

Normal Modes

As described in today's lecture, dihydrofolate reductase (DHFR) uses conformational changes to catalyze the reduction of dihydrofolate (DHF). Use the server

<http://midst.sabanciuniv.edu/anm/>

to calculate the normal modes for DHFR (use PDBc ode **4dfr**, chain **A**).

Which mode matches the fluctuations seen in the crystal structures in Bystroff & Kraut (1990)?

Where would you create a disulfide linkage that would minimally affect this mode?

Where would you create a disulfide linkage that would maximally suppress this mode?
