



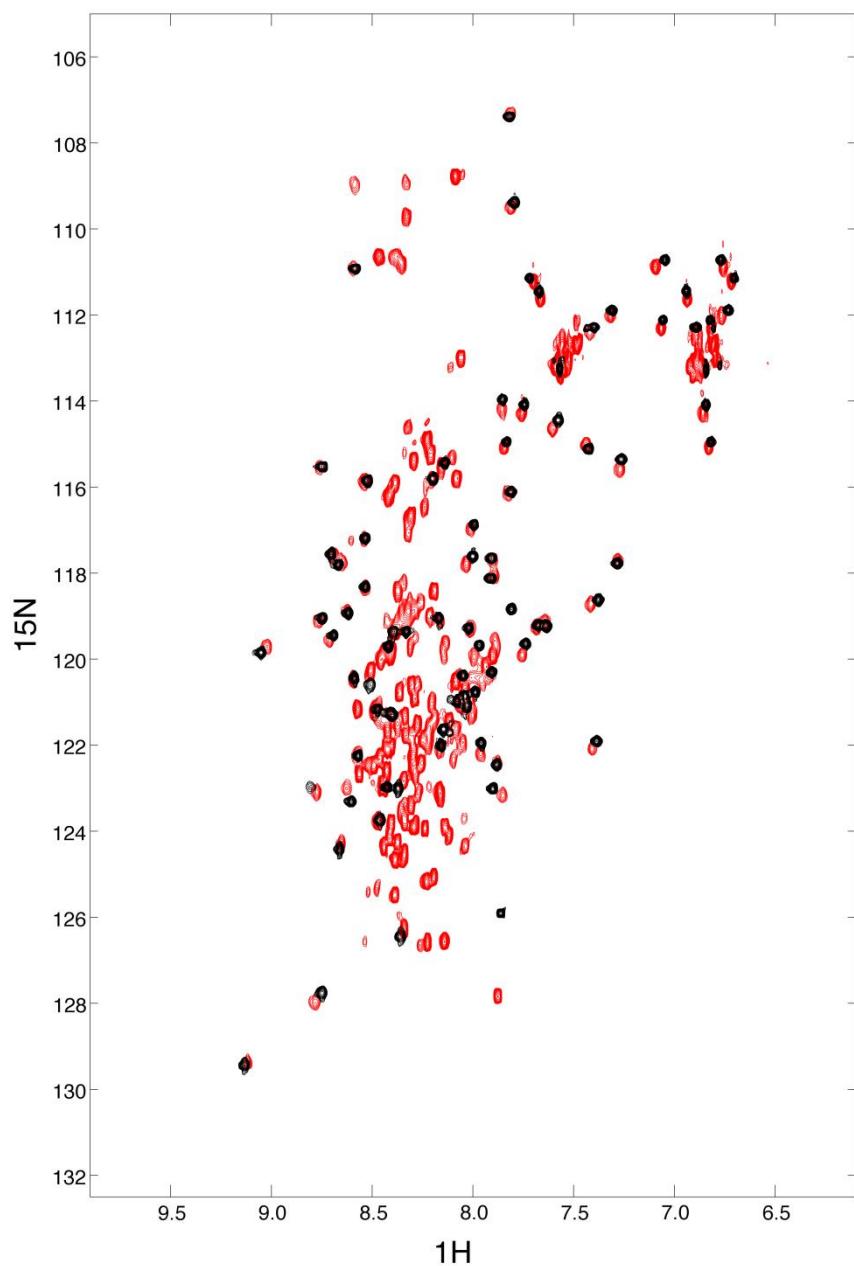
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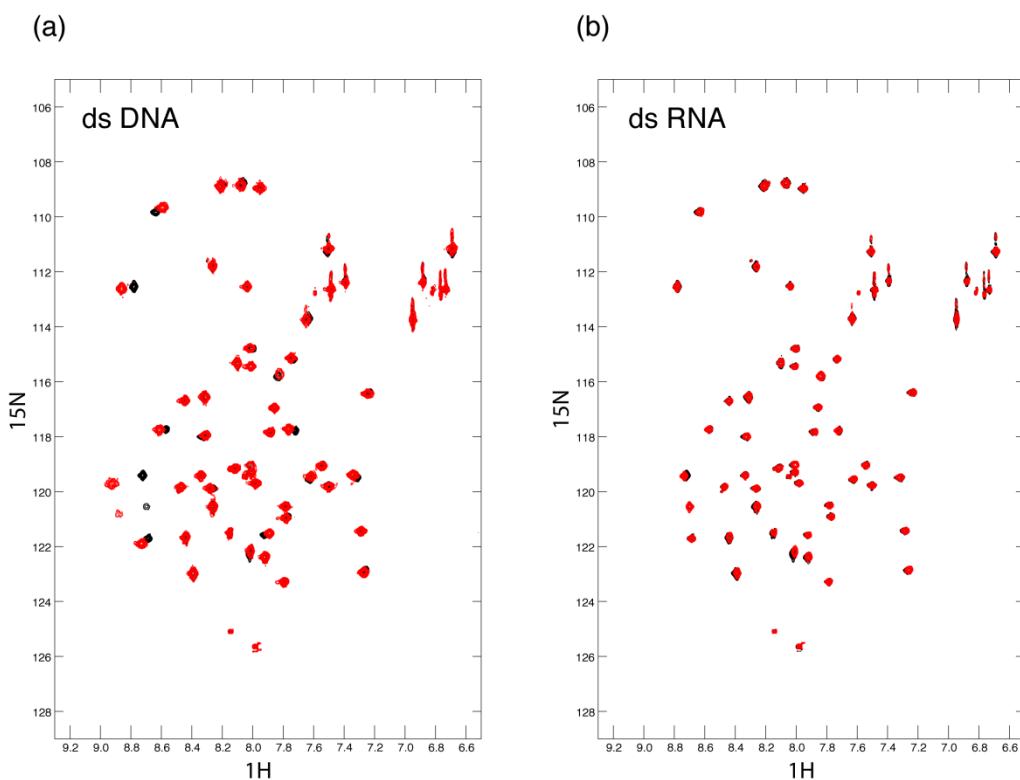
**High-resolution NMR structures of the domains of
Saccharomyces cerevisiae Tho1**

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Bycroft**

Figure S1

Superposition of ^{15}N -HSQC spectra for tho1 (residues 119-183 - black) and tho1 (residues 51-218 - red) in PBS. The additional amide resonances in the spectrum for the larger domain appear to fall in the region typically associated with disordered residues.

Figure S2



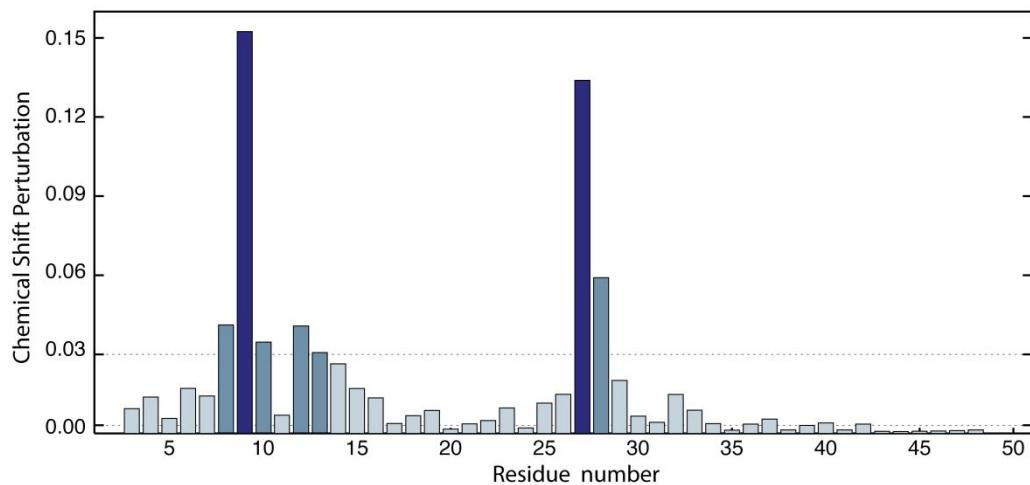
Superposition of ¹⁵N-HSQC spectra of Tho1 SAP domain (1-50) in PBS (black) with ¹⁵N-HSQC spectra of Tho1 SAP domain (1-50) in PBS with 200μM dsDNA and dsRNA (red). Whilst significant chemical shift perturbations were observed with dsDNA none were observed with dsRNA.

dsDNA 5'-TCCTGATCAGGA-3'

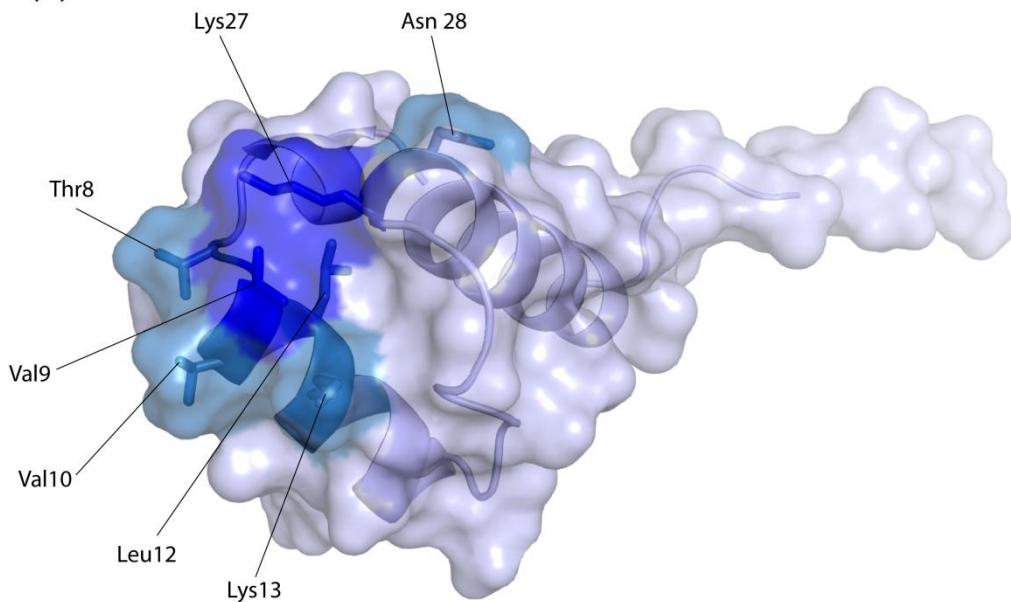
dsRNA 5'-GGACAGCUGUCCUUCGGGGACAGCUGUCC-3'

Figure S3

(a)



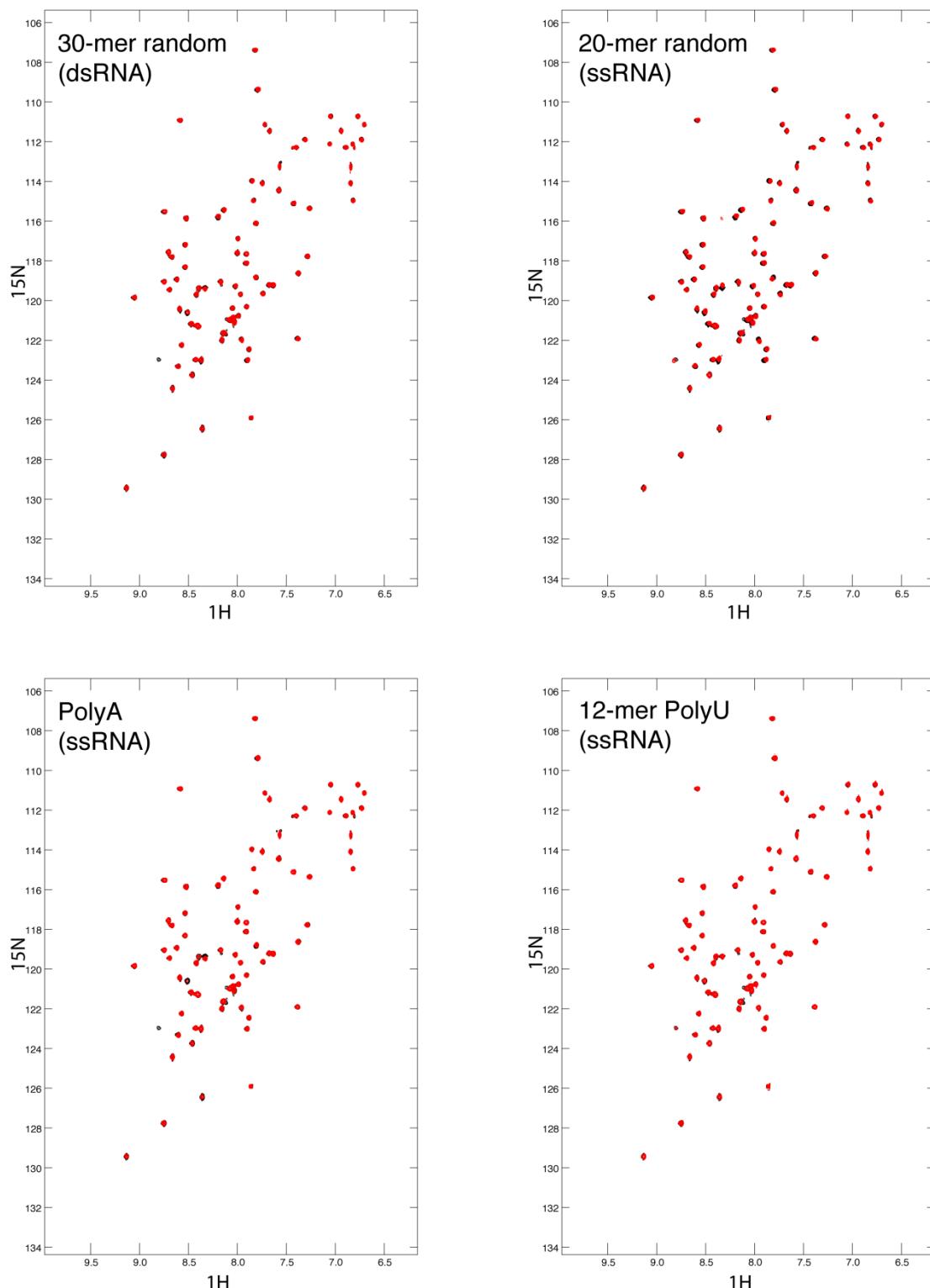
(b)



(a) CSP plot of *S. cerevisiae* Tho1 SAP domain on addition of 200 μ M 12-mer random dsDNA.

(b) CSP mapped on the structure of Tho1 SAP domain. Significant NCSPs were grouped and color-coded into two categories according to: medium (medium blue) if $2\sigma > \text{CSP} > 1\sigma$ and strong (dark blue) if $\text{CSP} > 2\sigma$, where σ is the standard deviation of the mean.

Figure S4



Superposition of ¹⁵N-HSQC spectra of tho1 (119-183) in PBS (black) with ¹⁵N-HSQC spectra of tho1 (118-183) in PBS with 200uM RNA (red). No significant chemical shift perturbations were observed.

random 30-mer dsRNA 5' -GGACAGCUGUCCCUUUCGGGGACAGCUGUCC-3'
random 20-mer ssRNA 5' -CUUGUACAUAGUUGGCCAUA-3'