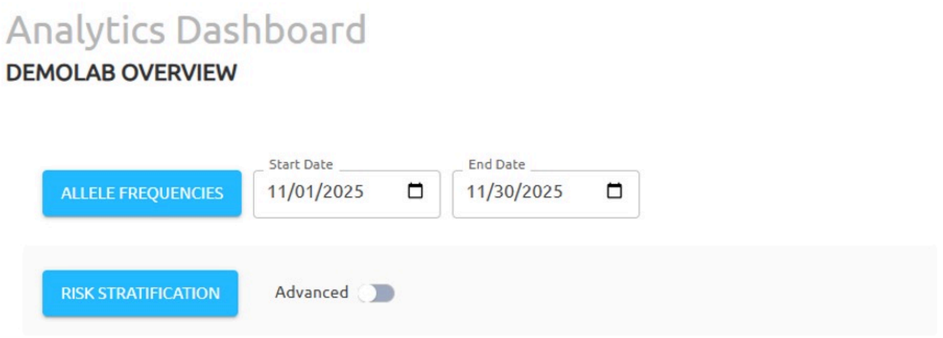
Analytics Dashboard
User Manual

Choosing the right medication requires evaluating multiple clinical factors, including the condition being treated, a patient's current medication list, age, organ function, comorbidities, and pharmacogenetic profile. When these factors are considered together, prescribers can reduce the risk of adverse events and improve treatment effectiveness.

While not every factor applies to every medication, pharmacogenetics plays a critical role for a defined set of drugs with strong evidence for clinically meaningful drug–gene interactions. Using prescription and patient data helps organizations identify who may benefit most from pharmacogenetic testing and other targeted clinical interventions.

To support this, **GenXys now offers the enhanced Analytics platform**, a web-based portal that allows you to upload clinical or prescription data and generate insights using powerful tools such as **risk stratification** and **allele frequency analysis.**

The platform is continuously expanding, with new modules and analytics capabilities being added to help organizations better understand their populations, optimize testing strategies, and drive data-informed decision-making.



Allele Frequencies:

The Allele Frequency Calculator provides a fast and accurate way to understand how common specific star alleles are within your tested population.

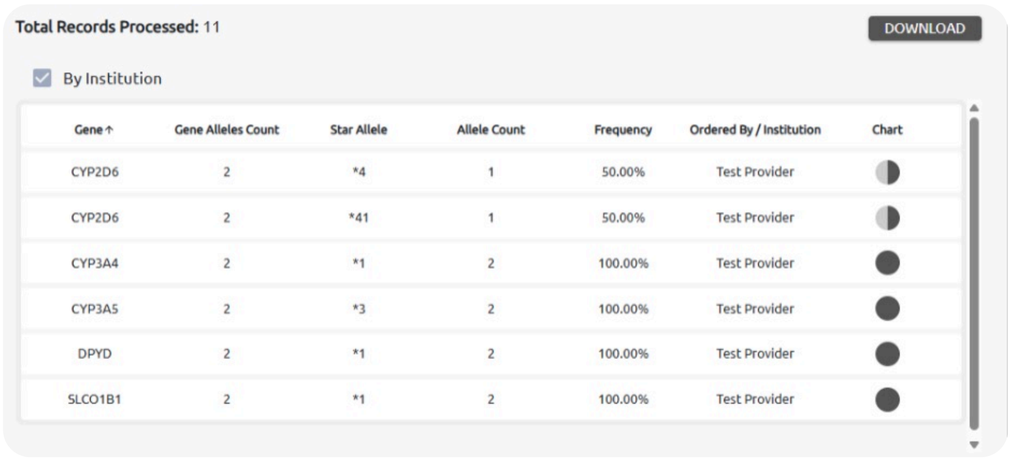
By analyzing uploaded genetic results, the tool calculates allele distribution patterns that can support clinical decision-making, panel design, population studies, and quality assurance.

The calculator reports three key values:

Gene Alleles Count: The total number of alleles observed for the selected gene across all individuals in the dataset.

Allele Count: The total number of times a specific star allele appears within the population.

Frequency: The percentage obtained by dividing the Allele Count by the Gene Alleles Count, representing how prevalent the allele is in your population.



Gene	Gene Alleles Count	Star Allele	Allele Count	Frequency	Ordered By / Institution	Chart
CYP2D6	2	*4	1	50.00%	Test Provider	
CYP2D6	2	*41	1	50.00%	Test Provider	
CYP3A4	2	*1	2	100.00%	Test Provider	
CYP3A5	2	*3	2	100.00%	Test Provider	
DPYD	2	*1	2	100.00%	Test Provider	
SLCO1B1	2	*1	2	100.00%	Test Provider	

GenXys PRESCRIBING SYSTEMS

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Report Components

1. **Total Records Processed**
   Shown at the top of the report, this number indicates how many individual test records were included in the calculation (e.g., 11 records processed).
2. **Grouping Option – "By Institution"**
   When enabled, results are organized by the ordering provider or institution. This allows users to compare allele frequencies across different clinics, labs, or provider groups.
3. **Data Table Columns**

- ***Gene***
  The gene for which allele frequency is being calculated (e.g., CYP2D6, CYP3A4).
- ***Gene Alleles Count***
  The total number of alleles observed for that gene across all individuals in the dataset.
- ***Star Allele***
  The specific star allele variant being measured (e.g., *4, *41, *1).
- ***Allele Count***
  The number of times this star allele appears across the tested population.
- ***Frequency***
  The percentage calculated as:
  (Allele Count ÷ Gene Alleles Count) × 100
  This represents how common the star allele is within the population.
- ***Ordered By / Institution***
  Indicates the provider or institution associated with the uploaded data. This helps users track allele frequencies at the clinic or lab level.
- ***Chart***
  A visual pie-style indicator showing the proportion of the allele within the gene's allele pool. Larger shaded portions represent higher allele frequencies.

Download Option

A Download button allows users to export the full dataset for further analysis, reporting, or integration with external workflows.

Risk Stratification

The Risk Stratification tool is designed to help organizations identify pharmacogenetic (PGx)–suitable candidates using validated, evidence-based criteria. Built on models tested against 1M+ patient records and over 10 million data calculations, the tool provides a reliable and scalable way to surface individuals who may benefit most from pharmacogenetic testing.

Using an intuitive query builder, users can define clinical conditions, medication thresholds, and logical AND/OR groupings to generate precise patient segments.

The tool also integrates with population health databases and includes evidence-based inappropriate prescribing detection, ensuring that high-risk or PGx-relevant cases are captured accurately. For user convenience, we have 13 pre-built queries.

Each query produces its own risk result, enabling organizations to prioritize follow-up, reduce medication-related harm, and support targeted interventions.

1. **File Preparation:** Prepare a CSV file of your data.
2. **File Upload:** Frag and drop or upload the file to run a query
3. **Results:** View the result and download the groups(s) of patients that you want to test.

File Preparation

The Risk Stratification import file must be a CSV file. It must contain a header row with the following names:

Column Name	Data Type (Maximum Length)
PatientId	String(50)
DrugName	String(512)

Risk Stratification determines the header row in the import file by first occurrence of the word: ***"PatientId".***
All the rows that follow the header row represent the data and must match the position of the header column.

The Risk Stratification import file supports comma or tab separators (but not both in the same file).
The Risk Stratification import file may contain other header columns and values; however, it ignores this information.

Here is an example of a Risk Stratification import file:

PatientId	DrugName
P1	PHENYTOIN
P1	RASBURICASE
P1	AMILORIDE
P1	CALAN
P1	BUSPIRONE
P1	TYLENOL
P2	PREDNISONE
P2	VALSARTAN
P2	AZITHROMYCIN

Two or more rows for one patient with the same drug name count as one drug in the results.

Risk Stratification uses only the data uploaded for current user's Risk Stratification job and no information is saved or stored.

The maximum size of aRisk Stratification data file is 5,000,000 bytes.

PatientId and DrugName values match using whole-word and case-insensitive comparisons.

The drug name values provided can be any drug and do not need to match drug names linked to cardiovascular disease, drug gene interactions, and mental health issues.

Once you have prepared your file log in to the portal and launch Analytics

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File Upload

To launch Risk Stratification, a user needs a valid license for TreatGx, ReviewGx, or LabGx.

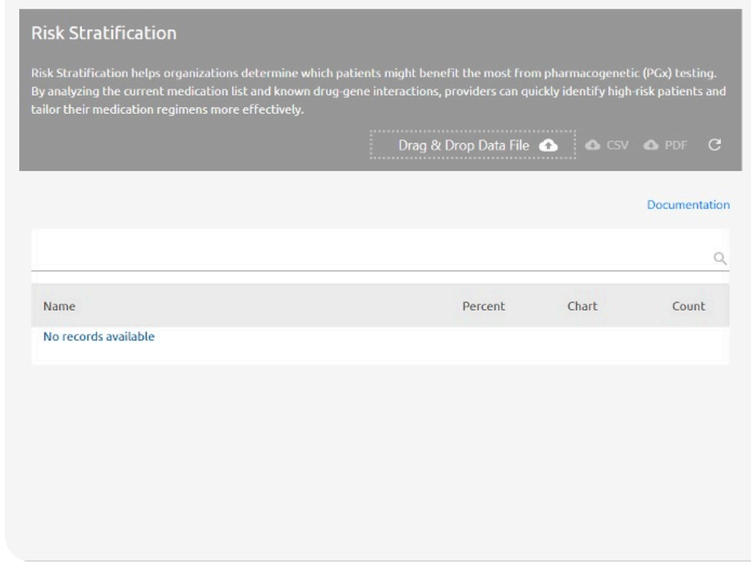
Log into the portal.

There you will see your products – click on ***"Launch" Analytics***

You will then need to upload your file.

Click on the Drag and Drop Data File to bring up the file window and select your file.

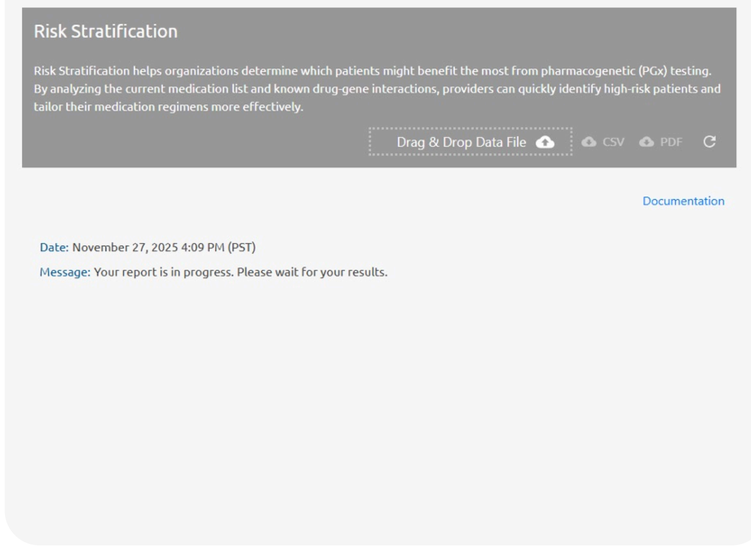
Confirm you want to upload the file.



The system will then start reviewing your data and analyzing it. If the data is not formatted correctly, the system will notify you. Analysis may take a couple of minutes to much longer, depending on the size of your file.

Results

As soon as the analysis is complete, the information is displayed.
These summary results can be saved by clicking the download file button next to the "Drag and Drop Data File" button.



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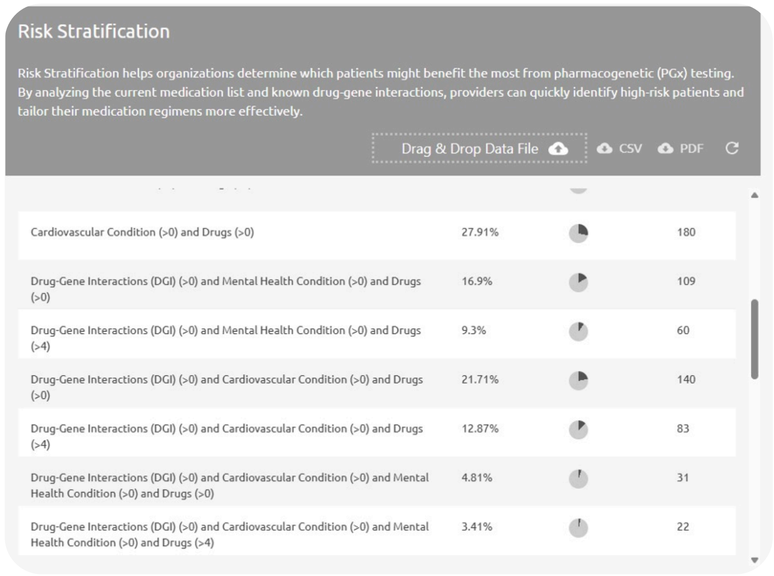
Finally, you can download the summary of the results in a CSV format by clicking the download icon next to the “drag and Drop” tab

A CSV file will be downloaded.

The first column is the criteria, the second is the percentage meeting that criteria, then the count, and in the fourth column, the patient IDs are separated by a comma.



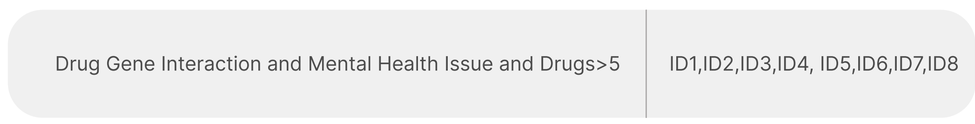
In this example, I am interested in patients

1. Taking a drug with known DGI,
2. Polypharmacy,
3. and also taking mental health drugs

Download the file which is a CSV and open it in Excel or similar.

You will then see the rows of criteria with the IDs in the next column.

If you wanted to look at those patients one way is to copy that cell with the Patient identifications of the patients and drop it into word, and then replace the comma with a line break.



Column D contains the patient IDs

Example:

Go down to row 12 that corresponds to the patients with

Drug Gene Interaction and Cardiovascular Disease and Mental Health Issue and Drugs (>0)

D12 has the Ids of all your patients. They are all in one cell - separated by commas.

To make them into a column of ID’s to look up on your EMR;

1. Copy that cell and paste it into word.
2. Highlight all those numbers in word.
3. Then apply the find and replace the comma with a paragraph mark and you will have your list of ids for the patients to look up on your EMR.