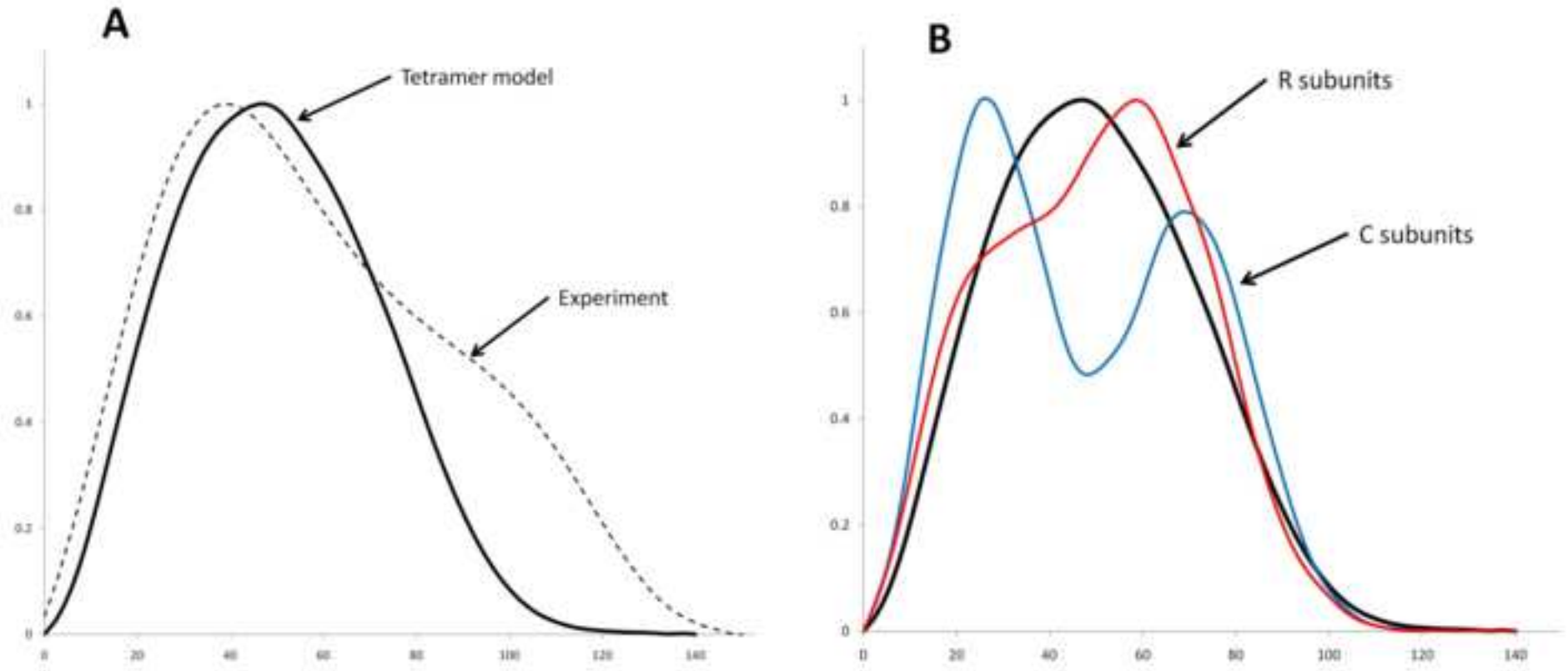
Supp Figure 1



Supporting text

Our model of the RIα tetrameric holoenzyme is based on the structure of the C-subunit bound to the RIα(91-379) mutant (Kim et al., 2007). Also in the RIα(91-379) construct the key Arg^{333} was mutated to lysine. This mutation blocks cAMP binding to the B-domain of the R-subunit that was important for crystallization of the complex. However, as it was shown earlier (Cheng et al., 2009), R333K mutation also changes the general form of the R:C heterodimer. Without mutation the complex has a substantial shoulder in its P(r) function in the long distance area. Mutation of the arginine leads to a complete disappearance of the shoulder that was explained by change of dynamics of the B-domain caused by the mutation. As shown in **Figure S1a** the same difference in P(r) function is observed for the tetrameric model in comparison to the full length wild type RIα holoenzyme. Obviously dynamic behavior of the B-domains in the complex has a substantial effect on the small angle X-ray scattering. The exact explanation of the long distance P(r) changes will require additional computational work that goes beyond the scope of the current paper. However, it is clear that the general shape of the proposed model is consistent with the SAXS experiments. Additionally we calculated separate P(r) functions for C and R-subunits (**Figure S1b**). Distance distribution function for the C-subunits in our model has two well separated peaks that is consistent with the previously reported SANS results (Heller et al., 2004).

Figure S1 legend

Figure S1, related to Figure 8. Distance distribution functions P(r) for the RIa holoenzyme model and its constituents. The tetramer model includes two C-subunits and two RIα(91-379) constructs (with R333K mutation) taken from the 2QCS structure bound to each other according to the interface shown on Figure 2. **A**) Comparison of the tetramer model (solid line) to experimental P(r) function for the full length wild type of RIα holoenzyme reported earlier (dashed line) (Heller et al., 2004).**B**) P(r) functions calculated separately for R-subunits (red line) and C-subunits (blue line) in the tetramer model.