

RMSD	TM-score	Score	SI%	SS%	Length
3.19	0.72	1738.79	52	63	777

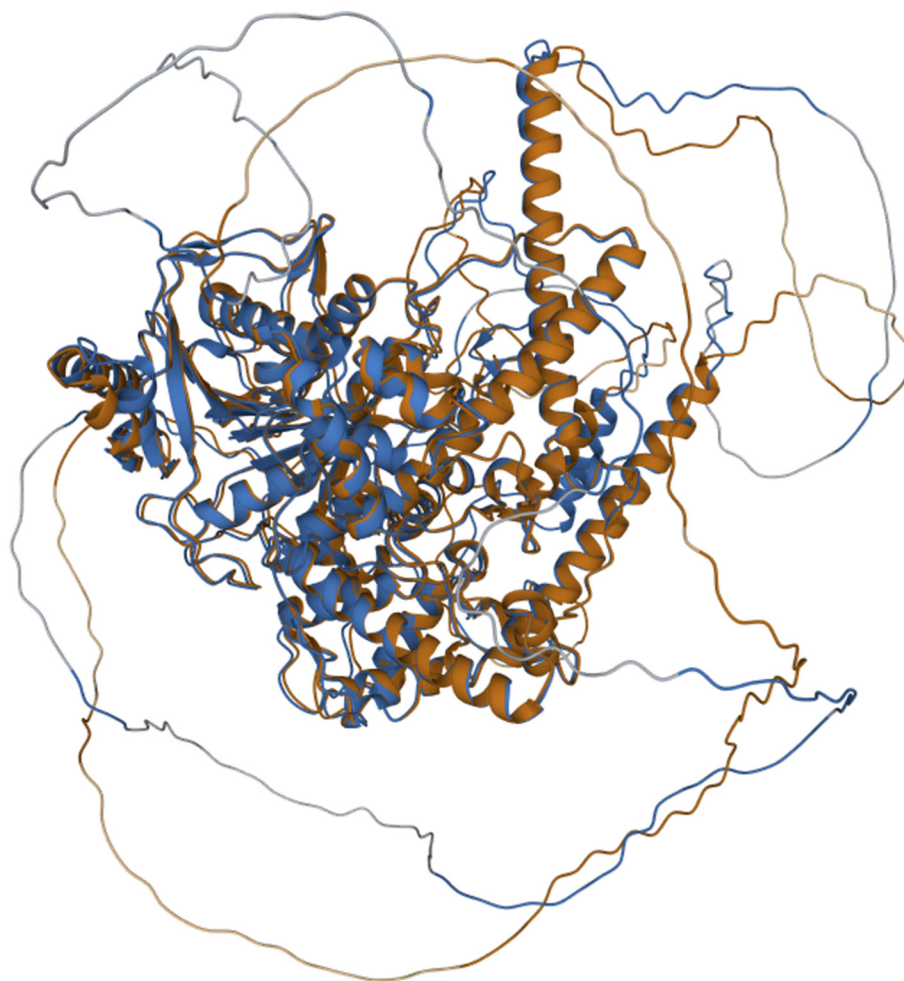


Figure S1. The pairwise structure alignment of two plant XRN proteins. The pairwise structure alignment of AtXRN3 (Orange) and OsXRN3 (Blue), displaying high similarity in the domains of alpha-helices and beta-sheets. The root mean square deviation (RMSD), TM-score, Score for structural similarity, sequence identity percentage (SI%), sequence similarity percentage (SS%) and the length of residue pairs structurally equivalent in the alignment were showed.

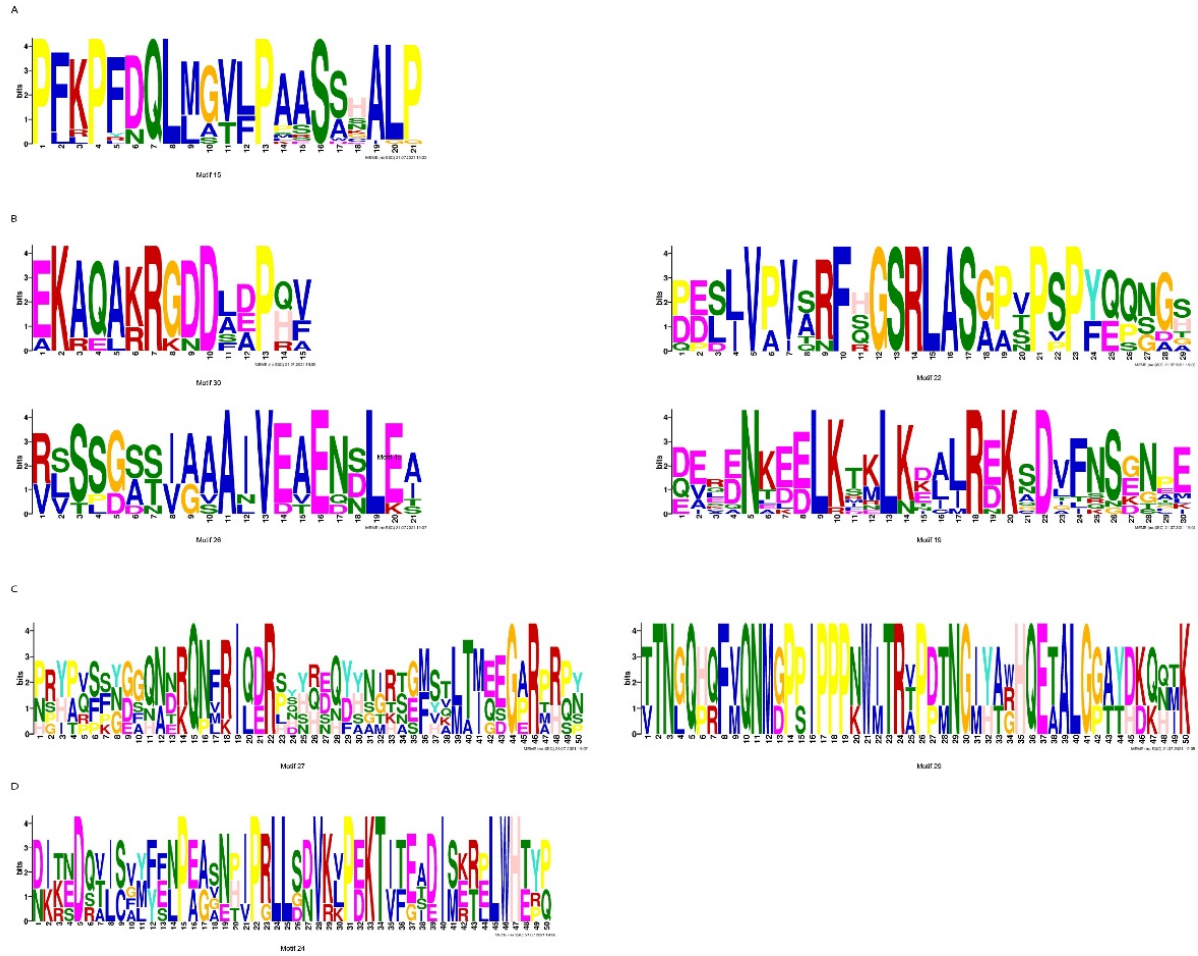


Figure S2. Visualization of the selected conserved motif sequences. (A) Motif 15, shared among all 23 XRNs. (B) Motifs 30, 22, 26 and 19 that were frequently lost in XRN4, XRN5 and a few of XRN3. (C) Motifs 27 and 29 specifically detected in XRN4 proteins. (D) Motif 24 specifically detected in XRN5 proteins.

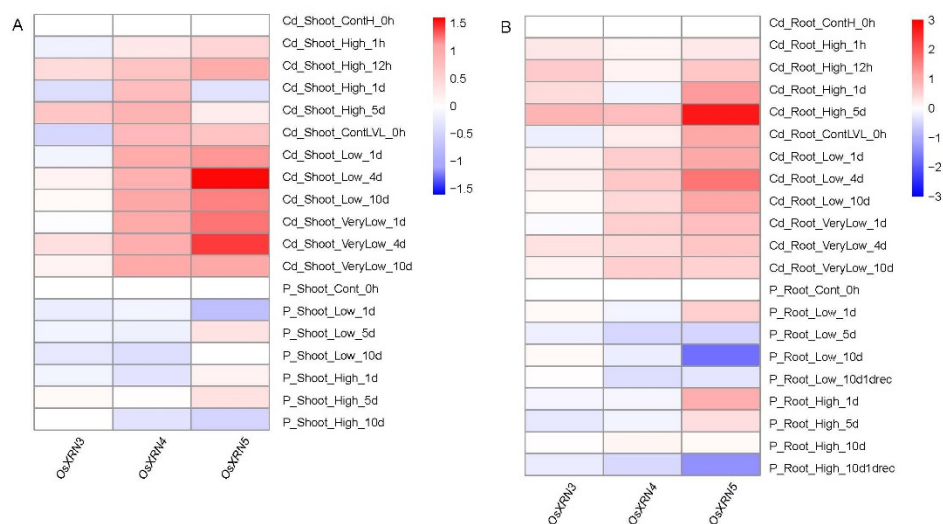


Figure S4. Cluster analysis of the *OsXRN*s expression pattern response to nutrition. Heat maps demonstrate the expression profiles of *OsXRN*s in response to Cd and P in rice shoot (A) and root (B).