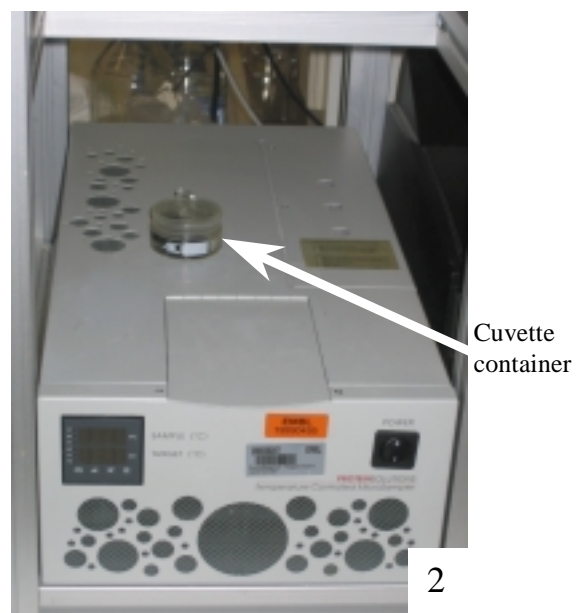
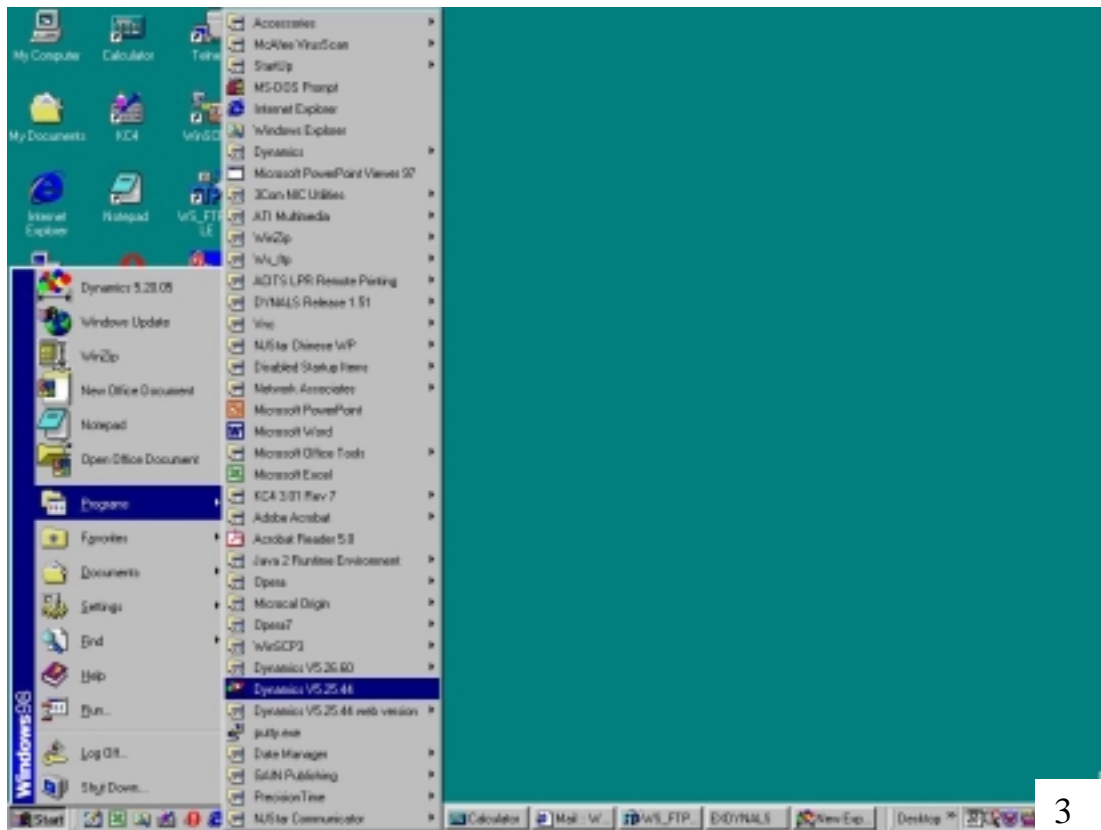


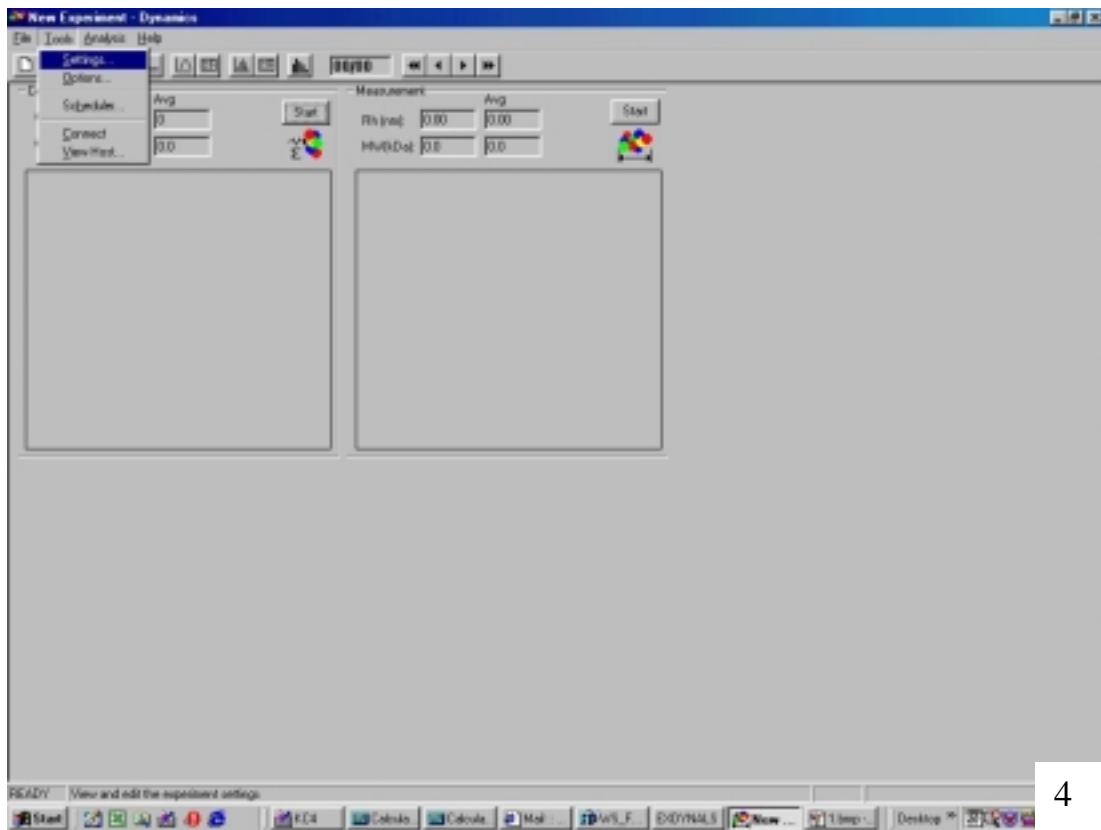
Dynamic light scattering (DLS):

- Turn on the machine by turning both switches on (**fig. 1, 2**).
- At the start menu in the programs folder choose Dynamics v5.25.44 (**fig. 3**). To set the temperature, choose *Tools* → *Settings* → *Temperature control unit* (**fig. 4, 5**), set the desired temperature (this can be done also directly from the machine) and wait some time until it is stabilized at the desired level (have in mind that cooling is much slower than heating so if you have more than one sample that require different temperatures it would be better if the ones that require the lowest temperature are measured first).
- There is a special cuvette that has to be used with this device and can be found in a small glass container over the DLS machine (**fig. 2**). To open the glass container turn the lid while trying to raise it (*be careful!* You should wear gloves, the liquid in the glass is toxic!) remove the cuvette, wash it thoroughly with millipore water and dry it using compressed air. Do not touch the bottom part of the cuvetes in any of the sides.
- Fill the cuvette with the sample using the special long tips making sure that there are no bubbles. Relatively low concentrations should be used, usually less than 1mg/ml. Dilute the sample with its buffer if necessary. Please note that it is recommended to remove large particles (dust) from the solution prior to the DLS experiment – you may do this using the airfuge (see manual).
- Place the cuvette in the holder by putting the frosted side to face the arrow.
- When you are done press *start* at the count rate window on the left of the screen (**fig. 6**). Generally the count rate should be between 300 and 1000. If you get very low numbers you should use a more concentrated sample.
- If everything is OK press start at the measurement window on the right of the screen (**fig. 6, 7**). [By choosing *tools* → *settings* → *data filtering* (**fig. 8**) the filtering limits can be chosen, if the MW model of the protein is known we can choose from the given ones under the *MW model* tab (**fig. 9**) (the *conditions* tab is not very important).]
- The blue measurements are the ones that are consistent with the filtering settings. When you have about 20 to 30 blue measurements it can be stopped.
- Then press the *cumulants catalog* button (**fig. 10, 11**) which shows the data. *All mono* is usually used for globular proteins but for long proteins it would be better to display them as *all bi*. At this point other measurements that do not seem reasonable or “good” can be excluded by using *mark*.
- The polydispersity index for all the measurements can be found at the bottom of the screen (obviously the lower the better). You can also print your results and receive them at the printer located on your right when you exit the main door of the wetlab.
- By pressing the *regularization histogram* (**fig. 12, 13**) button a graph of the measurements can be seen (it should look more or less like a gaussian distribution).

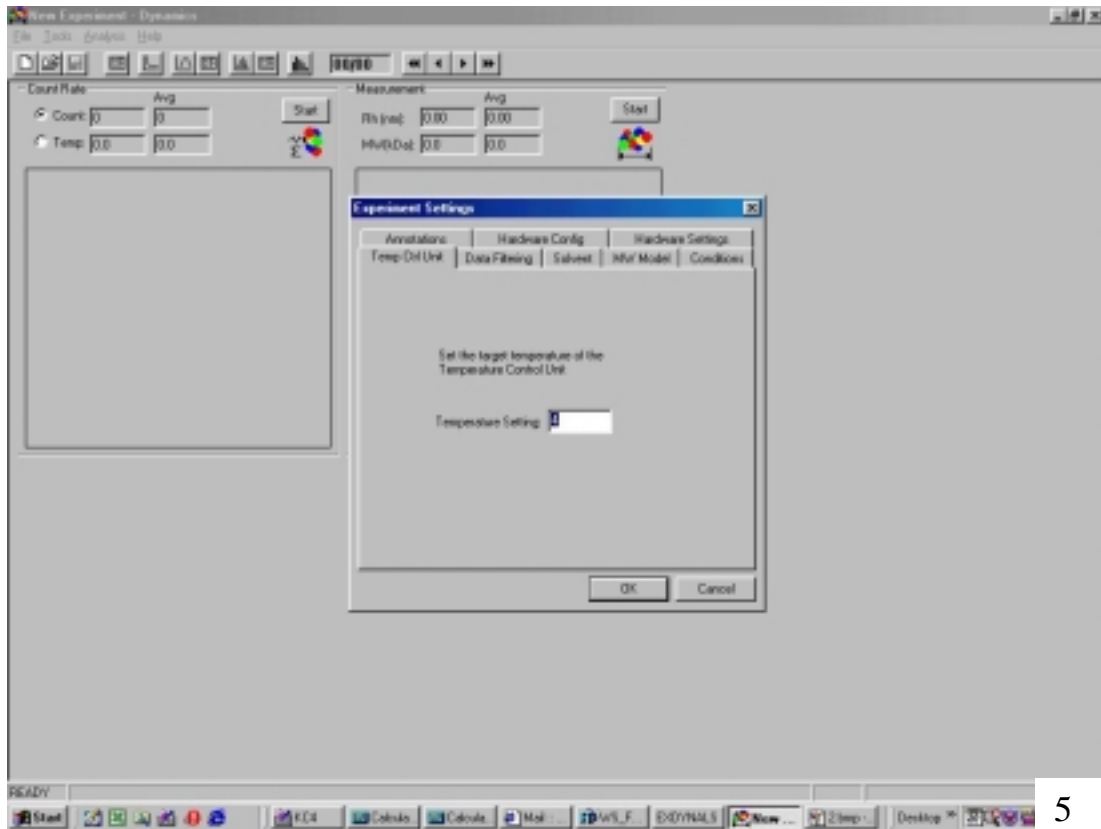




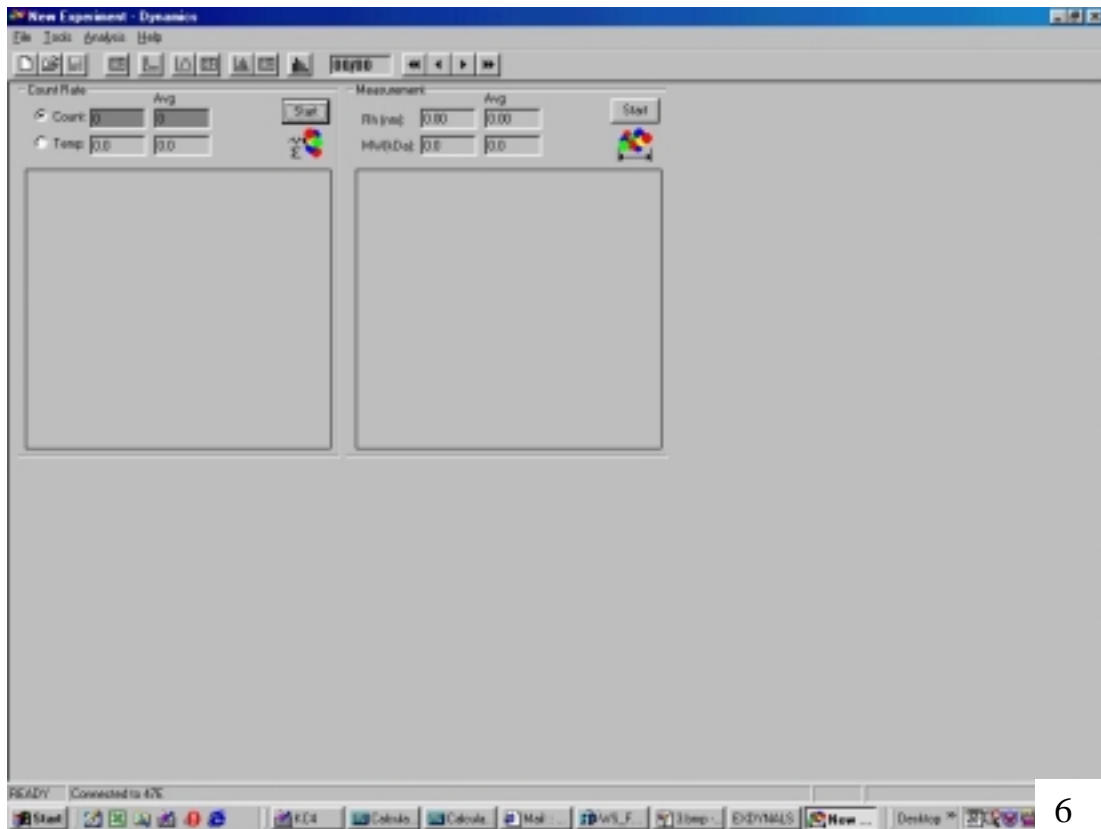
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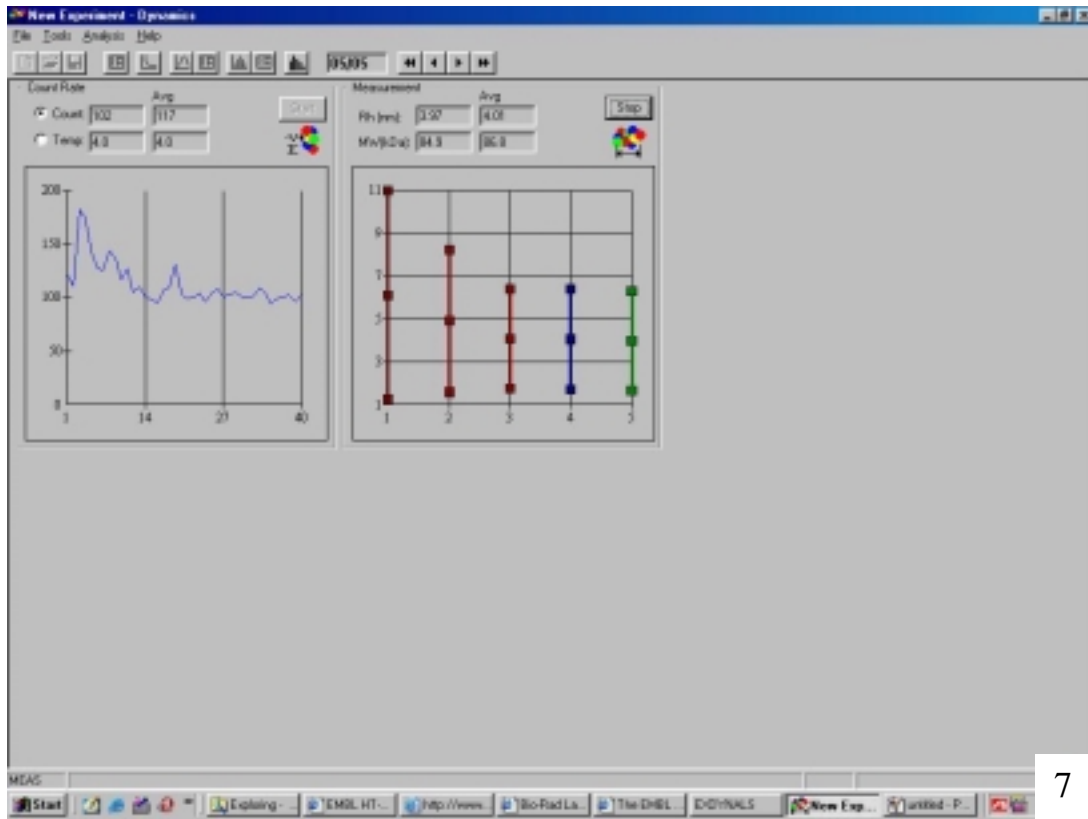
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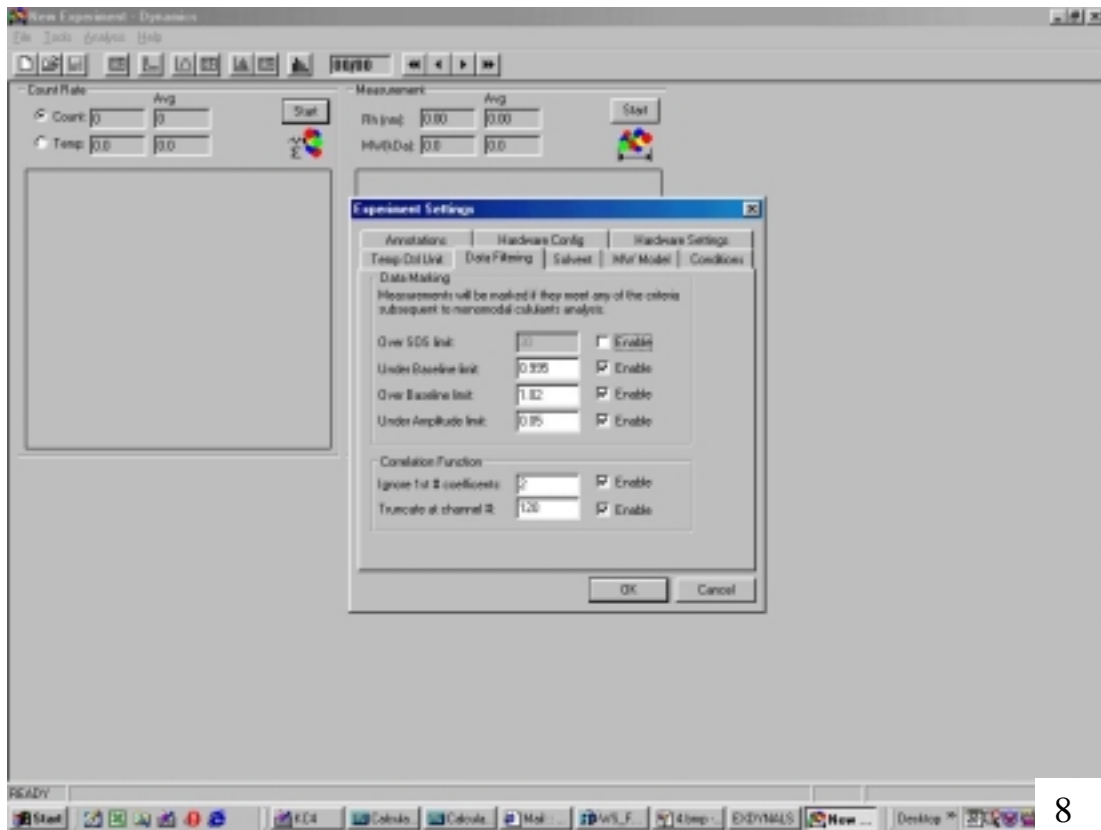
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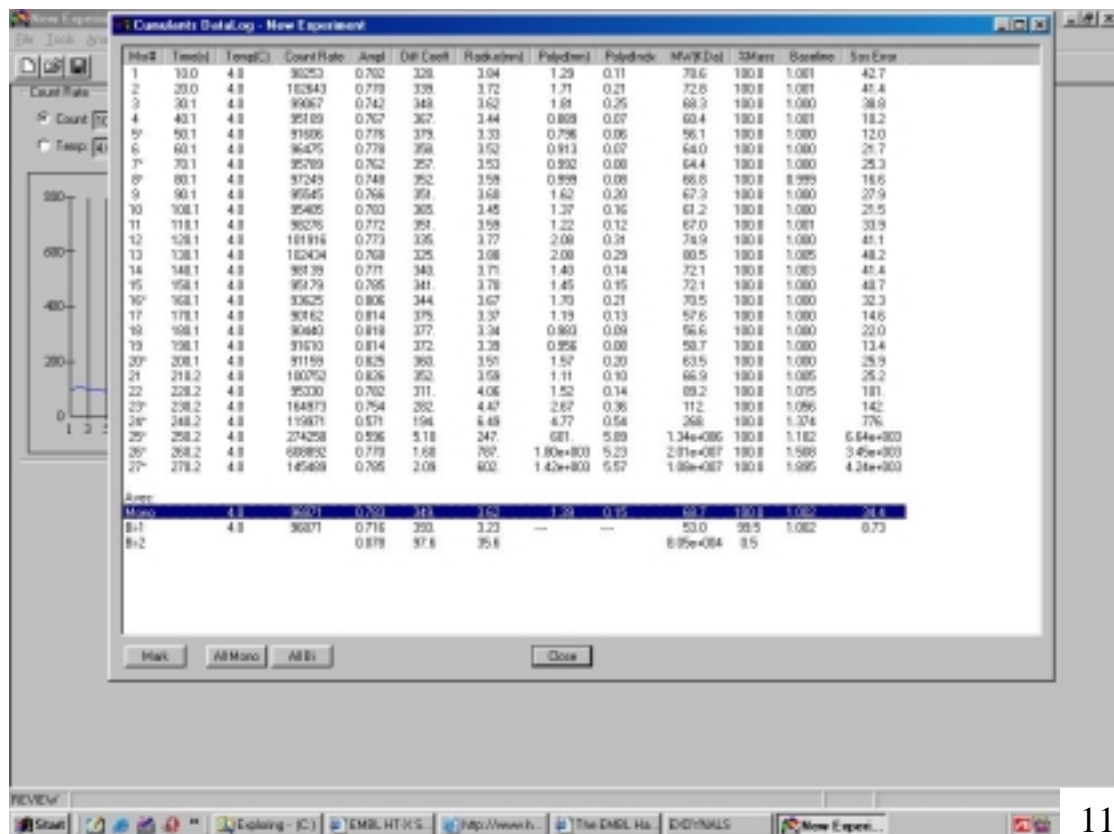
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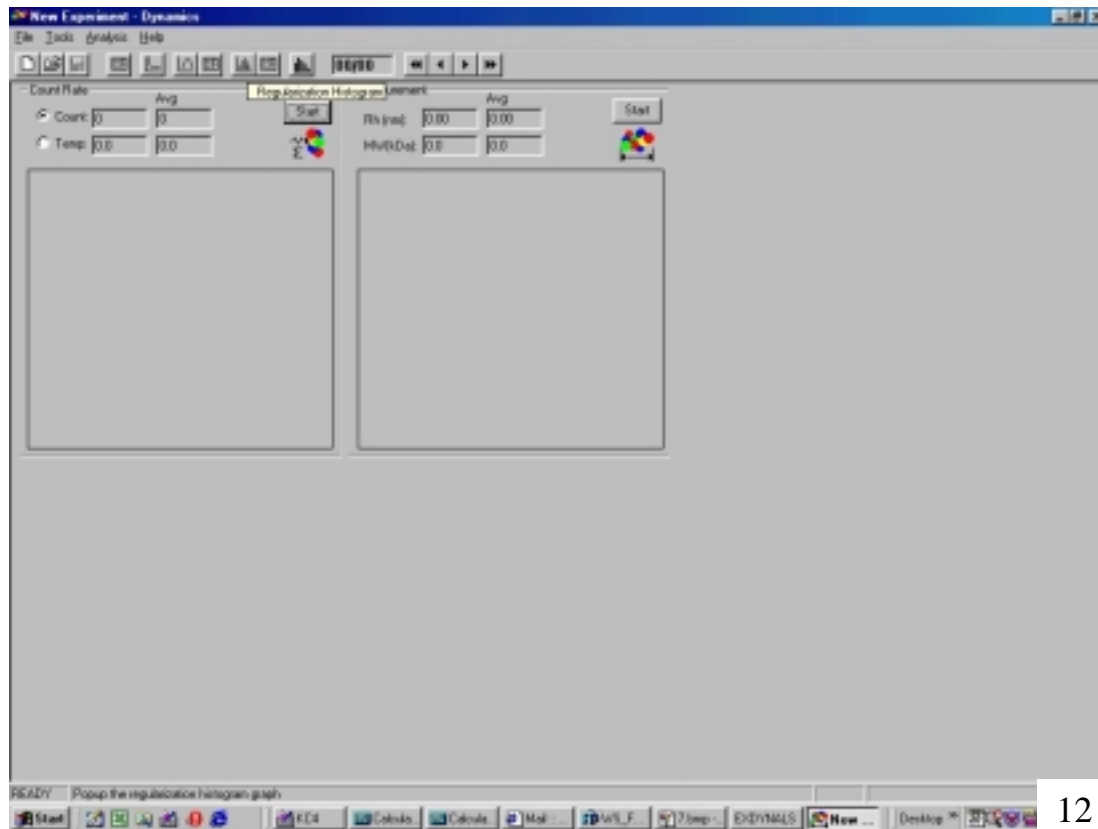
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