

Supporting Information

Peterson et al. 10.1073/pnas.0912718107

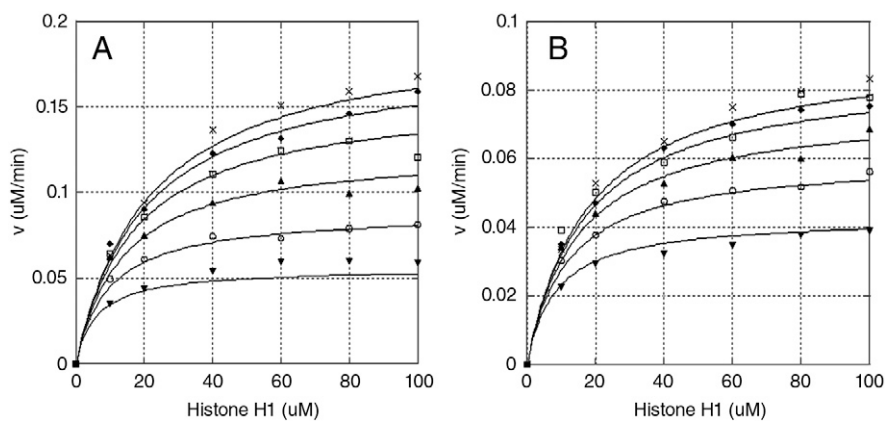


Fig. S1. Steady-state kinetic analysis of histone H1 phosphorylation by A) CDK5/p35 (0.33 nM) and B) CDK5/p25 (0.6 nM). Initial rates were obtained in response to varying both histone and ATP concentrations. Data were analyzed by global nonlinear regression fitting to give the best fit parameters in Table 1. In both A and B, ATP concentrations are (from top to bottom): 1 mM -x, 500 -◆, 250 -□, 125 -▲, 62.5 -○, 31 uM -▼

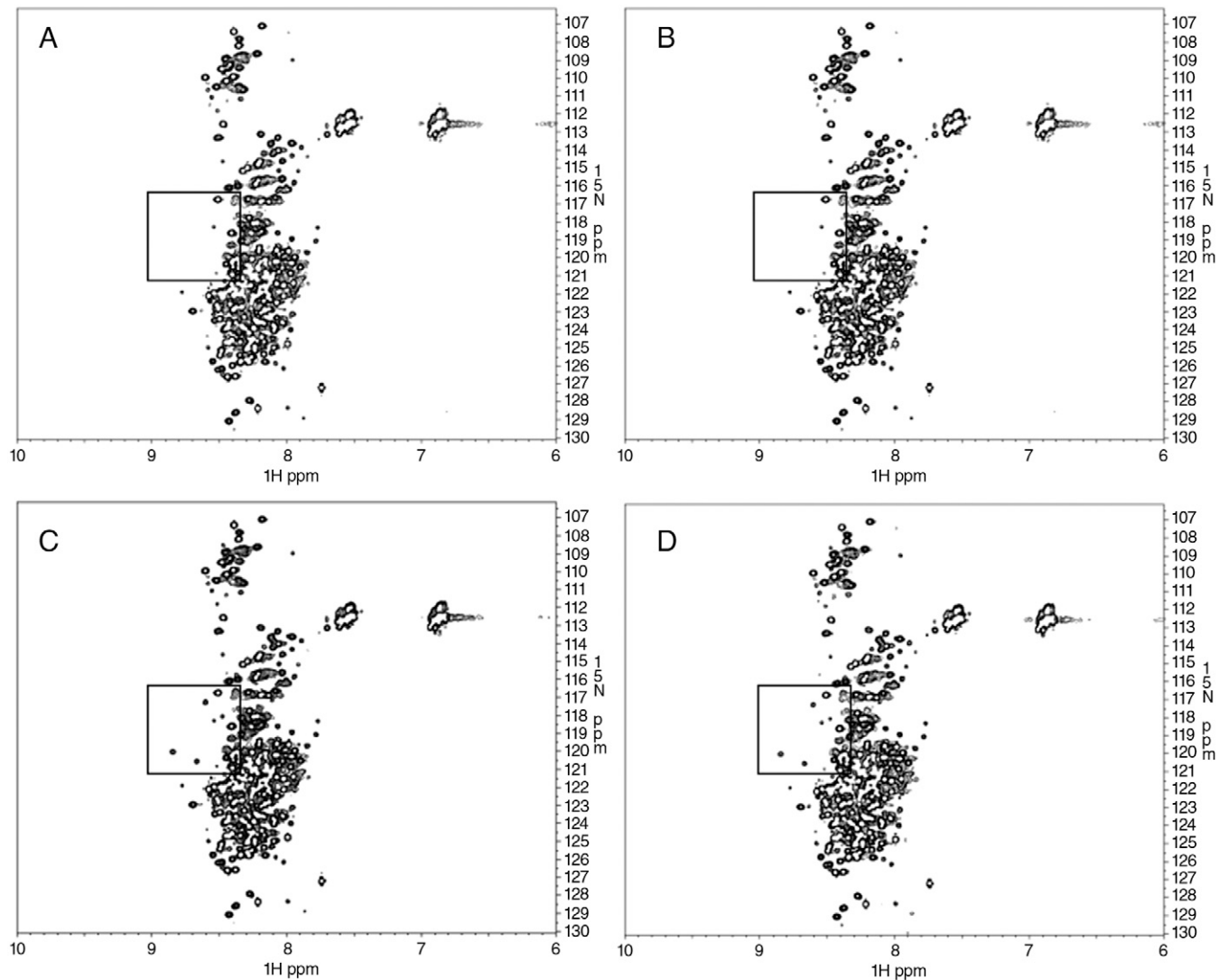


Fig. S2. ^1H - ^{15}N -HSQC spectra of tau phosphorylated with CDK5/p35 or CDK5/p25. Spectra of full-length human tau (441 amino acids) is shown in response to phosphorylation by: (A, C) CDK5/p35 (11 nM); (B, D) CDK5/p25 (11 nM); (A, B) after 30 min phosphorylation; (D, E) after 19 hr phosphorylation. Inset is shown as Fig. 3.