Upload Data

Click the Open Files icon in the main toolbar.

Add GenBank Files (GBK/SEQ) and/or Reference Files (SCF/AB1/ABI).

Note: Both GenBank and Reference files are optional when sequences map to genes of Homo sapiens.

Add Sample Files (SCF/AB1/ABI)

Click OK.
Double-click on the files in the Browser pane to view the trace data.
Analysis Settings

In the main toolbar select Process → Settings...

For first run analysis click Default then OK
Analyze Your Data!

Click Run icon in main toolbar.

You samples will be compared to references

The first window to appear is the Mutation Report.
By double-clicking a mutation cell in the **Mutation Report**, the **Graphical Analysis Display (GAD)** window appears.

- **Forward Reference Trace**
- **Forward Sample Trace**
- **Forward Comparison**
- **Reverse Comparison**
- **Reverse Sample Trace**
- **Reverse Reference Trace**
- **Mutation Table**
Click **Custom Report Builder** icon in main toolbar.

Default settings will group samples by Contig and pair Forward and Reverse samples.
Click **Display** menu in main toolbar and choose **Project Reviewer Report**.

Show All Contigs simultaneously, group traces by Sample ID, view information in many ways.
Print Clinical Report

- Click **Clinical Report** icon in main toolbar.
- Add a Custom **Header File**
- View and print a snapshot of each mutation call