Solution NMR studies reveal no global flexibility in the catalytic domain of CDC25B

Supplementary data

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FIGURE S1

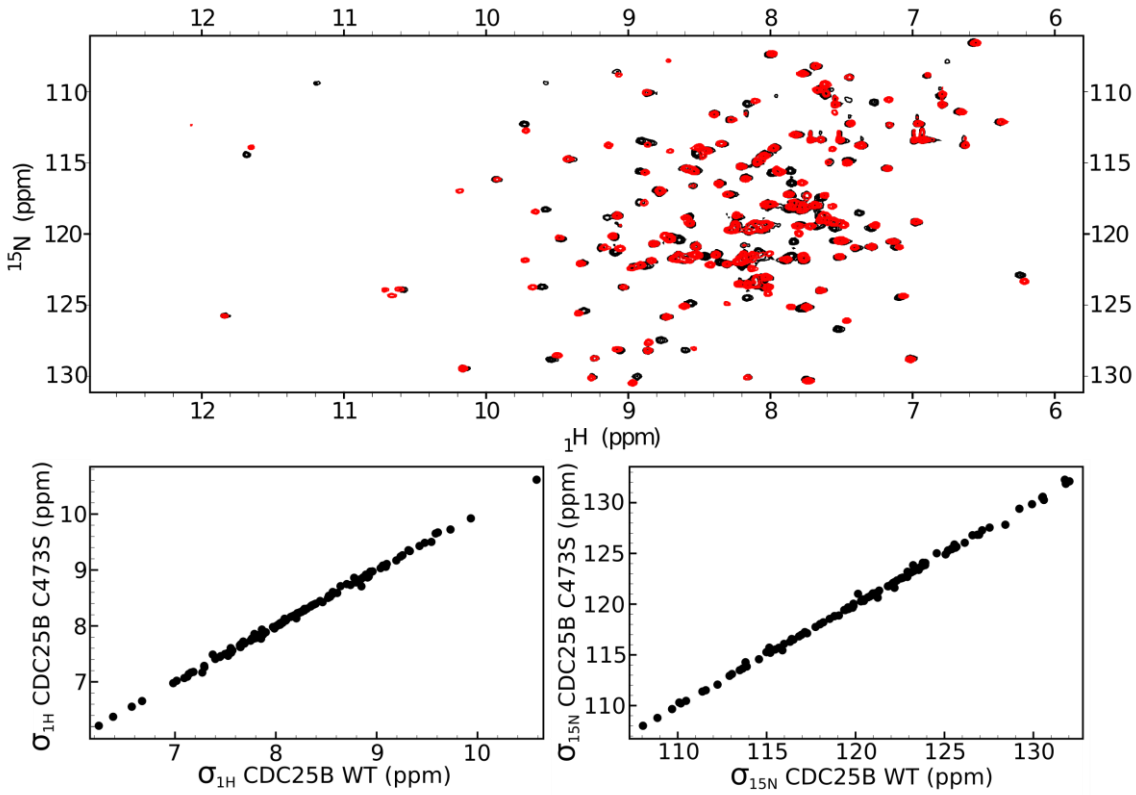

Figure S1. *Comparison of chemical shifts between CDC25B WT and the C473S mutant.* A) Overlap of $^{1}H^{15}N$-HSQC spectra for CDC25B WT (black) and C473S (red). B) Comparison of ^{1}H chemical shifts for the same residues in CDC25B WT and C473S mutant proteins from the $^{1}H^{15}N$-HSQC spectra. C) Same as in B, comparing ^{15}N chemical shifts. Analyses B and C omit 6 residues from the mutant protein including and immediately adjacent to the mutated residue (residues H472, S473, S476, S477, E478, and R479) that differed significantly enough in chemical shift such that they could not be definitely assigned in the WT spectrum.

FIGURE S2

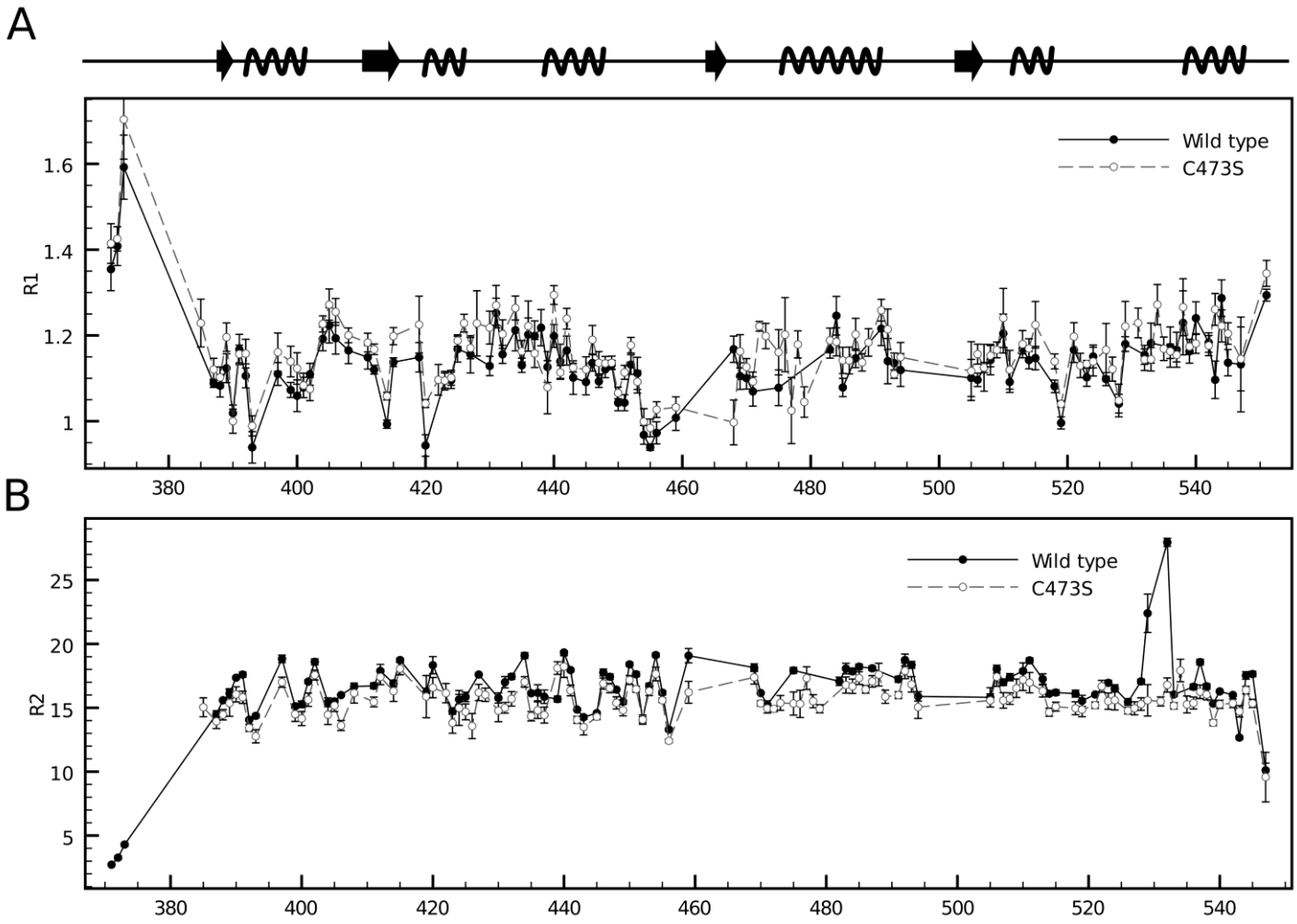

Figure S2. *Comparison of relaxation measurements between CDC25B WT and the C473S mutant.* A) R_1 values for CDC25B WT (black dots, solid line) and the C473S mutant (white dots, dotted line). A schematic of CDC25B secondary structure is shown above. B) Same as in A, comparing R_2 values.

FIGURE S3

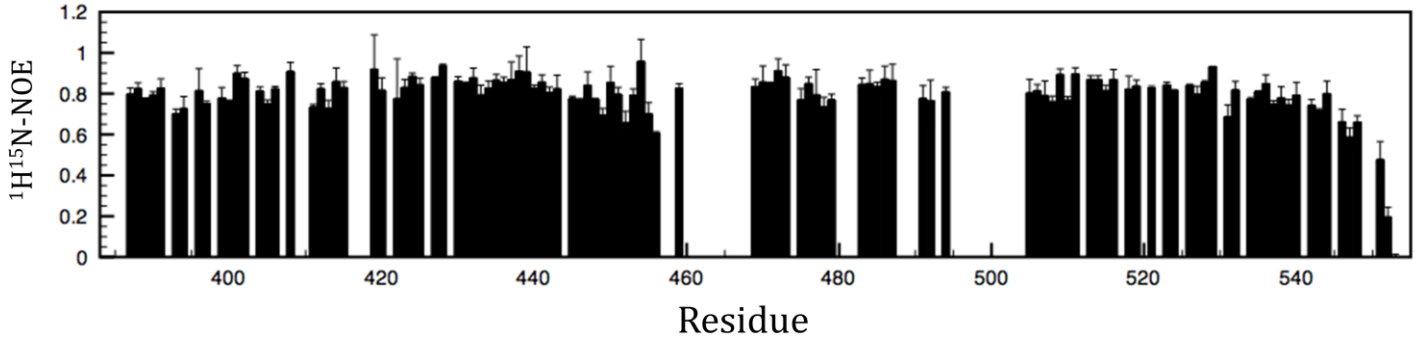

Figure S3. *$^{1}H^{15}N$-NOE measurements of the CDC25B C473S catalytic domain.* The ratios of the signals with and without saturation are shown in black bars for all assigned residues.

FIGURE S4

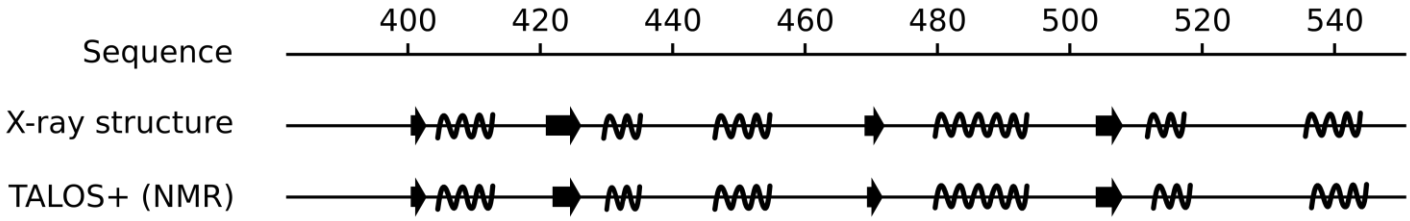

Figure S4. *Results of TALOS+ secondary structure prediction from the chemical shifts of the CDC25B C473S catalytic domain.* Graph shows a comparison of secondary structures determined from the crystal structure of CDC25B and predicted from TALOS+.