Supplementary Materials

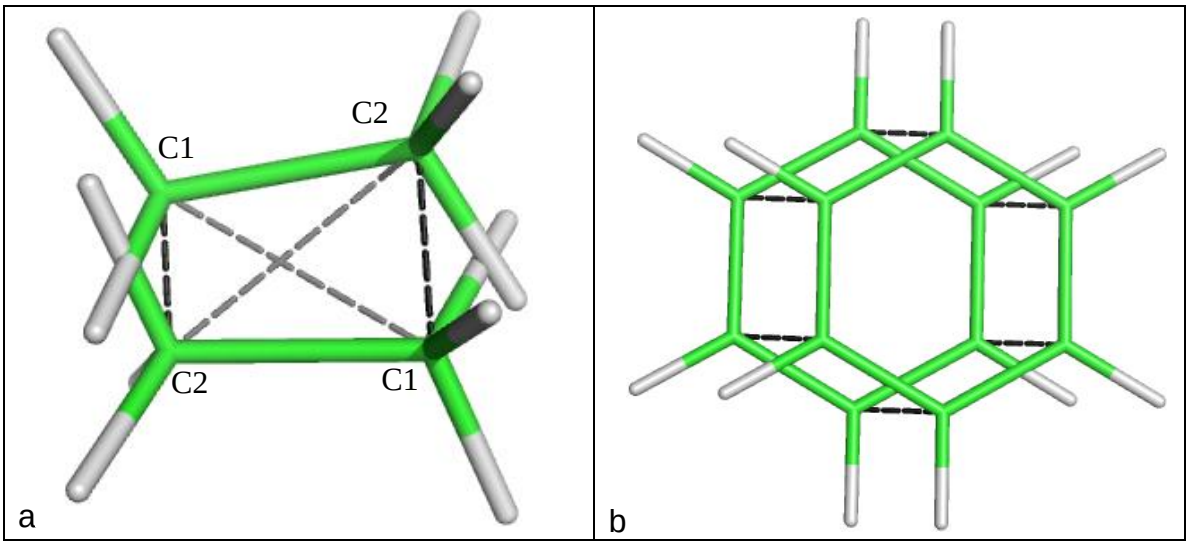

Fig. 1 Calculating the distance between probe molecules. a) The carbon atoms in an ethane molecule are indistinguishable but are labeled C1 and C2. We must examine all renamings of the carbons so that we calculate the correct (black) distances rather than the incorrect (grey) ones. b) Benzene exhibits a similar problem. The six carbons can be relabeled in 12 unique ways via symmetrically equivalent rotations and mirroring. We account for this in our symmetry-corrected RMSD calculations.

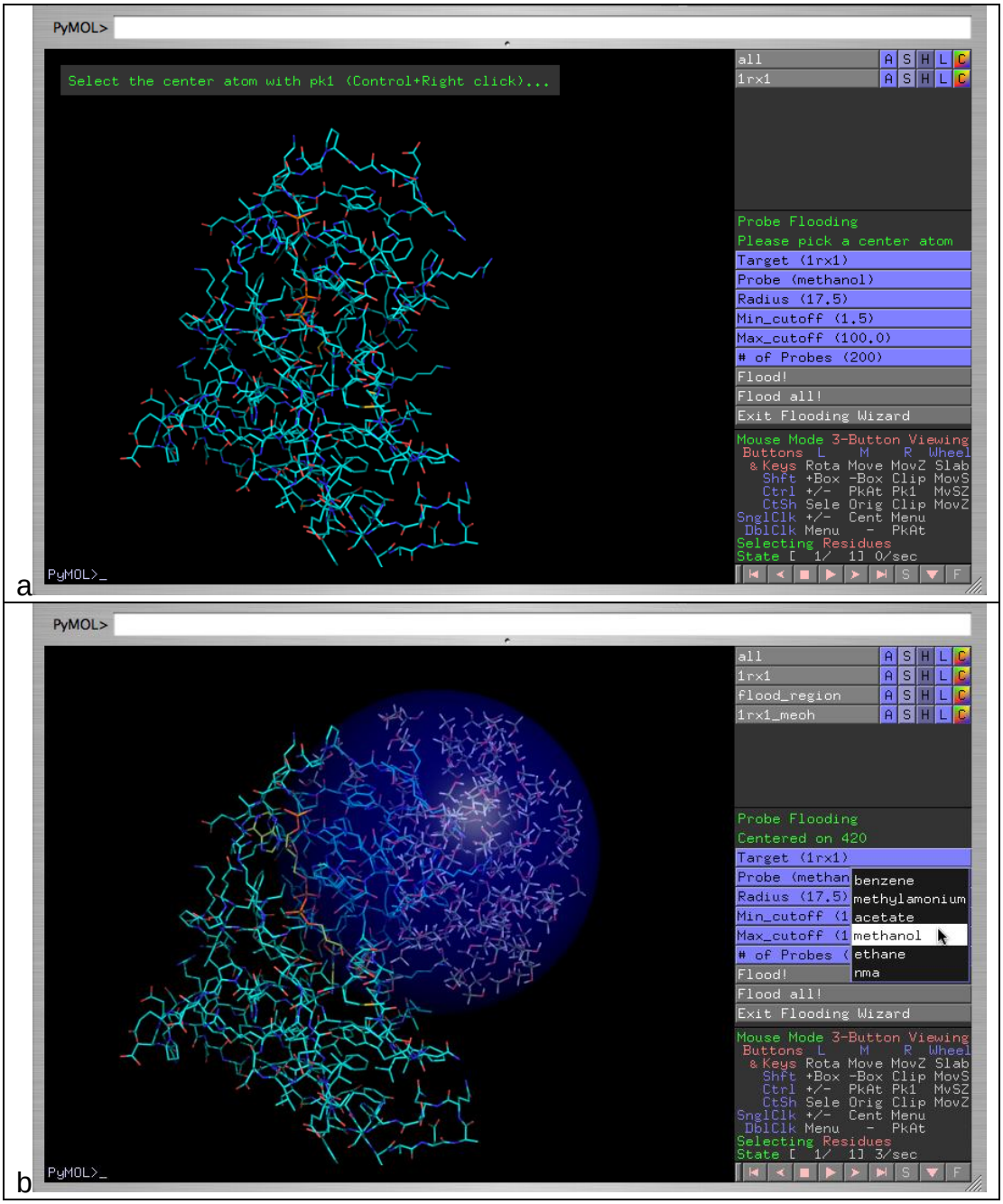

Fig. 2 The PyMOL flooding wizard. a) The initial wizard interface. Users may select the center of the flooding region, the probe with which to flood the protein surface, the radius of the flooding region, the minimum and maximum distances between individual probes and the protein surface, and the total number of probes with which to flood the protein surface. The "Flood!" button floods the protein surface with the chosen probe, and the "Flood all!" button floods the surface with all probe types individually. b) An example of a protein flooded with 200 methanols in random orientations and locations.