MIT | **B**iophysical
Instrumentation
Facility

JASCO Circular Dichroism Spectrometer

<u>Turning on the Jasco CD</u>

<u>Also see:https://jascoinc.com/training-video/converting-ellipticity-mrme/</u>

1. Turn on the nitrogen at the tank. (half turn of valve marked "1") Check the flow rate to see that the top of the black plug is above the red pointer at 10 L/min.
2. **Enter the time you do this into the logbook.**
3. Turn on the computer and wait until it is totally booted up.
4. If you'll be doing temperature work, turn on the chiller with the sliding black switch.
5. Turn on the CD power switch. (rocking toggle, left hand end of CD) Wait for the clicking noises to stop.
6. Double click on the Spectra Manager icon to open that software.
7. Choose Spectra Measurement and double-click it. The timer for 5 min. of nitrogen starts and then the lamp will light automatically. Check for its being lit. (If you just want to use the software and not the CD, click on the Cancel button. Skip would be used if the lamp has already been purged enough.)
8. Open the shutter with a single click on its icon. (a yellow door will appear when it's open)
9. Be sure the wavelength is set to 260-300 nm for watching the mdeg settle down.   (If you need to change the wavelength manually, go to the **nm** (with 2 blue arrows) icon in the toolbar. Click it and adjust the wavelength there.)
10. Watch the mdeg value on the lamp until it's stable. (a 0.4 mdeg **range** is good, takes about 10 min)
11. Hint: Don't send your parameters to the CD before the lamp has stabilized. That changes what's displayed and it will be difficult to assess lamp stability.

<u>Setting up Spectra Measurement </u>(for single scans at a single temp.)

1. Under Spectra Manager, double-click on Spectra Measurement.
2. Under the Measure button, pull down to Parameters.
3. In the **General** window, choose the number of channels you want to collect and name them from the drop-downs.
4. Choose a starting (high end) and ending (low end) wavelength.
5. Select a data pitch (frequency). 0.5 nm is the default. 1 nm is for quicker scans.
6. Start mode is Immediately unless your sample needs time in the darkness.

7. Scan mode is Continuous.
8. Scan speed: 50 nm/min is a good default. (correlates to the DIT)
9. Set the CD scale to 200 mdeg/1.0 dOD for proteins and most other work. If you have small CD signal, set it at 20 mdeg/1.0 dOD.
10. The FL scale setting is not applicable since we don't have that capability.
11. Start with a DIT (Digital Integration Time) of 4 sec. (scan speed x DIT should be < 200)
12. Set the bandwidth to be 1 nm as a good default.
13. If you want the machine to read replicates, put a number in the Accumulation box. If you want the software to average those replicates, leave the Accumulation box checked. If you want to do the averaging yourself (and see all the replicates separately), uncheck the box.
14. On the **Cell Unit** tab, enter the temp. and start condition you want, but no temp. control will occur.
15. In the **Control** window, choose whether you want the machine to keep your baseline to subtract from your samples. Check the Shutter open/close automatically box. If your samples are light-sensitive, also check the Shutter closed between samples box.
16. In the **Information** window, name your sample, its concentration, the solvent, whatever info you want to have in the file header. Check Display to be reminded to rename each new sample scan.
17. In the **Data** window, check Auto save so it will always save your data and give it your folder name from the Browse button. (You can make a personal folder in the JASCO data folder on the desktop.) Choose a Format for this from the drop-down. Also check Send data to Spectra Analysis.
18. To save all these parameters, click the Save button and give them a name so you can find them in your folder next time. This will be a .cdsp file.
19. When you're ready to scan, click the OK button and your parameters will be sent to the CD.
20. If you want the CD to keep your baseline to subtract from all your samples, click on **B** in the top toolbar. The temperature won't change until you start the first scan.
21. Once you hit **S** to start the measurement, the window for how many cells you have will open. You won't be able to name the samples separately but will have to keep track yourself of which sample was in which cell.

Converting data to a useful form

1. Open Spectra Manager.
2. Under Analysis, you'll see File Converter II. Double-click that to open it.
3. Your Source files are always Std. Ver. 2. In the Destination field, choose the format you want from the dropdown there.

4. Choose a Source folder by browsing for your main folder (in the Jasco Data folder on the desktop). If you're making your folder for the first time, also make a subfolder within it called Converted Data or something like that.
5. Choose the Destination folder to be the subfolder you built for receiving converted data.
6. Click the Convert button and it happens fast.
7. Go check that the correct file type made it into your destination folder.

Closing down the CD
1. To be able to record the HT voltage at 300 nm:
   a. Change the wavelength manually to 300 nm. (Click on the **nm** (with 2 blue arrows) icon in the toolbar and adjust the wavelength there.)
   b. Open the shutter.
   c. Record the voltage value in the log book.
2. Close all the Jasco software so the drivers can be terminated.
3. Switch off the CD.
4. Close the nitrogen tank. Record the time you do this in the logbook.
5. Turn off the chiller if you used it.
6. After you've sent your data to yourself, turn off the computer.

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