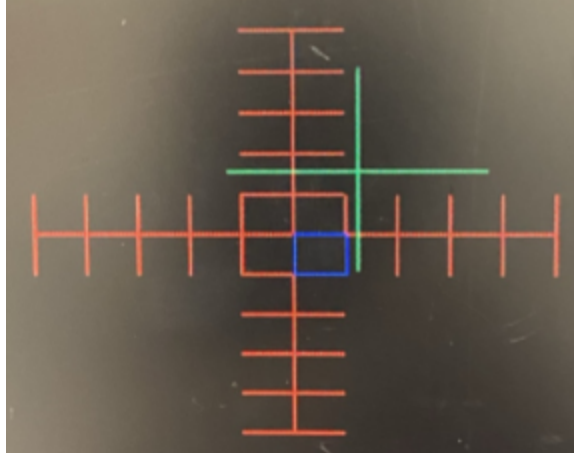


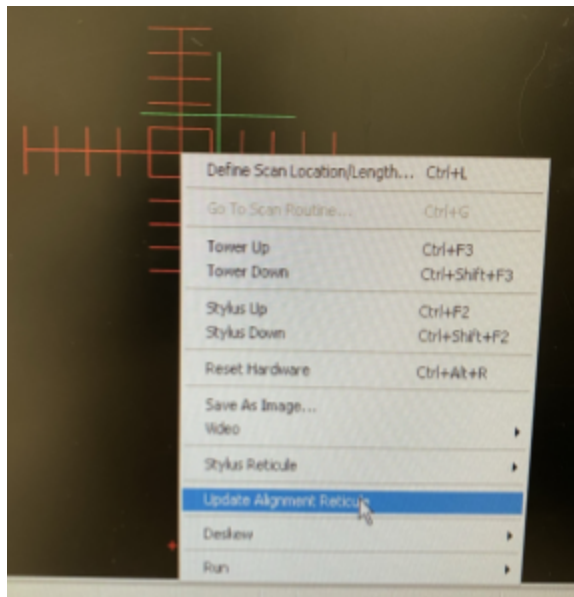
## Profilometer (Dektak 150)

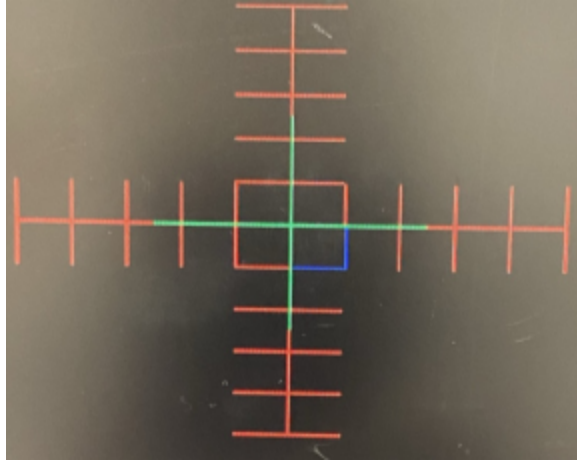
1. Initializing
  - a. "File"
  - b. "New"
2. Align the red reticle



a.

- b. Right click the center of red stylus reticle

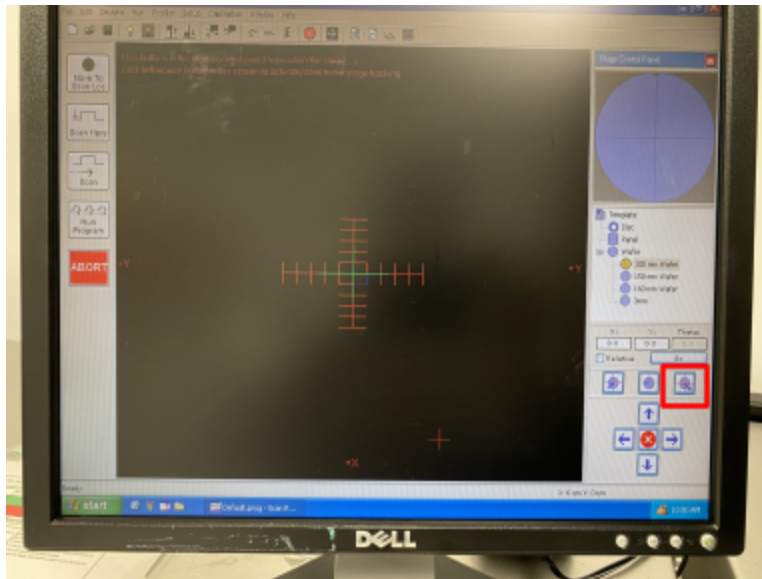




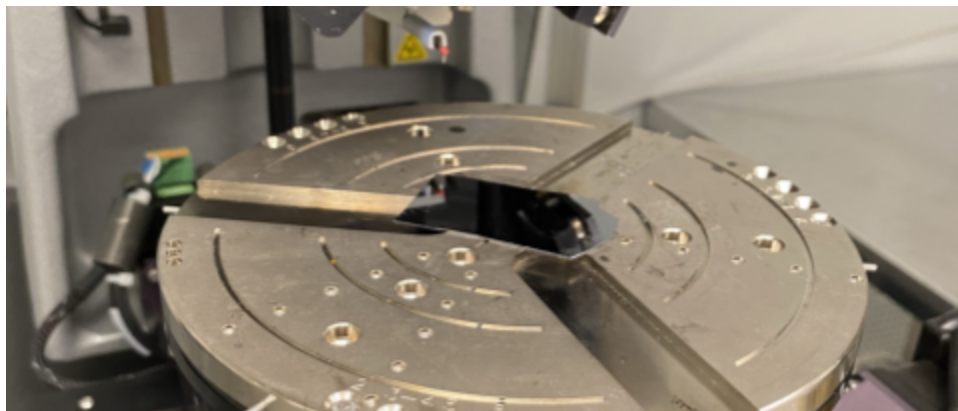
c.

### 3. Sampling loading

#### a. "Wafer unload"



#### b. Place a sample



- c. Turn on the knob “vacuum”

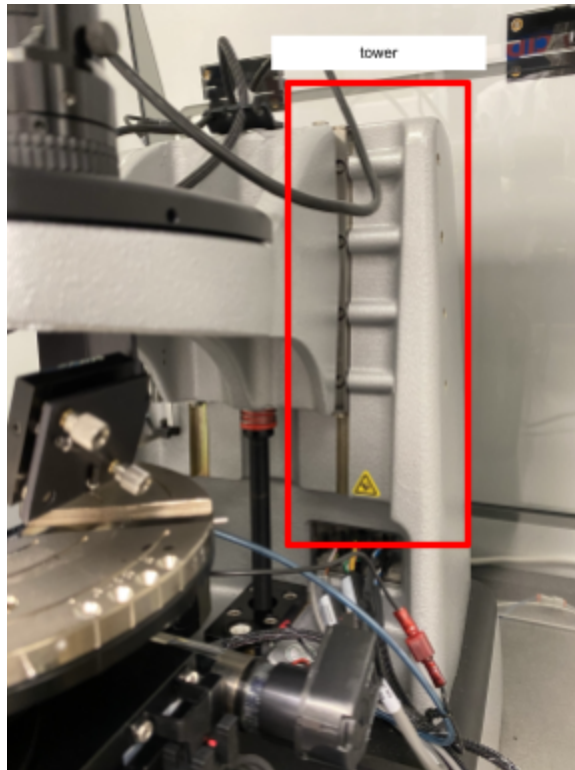
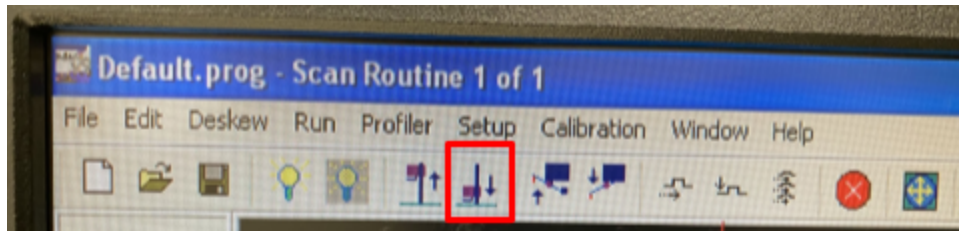


- d. “Wafer load”

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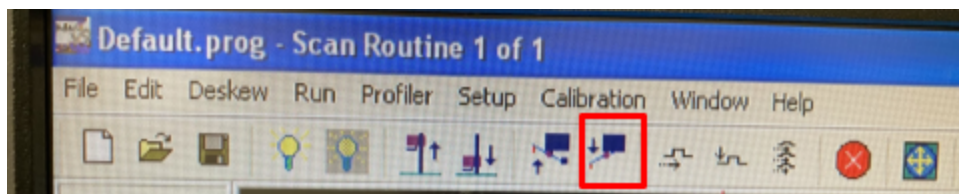
4. Measurement

a. "Tower down"



b. Find the position you want to measure using "X, Y stage control"

c. "Stylus down"



d. Check if the center of red stylus reticle matches with the tip of stylus  
i. If not, manually align them using manual knobs

- ii. If not, right click select "stylus"->"align"
  - e. "Window"->"scan routine"
  - f. Edit "scan parameters"
    - i. Structure height less than 1um, ->"measurement range: 6.5um"
    - ii. If the structure is over 1um (typically 3~4 um), -> "measurement range: 65um"
    - iii. If the structure is over 10um, -> "measurement range: 524um"
  - g. Go back to "window" - "sample positioning window"
  - h. "Scan here"
  - i. Measure step height and ASH (average step height)
    - i. "R" -> "Reference"
    - ii. "M" -> "Measure"
  - j. "Level" -> make two positions you think they are at the same level even
  - k. Save data  
Right click
- 

- 5. Sample unloading
    - a. "Wafer unload"
    - b. Turn off "vacuum"
- 

- 6. You can leave now:)