

# Voyager-DE Quick Start Instructions

by Laurie Parker, Ph.D.



**1. Sample Plate Spotting**

- 1.1. Mix sample and matrix at ~1:1—use ~ 1ul total per spot.
- 1.2. **Suggested matrices:**
  - 1.2.1. **DNA/RNA:** 2,5-dihydroxybenzoic acid (DHB) or THAP (15mg/1mL MeOH) + diammonium citrate (50mg/mL)
  - 1.2.2. **Peptides (MW up to ~10 kD):**  $\alpha$ -cyano-4-hydroxycinnamic acid (CHCA)
  - 1.2.3. **Peptides/Proteins (MW >10 kD):** sinapinic acid
- 1.3. When spotting samples do not touch the tip of the pipet to the sample plate.

**2. Sample Plate Loading**

- 2.1. Eject current sample plate/extend plate holder. In the Voyager Instrument Control Panel, select Eject from the Sample Plate menu. The Load/Eject Sample Plate dialog box is displayed. Click on “Eject.”
- 2.2. The plate holder arm will be extended out from the slot in the front of the instrument:



***NOTE: Do not leave the sample holder in the Eject position for more than a few seconds. Minimize the time the instrument is exposed to the atmosphere to reduce the time needed to reach high vacuum when you insert a new plate.***

- 2.3. Remove current plate by sliding out of holder (if no plate is there, check monitor screen for presence of plate in the instrument!!)



If there is no plate in the instrument, the monitor will show an empty sample stage:



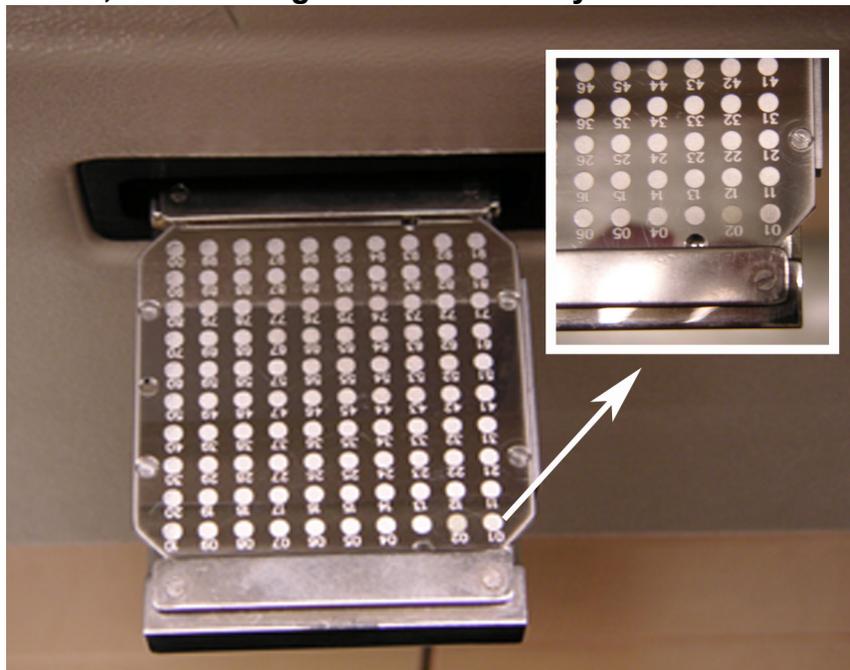
If a plate is still in there, it looks like this:

- If the sample plate is visible on the monitor you should click on “Load no plate” and try to eject again. If the plate still does not come out, notify the person responsible for the instrument service ([www.JBIscientific.com](http://www.JBIscientific.com)).
- **Do NOT load a plate if the monitor shows that one is already in the instrument!!**

- 2.4. Insert your plate by sliding in from the right side until ball bearings click in place



**Make sure orientation is correct!! See image below!! As you stand facing the instrument, sample spot #01 should be on the “south-east” corner, i.e. to the right and closest to you.**



***Note: If the sample plate does not snap into place, it may be inserted into the holder the wrong way, and it may jam inside the instrument. Remove the plate, slide it into the holder with the slanted underside of the plate facing to the left and toward the back of the instrument, and snap it into place.***

- 2.5. From the Sample Plate menu select “PlateID→ 100 well plate” and click “Load” to retract the sample plate and insert it into the main source chamber.
- 2.6. Wait approximately 2-3 minutes for source vacuum to go back down below  $10^{-6}$  (e.g.  $7-9 \times 10^{-7}$ ).

**3. Running samples**

- 3.1. Open Voyager Control Panel

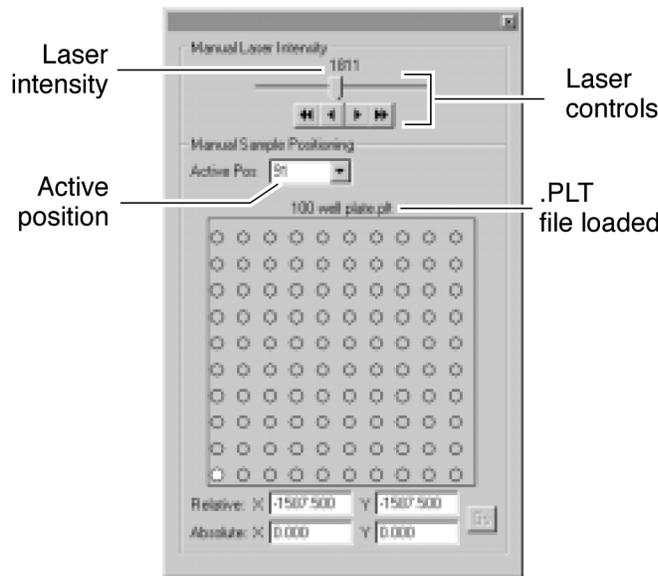


- 3.2. Turn on high voltage by clicking on icon:
- 3.3. Set directory and file name for saving data:
- 3.4. Acquisition methods are .bic files:



go to File → Instrument settings → C: drive→ Data → yourname → Bic → filename.bic, Select the .bic file that corresponds to the molecular weight range you are analyzing.

- 3.5. Select sample spot by entering spot position in box above plate image or by clicking on spot in plate image.



- 3.6. Fire laser at spot using the joystick (left button to start and stop firing) or with the icon.



- 3.7. To optimize detection and resolution, adjust instrument settings as detailed in the next section.
- 3.8. If you notice that the observed mass is significantly off from the expected value allow power supplies to warm up for ~30 minutes for best data. The power supplies are more stable after a significant warm up.

4. **Optimizing detection and resolution (quick instructions).**

- 4.1. Use the lowest laser intensity possible—e.g. if total ion counts is higher than  $10^4$ , turn down the laser in increments of  $\sim 100$ . Higher counts saturate the detector and negatively affect its ability to resolve isotopic peaks.
- 4.2. If there is no signal, double check which matrix you used (was it right for the mass of your material?) and the mass range settings and/or turn laser up.
- 4.3. In “Voltages” box (shows up when “Instrument Settings” window is open—should be default but if not visible you can open it by going to View → Instrument settings) you can adjust “accelerating,” “grid” and “guide wire” voltages and “delay time.”
  - 4.3.1. **Accelerating:** usually set at 20,000. This is normally fine.
  - 4.3.2. **Grid:** Grid voltage and delay time have an inverse association with each other on the results—raising the grid voltage might improve resolution or ions detected, but also increasing the delay time at the same time will take you back to where you were. In general, leave the grid voltage at the setting that was included in the .bic file for your mass range.
  - 4.3.3. **Guide wire:** This voltage helps to focus the ions as they travel up the flight tube. If you have very low ion counts (especially as seen for larger proteins etc.), increasing the guide wire voltage can improve sensitivity. However, resolution is sacrificed when you do this. For higher resolution at smaller masses, change guide wire voltage to zero.
  - 4.3.4. **Delay time:** This changes the amount of time that ions are allowed to accumulate before being accelerated along the flight tube. Allowing enough time for your ions to gather at the starting line can improve resolution a lot, and longer delay times are often required for larger proteins.  
**\*\*\*most useful parameters to try adjusting: guide wire and delay time\*\*\***

5. **Saving spectra:** Click on burning disk icon 

- 5.1. Files will be saved with the name you gave in the box below the directory selection

6. **Viewing spectra in Data Explorer**

- 6.1. For current spectrum, click on the “send to Data Explorer” icon (sorry, no pic available). Data Explorer program and saved .dat file will open.  
\*If this doesn’t work (or if you want to look at old data), quit Data Explorer and re-open from the desktop and then open your data file.

**For more info, see the full Getting Started Guide from AB Sciex, and the Voyager 5.1 User Guide.**