Supplementary Information

PhosIDP: a web tool to visualize the location of phosphorylation sites in disordered regions

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Supplementary Figure 1

Variation of window size for charge and fold propensity plots for Q14011. Sliding windows of the charge and fold propensity plots were changed to 5, 10 and 40, and displayed in comparison with the 21 amino acid window results.

Supplementary Figure 1
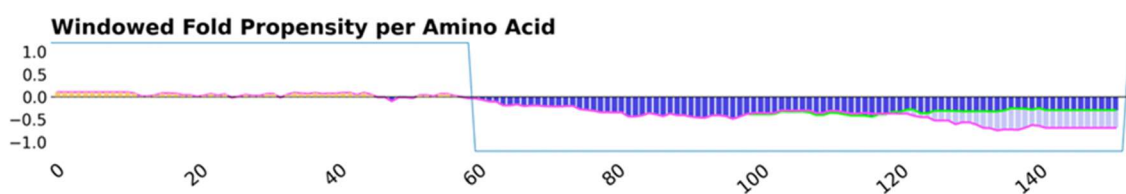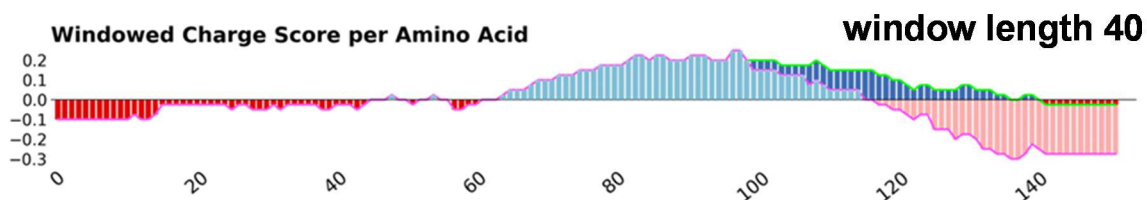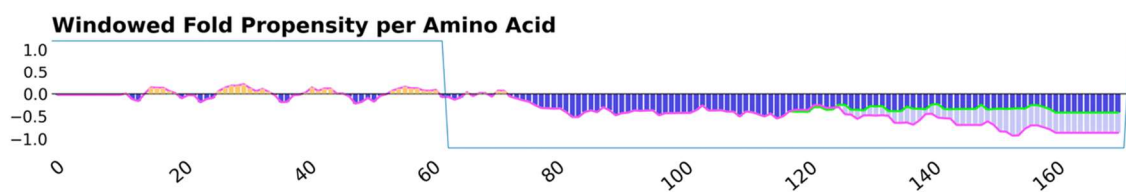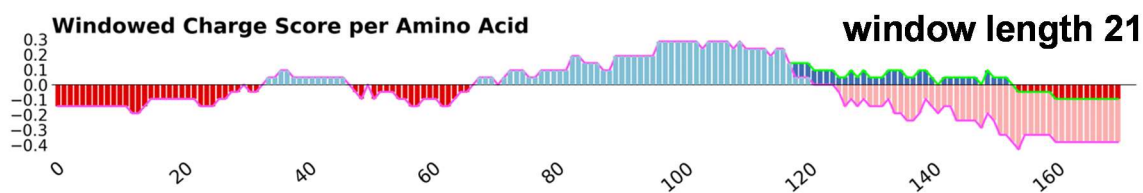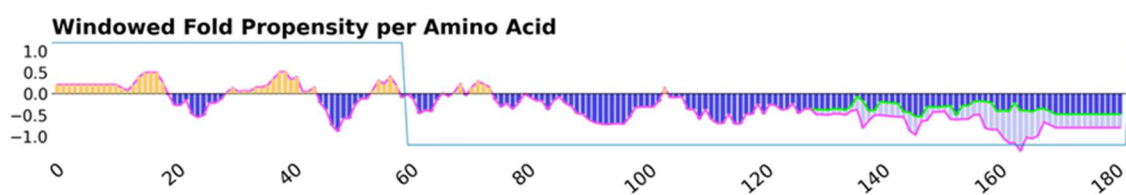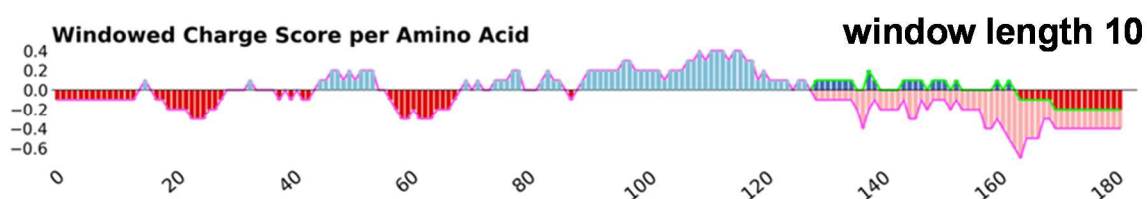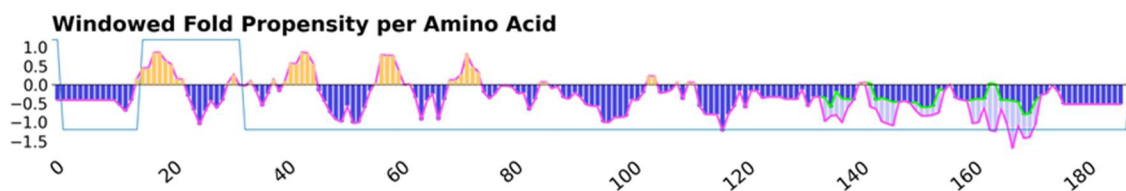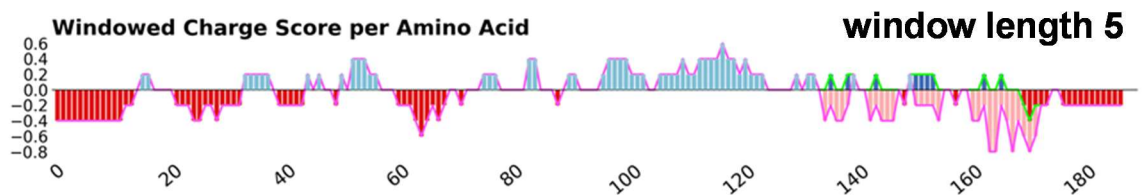
Supplementary Figure 2

Comparison of disorder prediction schemes, for CIRBP (Q14011) and nucleophosmin (P06748). Results from 4 predictors are shown, fold propensity as used in the phosIDP server, IUPred2-long, MetaDisorderMD, and PDisorder (see main text). Note that phosIDP and PDisorder predict disorder as negative, and IUPred2-Long and MetaDisorderMD predict disorder as positive, indicated with labels of IDR (disorder) and STR (ordered, structured).

Supplementary Figure 2