Supplementary Material

Solution structure and metal ion binding sites of the human CPEB3 ribozyme's P4 region

Miriam Skilandat[1], Magdalena Rowinska-Zyrek[1] and Roland K. O. Sigel*

phone: 41 44 635 4652
fax: 41 44 635 6802
✉ roland.sigel@chem.uzh.ch
Department of Chemistry, University of Zurich, Winterthurerstrasse 190, CH-8057 Zurich, Switzerland

[1] these authors contributed equally to this work
[*] to whom correspondence should be addressed

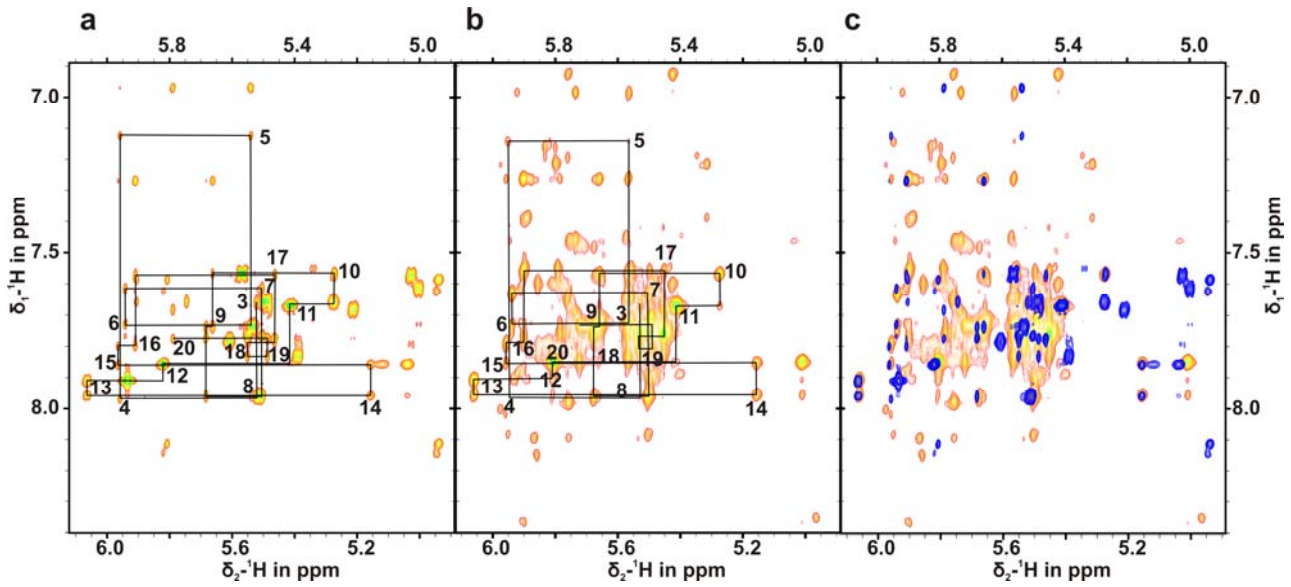

Figure S1. Comparison of the sequential walk regions of [^{1}H,^{1}H]-NOESY experiments (D_2O, 298 K, pD = 6.8) of (a) the P4 domain and (b) the full-length CPEB3. The sequential correlations of residues 3-20 of P4 are connected by black lines. (c) Overlay of (a) and (b): the CPEB3 P4 spectrum is shown in blue and the spectrum of the full-length CPEB3 ribozyme is shown in red-green. The chemical shifts and cross peak intensities of residues 3-20 of the P4 construct are in nice agreement with the corresponding signals of the full-length CPEB3.