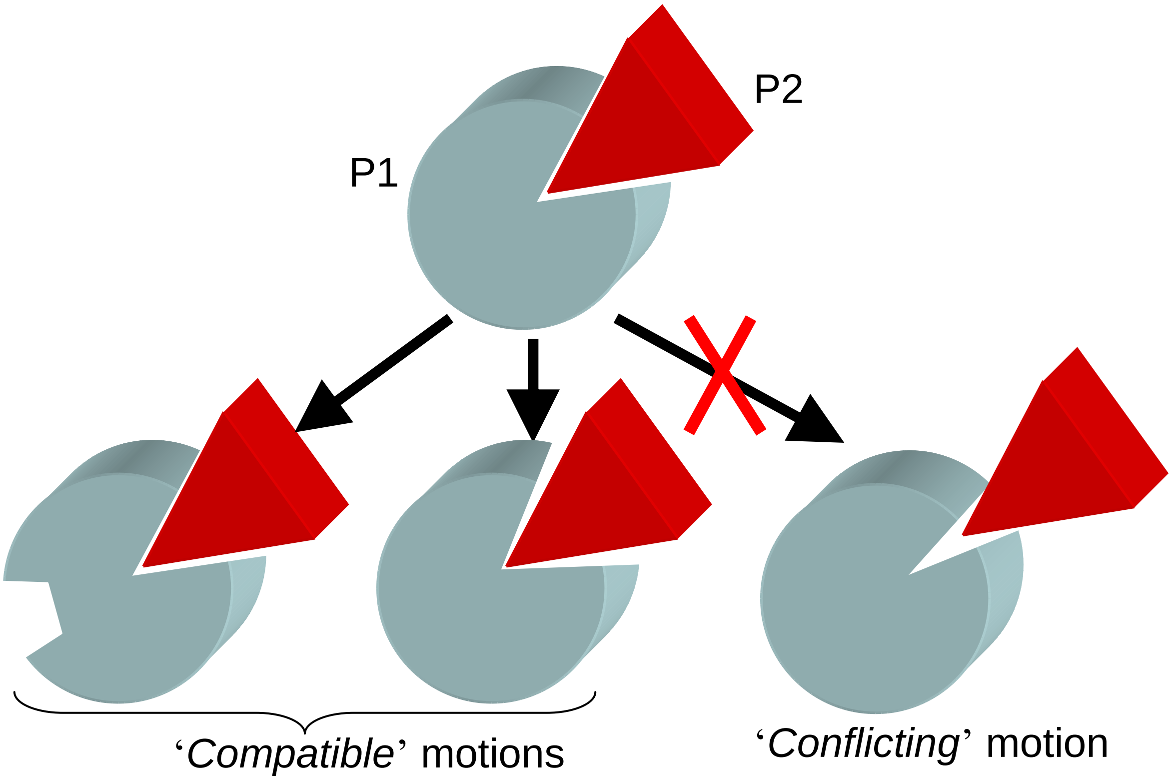
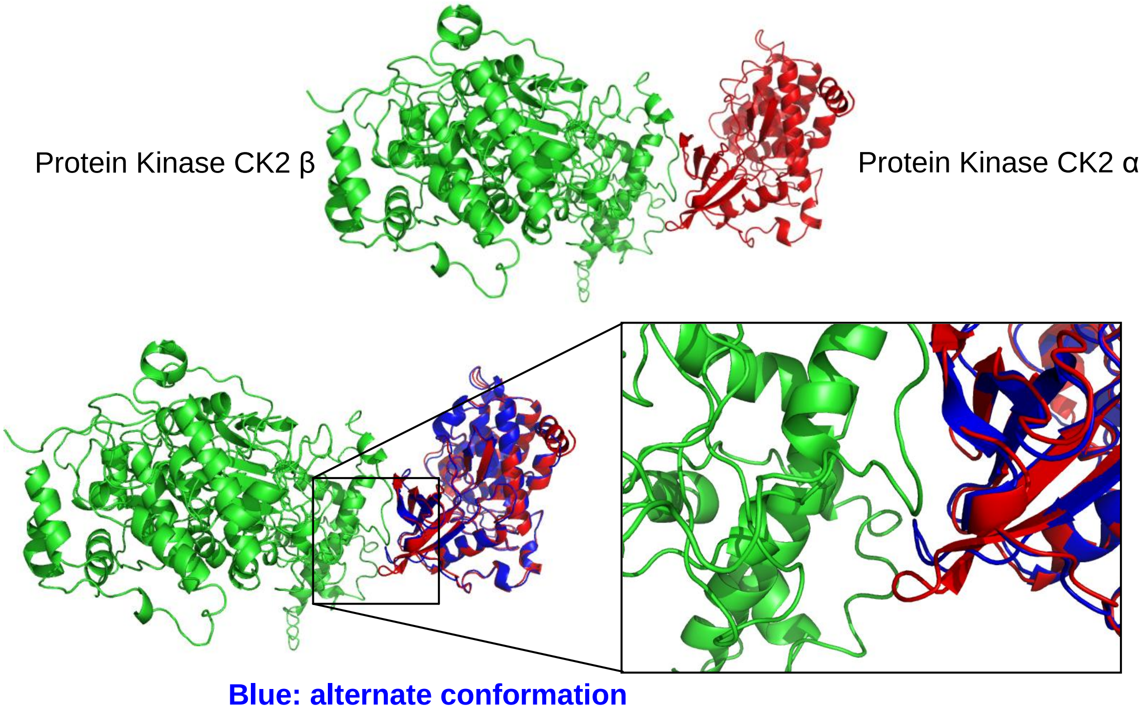
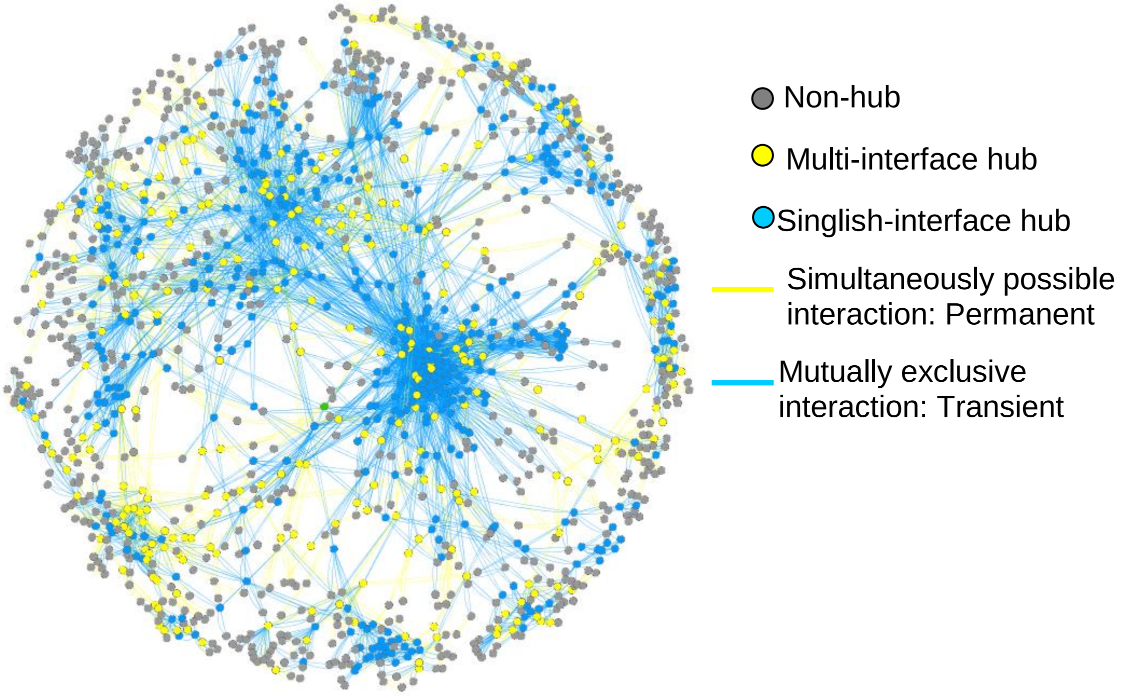
Supplementary Materials



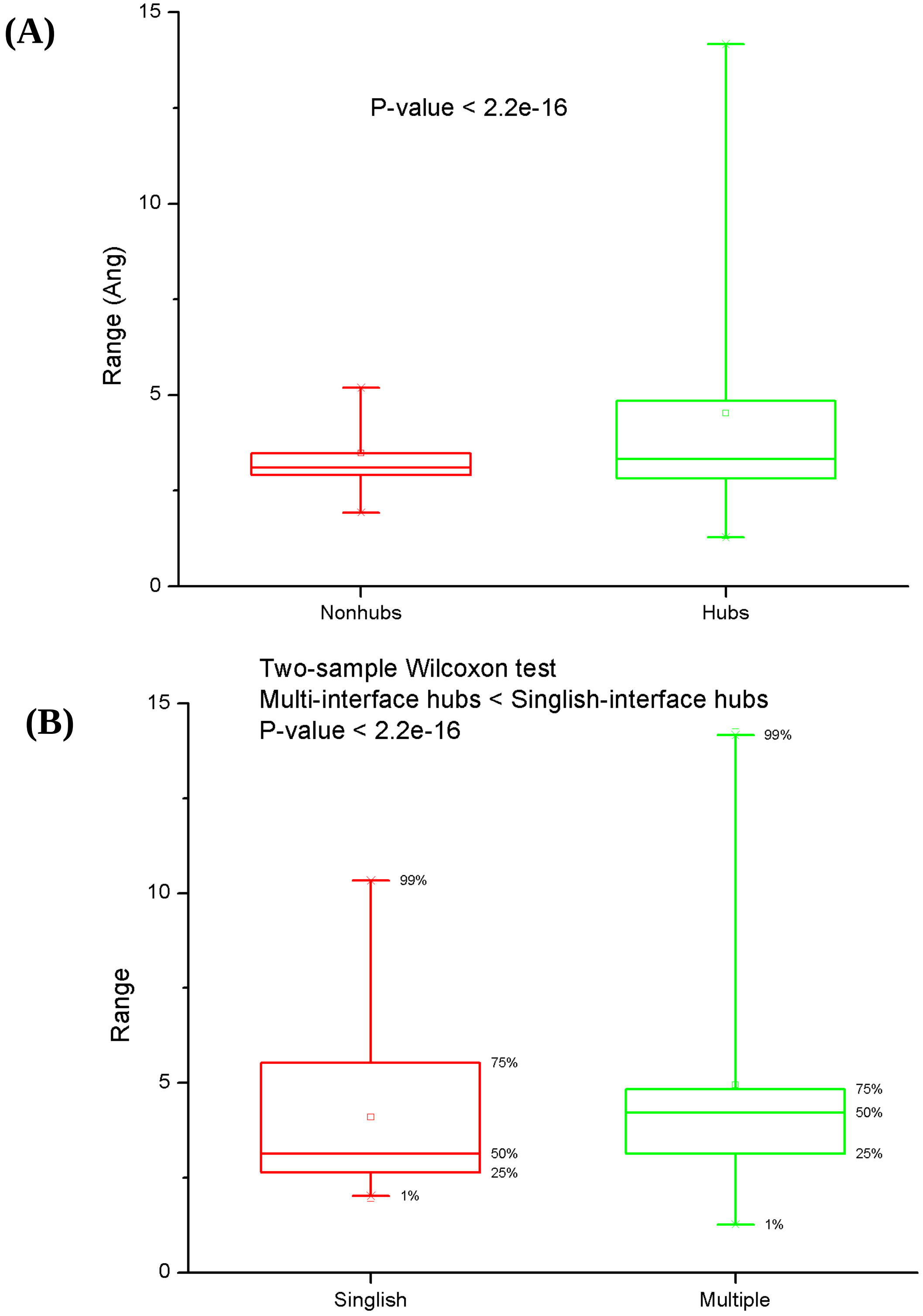
Supplementary Figure S1. Three scenarios of protein motions. Protein P1 shows motion, and of the three scenarios, there is one case for which the motion conflicts with the interaction between P1 and P2.



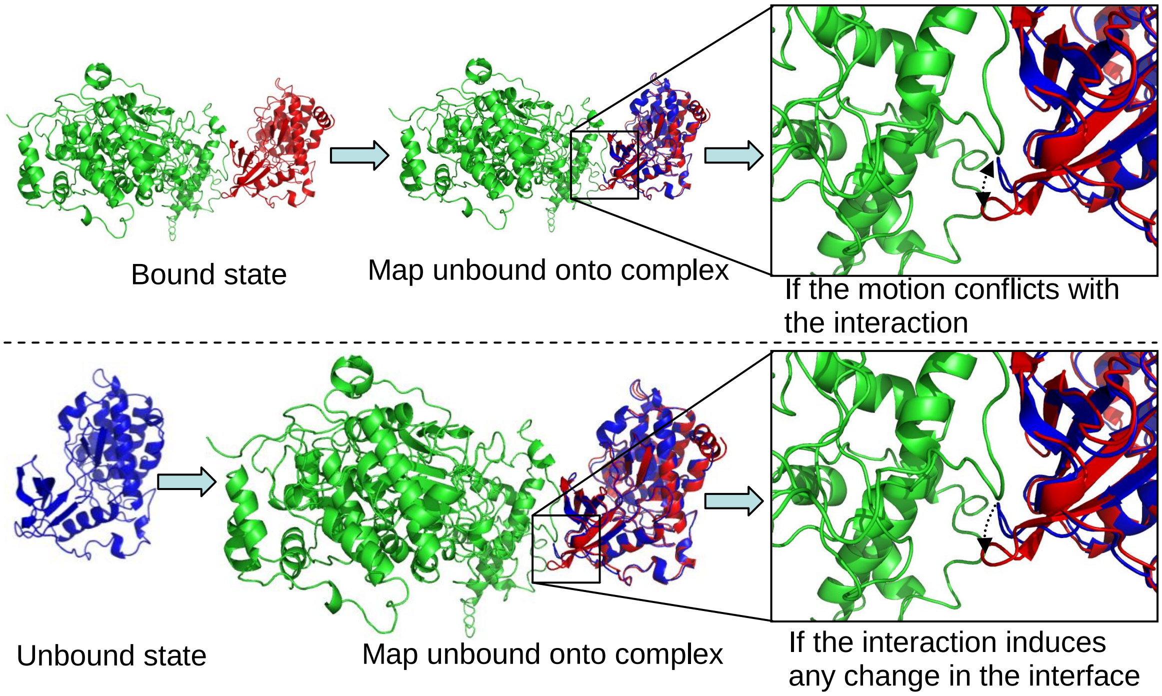
Supplementary Figure S2. A real example of protein motions that affects the interaction between two proteins. Protein Kinase CK2 α shows alternate an conformation (in blue). Alignment of the alternate conformation on the structure in complex with Protein Kinase CK2 β and close examination reveals that the alternate conformation conflicts with the interaction between this protein and Protein Kinase CK2 β.



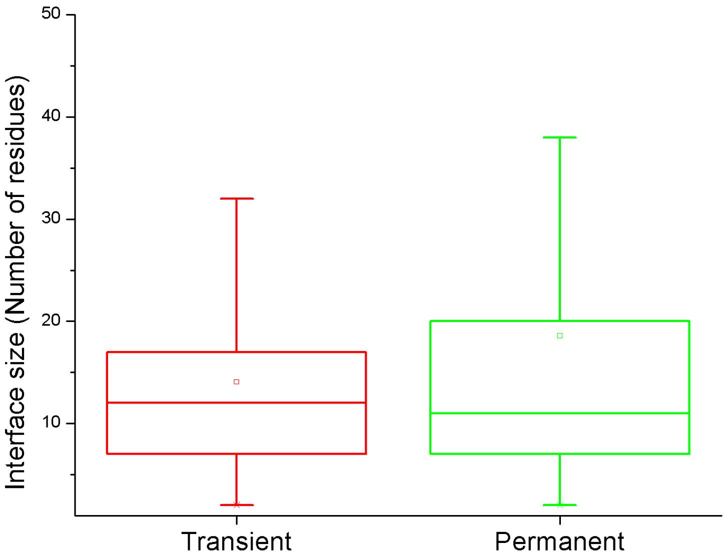
Supplementary Figure S3. Human Structural Interaction Network (SIN). Legends for nodes and edges are provided.



Supplementary Figure S4. Range of conformational changes for (A) Hubs and Non-hubs and (B) Singlish- and Multi-interface hubs for Human when the cases in which the protein showed less RMSD than the resolution in Å are removed.



Supplementary Figure S5. Alignment of unbound and complex structure reveals the conformational changes required for binding. By starting with the complex state and mapping the unbound structure with the conformation, as found in the complex, provides information on whether the alternate conformation conflicts with the interaction. On the other hand, if we start with the unbound state and then compare it with that in the complex state, it reveals the kind of conformational change that is required for the protein to interact with its partner.



Supplementary Figure S6: Size of the interfaces (in terms of the number of interfacial residues) that are involved in Transient and Permanent interactions.

Number of unique interfaces	Number of proteins
3	78
5	51
7	34
9	25
11	8

Supplementary Table S1: Number of proteins with a specific number of unique interfaces in Human.