



Instructions for Individual Projects in Kinemage form

(optional but required to earn an A)

Useful Files: [makeKinTut_inKiNG.pdf](#) , [FAQ](#) ,
[NonMolDemo.kin](#) , [Demo5_4b.kin](#) , [KiNG-manual.pdf](#) ,
[format-kinemage.pdf](#)

Choose a structural biology topic from your own particular interests or one from the list below. Search for known structures and the literature references to them, either directly in the Protein Data Bank or in the structure menu of PubMed, to make sure the information you will need is available for your topic (the minimum is one interesting PDB file and the literature reference that described that structure determination). Consider the method (xray, NMR, cryoEM), resolution and relationship of your structure(s) to ensure they are suitable for the question you want to address.

List of some possible topics:

- An integral membrane protein that forms a pore or an ion channel
- A DNA repair protein (not polymerase)
- Control of cell cycle enzymes (e.g., cyclin-kinase interactions)
- An enzyme complexed with a transition-state-analog inhibitor, vs apo or substrate
- A pair of structures showing an interesting conformation change
- A pair of distantly-similar proteins whose relationship was only recently recognized by combining genomics and known structures
- A ribozyme or riboswitch
- A large multiprotein or protein/nucleic acid “biological machine”

See one of us for help or suggestions if you're not sure about the suitability of a project idea. Also please be sure to ask for technical help if you need it! Jane Richardson is the primary contact for the projects (211 Nanaline Duke Bldg.; jsr@kinemage.biochem.duke.edu; 684-6010).

The final project report, in the form of a kinemage with both graphics and text, will be due after the end of this half-semester course and Fall Break. The date will be communicated in class. We need your kinemage file on a CD (or by email or other file transfer), plus a printout of the explanatory text for your kinemage.

Each student should work individually on their own project. We expect you to use the general information you learned in the course, but not to recapitulate specific examples already covered in detail. Similarly, you may certainly use the Branden & Tooze kinemages to get presentation ideas, but do not use them as direct starting-points.

The general idea is to learn more about a molecule (or a related pair) that interests you, and to present your findings in this format that lets us easily evaluate what you have learned. Using both the text window and especially the kinemage graphics, include:

- brief background about the molecule(s); PDB files used; papers cited.
- a description and illustration both of the overall 3-D structure(s) and of more details at the active, binding, or interaction site
- emphasis on at least one or two aspects of special interest (such as mechanisms of specificity, conformational changes, evolutionary relationships, unusual features, mutation results, etc.). Attribute the ideas (e.g., to a reference, or to something you noticed or measured in the structure)

- enough views, animations, special buttons or coloring, varied representations, etc. to make a good presentation for the kinemage reader; especially, include or emphasize in the graphics only those details that are relevant.

Other resources that can help you with your individual project are available from the course web site: There is a tutorial “makeKinTut_inKiNG.pdf”, using the toxin ricin as the example (PDB file 2AAI). You can either do the tutorial before making your own kinemages (it takes a couple of hours), or you can use it as a resource to learn how to do particular things that stump you otherwise. It also provides a general guide to what is required of you in this assignment, since a ricin kinemage file completed by the tutorial instructions with a well-written text window would resemble a quite excellent completed kinemage project.

The “[FAQ: Questions not covered in the tutorial](#)” gives answers to questions that have been asked by students doing kinemage projects similar to this one. It is worth scanning to start with, and then referring to later.

You should go to the [kinemage web site](#) software page and get the most up-to-date version of KiNG (and of Probe, Mage or Prekin if you use them) to work with, since features are being added and bugs fixed continually.

Cautions about saving files:

- Use file names that clearly identify what is in them, and end kinemage files with .kin Don't try to save over the old file – just change the name a little.
- Make sure you watch what directory you are saving the file into. If you can't see it later, do a search for its name. (In MSWindows the .kin extension may be dropped if you have defined it for program launch. The most failsafe organization in MSWindows is to put the programs in the same folder as all your working PDB and kinfiles.)

Stylistic Tips For Your Kinemages

- Look at the numerous available kinemage files for ideas.
- The first view seen when the kinemage is opened should be visually appealing and informative. It should be centered, mostly fill the window, and have something interesting visible and highlighted.
- Use a variety of views to show your subject not only from different directions but at different levels of detail. Give descriptive names to the views when you save them, so the reader has some idea of what the view shows before choosing it.
- Choose color schemes that match or blend nicely while providing the contrasts needed. Avoid multiple, bright primary colors for large features, but use them for small features you want to highlight. Refer to [Demo5_4b.kin](#) or the built-in palette kinemage for color suggestions.
- Give descriptive names to the buttons on the righthand button panel (i.e. the names of groups, subgroups, masters, etc.).
- Especially in a complicated kinemage, simplify the clutter of buttons using “no button” or “dominant” flags in the “Edit Hierarchy” dialog (see [FAQ](#)).
- If your protein has multiple identical subunits, usually you want to show details for just one. On the other hand, if your active site bridges subunits but the PDB file gives only one, download the “biological unit” instead.

Finally, keep trying things until you get the kinemage to really succeed in showing what you want it to show. Ask for help if you need it.