Supplementary Table 1. Structural statistics for the 20 lowest energy structures.

# Restraints	Z2-DPC-d_{38}	Z8-DPC-d_{38}	Z8-SDS-d_{25}	Z9-DPC-d_{38}	Z9-SDS-d_{25}
Unambiguous nOes	296	455	358	343	374
Ambiguous nOes	27	52	81	56	70
Unassigned nOes	0	0	0	0	0
Total nOes	323	507	439	399	444
# Dihedral Restraints	20	20	20	20	20
RMSD from ideal[a]					
Bonds (Å)	$8.97x10^{-4} \pm 7.81x10^{-5}$	$5.97x10^{-3} \pm 9.22x10^{-5}$	$3.85x10^{-3} \pm 5.46x10^{-5}$	$8.84x10^{-4} \pm 5.1x10^{-5}$	$3.96x10^{-3} \pm 3.1x10^{-4}$
Angles (Å)	$0.29 \pm 2.82x10^{-3}$	$0.54 \pm 1.17x10^{-2}$	$0.393 \pm 5.27x10^{-3}$	$0.274 \pm 2.2x10^{-3}$	$0.420 \pm 1.9x10^{-2}$
Impropers (deg)	$0.128 \pm 6.66x10^{-3}$	$0.45 \pm 1.54x10^{-2}$	$0.21 \pm 4.82x10^{-3}$	$9.93x10^{-2} \pm 7.3x10^{-3}$	$0.256 \pm 2.5x10^{-2}$
VDW (kcal·mol^{-1})	6.90 ± 0.69	39.03 ± 2.45	9.56 ± 0.66	4.98 ± 0.6	14.7 ± 0.92
Distance Restraints					
Unambiguous	$6.37x10^{-2} \pm 3.90x10^{-2}$	$6.67x10^{-2} \pm 1.91x10^{-2}$	$6.10x10^{-2} \pm 2.48x10^{-2}$	$8.84x10^{-2} \pm 1.7x10^{-2}$	$4.60x10^{-2} \pm 1.8x10^{-2}$
Ambiguous	$6.09x10^{-3} \pm 1.33x10^{-2}$	$1.05x10^{-2} \pm 1.84x10^{-3}$	$5.97x10^{-3} \pm 9.12x10^{-3}$	$8.05x10^{-3} \pm 1.1x10^{-2}$	$6.673x10^{-3} \pm 5.1x10^{-3}$
All dist. restraints	$6.09x10^{-2} \pm 3.69x10^{-2}$	$6.34x10^{-2} \pm 1.80x10^{-2}$	$5.55x10^{-2} \pm 2.22x10^{-2}$	$8.20x10^{-2} \pm 1.6x10^{-2}$	$4.228x10^{-2} \pm 1.6x10^{-2}$
Dihedral restraints (deg)	$2.08x10^{-2} \pm 3.33x10^{-2}$	0.66 ± 0.25	$2.63x10^{-2} \pm 4.00x10^{-2}$	$1.00x10^{-2} \pm 2.5x10^{-2}$	-
Nonbonded energies					
Elect. (kcal·mol^{-1})	-543.54 ± 36.94	-467.98 ± 52.09	-513.94 ± 34.36	-458.82 ± 49.8	-493.37 ± 35.6
VDW (kcal·mol^{-1})	-150.63 ± 4.02	-173.70 ± 3.67	-165.41 ± 2.83	-156.41 ± 4.0	-166.84 ± 2.0
Ramanchandran (%)[b, c]					
Most favoured	54.5	55.8	87.4	58.4	49.7
Additionally allowed	45.5	44.2	12.6	41.6	50.3
Generously allowed	0	0	0	0	0
Disallowed	0	0	0	0	0
Global RMSD[d]					
Backbone	(res. 3-19) 0.991	(res. 2-20) 0.514	(res. 4-17) 0.996	(res. 4-19) 0.849	(res. 4-19) 0.633
Heavy atoms	(res. 3-19) 1.364	(res. 2-20) 0.928	(res. 4-17) 1.587	(res. 4-19) 1.428	(res. 4-19) 1.027

a) The data in the Table are taken directly from the PROCHECK (41, 42) software output and do not imply an extremely high level of accuracy in the RMSD; b) Determined using PROCHECK (41,42); c) The relatively large number of residues that have backbone conformations in the additionally allowed regions, is quite frequently seen for structural ensembles of such linear helical peptides; typically these arise from residues near the N- and C-termini of the peptide, where the backbone structure is less well defined; d) Determined using MOLMOL (40).