SUPPLEMENTARY TABLE 4. HDX Data Summary and Experimental Parameters

Data Set	WT +/- GSK2830371	Hinge and flap deletions +/- GSK2830371		C-terminal truncations	Loop deletion
States analyzed	State 1: $PPM1D_{1-420}$ + DMSO State 2: $PPM1D_{1-420}$ + GSK	+DMSO State 1: $PPM1D_{1-420}$ State 3: $PPM1D_{\Delta flap}$ State 4: $PPM1D_{\Delta hinge}$	+GSK State 2: $PPM1D_{1-420}$ State 5: $PPM1D_{\Delta flap}$ State 6: $PPM1D_{\Delta hinge}$	State 1: $PPM1D_{1-420}$ State 7: $PPM1D_{1-377}$ State 8: $PPM1D_{1-400}$	State 1: $PPM1D_{1-420}$ State 9: $PPM1D_{\Delta loop}$
HDX reaction details [a]	Final D_2O concentration = 93.6%, pH_{read} = 7.1				
HDX time course	0.167, 1, 10, 60, 240 minutes				
Back-exchange	30-35%				
HDX controls	3 undeuterated + DMSO	8 undeuterated; 2-3 per state + DMSO		3 undeuterated; $PPM1D_{1-420}$	3 undeuterated; $PPM1D_{1-420}$
Number of peptides	79 followed, 102 identified	96 followed, 148 identified		128 followed, 193 identified	69 followed, 82 identified
Filtering parameters	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		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
Sequence coverage	91.2%	79%		92.9%	86.4%
Average peptide length	13.6	11.3		12.8	10.6
Redundancy	2.80	3.26		4.21	2.00
Replicates	1-2 technical for each state				
Repeatability	+/- 0.20 relative Da				
Significant differences	> 0.5 Da				

[a] 15-fold dilution with labeling buffer [20 mM HEPES, pD 7.5, 25 mM NaCl, 5 mM $MgCl_2$, 0.1 mM TCEP, 99.9% D_2O].
1:1 (v/v) dilution with quench buffer [0.8M guanidine hydrochloride, 0.8% formic acid, H_2O].