

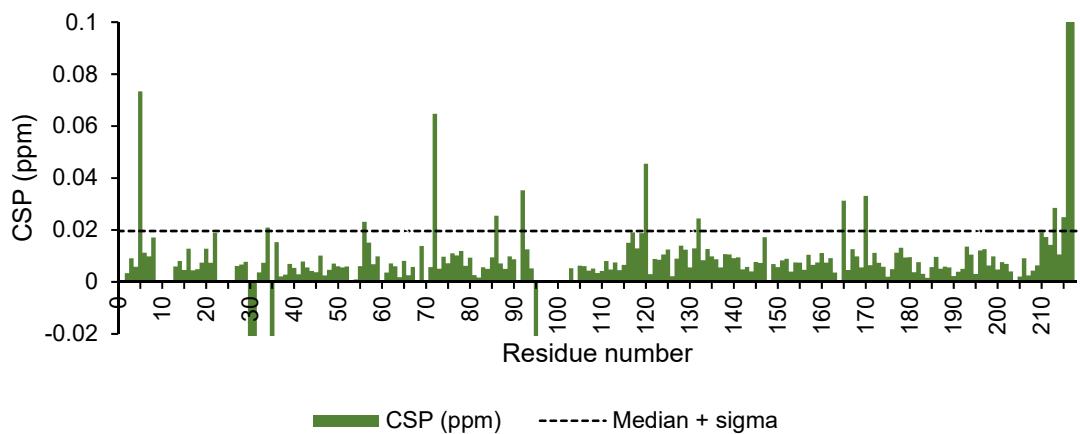
# ChemBioChem

## Supporting Information

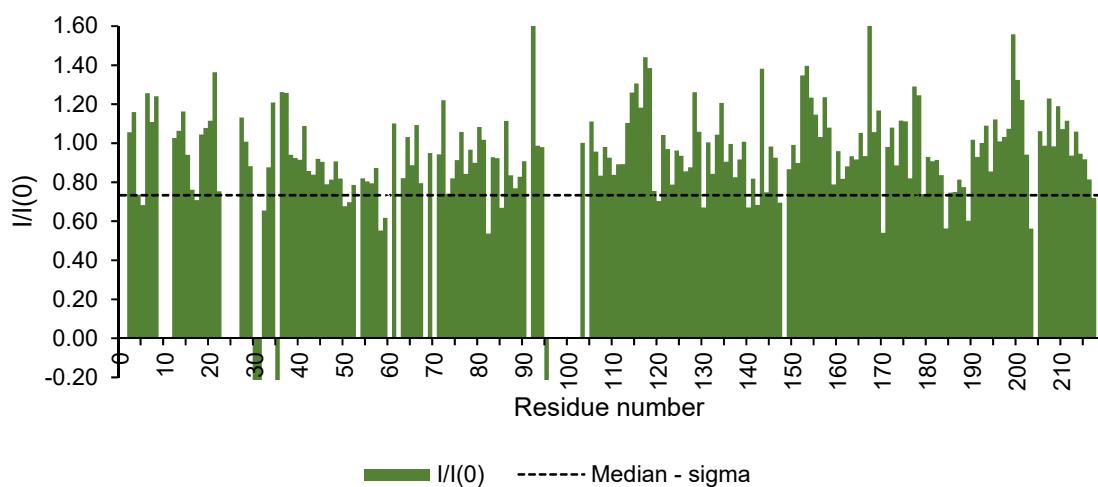
### The Charged Linker Modulates the Conformations and Molecular Interactions of Hsp90

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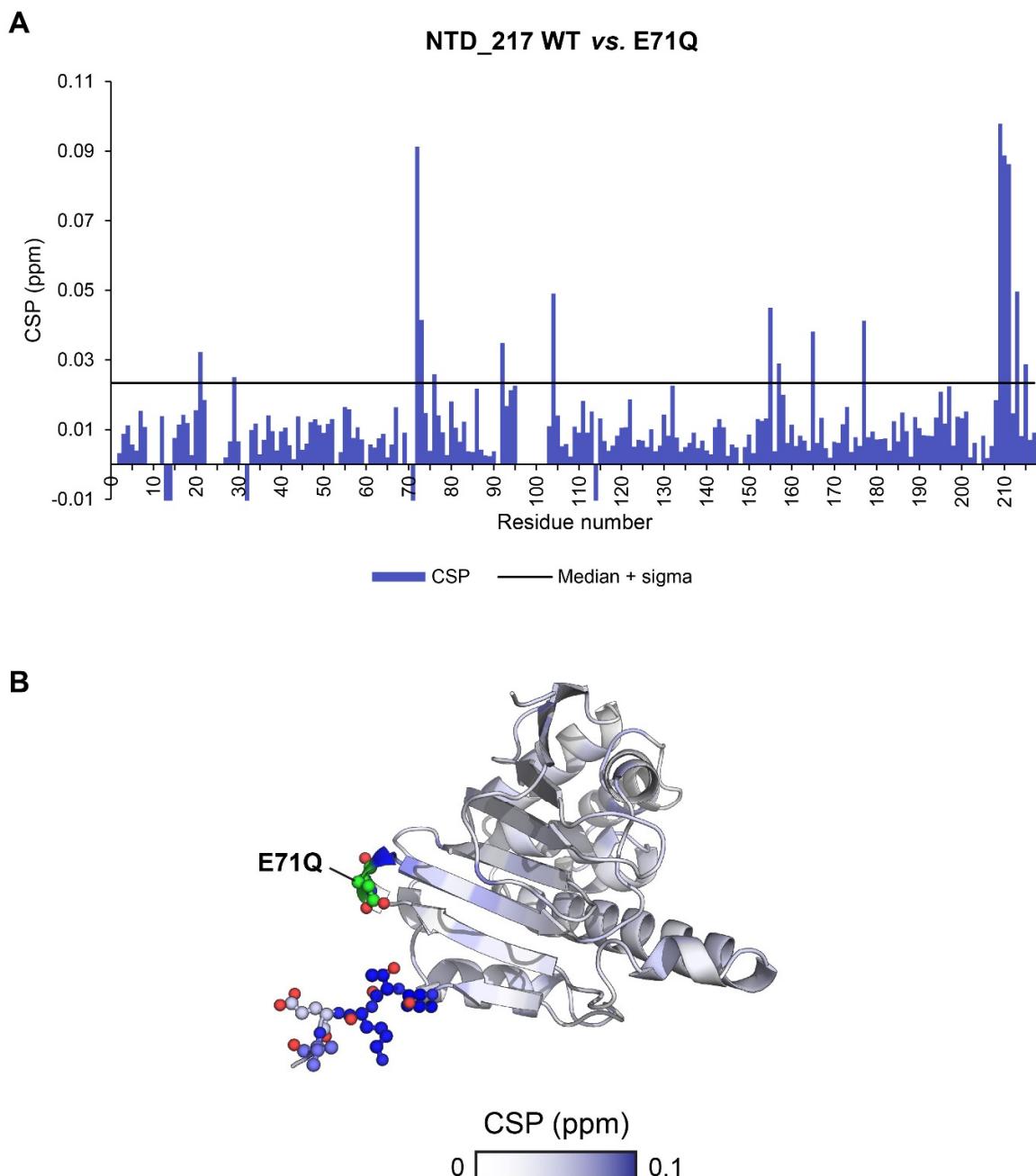
**CSP NTD\_252 vs. NTD\_217**



**I/I(0) NTD\_252 vs. NTD\_217**

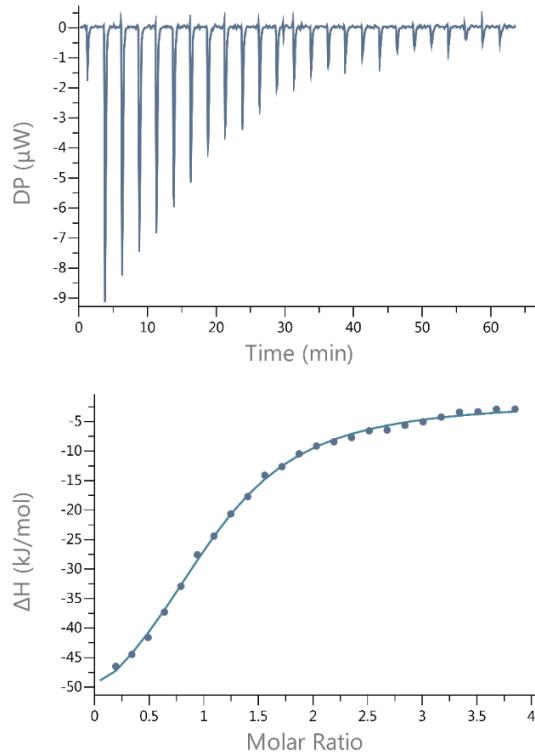


**Figure S1.** Comparison of NMR spectra of Hsp90 NTD constructs. The absence of significant CSP and intensity changes on the NTD between NTD\_252 and NTD\_217 indicates that only C-linker is responsible for interactions with N-linker and NTD.

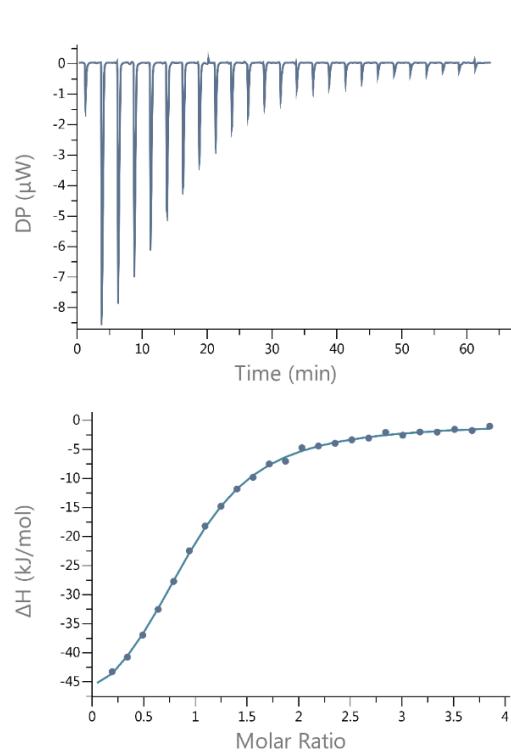


**Figure S2.** The  $\beta$ 2- $\beta$ 3 turn stabilizes the N-linker region. A) CSPs of NTD\_217 WT vs. E71Q shows strong perturbations on N-linker residues 209-213, indicating a charge-mediated interaction. B) Mapping of perturbations derived from E71Q mutation (green) on crystal structure of NTD bound to ATP (PDB 1AM1 [1]). Side chains of affected residues 209-215 are shown as sticks and spheres.

NTD\_217 + ADP



NTD\_274 + ADP



|             | $K_D$ ( $\mu\text{M}$ ) | stoichiometry     | $\Delta H$ ( $\text{kJ/mol}$ ) | $\Delta G$ ( $\text{kJ/mol}$ ) | $-T^*\Delta S$ ( $\text{kJ/mol}$ ) |
|-------------|-------------------------|-------------------|--------------------------------|--------------------------------|------------------------------------|
| NTD_217 ADP | $20.7 \pm 1.91$         | $1.04 \pm 0.017$  | $-60.2 \pm 2.21$               | -26.8                          | 33.5                               |
| NTD_274 ADP | $14.9 \pm 0.82$         | $0.912 \pm 0.009$ | $-54.8 \pm 1.05$               | -27.6                          | 27.3                               |

**Figure S3:** Summary of isothermal titration calorimetry experiments for nucleotide binding to NTD-linker constructs.

### Supplementary References

- [1] C. Prodromou, S. M. Roe, R. O'Brien, J. E. Ladbury, P. W. Piper, L. H. Pearl, *Cell* **1997**, *90*, 65-75.