

# CRDC Submission Portal APIs

## 1. Introduction

This document walks you through the basics of submitting data to CRDC Submission Portal using APIs. Information provide in CRDC Data Submission Instructions will not be included in this document. It is recommended to get familiar with CRDC Data Submission Instructions and submission workflow using CRDC Data Submission Portal before interacting with CRDC Submission APIs.

CRDC Submission Portal provides a set of Graphql APIs (<https://graphql.org/>). There is only one API endpoint, <https://hub.datacommons.cancer.gov/api/graphql>. Different functions are provided as separate API queries (read) and mutations (write). Users may use API tools like Postman as client to interact with the APIs. Users may also choose to write code in any popular programming languages to interact with the APIs.

All CRDC Submission Portal API queries and mutations use HTTP POST method. The APIs will always return HTTP code 200 (success) even when API call fails. The API returns data and errors in JSON format. If an API call succeeds, the returned data will be under “**data**” key. If any error occurs, the error information will be returned under “**error**” key (“**data**” key will be null).

CRDC Submission Portal API is authentication and authorization controlled. API tool (or your code) needs to be set up to send “Bearer Token” in “**Authorization**” header.

A Graphql API’s schema contains definitions of all queries, mutations and their parameters and return types. This document will only provide information that cannot be found in the Graphql schema.

## 2. Prerequisites

- A valid API token downloaded from Data Submission Portal.
- API testing tool, such as Postman or GraphiQL or custom code.
- Knowledge of using API tools and/or interacting with APIs in code.
- Basic knowledge of Graphql APIs (<https://graphql.org/>).

## 3. Conventions

A dot separated property name is used to describe the hierarchy in the data. For example, **submissions.\_id** means **\_id** property under **submissions** property. See screenshot below.

```

"total": 24,
"submissions": [
  {
    "_id": "de9f113c-1a9d-4740-9495-2c595976b440",
    "name": "DELETE-1025_Delete_1201",
    "submitterName": "crdc.g.submtr",
  }
]

```

## 4. Starting a new submission

Before creating a data submission, user needs to determine which study the data submission will be submitted to. To retrieve approved studies for a user's organization, call API query **getMyUser**.

API signature:

**getMyUser** : User

Sample Query	Sample graphql variables
<pre> query getMyUser {   getMyUser {     _id     studies {       _id     }   } } </pre>	

Important return values:

- **studies.\_id**: should be used as **studyID** parameter of **createSubmission** API.

To create a new data submission, call API mutation **createSubmission**.

API signature:

```

createSubmission (
  studyID: String!,
  dataCommons: String!,
  name: String!,
  intention: String!,
  dataType: String!
): Submission

```

Sample Query	Sample graphql variables
<pre> mutation createSubmission(\$studyID: String!, \$dataCommons: String!, \$name: String!, \$intention: String!, \$dataType: String!) {   createSubmission(     studyID: \$studyID     dataCommons: \$dataCommons     name: \$name     intention: \$intention     dataType: \$dataType   ) {     _id     status     createdAt   } } </pre>	<pre> {   "studyID": "4ab75167-0121-4fea-b515-94c01d8380cc",   "dataCommons": "ICDC",   "name": "API full workflow",   "intention": "New/Update",   "dataType": "Metadata and Data Files" } </pre>

Important parameters:

- **studyID:** `_id` field of an approved study
- **dataCommons:** data common's name such as "CTDC", "ICDC" etc. For General Commons the name should be "CDS"
- **name:** a user selected name for the submission
- **intention:** should be one of ["New/Update", "Delete"]
- **dataType:** should be one of ["Metadata Only", "Metadata and Data Files"]

Important return values:

- **`_id`:** submission's ID, aka. `submissionID`

## 5. Continuing an existing submission

### a. Retrieve a list of all submissions

To retrieve a list of all submissions a user has access to, call API query **listSubmissions**.

API signature:

```

listSubmissions(
  name: String,
  dbGaPID: String,
  dataCommons: String,
  submitterName: String,
  organization: String,
  status: [String],
  first: Int = -1,
  offset: Int = 0,
  orderBy: String = "updatedAt",
  sortDirection: String = "DESC"): ListSubmissions

```

Sample Query	Sample graphql variables
<pre> query listSubmissions(\$first: Int, \$offset: Int, \$orderBy: String, \$sortDirection: String, \$status: {String}) {   listSubmissions(     first: \$first     offset: \$offset     orderBy: \$orderBy     sortDirection: \$sortDirection     status: \$status   ){     total     submissions {       _id       name       submitterName       organization {         _id         name       }       dataCommons       studyAbbreviation       dbGaPID       modelVersion       status       conciergeName       createdAt       updatedAt       intention       dataFileSize {         formatted       }     }   } } </pre>	<pre> {   "status": "All",   "first": 2,   "offset": 0,   "sortDirection": "desc",   "orderBy": "updatedAt" } </pre>

Important parameters:

- **Name:** results will be filtered by data submission's name
- **dbGaPID:** results will be filtered by data submission's dbGaPID
- **dataCommons:** results will be filtered by data submission's data commons
- **submitterName:** results will be filtered by data submission's creator's name
- **organization:** results will be filtered by data submission's organization name, *this parameter is deprecated and will be removed in the future*
- **Status:** results will be filtered by this parameter if one or more of the following values is provided: ["New", "In Progress", "Submitted", "Released", "Completed", "Archived", "Canceled", "Rejected", "Withdrawn", "Deleted", "All"]. If "All" is provided, no filter will be applied.
- **first:** number of records to be returned, if -1 is sent, API will return all available data

- **offset:** skip given number of records before returning data
- **orderBy:** property name used to sort returned data
- **sortDirection:** should be one of ["ASC", "DESC"]

Important return values:

- **submissions.\_id:** submission's ID, aka. submissionID

## b. Retrieve information about a submission

To retrieve detailed information about a submission, call API query **getSubmission**.

API signature:

`getSubmission(_id: ID!): Submission`

Sample Query	Sample graphql variables
<pre> query getSubmission(\$id: ID!) {   getSubmission(_id: \$id) {     _id     name     submitterID     submitterName     organization {       _id       name     }     dataCommons     modelVersion     studyID     studyAbbreviation     dbGaPID     bucketName     rootPath     status     metadataValidationStatus     fileValidationStatus     crossSubmissionStatus     validationStarted     validationEnded     validationScope     validationType     deletingData     fileErrors {       submissionID       type       validationType       batchID </pre>	<pre> {   "id": "eea2a531-4860-4e09-bf8e-151f73d4c379" } </pre>

<pre> displayID submittedID severity uploadedDate validatedDate errors {   title   description } warnings {   title   description } } history {   status   reviewComment   dateTime   userID } conciergeName conciergeEmail intention dataType otherSubmissions createdAt updatedAt } </pre>	
--	--

Important parameters:

- **\_id**: submission's ID, aka. submissionID

To retrieve statistics of a submission, call API query **submissionStats**.

API signature:

`submissionStats(_id: ID!): SubmissionStats`

Sample Query	Sample graphql variables
<pre> query getSubmission(\$id: ID!) {   submissionStats(_id: \$id) {     stats {       nodeName       total       new       passed       warning       error     }   } } </pre>	<pre> {   "id": "eea2a531-4860-4e09-bf8e-151f73d4c379" } </pre>

Important parameters:

- **\_id**: submission's ID, aka. submissionID

To retrieve uploaded metadata, call API query **getSubmissionNodes**.

API signature:

```

getSubmissionNodes(
  submissionID: String!,
  nodeType: String!,
  status: String = "All",
  nodeID: String,
  first: Int = 10,
  offset: Int = 0,
  orderBy: String = "nodeID",
  sortDirection: String = "ASC"
): SubmissionNodes

```

Sample Query	Sample graphql variables
<pre> query getSubmissionNodes(\$_id: String!, \$nodeType: String!, \$status: String, \$submittedID: String, \$first: Int, \$offset: Int, \$orderBy: String, \$sortDirection: String) {   getSubmissionNodes(     submissionID: \$_id     nodeType: \$nodeType     status: \$status     nodeID: \$submittedID     first: \$first     offset: \$offset     orderBy: \$orderBy     sortDirection: \$sortDirection   ){     total     IDPropName     properties     nodes {       nodeID       nodeType       status       props     }   } } </pre>	<pre> {   "_id": "eea2a531-4860-4e09-bf8e-151f73d4c379",   "first": 20,   "offset": 0,   "sortDirection": "desc",   "orderBy": "studyID",   "nodeType": "study",   "status": "All",   "submittedID": "" } </pre>

Important parameters:

- **submissionID:** submission's ID
- **nodeType:** type of the metadata node to be returned
- **status:** should be one of ["All", "New", "Error", "Passed", "Warning"]. If "All" is provided. no filter will be applied, otherwise, return will be filtered by metadata's status.
- **nodeID:** if provided, return will be filtered by provided node ID, any node ID partially match given value will be returned.
- **first:** number of records to be returned, if -1 is sent, API will return all available data
- **offset:** skip given number of records before returning data
- **orderBy:** property name used to sort returned data
- **sortDirection:** should be one of ["ASC", "DESC"]

Important return values:

- **IDPropName:** name of the metadata node's ID property
- **Properties:** names of all metadata node's properties
- **Nodes.props:** a JSON string contains all properties of the metadata node, needs to be parsed as JSON in the code.

To get a summary of the submission, call API query **getSubmissionSummary**



API signature:

`getSubmissionSummary(submissionID: ID!): [nodeTypeSummary]`

Sample Query	Sample graphql variables
<pre>query getSubmissionSummary(\$submissionID: ID!) {   getSubmissionSummary(submissionID: \$submissionID) {     nodeType     new     updated     deleted   } }</pre>	<pre>{   "submissionID": "e356d430-70e4-40eb-8bde-6265fff1b46c" }</pre>

Important parameters:

- `submissionID`: submission's ID

Important return values:

- `nodeType`: node type
- `new`: number of new records that will be added
- `updated`: number of existing records that will be updated
- `deleted`: number of existing records that will be deleted

To download dbGaP load sheet, call API query **downloadDBGaPLoadSheet**

API signature:

`downloadDBGaPLoadSheet(submissionID:String!):String`

Sample Query	Sample graphql variables
<pre>query downloadDBGaPLoadSheet(\$submissionID: String!) {   downloadDBGaPLoadSheet(submissionID: \$submissionID) }</pre>	<pre>{   "submissionID": "e356d430-70e4-40eb-8bde-6265fff1b46c" }</pre>

Important parameters:

- `submissionID`: submission's ID

Important return values:

- A pre-signed URL that can be used to download the dbGaP load sheets in zip format.

### c. Edit a Submission

You can change the name of the submission by calling API **editSubmission**.

API signature:

```

editSubmission (
  _id: String!
  newName: String!
): Submission

```

Sample Query	Sample graphql variables
<pre> mutation EditSubmission(\$_id: String!, \$newName: String!) {   editSubmission(_id: \$_id, newName: \$newName) {     _id     name   } } </pre>	<pre> {   "_id": "{submissionID}",   "newName": "My new Submission Name" } </pre>

Important parameters:

- **\_id**: submission's ID
- **newName**: new submission name, maximum length is 25 characters.

## d. Uploading Files and Manifests

It is recommended to upload data files via Uploader CLI Tool. It is also possible to upload data files by writing code.

To retrieve an CLI configuration file, call API query **retrieveCLIConfig**. Returned data contains correct content and format (including line breaks and indentation). It is recommended to call this API in code and save returned string into a YAML file without modifying the content in anyway. For example, "my-cli-configuration.yml". API tools have their own way of displaying data contains line breaks, it will be hard to preserve original return data in an API tool.

API signature:

```

retrieveCLIConfig(
  submissionID: String!,
  apiURL: String!,
  dataFolder: String,
  manifest: String
  archive_manifest: String
): String

```

Sample Query	Sample graphql variables
<pre> query retrieveCLIConfig(\$submissionID: String!, \$apiURL: String!, \$dataFolder: String, \$manifest: String, \$archive_manifest: String) {   retrieveCLIConfig(     submissionID: \$submissionID     apiURL: \$apiURL     dataFolder: \$dataFolder     manifest: \$manifest     archive_manifest: \$archive_manifest </pre>	<pre> {   "submissionID": "0997c282-d3ac-47ab-a7f2-2dacd2ca7d7c",   "dataFolder": "/Users/user1/Desktop/datafiles/",   "manifest": "/Users/user1/Desktop/datafiles/manifest.tsv",   "archive_manifest": "/Users/user1/Desktop/datafiles/archive_manifest.tsv",   "apiURL": "https://hub-qa2.datacommons.cancer.gov/api/graphql" } </pre>

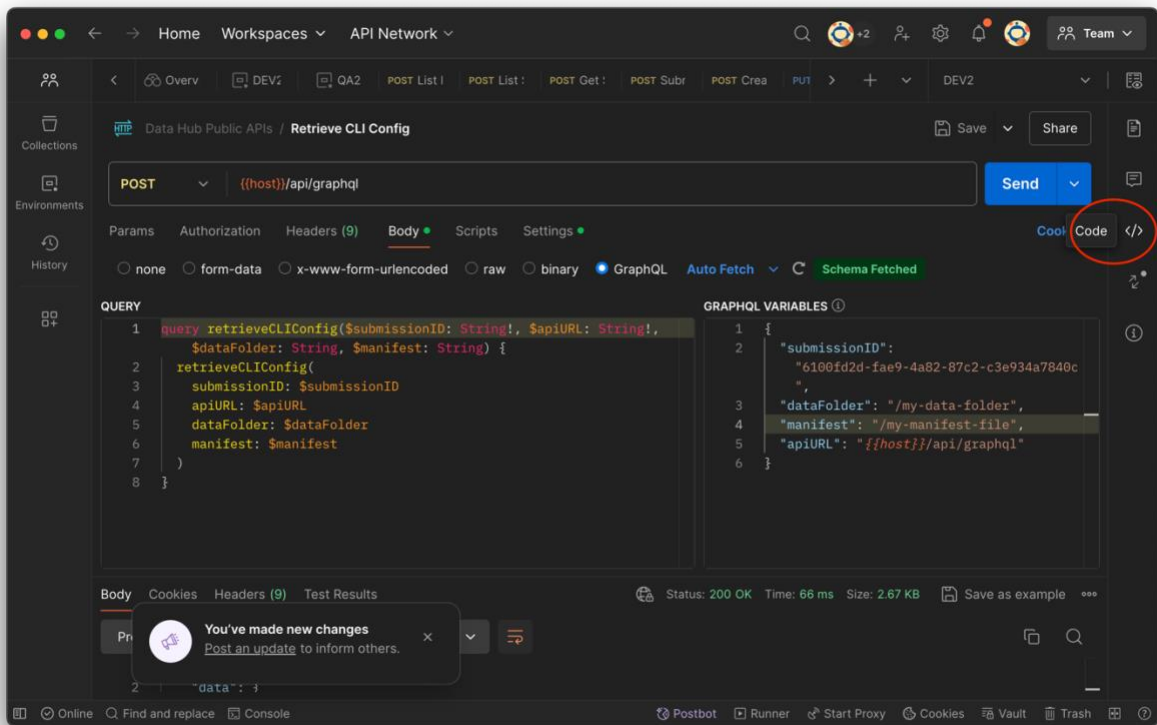
<pre> ) } </pre>	
------------------	--

Important parameters:

- **submissionID**: submission's ID
- **apiURL**: must be "**https://hub.datacommons.cancer.gov/api/graphql**"
- **dataFolder**: local path of data files folder, for example *"/Users/me/my-data-files-folder"*
- **manifest**: local path of manifest file, for example *"/Users/me/my-metadata-folder/my-file-manifest.tsv"*
- **archive\_manifest**: local path of archive manifest file, for example *"/Users/me/my-metadata-folder/archive-manifest.tsv"*

To save CLI configuration file retrieved as a file without writing code, follow steps below:

- Setup API request in Postman
- Click "Code" button (</>) on the right-side bar
- Copy and paste the command into a terminal (cmd on Windows), then add following code to end of the command  
`|jq -r '["data"]|["retrieveCLIConfig"]' > my-cli-configuration.yml`



If uploading data files in code is preferred, user may call API mutation **createTempCredentials** to retrieve a set of temporary credentials to use in the code.

API signature:

**createTempCredentials** (submissionID: ID!): TempCredentials

Sample Query	Sample graphql variables
<pre>mutation createTempCredentials (\$submissionID: ID!) {   createTempCredentials(submissionID: \$submissionID) {     accessKeyId     secretAccessKey     sessionToken   } }</pre>	<pre>{   "submissionID": "6100fd2d-fae9-4a82-87c2-c3e934a7840c" }</pre>

Important parameters:

- **submissionID**: submission's ID

Metadata templates can be uploaded via Uploader CLI Tool. It is also possible to upload metadata templates via API. If using API is preferred, it is recommended to perform following steps in code rather than in API tool:

- Step 1: create a "batch" by calling API mutation **createBatch**.
- Step 2: upload metadata templates using pre-signed URLs retrieved in step 1.

- Step 3: update upload results by calling API mutation **updateBatch**. API will take the input as is and store the status of the files in the database. An asynchronous essential validation will be triggered by the API call, and the batch's status will be updated based on validation result. If validations passed, metadata will be loaded into submission database and status will be set to “**Uploaded**”. Otherwise, batch status will be set to “**Failed**”. Note, individual file status will be based on the input, and will not be updated by essential validation service.
- Step 4: retrieve essential validation results by calling API query **listBatches**

### createBatch:

API signature:

```
createBatch (
  submissionID: ID!,
  type: String,
  files: [String!]!
): NewBatch
```

Sample Query	Sample graphql variables
<pre>mutation createBatch(\$submissionID: ID!, \$type: String, \$files: [String!]!) {   createBatch(submissionID: \$submissionID, type: \$type, files: \$files)   {     _id     submissionID     bucketName     filePrefix     type     fileCount     files {       fileName       signedURL     }     status     createdAt     updatedAt   } }</pre>	<pre>{   "submissionID": "0997c282-d3ac-47ab-a7f2-2dacd2ca7d7c",   "type": "metadata",   "files": ["program.tsv", "study.tsv", "participant.tsv", "sample.tsv"] }</pre>

Important parameters:

- **submissionID**: submission's ID
- **type**: should be one of ["metadata", "data file"]
- **files**: list of file names to be uploaded.

Important return values:

- **\_id**: batch's internal ID, aka batchID
- **files.signedURL**: S3 pre-signed URL that can be used to upload metadata templates

## updateBatch:

API signature:

updateBatch (batchID: ID!, files: [UploadResult]): Batch

Sample Query	Sample graphql variables
<pre>mutation updateBatch(\$batchID: ID!, \$files: [UploadResult]) {   updateBatch(batchID: \$batchID, files: \$files) {     _id     submissionID     type     fileCount     files {       filePrefix       fileName       size       status       errors       createdAt       updatedAt     }     status     createdAt     updatedAt   } }</pre>	<pre>{   "batchID": "13af4bee-bed8-42ce-8252-eb5a756185b9",   "files": [     {       "fileName": "program.tsv",       "succeeded": true,       "errors": null     }, {       "fileName": "study.tsv",       "succeeded": true,       "errors": null     }, {       "fileName": "participant.tsv",       "succeeded": true,       "errors": null     }, {       "fileName": "sample.tsv",       "succeeded": true,       "errors": null     }   ] }</pre>

Important parameters:

- **batchID**: batch's internal ID
- **files.skipped**: reserved for CLI use, should set to false

Important return values:

- **\_id**: batch's internal ID, aka batchID
- **displayID**: batch's UI ID
- **status**: current status of the batch. It will change after essential validation is finished (explained in previous sections). Please call **listBatches** to get the latest status.

To retrieve information about all batches, call API query **listBatches**.

API signature:

listBatches(  
 submissionID: ID!,  
 first: Int = 10,

```

offset: Int = 0,
orderBy: String = "updatedAt",
sortDirection: String = "DESC"
): ListBatches

```

Sample Query	Sample graphql variables
<pre> query listBatches(\$submissionID: ID!, \$first: Int, \$offset: Int, \$orderBy: String, \$sortDirection: String) {   listBatches(     submissionID: \$submissionID     first: \$first     offset: \$offset     orderBy: \$orderBy     sortDirection: \$sortDirection   ) {     total     batches {       _id       displayID       createdAt       updatedAt       submissionID       type       fileCount       files {         nodeType         filePrefix         fileName         size         status         errors         createdAt         updatedAt       }       status       errors     }   } } </pre>	<pre> {   "submissionID": "0997c282-d3ac-47ab-a7f2-2dacd2ca7d7c",   "first": 20,   "offset": 0,   "sortDirection": "desc",   "orderBy": "createdAt" } </pre>

Important parameters:

- **submissionID:** submission's ID
- **first:** number of records to be returned, if -1 is sent, API will return all available data
- **offset:** skip given number of records before returning data
- **orderBy:** property name used to sort returned data
- **sortDirection:** should be one of ["ASC", "DESC"]

Important return values:

- **batches.\_id**: batch's internal ID, aka batchID
- **batches.displayID**: batch's UI ID
- **batches.files.nodeType**: node type contained in the metadata file. This value is only available when the metadata file can be successfully read by the essential validation service. Otherwise, it will be null.

## e. Deleting data

To delete a metadata node, call API mutation **deleteDataRecords**.

API signature:

```
deleteDataRecords(  
  submissionID: String!,  
  nodeType: String!,  
  nodeIDs: [String!]  
): DataValidation
```

Sample Query	Sample graphql variables
<pre>mutation deleteDataRecords(\$_id: String!, \$nodeType: String!, \$nodeIDs: [String!]) {   deleteDataRecords(submissionID: \$_id, nodeType: \$nodeType, nodeIDs: \$nodeIDs) {     success     message   } }</pre>	<pre>{   "_id": "26000952-13c6-4cf5-9ac5-cf87b0c942f9",   "nodeType": "sample",   "nodeIDs": [     "allval_Samp_Sep18_01"   ] }</pre>

Important parameters:

- **submissionID**: submission's ID
- **nodeType**: type of the metadata node to be deleted, or "**data file**" if deleting data files from S3 bucket is desired.
- **nodeIDs**: a list of node IDs, API will delete metadata node that matches provided node IDs.

Important return values:

- **success**: a Boolean value indicates if a deletion operation has been successfully initialized, the deletion will be performed asynchronously.

To delete a data file from submission bucket, call API mutation **deleteDataRecords**.

API signature:

```
deleteDataRecords(  
  submissionID: String!,  
  nodeType: String!,
```



```
nodeIDs: [String!]
): DataValidation
```

Sample Query	Sample graphql variables
<pre>mutation deleteDataRecords(\$_id: String!, \$nodeType: String!, \$nodeIDs: [String!]) {   deleteDataRecords(submissionID: \$_id, nodeType: \$nodeType, nodeIDs: \$nodeIDs) {     success     message   } }</pre>	<pre>{   "_id": "26000952-13c6-4cf5-9ac5-cf87b0c942f9",   "nodeType": "data file",   "nodeIDs": [     "41_batchtextfiles.txt"   ] }</pre>

Important parameters:

- **submissionID**: submission's ID
- **nodeType**: must be "data file"
- **nodeIDs**: a list of file names to be deleted.

Important return values:

- **success**: a Boolean value indicates if a deletion operation has been successfully initialized, the deletion will be performed asynchronously.

## f. Running validations

To validate uploaded data, call API mutation **validateSubmission**.

API signature:

```
validateSubmission(
  _id: ID!,
  types: [String]
  scope: String
): DataValidation
```

Sample Query	Sample graphql variables
<pre>mutation validateSubmission(\$_id: ID!, \$types: [String], \$scope: String) {   validateSubmission(_id: \$_id, types: \$types, scope: \$scope) {     success   } }</pre>	<pre>{   "_id": "0997c282-d3ac-47ab-a7f2-2dacd2ca7d7c",   "types": [     "metadata", "data file"   ],   "scope": "All" }</pre>

Important parameters:

- **\_id**: submission's ID, aka. submissionID
- **types**: any combination of following values: ["metadata", "data file"]
- **scope**: should be one of ["New", "All"]

Important return values:

- **success**: a Boolean value indicates if a validation has been successfully initialized, it has no relationship to the validation's result.

To retrieve aggregated validation issues, call API query **aggregatedSubmissionQCResults**.

API signature:

```
aggregatedSubmissionQCResults(
  submissionID: ID!,
  severity: String = "all"
  first: Int = 20,
  offset: Int = 0,
  orderBy: String = "count"
  sortDirection: String = "DESC"): aggregatedQCResults
```

Sample Query	Sample graphql variables
<pre> <b>query</b> submissionQCResults(\$submissionID: ID!, \$severity: String, \$first: Int, \$offset: Int, \$orderBy: String, \$sortDirection: String) {   aggregatedSubmissionQCResults(     submissionID: \$submissionID     severity: \$severity     first: \$first     offset: \$offset     orderBy: \$orderBy     sortDirection: \$sortDirection   ) {     total     results {       title       severity       count       code     }   } } </pre>	<pre> {   "submissionID": "6100fd2d-fae9-4a82-87c2-c3e934a7840c",   "first": -1,   "offset": 0,   "sortDirection": "desc",   "orderBy": "displayID",   "severity": "All" } </pre>

Important parameters:

- **submissionID**: submission's ID
- **severities**: should be one of ["all", "error", "warning"] , return will be filtered by given issue severity. "all" means both errors and warnings.
- **first**: number of records to be returned, if -1 is sent, API will return all available data
- **offset**: skip given number of records before returning data
- **orderBy**: should be one of ["count", "title", "code", "severity"]
- **sortDirection**: should be one of ["ASC", "DESC"]

Important return values:

- **title**: title of the issue
- **severity**: either "Error" or "Warning"
- **count**: number of occurrences of the issue
- **code**: issue code that can be used in **submissionQCResults** API as **issueCode** parameter

To retrieve detailed validation issues, call API query **submissionQCResults**.

API signature:

```

submissionQCResults(
  _id: ID!,
  nodeTypes: [String],

```

```

batchIDs: [ID],
severities: String,
issueCode: String,

first: Int = 10,
offset: Int = 0
orderBy: String = "uploadedDate",
sortDirection: String = "DESC"
): QCResults

```

Sample Query	Sample graphql variables
<pre> <b>query</b> submissionQCResults(\$id: ID!, \$nodeTypes: [String], \$batchIDs: [ID], \$severities: <b>String</b>, \$first: <b>Int</b>, \$offset: <b>Int</b>, \$orderBy: <b>String</b>, \$sortDirection: <b>String</b>) {   submissionQCResults(     _id: \$id     nodeTypes: \$nodeTypes     batchIDs: \$batchIDs     severities: \$severities     first: \$first     offset: \$offset     orderBy: \$orderBy     sortDirection: \$sortDirection   ) {     total     results {       submissionID       <b>type</b>       validationType       batchID       displayID       submittedID       severity       uploadedDate       validatedDate       errors {         title         description       }       warnings {         title         description       }     }   } } </pre>	<pre> {   "id": "0997c282-d3ac-47ab-a7f2-2dacd2ca7d7c",   "first": -1,   "offset": 0,   "sortDirection": "desc",   "orderBy": "displayID",   "severities": "All" } </pre>

Important parameters:

- **\_id**: submission's ID, aka. submissionID
- **nodeTypes**: a list of metadata node types or "data file", return will be filtered by given metadata node types or file validation results if "data file" is given.
- **batchIDs**: a list of batches' internal IDs, return will be filtered by given batch internal IDs
- **severities**: should be one of ["All", "Error", "Warning"] , return will be filtered by given issue severity. "All" means both errors and warnings.
- **issueCode**: results will be filtered by the issue code
- **first**: number of records to be returned, if -1 is sent, API will return all available data
- **offset**: skip given number of records before returning data
- **orderBy**: property name used to sort returned data
- **sortDirection**: should be one of ["ASC", "DESC"]

Important return values:

- **validationType**: either "metadata" or "data file"
- **submittedID**: a metadata node's ID, or file name of a data file

## g. Submitting your Final Dataset

To submit a submission for review, call API mutation **submissionAction**.

API signature:

```
submissionAction (
  submissionID: ID!,
  action: String!
  comment: String
): Submission
```

Sample Query	Sample graphql variables
<pre>mutation submissionAction (\$submissionID: ID!, \$action: String!) {   submissionAction(submissionID: \$submissionID, action: \$action) {     _id     name     submitterID     submitterName     organization {       _id       name     }   }   dataCommons   modelVersion   studyID   studyAbbreviation   dbGaPID   bucketName   rootPath   status }</pre>	<pre>{   "submissionID": "0997c282-d3ac-47ab-a7f2-2dacd2ca7d7c",   "action": "Submit" }</pre>

<pre>metadataValidationStatus fileValidationStatus crossSubmissionStatus validationStarted validationEnded validationScope validationType deletingData fileErrors {   submissionID   type   validationType   batchID   displayID   submittedID   severity   uploadedDate   validatedDate   errors {     title     description   }   warnings {     title     description   } } history {   status   reviewComment   dateTime   userID } conciergeName conciergeEmail intention dataType otherSubmissions createdAt updatedAt } }</pre>	
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Important parameters:

- **submissionID**: submission's ID

- **action:** should be “**Submit**” for this use case. Valid value includes [“Submit”, “Withdraw”, “Cancel”]