BV-BRC API (1.0.0)

Download OpenAPI specification: [Download]

API documentation for BV-BRC

Retrieve content by ID

Fetches content details based on a given ID.

PATH PARAMETERS

⊣ `id` required	string ID of the content

Responses

— **200** Successfully retrieved content

— **404** Content not found

`GET` `/content/{id}` ⌄

Auto-generated summary for GET contentDirectory

Responses

— **200** Successful response

```
GET  /contentDirectory                                    ⌄
```

Auto-generated summary for GET *

Responses

— **200** Successful response

```
GET  /*                                                   ⌄
```

Auto-generated summary for POST *

Responses

— **200** Successful response

```
POST  /*                                                  ⌄
```

Add a new dataset entry

Creates a new dataset entry in the API.

REQUEST BODY SCHEMA: application/json
required

```
name          string

type          string
```

Responses

— **201** Successfully created dataset

— **400** Invalid data format

POST   /data   ⌄

Request samples

Payload

Content type
application/json

                                                        Copy

```json
{
    "name": "New dataset",
    "type": "genome"
}
```

Auto-generated summary for GET redis

Responses

— **200** Successful response

GET   /redis

Auto-generated summary for GET http_port

Responses

— **200** Successful response

GET   /http_port

Auto-generated summary for GET /summary_by_taxon/:taxon_id

Responses

— **200** Successful response

```
GET    /summary_by_taxon/:taxon_id                          ⌄
```

Auto-generated summary for GET /distinct/:collection/:field

Responses

— **200** Successful response

```
GET    /distinct/:collection/:field                         ⌄
```

Auto-generated summary for GET /taxon_category/

Responses

— **200** Successful response

```
GET   /taxon_category/                                    ⌄
```

Auto-generated summary for GET /subsystem_summary/:genome_id

Responses

— **200** Successful response

```
GET   /subsystem_summary/:genome_id                      ⌄
```

Retrieve available data types

Returns a list of all data types available in the API.

Responses

> **200** Successfully retrieved data types

```
GET   /data/type                                          ⌄

Response samples

  200

  Content type
  application/json

                                                        Copy

  [
      "genome"
  ]
```

Auto-generated summary for GET content-type

Responses

> — **200** Successful response

```
GET   /content-type                                       ⌄
```

Auto-generated summary for GET accept

Responses

— **200** Successful response

```
GET   /accept                                          ⌄
```

Auto-generated summary for PATCH /:target_id

Responses

— **200** Successful response

```
PATCH   /:target_id                                    ⌄
```

Auto-generated summary for POST /:target_id

Responses

— **200** Successful response

POST `/:target_id` ⌄

Retrieve API documentation

Serves API documentation in JSON format.

Responses

— **200** Successfully retrieved documentation

GET `/doc` ⌄

Auto-generated summary for GET publicURL

Responses

— **200** Successful response

GET `/publicURL` ⌄

Auto-generated summary for GET /

Returns general information about the API.

Responses

— **200** Successful response

```
GET    /                                              ⌄
```

Auto-generated summary for POST /

Responses

— **200** Successful response

```
POST   /                                              ⌄
```

Auto-generated summary for GET /:collection

Responses

— 200 Successful response

```
GET    /:collection                                      ⌄
```

Download a file

Allows downloading files from the API using a file ID.

QUERY PARAMETERS

┐ `fileId`
  required

string

ID of the file to download

Responses

— 200 File downloaded successfully

— 404 File not found

```
GET    /download                                         ⌄
```

Check genome permissions

Returns access permissions for a given genome.

QUERY PARAMETERS

⊣ genomeId
   required

string
ID of the genome

Responses

— **200** Successfully retrieved permissions

— **403** Access denied

GET /permissions/genome ⌄

Auto-generated summary for GET solr

Responses

— **200** Successful response

GET /solr ⌄

Search HPI data

Fetches data from the HPI search API using a search term.

QUERY PARAMETERS

⊣ term	string Search term for querying HPI data.

Responses

> **200** Successfully retrieved HPI search results

GET `/hpi/search` ⌄

Response samples

[200]

Content type
application/json

Copy   Expand all   Collapse all

```
{
-  "results": [
    +  { … }
    ]
}
```

Auto-generated summary for GET distributeURL

Responses

— **200** Successful response

```
GET   /distributeURL                                        ⌄
```

Auto-generated summary for GET /experiment

Responses

— **200** Successful response

```
GET   /experiment                                           ⌄
```

Auto-generated summary for GET /experiment/:id

Responses

— **200** Successful response

```
GET  /experiment/:id                                      ⌄
```

Auto-generated summary for GET /experiment/:id/id-list/:id_list

Responses

— **200** Successful response

```
GET  /experiment/:id/id-list/:id_list                     ⌄
```

Auto-generated summary for GET /experiment/:id/id-list/:id_list/ids

Responses

— **200** Successful response

`GET` `/experiment/:id/id-list/:id_list/ids` ⌄

Auto-generated summary for GET /api

Responses

— **200** Successful response

`GET` `/api` ⌄

Trigger data indexing

Initiates the indexing process for the API database.

Responses

— **200** Indexing started successfully

— **500** Error starting indexing

```
POST  /indexer                                                    ⌄
```

Auto-generated summary for GET queueDirectory

Responses

— **200** Successful response

```
GET  /queueDirectory                                              ⌄
```

Auto-generated summary for GET /:id

Responses

— **200** Successful response

```
GET  /:id                                                         ⌄
```

Auto-generated summary for POST /:type

Responses

— **200** Successful response

```
POST   /:type                                          ⌄
```

Retrieve JBrowse data

Fetches genomic visualization data for JBrowse.

QUERY PARAMETERS

⊣ genomeId
  required

string
Genome ID for JBrowse

Responses

— **200** Successfully retrieved JBrowse data

```
GET   /jbrowse                                         ⌄
```

Auto-generated summary for GET jbrowseAPIRoot

Responses

— **200** Successful response

```
GET   /jbrowseAPIRoot                                    ⌄
```

Auto-generated summary for GET type

Responses

— **200** Successful response

```
GET   /type                                              ⌄
```

Auto-generated summary for GET feature_type

Responses

— **200** Successful response

GET `/feature_type` ⌄

Auto-generated summary for GET /genome/2697049.107626/trackList

Responses

— **200** Successful response

GET `/genome/2697049.107626/trackList` ⌄

Auto-generated summary for GET /genome/:id/trackList

Responses

— **200** Successful response

```
GET   /genome/:id/trackList                                    ∨
```

Auto-generated summary for GET /genome/:id/tracks

Responses

— **200** Successful response

```
GET   /genome/:id/tracks                                       ∨
```

Auto-generated summary for GET /genome/:id/stats/global

Responses

— **200** Successful response

```
GET   /genome/:id/stats/global                                 ∨
```

Auto-generated summary for GET /genome/:id/stats/region/:sequence_id

Responses

— **200** Successful response

GET	/genome/:id/stats/region/:sequence_id	⌄

Auto-generated summary for GET /genome/:id/stats/regionFeatureDensities/:sequence_id

Responses

— **200** Successful response

GET	/genome/:id/stats/regionFeatureDensities/:sequence_id	⌄

Auto-generated summary for GET /genome/:id/features/:seq_accession

Responses

— **200** Successful response

```
GET   /genome/:id/features/:seq_accession                    ⌄
```

Auto-generated summary for GET /genome/:id/refseqs

Responses

— **200** Successful response

```
GET   /genome/:id/refseqs                                    ⌄
```

Auto-generated summary for GET /genome/:id/names/

Responses

— **200** Successful response

| GET | /genome/:id/names/ | ⌄ |

Execute multiple queries

Submits multiple queries to the API and returns combined results.

REQUEST BODY SCHEMA: application/json
required

⊣ queries ›   Array of objects

Responses

— **200** Successfully executed queries

— **400** Invalid query format

| POST | /query/multi | ⌄ |

Request samples

[Payload]

Content type
application/json

Copy   Expand all   Collapse all

```
{
  - "queries": [
      + { … }
    ]
```

```
  }
```

Execute an RPC request

Handles remote procedure calls (RPC) for various API functions.

REQUEST BODY SCHEMA: application/json
required

⌐ method   string

└ params   object

Responses

— **200** Successfully executed RPC call

— **400** Invalid request format

| POST | /rpc | ⌄ |

Request samples

[Payload]

Content type
application/json

Copy   Expand all   Collapse all

```json
{
    "method": "string",
    "params": { }
}
```