Pharmacogenomic Insights (PGXI) Website API Manual

For Pharmacogenomic Insights Website version 1.1

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Introduction

This document describes how to use the PGx Insights API. It will allow you to make educated decisions regarding what information you wish to translate into reports, what information you want to keep for your organization's management or healthcare system, what information you may need to provide should you need to engage with support, and what information you may feel comfortable discarding entirely.

Authentication Configuration File

To use the API, you must first authenticate to the Qiagen authentication server using credentials obtained by the PGxInsights server. Use the ClientID and Client Secret provided by your account representative to create a device code from the Server here: pgxinsights.com/getdevicecode. The final step of the device code wizard will provide a file called PGxI_Config.json with the credentials that your process can use to obtain an access token from the Qiagen server. The format of the request for an access token is in the cURL request that the device code process provides.


```
{
 "AuthServer": "https://apps-beta.ingenuity.com/qiaoauth/oauth/device/code",
 "TokenServer":        "https://apps-beta.ingenuity.com/qiaoauth/oauth/token",
 "ClientId":     "68946889-...",
 "ClientSecret":        "a09be592-...",
 "UserCode":   "EljIQ67r",
 "DeviceCode":        "b196d2f4-...",
 "CodeVerifier": "zZlURk...",
 "Credentials": "Njg5NDY4ODkt..."
}
```


In this file:

- **AuthServer** is the Qiagen authentication server that you obtained the device code from
- **TokenServer** is the Qiagen server where you will obtain an access token to use the API
- **ClientId** is the ID that you used to obtain the DeviceCode
- **ClientSecret** is the secret used to obtain the DeviceCode
- **UserCode** is the temporary code that used to obtain the DeviceCode
- **DeviceCode** is the code that used to obtain the access token
- **CodeVerifier** used by the Qiagen server to authenticate the DeviceCode
- Credentials are the base64 combination of ClientId and ClientSecret provided as a convenience

Calling the API

Step 1. Based on your JSON, ensure the following keys and values are present:

- **TokenServer**: https://apps-beta.ingenuity.com/qiaoauth/oauth/token
- **DeviceCode**: b1...
- **CodeVerifier**: zZ...
- **Credentials**: Nj... - (This is the Base64-encoded string of ClientId:ClientSecret.)

Important: You have already performed the device code request (and thus, have the **device_code**). You only need to exchange it for an access token.

Step 2. Construct Your Token Request.

Use an HTTP POST to the **TokenServer** URL. You must include:

- **Authorization header**:
  - Authorization: Basic <PGxI_Config.json.Credentials>
- **Content-Type header**:
  - Content-Type: application/x-www-form-urlencoded
- **Form fields**:
  - grant_type=urn:ietf:params:oauth:grant-type:device_code
  - device_code=<PGxI_Config.json.DeviceCode>
  - code_verifier=<PGxI_Config.json.CodeVerifier>

Step 3. Handle the Response.

If the Device Code is valid and the user is authorized, you should receive a JSON containing an access_token, token_type, expires_in, etc., for example:

```
{
 "access_token": "YOUR_ACCESS_TOKEN_HERE",
 "expires_in": 3600,
 "token_type": "Bearer",
 "refresh_token": "...",
 ...
}
```

Note Store the access token safely AND use the access_token in the Authorization header for subsequent API calls:

Common Errors

expired_token or **expired_device_code**: The Device Code is no longer valid. You must restart from the step where you request a fresh device code.

Once you have an access_token, you can call your protected APIs by adding Authorization: Bearer <access_token> to your requests.

API Request Structural Example

```
public class ApiRequest
{
  public string RequestId { get; set; }        // Unique ID for the request
  public DateTime RequestDateTime { get; set; }  // Request time and date
  public string? RequestNotes { get; set; }     // Any processing notes
  public List<ApiOutput> Outputs { get; set; }   // A list of input files
```

```
    public List<ApiInput> Inputs { get; set; }    // A list of output files
}
public class ApiInput
{
    public string  FileName { get; set; } = string.Empty;
    public string? FileType { get; set; } = string.Empty;    // Optional
    public int     FileTypeId { get; set; }                  // Optional
    public string  FileContent { get; set; } = string.Empty; // Base 64 encoded
    public string? Nomenclature { get; set; } = string.Empty;
}
public class ApiOutput
{
    public string OutputFileType { get; set; } = string.Empty;
}
```

API Responses

Responses to API requests will be JSON encoded with the following potential data types:

- **Variants JSON:** A list of variants determined from the input file and mapped to a canonical format. For each variant, the output provides:
    - SampleId
    - Gene
    - RSID
    - HGVS – the most common label for the variation
    - Build37Hgvs – the full HGVS designation for build 37
    - Build38Hgvs – the full HGVS designation for build 38
    - Chromosome
    - Zygosity – Wild Type (WT), Heterozygous (HET) or Homozygous Mut (MUT) or the number of copies reported by copy number variations
- **Variants CSV**: The same data is available in the Variants JSON file in tabular format, base 64 encoded.
- **Genotypes JSON:** A list of genotypes determined from the input file or based upon submitted variants. For each genotype, the output provides:
    - SampleId
    - Gene
    - Genotype – may be in star allele format for haplotyped genes or the genotype (e.g., c.421C>A C/C) when an individual gene variation is associated with clinical insights.
    - Phenotype – the phenotype associated with the genotype.
    - Activity Score – optional and only available for genes for which the activity score is relevant.
- **Genotypes CSV:** The same data is available in the Genotypes JSON file in tabular format, base 64 encoded.
- **Processing Notes (these are included with all output types)** – describe any errors or informational messages created while processing input files.

- **Insights JSON** – goes over the prescribing insights, Genetic Conditions, Potentially Impacted Medications and overall test summary of the processed sample. Details regarding the output of the Insights JSON output listed below.

Insights JSON

Prescribing Insights

This section describes the content of the prescribing insights returned from API requests.

- The case ID number is associated with the case information in the knowledge base.
- Drug – This is the generic name of the drug.
- GeneticCause is the genetic variation or phenotype that is relevant to the gene-drug interaction.
  TradeNames – these are the brand names of the drug.
- CaseMnemonic – this is a mnemonic used to identify the case.
- Primary Source – this indicates where the primary source of information for the Prescribing Insights comes from.
- Acronym – this is the acronym for the primary source field.
- Severity – this indicates the criticality or importance of the information present. Severity may be 'Informational,' 'Warning,' or 'Critical.'
- Evidence Level—this is the level of evidence accumulated to back up the claims that Prescribing Insights recommends. Levels are 'weak,' 'moderate,' and 'strong.'
- Population – this is the population type that is affected by this.
- Type—this is the type of information that the item being referenced relates to (PGx, Genetic Condition, etc.)
- Title – this is the title that briefly describes the gene-drug interaction.
- BriefDescription – this provides a brief description of the recommendations contained in literature.
- IssueDescription: this will give an overview as to what the problem related to the mediation may be – ex: 'efficacy'
- FullDescription – this will expand on the issue description and give a full explanation of what, if any, the concerns are for the gene and drug in relation to the results of this specific test.
- ApproachDescription – this will provide a recommendation that should be examined when considering applying this drug to a given sample with these genetic results.
- Content – this section will contain a series of follow up information that can be utilized in reporting.
  - Genetic Interpretation – goes over genetic information that may be of value in explaining why there may be concerns in utilizing a given medication; it can also recommend that the medication will function as normal.
  - Prescribing Insights – this gives feedback and warnings regarding what side effects may occur should this given medication be prescribed; it can also recommend that the medication will function as normal.
  - Clinical Consequences – this will indicate whether there may be some kind of consequence when this drug is metabolized under the test result genetic makeup.

- References – this provides references used to build the overall case for the drug-gene association and prescribing recommendations.
    - Title – the title of the article being referenced.
    - Citation – the source of the information, individuals involved in research, developing organization(s), etc.
    - URL – URL to the location of the data being referenced (if available).
    - PubMedId – if available through the National Institute of Health (NIH), this is the library ID used.
    - IsReported – this was previously used to restrict references to include on reports. If it is listed as 'true' it is considered a key reference to utilize.

Genetic Conditions

This section reviews any genetic conditions indicated by the genetic test results.

- CaseId – this is the case identifier in the knowledgebase.
- Condition – the name of the genetic condition.
- Genetic Cause – the genetic marker that causes the genetic condition to occur.
- CaseMnemonic – this is a quick Mnemonic to identify the specific case.
- PrimarySource – this is the primary source of information regarding this genetic condition.
- Acronym – the acronym of the primary source.
- Severity – the severity of the genetic condition in relation to the test results. The possible results, like above, are 'Informational', 'Warning', and 'Critical'.
- Evidence Level – this is the level of evidence ascribed to the information used to develop the case. Levels are 'weak,' 'moderate,' and 'strong.'
- Population – the population demographic type that can be affected by this condition.
- Type – Condition for Genetic Conditions
- Title – If the genetic test results show this condition present, this is the title for this reporting section.
- BriefDescription – A brief overview and cause of this condition based on the genetic test results of the sample.
- GeneticConditions – This section provides detailed information about the genetic condition.
    - Category – these are the titles of the various information pieces that will be provided on the genetic condition based on the genetic test results returned from the given sample, including:
        - Risk Interpretation
        - Genotype/Phenotype Summary
        - Risk Classification
        - Genetic Interpretation

Note Each category has text associated with it

- References – this section covers the references that were utilized to generate the Genetic Condition section and its enclosed data.
    - Title – the title of the article or paper that was being utilized.
    - PubMedId – if the article comes from the NIH, this is the reference number for the article.
    - Citation – all individuals, organizations, and literature involved in the article.

- URL – where the article can be found on the internet.
- IsReported – a database flag indicating whether it is considered key information in generating results.

Potentially Impacted Medications (PIM) Table

This section provides a summary view of medications based on the PGx test results. It is meant as a quick reference section to see the implications of the test on drugs based on their therapeutic class. The repercussions are categorized as 'Informational,' 'Warning,' and 'Critical.'

- Category – this is the indication that drugs treat.
- TherapeuticClass is the classification of drugs based on their intended effect or therapeutic use.
- SeverityList – this section categorizes the severity of drug-gene interactions into Informational, Warning, or Critical issues. Each severity contains a list of drugs and includes:
  - DrugId: The identification number of the drug in the PGxI Database.
  - Drug Name: The generic name of the drug. (ex: acetaminophen)
  - TradeNames: The brand names of the drugs (ex: Tylenol).
  - IsPgx: value 1 means it has actual PGx guidance. Value 0 means it is just an alternative not affected by genetics.

Test Summary

This section summarizes the genetic test results in the file and associates them with known clinical consequences.

- PID: This is the name of the sample from the file. It may also be referred to as the test accession number.
- Gene: The name of the gene that was being tested.
- Genotype: The genotype called for the gene in question.
- Phenotype: The phenotype of the gene listed against the sample.
- Clinical Consequences: A summary of the implications of the phenotypes.

Document Revision History

Revision	Description
May 2025	Initial release for Pharmacogenomic Insights Website version 1.1