

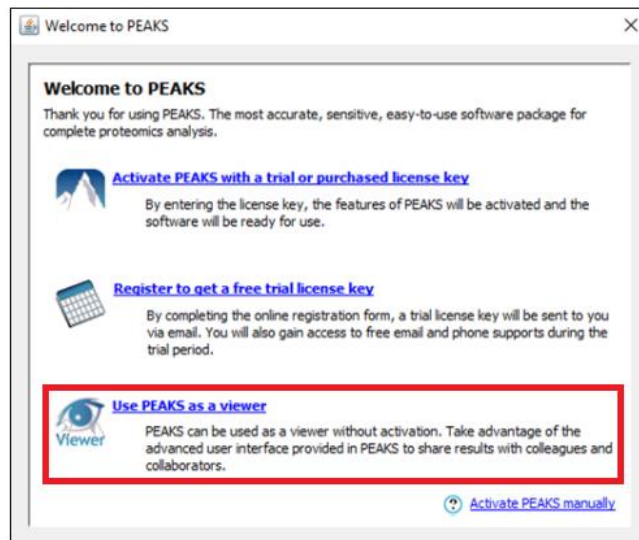
What is PEAKS Viewer?

PEAKS Viewer is a way to share your PEAKS Studio results with researchers, colleagues, and collaborators around the world. The Viewer allows you to open completed PEAKS projects to view, filter and export, just like you are using the licensed version!

Note: For projects created in PEAKS 8.5 and newer, the results can be viewed in the same version of PEAKS or newer. For example, PEAKS 8.5 projects can be viewed in the PEAKS 8.5, X, X+ or Xpro Viewer, but projects created in a newer version of PEAKS cannot be viewed in an older PEAKS Studio version Viewer. For projects created in PEAKS 8.0 and older, the same version that the PEAKS project was created on needs to be used to view the results in PEAKS Viewer.

How to Setup PEAKS Viewer?

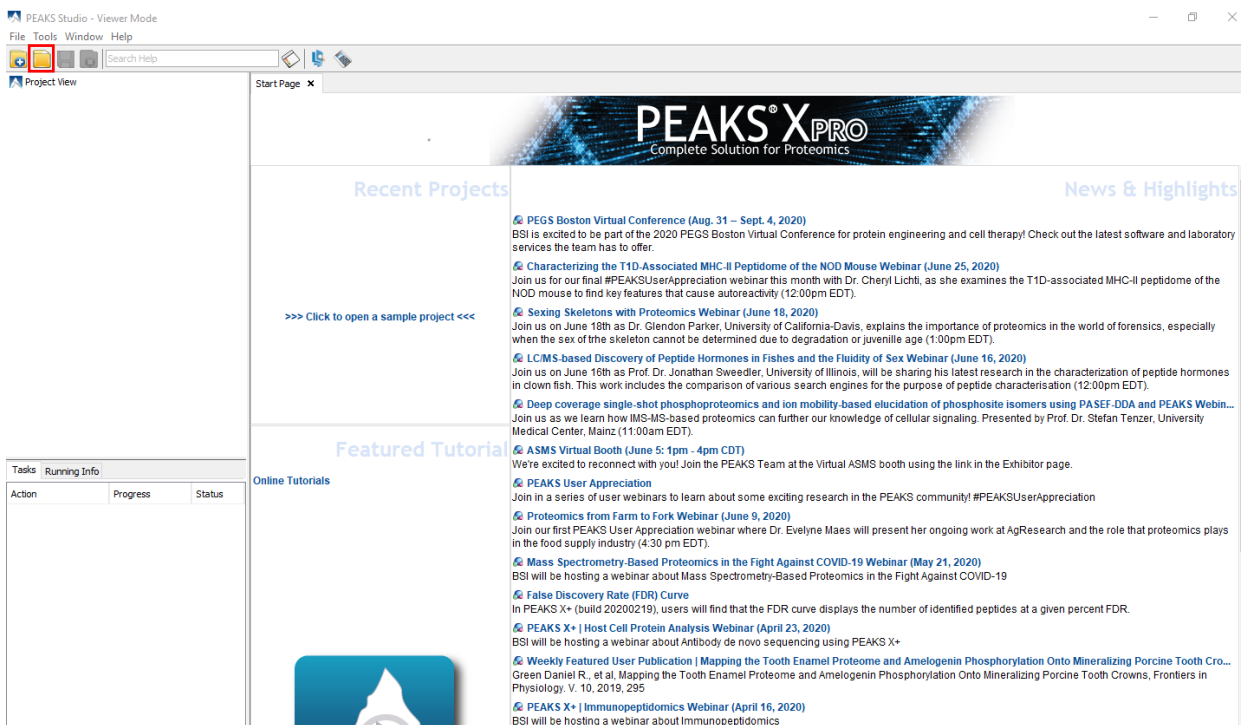
1. Download PEAKS Studio from the Bioinformatics Solutions Inc. website.
(<http://www.bioinfor.com/download-peaks-studio/>)
2. Run the PEAKS Studio Installer by double-clicking on the file that was just downloaded.
3. Install the program by following the on-screen instructions. PEAKS will by default install into the C:\ drive and will generate a folder called C:\PEAKSStudio[version].
4. Now that PEAKS is installed, you can launch the software by going to the Start menu and selecting PEAKS Studio.
5. When PEAKS Studio opens, the License Wizard will appear. Please select the third option as seen below.



6. PEAKS Viewer will then open and allow you to open your PEAKS Studio project.

Navigating through PEAKS Viewer

1. To open a project, click on the Open Project icon, or choose File > Open Project from the menu bar.
 - A dialogue box will appear. Browse to the location where your PEAKS project is stored, select the entire folder, and click open.



2. In the Project View pane located in the upper left-hand side of the window, you will see your PEAKS project organized in a tree graph with different nodes like the Data refine node.
3. Double clicking on the results node will open a summary page on the right side of your screen. The Summary page will provide an overview of the data searched with filters that can be adjusted. Moreover, the results can then be exported by clicking on the “Export” button.
4. The Summary page will also display several tabs:
 - The Feature tab contains a list of all detectable features that passed the filters. Each feature will list all the MS/MS scans associated with it.

- The Protein tab will display a list of the identified proteins and a visual representation of the coverage of each protein.
- The Peptide tab shows all the peptides identified as well as spectrum details and MS/MS fragmentation details.
- The De novo Only tab contains all the peptides that were generated by De novo sequencing that were not matched to the database.