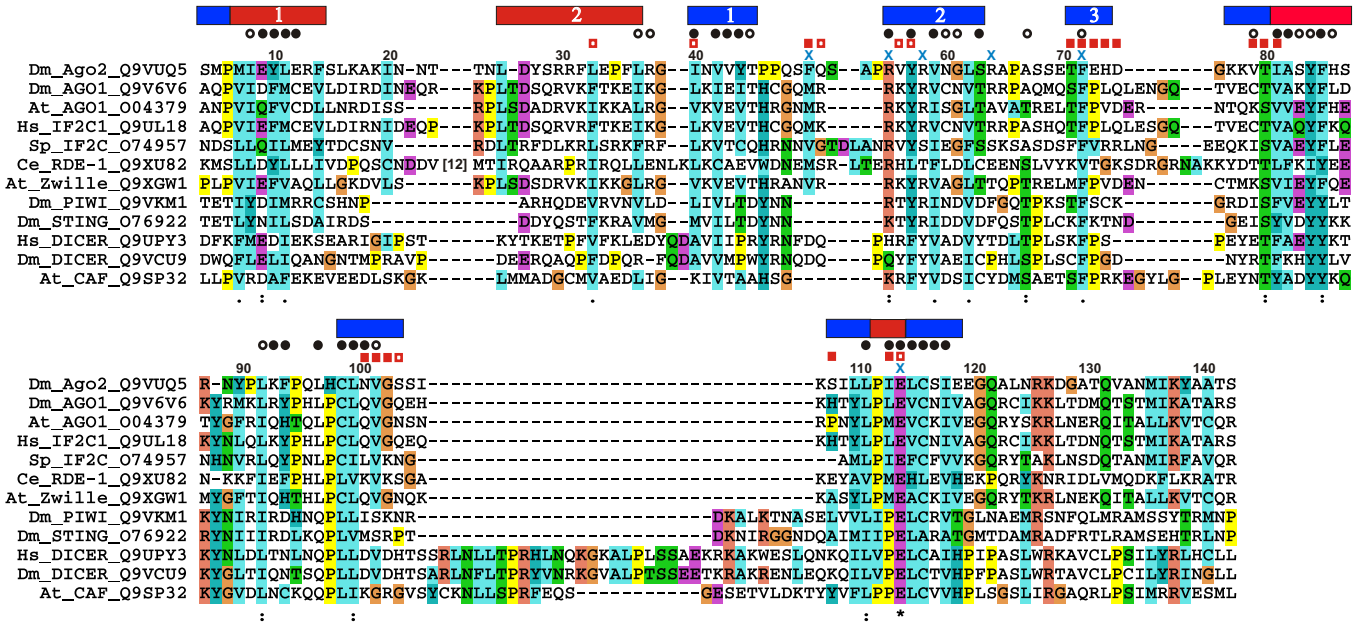
Figure S1 Multiple sequence alignment of PAZ domains.



Accession numbers are indicated on the left. Abbreviations are: Dm *Drososphila melanogaster*, At *Arabidopsis thaliana*, Hs *Homo sapiens*, Sp *Schizosaccharomyces pombe*. Residue numbers, secondary structure, protein-RNA contacts (open/filled red squares for medium/strong chemical shift perturbation, see Fig. 2c,d), and solvent-protected amide protons (open/filled circles for medium/slow H/D exchange in NMR measurements) and mutations (blue "X") are shown on top. Partial, high or complete residue conservations are shown below the alignment with ".", ":" and "*" and residues are color-coded according to CLUSTALX (Jeanmougin, F., Thompson, J. D., Gouy, M., Higgins, D. G. & Gibson, T. J. Trends Biochem. Sci. 1998, 23, 403-5).

Note, that residues 120-143, following the last strand (7) are unstructured even in protein constructs extended N- and C-terminally, and a PAZ domain comprising residues 1-123 is structurally intact (data not shown).