

Proteograph™ Analysis Suite Quick Reference

Proteogenomics Workflow

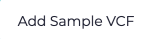



Variant Peptide Search Set-Up

1. Add variant call files (VCF)


Navigate to  **Data Files** then **VCF Files** and upload a VCF for each sample.

Single VCF upload

To upload a .vcf for a single sample, select  and either select an existing sample from the drop down menu or input a custom sample name corresponding to the sample name used in a plate map file. Select  to add the corresponding .vcf file.

-OR-

Batch VCF upload

To upload multiple samples, select  and choose files to upload. Additionally, provide a .csv file containing the mapping of the sample name to the .vcf file name.

Batch Upload


2. Analysis setup

Optionally, add a plate or link to a plate.


Create a Project and proceed to **Step 3** prior to launching analysis.

For more details, see the *Proteograph Analysis Suite Quick Reference: Add a plate, Link to a plate, and Create Project from plates.*

3. Launch analysis

Navigate to  **Projects** and select previously created Proteogenomic Project(s) containing samples with added .vcf files.

Select  to analyze samples.

Ensure the  **Proteogenomics Analysis Protocol** is selected and verify a .vcf is uploaded for each sample in the Project.

Proteogenomics Analysis Results

Navigate to  **Analyses** and select completed proteogenomics analyses-of-interest.

1. Variant Peptide Browser


Navigate to **Variant Peptide Browser** and examine variant peptide search results (left table) and counts per sample (right bar graph).

To browse data, click on a variant (left table) to view reference and variant peptide intensity per sample.

Select a variant ID (e.g., [T94380925A:E5V](#)) to view a variant peptide in the Proteogenomics Data Explorer.




2. Proteogenomics Data Explorer

Navigate to **Proteogenomics Data Explorer** to view peptides in a genomic space.

Select   to view peptides with respect to genomic coordinates.

Select  to expand results by sample.

Select  **Display Introns** to display/hide introns.

Select    to navigate across a protein sequence.