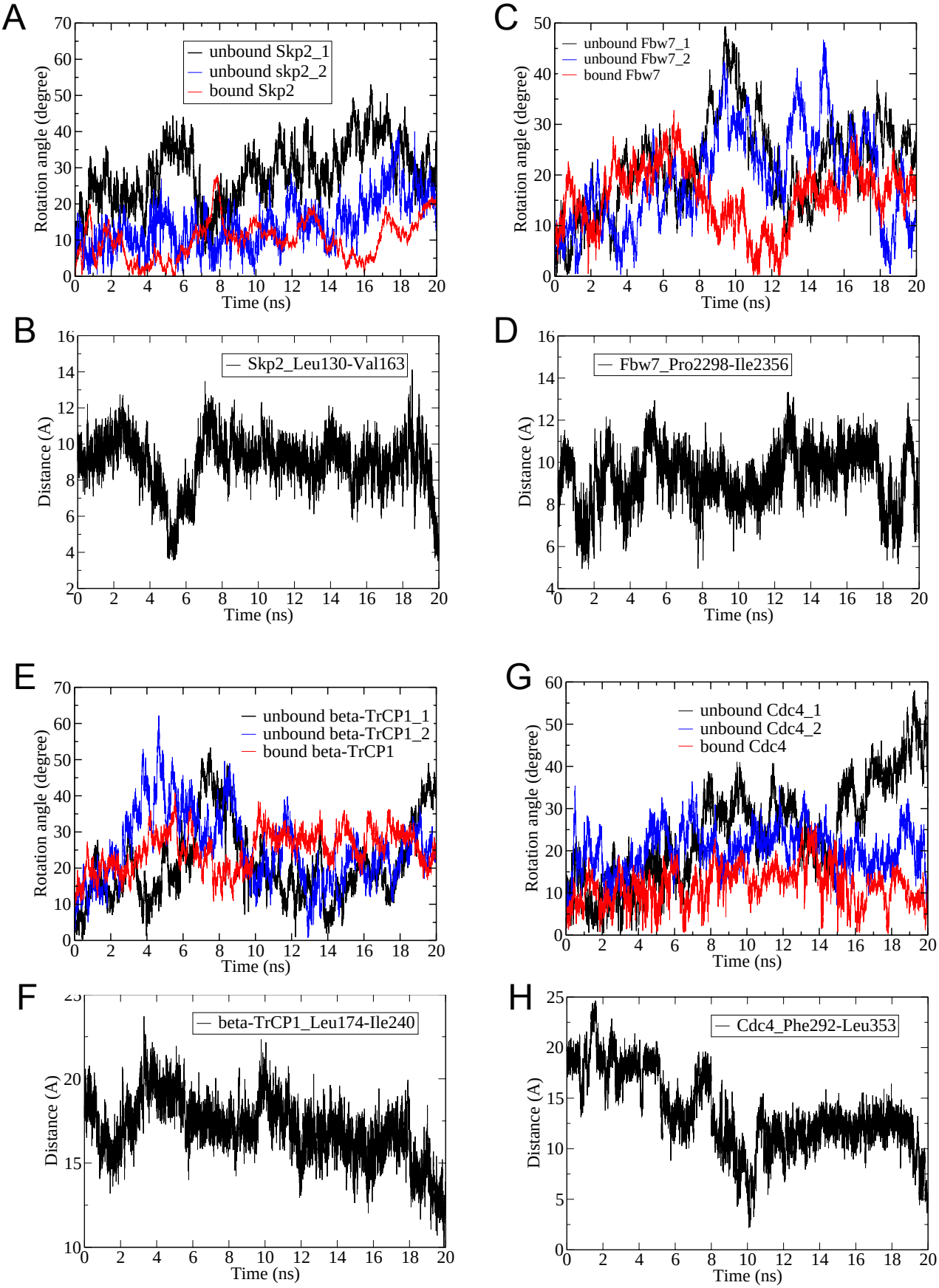
A
unbound Skp2_1
unbound skp2_2
bound Skp2
Rotation angle (degree)
Time (ns)
B
Skp2_Leu130-Val163
Distance (A)
Time (ns)
C
unbound Fbw7_1
unbound Fbw7_2
bound Fbw7
Rotation angle (degree)
Time (ns)
D
Fbw7_Pro2298-Ile2356
Distance (A)
Time (ns)
E
unbound beta-TrCP1_1
unbound beta-TrCP1_2
bound beta-TrCP1
Rotation angle (degree)
Time (ns)
F
beta-TrCP1_Leu174-Ile240
Distance (A)
Time (ns)
G
unbound Cdc4_1
unbound Cdc4_2
bound Cdc4
Rotation angle (degree)
Time (ns)
H
Cdc4_Phe292-Leu353
Distance (A)
Time (ns)

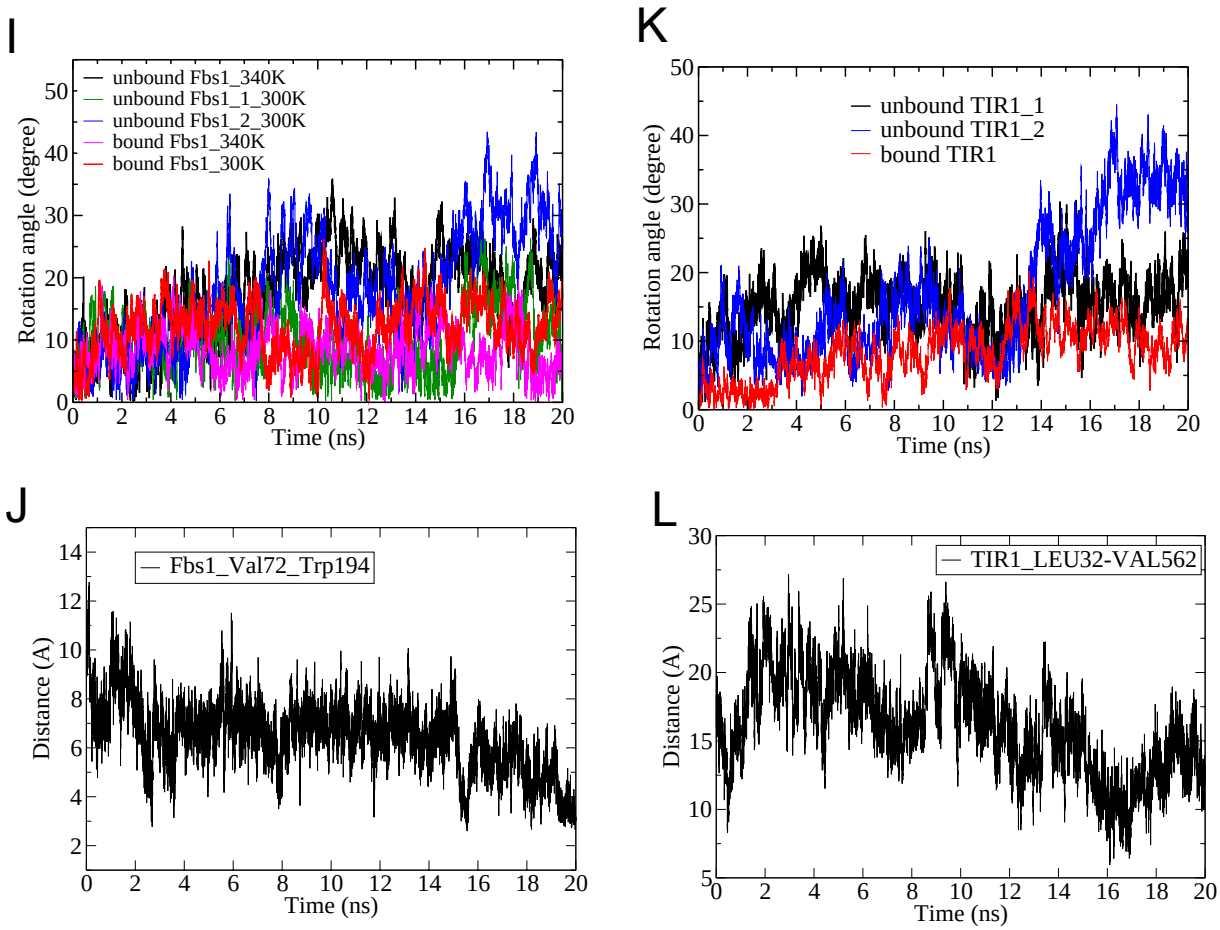

Figure S1. Angle rotation graphs of unbound trajectory 1 (black), trajectory 2 (blue) and bound (red) forms for (A) Skp2, (C) Fbw7, (E) β-TrCP1, (G) Cdc4, (I) Fbs1, and (K) TIR1. The graphs of changes in the distances between hydrophobic residues from box domain and linker are shown for the unbound form trajectory 1 of (B) Skp2, (D) Fbw7, (F) β-TrCP1, (H) Cdc4, (J) Fbs1 and (L) TIR1.