In CCPNMRV3 :

> Assign > Assignment Inspector > Right clic on the header > Column Settings...

Check only : Value(ppm), NmrAtom, SequenceCode, ResidueType, AtomName, Total Peak Count

> Save > Close > ctrl a > right clic> Export visible Table > save it in .cvs
> In View>Peak Table> select the N or C NOESY spectra

Check only in columns Settings : POS F1, POS F2, POS F3 and Volume

> Save > Close > ctrl a > right clic> Export visible Table > save it in .cvs

Do the same for the other NOESY.

The CSV of the full attribution of the protein extract from CCPNMRV3

The CSV of the peak of NOE extract from CCPNMRV3
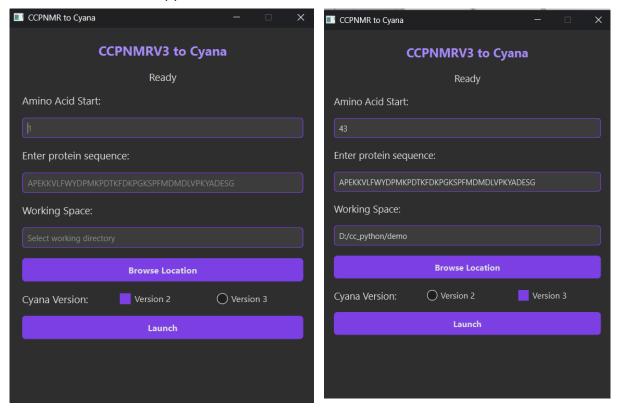
For CCPNMRV3_to_cyana

Creat a File with the three csv files and name it 13C.csv 15N.cvs and attrib.csv.

My file is demo for the exemple.

In the file of the software execute main.py via the terminal :

$python3 main.py

This windos should appear.

File the different information on the right the parameters for the demo.

Clic on Launch and 3 new files are creat in the working space: prot.seq, attib_cyana.prot, 15N.peaks and 13C.peaks.