**Remarks on the FRET window and chromophore labeling in MMM**

1. Chromophores should be clearly distinguished from spin labels. For that, rot\_lib.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. In labeling\_conditions\_chromophore.m, function handles=initialize\_popup(handles)

You must replace class nitroxide by class chromophore. The same applies in function popupmenu\_library\_CreateFcn.

4. The site scan window for chromophores does not support dynamic native side chain rotamers by SCWRL4.

5. The labeling conditions window for chromophores does not have temperature selection.

6. Attachment of chromophores is currently supported only for peptides (proteins).

7. Maybe we should block selection of more than two chromophores in the FRET window, since computation is implemented only for pairs