FIGURE S2 Singular value decomposition (SVD) analyses of RDC data (^{1}H-^{15}N) for PEA-15 DED in ERK2-bound form measured from two distinct media as labeled. The crystal structure of PEA-15 DED bound to unphosphorylated ERK2, PDB 4IZ7, was used in all analyses. The secondary α-helical structures are indicated on top of the plot. Experimental RDC values are shown in red and simulated values in blue. (A) and (B) SVD analyses of RDC data for all DED residues (1-90); (C) and (D) SVD analyses of RDC data for helices α1, α5, and α6. A reasonable match between the predicted and experimental RDC values could be obtained in both media, and the order tensor matrix generated by the SVD was used in the back calculations of predicted RDC values as shown in the main manuscript. (E) and (F) SVD analyses of RDC data for helices α2, α3, and α4. The predicted and experimental RDCs do not match well in this region, suggesting conformational variations between crystal structure and solution state, attributed to crystal packing artifacts.