

**Supplementary Table 5: HDX Data Summary and Experimental Parameters**

Data Set	PPM1D <sub>(1-420)</sub>	Hinge and flap deletions
<b>Related Figures</b>	Figures 4A, 4B, 5A, 5B	Figures 4C, 4D, 4E, 4F, 6B, 6D, Supp. 5F
<b>States analyzed</b>	PPM1D <sub>(1-420)</sub> + DMSO PPM1D <sub>(1-420)</sub> + GSK	+DMSO PPM1D <sub>(1-420)</sub> PPM1D <sub>Δflap</sub> PPM1D <sub>Δhinge</sub> +GSK PPM1D <sub>(1-420)</sub> PPM1D <sub>Δflap</sub> PPM1D <sub>Δhinge</sub>
<b>HDX reaction details (a)</b>	Final D <sub>2</sub> O concentration = 93.6%, 1:1 (v/v) dilution with quench buffer [0.8M guanidine hydrochloride, 0.8% formic acid, H <sub>2</sub> O].	
<b>HDX time course</b>	0.167, 1, 10, 60, 240 minutes	
<b>Back-exchange (b)</b>	~35%	
<b>HDX controls</b>	3 undeuterated + DMSO	8 undeuterated; 2-3 per state + DMSO
<b>Number of peptides</b>	79 followed, 102 identified	96 followed, 148 identified
<b>Filtering parameters</b>	0.3 products per a.a. 3 consecutive products 8 ppm error File threshold of 2	0.3 products per a.a. 3 consecutive products 10 ppm error File threshold of 4
<b>Sequence coverage</b>	91.2%	79%
<b>Average peptide length</b>	13.6	11.3
<b>Redundancy</b>	2.8	3.26
<b>Replicates</b>	1-3 technical replicates for each state	
<b>Repeatability (c)</b>	+/- 0.20 relative Da	
<b>Significant differences (d)</b>	> 0.5 Da	

(a) 15-fold dilution with labeling buffer [20 mM HEPES, pH 7.5, 25 mM NaCl, 5 mM MgCl<sub>2</sub>, 0.1 mM TCEP, 99.9% D<sub>2</sub>O].

1:1 (v/v) dilution with quench buffer [0.8M guanidine hydrochloride, 0.8% formic acid, H<sub>2</sub>O].

(b) Back exchange estimated using peptides from the loop region of PPM1D, specifically peptides covering residues 45-60.

(c) Average standard deviation across all replicate measurements for all peptides and timepoints for each state analyzed.

(d) Global  $|\Delta\text{HX}|$  significance threshold was calculated from experimental standard deviations to be 0.405 Da (Hageman et al., 2014).

C-terminal truncations	Loop deletion
Figure 7D	Supplementary Figure 6B
PPM1D <sub>(1-420)</sub> PPM1D <sub>(1-400)</sub> PPM1D <sub>(1-377)</sub>	PPM1D <sub>(1-420)</sub> PPM1D <sub>Δloop</sub>
pH <sub>read</sub> = 7.1	
tes	
3 undeuterated; PPM1D <sub>(1-420)</sub>	3 undeuterated; PPM1D <sub>(1-420)</sub>
128 followed, 193 identified	69 followed, 82 identified
0.3 products per a.a. 3 consecutive products 9 ppm error File threshold of 2	0.3 products per a.a. 3 consecutive products 10 ppm error File threshold of 3
92.9%	86.4%
12.8	10.6
4.21	2
ch state	

91.

TS and Weis DD. *Anal Chem* 91, 8008-8016, 2019).