

Figure S3

Distribution of the distance in the structures generated by HADDOCK (A) after the first rigid body step (it0), (B) after the semiflexible simulated annealing step between the two pSer and pThr binding sites. This distance was evaluated from the distance between the OG atom of Ser42 (corresponding to the conserved Ser in contact with the pThr in complexes of FHA domains) and the NH atom of Cys119 (predicted to be in contact with the pSer of the tandem BRCT).

