



Residues discussed in the text are annoated. The view is rotated 180° along the y-axis compared to Fig.2. **a**, Surface representation of the PAZ domain colored by sequence conservation. A conservation score was generated using CLUSTAL X (Jeanmougin, F., Thompson, J. D., Gouy, M., Higgins, D. G., and Gibson, T. J. (1998) Multiple sequence alignment with Clustal X. *Trends Biochem. Sci.* **23**, 403-405). High to low sequence conservation is indicated by magenta to white coloring.

b, Surface representation of the PAZ domain colored by electrostatic charge. White, blue and red corresponds to neutral, positive and negative electrostatic potential, respectively.

c, RNA binding site on the PAZ domain based on the NMR titration shown in Fig. 1c. Residues where amide signals could not analyzed due to signal overlap are shown in yellow, residues where signals disappear at 1:5 molar ratio of protein:RNA are colored green, other residues are colored with a gradient from green to white according to the degree of chemical shift changes.