolean data. Ex: True
resource_uri	Unicode string data. Ex: “Hello World”
libraryPrepTypeDisplayedName	Unicode string data. Ex: “Hello World”
reverse3primeadapter	Unicode string data. Ex: “Hello World”

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 111,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/plannedexperiment/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "planDisplayedName": "Ion AmpliSeq HD for Tumor - DNA",
            "autoAnalyze": true,
            "endBarcodeKitName": "",
            "templatingKitBarcode": null,
            "preAnalysis": true,
            "thumbnailanalysisargs": "Analysis --args-json /opt/ion/config/args_540_
↪analysis.json --thumbnail true",
            "applicationGroup": "/rundb/api/v1/applicationgroup/1/",
            "mixedTypeRNA_hotSpotRegionBedFile": "",
            "mixedTypeRNA_targetRegionBedFile": "",
            "platform": "",
            "categories": "onco_solidTumor;onco_heme;",
            "planPGM": null,
            "prebasecallerargs": "BaseCaller --barcode-filter-minreads 10 --phasing-
↪residual-filter=2.0 --max-phasing-levels 2 --wells-normalization on --read-
↪structure AmpliseqHD --tag-filter-method need-prefix",
            "alignmentargs": "tmap mapall -g 0 ... --context stage1 map4",
            "thumbnailbasecallerargs": "BaseCaller --barcode-filter-minreads 10 --
↪phasing-residual-filter=2.0 --wells-normalization on --read-structure AmpliseqHD",
            "libkit": null,
            "projects": [],
            "notes": "",
            "sequencekitname": "Ion S5 Sequencing Kit",
            "base_recalibration_mode": "standard_recal",
            "storageHost": null,
            "expName": "",
            "thumbnailionstatsargs": "ionstats alignment",
            "cycles": null,
            "isReverseRun": false,
            "storage_options": "A",
            "thumbnailalignmentargs": "tmap mapall -g 0 ... --context stage1 map4",
            "chipType": "540",
            "library": "hg19",
            "runMode": "single",
            "sampleTubeLabel": "",
            "seqKitBarcode": null,
            "barcodeId": "Ion AmpliSeq HD Dual Barcode Kit 1-24",
            "isPlanGroup": false,
            "realign": false,
            "sampleGroupingName": "Self",
            "experiment": "/rundb/api/v1/experiment/136/",
            "bedfile": "/results/uploads/BED/2/hg19/unmerged/detail/AmpliSeqExome.
↪20141113.designed.bed",
            "applicationCategoryDisplayedName": "Oncology - Solid Tumor | Oncology -␣
↪HemeOnc",
            "isReusable": false,
```

```
            "isDuplicateReads": false,
            "sampleSets": [],
            "thumbnailbeadfindargs": "justBeadFind --args-json /opt/ion/config/args_
↪540_beadfind.json --thumbnail true",
            "librarykitname": "Ion AmpliSeq HD Library Kit",
            "sseBedFile": "",
            "adapter": null,
            "basecallerargs": "BaseCaller --barcode-filter-minreads 10 --phasing-
↪residual-filter=2.0 --max-phasing-levels 2 --num-unfiltered 1000 --barcode-filter-
↪postpone 1 --wells-normalization on --read-structure AmpliseqHD",
            "earlyDatFileDeletion": false,
            "parentPlan": null,
            "origin": "gui|5.10.0.RC4",
            "forward3primeadapter": "ATCACCGACTGCCCATAGAGAGGCTGAGAC",
            "planStatus": "pending",
            "isCustom_kitSettings": false,
            "samplePrepKitName": null,
            "applicationGroupDisplayedName": "DNA",
            "metaData": {
                "fromTemplate": "Ion_AmpliSeq_HD_for_Tumor_-_DNA",
                "fromTemplateSource": "ION"
            },
            "isFavorite": false,
            "qcValues": [
                {
                    "threshold": 30,
                    "plannedExperiment": "/rundb/api/v1/plannedexperiment/143/",
                    "id": 407,
                    "qcType": {
                        "description": "",
                        "minThreshold": 1,
                        "maxThreshold": 100,
                        "defaultThreshold": 30,
                        "qcName": "Key Signal (1-100)",
                        "id": 2,
                        "resource_uri": "/rundb/api/v1/qctype/2/"
                    },
                    "resource_uri": "/rundb/api/v1/plannedexperimentqc/407/"
                },
                {
                    "threshold": 30,
                    "plannedExperiment": "/rundb/api/v1/plannedexperiment/143/",
                    "id": 408,
                    "qcType": {
                        "description": "",
                        "minThreshold": 0,
                        "maxThreshold": 100,
                        "defaultThreshold": 30,
                        "qcName": "Usable Sequence (%)",
                        "id": 3,
                        "resource_uri": "/rundb/api/v1/qctype/3/"
                    },
                    "resource_uri": "/rundb/api/v1/plannedexperimentqc/408/"
                },
                {
                    "threshold": 30,
                    "plannedExperiment": "/rundb/api/v1/plannedexperiment/143/",
                    "id": 406,
```

```
                    "qcType": {
                        "description": "",
                        "minThreshold": 0,
                        "maxThreshold": 100,
                        "defaultThreshold": 30,
                        "qcName": "Bead Loading (%)",
                        "id": 1,
                        "resource_uri": "/rundb/api/v1/qctype/1/"
                    },
                    "resource_uri": "/rundb/api/v1/plannedexperimentqc/406/"
                }
            ],
            "analysisargs": "Analysis --args-json /opt/ion/config/args_540_analysis.
↪json",
            "thumbnailcalibrateargs": "Calibration",
            "templatingKitName": "Ion Chef S540 V1",
            "runType": "AMPS_HD_DNA",
            "username": "ionadmin",
            "planShortID": "SP1XE",
            "sampleDisplayedName": "",
            "prethumbnailbasecallerargs": "BaseCaller --barcode-filter-minreads 10 --
↪phasing-residual-filter=2.0 --wells-normalization on --read-structure AmpliseqHD --
↪tag-filter-method need-prefix",
            "controlSequencekitname": null,
            "tfKey": "ATCG",
            "mixedTypeRNA_reference": "",
            "childPlans": [],
            "pairedEndLibraryAdapterName": "",
            "reverselibrarykey": "",
            "irworkflow": "",
            "planExecuted": false,
            "project": "",
            "usePostBeadfind": false,
            "libraryReadLength": 200,
            "runname": null,
            "chefInfo": {},
            "planGUID": "1d75abf5-4d15-43f5-bb08-1c89d7344175",
            "ionstatsargs": "ionstats alignment",
            "samplePrepProtocol": "",
            "sample": "",
            "planExecutedDate": null,
            "reverse_primer": null,
            "id": 143,
            "barcodedSamples": {
                "Sample 10": {
                    "dualBarcodes": [],
                    "barcodeSampleInfo": {
                        "IonHDdual_0110": {
                            "description": "",
                            "reference": "hg19",
                            "targetRegionBedFile": "/results/uploads/BED/2/hg19/
↪unmerged/detail/AmpliSeqExome.20141113.designed.bed",
                            "hotSpotRegionBedFile": "",
                            "nucleotideType": "DNA",
                            "controlSequenceType": "",
                            "externalId": "",
                            "endBarcode": "",
                            "controlType": "",
```

```
                            "sseBedFile": ""
                        }
                    },
                    "barcodes": [
                        "IonHDdual_0110"
                    ]
                },
                "Sample 8": {
                    "dualBarcodes": [],
                    "barcodeSampleInfo": {
                        "IonHDdual_0108": {
                            "description": "",
                            "reference": "hg19",
                            "targetRegionBedFile": "/results/uploads/BED/2/hg19/
↪unmerged/detail/AmpliSeqExome.20141113.designed.bed",
                            "hotSpotRegionBedFile": "",
                            "nucleotideType": "DNA",
                            "controlSequenceType": "",
                            "externalId": "",
                            "endBarcode": "",
                            "controlType": "",
                            "sseBedFile": ""
                        }
                    },
                    "barcodes": [
                        "IonHDdual_0108"
                    ]
                },
                "Sample 9": {
                    "dualBarcodes": [],
                    "barcodeSampleInfo": {
                        "IonHDdual_0109": {
                            "description": "",
                            "reference": "hg19",
                            "targetRegionBedFile": "/results/uploads/BED/2/hg19/
↪unmerged/detail/AmpliSeqExome.20141113.designed.bed",
                            "hotSpotRegionBedFile": "",
                            "nucleotideType": "DNA",
                            "controlSequenceType": "",
                            "externalId": "",
                            "endBarcode": "",
                            "controlType": "",
                            "sseBedFile": ""
                        }
                    },
                    "barcodes": [
                        "IonHDdual_0109"
                    ]
                },
                "Sample 6": {
                    "dualBarcodes": [],
                    "barcodeSampleInfo": {
                        "IonHDdual_0106": {
                            "description": "",
                            "reference": "hg19",
                            "targetRegionBedFile": "/results/uploads/BED/2/hg19/
↪unmerged/detail/AmpliSeqExome.20141113.designed.bed",
                            "hotSpotRegionBedFile": "",
```

```
                            "nucleotideType": "DNA",
                            "controlSequenceType": "",
                            "externalId": "",
                            "endBarcode": "",
                            "controlType": "",
                            "sseBedFile": ""
                        }
                    },
                    "barcodes": [
                        "IonHDdual_0106"
                    ]
                },
                "Sample 7": {
                    "dualBarcodes": [],
                    "barcodeSampleInfo": {
                        "IonHDdual_0107": {
                            "description": "",
                            "reference": "hg19",
                            "targetRegionBedFile": "/results/uploads/BED/2/hg19/
↪unmerged/detail/AmpliSeqExome.20141113.designed.bed",
                            "hotSpotRegionBedFile": "",
                            "nucleotideType": "DNA",
                            "controlSequenceType": "",
                            "externalId": "",
                            "endBarcode": "",
                            "controlType": "",
                            "sseBedFile": ""
                        }
                    },
                    "barcodes": [
                        "IonHDdual_0107"
                    ]
                },
                "Sample 4": {
                    "dualBarcodes": [],
                    "barcodeSampleInfo": {
                        "IonHDdual_0104": {
                            "description": "",
                            "reference": "hg19",
                            "targetRegionBedFile": "/results/uploads/BED/2/hg19/
↪unmerged/detail/AmpliSeqExome.20141113.designed.bed",
                            "hotSpotRegionBedFile": "",
                            "nucleotideType": "DNA",
                            "controlSequenceType": "",
                            "externalId": "",
                            "endBarcode": "",
                            "controlType": "",
                            "sseBedFile": ""
                        }
                    },
                    "barcodes": [
                        "IonHDdual_0104"
                    ]
                },
                "Sample 5": {
                    "dualBarcodes": [],
                    "barcodeSampleInfo": {
                        "IonHDdual_0105": {
```

```
                            "description": "",
                            "reference": "hg19",
                            "targetRegionBedFile": "/results/uploads/BED/2/hg19/
↪unmerged/detail/AmpliSeqExome.20141113.designed.bed",
                            "hotSpotRegionBedFile": "",
                            "nucleotideType": "DNA",
                            "controlSequenceType": "",
                            "externalId": "",
                            "endBarcode": "",
                            "controlType": "",
                            "sseBedFile": ""
                        }
                    },
                    "barcodes": [
                        "IonHDdual_0105"
                    ]
                },
                "Sample 2": {
                    "dualBarcodes": [],
                    "barcodeSampleInfo": {
                        "IonHDdual_0102": {
                            "description": "",
                            "reference": "hg19",
                            "targetRegionBedFile": "/results/uploads/BED/2/hg19/
↪unmerged/detail/AmpliSeqExome.20141113.designed.bed",
                            "hotSpotRegionBedFile": "",
                            "nucleotideType": "DNA",
                            "controlSequenceType": "",
                            "externalId": "",
                            "endBarcode": "",
                            "controlType": "",
                            "sseBedFile": ""
                        }
                    },
                    "barcodes": [
                        "IonHDdual_0102"
                    ]
                },
                "Sample 3": {
                    "dualBarcodes": [],
                    "barcodeSampleInfo": {
                        "IonHDdual_0103": {
                            "description": "",
                            "reference": "hg19",
                            "targetRegionBedFile": "/results/uploads/BED/2/hg19/
↪unmerged/detail/AmpliSeqExome.20141113.designed.bed",
                            "hotSpotRegionBedFile": "",
                            "nucleotideType": "DNA",
                            "controlSequenceType": "",
                            "externalId": "",
                            "endBarcode": "",
                            "controlType": "",
                            "sseBedFile": ""
                        }
                    },
                    "barcodes": [
                        "IonHDdual_0103"
                    ]
```

```
                },
                "Sample 1": {
                    "dualBarcodes": [],
                    "barcodeSampleInfo": {
                        "IonHDdual_0101": {
                            "description": "",
                            "reference": "hg19",
                            "targetRegionBedFile": "/results/uploads/BED/2/hg19/
↪unmerged/detail/AmpliSeqExome.20141113.designed.bed",
                            "hotSpotRegionBedFile": "",
                            "nucleotideType": "DNA",
                            "controlSequenceType": "",
                            "externalId": "",
                            "endBarcode": "",
                            "controlType": "",
                            "sseBedFile": ""
                        }
                    },
                    "barcodes": [
                        "IonHDdual_0101"
                    ]
                }
            },
            "custom_args": false,
            "regionfile": "",
            "selectedPlugins": {
                "coverageAnalysis": {
                    "userInput": {},
                    "version": "5.8.0.8",
                    "features": [],
                    "name": "coverageAnalysis",
                    "id": 41
                },
                "variantCaller": {
                    "userInput": {
                        "meta": {
                            "configuration": "ampliseq_hd_ffpe"
                        }
                    },
                    "version": "5.8.0.19",
                    "features": [],
                    "name": "variantCaller",
                    "id": 36
                }
            },
            "beadfindargs": "justBeadFind --args-json /opt/ion/config/args_540_
↪beadfind.json",
            "isSystemDefault": false,
            "autoName": null,
            "libraryKey": "TCAG",
            "flows": 500,
            "date": "2018-04-13T22:17:13.000108+00:00",
            "isSystem": false,
            "variantfrequency": "",
            "planName": "Ion_AmpliSeq_HD_for_Tumor_-_DNA",
            "calibrateargs": "Calibration",
            "flowsInOrder": "",
            "libraryPrepType": "",
```

```
            "sampleGrouping": "/rundb/api/v1/samplegrouptype_cv/2/",
            "chipBarcode": "",
            "sampleSetDisplayedName": "",
            "usePreBeadfind": true,
            "resource_uri": "/rundb/api/v1/plannedexperiment/143/",
            "libraryPrepTypeDisplayedName": "",
            "reverse3primeadapter": ""
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Planned Experiment Db Resource

Resource URL `http://mytorrentserver/rundb/api/v1/plannedexperimentdb/`
Schema URL `http://mytorrentserver/rundb/api/v1/plannedexperimentdb/schema/`

Resource Fields

field	help text
origin	Unicode string data. Ex: “Hello World”
isReverseRun	Boolean data. Ex: True
planDisplayedName	Unicode string data. Ex: “Hello World”
storage_options	Unicode string data. Ex: “Hello World”
preAnalysis	Boolean data. Ex: True
planShortID	Unicode string data. Ex: “Hello World”
username	Unicode string data. Ex: “Hello World”
planStatus	Unicode string data. Ex: “Hello World”

Table 2.17 – continued from previous page

field	help text
runMode	Unicode string data. Ex: “Hello World”
isCustom_kitSettings	Boolean data. Ex: True
sampleTubeLabel	Unicode string data. Ex: “Hello World”
planExecutedDate	A date & time as a string. Ex: “2010-11-10T03:07:43”
samplePrepKitName	Unicode string data. Ex: “Hello World”
reverse_primer	Unicode string data. Ex: “Hello World”
applicationGroup	A single related resource. Can be either a URI or set of nested resource data.
seqKitBarcode	Unicode string data. Ex: “Hello World”
id	Integer data. Ex: 2673
metaData	Unicode string data. Ex: “Hello World”
sampleSets	Many related resources. Can be either a list of URIs or list of individually nested resource data.
isFavorite	Boolean data. Ex: True
qcValues	Many related resources. Can be either a list of URIs or list of individually nested resource data.
samplePrepProtocol	Unicode string data. Ex: “Hello World”
isPlanGroup	Boolean data. Ex: True
experiment	A single related resource. Can be either a URI or set of nested resource data.
projects	Many related resources. Can be either a list of URIs or list of individually nested resource data.
runType	Unicode string data. Ex: “Hello World”
templatingKitBarcode	Unicode string data. Ex: “Hello World”
templatingKitName	Unicode string data. Ex: “Hello World”
planPGM	Unicode string data. Ex: “Hello World”
isSystemDefault	Boolean data. Ex: True
autoName	Unicode string data. Ex: “Hello World”
isReusable	Boolean data. Ex: True
controlSequencekitname	Unicode string data. Ex: “Hello World”
date	A date & time as a string. Ex: “2010-11-10T03:07:43”
isSystem	Boolean data. Ex: True
libkit	Unicode string data. Ex: “Hello World”
categories	Unicode string data. Ex: “Hello World”
planName	Unicode string data. Ex: “Hello World”
parentPlan	Unicode string data. Ex: “Hello World”
childPlans	A list of data. Ex: [’abc’, 26.73, 8]
pairedEndLibraryAdapterName	Unicode string data. Ex: “Hello World”
sampleGrouping	A single related resource. Can be either a URI or set of nested resource data.
adapter	Unicode string data. Ex: “Hello World”
irworkflow	Unicode string data. Ex: “Hello World”
planExecuted	Boolean data. Ex: True
project	Unicode string data. Ex: “Hello World”
usePostBeadfind	Boolean data. Ex: True
storageHost	Unicode string data. Ex: “Hello World”
expName	Unicode string data. Ex: “Hello World”
libraryReadLength	Integer data. Ex: 2673
runname	Unicode string data. Ex: “Hello World”
usePreBeadfind	Boolean data. Ex: True
planGUID	Unicode string data. Ex: “Hello World”
cycles	Integer data. Ex: 2673
resource_uri	Unicode string data. Ex: “Hello World”

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 111,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/plannedexperimentdb/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "origin": "gui|5.10.0.RC4",
            "isReverseRun": false,
            "planDisplayedName": "Ion AmpliSeq HD for Tumor - DNA",
            "storage_options": "A",
            "preAnalysis": true,
            "planShortID": "SP1XE",
            "username": "ionadmin",
            "planStatus": "pending",
            "runMode": "single",
            "isCustom_kitSettings": false,
            "sampleTubeLabel": "",
            "planExecutedDate": null,
            "samplePrepKitName": null,
            "reverse_primer": null,
            "applicationGroup": "/rundb/api/v1/applicationgroup/1/",
            "seqKitBarcode": null,
            "id": 143,
            "metaData": {
                "fromTemplate": "Ion_AmpliSeq_HD_for_Tumor_-_DNA",
                "fromTemplateSource": "ION"
            },
            "sampleSets": [],
            "isFavorite": false,
            "qcValues": [
                {
                    "threshold": 30,
                    "plannedExperiment": "/rundb/api/v1/plannedexperiment/143/",
                    "id": 407,
                    "qcType": {
                        "description": "",
                        "minThreshold": 1,
                        "maxThreshold": 100,
                        "defaultThreshold": 30,
                        "qcName": "Key Signal (1-100)",
                        "id": 2,
                        "resource_uri": "/rundb/api/v1/qctype/2/"
                    },
                    "resource_uri": "/rundb/api/v1/plannedexperimentqc/407/"
                },
                {
                    "threshold": 30,
                    "plannedExperiment": "/rundb/api/v1/plannedexperiment/143/",
                    "id": 408,
                    "qcType": {
                        "description": "",
                        "minThreshold": 0,
```

```
                    "maxThreshold": 100,
                    "defaultThreshold": 30,
                    "qcName": "Usable Sequence (%)",
                    "id": 3,
                    "resource_uri": "/rundb/api/v1/qctype/3/"
                },
                "resource_uri": "/rundb/api/v1/plannedexperimentqc/408/"
            },
            {
                "threshold": 30,
                "plannedExperiment": "/rundb/api/v1/plannedexperiment/143/",
                "id": 406,
                "qcType": {
                    "description": "",
                    "minThreshold": 0,
                    "maxThreshold": 100,
                    "defaultThreshold": 30,
                    "qcName": "Bead Loading (%)",
                    "id": 1,
                    "resource_uri": "/rundb/api/v1/qctype/1/"
                },
                "resource_uri": "/rundb/api/v1/plannedexperimentqc/406/"
            }
        ],
        "samplePrepProtocol": "",
        "isPlanGroup": false,
        "experiment": "/rundb/api/v1/experiment/136/",
        "projects": [],
        "runType": "AMPS_HD_DNA",
        "templatingKitBarcode": null,
        "templatingKitName": "Ion Chef S540 V1",
        "planPGM": null,
        "isSystemDefault": false,
        "autoName": null,
        "isReusable": false,
        "controlSequencekitname": null,
        "date": "2018-04-13T22:17:13.000108+00:00",
        "isSystem": false,
        "libkit": null,
        "categories": "onco_solidTumor;onco_heme;",
        "planName": "Ion_AmpliSeq_HD_for_Tumor_-_DNA",
        "parentPlan": null,
        "childPlans": [],
        "pairedEndLibraryAdapterName": "",
        "sampleGrouping": "/rundb/api/v1/samplegrouptype_cv/2/",
        "adapter": null,
        "irworkflow": "",
        "planExecuted": false,
        "project": "",
        "usePostBeadfind": false,
        "storageHost": null,
        "expName": "",
        "libraryReadLength": 200,
        "runname": null,
        "usePreBeadfind": true,
        "planGUID": "1d75abf5-4d15-43f5-bb08-1c89d7344175",
        "cycles": null,
        "resource_uri": "/rundb/api/v1/plannedexperimentdb/143/"
```

```
        }
    ]
}
```

Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Planned Experiment Qc Resource

Resource URL `http://mytorrentserver/rundb/api/v1/plannedexperimentqc/`
Schema URL `http://mytorrentserver/rundb/api/v1/plannedexperimentqc/schema/`

Resource Fields

field	help text	default	nullable	readonly	blank	unique	type
threshold	Integer data. Ex: 2673	0	false	false	false	false	integer
plannedExperiment	A single related resource. Can be either a URI or set of nested resource data.	n/a	false	false	false	false	related
id	Integer data. Ex: 2673		false	false	true	true	integer
qcType	A single related resource. Can be either a URI or set of nested resource data.	n/a	false	false	false	false	related
resource_uri	Unicode string data. Ex: “Hello World”	n/a	false	true	false	false	string

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 318,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/plannedexperimentqc/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "threshold": 30,
            "plannedExperiment": "/rundb/api/v1/plannedexperiment/43/",
            "id": 127,
            "qcType": {
                "description": "",
                "minThreshold": 0,
                "maxThreshold": 100,
                "defaultThreshold": 30,
                "qcName": "Bead Loading (%)",
                "id": 1,
                "resource_uri": "/rundb/api/v1/qctype/1/"
            },
            "resource_uri": "/rundb/api/v1/plannedexperimentqc/127/"
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Plan Template Basic Info Resource

Resource URL `http://mytorrentserver/rundb/api/v1/plantemplatebasicinfo/`
Schema URL `http://mytorrentserver/rundb/api/v1/plantemplatebasicinfo/schema/`

Resource Fields

field	help text
origin	Unicode string data. Ex: “Hello World”
isReverseRun	Boolean data. Ex: True
planDisplayedName	Unicode string data. Ex: “Hello World”
storage_options	Unicode string data. Ex: “Hello World”
preAnalysis	Boolean data. Ex: True
reference	Unicode string data. Ex: “Hello World”
planShortID	Unicode string data. Ex: “Hello World”
hotSpotRegionBedFile	Unicode string data. Ex: “Hello World”
planStatus	Unicode string data. Ex: “Hello World”
runMode	Unicode string data. Ex: “Hello World”
isCustom_kitSettings	Boolean data. Ex: True
sampleTubeLabel	Unicode string data. Ex: “Hello World”
planExecutedDate	A date & time as a string. Ex: “2010-11-10T03:07:43”
samplePrepKitName	Unicode string data. Ex: “Hello World”
reverse_primer	Unicode string data. Ex: “Hello World”
applicationGroup	A single related resource. Can be either a URI or set of nested resource data.
applicationGroupDisplayedName	Unicode string data. Ex: “Hello World”
id	Integer data. Ex: 2673
metaData	Unicode string data. Ex: “Hello World”
isFavorite	Boolean data. Ex: True
seqKitBarcode	Unicode string data. Ex: “Hello World”
samplePrepProtocol	Unicode string data. Ex: “Hello World”
isPlanGroup	Boolean data. Ex: True
sampleGroupName	Unicode string data. Ex: “Hello World”
experiment	A single related resource. Can be either a URI or set of nested resource data.
projects	Many related resources. Can be either a list of URIs or list of individually nested resource da
barcodeKitName	Unicode string data. Ex: “Hello World”
runType	Unicode string data. Ex: “Hello World”
templatingKitBarcode	Unicode string data. Ex: “Hello World”
templatingKitName	Unicode string data. Ex: “Hello World”
planPGM	Unicode string data. Ex: “Hello World”
isSystemDefault	Boolean data. Ex: True
applicationCategoryDisplayedName	Unicode string data. Ex: “Hello World”
autoName	Unicode string data. Ex: “Hello World”
isReusable	Boolean data. Ex: True
controlSequencekitname	Unicode string data. Ex: “Hello World”
sequencingInstrumentType	Unicode string data. Ex: “Hello World”
date	A date & time as a string. Ex: “2010-11-10T03:07:43”
eas	A single related resource. Can be either a URI or set of nested resource data.
isSystem	Boolean data. Ex: True
libkit	Unicode string data. Ex: “Hello World”
categories	Unicode string data. Ex: “Hello World”
planName	Unicode string data. Ex: “Hello World”
irAccountName	Unicode string data. Ex: “Hello World”
templatePrepInstrumentType	Unicode string data. Ex: “Hello World”

Table 2.18 – continued from previous page

field	help text
pairedEndLibraryAdapterName	Unicode string data. Ex: “Hello World”
targetRegionBedFile	Unicode string data. Ex: “Hello World”
adapter	Unicode string data. Ex: “Hello World”
irworkflow	Unicode string data. Ex: “Hello World”
planExecuted	Boolean data. Ex: True
username	Unicode string data. Ex: “Hello World”
usePostBeadfind	Boolean data. Ex: True
storageHost	Unicode string data. Ex: “Hello World”
expName	Unicode string data. Ex: “Hello World”
libraryReadLength	Integer data. Ex: 2673
runname	Unicode string data. Ex: “Hello World”
usePreBeadfind	Boolean data. Ex: True
planGUID	Unicode string data. Ex: “Hello World”
cycles	Integer data. Ex: 2673
notes	Unicode string data. Ex: “Hello World”
resource_uri	Unicode string data. Ex: “Hello World”

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 96,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/plantemplatebasicinfo/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "origin": "|5.10.0.RC4",
            "isReverseRun": false,
            "planDisplayedName": "Ion AmpliSeq HD for Tumor - DNA and Fusions -␣
↪Separate Libraries",
            "storage_options": "A",
            "preAnalysis": true,
            "reference": "hg19",
            "planShortID": "A628Z",
            "hotSpotRegionBedFile": "",
            "planStatus": "planned",
            "runMode": "single",
            "isCustom_kitSettings": false,
            "sampleTubeLabel": null,
            "planExecutedDate": null,
            "samplePrepKitName": null,
            "reverse_primer": null,
            "applicationGroup": "/rundb/api/v1/applicationgroup/5/",
            "applicationGroupDisplayedName": "DNA and Fusions (Separate Libraries)",
            "id": 141,
            "metaData": {},
            "isFavorite": false,
            "seqKitBarcode": null,
            "samplePrepProtocol": "",
            "isPlanGroup": false,
```

```
            "sampleGroupName": "DNA and Fusions",
            "experiment": "/rundb/api/v1/experiment/134/",
            "projects": "",
            "barcodeKitName": "Ion AmpliSeq HD Dual Barcode Kit 1-24",
            "runType": "AMPS_HD_DNA_RNA",
            "templatingKitBarcode": null,
            "templatingKitName": "Ion Chef S540 V1",
            "planPGM": "",
            "isSystemDefault": false,
            "applicationCategoryDisplayedName": "Oncology - Solid Tumor | Oncology -␣
↪HemeOnc",
            "autoName": null,
            "isReusable": true,
            "controlSequencekitname": null,
            "sequencingInstrumentType": "s5",
            "date": "2018-04-12T05:54:10.000222+00:00",
            "eas": "/rundb/api/v1/experimentanalysissettings/133/",
            "isSystem": true,
            "libkit": null,
            "categories": "onco_solidTumor;onco_heme;",
            "planName": "Ion_AmpliSeq_HD_for_Tumor_-_DNA_and_Fusions_-_Separate_
↪Libraries",
            "irAccountName": "",
            "templatePrepInstrumentType": "IonChef",
            "pairedEndLibraryAdapterName": null,
            "targetRegionBedFile": "",
            "adapter": null,
            "irworkflow": "",
            "planExecuted": false,
            "username": null,
            "usePostBeadfind": false,
            "storageHost": null,
            "expName": "",
            "libraryReadLength": 200,
            "runname": null,
            "usePreBeadfind": true,
            "planGUID": "e52fac66-4086-433e-b8e7-ad1d1403946f",
            "cycles": null,
            "notes": "",
            "resource_uri": "/rundb/api/v1/plantemplatebasicinfo/141/"
        }
    ]
}
```


Allowed list HTTP methods

- GET

Allowed detail HTTP methods

- GET

Plan Template Summary Resource

Resource URL `http://mytorrentserver/rundb/api/v1/plantemplatesummary/`
Schema URL `http://mytorrentserver/rundb/api/v1/plantemplatesummary/schema/`

Resource Fields

field	help text	default	nullable	readonly	bla
origin	Unicode string data. Ex: “Hello World”		true	false	fals
isReverseRun	Boolean data. Ex: True	false	false	false	tru
planDisplayedName	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
storage_options	Unicode string data. Ex: “Hello World”	A	false	false	fals
preAnalysis	Boolean data. Ex: True	true	false	false	tru
planShortID	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
planStatus	Unicode string data. Ex: “Hello World”		false	false	tru
runMode	Unicode string data. Ex: “Hello World”		false	false	tru
isCustom_kitSettings	Boolean data. Ex: True	false	false	false	tru
sampleTubeLabel	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
planExecutedDate	A date & time as a string. Ex: “2010-11-10T03:07:43”	n/a	true	false	fals
samplePrepKitName	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
reverse_primer	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
seqKitBarcode	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
id	Integer data. Ex: 2673		false	false	tru
metaData	Unicode string data. Ex: “Hello World”	{}	false	false	tru
isFavorite	Boolean data. Ex: True	false	false	false	tru
samplePrepProtocol	Unicode string data. Ex: “Hello World”		true	false	fals
isPlanGroup	Boolean data. Ex: True	false	false	false	tru
templatingKitName	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
runType	Unicode string data. Ex: “Hello World”	GENS	false	false	fals
templatingKitBarcode	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
planPGM	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
isSystemDefault	Boolean data. Ex: True	false	false	false	tru
autoName	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
isReusable	Boolean data. Ex: True	false	false	false	tru
controlSequencekitname	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
date	A date & time as a string. Ex: “2010-11-10T03:07:43”	n/a	true	false	fals
isSystem	Boolean data. Ex: True	false	false	false	tru
libkit	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
categories	Unicode string data. Ex: “Hello World”		true	false	fals
planName	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
pairedEndLibraryAdapterName	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
adapter	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
irworkflow	Unicode string data. Ex: “Hello World”		false	false	tru
planExecuted	Boolean data. Ex: True	false	false	false	tru
username	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
usePostBeadfind	Boolean data. Ex: True	true	false	false	tru
storageHost	Unicode string data. Ex: “Hello World”	n/a	true	false	fals
expName	Unicode string data. Ex: “Hello World”		false	false	tru

Table 2.19 – continued from previous page

field	help text	default	nullable	readonly	bla
libraryReadLength	Integer data. Ex: 2673	0	false	false	fal
runname	Unicode string data. Ex: “Hello World”	n/a	true	false	fal
usePreBeadfind	Boolean data. Ex: True	true	false	false	tru
planGUID	Unicode string data. Ex: “Hello World”	n/a	true	false	fal
cycles	Integer data. Ex: 2673	n/a	true	false	fal
resource_uri	Unicode string data. Ex: “Hello World”	n/a	false	true	fal

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 103,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/plantemplatesummary/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "origin": "|5.10.0.RC4",
            "isReverseRun": false,
            "planDisplayedName": "Ion AmpliSeq HD for Tumor - DNA and Fusions -␣
↪Separate Libraries",
            "storage_options": "A",
            "preAnalysis": true,
            "planShortID": "A628Z",
            "planStatus": "planned",
            "runMode": "single",
            "isCustom_kitSettings": false,
            "sampleTubeLabel": null,
            "planExecutedDate": null,
            "samplePrepKitName": null,
            "reverse_primer": null,
            "seqKitBarcode": null,
            "id": 141,
            "metaData": {},
            "isFavorite": false,
            "samplePrepProtocol": "",
            "isPlanGroup": false,
            "templatingKitName": "Ion Chef S540 V1",
            "runType": "AMPS_HD_DNA_RNA",
            "templatingKitBarcode": null,
            "planPGM": "",
            "isSystemDefault": false,
            "autoName": null,
            "isReusable": true,
            "controlSequencekitname": null,
            "date": "2018-04-12T05:54:10.000222+00:00",
            "isSystem": true,
            "libkit": null,
            "categories": "onco_solidTumor;onco_heme;",
            "planName": "Ion_AmpliSeq_HD_for_Tumor_-_DNA_and_Fusions_-_Separate_
↪Libraries",
            "pairedEndLibraryAdapterName": null,
```

```
            "adapter": null,
            "irworkflow": "",
            "planExecuted": false,
            "username": null,
            "usePostBeadfind": false,
            "storageHost": null,
            "expName": "",
            "libraryReadLength": 200,
            "runname": null,
            "usePreBeadfind": true,
            "planGUID": "e52fac66-4086-433e-b8e7-ad1d1403946f",
            "cycles": null,
            "resource_uri": "/rundb/api/v1/plantemplatesummary/141/"
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Plugin Resource

Resource URL `http://mytorrentserver/rundb/api/v1/plugin/`
Schema URL `http://mytorrentserver/rundb/api/v1/plugin/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
active	Boolean data. Ex: True	true	false	false	true	false	boolean
availableVersions	A list of data. Ex: ['abc', 26.73, 8]	[]	false	true	false	false	list
id	Integer data. Ex: 2673		false	false	true	true	integer
isPlanConfig	Boolean data. Ex: True	n/a	false	true	false	false	boolean
isSupported	Boolean data. Ex: True	n/a	false	true	false	false	boolean
script	Unicode string data. Ex: "Hello World"		false	false	true	false	string
selected	Boolean data. Ex: True	false	false	false	true	false	boolean
requires_configuration	Boolean data. Ex: True	false	false	false	true	false	boolean
version	Unicode string data. Ex: "Hello World"	n/a	false	false	false	false	string
hasAbout	Boolean data. Ex: True	n/a	false	true	false	false	boolean
input	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string
majorBlock	Boolean data. Ex: True	false	false	false	true	false	boolean
status	Unicode string data. Ex: "Hello World"		true	false	false	false	string
description	Unicode string data. Ex: "Hello World"		false	false	true	false	string
defaultSelected	Boolean data. Ex: True	false	false	false	true	false	boolean
pluginsettings	Unicode string data. Ex: "Hello World"		true	false	false	false	string
date	A date & time as a string. Ex: "2010-11-10T03:07:43"	true	false	false	true	false	datetime
path	Unicode string data. Ex: "Hello World"		false	false	true	false	string
isConfig	Boolean data. Ex: True	n/a	false	true	false	false	boolean
isInstance	Boolean data. Ex: True	n/a	false	true	false	false	boolean
name	Unicode string data. Ex: "Hello World"	n/a	false	false	false	false	string
userinputfields	Unicode string data. Ex: "Hello World"	{}	true	false	false	false	string
url	Unicode string data. Ex: "Hello World"		false	false	true	false	string
config	Unicode string data. Ex: "Hello World"		true	false	false	false	string
packageName	Unicode string data. Ex: "Hello World"		false	false	true	false	string
versionedName	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string
isUpgradable	Boolean data. Ex: True	false	false	true	false	false	boolean

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 16,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/plugin/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "active": true,
            "availableVersions": [
                "5.8.0.0"
```

```
            ],
            "id": 30,
            "isPlanConfig": true,
            "isSupported": true,
            "script": "smallRNA.py",
            "selected": true,
            "requires_configuration": false,
            "version": "5.8.0.0",
            "hasAbout": false,
            "input": "/configure/plugins/plugin/30/configure/report/",
            "majorBlock": true,
            "status": {},
            "description": "Run the small RNA pipeline.",
            "defaultSelected": false,
            "pluginsettings": {
                "depends": [],
                "features": [],
                "runtypes": [
                    "wholechip",
                    "thumbnail",
                    "composite"
                ],
                "runlevels": [
                    "default"
                ]
            },
            "date": "2017-12-05T00:11:04.000271+00:00",
            "path": "/results/plugins/smallRNA",
            "isConfig": true,
            "isInstance": true,
            "name": "smallRNA",
            "userinputfields": {},
            "url": "",
            "config": {},
            "packageName": "ion-plugin-smallrna",
            "versionedName": "smallRNA--v5.8.0.0",
            "resource_uri": "/rundb/api/v1/plugin/30/",
            "isUpgradable": false
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET

- POST
- PUT
- DELETE
- PATCH

Plugin Result Resource

Resource URL `http://mytorrentserver/rundb/api/v1/pluginresult/`
Schema URL `http://mytorrentserver/rundb/api/v1/pluginresult/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
major	Boolean data. Ex: True	n/a	false	true	false	false	boolean
can_terminate	Boolean data. Ex: True	n/a	false	true	false	false	boolean
resultName	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string
pluginVersion	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string
result	A single related resource. Can be either a URI or set of nested resource data.	n/a	false	false	false	false	related
owner	A single related resource. Can be either a URI or set of nested resource data.	n/a	false	false	false	false	related
id	Integer data. Ex: 2673		false	false	true	true	integer
size	Unicode string data. Ex: "Hello World"	-1	false	false	false	false	string
validation_errors	Unicode string data. Ex: "Hello World"	{}	false	false	true	false	string
state	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string
store	Unicode string data. Ex: "Hello World"	{}	false	false	true	false	string
files	A list of data. Ex: ['abc', 26.73, 8]	n/a	false	true	false	false	list
URL	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string
plugin_result_jobs	Many related resources. Can be either a list of URIs or list of individually nested resource data.	n/a	false	false	false	false	related
path	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string
endtime	A date & time as a string. Ex: "2010-11-10T03:07:43"	n/a	false	true	false	false	datetime
apikey	Unicode string data. Ex: "Hello World"	n/a	true	false	false	false	string
plugin	A single related resource. Can be either a URI or set of nested resource data.	n/a	false	false	false	false	related
reportLink	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string
pluginName	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string
starttime	A date & time as a string. Ex: "2010-11-10T03:07:43"	n/a	false	true	false	false	datetime
inodes	Unicode string data. Ex: "Hello World"	-1	false	false	false	false	string
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 17,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/pluginresult/?offset=1&limit=1&format=json"
    },
    "objects": [
```

```
        {
            "major": true,
            "can_terminate": false,
            "resultName": "Auto_user_CB1-42-r9723-314wfa-tl_94",
            "pluginVersion": "5.8.0.0",
            "result": "/rundb/api/v1/results/6/",
            "owner": "/rundb/api/v1/user/2/",
            "id": 24,
            "size": "344884433",
            "validation_errors": {
                "validation_errors": []
            },
            "state": "Error",
            "store": {
                "reference": "/results/referenceLibrary/tmap-f3/hg19/hg19.fasta",
                "barcoded": false,
                "Error": "Failed running run_rnaseqanalysis.py.",
                "genome": "hg19",
                "launch_mode": "Manual",
                "fpkm_thres": "0.3",
                "cutadapt": "None",
                "fraction_of_reads": "1"
            },
            "files": [
                "RNASeqAnalysis.html"
            ],
            "URL": "/output/Home/Auto_user_CB1-42-r9723-314wfa-tl_94_006/plugin_out/
↪RNASeqAnalysis_out.24/",
            "plugin_result_jobs": [
                {
                    "grid_engine_jobid": 517,
                    "id": 24,
                    "state": "Error",
                    "starttime": "2018-04-25T22:22:52.000576+00:00",
                    "endtime": "2018-04-25T22:28:47.000816+00:00",
                    "config": {
                        "cutadapt": "None",
                        "fraction_of_reads": "1",
                        "reference": "/results/referenceLibrary/tmap-f3/hg19/hg19.
↪fasta",
                        "genome": "hg19",
                        "launch_mode": "Manual"
                    },
                    "run_level": "default",
                    "resource_uri": "/rundb/api/v1/PluginResultJob/24/"
                }
            ],
            "path": "/results/analysis/output/Home/Auto_user_CB1-42-r9723-314wfa-tl_
↪94_006/plugin_out/RNASeqAnalysis_out.24",
            "endtime": "2018-04-25T22:28:47.000816+00:00",
            "apikey": "5a4f5fb12ef3d6c5490b3a41501097a506cd8d85",
            "plugin": "/rundb/api/v1/plugin/29/",
            "reportLink": "/output/Home/Auto_user_CB1-42-r9723-314wfa-tl_94_006/",
            "pluginName": "RNASeqAnalysis",
            "starttime": "2018-04-25T22:22:52.000576+00:00",
            "inodes": "33",
            "resource_uri": "/rundb/api/v1/pluginresult/24/"
        }
```

```
    ]
}
```

Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Plugin Result Job Resource

Resource URL `http://mytorrentserver/rundb/api/v1/PluginResultJob/`
Schema URL `http://mytorrentserver/rundb/api/v1/PluginResultJob/schema/`

Resource Fields

field	help text	default	nullable	readonly	blank	unique	type
grid_engine_jobid	Integer data. Ex: 2673	n/a	true	false	false	false	integer
id	Integer data. Ex: 2673		false	false	true	true	integer
state	Unicode string data. Ex: “Hello World”	n/a	false	false	false	false	string
starttime	A date & time as a string. Ex: “2010-11-10T03:07:43”	n/a	true	false	false	false	datetime
endtime	A date & time as a string. Ex: “2010-11-10T03:07:43”	n/a	true	false	false	false	datetime
config	Unicode string data. Ex: “Hello World”		false	false	true	false	string
run_level	Unicode string data. Ex: “Hello World”	n/a	false	false	false	false	string
resource_uri	Unicode string data. Ex: “Hello World”	n/a	false	true	false	false	string

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 17,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/PluginResultJob/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "grid_engine_jobid": -1,
            "id": 19,
            "state": "Completed",
            "starttime": "2017-08-09T20:26:03.000549+00:00",
            "endtime": "2017-08-09T20:30:11.000942+00:00",
            "config": {
                "compressedType": "zip",
                "bamCreate": "on",
                "xlsCreate": "off",
                "zipFASTQ": "off",
                "vcfCreate": "on",
                "zipXLS": "off",
                "delimiter_select": ".",
                "zipVCF": "on",
                "zipBAM": "on",
                "fastqCreate": "off",
                "select_dialog": [
                    "run_name",
                    "samplename",
                    "instrument",
                    "",
                    "",
                    "",
                    ""
                ]
            },
            "run_level": "last",
            "resource_uri": "/rundb/api/v1/PluginResultJob/19/"
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Project Resource

Resource URL `http://mytorrentserver/rundb/api/v1/project/`
Schema URL `http://mytorrentserver/rundb/api/v1/project/schema/`

Resource Fields

field	help text	default	nullable	readonly	blank	unique	type
name	Unicode string data. Ex: "Hello World"	n/a	false	false	false	true	string
creator	A single related resource. Can be either a URI or set of nested resource data.	n/a	false	false	false	false	related
created	A date & time as a string. Ex: "2010-11-10T03:07:43"	true	false	false	true	false	datetime
modified	A date & time as a string. Ex: "2010-11-10T03:07:43"	true	false	false	true	false	datetime
id	Integer data. Ex: 2673		false	false	true	true	integer
resultsCount	Integer data. Ex: 2673	n/a	false	true	false	false	integer
public	Boolean data. Ex: True	true	false	false	true	false	boolean
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 2,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/project/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "name": "demo",
            "creator": "/rundb/api/v1/user/1/",
            "created": "2017-07-22T06:59:07.000475+00:00",
            "modified": "2018-02-28T17:32:01.000703+00:00",
```

```
            "id": 1,
            "resultsCount": 6,
            "public": true,
            "resource_uri": "/rundb/api/v1/project/1/"
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Project Results Resource

Resource URL `http://mytorrentserver/rundb/api/v1/projectresults/`
Schema URL `http://mytorrentserver/rundb/api/v1/projectresults/schema/`

Resource Fields

field	help text	default	nullable	readonly	blank	unique	type
reference	Unicode string data. Ex: "Hello World"	n/a	true	false	false	false	string
reportStatus	Unicode string data. Ex: "Hello World"	Nothing	true	false	false	false	string
runid	Unicode string data. Ex: "Hello World"		false	false	true	false	string
id	Integer data. Ex: 2673		false	false	true	true	integer
metaData	Unicode string data. Ex: "Hello World"	{}	false	false	true	false	string
log	Unicode string data. Ex: "Hello World"		false	false	true	false	string
timeStamp	A date & time as a string. Ex: "2010-11-10T03:07:43"	true	false	false	true	false	datetime
resultsName	Unicode string data. Ex: "Hello World"	n/a	false	false	false	false	string
status	Unicode string data. Ex: "Hello World"	n/a	false	false	false	false	string
processedflows	Integer data. Ex: 2673	n/a	false	false	false	false	integer
processedCycles	Integer data. Ex: 2673	n/a	false	false	false	false	integer
representative	Boolean data. Ex: True	false	false	false	true	false	boolean
diskusage	Integer data. Ex: 2673	n/a	true	false	false	false	integer
projects	Many related resources. Can be either a list of URIs or list of individually nested resource data.	n/a	false	false	false	false	related
resultsType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
parentIDs	Unicode string data. Ex: "Hello World"		false	false	true	false	string
timeToComplete	Unicode string data. Ex: "Hello World"	n/a	false	false	false	false	string
reportLink	Unicode string data. Ex: "Hello World"	n/a	false	false	false	false	string
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string
framesProcessed	Integer data. Ex: 2673	n/a	false	false	false	false	integer
autoExempt	Boolean data. Ex: True	false	false	false	true	false	boolean
analysisVersion	Unicode string data. Ex: "Hello World"	n/a	false	false	false	false	string

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 7,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/projectresults/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "reference": "",
            "reportStatus": "Nothing",
            "runid": "MJMQ3",
            "id": 3,
            "metaData": {},
            "log": "/output/Home/Auto_S5-540_WholeTranscriptomeRNA_91_003/log.html",
            "timeStamp": "2017-07-22T13:15:56.000197+00:00",
            "resultsName": "Auto_S5-540_WholeTranscriptomeRNA_91",
            "status": "Completed",
            "processedflows": 0,
            "processedCycles": 0,
            "representative": false,
            "diskusage": 229301,
            "projects": [
                "/rundb/api/v1/project/1/"
            ],
            "resultsType": "",
            "parentIDs": "",
            "timeToComplete": "0",
            "reportLink": "/output/Home/Auto_S5-540_WholeTranscriptomeRNA_91_003/",
            "resource_uri": "/rundb/api/v1/projectresults/3/",
            "framesProcessed": 0,
            "autoExempt": false,
            "analysisVersion": "db:5.6.18-1,an:5.6.5-1,"
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST

- PUT
- DELETE
- PATCH

Publisher Resource

Resource URL `http://mytorrentserver/rundb/api/v1/publisher/`
Schema URL `http://mytorrentserver/rundb/api/v1/publisher/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
name	Unicode string data. Ex: "Hello World"	n/a	false	false	false	true	string
version	Unicode string data. Ex: "Hello World"	n/a	false	false	false	false	string
global_meta	Unicode string data. Ex: "Hello World"	{}	false	false	true	false	string
date	A date & time as a string. Ex: "2010-11-10T03:07:43"	n/a	false	false	false	false	date-time
path	Unicode string data. Ex: "Hello World"	n/a	false	false	false	false	string
id	Integer data. Ex: 2673		false	false	true	true	integer
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 2,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/publisher/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "name": "BED",
            "version": "1.0",
            "global_meta": {},
            "date": "2017-07-22T21:17:13.000054+00:00",
            "path": "/results/publishers/BED",
            "id": 2,
            "resource_uri": "/rundb/api/v1/publisher/BED/"
        }
    ]
}
```

Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Qc Type Resource

Resource URL `http://mytorrentserver/rundb/api/v1/qctype/`
Schema URL `http://mytorrentserver/rundb/api/v1/qctype/schema/`

Resource Fields

field	help text	default	nullable	readonly	blank	unique	type
description	Unicode string data. Ex: "Hello World"		false	false	true	false	string
minThreshold	Integer data. Ex: 2673	0	false	false	false	false	integer
maxThreshold	Integer data. Ex: 2673	100	false	false	false	false	integer
defaultThreshold	Integer data. Ex: 2673	0	false	false	false	false	integer
qcName	Unicode string data. Ex: "Hello World"	n/a	false	false	false	true	string
id	Integer data. Ex: 2673		false	false	true	true	integer
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string

Example Response

```
{
    "meta": {
        "previous": null,
        "total_count": 3,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/qctype/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "description": "",
            "minThreshold": 0,
            "maxThreshold": 100,
            "defaultThreshold": 30,
            "qcName": "Bead Loading (%)",
            "id": 1,
            "resource_uri": "/rundb/api/v1/qctype/1/"
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Quality Metrics Resource

Resource URL `http://mytorrentserver/rundb/api/v1/qualitymetrics/`
Schema URL `http://mytorrentserver/rundb/api/v1/qualitymetrics/schema/`

Resource Fields

field	help text	default	nullable	re
q0_reads	Integer data. Ex: 2673	n/a	false	fa
q17_max_read_length	Integer data. Ex: 2673	n/a	false	fa
q20_median_read_length	Integer data. Ex: 2673	0	false	fa
q20_reads	Integer data. Ex: 2673	n/a	false	fa
report	A single related resource. Can be either a URI or set of nested resource data.	n/a	false	fa
q17_mean_read_length	Floating point numeric data. Ex: 26.73	n/a	false	fa
q17_100bp_reads	Integer data. Ex: 2673	n/a	false	fa
resource_uri	Unicode string data. Ex: “Hello World”	n/a	false	tr
q0_max_read_length	Integer data. Ex: 2673	n/a	false	fa
q20_100bp_reads	Integer data. Ex: 2673	n/a	false	fa
id	Integer data. Ex: 2673		false	fa
q20_mean_read_length	Integer data. Ex: 2673	n/a	false	fa
q20_150bp_reads	Integer data. Ex: 2673	n/a	false	fa
q0_bases	Unicode string data. Ex: “Hello World”	n/a	false	fa
q20_50bp_reads	Integer data. Ex: 2673	n/a	false	fa
q17_reads	Integer data. Ex: 2673	n/a	false	fa
q17_50bp_reads	Integer data. Ex: 2673	n/a	false	fa
q17_median_read_length	Integer data. Ex: 2673	0	false	fa
q0_50bp_reads	Integer data. Ex: 2673	n/a	false	fa
q17_150bp_reads	Integer data. Ex: 2673	n/a	false	fa
q0_150bp_reads	Integer data. Ex: 2673	0	false	fa
q0_mean_read_length	Floating point numeric data. Ex: 26.73	n/a	false	fa
q17_bases	Unicode string data. Ex: “Hello World”	n/a	false	fa
q0_mode_read_length	Integer data. Ex: 2673	0	false	fa
q20_mode_read_length	Integer data. Ex: 2673	0	false	fa
q20_max_read_length	Floating point numeric data. Ex: 26.73	n/a	false	fa
q20_bases	Unicode string data. Ex: “Hello World”	n/a	false	fa
q0_median_read_length	Integer data. Ex: 2673	0	false	fa
q0_100bp_reads	Integer data. Ex: 2673	n/a	false	fa
q17_mode_read_length	Integer data. Ex: 2673	0	false	fa

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 6,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/qualitymetrics/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "q0_reads": 93969124,
            "q17_max_read_length": 361,
            "q20_median_read_length": 149,
            "q20_reads": 93969124,
            "report": "/rundb/api/v1/results/3/",
            "q17_mean_read_length": 149.579903660696,
            "q17_100bp_reads": 82389255,
            "resource_uri": "/rundb/api/v1/qualitymetrics/1/",
            "q0_max_read_length": 361,
```

```
            "q20_100bp_reads": 82389255,
            "id": 1,
            "q20_mean_read_length": 149,
            "q20_150bp_reads": 46834701,
            "q0_bases": "14055892515",
            "q20_50bp_reads": 91801424,
            "q17_reads": 93969124,
            "q17_50bp_reads": 91801424,
            "q17_median_read_length": 149,
            "q0_50bp_reads": 91801424,
            "q17_150bp_reads": 46834701,
            "q0_150bp_reads": 46834701,
            "q0_mean_read_length": 149.579903660696,
            "q17_bases": "12627160533",
            "q0_mode_read_length": 141,
            "q20_mode_read_length": 141,
            "q20_max_read_length": 361,
            "q20_bases": "11916010889",
            "q0_median_read_length": 149,
            "q0_100bp_reads": 82389255,
            "q17_mode_read_length": 141
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Reference Genome Resource

Resource URL `http://mytorrentserver/rundb/api/v1/referencegenome/`
Schema URL `http://mytorrentserver/rundb/api/v1/referencegenome/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
status	Unicode string data. Ex: "Hello World"		false	false	true	false	string
reference_path	Unicode string data. Ex: "Hello World"		false	false	true	false	string
name	Unicode string data. Ex: "Hello World"	n/a	false	false	false	false	string
short_name	Unicode string data. Ex: "Hello World"	n/a	false	false	false	false	string
index_version	Unicode string data. Ex: "Hello World"		false	false	true	false	string
notes	Unicode string data. Ex: "Hello World"		false	false	true	false	string
enabled	Boolean data. Ex: True	true	false	false	true	false	boolean
species	Unicode string data. Ex: "Hello World"		false	false	true	false	string
identity_hash	Unicode string data. Ex: "Hello World"	None	true	false	false	false	string
source	Unicode string data. Ex: "Hello World"		false	false	true	false	string
version	Unicode string data. Ex: "Hello World"		false	false	true	false	string
celery_task_id	Unicode string data. Ex: "Hello World"		false	false	true	false	string
date	A date & time as a string. Ex: "2010-11-10T03:07:43"	2018-06-19T20:40:12.000844+00:00	false	false	false	false	date-time
verbose_error	Unicode string data. Ex: "Hello World"		false	false	true	false	string
id	Integer data. Ex: 2673		false	false	true	true	integer
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 6,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/referencegenome/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "status": "complete",
            "reference_path": "/results/referenceLibrary/tmap-f3/AmpliSeq_Mouse_
↪Transcriptome_v1",
            "name": "AmpliSeq Mouse Transcriptome v1",
            "short_name": "AmpliSeq_Mouse_Transcriptome_v1",
```

```
            "index_version": "tmap-f3",
            "notes": "",
            "enabled": true,
            "species": "",
            "identity_hash": "92e672f416392e46e3137388d878efe7",
            "source": "http://ionupdates.com/reference_downloads/AmpliSeq_Mouse_
↪Transcriptome_v1.zip",
            "version": "",
            "celery_task_id": "370dd08d-d9d0-4f9f-8965-d0563a4461b7",
            "date": "2018-01-23T22:42:16.000613+00:00",
            "verbose_error": "",
            "id": 4,
            "resource_uri": "/rundb/api/v1/referencegenome/4/"
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Results Resource

Resource URL `http://mytorrentserver/rundb/api/v1/results/`
Schema URL `http://mytorrentserver/rundb/api/v1/results/schema/`

Resource Fields

field	help text	default	nul
reference	Unicode string data. Ex: “Hello World”	n/a	true
processedflows	Integer data. Ex: 2673	n/a	fals
reportStatus	Unicode string data. Ex: “Hello World”	Nothing	true

Table 2.21 – continued from previous page

field	help text	default	nul
reportstorage	A single related resource. Can be either a URI or set of nested resource data.	n/a	fals
analysisVersion	Unicode string data. Ex: “Hello World”	n/a	fals
runid	Unicode string data. Ex: “Hello World”		fals
id	Integer data. Ex: 2673		fals
filesystempath	Unicode string data. Ex: “Hello World”	n/a	fals
metaData	Unicode string data. Ex: “Hello World”	{}	fals
log	Unicode string data. Ex: “Hello World”		fals
timeStamp	A date & time as a string. Ex: “2010-11-10T03:07:43”	true	fals
libmetrics	Many related resources. Can be either a list of URIs or list of individually nested resource data.	n/a	fals
experiment	A single related resource. Can be either a URI or set of nested resource data.	n/a	true
resultsName	Unicode string data. Ex: “Hello World”	n/a	fals
status	Unicode string data. Ex: “Hello World”	n/a	fals
planShortID	Unicode string data. Ex: “Hello World”	n/a	fals
processedCycles	Integer data. Ex: 2673	n/a	fals
bamLink	Unicode string data. Ex: “Hello World”	n/a	fals
representative	Boolean data. Ex: True	false	fals
pluginState	A dictionary of data. Ex: {‘price’: 26.73, ‘name’: ‘Daniel’}	n/a	fals
qualitymetrics	Many related resources. Can be either a list of URIs or list of individually nested resource data.	n/a	fals
diskusage	Integer data. Ex: 2673	n/a	true
eas	A single related resource. Can be either a URI or set of nested resource data.	n/a	true
projects	Many related resources. Can be either a list of URIs or list of individually nested resource data.	n/a	fals
pluginStore	A dictionary of data. Ex: {‘price’: 26.73, ‘name’: ‘Daniel’}	n/a	fals
resultsType	Unicode string data. Ex: “Hello World”		fals
tfmetrics	Many related resources. Can be either a list of URIs or list of individually nested resource data.	n/a	fals
parentIDs	Unicode string data. Ex: “Hello World”		fals
analysismetrics	Many related resources. Can be either a list of URIs or list of individually nested resource data.	n/a	fals
timeToComplete	Unicode string data. Ex: “Hello World”	n/a	fals
reportLink	Unicode string data. Ex: “Hello World”	n/a	fals
pluginresults	Many related resources. Can be either a list of URIs or list of individually nested resource data.	n/a	fals
framesProcessed	Integer data. Ex: 2673	n/a	fals
autoExempt	Boolean data. Ex: True	false	fals
resource_uri	Unicode string data. Ex: “Hello World”	n/a	fals

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 7,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/results/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "reference": "",
            "processedflows": 0,
            "reportStatus": "Nothing",
            "reportstorage": {
                "name": "Home",
                "default": true,
```

```
                "webServerPath": "/output",
                "dirPath": "/results/analysis/output",
                "id": 1,
                "resource_uri": ""
            },
            "analysisVersion": "db:5.6.18-1,an:5.6.5-1,",
            "runid": "MJMQ3",
            "id": 3,
            "filesystempath": "/results/analysis/output/Home/Auto_S5-540_
↪WholeTranscriptomeRNA_91_003",
            "metaData": {},
            "log": "/output/Home/Auto_S5-540_WholeTranscriptomeRNA_91_003/log.html",
            "timeStamp": "2017-07-22T13:15:56.000197+00:00",
            "libmetrics": [
                "/rundb/api/v1/libmetrics/1/"
            ],
            "experiment": "/rundb/api/v1/experiment/91/",
            "resultsName": "Auto_S5-540_WholeTranscriptomeRNA_91",
            "status": "Completed",
            "planShortID": "RI63N",
            "processedCycles": 0,
            "bamLink": "/output/Home/Auto_S5-540_WholeTranscriptomeRNA_91_003/
↪download_links/S5-540_WholeTranscriptomeRNA_Auto_S5-540_WholeTranscriptomeRNA_91.bam
↪",
            "representative": false,
            "qualitymetrics": [
                "/rundb/api/v1/qualitymetrics/1/"
            ],
            "diskusage": 229301,
            "eas": "/rundb/api/v1/experimentanalysissettings/90/",
            "projects": [
                "/rundb/api/v1/project/1/"
            ],
            "resultsType": "",
            "tfmetrics": [
                "/rundb/api/v1/tfmetrics/2/",
                "/rundb/api/v1/tfmetrics/1/"
            ],
            "parentIDs": "",
            "analysismetrics": [
                "/rundb/api/v1/analysismetrics/1/"
            ],
            "timeToComplete": "0",
            "reportLink": "/output/Home/Auto_S5-540_WholeTranscriptomeRNA_91_003/",
            "pluginresults": [
                "/rundb/api/v1/pluginresult/9/",
                "/rundb/api/v1/pluginresult/8/",
                "/rundb/api/v1/pluginresult/3/"
            ],
            "framesProcessed": 0,
            "autoExempt": false,
            "resource_uri": "/rundb/api/v1/results/3/"
        }
    ]
}
```

Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Rig Resource

Resource URL `http://mytorrentserver/rundb/api/v1/rig/`
Schema URL `http://mytorrentserver/rundb/api/v1/rig/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
display_state	Unicode string data. Ex: "Hello World"		false	false	true	false	string
name	Unicode string data. Ex: "Hello World"	n/a	false	false	false	true	string
state	Unicode string data. Ex: "Hello World"		false	false	true	false	string
version	Unicode string data. Ex: "Hello World"	{}	false	false	true	false	string
ftprootdir	Unicode string data. Ex: "Hello World"	results	false	false	false	false	string
last_clean_date	Unicode string data. Ex: "Hello World"		false	false	true	false	string
updatehome	Unicode string data. Ex: "Hello World"	192.168.201.1	false	false	false	false	string
ftpserver	Unicode string data. Ex: "Hello World"	192.168.201.1	false	false	false	false	string
comments	Unicode string data. Ex: "Hello World"		false	false	true	false	string
last_experiment	Unicode string data. Ex: "Hello World"		false	false	true	false	string
ftppassword	Unicode string data. Ex: "Hello World"	ionguest	false	false	false	false	string
updateflag	Boolean data. Ex: True	false	false	false	true	false	boolean
location	A single related resource. Can be either a URI or set of nested resource data.	n/a	true	false	true	false	related
last_init_date	Unicode string data. Ex: "Hello World"		false	false	true	false	string
updateCommand	Unicode string data. Ex: "Hello World"	{}	false	false	true	false	string
alarms	Unicode string data. Ex: "Hello World"	{}	false	false	true	false	string
serial	Unicode string data. Ex: "Hello World"	n/a	true	false	false	false	string
host_address	Unicode string data. Ex: "Hello World"		false	false	true	false	string
type	Unicode string data. Ex: "Hello World"		false	false	true	false	string
ftpusername	Unicode string data. Ex: "Hello World"	ionguest	false	false	false	false	string
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 4,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/rig/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "display_state": "",
            "name": "default",
            "state": "",
            "version": {},
            "ftprootdir": "results",
            "last_clean_date": "",
            "updatehome": "192.168.201.1",
            "ftpserver": "192.168.201.1",
```

```
            "comments": "This is a model PGM.  Do not delete.",
            "last_experiment": "",
            "ftppassword": "ionguest",
            "updateflag": false,
            "location": {
                "name": "Home",
                "resource_uri": "/rundb/api/v1/location/1/",
                "defaultlocation": true,
                "comments": "",
                "id": 1
            },
            "last_init_date": "",
            "updateCommand": {},
            "alarms": {},
            "serial": null,
            "host_address": "",
            "type": "",
            "ftpusername": "ionguest",
            "resource_uri": "/rundb/api/v1/rig/default/"
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Run Type Resource

Resource URL `http://mytorrentserver/rundb/api/v1/runtype/`
Schema URL `http://mytorrentserver/rundb/api/v1/runtype/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
applicationGroups	Many related resources. Can be either a list of URIs or list of individually nested resource data.	n/a	true	false	false	false	related
description	Unicode string data. Ex: "Hello World"		false	false	true	false	string
nucleotideType	Unicode string data. Ex: "Hello World"	dna	false	false	true	false	string
barcode	Unicode string data. Ex: "Hello World"		false	false	true	false	string
meta	Unicode string data. Ex: "Hello World"		true	false	false	false	string
alternate_name	Unicode string data. Ex: "Hello World"		true	false	false	false	string
runType	Unicode string data. Ex: "Hello World"	n/a	false	false	false	true	string
id	Integer data. Ex: 2673		false	false	true	true	integer
isActive	Boolean data. Ex: True	true	false	false	true	false	boolean
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 15,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/runtype/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "applicationGroups": [
                "/rundb/api/v1/applicationgroup/1/",
                "/rundb/api/v1/applicationgroup/3/",
                "/rundb/api/v1/applicationgroup/4/"
            ],
            "description": "Generic Sequencing",
            "nucleotideType": "dna",
            "barcode": "",
            "meta": {},
            "alternate_name": "Other",
            "runType": "GENS",
            "id": 1,
            "isActive": true,
            "resource_uri": "/rundb/api/v1/runtype/1/"
        }
    ]
}
```

Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Sample Resource

Resource URL `http://mytorrentserver/rundb/api/v1/sample/`
Schema URL `http://mytorrentserver/rundb/api/v1/sample/schema/`

Resource Fields

field	help text	default	nullable	readonly	blank	unique	type
status	Unicode string data. Ex: "Hello World"		false	false	true	false	string
sampleSets	Many related resources. Can be either a list of URIs or list of individually nested resource data.	n/a	true	false	true	false	related
description	Unicode string data. Ex: "Hello World"	n/a	true	false	false	false	string
displayedName	Unicode string data. Ex: "Hello World"	n/a	true	false	false	false	string
experiments	Many related resources. Can be either a list of URIs or list of individually nested resource data.	n/a	true	false	true	false	related
externalId	Unicode string data. Ex: "Hello World"		true	false	false	false	string
date	A date & time as a string. Ex: "2010-11-10T03:07:43"	true	true	false	false	false	datetime
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string
id	Integer data. Ex: 2673		false	false	true	true	integer
name	Unicode string data. Ex: "Hello World"	n/a	true	false	false	false	string

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 23,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/sample/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "status": "run",
            "sampleSets": [],
            "description": null,
            "displayedName": "e5272-wfa-l165",
            "experiments": [
                "/rundb/api/v1/experiment/94/"
            ],
            "externalId": "",
            "date": "2017-08-23T21:42:01.000299+00:00",
            "resource_uri": "/rundb/api/v1/sample/4/",
            "id": 4,
            "name": "e5272-wfa-l165"
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT

Allowed detail HTTP methods

- GET
- POST
- PUT

Sample Annotation Cv Resource

Resource URL `http://mytorrentserver/rundb/api/v1/sampleannotation_cv/`
Schema URL `http://mytorrentserver/rundb/api/v1/sampleannotation_cv/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
annotationType	Unicode string data. Ex: "Hello World"	n/a	false	false	false	false	string
uid	Unicode string data. Ex: "Hello World"	n/a	false	false	false	true	string
isIRCompatible	Boolean data. Ex: True	false	false	false	true	false	boolean
sampleGroupType_CV	A single related resource. Can be either a URI or set of nested resource data.	n/a	true	false	true	false	related
value	Unicode string data. Ex: "Hello World"		false	false	true	false	string
iRValue	Unicode string data. Ex: "Hello World"	n/a	true	false	false	false	string
iRAnnotationType	Unicode string data. Ex: "Hello World"	n/a	true	false	false	false	string
id	Integer data. Ex: 2673		false	false	true	true	integer
isActive	Boolean data. Ex: True	true	false	false	true	false	boolean
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 50,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/sampleannotation_cv/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "annotationType": "relationshipRole",
            "uid": "SAMPLEANNOTATE_CV_0006",
            "isIRCompatible": true,
            "sampleGroupType_CV": "/rundb/api/v1/samplegrouptype_cv/4/",
            "value": "Father",
            "iRValue": "Father",
            "iRAnnotationType": "Relation",
            "id": 6,
            "isActive": true,
            "resource_uri": "/rundb/api/v1/sampleannotation_cv/6/"
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT

- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Sample Attribute Resource

Resource URL `http://mytorrentserver/rundb/api/v1/sampleattribute/`
Schema URL `http://mytorrentserver/rundb/api/v1/sampleattribute/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
description	Unicode string data. Ex: “Hello World”	n/a	true	false	false	false	string
dataType_name	Unicode string data. Ex: “Hello World”	n/a	true	true	true	false	string
dataType	A single related resource. Can be either a URI or set of nested resource data.	n/a	true	false	true	false	related
displayedName	Unicode string data. Ex: “Hello World”	n/a	false	false	false	true	string
isMandatory	Boolean data. Ex: True	false	false	false	true	false	boolean
sampleCount	Integer data. Ex: 2673	n/a	false	true	false	false	integer
lastModifiedDate	A date & time as a string. Ex: “2010-11-10T03:07:43”	true	false	false	true	false	datetime
creationDate	A date & time as a string. Ex: “2010-11-10T03:07:43”	true	false	false	true	false	datetime
id	Integer data. Ex: 2673		false	false	true	true	integer
isActive	Boolean data. Ex: True	true	false	false	true	false	boolean
resource_uri	Unicode string data. Ex: “Hello World”	n/a	false	true	false	false	string

Example Response

```
{
    "meta": {
        "previous": null,
        "total_count": 0,
```

```
        "offset": 0,
        "limit": 1,
        "next": null
    },
    "objects": []
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Sample Attribute Data Type Resource

Resource URL `http://mytorrentserver/rundb/api/v1/sampleattributedatatype/`
Schema URL `http://mytorrentserver/rundb/api/v1/sampleattributedatatype/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
dataType	Unicode string data. Ex: "Hello World"	n/a	false	false	false	true	string
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string
description	Unicode string data. Ex: "Hello World"	n/a	true	false	false	false	string
isActive	Boolean data. Ex: True	true	false	false	true	false	boolean
id	Integer data. Ex: 2673		false	false	true	true	integer

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 2,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/sampleattributedatatype/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "dataType": "Text",
            "resource_uri": "/rundb/api/v1/sampleattributedatatype/1/",
            "description": "Up to 1024 characters",
            "isActive": true,
            "id": 1
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Sample Group Type Cv Resource

Resource URL `http://mytorrentserver/rundb/api/v1/samplegrouptype_cv/`
Schema URL `http://mytorrentserver/rundb/api/v1/samplegrouptype_cv/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
isIRCompatible	Boolean data. Ex: True	false	false	false	true	false	boolean
description	Unicode string data. Ex: "Hello World"	n/a	true	false	false	false	string
sampleAnnotation_set	Many related resources. Can be either a list of URIs or list of individually nested resource data.	n/a	true	false	true	false	related
displayedName	Unicode string data. Ex: "Hello World"	n/a	false	false	false	true	string
iRValue	Unicode string data. Ex: "Hello World"	n/a	true	false	false	false	string
iRAnnotationType	Unicode string data. Ex: "Hello World"	n/a	true	false	false	false	string
uid	Unicode string data. Ex: "Hello World"	n/a	false	false	false	true	string
sampleSets	Many related resources. Can be either a list of URIs or list of individually nested resource data.	n/a	true	false	true	false	related
id	Integer data. Ex: 2673		false	false	true	true	integer
isActive	Boolean data. Ex: True	true	false	false	true	false	boolean
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 7,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/samplegrouptype_cv/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "isIRCompatible": true,
            "description": "",
            "sampleAnnotation_set": [
                "/rundb/api/v1/sampleannotation_cv/1/",
                "/rundb/api/v1/sampleannotation_cv/2/"
            ],
            "displayedName": "Sample_Control",
            "iRValue": "Paired_Sample|Sample_Control",
            "iRAnnotationType": "RelationshipType",
            "uid": "SAMPLEGROUP_CV_0001",
            "sampleSets": [],
            "id": 1,
            "isActive": true,
            "resource_uri": "/rundb/api/v1/samplegrouptype_cv/1/"
        }
    ]
}
```

Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Sample Prep Data Resource

Resource URL `http://mytorrentserver/rundb/api/v1/sampleprepdata/`
Schema URL `http://mytorrentserver/rundb/api/v1/sampleprepdata/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
instrumentName	Unicode string data. Ex: "Hello World"		false	false	true	false	string
kitType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
tipRackBarcode	Unicode string data. Ex: "Hello World"		false	false	true	false	string
remainingSeconds	Integer data. Ex: 2673	n/a	true	false	false	false	integer
reagentsExpiration	Unicode string data. Ex: "Hello World"		false	false	true	false	string
instrumentStatus	Unicode string data. Ex: "Hello World"		false	false	true	false	string
solutionsExpiration	Unicode string data. Ex: "Hello World"		false	false	true	false	string
message	Unicode string data. Ex: "Hello World"		false	false	true	false	string
id	Integer data. Ex: 2673		false	false	true	true	integer
reagentsPart	Unicode string data. Ex: "Hello World"		false	false	true	false	string
packageVer	Unicode string data. Ex: "Hello World"		false	false	true	false	string
progress	Floating point numeric data. Ex: 26.73	0	false	false	true	false	float
lastUpdate	A date & time as a string. Ex: "2010-11-10T03:07:43"	n/a	true	false	false	false	datetime
logPath	Unicode string data. Ex: "Hello World"	n/a	true	false	false	false	string
solutionsLot	Unicode string data. Ex: "Hello World"		false	false	true	false	string
scriptVersion	Unicode string data. Ex: "Hello World"		false	false	true	false	string
startTime	A date & time as a string. Ex: "2010-11-10T03:07:43"	n/a	true	false	false	false	datetime
operationMode	Unicode string data. Ex: "Hello World"		false	false	true	false	string
samplePrepDataType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
solutionsPart	Unicode string data. Ex: "Hello World"		false	false	true	false	string
reagentsLot	Unicode string data. Ex: "Hello World"		false	false	true	false	string
endTime	A date & time as a string. Ex: "2010-11-10T03:07:43"	n/a	true	false	false	false	datetime
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 0,
        "offset": 0,
        "limit": 1,
        "next": null
    },
    "objects": []
}
```

Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Sample Set Resource

Resource URL `http://mytorrentserver/rundb/api/v1/sampleset/`
Schema URL `http://mytorrentserver/rundb/api/v1/sampleset/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
status	Unicode string data. Ex: "Hello World"		false	false	true	false	string
libraryPrepInstrument	Unicode string data. Ex: "Hello World"		false	false	true	false	string
libraryPrepType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
libraryPrepPlateType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
description	Unicode string data. Ex: "Hello World"	n/a	true	false	false	false	string
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string
sampleCount	Integer data. Ex: 2673	n/a	false	true	false	false	integer
displayedName	Unicode string data. Ex: "Hello World"	n/a	false	false	false	true	string
SampleGroupType_CV	A single related resource. Can be either a URI or set of nested resource data.	n/a	true	false	true	false	related
pcrPlateSerialNum	Unicode string data. Ex: "Hello World"		true	false	false	false	string
libraryPrepInstrumentData	A single related resource. Can be either a URI or set of nested resource data.	n/a	true	false	true	false	related
libraryPrepKitName	Unicode string data. Ex: "Hello World"	n/a	true	false	false	false	string
samples	Many related resources. Can be either a list of URIs or list of individually nested resource data.	n/a	true	false	true	false	related
lastModifiedDate	A date & time as a string. Ex: "2010-11-10T03:07:43"	true	false	false	true	false	datetime
sampleGroupTypeName	Unicode string data. Ex: "Hello World"	n/a	true	true	true	false	string
combinedLibraryTubeLabel	Unicode string data. Ex: "Hello World"		false	false	true	false	string
creationDate	A date & time as a string. Ex: "2010-11-10T03:07:43"	true	false	false	true	false	datetime
libraryPrepTypeDisplayedName	Unicode string data. Ex: "Hello World"	n/a	true	true	true	false	string
id	Integer data. Ex: 2673		false	false	true	true	integer
libraryPrepKitDisplayedName	Unicode string data. Ex: "Hello World"	n/a	true	true	true	false	string

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 2,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/sampleset/?offset=1&limit=1&format=json"
```

```
    },
    "objects": [
        {
            "readyForPlanning": true,
            "status": "created",
            "libraryPrepInstrument": "",
            "libraryPrepType": "",
            "libraryPrepPlateType": "",
            "description": "",
            "resource_uri": "/rundb/api/v1/sampleset/1/",
            "sampleCount": 8,
            "displayedName": "Ampliseq on Chef",
            "SampleGroupType_CV": null,
            "pcrPlateSerialNum": "",
            "libraryPrepInstrumentData": null,
            "libraryPrepKitName": "",
            "samples": [
                "/rundb/api/v1/samplesetitem/3/",
                "/rundb/api/v1/samplesetitem/5/",
                "/rundb/api/v1/samplesetitem/7/",
                "/rundb/api/v1/samplesetitem/9/",
                "/rundb/api/v1/samplesetitem/11/",
                "/rundb/api/v1/samplesetitem/13/",
                "/rundb/api/v1/samplesetitem/15/",
                "/rundb/api/v1/samplesetitem/17/"
            ],
            "lastModifiedDate": "2017-08-28T21:21:14.000027+00:00",
            "sampleGroupTypeName": "",
            "combinedLibraryTubeLabel": "",
            "creationDate": "2017-08-28T21:21:14.000027+00:00",
            "libraryPrepTypeDisplayedName": "",
            "id": 1,
            "libraryPrepKitDisplayedName": ""
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE

- PATCH

Sample Set Item Resource

Resource URL `http://mytorrentserver/rundb/api/v1/samplesetitem/`
Schema URL `http://mytorrentserver/rundb/api/v1/samplesetitem/schema/`

Resource Fields

field	help text	default	nullable	readonly	blank	unique	type
sample	A single related resource. Can be either a URI or set of nested resource data.	n/a	true	false	true	false	related
cellNum	Unicode string data. Ex: “Hello World”		true	false	false	false	string
biopsyDays	Integer data. Ex: 2673	0	true	false	false	false	integer
resource_uri	Unicode string data. Ex: “Hello World”	n/a	false	true	false	false	string
nucleotideType	Unicode string data. Ex: “Hello World”		false	false	true	false	string
gender	Unicode string data. Ex: “Hello World”	n/a	true	false	false	false	string
relationshipGroup	Integer data. Ex: 2673	n/a	false	false	false	false	integer
coupleId	Unicode string data. Ex: “Hello World”		true	false	false	false	string
cellularityPct	Integer data. Ex: 2673	n/a	true	false	false	false	integer
id	Integer data. Ex: 2673		false	false	true	true	integer
relationshipRole	Unicode string data. Ex: “Hello World”	n/a	true	false	false	false	string
pcrPlateColumn	Unicode string data. Ex: “Hello World”		true	false	false	false	string
cancerType	Unicode string data. Ex: “Hello World”	n/a	true	false	false	false	string
controlType	Unicode string data. Ex: “Hello World”		true	false	false	false	string
sampleSet	A single related resource. Can be either a URI or set of nested resource data.	n/a	true	false	true	false	related
lastModifiedDate	A date & time as a string. Ex: “2010-11-10T03:07:43”	true	false	false	true	false	datetime
dnabarcode	A single related resource. Can be either a URI or set of nested resource data.	n/a	true	false	true	false	related
pcrPlateRow	Unicode string data. Ex: “Hello World”		true	false	false	false	string
creationDate	A date & time as a string. Ex: “2010-11-10T03:07:43”	true	false	false	true	false	datetime
embryoId	Unicode string data. Ex: “Hello World”		true	false	false	false	string
description	Unicode string data. Ex: “Hello World”		true	false	false	false	string

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 16,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/samplesetitem/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "sample": "/rundb/api/v1/sample/8/",
            "cellNum": "",
            "biopsyDays": 0,
            "resource_uri": "/rundb/api/v1/samplesetitem/3/",
            "nucleotideType": "",
            "gender": "",
            "relationshipGroup": 0,
            "coupleId": "",
            "cellularityPct": null,
            "id": 3,
            "relationshipRole": "",
            "pcrPlateColumn": "",
            "cancerType": "",
            "controlType": "",
            "sampleSet": "/rundb/api/v1/sampleset/1/",
            "lastModifiedDate": "2017-11-01T16:19:12.000420+00:00",
            "dnabarcode": null,
            "pcrPlateRow": "",
            "creationDate": "2017-11-01T16:19:12.000420+00:00",
            "embryoId": "",
            "description": ""
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE

- PATCH

Sample Set Item Info Resource

Resource URL `http://mytorrentserver/rundb/api/v1/samplesetiteminfo/`
Schema URL `http://mytorrentserver/rundb/api/v1/samplesetiteminfo/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
relationshipGroup	Integer data. Ex: 2673	n/a	true	true	true	false	integer
sampleDescription	Unicode string data. Ex: "Hello World"	n/a	true	true	true	false	string
dnabarcodeKit	Unicode string data. Ex: "Hello World"	n/a	true	true	true	false	string
sample	A single related resource. Can be either a URI or set of nested resource data.	n/a	true	false	true	false	related
pcrPlateColumn	Unicode string data. Ex: "Hello World"		true	false	false	false	string
cancerType	Unicode string data. Ex: "Hello World"	n/a	true	false	false	false	string
id	Integer data. Ex: 2673		false	false	true	true	integer
sampleDisplayedName	Unicode string data. Ex: "Hello World"	n/a	true	true	true	false	string
cellNum	Unicode string data. Ex: "Hello World"		true	false	false	false	string
sampleExternalId	Unicode string data. Ex: "Hello World"	n/a	true	true	true	false	string
coupleId	Unicode string data. Ex: "Hello World"		true	false	false	false	string
pcrPlateRow	Unicode string data. Ex: "Hello World"		true	false	false	false	string
sampleSetPk	Integer data. Ex: 2673	n/a	true	true	true	false	integer
sampleSetStatus	Unicode string data. Ex: "Hello World"	n/a	true	true	true	false	string
embryoId	Unicode string data. Ex: "Hello World"		true	false	false	false	string
sampleSet	A single related resource. Can be either a URI or set of nested resource data.	n/a	true	false	true	false	related
description	Unicode string data. Ex: "Hello World"		true	false	false	false	string
lastModifiedDate	A date & time as a string. Ex: "2010-11-10T03:07:43"	true	false	false	true	false	datetime
relationshipRole	Unicode string data. Ex: "Hello World"	n/a	true	true	true	false	string
samplePk	Integer data. Ex: 2673	n/a	true	true	true	false	integer
dnabarcode	A single related resource. Can be either a URI or set of nested resource data.	n/a	true	true	true	false	related
creationDate	A date & time as a string. Ex: "2010-11-10T03:07:43"	true	false	false	true	false	datetime
biopsyDays	Integer data. Ex: 2673	0	true	false	false	false	integer
nucleotideType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
gender	Unicode string data. Ex: "Hello World"	n/a	true	false	false	false	string
cellularityPct	Integer data. Ex: 2673	n/a	true	false	false	false	integer
controlType	Unicode string data. Ex: "Hello World"		true	false	false	false	string
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 16,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/samplesetiteminfo/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "relationshipGroup": 0,
            "sampleDescription": "",
            "dnabarcodeKit": "",
            "sample": "/rundb/api/v1/sample/8/",
            "pcrPlateColumn": "",
            "cancerType": "",
            "attribute_dict": {},
            "id": 3,
            "sampleDisplayedName": "1",
            "cellNum": "",
            "sampleExternalId": "",
            "coupleId": "",
            "pcrPlateRow": "",
            "sampleSetPk": 1,
            "sampleSetStatus": "created",
            "embryoId": "",
            "sampleSet": "/rundb/api/v1/sampleset/1/",
            "description": "",
            "lastModifiedDate": "2017-11-01T16:19:12.000420+00:00",
            "sampleSetGroupType": "",
            "relationshipRole": "",
            "samplePk": 8,
            "dnabarcode": "",
            "creationDate": "2017-11-01T16:19:12.000420+00:00",
            "biopsyDays": 0,
            "nucleotideType": "",
            "gender": "",
            "cellularityPct": null,
            "controlType": "",
            "resource_uri": "/rundb/api/v1/samplesetiteminfo/3/"
        }
    ]
}
```


Allowed list HTTP methods

- GET

Allowed detail HTTP methods

- GET

Sequencing Kit Info Resource

Resource URL `http://mytorrentserver/rundb/api/v1/sequencingkitinfo/`
Schema URL `http://mytorrentserver/rundb/api/v1/sequencingkitinfo/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
isActive	Boolean data. Ex: True	true	false	false	true	false	boolean
samplePrep_instrumentType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
kitType	Unicode string data. Ex: "Hello World"	n/a	false	false	false	false	string
defaultFlowOrder	A single related resource. Can be either a URI or set of nested resource data.	n/a	true	false	false	false	related
name	Unicode string data. Ex: "Hello World"	n/a	false	false	false	true	string
nucleotideType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
defaultCartridgeUsageCount	Integer data. Ex: 2673	n/a	true	false	false	false	integer
instrumentType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
chipTypes	Unicode string data. Ex: "Hello World"		false	false	true	false	string
runMode	Unicode string data. Ex: "Hello World"		false	false	true	false	string
parts	Many related resources. Can be either a list of URIs or list of individually nested resource data.	n/a	false	false	false	false	related
flowCount	Integer data. Ex: 2673	n/a	false	false	false	false	integer
applicationType	Unicode string data. Ex: "Hello World"		true	false	false	false	string
cartridgeExpirationDayLimit	Integer data. Ex: 2673	n/a	true	false	false	false	integer
libraryReadLength	Integer data. Ex: 2673	0	false	false	false	false	integer
cartridgeBetweenUsageAbsoluteMaxDayLimit	Integer data. Ex: 2673	n/a	true	false	false	false	integer
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string
uid	Unicode string data. Ex: "Hello World"	n/a	false	false	false	true	string
id	Integer data. Ex: 2673		false	false	true	true	integer
categories	Unicode string data. Ex: "Hello World"		true	false	false	false	string
description	Unicode string data. Ex: "Hello World"		false	false	true	false	string

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 28,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/sequencingkitinfo/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "isActive": true,
            "samplePrep_instrumentType": "OT_IC",
            "kitType": "SequencingKit",
            "defaultFlowOrder": null,
            "name": "IonPGMInstallKit",
            "nucleotideType": "",
            "defaultCartridgeUsageCount": null,
            "instrumentType": "pgm",
            "chipTypes": "",
            "runMode": "",
            "parts": [
                {
                    "barcode": "4480217",
                    "id": 20019,
                    "resource_uri": "/rundb/api/v1/kitpart/20019/",
                    "kit": "/rundb/api/v1/kitinfo/20020/"
                },
                {
                    "barcode": "4480282",
                    "id": 20020,
                    "resource_uri": "/rundb/api/v1/kitpart/20020/",
                    "kit": "/rundb/api/v1/kitinfo/20020/"
                },
                {
                    "barcode": "4480284",
                    "id": 20021,
                    "resource_uri": "/rundb/api/v1/kitpart/20021/",
                    "kit": "/rundb/api/v1/kitinfo/20020/"
                }
            ],
            "flowCount": 100,
            "applicationType": "",
            "cartridgeExpirationDayLimit": null,
            "libraryReadLength": 0,
            "cartridgeBetweenUsageAbsoluteMaxDayLimit": null,
            "resource_uri": "/rundb/api/v1/sequencingkitinfo/20020/",
            "uid": "SEQ0006",
            "id": 20020,
            "categories": "readLengthDerivableFromFlows;",
            "description": "Ion PGM Install Kit"
        }
    ]
}
```

Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Sequencing Kit Part Resource

Resource URL `http://mytorrentserver/rundb/api/v1/sequencingkitpart/`
Schema URL `http://mytorrentserver/rundb/api/v1/sequencingkitpart/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string
barcode	Unicode string data. Ex: "Hello World"	n/a	false	false	false	true	string
defaultFlowOrder	A single related resource. Can be either a URI or set of nested resource data.	n/a	true	false	false	false	related
kit	A single related resource. Can be either a URI or set of nested resource data.	n/a	false	false	false	false	related
id	Integer data. Ex: 2673		false	false	true	true	integer

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 104,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/sequencingkitpart/?offset=1&limit=1&format=json"
```

```
    },
    "objects": [
        {
            "resource_uri": "/rundb/api/v1/sequencingkitpart/20021/",
            "barcode": "4480284",
            "defaultFlowOrder": null,
            "kit": "/rundb/api/v1/kitinfo/20020/",
            "id": 20021
        }
    ]
}
```


Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Support Upload Resource

Resource URL `http://mytorrentserver/rundb/api/v1/supportupload/`
Schema URL `http://mytorrentserver/rundb/api/v1/supportupload/schema/`

Resource Fields

field	help text	default	nullable	readonly	blank	unique	type
ticket_id	Unicode string data. Ex: "Hello World"		false	false	true	false	string
updated	A date & time as a string. Ex: "2010-11-10T03:07:43"	true	false	false	true	false	datetime
local_message	Unicode string data. Ex: "Hello World"		false	false	true	false	string
description	Unicode string data. Ex: "Hello World"		false	false	false	false	string
created	A date & time as a string. Ex: "2010-11-10T03:07:43"	true	false	false	true	false	datetime
ticket_status	Unicode string data. Ex: "Hello World"		false	false	true	false	string
contact_email	Unicode string data. Ex: "Hello World"		false	false	false	false	string
result	A single related resource. Can be either a URI or set of nested resource data.	n/a	false	false	false	false	related
file	A single related resource. Can be either a URI or set of nested resource data.	n/a	true	false	false	false	related
celery_task_id	Unicode string data. Ex: "Hello World"		false	false	true	false	string
ticket_message	Unicode string data. Ex: "Hello World"		false	false	true	false	string
id	Integer data. Ex: 2673		false	false	true	true	integer
local_status	Unicode string data. Ex: "Hello World"		false	false	true	false	string
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string

Example Response

```
{
    "meta": {
        "previous": null,
        "total_count": 0,
        "offset": 0,
        "limit": 1,
        "next": null
    },
    "objects": []
}
```

Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Template Resource

Resource URL `http://mytorrentserver/rundb/api/v1/template/`
Schema URL `http://mytorrentserver/rundb/api/v1/template/schema/`

Resource Fields

field	help text	default	nullable	readonly	blank	unique	type
isofficial	Boolean data. Ex: True	true	false	false	true	false	boolean
name	Unicode string data. Ex: “Hello World”	n/a	false	false	false	false	string
sequence	Unicode string data. Ex: “Hello World”		false	false	true	false	string
comments	Unicode string data. Ex: “Hello World”		false	false	true	false	string
key	Unicode string data. Ex: “Hello World”	n/a	false	false	false	false	string
id	Integer data. Ex: 2673		false	false	true	true	integer
resource_uri	Unicode string data. Ex: “Hello World”	n/a	false	true	false	false	string

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 6,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/template/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "isofficial": true,
            "name": "TF_A",
            "sequence":
↪"TGTTTTAGGGTCCCCGGGGTTAAAAGGTTTCGAACTCAACAGCTGTCTGGCAGCTCGCTCTACGATCTGAGACTGCCAAGGCACACAGGGGATAGG
↪",
            "comments": " ",
```

```
            "key": "ATCG",
            "id": 1,
            "resource_uri": "/rundb/api/v1/template/1/"
        }
    ]
}
```

Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Tf Metrics Resource

Resource URL `http://mytorrentserver/rundb/api/v1/tfmetrics/`
Schema URL `http://mytorrentserver/rundb/api/v1/tfmetrics/schema/`

Resource Fields

field	help text	default	nullable	readonly	blank	unique	type
corrHPSNR	Unicode string data. Ex: "Hello World"		false	false	true	false	string
Q10Mean	Floating point numeric data. Ex: 26.73	n/a	false	false	false	false	float
SysSNR	Floating point numeric data. Ex: 26.73	n/a	false	false	false	false	float
HPAccuracy	Unicode string data. Ex: "Hello World"		false	false	true	false	string
Q17ReadCount	Floating point numeric data. Ex: 26.73	n/a	false	false	false	false	float
sequence	Unicode string data. Ex: "Hello World"	n/a	false	false	false	false	string
Q17Histo	Unicode string data. Ex: "Hello World"		false	false	true	false	string
name	Unicode string data. Ex: "Hello World"	n/a	false	false	false	false	string
aveKeyCount	Floating point numeric data. Ex: 26.73	n/a	false	false	false	false	float
number	Floating point numeric data. Ex: 26.73	n/a	false	false	false	false	float
id	Integer data. Ex: 2673		false	false	true	true	integer
keypass	Floating point numeric data. Ex: 26.73	n/a	false	false	false	false	float
Q10ReadCount	Floating point numeric data. Ex: 26.73	n/a	false	false	false	false	float
report	A single related resource. Can be either a URI or set of nested resource data.	n/a	false	false	false	false	related
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string
Q17Mean	Floating point numeric data. Ex: 26.73	n/a	false	false	false	false	float
Q10Histo	Unicode string data. Ex: "Hello World"		false	false	true	false	string

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 10,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/tfmetrics/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "corrHPSNR": "",
            "Q10Mean": 92,
            "SysSNR": 8.90596237826753,
            "HPAccuracy": "0 : 92614661/92987980, 1 : 66459432/67074439, 2 : 2982150/
↪3047963, 3 : 0/0, 4 : 701514/761937, 5 : 0/0, 6 : 0/0, 7 : 0/0",
            "Q17ReadCount": 663166,
            "sequence":
↪"TACGAGCGTGTAGACGTGTCGTACGTGCGACGTAGTGAGTATACATGCTCTGACACTATGTACGATCTGAGACTGCCAAGGCACACAGGGGATAGG
↪",
            "Q17Histo": "6186 2376 12408 3441 8 196 6739 944 62 3088 1321 1740 5837␣
↪11552 5171 6973 3499 3109 2311 5441 1418 861 889 476 632 693 1993 587 208 2048 844␣
↪951 799 535 202 53 989 443 213 222 160 499 378 235 56 39 90 71 81 57 2773 919 753␣
↪845 411 2087 578 481 895 330 492 337 365 1146 474 624 457 442 282 657 888 422 270␣
↪290 412 457 1321 78 431 97 612 84 734 210 135 550 274 1025 151 1225 20936 9776 1625␣
↪338 780 18329 551335 35033 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0␣
↪0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0␣
↪0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0␣
↪0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0␣
↪0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0␣
↪0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0␣
↪0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
```

```
            "name": "TF_C",
            "aveKeyCount": 95,
            "number": 762290,
            "id": 1,
            "keypass": 762290,
            "Q10ReadCount": 732661,
            "report": "/rundb/api/v1/results/3/",
            "resource_uri": "/rundb/api/v1/tfmetrics/1/",
            "Q17Mean": 83,
            "Q10Histo": "1963 514 2070 833 2 15 20 52 29 47 959 452 1823 2178 2099␣
↪2088 1338 678 623 514 695 769 435 231 218 209 304 449 377 132 307 482 698 667 494␣
↪262 254 250 389 312 653 356 312 392 457 376 233 206 171 242 355 428 368 376 328 274␣
↪160 128 127 117 208 147 128 140 112 122 101 86 101 116 167 130 137 107 110 134 188␣
↪165 147 120 189 174 179 153 208 284 358 416 548 1770 22262 10956 4925 3780 3745␣
↪21341 555735 39369 18315 11400 8819 7006 5487 4258 3206 1865 586 0 0 0 0 0 0 0 0 0␣
↪0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0␣
↪0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0␣
↪0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0␣
↪0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0␣
↪0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0␣
↪0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0␣
↪0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0"
        }
    ]
}
```

Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Three Prime Adapter Resource

Resource URL `http://mytorrentserver/rundb/api/v1/threeprimeadapter/`
Schema URL `http://mytorrentserver/rundb/api/v1/threeprimeadapter/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
direction	Unicode string data. Ex: "Hello World"	Forward	false	false	false	false	string
description	Unicode string data. Ex: "Hello World"		false	false	true	false	string
sequence	Unicode string data. Ex: "Hello World"	n/a	false	false	false	false	string
chemistryType	Unicode string data. Ex: "Hello World"		false	false	true	false	string
runMode	Unicode string data. Ex: "Hello World"	single	false	false	true	false	string
isActive	Boolean data. Ex: True	true	false	false	true	false	boolean
uid	Unicode string data. Ex: "Hello World"	n/a	false	false	false	true	string
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string
id	Integer data. Ex: 2673		false	false	true	true	integer
isDefault	Boolean data. Ex: True	false	false	false	true	false	boolean
name	Unicode string data. Ex: "Hello World"	n/a	false	false	false	true	string

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 8,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/threeprimeadapter/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "direction": "Forward",
            "description": "Default forward adapter",
            "sequence": "ATCACCGACTGCCCATAGAGAGGCTGAGAC",
            "chemistryType": "",
            "runMode": "single",
            "isActive": true,
            "uid": "FWD_0001",
            "resource_uri": "/rundb/api/v1/threeprimeadapter/1/",
            "id": 1,
            "isDefault": true,
            "name": "Ion P1B"
        }
    ]
}
```

Allowed list HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Allowed detail HTTP methods

- GET
- POST
- PUT
- DELETE
- PATCH

Torrent Suite Resource

Resource URL `http://mytorrentserver/rundb/api/v1/torrentsuite/`
Schema URL `http://mytorrentserver/rundb/api/v1/torrentsuite/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
meta_version	Unicode string data. Ex: "Hello World"	n/a	true	true	true	false	string
locked	Unicode string data. Ex: "Hello World"	n/a	true	true	true	false	boolean
logs	Unicode string data. Ex: "Hello World"	n/a	true	true	true	false	boolean
versions	Unicode string data. Ex: "Hello World"	n/a	true	true	true	false	string

Example Response


```
{
    "meta_version": "5.10.0",
    "locked": false,
    "logs": false,
    "versions": {
        "ion-docs": "5.10.2",
        "ion-gpu": "5.10.0-1",
        "ion-pipeline": "5.10.8-1",
        "ion-torrentpy": "5.10.8-1",
```

```
        "ion-tsconfig": "5.10.4-1",
        "ion-chefupdates": "5.10.0",
        "ion-rsmts": "5.6.1-1",
        "ion-sampledata": "1.2.0-1",
        "ion-publishers": "5.10.2-1",
        "ion-dbreports": "5.10.26-1",
        "ion-analysis": "5.10.10-1",
        "ion-onetouchupdater": "5.0.2-1",
        "ion-torrentr": "5.10.9-1",
        "ion-plugins": "5.10.12-1",
        "ion-referencelibrary": "2.2.0"
    }
}
```


Allowed list HTTP methods

- GET
- PUT

Allowed detail HTTP methods

None

User Resource

Resource URL `http://mytorrentserver/rundb/api/v1/user/`
Schema URL `http://mytorrentserver/rundb/api/v1/user/schema/`

Resource Fields

field	help text	default	nullable	read-only	blank	unique	type
profile	A single related resource. Can be either a URI or set of nested resource data.	n/a	false	false	false	false	related
username	Required. 30 characters or fewer. Letters, numbers and @/./+/-/_ characters	n/a	false	false	false	true	string
first_name	Unicode string data. Ex: "Hello World"		false	false	true	false	string
last_name	Unicode string data. Ex: "Hello World"		false	false	true	false	string
is_active	Designates whether this user should be treated as active. Unselect this instead of deleting accounts.	true	false	false	true	false	boolean
email	Unicode string data. Ex: "Hello World"		false	false	true	false	string
last_login	A date & time as a string. Ex: "2010-11-10T03:07:43"	2018-06-19T20:40:18.000722+00:00	false	false	false	false	datetime
full_name	Unicode string data. Ex: "Hello World"	n/a	false	false	false	false	string
resource_uri	Unicode string data. Ex: "Hello World"	n/a	false	true	false	false	string
id	Integer data. Ex: 2673		false	false	true	true	integer
date_joined	A date & time as a string. Ex: "2010-11-10T03:07:43"	2018-06-19T20:40:18.000722+00:00	false	false	false	false	datetime

Example Response


```
{
    "meta": {
        "previous": null,
        "total_count": 6,
        "offset": 0,
        "limit": 1,
        "next": "/rundb/api/v1/user/?offset=1&limit=1&format=json"
    },
    "objects": [
        {
            "profile": {
                "phone_number": "",
                "name": "",
                "title": "Lab Contact",
                "last_read_news_post": "1984-11-06T00:00:00+00:00",
                "note": "",
                "id": 3,
                "resource_uri": ""
            },
            "username": "lab_contact",
            "first_name": "",
            "last_name": "",
            "is_active": true,
            "email": "ionuser@iontorrent.com",
            "last_login": "2017-07-22T06:43:37.000251+00:00",
            "full_name": "",
            "resource_uri": "/rundb/api/v1/user/3/",
```

```
            "id": 3,
            "date_joined": "2017-07-22T06:43:37.000251+00:00"
        }
    ]
}
```

Allowed list HTTP methods

- GET

Allowed detail HTTP methods

- GET

API Examples

See *API Reference* for a listing of all available APIs. This section has the setup common to all the API examples. See *Authentication* for more information on the authentication header. All examples use the third-party python library requests.

```
import requests

BASE_URL = "http://example.xyz"
USERNAME = "ionadmin"
API_KEY = "efb7a14021732d773a4258b69d9452042a31a6b6"
```

Fetching all Chips

Using the *Chip Resource* API.

```
headers = {"Authorization": "ApiKey " + USERNAME + ":" + API_KEY}
object_list = []

next_url = "/rundb/api/v1/chip/"
while next_url:
    response = requests.get(BASE_URL + next_url, headers=headers, params={})
    response.raise_for_status()
    response_data = response.json()

    object_list += response_data["objects"]
    next_url = response_data["meta"]["next"] or None

print object_list
```

```
[...]
```

Adding Filters

Using the *Chip Resource* API.

```
headers = {"Authorization": "ApiKey " + USERNAME + ":" + API_KEY}
object_list = []

next_url = "/rundb/api/v1/chip/"
while next_url:
    response = requests.get(BASE_URL + next_url, headers=headers, params={"name__
↪startswith": "31"})
    response.raise_for_status()
    response_data = response.json()

    object_list += response_data["objects"]
    next_url = response_data["meta"]["next"] or None

for chip in object_list[0:3]:
    print chip["name"]
```

```
314
316
318
```

Completed Runs and Reports

Using the *Composite Experiment Resource* API.

```
headers = {"Authorization": "ApiKey " + USERNAME + ":" + API_KEY}
object_list = []

next_url = "/rundb/api/v1/compositeexperiment/"
while next_url:
    response = requests.get(BASE_URL + next_url, headers=headers)
    response.raise_for_status()
    response_data = response.json()

    object_list += response_data["objects"]
    next_url = response_data["meta"]["next"] or None

for experiment in object_list[0:3]:
    print experiment["displayName"]
    for report in experiment["results"]:
        print "    " + report["resultsName"] + " " + report["status"]
```

```
S5-530 cfDNA
    Reanalyze Completed
    S5-530_cfDNA Completed
    Auto_S5-530_cfDNA_89 Completed
S5-540 AmpliSeqExome
    S5-540_AmpliSeqExome Importing Failed
    Auto_S5-540_AmpliSeqExome_90 Completed
S5-540 WholeTranscriptomeRNA
    Auto_S5-540_WholeTranscriptomeRNA_91 Importing Failed
```

Fetching a Report

Using the *Results Resource* API.

```
headers = {"Authorization": "ApiKey " + USERNAME + ":" + API_KEY}

report_response = requests.get(BASE_URL + "/rundb/api/v1/results/3/", headers=headers)
report_response.raise_for_status()
report_response_data = report_response.json()

print report_response_data["resultsName"]

for plugin_name, plugin_status in report_response_data["pluginState"].items():
    print "    " + plugin_name, plugin_status

lib_metrics_response = requests.get(BASE_URL + report_response_data["libmetrics"][0],␣
↪headers=headers)
lib_metrics_response.raise_for_status()
lib_metrics_response_data = lib_metrics_response.json()

print "%.1f million reads" % (lib_metrics_response_data["totalNumReads"]/1000000.0)
```

```
Auto_S5-540_WholeTranscriptomeRNA_91
    DataExport Completed
    ERCC_Analysis Completed
    sampleID Error
    coverageAnalysis Error
    AssemblerSPAdes Started
    FilterDuplicates Completed
    RunTransfer Completed
94.0 million reads
```

Planning a Non-barcoded Run

Using the *Planned Experiment Resource* API.

```
headers = {"Authorization": "ApiKey " + USERNAME + ":" + API_KEY}
plan_json = {
    "library": "hg19",
    "planName": "DOCS_my_plan",
    "sample": "my_sample",
    "chipType": "520",
    "sequencekitname": "Ion S5 Sequencing Kit",
    "librarykitname": "Ion Xpress Plus Fragment Library Kit",
    "templatingKitName": "Ion 520/530 Kit-OT2"
}
response = requests.post(BASE_URL + "/rundb/api/v1/plannedexperiment/",␣
↪headers=headers, json=plan_json)
response.raise_for_status()
print response.status_code
```

```
201
```

Planning a Barcoded Run

Using the *Planned Experiment Resource* API.

```
headers = {"Authorization": "ApiKey " + USERNAME + ":" + API_KEY}
plan_json = {
    "library": "hg19",
    "planName": "DOCS_my_plan",
    "sample": "my_sample",
    "chipType": "520",
    "sequencekitname": "Ion S5 Sequencing Kit",
    "librarykitname": "Ion Xpress Plus Fragment Library Kit",
    "templatingKitName": "Ion 520/530 Kit-OT2",
    "barcodeId": "IonXpress",
    "barcodedSamples": {
        'demo sample 1': {
            'barcodeSampleInfo': {
                'IonXpress_003': {
                    'description': 'description here',
                    'hotSpotRegionBedFile': '',
                    'nucleotideType': 'DNA',
                    'reference': 'hg19',
                    'targetRegionBedFile': ''
                }
            },
            'barcodes': ['IonXpress_003']
        },
        'demo sample 2': {
            'barcodeSampleInfo': {
                'IonXpress_004': {
                    'description': 'description here',
                    'hotSpotRegionBedFile': '',
                    'nucleotideType': 'DNA',
                    'reference': 'hg19',
                    'targetRegionBedFile': ''
                }
            },
            'barcodes': ['IonXpress_004']
        }
    }
}
response = requests.post(BASE_URL + "/rundb/api/v1/plannedexperiment/",␣
↪headers=headers, json=plan_json)
response.raise_for_status()
print response.status_code
```

```
201
```

CHAPTER 3

Legal

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