Supporting Information

Polyamines Mediate Folding of Primordial Hyperacidic Helical Proteins

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Supporting Figures



Figure S1. Circular dichroism spectra of Acidic-(HhH)² **upon incubation with spermine (SPM).** Spectra were taken immediately after addition of 0.05 mM spermine and again after 1 h and 24 h of incubation. The resulting spctrea are very similar, demonstrating that for Acidic-(HhH)² polyamine-induced structure formation is very fast.





Figure S2. Spermine titration of acidified Primordial-(HhH)₂. Shown are titrations of 5 μ M protein with spermine (SPM); the protein sequences are shown above the respective titrations graphs. **A.** Complete acidification of Primordial-(HhH)₂ (replacement of all Arg residues to Glu) resulted in an unfolded protein that is only weakly responsive to spermine addition. **B.** Based on previous experience with the (HhH)₂ fold (see *Main Text*) we reverted two positions to arginine (colored blue in the sequence), which resulted in acquisition of an α -helical structure upon addition of spermine.



Figure S3. A 2D ¹H NMR TOCSY spectrum of Acidic-(HhH)₂ in the presence of 250 fold excess spermine at 293 K. The spectrum was acquired on a 600 MHz NMR spectrometer using 120-ms mixing time and reports on intra-residue interactions of amide groups with aliphatic groups as well as interactions within aromatic sidechains. The fingerprints region of the spectrum, revealing intra-residue ¹HN-¹H^{α} correlations, is marked with a box (see the main text).



Figure S4: Titration of Acidic-(HhH)₂ with various polyamines. Circular dichroism spectra of 10 μ M Ni-NTA-purified Acidic-(HhH)₂ were collected upon addition of various concentrations of polyamines. Plotted here is the CD signal at 222 nm, a reporter of α -helical structure, after buffer subtraction and dilution correction. Estimated midpoint concentrations are: spermine = 0.09 mM, spermidine = 0.6 mM, putrescine = 23 mM; these values and the midpoints concentrations from the independent titration in Figure 5 are within ±20% (the midpoint for propylamine could not be reliably estimated from this dataset, but the plot is qualitatively very similar to the titration in Figure 5). Midpoint values were estimated from a linear interpolation between points and assuming a saturated folded signal of -19 mdeg at 222 nm.



Figure S5. Circular dichroism spectra of Acidic-(HhH)₂ titrated with salts and polyamines. Circular dichroism spectra of 5 μ M Acidic-(HhH)₂ were monitored upon addition of: A, MgCl₂; B, CaCl₂; C, NaCl; D, propylamine (PA); E, putrescine (Put); F, spermidine (SPD). Spectra from the titration with spermine are presented in Figure 3. Each curve represents the average of two spectra after buffer subtraction and correction for dilution due to titration. Data points exceeding 700 V of applied voltage to the photomultiplier tube (PMT) were discarded. These data were used to generate the titration curves presented in Figure 5.