



Zurich, 30 October 2019

Dear Editor Wu,

We are pleased to submit our revised manuscript, "*Quaternary structure modeling through chemical cross-linking mass spectrometry: Extending TX-MS Jupyter reports*", for consideration by JoVE. The manuscript describes a method to enable biologists with minimal technical skills to analyze structural models and the supporting MS data in more depth compared to the standard report produce by the TX-MS method which we recently published in Nature Communications¹. All the changes to the manuscript were tracked and each point raised by reviewers addressed in a separate rebuttal letter. We have uploaded high-resolution versions of the figures. Given the easily addressed reviewer comments, we are cautiously optimistic that the manuscript will be accepted, and we are looking forward to the next steps.

Sincerely,

A handwritten signature in blue ink, appearing to be 'LM'.

Dr. Lars Malmström
University of Zurich

1. Hauri, S. *et al.* Rapid determination of quaternary protein structures in complex biological samples. *Nat Commun* **10**, 192 (2019).