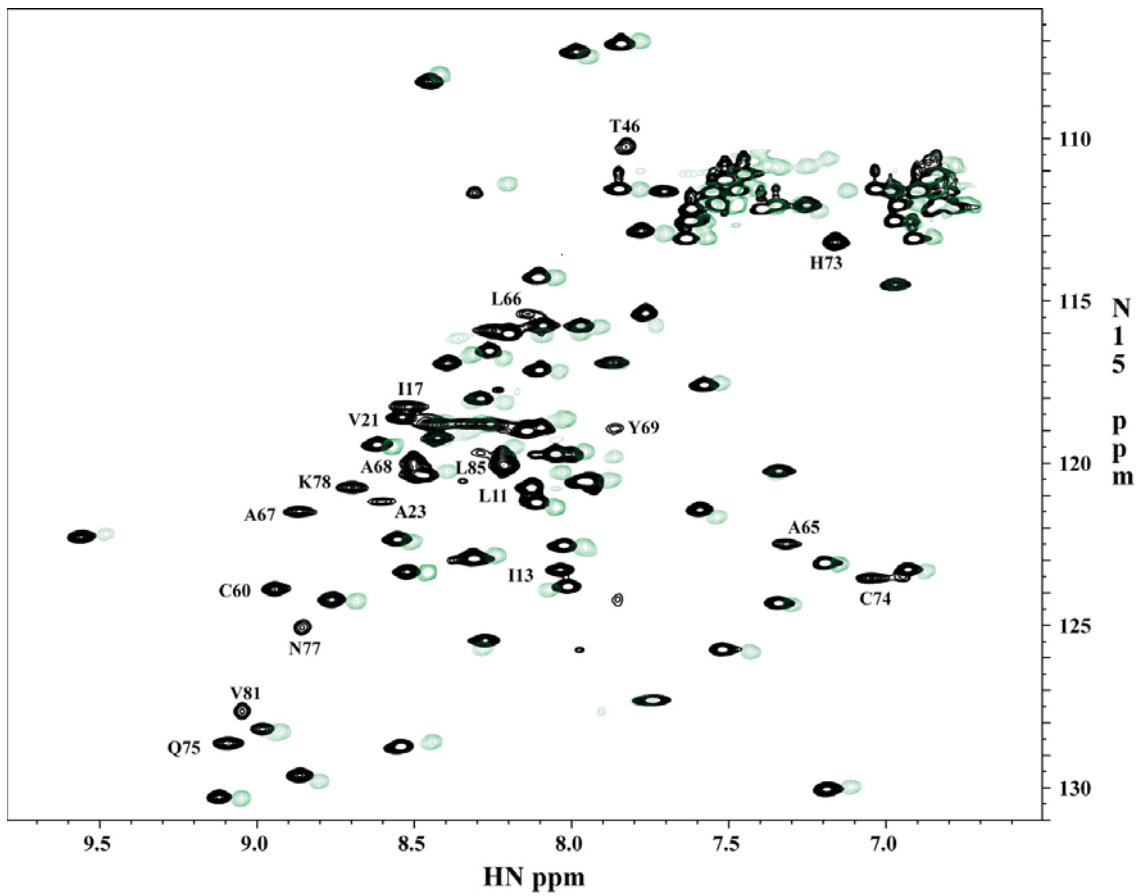


## Supplementary Figures

### Structural Basis for p300 Taz2/p53 TAD1 Binding and Modulation by Phosphorylation

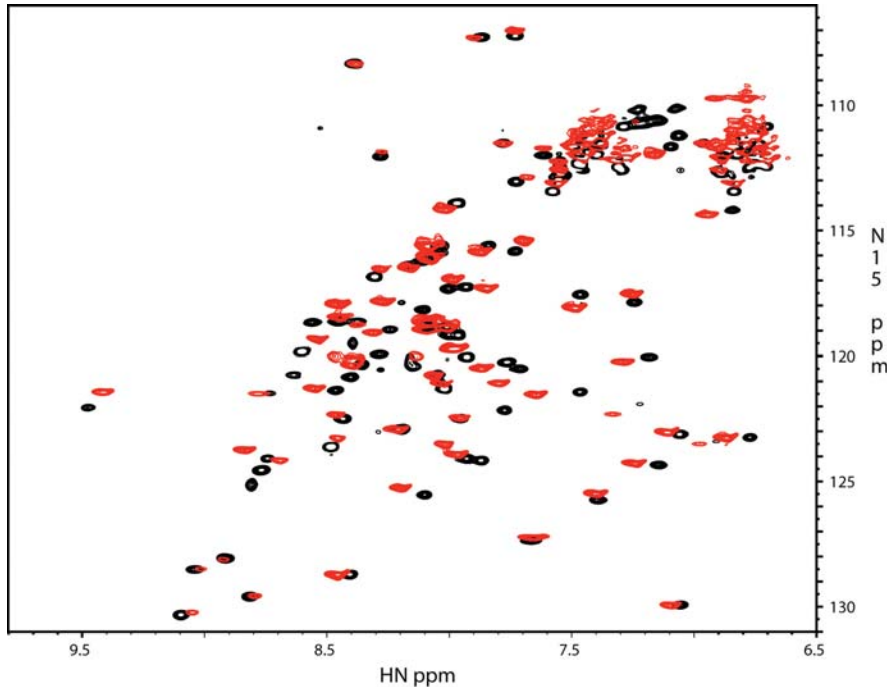
Hanqiao Feng, Lisa M. Miller Jenkins, Stewart R. Durell, Ryo Hayashi, Sharlyn J. Mazur, Scott Cherry, Joseph E. Tropea, Maria Miller, Alexander Wlodawer, Ettore Appella, Yawen Bai

**Figure S1. Optimization of the Buffer Conditions for NMR Spectroscopy.** Overlay of the HSQC of the Taz2-p53<sub>2-39</sub> complex in 50 mM MES buffer pH 6.3 (black) and in 25 mM sodium acetate buffer pH 5.8 (green). Peaks that are observed at pH 6.3 but not at pH 5.8 are labeled.

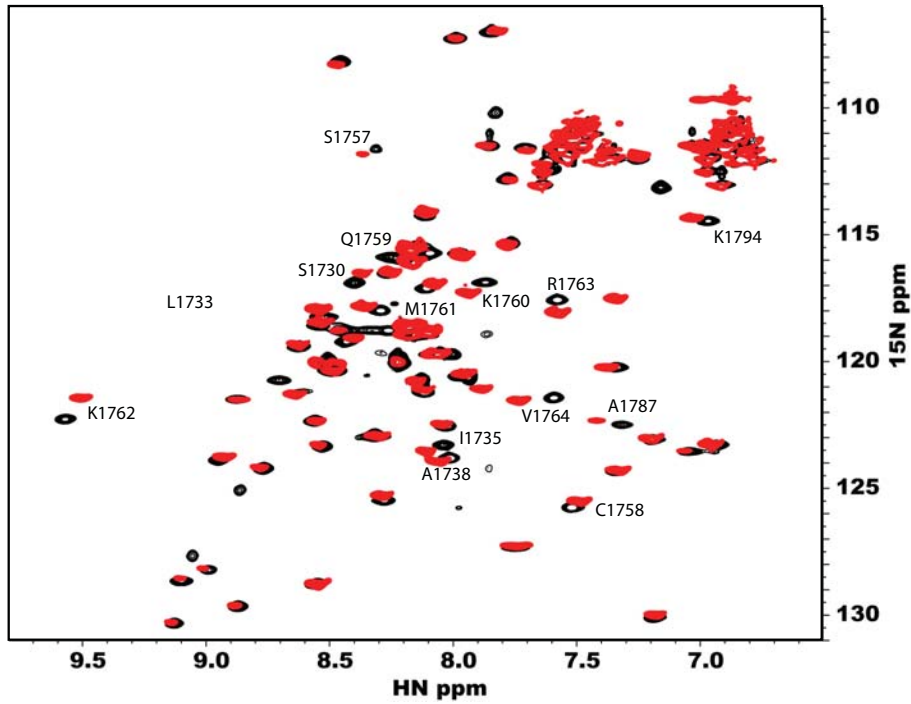


**Figure S2. Changes in Taz2 Chemical Shift upon Addition of p53<sub>35-59</sub>.** (A) Overlay of the HSQC of Taz2 (black) and the Taz2-p53<sub>35-59</sub> complex (red). (B) Overlay of the HSQC of the Taz2-p53<sub>23-39</sub> complex (black) and the Taz2-p53<sub>35-59</sub> complex (red).

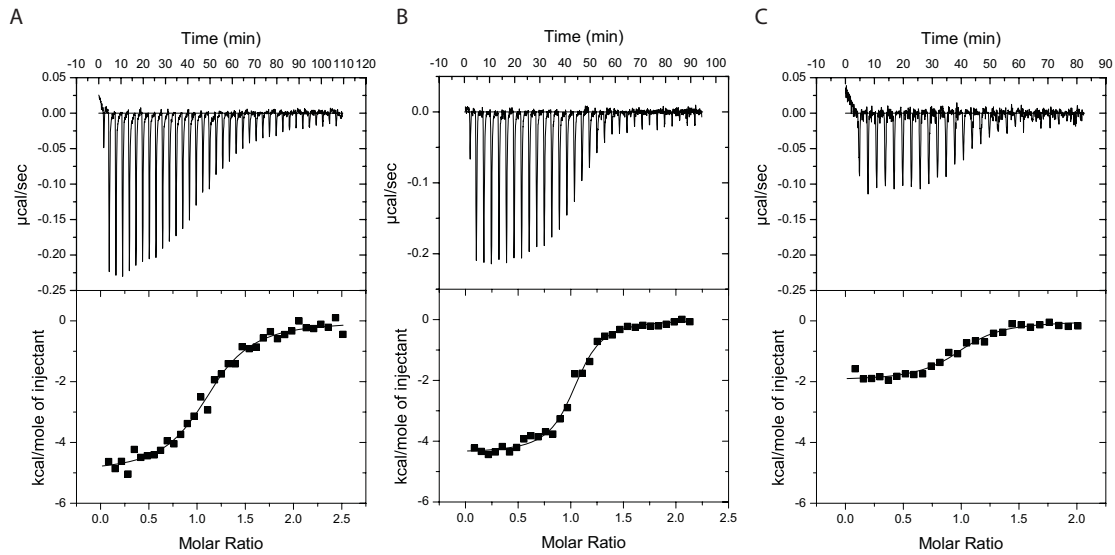
A



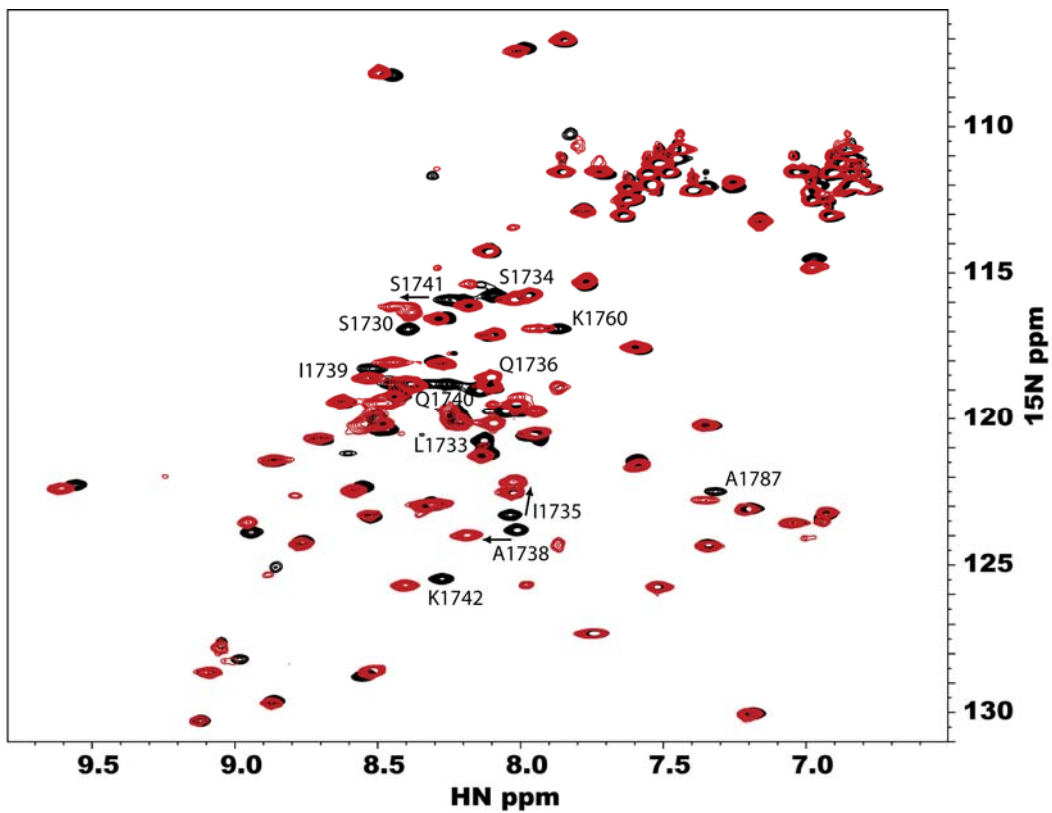
B



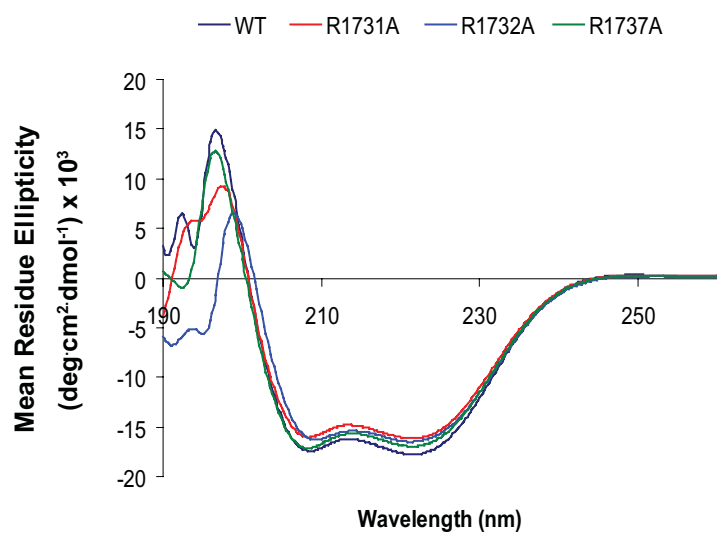
**Figure S3. ITC Titrations of Phosphorylated p53<sub>1-39</sub> into Taz2.** ITC curves of the interaction of p53<sub>1-39</sub>15pS (A), p53<sub>1-39</sub>18pT (B), and p53<sub>1-39</sub>15pS,18pT (C) with Taz2. Data are shown for a representative experiment in which p53 was titrated into Taz2 at 35 °C. In each panel, the top figure represents the raw data and the lower figure the normalized, integrated injection heats for each point. The solid curves are derived from a 1:1 binding model.



**Figure S4. Changes in Taz2 Chemical Shift upon Addition of Phosphorylated p53.** Overlay of the HSQC of the Taz2-p53<sub>2-39</sub> complex (black) and the Taz2-p53<sub>1-39</sub>18pT complex (red).

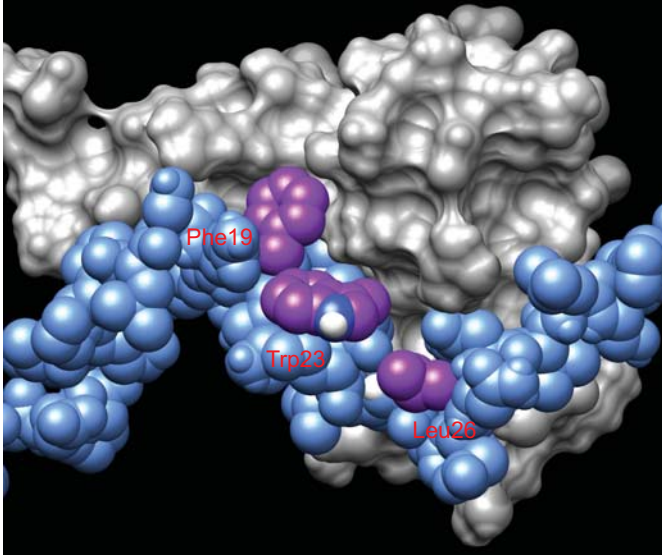


**Figure S5. CD Spectra of Taz2 Mutants.** CD spectra of native Taz2 (black), Taz2(R1731A) (red), Taz2(R1732A) (blue), and Taz2(R1737A) (green).



**Figure S6. Position of p53 Residues in Complex with Taz2 or MDM2 that are Integral for Binding.** (A) Model of the Taz2 (gray)-p53<sub>2-39</sub> (blue) complex showing the side chains of Phe<sub>19</sub>, Trp<sub>23</sub>, and Leu<sub>26</sub>. (B) Model of the MDM2 (transparent gray)-p53<sub>15-29</sub> (blue) showing the side chains of Phe<sub>19</sub>, Leu<sub>22</sub>, Trp<sub>23</sub>, Leu<sub>25</sub>, and Leu<sub>26</sub>. The model is based upon PDB 1YCR.

A



B

