**From:** Thomas Schubert [<mailto:schubert@2bind.de>]   
**Sent:** Friday, August 26, 2016 6:07 AM  
**To:** Sudipto Munshi <[sudipto.munshi@pmc-at.com](mailto:sudipto.munshi@pmc-at.com)>  
**Subject:** RE: quote

We can definitely try work in the labelfree system. THe protein contains tryptophans and the affinity to the various ligands is not too good. Important will be to check if the ligands do show background fluorescence at the very high conc. need to determine the Kd. This is basically the bottleneck. If the ligands do not show background I do not see any issue with the labelfree system. If they show background we are not able to use the labelfree system and have to switch to the fluorescent assay.

I do understand your concerns about labelling. I just want to remind you that this type of chemistry is routinely used in different other technologies as well (such as SPR Biacore).

During the years of working with MST we had probably two cases where the labelling really mattered. So usually it is not a problem.

In other words, we will test the labelfree system first and check if we can use it at all. If yes, we will continue in this system. If not, we will inform you and would recommend to work in the labelled assay version.

Is this procedure of interest for you?

thanks for the info.

**We made the initial tests in the labelfree. Unfortunately three of the four ligands show significant background in the labelfree system. Currently there is no possibility to use this assay type. Please see the document in the attachment. (Each peak indicates one substance)**

One solution we can offer is to label the protein.

Please confirm that we should go that way.