Comments to the Author:
The authors have addressed the comments by the two referees very well. This is an interesting study reporting an unusual ligand binding mode. It is very well suited for the Rob Kaptein Festschrift. The paper is essentially ready for publication, after resolving a few editorial formatting requests. In addition, please also address the following minor revision.

- The overall finding that the bound ligand populates a conformational ensemble in the hydrophobic pocket of the protein strongly resembles the ligand interaction mode described in Takeuchi et al, Scientific Reports 4, 6922 (2014). Please cite that paper and briefly compare the two cases in the discussion.

We have cited this interesting and relevant paper, and included a sentence relating it to our study in the discussion section. Essentially the study by Takeuchi and co-workers focusses on dynamics within the protein, and ours on dynamics within the ligand.

Non-public comments to the author:
Please make the following formatting changes:

- Figure 2 A, B, C: y-axes need a proper label including units (probably Fluorescence intensity (a.u.) and [CaM]/[idoxifene])

All done

- Figures 3, S2 label both axes, with property and unit.

All done. Note y-axis of Fig 3 and the x-axes of both Figs are unitless.

- Figures 2C, 4, 5, S1, please label axes that shows chemical shifts with labels like delta(1H) [ppm] or omega_X(1H) [ppm], where X is the dimension number.

All done

- Please doublecheck all Figures and Supplementary Figures for proper axes labeling. If self-explanatory, the description of these labels may then be removed from the respective Figure captions to make captions more concise.

We have shortened the caption to Fig 2 accordingly, and haven't spotted any other issues relating to axes labelling.