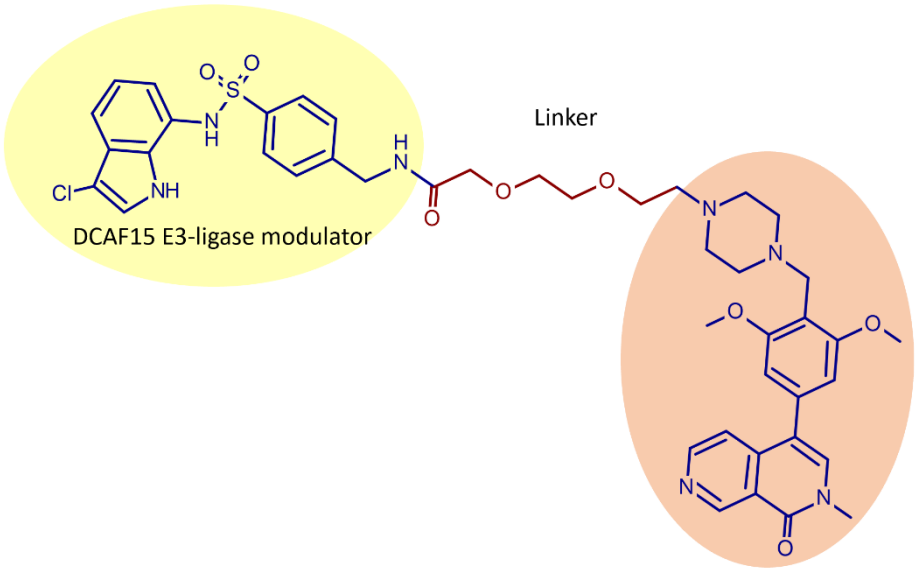
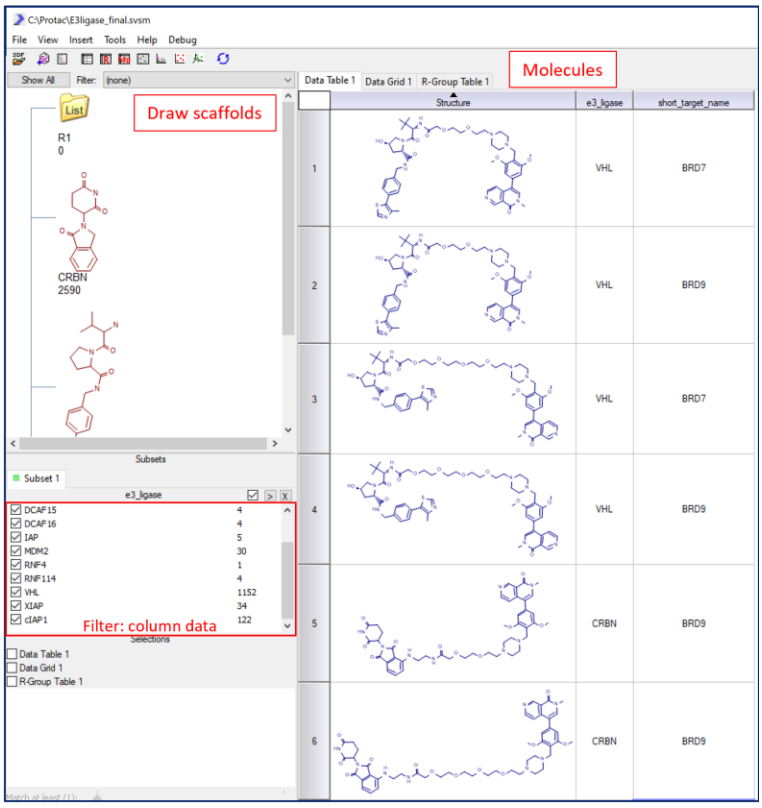
PROTAC Analysis tool

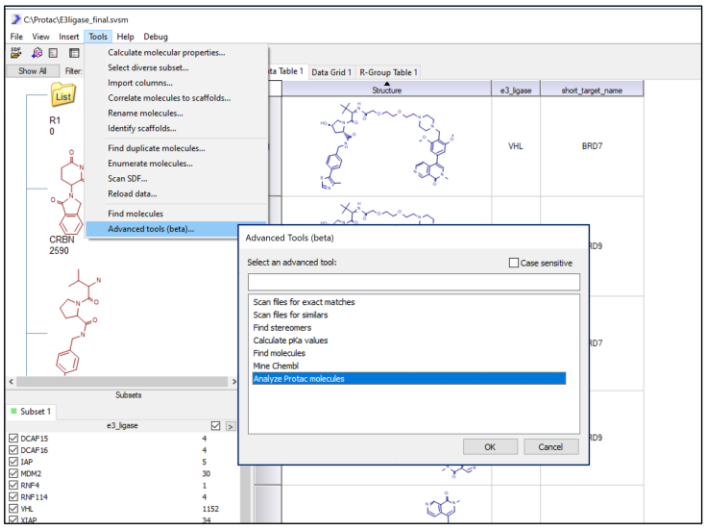


The PROTAC analysis tool breaks up PROTAC-molecules into their constituent parts. The algorithm identifies the linker that joins the two ligands. It compares the ligands against a known list of PROTAC modulators to identify the E3 ligase modulator as 'R1' positions it on the left side of molecule, extends the linker horizontally in the middle of the molecule, and identifies the remaining ligand as the warhead ('R2') placing on the right-hand side of the molecules. Using ***SARvision|SM***, molecules can be readily browsed, filtered and molecule properties calculated. In a folder name 'R1' in the scaffold tree, the user can add any new or proprietary E3 ligase molecules that the algorithm is not identifying by placing into the 'R1' column.

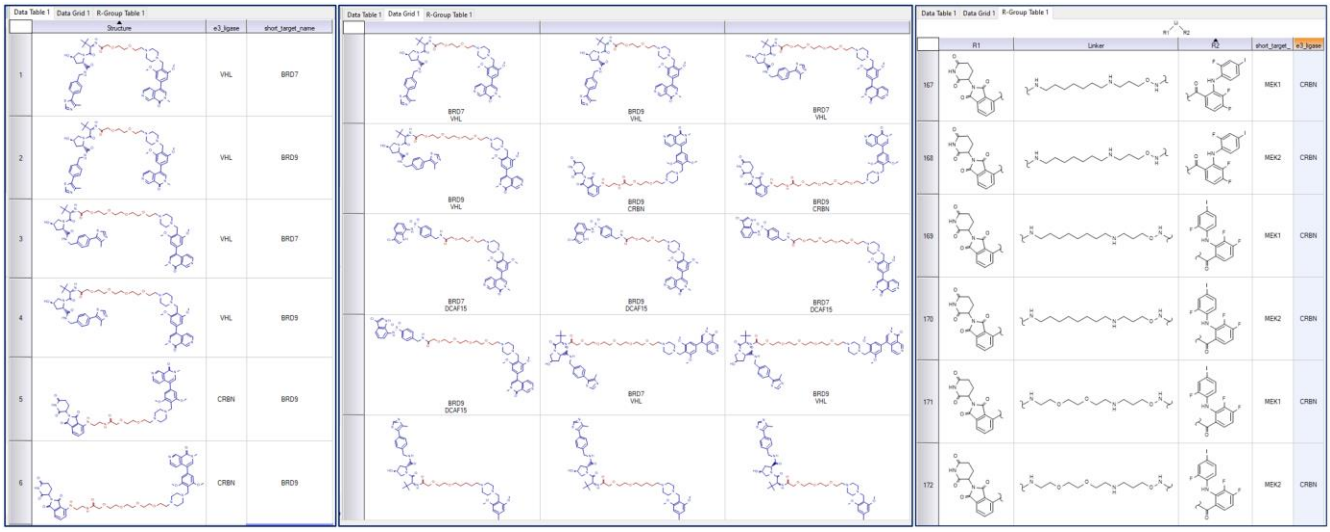
1. Open a set of PROTAC molecules for study (file->open sdf or project file).



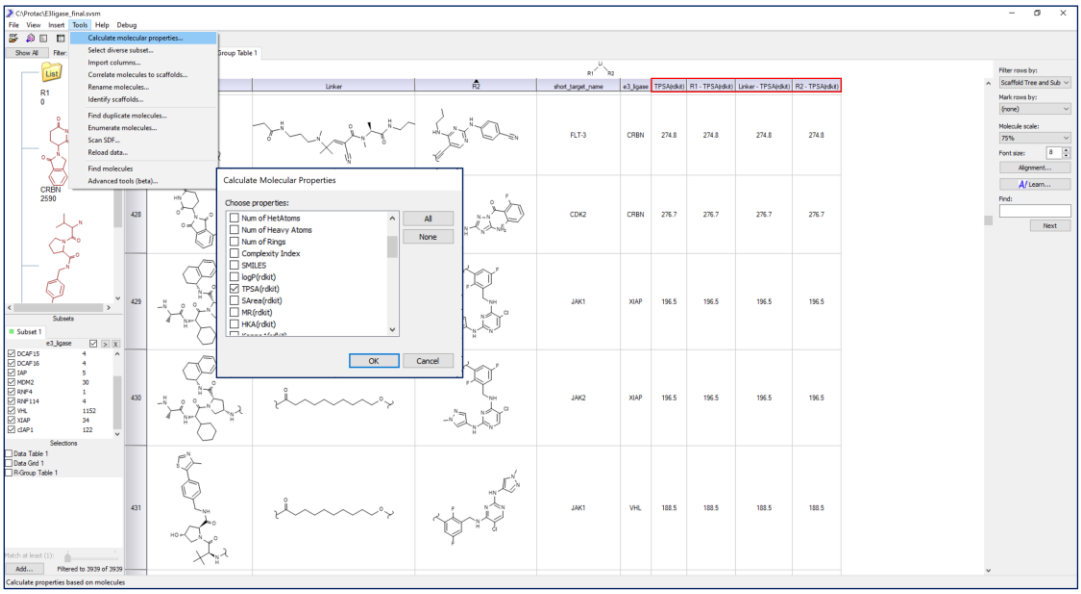
2. Under tools->Advanced tools->Analyze PROTACs implements an algorithm to break PROTACs into their constituent parts. This should process ~400 molecules a second…give a few seconds.



3. Three different table views of the data. The E3 ligase modulator is oriented on the right, the linker should be extended horizontally in the middle and identified in red, and the warhead or targeting ligand should be located on the right. In the R-Group Table these are labeled ‘R1’, ‘Linker’ and ‘R2’ respectively.



4. Calculate property columns for entire PROTAC and for each part of the molecule:Tools->Calculate molecular properties.



5. Filter by E3 ligase or any column of data in the dataset.