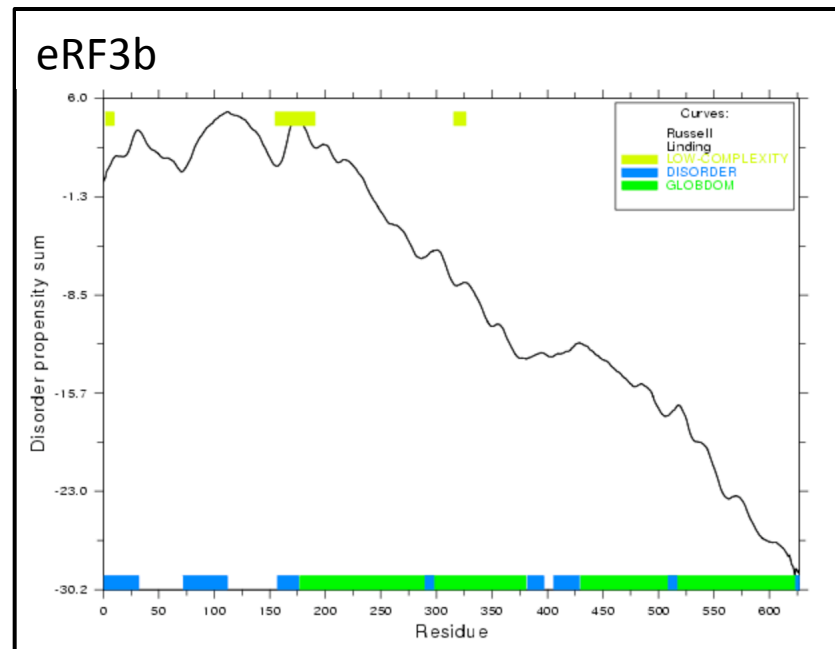
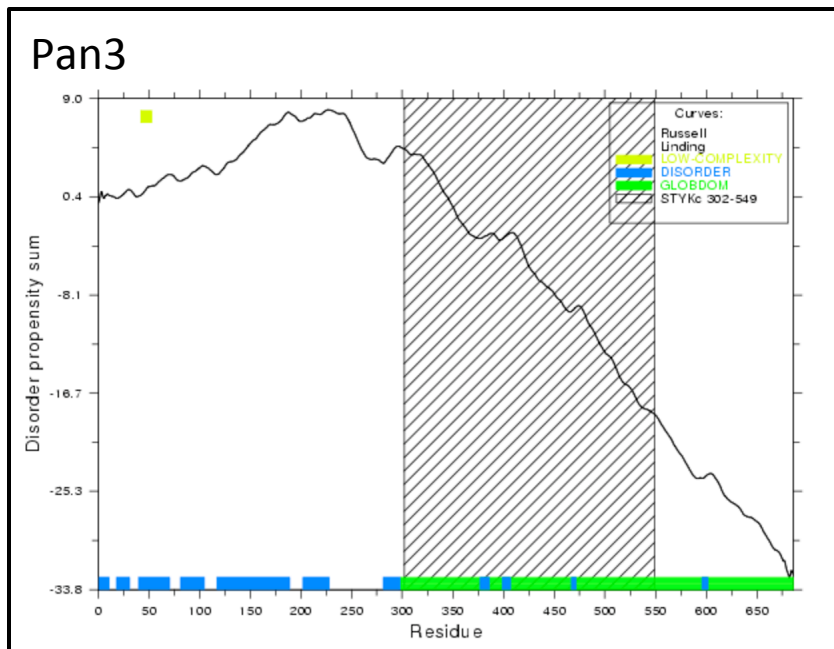
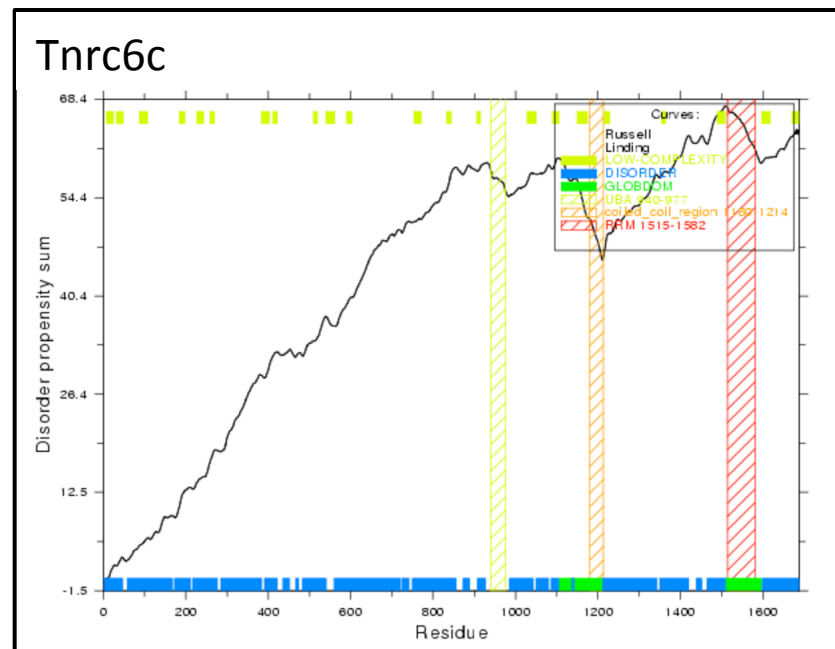
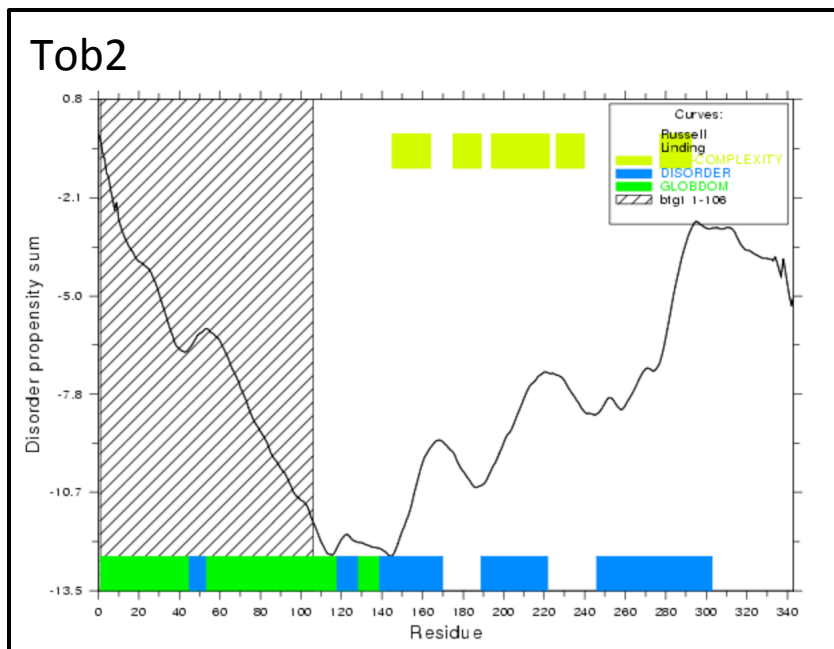
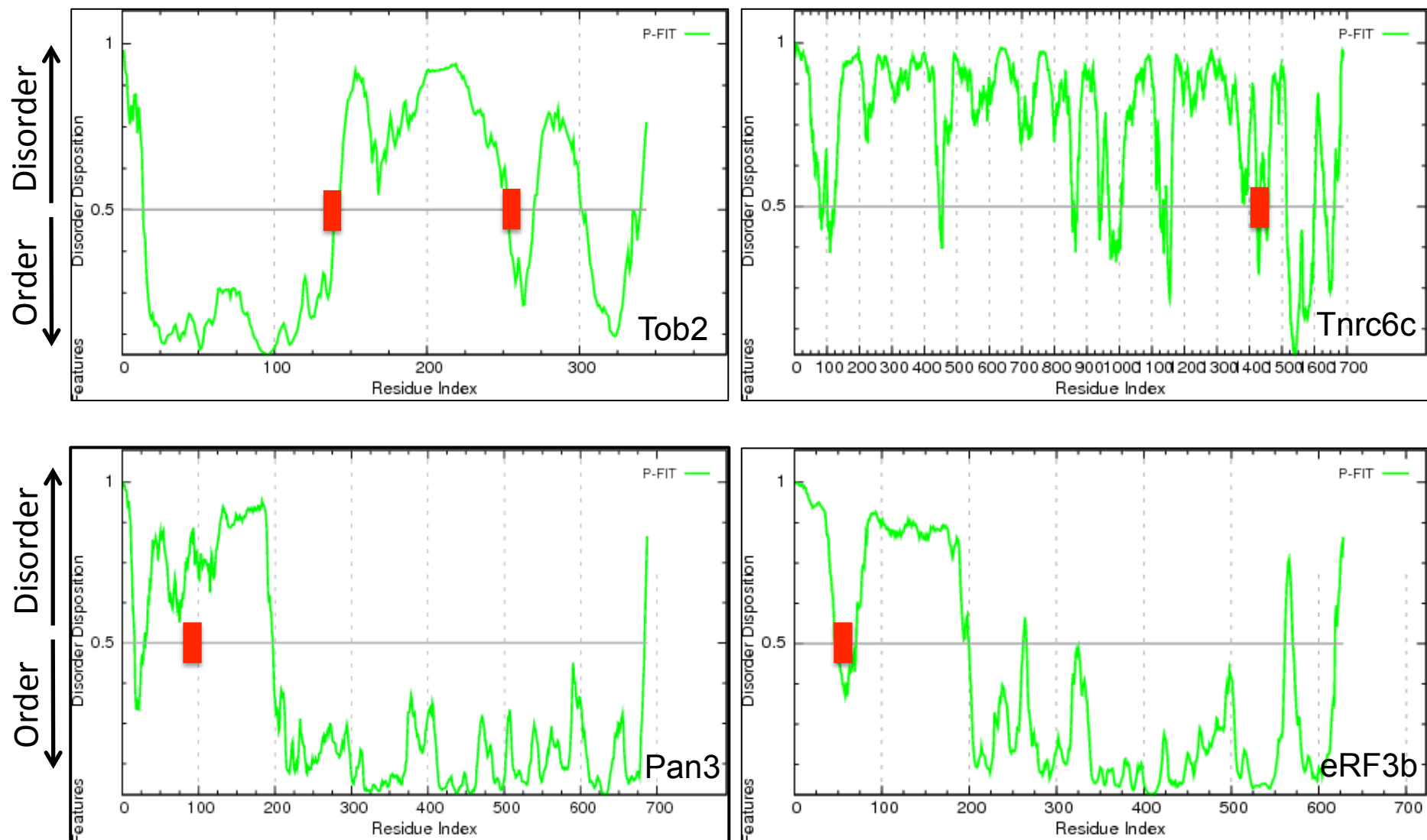


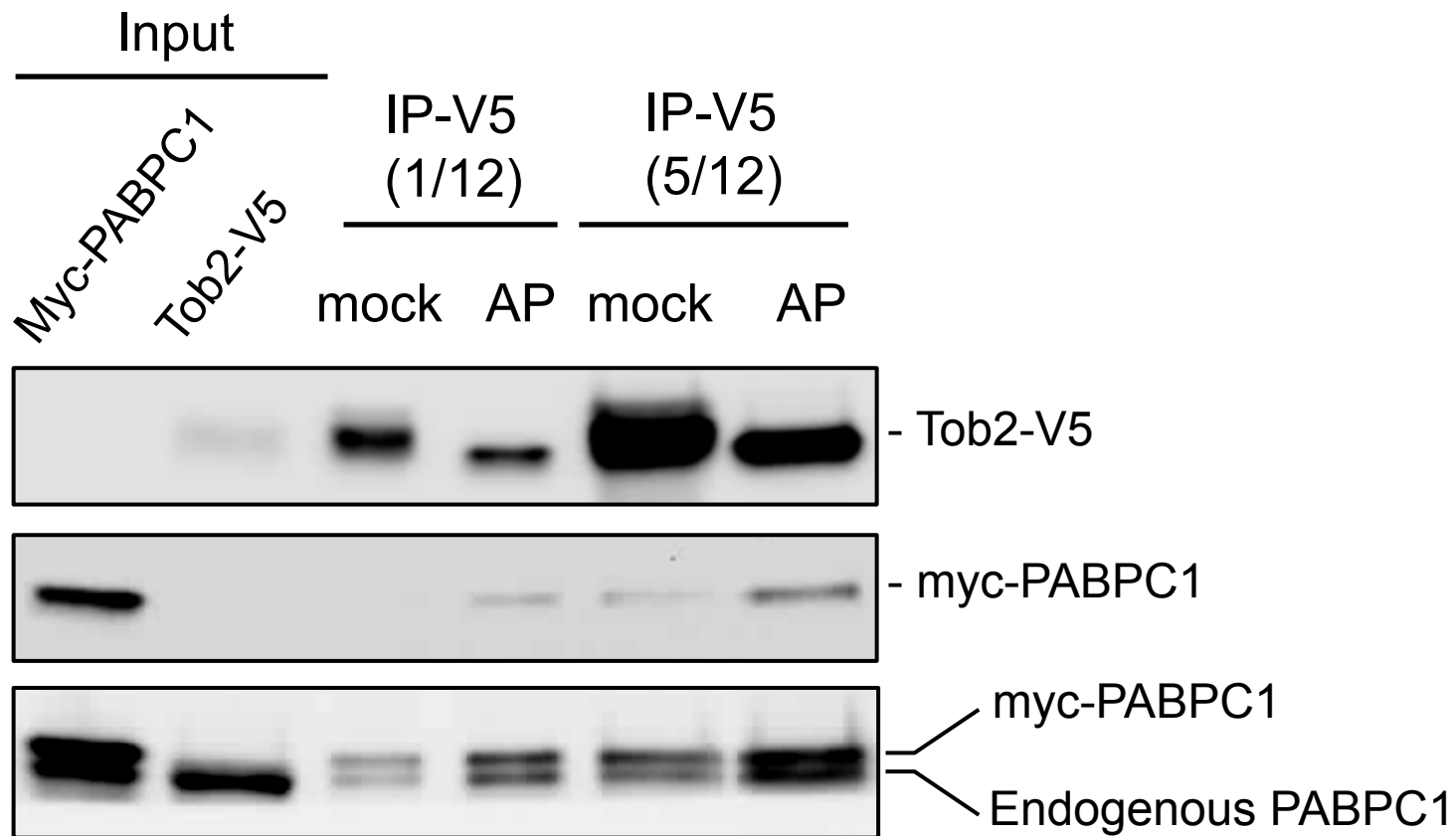
A



B

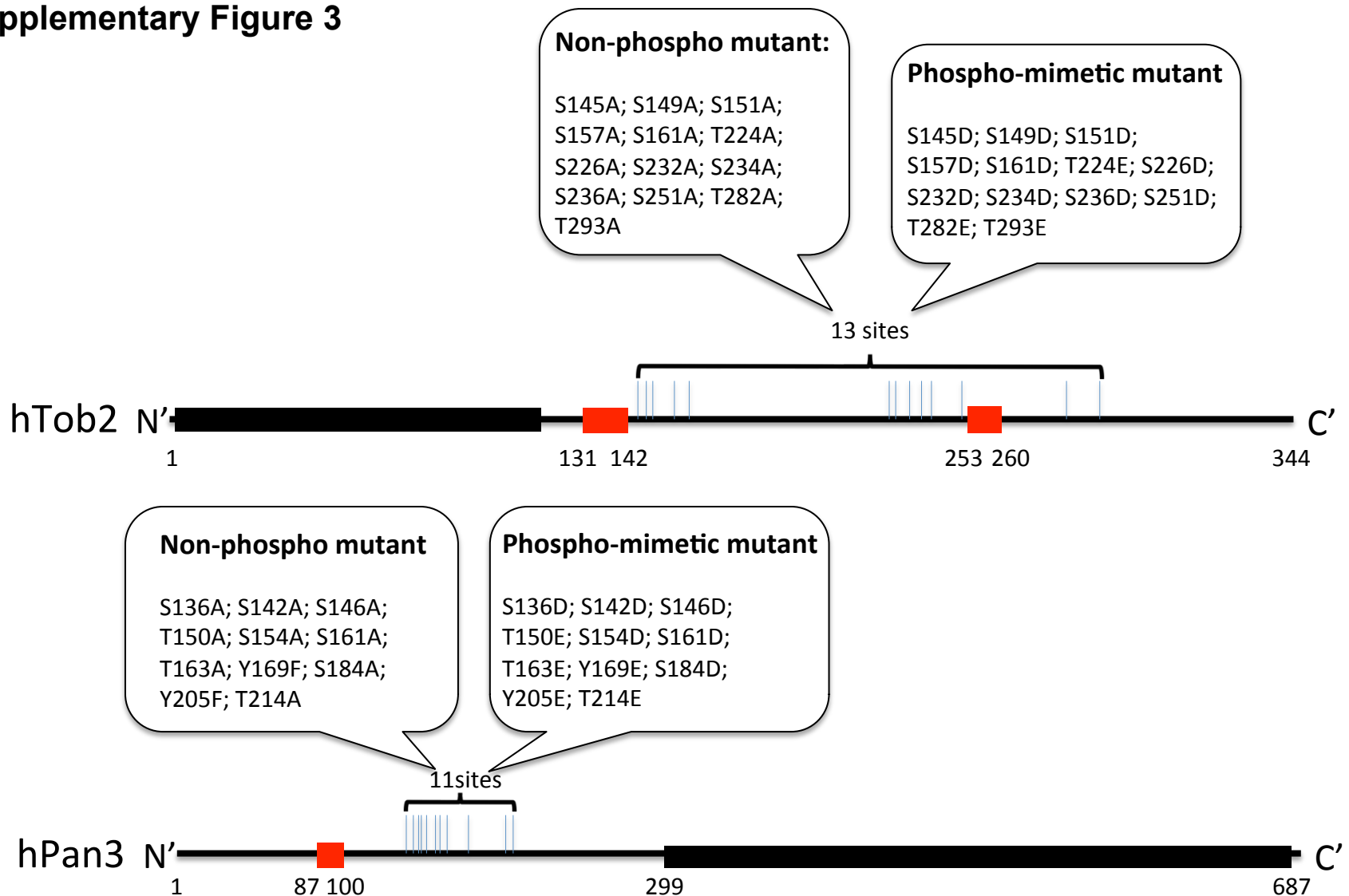
 PAM2 motif

Supplementary Fig. 1. PAM2 motif-containing proteins contain extensive regions of intrinsic disorder. Human Tob2, Pan3, Tnrc6c and eRF3b protein sequences were analyzed for intrinsically disordered or unstructured regions (IDR) by Globplot (A) or PONDER (B) predictor. The websites are listed in the text. Note that in panel a, blue boxes at the bottom of each plot depict the predicted IDRs for each protein while structured domains were shown as green boxes. In panel b, green lines above 0.5 is considered IDRs by PONDR. Also indicated are the position of PAM2 motif in each protein analyzed (red box).



Supplementary Figure 2. Effects of alkaline phosphatase treatment on Tob2's interaction with PABPC1. 1/12 or 5/12 of the total immunoprecipitated Tob2-V5 was treated with alkaline phosphatase (AP) or without AP treatment (mock). Treated samples were further incubated with the lysate made from cells expressing myc-PABPC1 for co-IP. Western blot analysis showed that phosphatase treated Tob2-V5 pulls down much more myc-PABPC1 than does mock-treated Tob2-V5. Cell extracts for IP experiments were prepared from NIH3T3 cells that were transiently transfected with the plasmids encoding the proteins indicated.

Supplementary Figure 3



Note that the cluster of potential phosphorylation sites shown above for Pan3 includes two tyrosine residues that were also mutated to phenylalanines or glutamates in the respective NP or PM mutant of Pan3.

Supplementary Figure 3

Non-Phospho mutant:

S1225A; S1229A; S1233A; S1237A; S1240A; T1244A;
S1257A; T1261A; S1286A; S1291A; S1293A; S1314A;

S1338A; S1339A; S1343A; Y1344F; Y1347F; S1355A;
S1358A; S1366A; S1368A; S1372A; S1374A; S1378A;

T1410A; S1413A; S1439A; S1443A; S1446A; S1447A;
S1468A; S1469A; S1484A; S1485A; S1490A; S1500A;
S1502A; S1508A; S1509A;

S1603A; S1607A; S1609A; S1611A; S1612A; S1617A;
S1621A; S1663A; S1672A; S1686A; S1689A

Phospho-mimetic mutant:

S1225D; S1229D; S1233D; S1237D; S1240D; T1244E;
S1257D; T1261E; S1286D; S1291D; S1293D; S1314D;

S1338D; S1339D; S1343D; Y1344E; Y1347E; S1355D;
S1358D; S1366D; S1368D; S1372D; S1374D; S1378D;

T1410E; S1413D; S1439D; S1443D; S1446D; S1447D;
S1468D; S1469D; S1484D; S1485D; S1490D; S1500D;
S1502D; S1508D; S1509D;

S1603D; S1607D; S1609D; S1611D; S1612D; S1617D;
S1621D; S1663D; S1672D; S1686D; S1689D



■ Structured region

■ PAM2 motif

| Phosphorylation sites