**Remarks on the FRET window in MMM**

1. Chromophores should be clearly distinguished from spin labels. For that, rotlib.class should be set to “chromophore”.

2. I strongly suggest to not “attach” chromophores, i.e. to not generate explicit coordinates in the structure (too many atoms, too many rotamers). The new MMM will not do this for spin labels either. The FRET window will compute distributions “on the fly” from “virtual” rotamers, as is done in RigiFlex. This also save me from adapting the DEER window. If chromophores are not attached, the DEER window will be blind to them.

3. Chromophores need their own equivalent of the “Labeling conditions” window. It does not make sense to have them under “EPR” and to select from a set of libraries that contain both spin labels and chromophores.

4. We need to decide whether we want to have a “Site scan” window or we just compute rotamers for selected sites. In any case, we shall use the same site scan function as for spin labels (and cofactors), just with a different option.