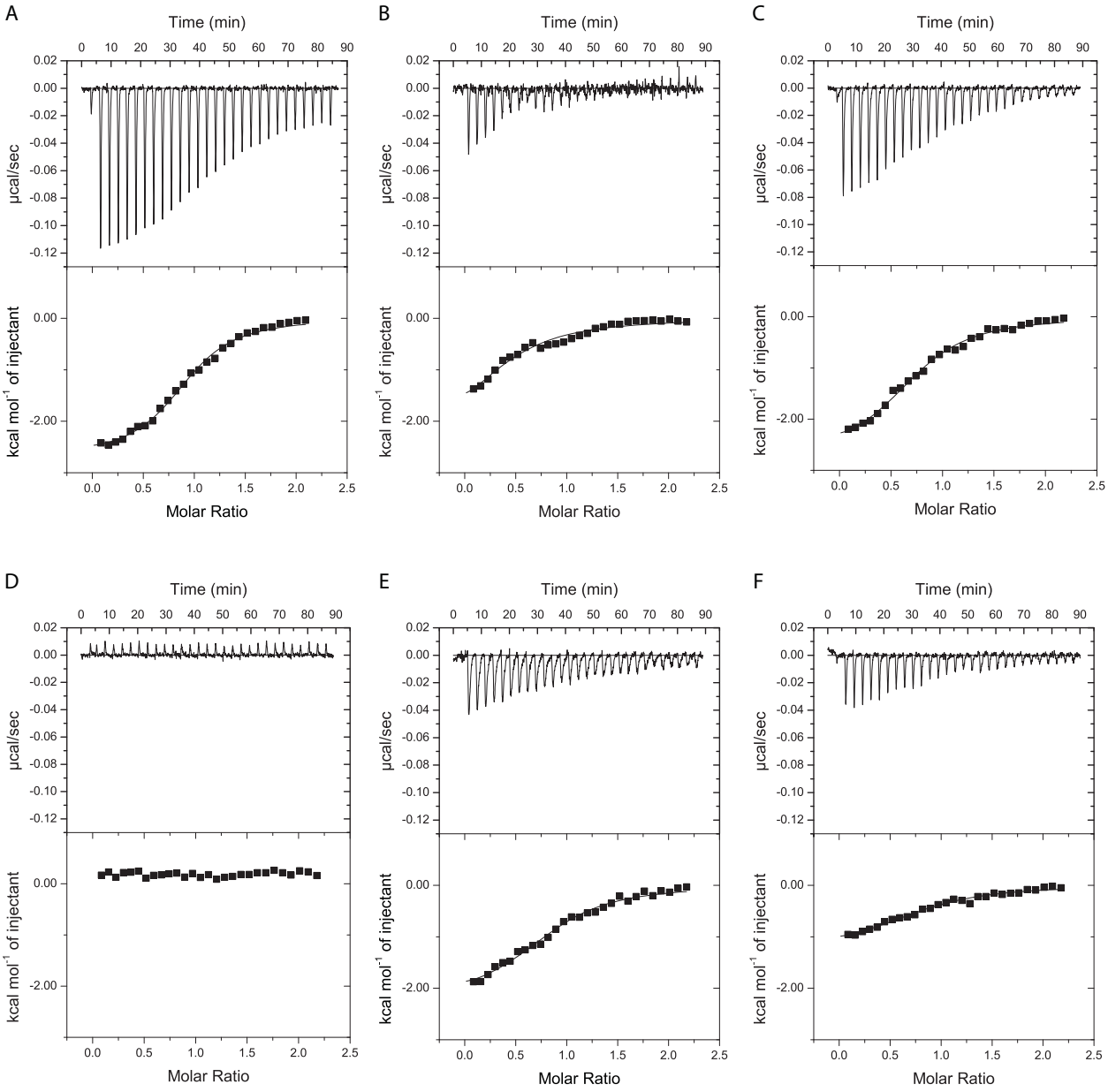
Supporting Figure 1. ITC characterization of the interaction of p53(35-59) with Taz2. Representative binding isotherms for the titration of p53(35-59) (A); p53(35-59) I50A (B); p53(35-59) E51Q (C); p53(35-59) W53Q (D); p53(35-59) F54S (E) into wild-type Taz2 or p53(35-59) into Taz2 R1731A (F). In each panel, the raw data is displayed in the upper figure and the normalized, integrated injection heats are displayed in the lower panel. The solid lines in the lower figures of both panels reflect the best fit of a one-site binding model.



Supporting Figure 2. Comparison of the p53(35-59) binding site on p300 Taz2 with the high- and low-affinity sites for p53(38-61) binding to CBP Taz2 determined from a multi-dimensional analysis of chemical shifts by Arai et al. (Arai, M., Ferreon, J.C., and Wright, P.E. (2012). J Am Chem Soc 134, 3792-3803). The p300 Taz2 component of the complex is represented in a space-filling format, and the p53(35-59) peptide is represented in a ribbon style. Residues of p300 Taz2 analogous to those of CBP Taz2 that undergo chemical shifts associated with the two binding sites are color-coded with the same scheme used by Arai et al. (A) High-affinity binding site: (red) average chemical shift difference (Δδav) greater than mean + 2SD, (orange) mean + 1SD to mean + 2SD, (yellow) mean to mean + 1SD. (B) Low affinity binding site: (blue) Δδav greater than mean + 2SD, (cyan) mean + 1SD to mean + 2SD, (green) mean to mean + 1SD. (gray) defines residues with Δδav less than mean, and (purple) defines signal broadened beyond analysis. (C) View of low-affinity site rotated to display the winding of the N-terminal of the p53(35-59) peptides around the core of p300 Taz2.