## Comments on Review B

This review expresses the strong opinion that “despite 30+ years of computational structural biology, there are few success stories of how the computational tools really impact significant biological discoveries”. Moreover, the reviewer claims that folding and docking have far too much complexity to be identified visually. We believe that these claims are too strong and that the computational tools can significantly contribute to the understanding of the molecular structures and their function. This was also confirmed by numerous publications citing such tools (only the publication about CAVER algorithm has currently 139 citations in WoS). It should be also stated that the tools nor the visual representations of their results do not aim to replace the work of the biochemist – they serve as a guidance but the final decision has to be and always will be on the domain expert. So as we have different opinions on the basic research domains we are working in, it is very hard to address individual comments of the reviewer.