Supplementary Figure S1, Related to Figure 1. Sequence coverage of full length PR-A and PR-B at different stages of HDX experiments. (a) MSMS sequence coverage of PR-B and PR-A. Letters in red are amino acid sequence detected by analyzing pepsin digested MS/MS spectra using MASCOT. (b) Sequence coverage (%) obtained during MS/MS, 0 second time point injection (t0) and on-exchange experiments of full length and N terminal domain of PR-B and PR-A.

Supplementary Figure S2, Related to Figure 1. Solution state conformational flexibility of agonist bound full length PR-B with different domains indicated by arrow head. The back exchange corrected average % of deuterium incorporation across six different time points (0,10,30,60,300,900 and 3600 sec) are represented is sequence lay out format where each horizontal bar represents each peptide. Colors are according to the color bar at the bottom of the figure.

Supplementary Figure S3, Related to Figure 1. Solution state conformational flexibility of agonist bound full length PR-A with different domains indicated by arrow head. The back exchange corrected average % of deuterium incorporation across six different time points (0,10,30,60,300,900 and 3600 sec) are represented is sequence lay out format where each horizontal bar represents each peptide. Colors are according to the color bar at the bottom of the figure.

Supplementary Figure S4, Related to Figure 4. Solution state conformational flexibility of TBPc. The back exchange corrected average % of deuterium incorporation across six different time points (0,10,30,60,300,900 and 3600 sec) are represented is sequence lay out format where each horizontal bar represents each peptide. Colors are according to the color bar at the bottom of the figure.

Supplementary Figure S5, Related to Figure 4. Differential HDX of isolated N terminal domain (PR-A) showed no perturbation upon interaction with $TBP_{C.}$

(a)

PR-B

MTE**LKAKGPRAPHVAGGPPSPEVGSPLLCRPAAGPFPGSQTSDTLPEVSAIPISLDGLLFPRPCQGQDPSDEKTQDQQSLSDVEGAYSRAEATRGAGGSSSSPPEKDSGLLDSVLDTLLAPSGPGQSQPSPPACEVTSSWCLFGPELPEDPPAAPATQRVLSPLM**SRSGCKVGDSSGTAAAHKVLPRGLSPARQLLLPASESPHWSGAPVKPSPQAAAVEVEEEDGSESEESAGPLLKGKPRALGGAAAGGGAAAVPPGAAAGG**VALVPKEDSRFSAPRVALVEQDAPMAPGRSPLATTVMDFIHVPILPLNHALLAARTRQLLEDESYDGGAGAASAFAPPRSSPCASSTPVA**VGDFPDCAYPPDAEPKDDAYPLY**SDFQPPALKIKEEEEGAEASARSPRSYLVAGANPAAFPDFPLGPPPPLPPRATPSRPGEAAVTAAPASASVSSASSSGSTL**ECILYKAEGAPPQQGPFAPPPCKAPGASGCLL**PRDGLPSTSASAAAAGAAPALYPALGLNGLPQLGYQAAVLKEGLPQVYPPYLNYLRPDSEASQSPQYSFESLPQKICLICGDEASGCHYGVLTCGSCKVFFKRAMEGQHNYLCAGRNDCIVD**KIRRKNCPACRLRKCCQAGMVLGGRKFKKFNKVRV**VRALDAVALPQPVGVPNESQALSQRFTFSPGQDIQLIPPLINLLMSIEPDVIYAGHDNTKPDTSSSLLTSLNQLGERQLLSVVKWSKSLPGFRNLHIDD**QITLI**QYSWMSLMVFGLGWRSYKHVSGQMLYFAPDLILNEQRMKESSF**YSLCL**TMWQIPQEFVKLQVSQEEFLCMKVLLLLNTIPLEGLRSQTQFEEMRSSYIRELIKAIGLRQKGVVSSSQRFYQLTKLLDNLHDLVKQLHLYCLNTFIQSRALSVEFPEMMSEVIAAQLPKILAGMVKPLLFHKK**

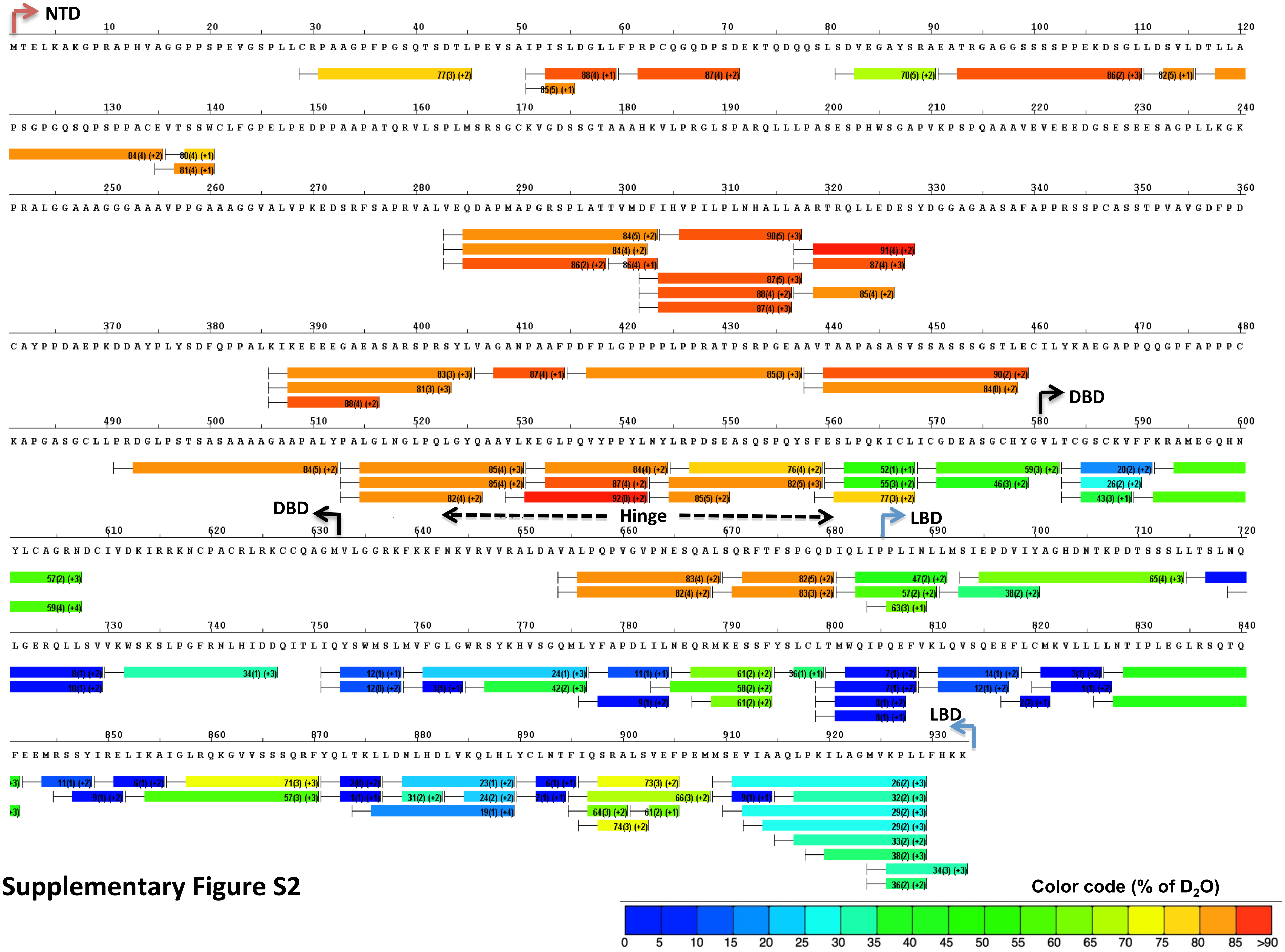
PR-A

MSRSGCKVGDSSGTAAAHKVLPRGLSPARQ**LLLPASESPHWSGAPVKPSPQAAA**VEVEEEDGSESEESAGPLLKGKPRALGGAAAGGGAAAVPPGAAAGG**VALVPKEDSRFSAPRVALVEQDAPMAPGRSPLATTVMDFIHVPILPLNHALLAARTRQLLEDESYDGGAGAASAFAPPRSSPCA**SSTPVAVGDFPDCAYPPDAEPKDDAYPLY**SDFQPPALKIKEEEEGAEASARSPRSYLVAGANPAAFPDFPLGPPPPLPPRATPSRPGEAAVTAAPASASVSSASSSGSTLE**CILYKAEGAPPQQGPFAPPPCKAPGASGCLL**PRDGLPSTSASAAAAGAAPALYPALGLNGLPQLGYQAAVLKEGLPQVYPPYLNYLRPDSEASQSPQYSFESLPQKICLICGDEASGCHYGVLTCGSCKVFFKRAMEGQHNYLCAGRNDCIVD**KIRRKNCPACRLRKCCQAGMVLGGRKFKKFNKVRV**VRALDAVALPQPVGVPNESQALSQRFTFSPGQDIQLIPPLINLLMSIEPDVIYAGHDNTKPDTSSSLLTSLNQLGERQLLSVVKWSKSLPGFRNLHIDD**QITL**IQYSWMSLMVFGLGWRSYKHVSGQMLYFAPDLILNEQRMKESSF**YSLCL**TMWQIPQEFVKLQVSQEEFLCMKVLLLLNTIPLEGLRSQTQFEEMRSSYIRELIKAIGLRQKGVVSSSQRFYQLTKLLDNLHDLVKQLHLYCLNTFIQSRALSVEFPEMMSEVIAAQLPKILAGMVKPLLFHKK**

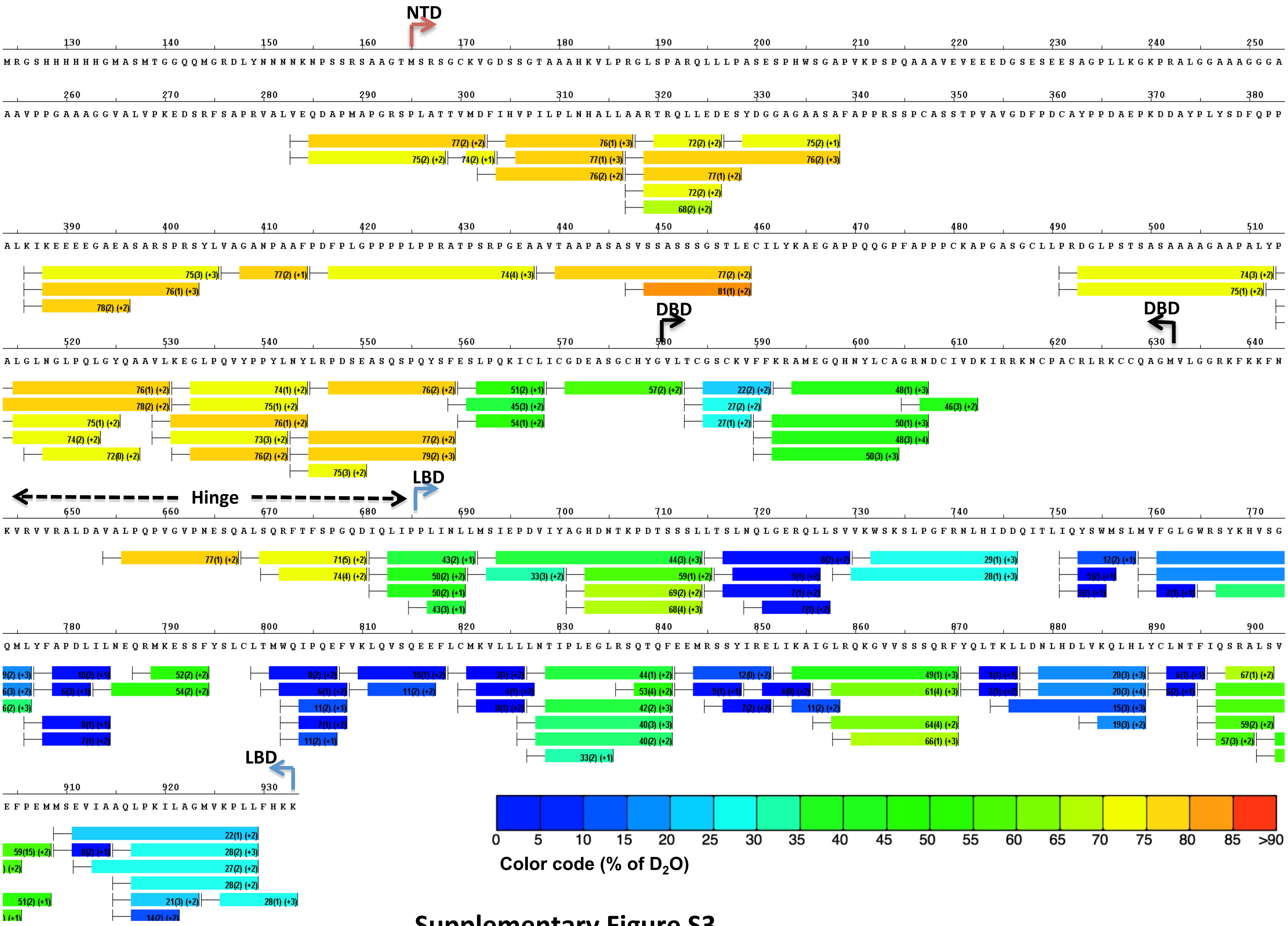
(b)

Isoform	MSMS	t0 (FL)	t0 (NTD only)	On exchange (FL)	On exchange (NTD only)
PR-A	75	72	59	68.7	47
PR-B	78	75	69	65.9	53

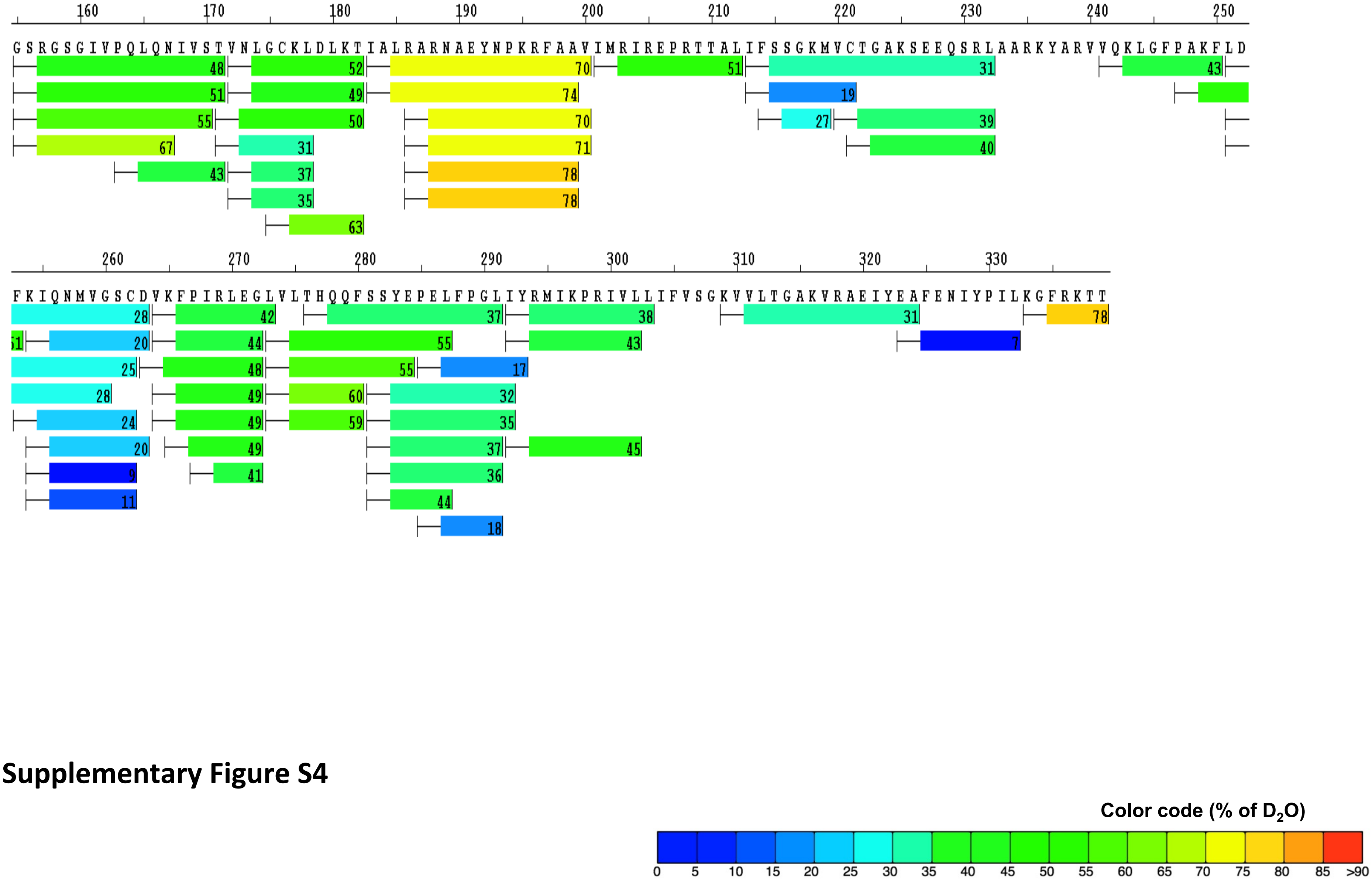
Supplementary Figure S1



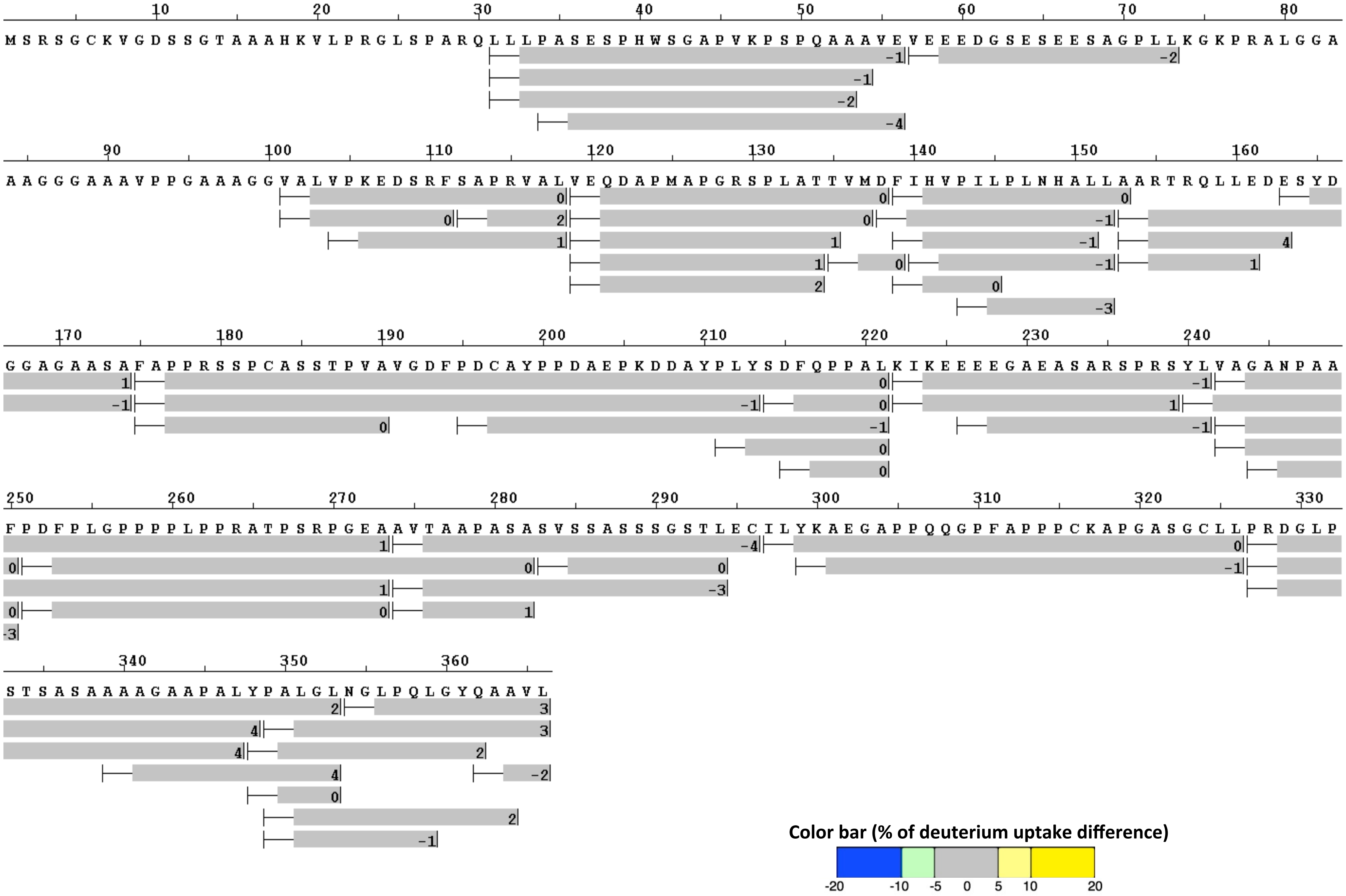
Supplementary Figure S2



Supplementary Figure S3



Supplementary Figure S4



Supplementary Figure S5