

**Conserved binding of GCAC motifs by MEC-8,  
couch potato and the RBPMS protein family**

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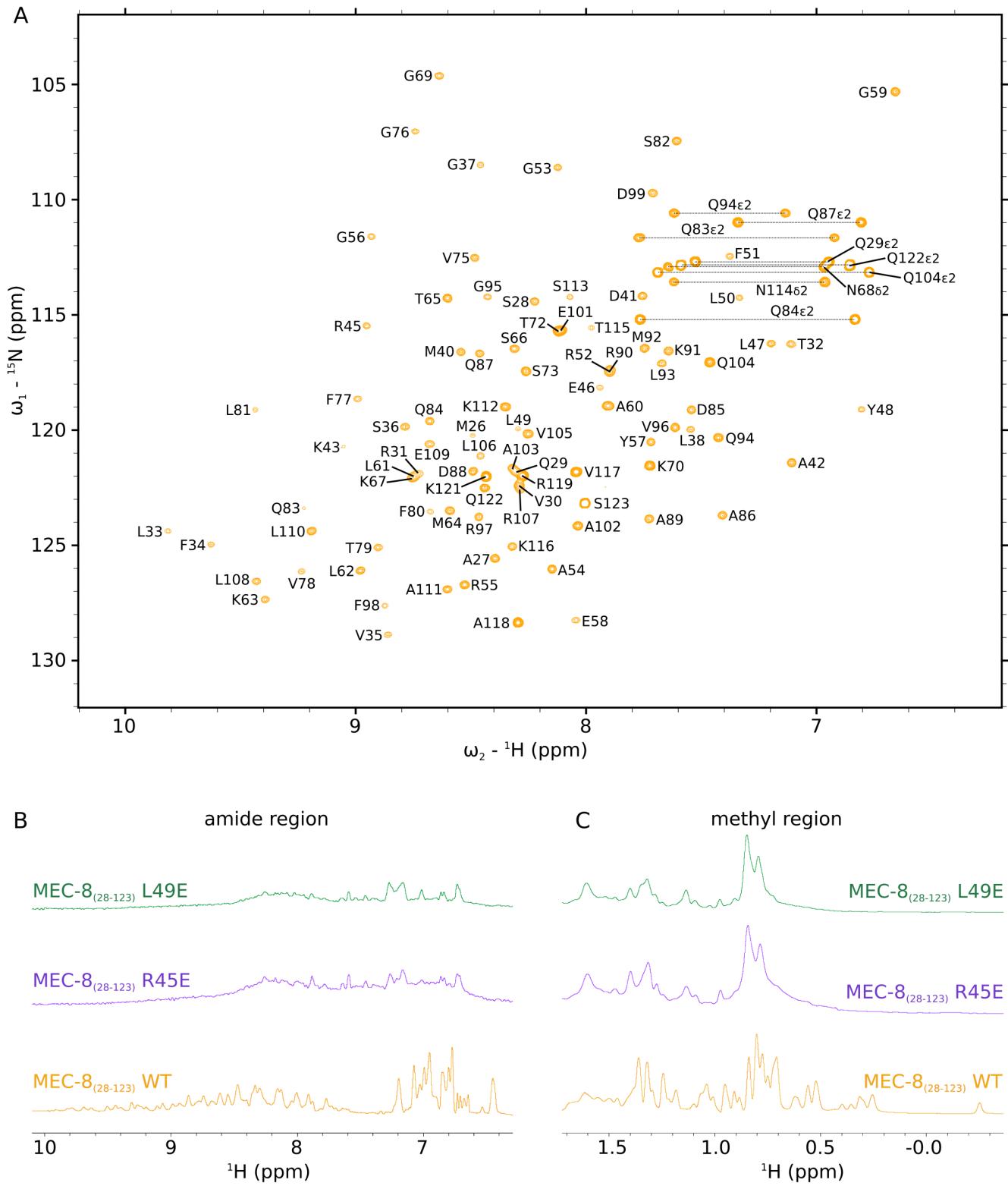
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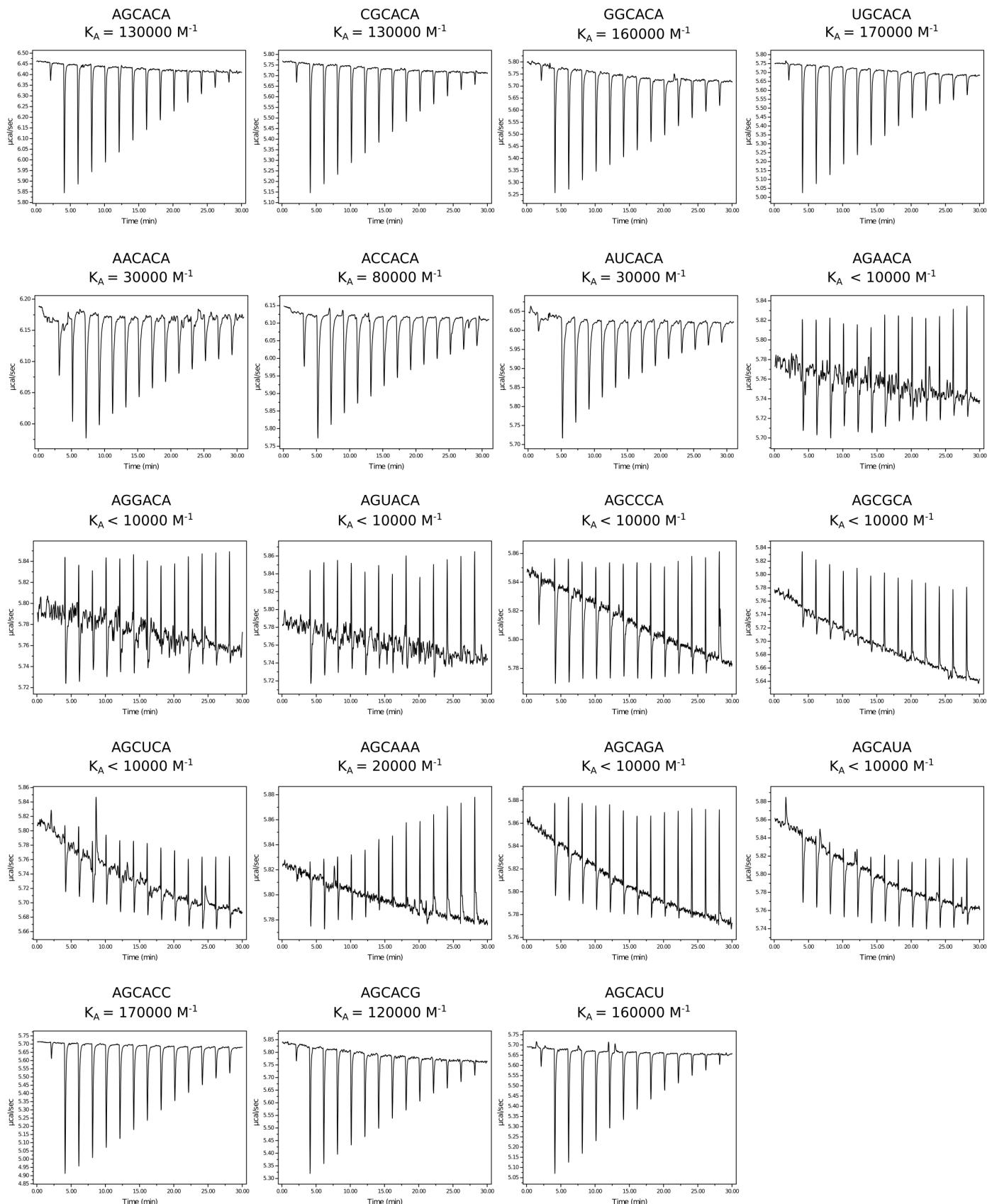
**SUPPLEMENTARY TABLE S1.** Data collection and refinement statistics.

	MEC-8 RRM1	MEC-8 RRM1 + AGCACATTTTTTAGCACA
PDB ID	5BJR	5TKZ
Data collection		
Beamline	ESRF ID23-2	ESRF ID23-2
Space group	<i>I</i> 2 2 2	<i>P</i> 32 2 1
Cell dimensions		
<i>a</i> , <i>b</i> , <i>c</i> (Å)	52.59, 96.42, 109.99	52.19, 52.19, 156.53
$\alpha$ , $\beta$ , $\gamma$ (°)	90, 90, 90	90, 90, 120
Wavelength (Å)	0.873	0.873
Resolution (Å) <sup>a</sup>	35.36–2.60 (2.69–2.60)	25.74–1.53 (1.58–1.53)
R <sub>merge</sub> (%) <sup>a</sup>	8.5 (34.4)	3.4 (35.9)
<i>I</i> / $\sigma$ <i>I</i> <sup>a</sup>	6.00 (2.68)	8.03 (2.26)
Observations <sup>a</sup>	17121 (1703)	76451 (7524)
Unique reflections <sup>a</sup>	8854 (872)	38386 (3768)
Completeness (%) <sup>a</sup>	99.06 (99.54)	99.99 (100.00)
Multiplicity <sup>a</sup>	1.9 (2.0)	2.0 (2.0)
Refinement		
Resolution (Å) <sup>a</sup>	35.36–2.60 (2.76–2.60)	25.74–1.53 (1.58–1.53)
Number of reflections	8842	38385
R <sub>work</sub> /R <sub>free</sub> (%) <sup>a</sup>	23.7/28.5	23.3/27.1
Unit cell content / No. atoms		
Protein/nucleic acid	1328	1606
Solvent	37	134
Ions (NH <sub>4</sub> )	15	
Average B, all atoms (Å <sup>2</sup> )	48.5	38.4
R.m.s. deviations		
Bond lengths (Å)	0.002	0.009
Bond angles (°)	0.571	1.177
Ramachandran plot		
Favored (%)	100	99.43
Allowed (%)	0	0.57
Outliers (%)	0	0

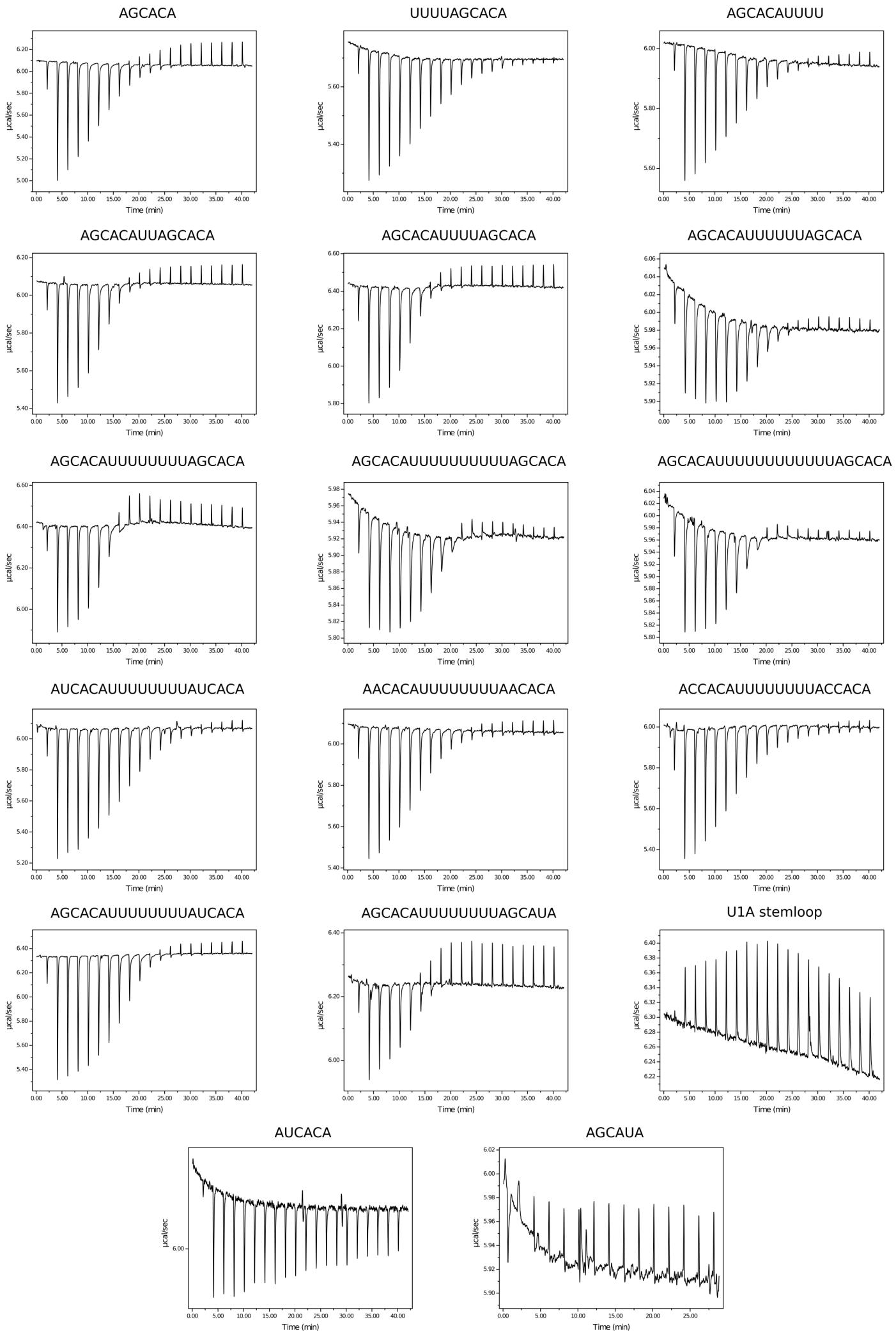
<sup>a</sup> Data in parentheses refer to the highest resolution shell



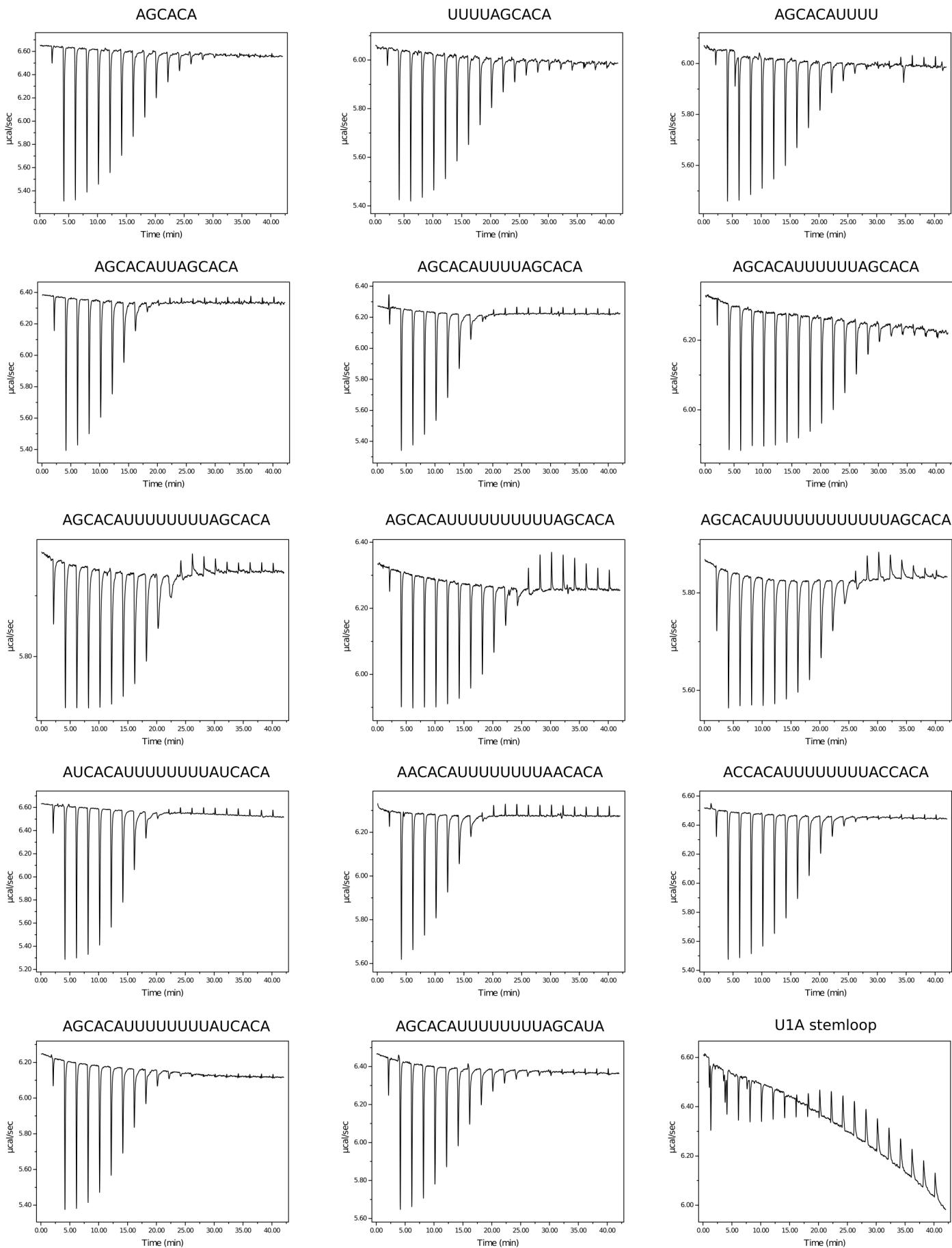
**SUPPLEMENTARY FIGURE S1.** NMR spectroscopy data for MEC-8 RRM1. (A)  $^1\text{H}$ , $^{15}\text{N}$ -HSQC spectrum at 298 K for 500  $\mu\text{M}$   $^{15}\text{N}$  MEC-8<sub>(28-123)</sub> in 50 mM TRIS (pH 7.5) and 150 mM NaCl, with 10% D<sub>2</sub>O (v/v). Crosspeaks for backbone amides, as well as sidechain asparagine and glutamine amides, have been annotated with residue type and number. (B,C) Selected regions of 1D  $^1\text{H}$  spectra for wildtype MEC-8<sub>(28-123)</sub>, as well as mutants Arg45Glu and Leu49Glu. Both dimerization surface mutants result in destabilization of the protein fold.



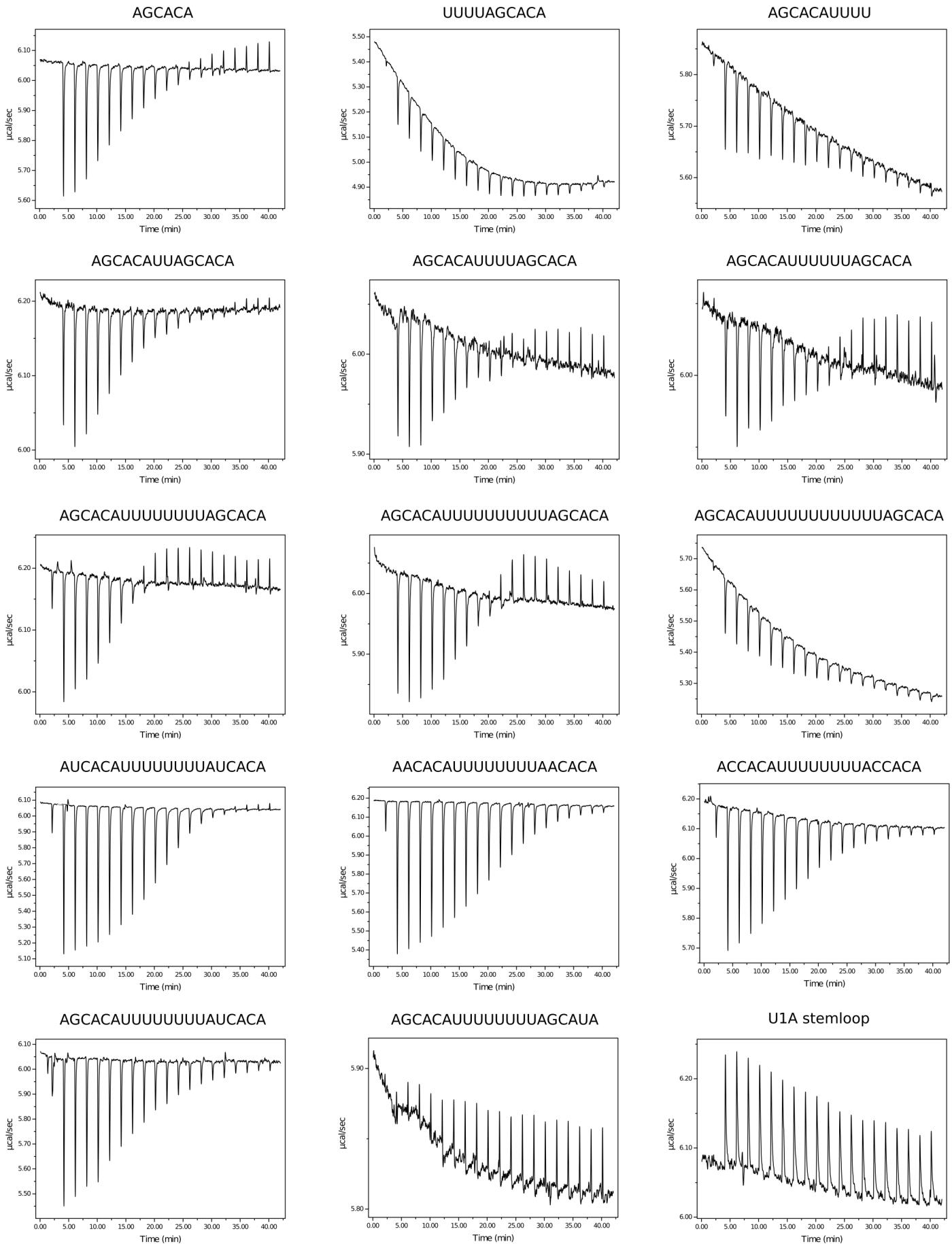
**SUPPLEMENTARY FIGURE S2.** Representative raw ITC data and derived  $K_A$  values used to define the initial affinity-weighted sequence motif of MEC-8 RRM1 as shown in Fig. 1F.



**SUPPLEMENTARY FIGURE S3.** Representative raw ITC data for RNA ligand binding by MEC-8 RRM1 from Table 1.



**SUPPLEMENTARY FIGURE S4.** Representative raw ITC data for RNA ligand binding by couch potato RRM from Table 2.



**SUPPLEMENTARY FIGURE S5.** Representative raw ITC data for RNA ligand binding by RBPMS RRM from Table 2.