Biophysical techniques that provide structural information at the mesoscale, such as cryo-electron microscopy and 3D tomography, are now sufficiently mature that they merit their own online repository called the EMDataBank (EMDB). We have developed a continuum mechanics description of proteins which uses this new experimental data as input to the simulations. The model is a Finite Element algorithm which we have generalised to include thermal fluctuations, and which is therefore known as Fluctuating Finite Element Analysis (FFEA) [1]. FFEA is a new algorithm for biomolecular modelling which provides trajectory equivalent to that obtained by conventional molecular dynamics simulations, but which shows how the global shape of the protein changes during the simulation, rather than providing information on the fluctuations of individual atomic positions. We describe the theoretical background to FFEA, its relationship to established biomolecular modelling techniques and provide examples of its application to mesoscale biomolecular dynamics.