**Panel Space: Please use this space for exploriation purposes. There are three endpoints associated with panel space as follows**

**1. GET /panels**

**Description**  
Returns **data** based on an input identifier (Panel\_ID, Rcode, or HGNC\_ID(s)). Providing multiple parameters will return a custom error message due to the complexity of handling these requests. It can also handle partial matches if the user sets Similar\_Matches=true (defaults to False). However, this is still not implemented for HGNC ID. Please see below for the accepted format

**Accepted Query Parameters**

* **Panel\_ID** (string/number, optional)  
  Provide a numeric Panel ID (e.g., 123).
* **Rcode** (string, optional)  
  Provide a code like R208.
* **HGNC\_ID** (string, optional)  
  Provide a single HGNC ID (e.g., HGNC:1100) or comma-separated multiple IDs (e.g., HGNC:1100,HGNC:2200,…).
* **Similar\_Matches** (boolean, optional)  
  If true, the endpoint attempts partial or “similar” matching (like LIKE queries in the DB). Defaults to false. This is not implemented when providing HGNC IDs and will raise an internal server error with 500 status code.
* **Confidence** (Choice (string), required)  
  Based on the value, retrieves only genes that match the criteria, i.e, Green/Amber/Red or ALL (default value)

**Return Format (JSON)**

If one valid identifier is provided and matches the database records The API provides data based on the input parameter as follows:

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  Description automatically generatedIf Panel ID:
* A screenshot of a computer program

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Returns a Json object with each element representing a gene information (HGNC ID, symbol, Grch 38/37 chromosome, start and stop ), Any R code that utilises this panel ID and its associated version and the confidence of the gene within that R code.

* A screenshot of a computer screen

  Description automatically generatedIf R Code provided:

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Returns a Json object with each element representing a gene information (HGNC ID, symbol, Grch 38/37 chromosome, start and stop ), all Panel IDs withing this rcode and its associated version and the confidence of the gene within that R code.

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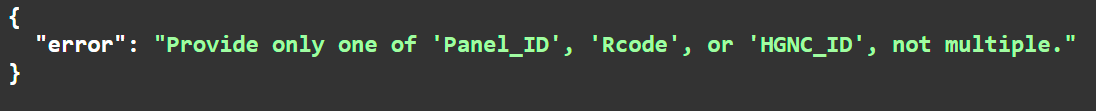
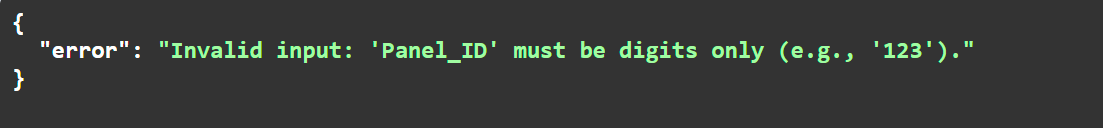
  Description automatically generatedIf HGNC ID(s) provided:

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Description automatically generated

Returns a Json object with all the associated panel IDs and R codes

* If **no matches** are found, you typically get:
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  Description automatically generatedReturns a custom message to inform users of not matches found but with a 200 reponse
* If you **pass multiple identifiers** at once (e.g., Panel\_ID **and** Rcode), we raise a custom message with a 400 reposne as follows:
* If you **pass an invalid identifiers** with formatting issues, we raise custom error messages with 400 response to users to showcase the correc format

**2. GET /panels/download**

**Description**  
Generates and **returns a BED file** representing exome data from an **external** API call (e.g., the VariantValidator gene2transcripts\_v2 endpoint). This means it queries an online service for each gene and then formats the result into a **BED** file.

**Accepted Query Parameters**

* **Panel\_ID** or **Rcode** or **HGNC\_ID**
  + Exactly one of these should be provided.
  + HGNC\_ID can be a single ID or multiple comma-separated IDs.
* **Similar\_Matches** (boolean, optional)
  + Same logic as /panels for partial matching. This does not raise an error and only matches the exact HGNC ID(s) when provided.
* **genome\_build** (Choice(string), required)
  + Typically "GRCh38" or "GRCh37". Default is "GRCh38".
* **transcript\_set** (Choice(string), required)
  + Usually "all", "refseq", or "ensembl".
  + Default is "all". Please see visti [] for more informaiton.
* **limit\_transcripts** (string, optional)
  + e.g., "mane\_select", "mane\_plus\_clinical", "all".
  + Default will be "mane\_select".
  + "all" is equivalent to select option in variant validator api. Please visit [] for more information

**Return Format**

* **On success**:
  + A **BED file** (MIME type: text/plain) is returned as a downloadable attachment. Please copy the complete endpoint url and paste it into a new tab to download the file. This file should contain all the genes that make up a panel/rcode. IF HGNC ID(s) provided, it will retrieve only user-specified genes
  + Data consists of Chromosome, start, stop, <gene>\_<exon>\_<transcript id> , strandedness
  + The filename typically follows the user provided parameters.

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* **On error**: returns a **JSON** with an "error" message and HTTP code **400** or **500**

**3. GET /panels/download/local**

**Description**  
Similar to the **“download”** endpoint above, but uses a **local** BED records stored in our own database tables (bed37 or bed38). This does **not** call an external API. It relies on local copies of BED data. This endpoints should be used if contacting variant validator fails.

**Accepted Query Parameters**

* **Panel\_ID** or **Rcode** or **HGNC\_ID**
  + Must provide exactly one.
  + HGNC\_ID (s) can be comma-separated.
* **Similar\_Matches** (boolean, optional)
  + If true, partial matching for only Panel\_ID or Rcode.
* **genome\_build** (string, optional)
  + Either "GRCh37" or "GRCh38". If not specified, often defaults to "GRCh38".
* Possibly your code also requires:
  + **transcript\_set** (e.g., "all")
  + **limit\_transcripts** (e.g., "all")  
    (Check your parser logic; these might be mandatory or defaulted.)

**Return Format**

* **On success**:
  + A screenshot of a computer

    Description automatically generated**A BED file** (MIME type text/plain) with local database data. However, the format is slightly different. As shown below:
  + Return data consists of : chromosome, start, end , <gene>\_<exon>, strandedness, transcript id (Gencode only), type (options[mane select (ms), mane plus clinical (mpc), canonical (can)], HGNC ID.

Note: Type was used to simplify database creation of all bed records. GTF was used to extract all the necessary genes information. However, the complexity of having many transcript records resulted in having multiple records for some exons, which can be confusing. To overcome this more simply. The records were filtered based on priority. If ms is found for a given exon, the database will only have these records and ignores mpc and can. If ms not found, the database will then try to get any mpc records if exist and will ignore canonical. Finally If neither records were found then the database will only retrieve any canonical records. This prevents creating duplicate records which can interfere with sorting downstream. It is also important to note that ms and mpc can also be considered canonical.

* + if no data found or missing parameters returns a custom message.

**4. GET /patient**

**Description**  
Returns **patient test records**. If only a Patient ID is given, it lists **all R codes** (plus versions/dates) that patient has. If only an R code is given, it lists **all patients** who have that code. (Originally, it can also handle version comparisons, but we’re skipping that scenario if data is always up to date.)

**Accepted Query Parameters**

* **Patient ID** (string, optional)
  + e.g., T123.
* **R code** (string, optional)
  + e.g., R208.

**Return Format (JSON)**

**A) Only Patient ID Provided**

json

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{

"Patient ID": "T123",

"patient records": {

"0": {

"2023-12-30": ["R208", 2.5]

},

"1": {

"2022-05-16": ["R167", 1.5]

}

}

}

* Each key in "patient records" can be an index (0, 1, 2...) whose value is a date → [Rcode, version].

**B) Only R code Provided**

json

Copy code

{

"R code": "R208",

"Records": {

"0": {

"2023-12-30": ["T123", 2.5]

},

"1": {

"2023-04-10": ["T456", 1.0]

}

}

}

* Each key in "Records" is an index (0, 1, 2...) whose value is a date → [Patient\_ID, version].

**C) Both Provided**

*(Your code might do version checks or simply return a “no version change” message if everything is up to date.)*

json

Copy code

{

"disclaimer": "Panel comparison up to date",

"status": "No version change since last T456 had R100",

"Version": "5.0",

"Panel content": {

"HGNC:132": 3,

"HGNC:20000": 2

}

}

*(If you are skipping version changes entirely, you might always see the “no version change” format, or just a fallback message.)*

**D) Edge Cases**

* **If neither Patient ID nor R code is given**: Some code returns a **200** with:

json

Copy code

{

"Patient ID": null,

"patient records": {}

}

or you might choose to return a **400** if you want to enforce that at least one param is required.

**5. GET /patient/bed**

* **Purpose**
  + **Creates a BED file for a given patient and optionally a specific R code & version, calling the VariantValidator API. Note that, it only returns a bed file if the patient has a single instance of record or else asks user to be more specific based on scenarios.**
  + **Similar to /panels/download but specifically for a patient’s previously recorded R code and version.**
* **Query Parameters (Required)**
  + **Patient ID (string)**
  + **genome\_build = GRCh37 or GRCh38**
  + **transcript\_set = refseq, ensembl, or all**
  + **limit\_transcripts = 'mane\_select + mane\_plus\_clinical', 'mane\_select', 'canonical'**
* **Query Parameters (Optional)**
  + **R code (string)**
  + **version (string, e.g. 2.5)**
  + **Padding (int, default=0, max=250) for adding bases around intervals.**
* **Logic Flow:**
  + - **If Patient id provided and R code/version missing, tries to auto-detect all records from the database records records and returns a json object with multiple records (if present) or a bed file if only a single associated record is identified. If multiple or none → returns a custom message to guide user to provide more parameters.**
    - **If R code provided and version missing but multiple versions records were associated with the patient → returns a message to specify the version the user would like to create the bed for.**
    - **If both provided → checks that (patient\_id, r\_code, version) actually exists in patient\_data.**
    - **Checks whether version is out of date vs. DB’s newest version. If older → uses archived genes from panel\_genes\_archive; if current → uses panel\_genes to create a list of genes.**
    - **Calls VariantValidator with the final gene list.**
    - **Returns a .bed file named: "<patient\_id>\_<r\_code>\_<genome\_build>\_<limit\_transcripts>.bed".**
* **Response Examples**
  + **A screenshot of a computer screen

    Description automatically generatedSuccessful: HTTP 200, text/plain with BED data. Patient ID: T123 with a single R208 records:**
  + **A screen shot of a computer program

    Description automatically generatedMultiple records found when no R code was provided: Patient ID:**
  + **A black screen with white text

    Description automatically generated If patient ID does not match our records the json object consists of following message:**
  + **No BED failed to generate for some reason will return :**

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* + - **Please report this by raising an issue as this needs to be investigated**
  + **External API error custom API error with the following message:**

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* + - **(HTTP 400 or 500 depending on the cause.)**

**Usage Summary**

1. **GET /panels**: Query by Panel\_ID, Rcode, or HGNC\_ID to retrieve basic panel info in **JSON**.
2. **GET /panels/download**: Download a **BED file** from an **online** gene/transcript service for your specified panel/gene.
3. **GET /panels/download/local**: Download a **BED file** from a **local** DB table (bed37, bed38) rather than the online service.
4. **GET /patient**: Query by Patient ID or R code to see who had that code or what codes that patient had. Returns **JSON** with historical test data.