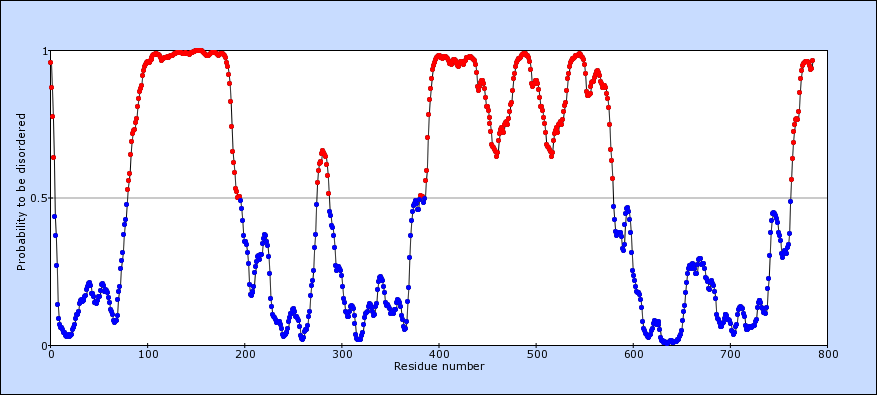
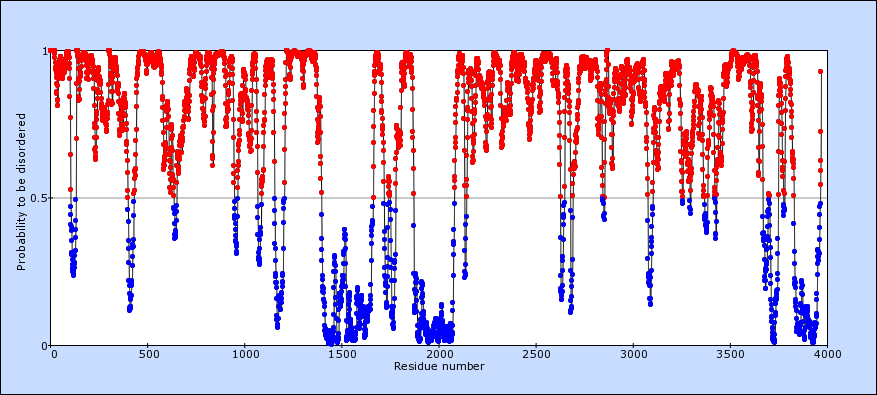
**Supplementary material 12.** Predicted disordered regions of all analysed CBPs (disordered regions were predicted by IsUnstruct tool [31]

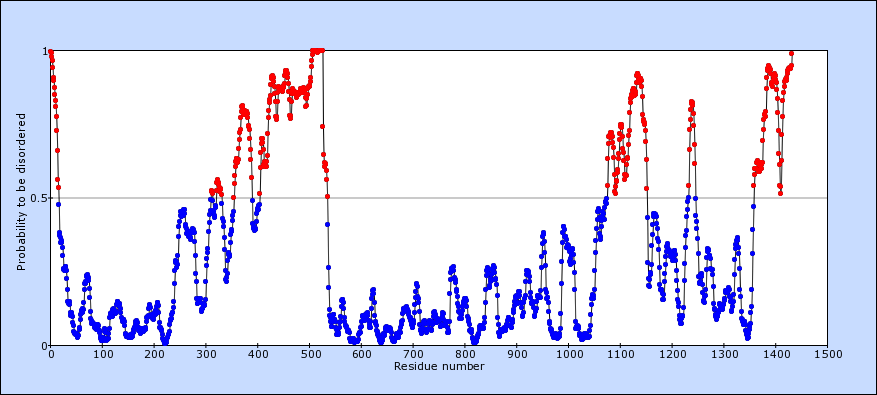
**IFI16** (43.18 % AA predicted to be disordered by previous program (PrDOS [30])



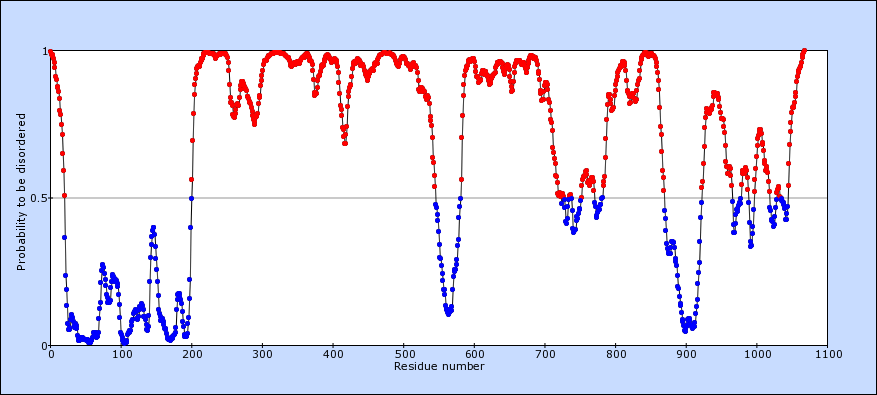
**KMT2A** (not predicted by previous program – too long protein sequence)



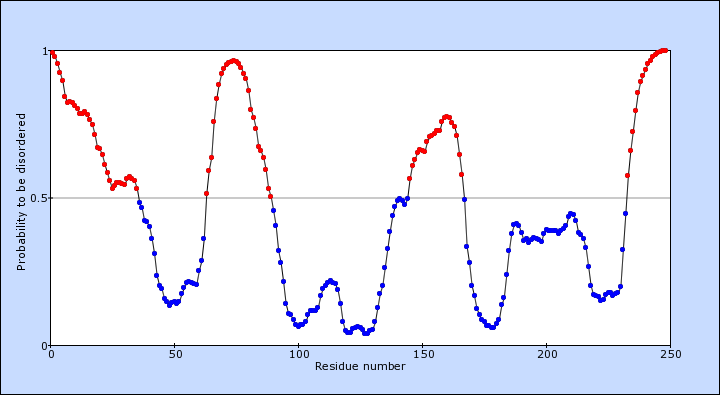
**WRN** (29.82 % AA predicted to be disordered by previous program)

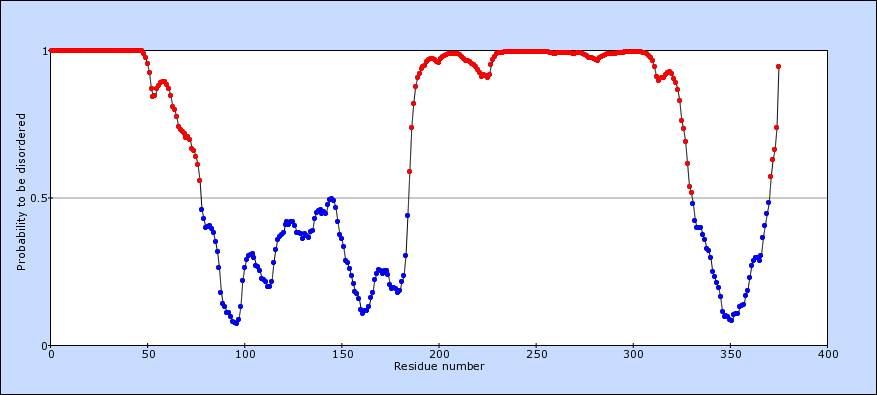


**AF10** (65.92 % AA predicted to be disordered by previous program)

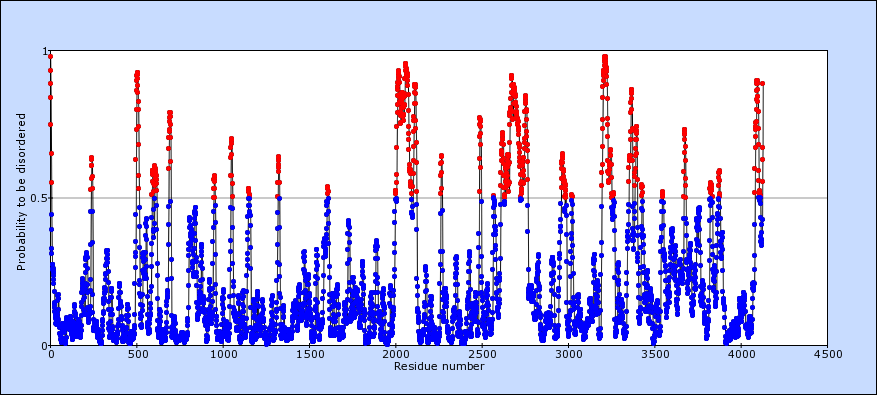


**14-3-3 sigma** (11.29 % AA predicted to be disordered by previous program)

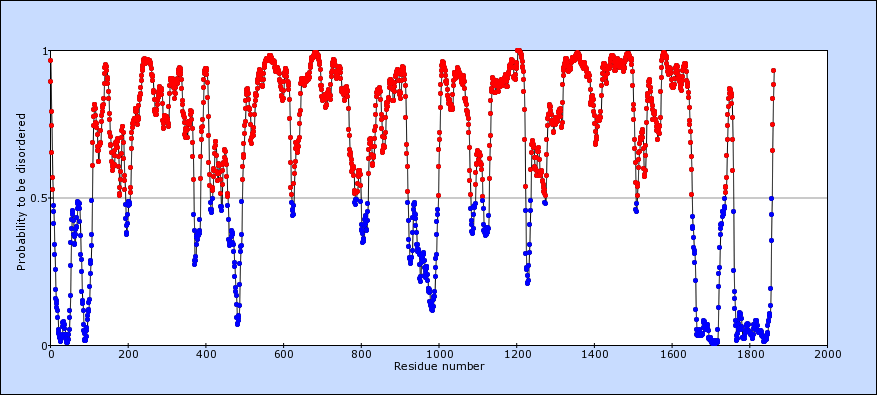


**DEK** (54.93 % AA predicted to be disordered by previous program)

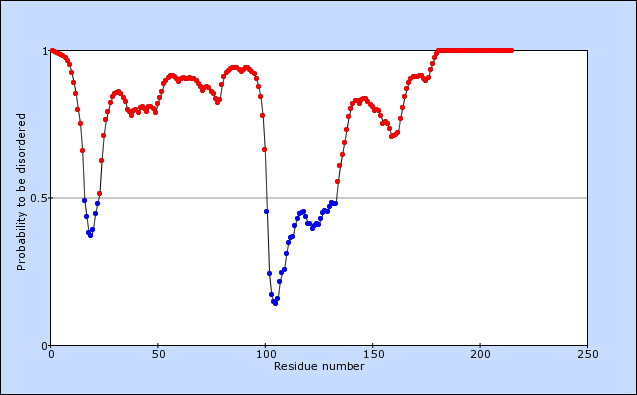
**PRKDC** (not predicted by previous program – too long protein sequence)



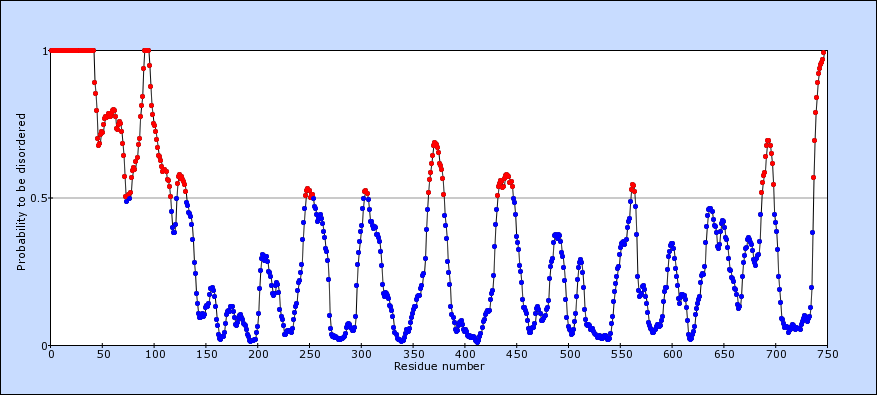
**BRCA1** (65.75 % AA predicted to be disordered by previous program)



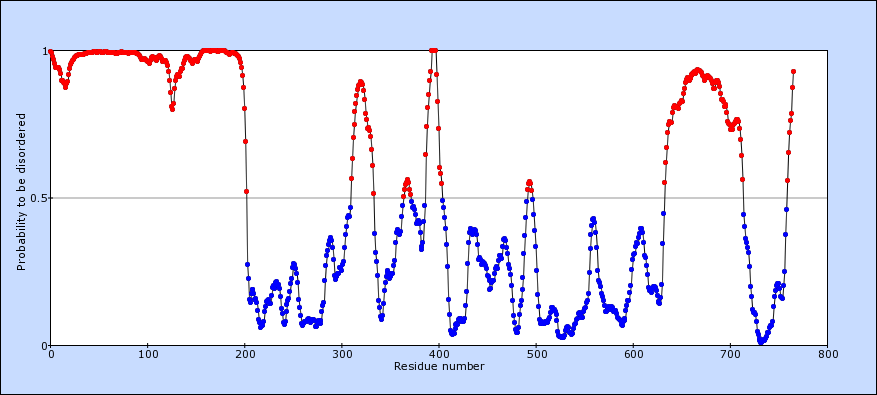
**HMGB1** (34.42 % AA predicted to be disordered by previous program)



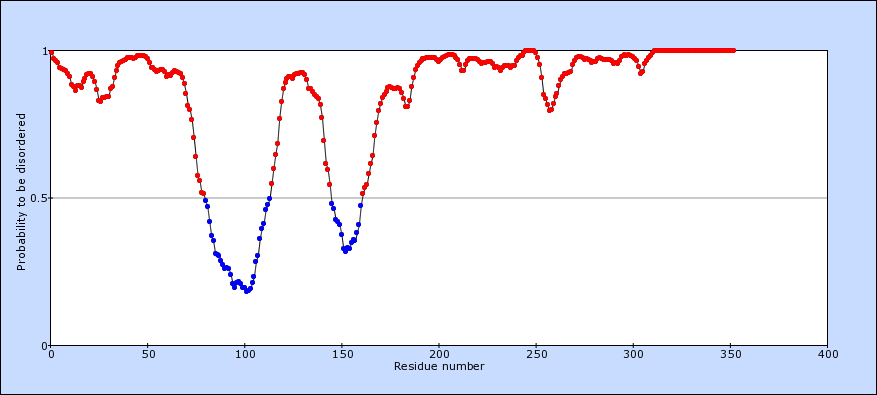
**RAD54L** (20.62 % AA predicted to be disordered by previous program)



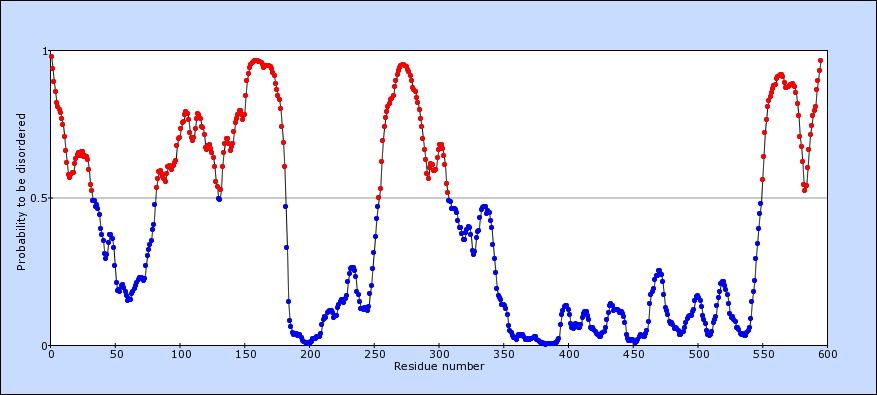
**TOP1** (35.82 % AA predicted to be disordered by previous program)



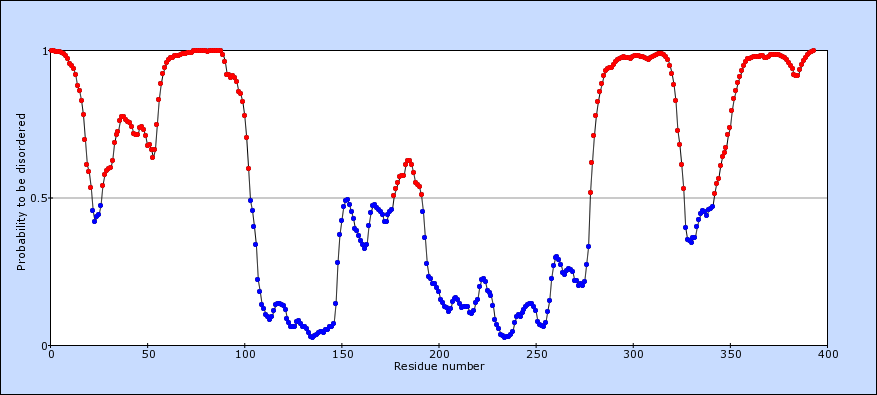
**R51A1** (73.86 % AA predicted to be disordered by previous program)



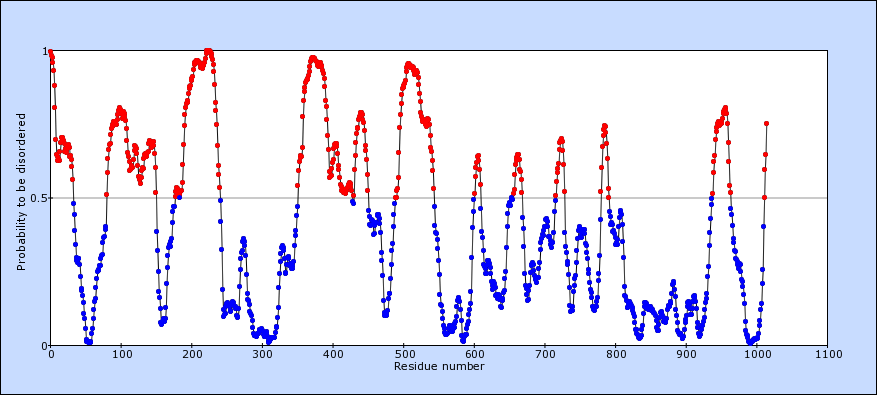
**ESR1** (40.5 % AA predicted to be disordered by previous program)



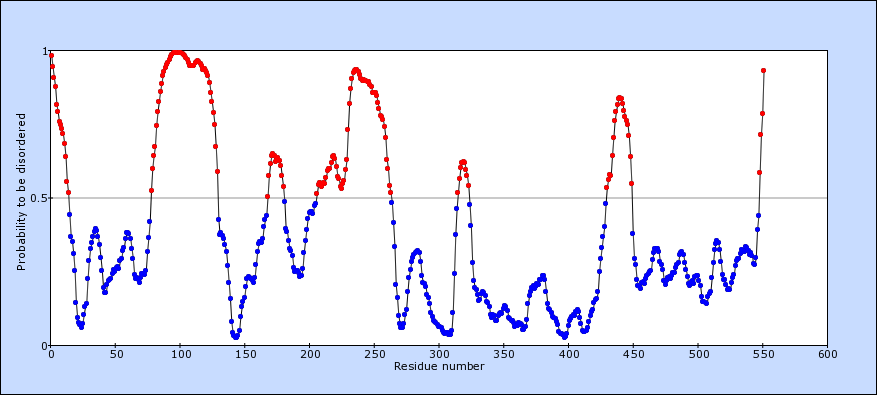
**P53** (35.11 % AA predicted to be disordered by previous program)



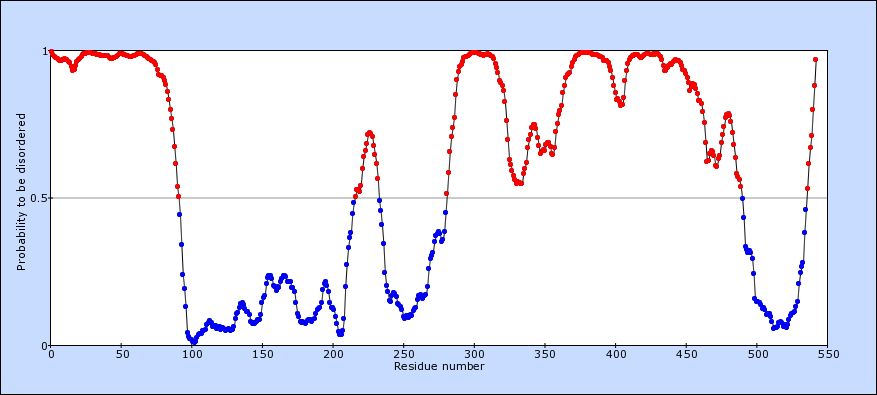
**PARP1** (17.55 % AA predicted to be disordered by previous program)



**MUS81** (25.23 % AA predicted to be disordered by previous program)



**TERF2** (46.86 % AA predicted to be disordered by previous program)



**XPF** (26.86 % AA predicted to be disordered by previous program)

