

## "Backbone Dynamics of Calmodulin Studied by $^{15}\text{N}$ Relaxation Using Inverse Detected Two-Dimensional NMR Spectroscopy: The Central Helix Is Flexible"

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This paper relates to how NMR relaxation measurements can be used to study **motions** of protein molecules, i.e. **dynamics**, on a picosecond/nanosecond timescale. In this case, the researchers are studying the solution dynamics of the linker connecting the two domains of  $\text{Ca}^{2+}$ -calmodulin, as well as the dynamics of the two domains themselves. In X-ray crystallography studies this linker is helical and forms an apparently rigid connection between the two domains. As an aid in understanding this paper, I have handed out some notes on the analysis of relaxation measurements in terms of dynamics (p. D-1 to D-6). Please read these as a companion to the article!

### **What I want you to get out of this paper:**

I don't expect you to understand this paper in its entirety--it is rather technical and difficult. Focus on a good understanding of Figure 4. I also want you to consider how the characterization of **motional anisotropy** (i.e. different rates of tumbling with respect to the x,y and z axes) relates to the issue of the flexibility of the central linker. For **Thursday, Mar 6**, focus on being prepared to answer the questions below:

- >Apart from the central helix, what other part of the protein seems to be most flexible?
- >Explain Figure 4d, in terms of the general decrease in correlation time over the length of the sequence. What does this mean in terms of the motion of the two domains?
- >What does the lack of motional anisotropy imply?