

Table S1. Comparison of statistics for the Ca²⁺-CRC-C/K₁₉ and Ca²⁺-LC-HsCen2 structures

	Ca ²⁺ -CRC-C/K ₁₉ (1OQP)	Ca ²⁺ -LC-HsCen2 (1M39)
A. NOE-based distance restraints		
Total	1571 (19.1 per residue ^a)	1062 (15.4 per residue ^a)
Intraresidue	527	337
Sequential	309	243
Medium range (2≤ i-j <5)	306	234
Long range (i-j ≥5)	429 ^b	248
B. Average number of distance restraint violations per structure		
0.1 Å < d < 0.2 Å	0.8	N/A
d > 0.2 Å	0	4.1
C. Ensemble Ramachandran Plot^a		
Residues in most-favored regions	91.0%	86.2%
Residues in additionally allowed regions	8.3%	10.6%
Residues in generously allowed regions	0.6%	1.4%
Residues in disallowed regions	0.1%	1.8%
D. Average backbone RMSD from the mean structure (Å)		
All ^a	0.41	0.92
All helices ^c	0.33	0.81
Helices I through IV	0.25	0.49
^a For the structured regions only: (CRC-C/K ₁₉) residues 99-169 in CRC-C and 5-15 in K ₁₉ ; (LC-HsCen2) residues 86-94 and 105-164.		
^b Including 298 long range NOEs and 131 intermolecular NOEs		
^c Helices are defined as: (CRC-C) Helix I, 99-110; Helix II, 120-130; Helix III, 136-146; Helix IV, 156-165; (K ₁₉) Helix I', 5-15; (LC-HsCen2) Helix I (E), 105-113; Helix II (F), 123-132; Helix III (G), 139-148; Helix IV (H), 159-164; Helix I' (D) 86-94.		