Table 1: Estimates on the total number of phosphoproteins and p-sites for the various species, based on different analyses.

		Human	Mouse	Arabidopsis	Yeast
Proteins	current	10 456	6512	4930	2587
	current_3X	6683	3827	1815	1630
	Rcapture_HTP_vs_LTP	12 844	11 190	NA	2951
	Rcapture_1 %_noise	10 239	8346	6531	2772
	CF_1 %_noise	9160	7213	4292	2373
	CF_3X	7582	6789	NA	2297
	CF_best_start_1 %_noise	8803	7167	4558	2328
	CF_best_end_1 %_noise	8775	7099	4292	2304
	CF_half_exp_1 %_noise	7885	6329	2373	2257
P-sites	current	86 181	36 438	14 796	13244
	current_3X	27 110	10 384	3078	4156
	Rcapture_HTP_vs_LTP	229 616	155 668	NA	40350
	Rcapture_1 %_noise	124 985	71 456	27 815	21343
	CF_1 %_noise	94 670	54 031	23 531	14533
	CF_3X	91 500	NA	34 457	NA
	CF_best_start_1 %_noise	82 092	45 797	15 122	12962
	CF_best_end_1 %_noise	86 723	49 122	23 531	14496
	CF_half_exp_1 %_noise	89 639	36 615	6016	11980

Second column denotes the analysis and datasets: current: experimentally identified; current_3X: experimentally identified in three or more experiments; Rcapture_HTP_vs_LTP: The Capture-Recapture analysis that used the HTP compendium and the LTP compendium (shown in **bold** as the most reliable estimate); Rcapture_1 %_noise: The Capture-Recapture analysis assuming 1 % noise in each dataset; CF_1 %_noise: The Curve-Fitting analysis assuming 1 % noise; CF_3X: The Curve-Fitting analysis based on the datasets that have been identified in three or more experiments. CF_best_start_1 %_noise: The Curve-Fitting analysis assuming 1 % noise and changing the order of the largest experiment as first; CF_best_end_1 %_noise: The Curve-Fitting analysis assuming 1 % noise and changing the order of the largest experiment as last; CF_half_exp_1 %_noise: The Curve-Fitting analysis assuming 1 % noise and using only the first half of experiments.